PHYSICAL ANTHROPOLOGY

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Preface to the 3rd Edition

A host of informations have gathered during the last decade in practically all the spheres of human biology. Palaeoanthropology, which was previously based on morphological and derived anatomical studies of human fossils, is being influenced to a great extent by the genetic datas. Mitochondrial DNA, y-chromosomal DNA and nuclear DNA have been extracted from a number of fossils and their sequencing done and compared and contrasted with extinct and extant group of humans. There has been largescale use of genetic engineering and generation of haplotypes in comparing and contrasting different ethnic groups to unravel various mysteries that surround human evolution. Not visiting these areas of novel acquisitions in the field of human biology shall be injustice to students. I, therefore, have tried to include such developments in these areas and make the course content up-to-date as far as possible. In total 25 pages have been changed and 25 new pages inserted, besides some changes in other pages. I have tried to justify the confidence reposed in me by my readers and I assure them that such will be my endeavour for all time to come.

In the mean time, there has been some departures from, and some new arrivals, in my family. I lost my mother and in-laws a few years ago. My sister-in-laws, sarita and Rinku are new arrivals so are the nephews Adi, Shaurya, Surya, Varun and nieces Lucky and Naina, the last being the darling of the house. They all are inspiration to me.

I am thankful to my sons, Rohan & Rohit, who searched the NET for informations on some of the topics of the book and typed some chapter. I am also thankful to A. K. Lal, my cousin, for the same. I am also thankful to my wife who ungrudgingly went through the solitude during revision of the book. I am also thankful to Mr. Chandan Guha, Patna Offsetters, Patna for his keen interest in printing this book.

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P. Nath

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समर्पण :

नन्हें-नन्हें हाथों में ।
सागर-तट पर बनाते हैं जो,
बालू के हरौंदे ।
मुठ्ठी में भर लेते हैं,
सीप और घोंघे ।

पी० नाथ

PREFACE TO THE 1st EDITION

Honestly speaking, it is beyond capability of one individual to justify the diverse topics included in the subject. As a teacher of genetics, evolution and human evolution for the last twenty years at the graduate and postgraduate level, I have realised the problems being faced by students. Syllabi of UPSC and some Universities have been restructured this year and several current topics have been included. Examinees were facing difficulties in preparing for the examination. I thought it proper to come out with whatever material available with me. Examinees of this year have been main concern hence there has been a very quick compilation of the book. This is not an excuse for any error that may have crept due to rapid proof-reading and printing and I, honestly, own all such mistakes. One should not expect much sophistication in first aid-its timing is crucial. In many ways, one will find this book more than the first aid.

I must thank my parents, teacher Dr. A. Nath, Deptt. of Zoology, Patna University, Father-in-law Dr. S.P. Lall, Deptt. of Botany, College of Commerce, Patna for their kind blessings and support. I also sincerely thank my wife Shobha, brothers Prem, Om, Anant, Anand, Rajesh, Kamal, and sisters Meera, Ira, Ranjana, Rashmi, Rajat, Smriti, and sister-in-law Sunita, sons Rohan and Rohit and nephews Rishi and Gungun for their material and moral support. Anant Prakash, who has successfully competed in Allied Group "A" Services with anthropology as one of the optional, has spared time for proof-reading of this book.

PATNA
10-08-1995

P. NATH

PREFACE TO THE 2nd EDITION

I am thankful to teachers and students of anthropology who liked the book and made first edition of the book a success. This has inspired me to go in for a second edition. A whole new section on demography and many topics in applied anthropology has been added. It will certainly help students to a great extent. The chapters on evolution has completely been recasted and made more understandable. In addition, several topics in the area of human ecology and human genetics have either been trimmed in order to make it more relevant or, expanded in order to justify their full implications. The book is now in the hands of readers to judge.

There have been new arrivals of persons in my family namely sisters-in-law Puja, Shubhra and Aradhana; nieces Shristi, Anjali, Tanvi and Aishwarya and nephews Adarsh and twins Luv-Kush. They all have proved refreshing amid long hours of work. Departure of my loving sister, Ira, and her husband Sachida, however, has been a setback.

I am thankful to my father, who happens to be the publisher of this book, for having opted for a quick, second revision of this book. I am also thankful to Dr. S.P. Sinha who provided some materials on genetics.

I, finally, wish good luck to CS aspirants whose success in the subject, and overall success, has been the main driving force for me.

PATNA
17-09-2003

P. NATH

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BRANCHES OF HUMAN GENETICS

Mendel is regarded as father of genetics because he discovered "Laws of Inheritance". It does not mean that study of genetics did not exist prior to Mendel. Maupertuis, born in France in 1698, studied inheritance of albinism and polydactyly in the eighteenth century. Otto's account in 1803 of haemophilia in a New Hampshire family was apparently the earliest clear description of the clinical features and mode of inheritance of this disease ; it was transmitted by healthy carrier females to their sons but never by an affected father to his son. This mode of inheritance was also noted in the case of colour blindness by John Dalton, an English Scientist.

Joseph Adams was, perhaps, the real founder of human genetics. A physician by profession, he published a book entitled "A Treatise on the Supposed Hereditary Properties of Diseases" in 1814 in which he showed considerable insight into many of the principles of medical genetics. On the basis of pedigree patterns, he clearly distinguished familial (recessive) from hereditary (dominant) disorders; he emphasised the interaction between hereditary susceptibility and precipitating environmental factors.

Most earlier investigators of human heredity were mainly interested in tracing pedigrees. Other aspects of human genetics received very little attention, except for a few studies on the effects of cousin marriages. One of the first scientists to become interested in the effects of inbreeding was Charles Darwin, who himself married a first cousin. The results of his plant breeding experiment led him to conclude that the progeny of crosses between unrelated organisms (outbreeding) were more vigorous than the progeny of crosses between related organisms (inbreeding). The French neurologist, Meniere, in 1856, suggested that in man deaf-mutism was more common in the children of cousin marriages. By the end of nineteenth century, human genetics was still in its infancy.

Besides human pedigrees and consanguineous marriages, another aspect of human genetics that had occupied the minds of workers in the beginning of 20th century was nature versus nurture controversy.

In man, the distinction between the effects of nature and nurture were made clear for the first time in 1875 by Sir Francis Galton, uncle of Charles Darwin. Galton argued that, since identical twins have the same genetic constitution, any difference between

them must be due to environment. Galton was especially interested in the inheritance of physique and special talents. In pursuing this interest, he studied families of wrestlers in the north of England. As a means of estimating the degree of resemblance between various relatives he introduced to genetics the statistical concept of the regression coefficient. He also introduced concept of selective breeding and "eugenics" which however, has no bright prospect with human beings. After rediscovery of Mendelism in 1900 much effort was made to apply these findings to man. Unfortunately, many of the earlier investigators oversimplified things. These early investigators not only believed that many human diseases were explicable in terms of the effects of single genes but that all disorders were due either to heredity or environment. This again was an oversimplificdation. Nevertheless, inauguration of human genetics can be said to have occurred with the Garrod's data of inborn errors of metabolism in 1901. It developed slowly in the first half of 20th century during which time populational studies dominated. Human genetics has no facilities of controlled breeding hence most of the human geneticists satisfied themselves with pedigree analysis. However, with the discovery of new instruments to analyse sub cellular components, and, discovery of the genetic material itself in the later half of 20th century. We find an accelerated growth of human genetics which has now ramified in diverse directions. Some of the important branches of human genetics follow in next sections.

1. Biochemical And Clinical Genetics

Alkaptonuria is a very rare condition in which affected persons excrete dark-coloured urine. The disease is usually recognised in infancy because the nappies are darkly stained and, in fact, washing with soap tends to make these stains even more intense. The dark colour is due to the presence of homogentisic acid which is broken down in normal persons and so does not appear in the urine.

Sir Archibald Garrod, in 1901, presented a paper in which he studied four families affected with the disease, the disease appearing in the offspring of cousin marriages most of the time Bateson suggested to him that Alkaptonuria was a recessive disorder hence appeared most often in the offspring of cousin marriages. Till 1900 genetics was studied in terms of structural traits. It was for the first time that Garrod implicated a biochemical substance in the action of gene, designated by Garrod as "inborn

error of metabolism".

This was the beginning of biochemical genetics and the idea that genes control the synthesis of enzymes, which in turn are responsible for carrying out specific biochemical processes. Beadle and Tatum provided experimental evidence for these ideas from breeding experiments with the bread mould *Neurospora crassa* for which they were awarded the Nobel Prize for Medicine and Physiology in 1958.

The modern era of human biochemical genetics began in the 1940s when the techniques of paper chromatography resulted in the discovery and clarification of a number of inborn errors of metabolism associated with the excretion of abnormal quantities of amino acids. These techniques are still producing new discoveries of additional genetic diseases resulting from blocks in the intermediary metabolism of amino acids and carbohydrates. One example of such inborn errors is phenylketonuria, which is caused by the absence of activity of the enzyme phenylalanine hydroxylase, and which results in mental retardation in the homozygote. By means of a variety of screening programmes, affected individuals for a number of these defects can be discovered at birth, and, if it is feasible, receive special treatment to avoid the ill effects of the mutant gene. This has been attempted and has been partially successful in the case of several inborn errors. The list of newly discovered inborn errors grows constantly. (List is following). This is of course, only to be expected since it is well known from lower organisms that mutation is a constant and fairly random event. Clinical abnormalities produced by such mutations may result from a variety of mechanisms, including deficiency of the product of the affected enzyme, accumulation of immediate or less immediate precursors, the overloading of alternate pathways leading to overproduction of another product, or the production of an abnormal intra-or extracellular structural component.

Table : *Characteristics and some inborn errors of metabolism (AR and AD = autosomal recessive and dominant. XR and XD = X-linked recessive or dominant)*

Type of defect	Genetics (Usual)	Deficient enzyme of defect	Main clinical features
Amino acid			
Albinism	AR	tyrosinase	lack of skin and hair pigment eye defect

Alkaptonuria	AR	homogentisic acid oxidase	arthritis
Homocystinuria	AR	Cystathgionine synthetase	mental retardation, dislocation of lens, thrombosis, skeletal abnormalities
Maple syrup urine disease	AR	branched-chain alpha-ketoacid decarboxylase	mental retardation
Phenylketonuria	AR	phenylalanine hyroxylase	mental retardation, fair skin eczema, epilepsy
Carbohydrate			
Galactosaemia	AR	galactose-1 phosphare uridyl transferase	cataracts, mental retardation, cirrhosis
Transport protein			
Cystinuria	AR	renal transport defect of cystine	kidney stones
Familial hypercholesterolaemia	AD	defect in cell surface receptor for low-denisty lipoprotein	early coronary artery disease
Vitamin-D resistant rickets	XD	renal defect in phosphate reabsorption	rickets
Lysosomal storage disorders			
Glycogen			
Mcardle's syndrome	AR	muslce phosphorylase	muscle cramps
Pompe's.	AR	lysosomal, 4-glucosidase	heart failure, muscle weakness
Mucopolysaccharide			
Hunter-s syndrome	AR	iduronidase	as hunter's syndrome plus corneal clouding
Sphingolipid			
Niemann-Pick disease	AR	sphingomyelinase	mental retardation
Tay-Sachs disease	AR	hexosaminidase-A	fits, mental retradation, blindness
Urea cycle			

Ornithine transcarbamylase deficiency	XR	ornithine transcarbamylase	hyperammonaemia, death in early infancy
Purine/pryimidine metabolism			
Leasch-Nyhan disease	XR	hypoxanthine phosphoribosyltransferase	mental retardation, uncontrolled movements, self-mutilation
Porphyrias			
Acute intermittent porphyria	AD	prophobilinogen deaminase	abdominal pain, CNS effects
Organic acids			
Methylmalonic acidaemia	AR	methylmalonyl-CoA mutase	hypotonia, poor feeding developmental delay
Endocrine			
Diabetes insipidus	AD	ADH	Polyuria
Adrenogential syndrome	AR	21-hyroxylase	virilisation
Miscellaneous			
Cystic fibrosis	AR	α-1 antitrypsin	lung disease

a. Haemoglobins : In 1949, Pauling and his co-workers established that sickle-cell haemoglobin had a different net charge from normal haemoglobin, and with this finding they coined the term "molecular disease". This was also the first use of the technique which has become one of the most productive in the study of biochemical genetics, that of electrophoresis, or the separation of proteins by differences in charge. In 1957, Ingram was able to show that this difference in charge was due to the substitution of the amino acid valine for glutamic acid at the sixth position of the amino acid sequence of the beta chain of haemoglobin. He achieved this by breaking up the protein chains with enzymes such as trypsin, separating the oligopeptides from each other by electrophoresis and chromatography, the latter method being dependent upon differences in solubility rather than charges, and searching for a peptide which had changes in its position. Once the altered peptide was located, it and its normal counterpart could be extracted from the paper chromatograms and their amino acid sequences determined. This technique has since resulted in the identification of over 100 different mutations

occurring in the two chains of adult haemoglobin.

b. Serum Proteins : The technique for the efficient detection of polymorphic variants of proteins and enzymes was discovered in the 1950s by Smithies and is called starch gel elctrophoresis. The samples to be studied are inserted into a slab of gel made by combining colloidal starch with buffer, and an electric current is then sent through the gel. This technique will not only separate different proteins by their difference in charge, which can be achieved in any electrophoretic medium such as paper, but will also separate them according to their molecular size. This is due to the fact that the starch acts as a sieve, slowing down the movement of the molecules proportionately to their size. The technique results in the separation of serum proteins into over 30 major components instead of the 5 previously detectable by paper electrophoresis.

Using this method, Smithies described two polymorphisms for common serum proteins. One of these is haptoglobin, which serves the function of binding haemoglobin abnormally released from red cells.

The other protein initially discovered to be polymorphic by Smithies was the iron-binding protein of serum, called transferrin. Since then, there have been over 20 different transferrins found in different individuals and their families . These, like haemoglobins, seem to differ from each other by single amino acid substitutions. Although it is difficult enough to understand how such enormous variability can exist in an essential structural protein without affecting its function, it is even more amazing to observe this variability in many enzymes, substances known to be critical in maintaining normal metabolism. In his search for genetic variation of enzymes demonstrable by starch gel electrophoresis, Harris at the Galton Laboratory at University College in London discovered that over half of the enzymes screened showed such variation, with many of these demonstrating marked polymorphism. Polymorphism here is defined as the existence of two or more variants of an enzyme, each occurring with a gene frequency of greater than 1 percent. Although most of this variation does not seem to affect the function of the enzymes, sometimes their activity will be altered, and it is, of course, these situations which we call inborn errors of metabolism.

c. Enzymes Of RBC : Most of the enzymes which have been studied for genetic polymorphism are those found in red blood cells, since this tissue is the most easily available. Among

the polymorphic enzymes found in the red blood cells are a number essential for the survival of the cell due to their activity in carbohydrate metabolism. These include phosphoglucomutase, which has been shown to be produced by three separate unlinked genes each of which shows genetic variation, 6-phosphogluconate dehydrogenase, and glucose 6-phosphate dehydrogenase, the latter coded by extremely mutable gene on the X-chromosome.

A few special things should be said about the sex-linked gene for glucose-6-phosphate dehydrogenase (G-6-PD).

The initial proof in man of the validity of the Lyon hypothesis of genetic inactivation of one X in female cells was demonstrated in cultured skin fibroblasts derived from women heterozygous for two electrophoretic types of G-6-PD.While an extract of a population of these fibroblasts demonstrated both types of enzymes, extracts derived from clones of cells grown from single fibroblasts showed only one or the other variant of this enzyme. This means that despite the presence of two x chromosomes carrying different genes for G-6-PD only one of these is expressed in any one cell and in all of its offspring. This finding has aided in settling some fundamental questions regarding the origin of certain tumours. It has long been argued whether cancers arise from a single event in a single cell or whether they are multiclonal in origin. Gartler has been able to resolve this question for at least some situations by studying some tumours in women heterozygous for two forms of G-6-PD. For example he found that fibroid tumours of the uterus each derived from a single cell, since the tissue of single tumours demonstrated only one or the other of the G-6-PD variants. An even more interesting finding was that all the peripheral blood cells of patients with chronic myelogenous leukaemia, and carrying the Philadelphia chromosome, showed only one or the other of the two G-6-PD variants, although tissue derived from skin biopsy showed both variants to be present in the patients. This not only indicates that the disease derives from a single event in one cell (probably the chromosomal alteration producing the Philadelphia chromosome) but that the responsible cell is a common precursor for the red cell, white cell, and platelet components of blood and that its offspring replace the entire bone marrow and, thereby, the peripheral blood of the affected individual. This is one of the many examples in which studies in human genetics can help to resolve problems in other fields, in this case those of cancer research.

d. Placental Enzymes : Another tissue commonly used in

these studies is the placenta. It has been shown that a number of enzymes present in the placenta are the product of foetal genes. It thereby becomes possible to obtain large quantities of foetal tissue for study without having to obtain it directly from a newborn child. such a study resulted, for example, in the discovery that placental alkaline phoshpatase, an enzyme restricted to the placenta and not found in any other tissues, is under genetic control. In Harris' studies it became apparent that placentas derived from nonidentical twins were sometimes alike in their alkaline phosphatase phenotype is determined by the foetus and not by the mother, since the latter situation would have resulted in identical phenotypes in both twins. By studying a series of randomly chosen placentas and calculating the hypothetical gene frequency for the three alleles postulated to cause this variation, it became possible to predict the distribution of the six common phenotypes among nonidentical twins. This predicted distribution agreed so will with the observed findings that it became apparent the variation in this enzyme was in fact due to a genetic polymorphism. This type of genetic analysis, called sib-pair analysis, is very useful when it is impossible to do pedigree studies.

2. Immunogenetics

a. Blood Cell Antigens : Another prediction of complete individual variability was made by Landsteiner when he discovered the ABO blood groups. He believed that adequate immunological techniques would demonstrate that each individual's tissues would be antigenically different from those of any other individual, again with the exception of identical twins. Studies brought out more and more variation in antigens present on the red blood cell, resulting in more accurate blood transfusion techniques. Even red cell variation alone comes close to Landsteiner prediction, but he has been proved completely correct by the discovery of histocompatibility antigens on other tissues, primarily studied in blood lymphocytes. As is known from the difficulties encountered in organ transplantation. individual variability of these antigens is enormous

To understand the genetics of antigenic differences. it is useful to analyze the mechanisms involved in the ABO blood group system. which is the best studied of all. In the 1920s. genetic analysis showed that the four genotypes.A. B. AB. and O. were due to three alleles at one locus. O individuals are

homozygotes for a recessive gene and lack A or B specificity. Differentiation of these types is also possible due to the existence of naturally occurring antibodies in the sera of normal individuals. People with blood type A have anti-B antibodies; those with B have anti-A ; those with O have anti A and anti B; and those with AB have neither (Table). These antibodies are capable of agglutinating the red cells of the type against which they are directed, and this is the basis of blood typing.

Table : *ABO blood groups*

Phenotype	Genotype	Antibodies in serum
A	AA. AO	Anti-B
B	BB. BO	Anti-A
AB	AB	Neither
O	OO	Anti-A and anti-B

Another famous blood group showing genetic variation is Rh this blood group system, for which no naturally occurring antibodies occur in humans, nevertheless is strongly antigenic. For this reason, transfusion of blood containing a major Rh antigen into an individual missing this antigen produces an immunologic response, so that the recipient now makes anti-Rh antibodies, which will cause a transfusion reaction if he is again transfused with Rh-positive blood. This situation became even more critical when it was realized that Rh-negative women married to men having this antigen could be sensitized while pregnant with children who inherited the Rh-positive gene from their father. Such sensitization occurs at the end of the first pregnancy by means of a leak of foetal blood into the maternal circulation. Subsequent pregnancies in which the children are Rh-positive are then affected by the antibodies produced in the mother due to the initial sensitization. These antibodies can cross the placenta and severely damage the child, frequently resulting in stillbirth, severe jaundice, or mental retardation. Initially, the treatment for this situation consisted of removal of the child before the end of pregnancy and an exchange transfusion with normal blood. While this saved many of the affected children, many others died or remained damaged

It was also recognized that not all Rh-incompatible pregnancies resulted in maternal immunization. Careful analysis of the affected and unaffected families revealed that if the mother, in addition to her Rh incompatibility, also was incompatible with her offspring insofar as the ABO blood groups are concerned. this

reduced the risk of Rh disease. The particular incompatibility that was most effective in prevention was a type O mother with type A or B offspring. Since it was known that type O individuals have naturally occurring anti-A and anti-B antibodies, it was assumed that the protective mechanism depends upon the rapid elimination of the incompatible foetal cells by maternal antibodies before the Rh antigen of these foetal cells could act to sensitize the mother. On this basis, therapy was instituted consisting of the injection into the mother of anti-Rh antibody shortly after delivery of her first Rh-incompatible child. It was hoped that this antibody would rapidly destroy the foetal cells and prevent sensitization. This form of therapy has been essentially perfect in the prevention of Rh disease. Here again co-operation between geneticists, immunologists, and clinicians has produced not only greater understanding of human biology but specific therapy for a genetic disease.

b. HLA System : Increased activity in the field of organ transplantation initiated the accelerated study of human histocompatibility antigens. Within few years the use of techniques derived from the study of mouse histocompatibility genes made it apparent that the major histocompatibility differences between people are the result of differences at one major locus. This is identical to the situation in other mammals in which it has been studied. This locus, referred to as HLA, has many alleles, each responsible for the production of several antigens. It is highly unlikely, because of this complexity, that any two unrelated individuals will be completely identical at this locus. It is apparent that unrelated individuals would rarely, if ever, be sufficiently compatible to accept grafts form each other without danger of rejection. It would appear, however, that the greater the similarity at this locus, the more likely it is that a transplanted organ will not be rejected. In addition to the obvious practical application of studies of HLA, there is a great unresolved theoretical problem. What is the purpose of such enormous individual variability at one locus dealing with antigenic specificity? A variety of explanations has been offered. One of these proposes that this variability is associated with very refined recognition processes which may act in the form of surveillance within the body for mutant cells displaying changes in their surface antigens. Since such changes are thought to be typical of malignant transformation, recognition and elimination of such altered cells may be a defense against neoplasia.

 DEGAM

c. Variability Of Immunoglobulins : Immunogenetics is concerned with variability of the recognition molecules themselves. The serum proteins known as immunoglobulins, gamma globulins, or antibodies fall into 5 classes. These are IgD, IgE, IgG, IgA and IgM. Each of these consists of two pairs of identical chains called H (heavy) and L (light). The heavy chain determines the class of immunoglobulin. The light chains, of which there are two types, called kappa and lambda, are made up of over 200 amino acids about half of which are constant.

The other half of each light chain varies from molecule to molecule to an almost unlimited extent, and this variability in part determines the antibody specificity of the molecule. Similarly, it appears that three-quarters of the heavy chain is constant again with occasional amino acid substitutions due to genetic variation, and one-quarter, about 110 amino acids long, is extremely variable. This end of the chain, together with the variable end of the light chain, makes up the specific antibody site which combines with a specific antigen.

Accurate analysis of the sequence of amino acids in these portions of immunoglobulins has shown that there is a great deal of homology between the variable and constant halves of the light chains, indicating that they emerged from a common ancestral gene. In addition, it appears that the heavy chain is made up of four homologous copies of the same gene originally coding for half of the light chain. There are several hundreds genes from which a few are selected to form antibodies. This is the main reason of antibody diversity.

From this review of current problems in human genetics, it can be seen that the many new techniques developed in the field have already produced numerous advances. The major conclusion form this progress is that there is virtually unlimited genetic variability in man, certainly enough to assure each of us of being a unique individual, biochemically and antigenically different from all others, except in the case of identical twins. The major problem to be resolved now is how this enormous heterogeneity has come about, how it is maintained, and what may be its function in our survival as a species.

3. Developmental Genetics

The Zygote, the fusion product of sperm and ovum, undergoes mitotic divisions and thus cell number increases.

Initially, all cells are alike, called embryonic type (without specialised function). But later on such embryonic cells become differentiated to perform specialized functions. Developmental genetics is concerned with the process of differentiation of cells.

There exists a relationship between DNA and proteins synthesized in the cell because it is DNA that directs protein synthesis through mRNA. It is protein that characterizes a cell. Hence, it is DNA which should ultimately be held as the factor for differentiation.

a. Totipotency And Nuclear Transplantation : There is no loss of DNA as mitotic divisions continue and there is ample proof that DNA content of the zygote is the same as that of later cells. Differentiation, thus, is not caused due to loss of any DNA in any of the differentiated cells. All cells have same DNA and equally capable of causing growth.

John Gurdon's experiments of nuclear transplantations in the 1960s clearly established that all cells of body are equally 'totipotent' and capable of causing growth of a zygote. It was shown that if nucleus of a toad's zygote is destroyed and replaced by its skin cell, the skin cell's nucleus is capable of causing complete growth of zygote. The experiment also proved that cytoplasm is a potent force in development because it can make the genes 'on' or 'off'. The genes 'on' in the skin cells were different. When the nucleus of skin cells was transplanted into zygote, the cytoplasm of the zygote switched the prior active genes 'off' and another class of genes 'on'. Development, at the genetic level, is thus considered an interaction between cytoplasm and genes during which certain genes are switched 'on' and 'off' (derepressed and repressed respectively).

b. House Keeping And Luxury Genes : From development point of view genes are divided into housekeeping and luxury classes - the former concerned with elaboration of those substances that are essential for all cells eg. membrane proteins. Such genes are switched "on" in all the cells. Luxury genes are concerned with specialised function of the cell, hence switched 'on' differently in different cell. There is a definite sequence in which different genes are activated and this is largely a function of induction that organises the embryo.

Once a cell is differentiated, it secretes certain substances, called inducer for other cells to differentiate. The chemical nature of such substances seem to be nucleo-proteinous.

Development, however, does not involve only differentiation of cells. Region formation is an equally important aspect which is probably brought about by homeotic genes.

c. Homoeotic Genes : From development point of view genes can be grouped as :

a. Highest order genes - that define axes

b. Middle order genes - that define segments

c. Lower order genes - that give identity to segment.

Homoeotic genes are lower order genes. In *Drosophila*, where they have been studied in most detail, they appear to specify the diversity of the different body segments and their expression can often be shown to occur at a particular time of development, in a defined region of the developing organism. The homoeobox or Hox genes have been shown to be closely related a structure, in that the protein produced has a closely conserved sequence of approximately 60 amino acids which has been called the homoeobox domain. The Hox genes appear to code for proteins involved in the regulation of gene expressions as transcription factors and almost certainly act by binding particular DNA sequences. It is interesting that the homoeobox genes in certain species have been found to map to a single chromosomal cluster and the order of the loci of the homoeotic genes on the chromosome is the same as the order of the physical segments in the animal concerned. Homoeotic sequences have been identified in man and have been shown to be expressed in spinal cord during embryonic development (Simeone et al 1986) but their role in development is not yet clear. Deubtless this area of research in the next decade will provide the means to begin to understand some of the genetic factors controlling development.

d. Developmental Anomalies In Humans : Human developmental genetics is concerned not only with unfolding the genetic mystery of normal development but seek causes and explanation on its background for any developmental anomaly witnessed in humans. Many examples are known, both in animals and man, of mutations and teratogens that interfere with the normal development. Teratogen is an agent that causes congenital abnormalities. Mutations, particular during phenocritical period, are likely to disrupt normal embryogenesis because all the stages thereafter become disorderly.

In man, teratogenic agents include radiation during pregnancy, maternal infection with rubella, treatment during

pregnancy with certain drugs and substances.

The developmental genetics is inseparably linked with science of embryology. Almost all experiments in developmental genetics is confined to womb of a mother in which embryo is developing. It is only with the help of embryology that one can identify various tissue types, its structure and relationship with other tissues. It is only through the embryonic tissue that we can identify whether gene is switched "on" or "off". While studying effect of mutations and teratogenic agents, it is science of embryology can tell us about the nature of the changes undergone during defects so that a plausible explanation can be sought for from the science of genetics.

4. Pharmacogenetics

Drugs can be used to reveal genetic variations of organisms e.g. certain bacteria are resistant to certain antibiotics; certain insects are resistant to the DDT and organophosphorus insecticides. Human beings, too, reveal certain variations in response to certain drugs. The term pharmacogenetics was introduced by Vogel in 1959 for the study of genetically determined variations that are revealed solely by the effects of drugs. Such a definition excludes those hereditary disorders in which symptoms may occur spontaneously but which are often precipitated or aggravated by drugs. Nowadays many investigators also include these latter diseases within the sphere of pharmacogenetics. For many years it has been known that some individuals may be especially sensitive to the effects of a particular drug whereas others may be quite resistant. Such individual variations may be the result of factors which are not genetic and such variations do not come within the scope of pharmacogenetics which is only concerned with genetically determined variations in drug response.

Once a drug is taken orally, it is broken down into five particles and absorbed in the gut from where it reaches blood stream. From blood, it is distributed to most of the tissues and tissue fluid. A small part of it really reaches the target tissue and the rest is either excreted unchanged or first metabolized then excreted. In due course, either directly or through metabolism, all the drug is excreted out. The metabolism of many drugs involves biochemical modifications, usually taking place in liver, during which the drug is linked to another molecule.

a. Known Paths Of Metabolism : Persons vary in the way

they metabolize the drug and this can be genetically determined. Biochemical steps of many such metabolism is well worked out and understood. For example, take the case of isoniazid, an antituberculosis drug. The drug is metabolized by the process of acetylation which takes place in liver. Persons differ on the basis of rate of inactivation, being rapid or slow inactivators. Take another example. Succinylcholine is a muscle relaxant. Some persons are found to be sensitive to the relaxant because of an abnormal plasma enzyme called pseudocholinesterase. Similarly, persons vary in their reaction to malarial drug, Primaquine. Some develop haemolytic anaemia (anaemia due to break down of RBC) due to deficiency of the enzyme glucose 6 phosphate dehydrogenase in their RBC. You will find a few facts about this enzyme in biochemical genetics.

Thiopurine drugs are used in treatment of certain forms of Cancer. About 0.3% of population are unable to properly metabolize the drug hence develop serious side effects. The deficiency seems to be of an enzyme of RBC, TMPT (thiopurine methyl transferase) which has genetic basis.

Debrisoquine, a drug used in treatment of hypertension, is not metabolized by 5-10% of British subjects. Though initially the subjects were supposed to be homozygotes for a recessive gene, recent observations have revealed at least four different mutations, and that too in introns that result in faulty mRNA splicings.

Organophosphates are widely used in agriculture and industry. The enzyme that metabolizes the substance is paraoxonase, a product of two allele polymorphic systems. Some can metabolize the drug faster than others.

b. Unknown Paths Of Metabolism : Coumarin is an anticoagulant drug which is used in treatment of myocardial infarction to prevent the blood from clotting. Some persons require 20 times the usual dose prescribed for normal patients. In rats, if has been shown to be due to high levels of vit K which counteracts the drug.

Malignant hyperpyrexia is a rare complication of anaesthesia during which muscles remain rigid while temperature runs as high as 108^0F. The condition seems to be inherited as autosomal dominant trait. Patients often have raised serum level of creatine kinase and are sensitive to caffeine and some other chemicals. The real cause has not been ascertained, though it seems that there is basic defect of reduced uptake and binding of calcium ions to the

sarcoplasmic reticulum of muscles.

Persons also differ in metabolism of Alcohol. It is metabolized in liver by enzymes ADH and ALDH (alcohol dehydrogenase and aldehyde dehydrogenase respectively). There is a typical allele, distributed more commonly in oriental region, of ADH which rapidly forms acetaldehyde, and results in unpleasant symptoms. In Europeans, a normal allele of ADH is more prevalent which slowly metabolize alcohol and hence it is not unpleasant. The situation, however, has some more complexities. There are many variations due to altered drug response e.g. Porphyria variegata, some haemoglobino pathies, diabetes, gout etc. In many cases, aetiology is not clear but biochemical evidence of variation in response to drugs suggest a genetic contribution. Cases in which variable forms of a disease, such as depression, has response to drugs can indicate to the genetic reasons of the disease. It is difficult to explain origin of such variation in drug response.

In the case of G6PD deficiency there is evidence which suggest that a deficiency of this enzyme may confer some protection against one form of malaria. But with regard to the other examples of hereditary variations in response to drugs we have very little idea. It is possible that in the past some metabolic variations may have conferred selective advantages under certain dietary conditions. Another possibility is that some might have conferred resistance to particular infections. However, at present we really have very less evidence.

This branch of genetics is inseparably linked to pharmacology. It is in pharmacology that we study molecular structure of drugs and their target tissue and mechanism of action of the drug. When a drug does not show a predicted mechanism of action, it becomes necessary to explain the reasons. It is where pharmacogenetics steps in and analyses the variations and its probable genetic reasons.

5. Population Genetics

Evolutionary action takes place at the level of population. This is not to deny the fundamental, underlying importance of molecular, chromosomal, cellular or organismal events. Population genetics stresses that evolution operates on groups of organisms, not on individuals or their component parts. All organisms have descent with modifications and it is meaningful in context of a

group within which there is genetic exchange.

In population genetics, individual genes have no meaning. It is the gene pool of the population that matters. The gene-pool consists of all the genes, in all their allelic forms, in the reproductive gametes of the population. Changes in the gene pool will reflect changes in the population. The more rapid or extreme the gene pool shifts, the faster the population undergoes change. One cannot study the entire gene pool. Even if one possessed the tool to identify all of the genes of a gene pool the amount of work would become prohibitive and burdensome. Population genetics, thus, selects a phenotypically measurable gene-marker and studies its frequency over a period of time. Gene frequency of a given allele is a function of percent of individuals in the population who have that gene and thus its value may range from zero to 100 percent. A stable gene pool is one in which frequency of a allele remains stable, whatever its value.

Population genetics, thus, considers frequency of genes in the population and studies effects of various forces such as mutation, selection, drift, migration, non random mating etc. that destabilizes the genetic equilibrium and thus causes evolution. Stability of the genetic equilibrium means that population is experiencing no change. In such a population the relative proportions of the different genotypes remain constant from one generation to another. This is known as the Hardy Weinberg principle which was put forward independently by an English mathematician, G H. Hardy, and a German physician, W. Weinberg, in 1908. It will be seen that gene and genotype frequency remains the same every generation, if Hardy-Weinberg conditions exists.

Theoretical And Practical Values : Study and analysis of gene frequency and changes in them have both theoretical and practical value.

1. They provide insight into mechanism of evolution, and they may often reveal evolutionary change in progress. It can reveal where the population came from in terms of taxonomic relationships and where it is going in terms of adaptive change. Studies of Gene frequency of populations of many islands have indicated the population of the mainland it came from, along with its degree of variance. Population genetics, thus, can reveal roots of a population, besides estimating its evolutionary progress.

2. Observable changes in the frequency of a gene that entail physical handicaps is often useful for national agencies that are

esponsible for anticipating future needs of a society in terms of health care, educational programmes, man-power planning etc.

3 By applying rules of population genetics one can know the status of carriers of a disease, and by working out the degree of inbreeding, the probable percentage of persons affected with certain autosomal recessive diseases. For example, if frequency of alkaptonuria is known the status of carriers in the population can be calculated in this way.

Alkaptonuria affects about one child in every 1000 000. Therefore,

$$q^2 = 1/1\,000\,000$$

$$\text{therefore} \quad q = 1/1000$$

$$\text{but} \quad p = 1 - q$$

$$\text{therefore} \quad p = 1 - 1/1000$$

$$= 1$$

$$\text{The frequency of carriers} = 2pq$$

$$= 2 . 1/1000$$

$$= 1/500$$

This example also illustrates another important point, which is that in the general population carriers are very much more common than affected individuals for any autosomal recessive disorder. If the status of carriers becomes known national agencies can work out number of probable sufferers in the future and the resources needed to meet such a situation.

4. Population genetics helps not only in discovering "roots" of a population but also "routes" of a population. Study of gene frequencies of ABO system has provided valuable information regarding the routes of migration of people in the prehistoric times and has supported results obtained form anthropological studies and comparative linguistics.

5. Tools and analyses of population genetics has aided in blasting away myth of racial superiority and thus has become important weapons in ideological war against those who support racism. No race can claim to be genetically pure, it is the frequency variations of different alleles that make populations appear different. All populations have deleterious recessive genes hidden from natural selection in heterozygotes and it will be carried so for a long time transgressing all the political divide.

6 Population genetics raises some ethical questions too.

Should a haemophiliac transfused with artificially synthesized factor VIII in order to prolong its life span and reproductive time ? Individual concern reply in 'Yes'. Would the answer remain same if well-being of population is concerned ? Possessor of such recessive deleterious gene will only add to the genetic burden of the population in the long-run. Population genetics does not suggest a way out, though it nonetheless provides with the opportunity to calculate cost benefit of the situation.

Methods Of Study : The discovery of the Hardy Weinberg law resulted in study on frequencies of genetically determined variations. Data on genotype, or phenotype, or gene-allele, or chromosome structure are collected from field study or laboratory experiments on a population basis. The observed number is compared with expected number and the difference is tested for significance by the chi- square test. It answers the question that whether something has or has not any effect on difference between expected and observed frequency.

The population genetics, thus is concerned with describing the genetic constitution of the population. When evolutionary differences between populations become significant, a study of changes in the gene frequency becomes study of microevolution.

Population genetics embraces four fields - anthropological and cytological studies for the collection of datas, and mathematical and statistical formulations for interpretation of these datas inorder to comprehend its significance.

6. Radiation-Genetics

Ionizing radiations include electromagnetic waves of very short wave lengths such as X-rays and gamma rays, and high-energy particles such as alpha and ta particles and neutrons. Natural sources of ionising radiation include cosmic rays and external and internal radiation from naturally occurring radioactive elements in the environment. Artificial sources of radiation include those resulting from diagnostic radiological procedures, radiotherapy, occupational exposure and nuclear accidents and explosions.

In 1927, H.J. Muller demonstrated that exposure of colonies of *Drosphila* to X-rays resulted in an increase in the number of mutations in excess of those occurring spontaneously. He thus showed that X-rays are mutagenic and for his work in the field of radiation genetics he was awarded the Nobel prize in 1946. Further

experiments on *Drosophila* have shown that ionising radiation may cause mutations in both the sex cells and body cells. Mutations induced in the body cells are termed somatic mutations. It is with mutations in the sex cells that the geneticist is most concerned because they can be transmitted to future progeny.

Effects Of Radiation

1. Somatic Effects : Those near the site of atomic explosion in Japan in 1945, many were killed immediately by the blast and may suffered from the effects of having received an enormous dose of radiation. Some died within 10 days, others were ill for several weeks. Those exposed, lost their hair and their bone marrow activity was greatly reduced so that the number of circulating leucocytes was considerably diminished and their resistance to infection was therefore severely impaired. Among those who recovered from the immediate effects, some of them later developed leukaemia.

The somatic effects of a high dose of radiation to a localised volume of tissue are local tissue necrosis (radiation burn) and general malaise with some nausea and vomitting (radiation sickness).

2. Genetic Effects : Mutations occur very rarely under natural conditions. (spontaneous mutations). Natural background level of radiation are too low to account for the vast majority of spontaneously occurring mutations. The genetic effects of radiation are not easy to assess for they are not manifest in the generation which is exposed to radiation but in subsequent generations. If a dominant mutation is produced then it will be manifest in the next generation but a recessive mutation is only likely to be manifest when two heterozygotes marry and have children. If the recessive mutant allele is very rare then the chance of this happening will be small. Several lines of experiments have been devised to assess genetic effects of radiation.

a. Offspring Of Parents Exposed To Radiation : The earliest one was by Neel and Schull who believed that radiations in Hiroshima Nagasaki due to atomic bomb has affected x-chromosome of parents and has resulted in altered sex-ratio. They designed experiments in which female and male parents were exposed to radiation . X-linked mutation in females meant lesser number of boys born to them, and x-linked mutations in males meant greater number of boys born to them. They found evidence for greater number of boys, i.e. high sex-ratio (number of boys to

girls).Careful studies by Kato (1975), however, has refuted such claim of alteration in sex-ratio. Animal studies have also failed to demonstrate any significant genetic effects of the increased amounts of background radiation in Kerala in (India) though there is a suggestion that the incidence of Down's syndrome have been increased in this region (Kochupillai et al.1976).

b. Offspring Of Parents Who Received Pelvic Radiotherapy: The results of such studies were similar to those obtained in the earlier Japanese study ; there was a slight increase in the sex ratio (more males) when the father was the irradiated parent and a slight decrease when the mother was the irradiated parent. However the results of such studies have to be accepted with caution because many factors other than radiation may influence the sex ratio. such as paternal age, birth order etc.

c. Offspring Of Radiologists : In the United States the incidence of abortions, stillbirths and congenital malformations in the offspring of other medical professionals have been compared. The assumption made was that radiologists are exposed to more radiation than are other physicians. The results of these studies showed that there were slightly more foetal deaths but the differences were not statistically significant.

d. Offspring Of Nuclear Power Station Workers : The results of such studies suggested that exposure to ionising radiation in some way led to leukaemia, possibly by inducing mutations in the germ cells of the fathers, though leukaemia is not strictly a genetic disorder. It will be instructive to see if in future there is any increase of genetic disorders in the offspring of such fathers, though so far there is no evidence of this (Gardner et.al 1990).

Experiments on other organisms have shown clearly that ionising radiations do cause mutations, the vast majority of which are harmful. The important point as far as man in concerned is that induced mutations may harm individuals in future generations. The hazard is not so much to ourselves as to our descendants. In man we do not have any precise way of estimating the amount of genetic damage caused by radiation. A direct way is to study the birth incidences of disorders if there has been any significant change over time. Such an approach would only be likely to yield meaningful results if precise incidence figures were available. Committee on the Biological Effects of Ionizing Radiations (1980), US has calculated such precise risk.

The International Commission of Radiological Protection (ICRP), working in close liaison with various agencies of the United

Nations has been mainly responsible for defining what is referred to as the maximum permissible dose of radiation. The commission has fixed 50 mSv/year, though it varies from country to country, the lowest being of those fixed by UK, 15 mSV. To put this into perspective, 1mSv is roughly 50 times the dose received in a single chest X-ray.

The rad (radiation absorbed dose) is a measure of the amount of any ionising radiation which is actually absorbed by a tissue and is equivalent to 100 ergs of energy per gram of tissue. A rem (Roentgen equivalent for man) is a measure of any radiation in terms of X-rays and is that absorbed dose which produces in a given tissue the same biological effect as one rad of X-rays. In SI units 100 rem is equivalent to 1 sievert (Sv).

7. Ecogenetics

Though the term is new, first given by Brewer in 1971, the concept has been an old one, followed much ago in past, and developed in the second half of 20th Century by such workers as kettlewell, E.B. Ford, Sheppard, Dobzhansky, Dowdeswell etc who worked mainly with animal populations. The term ecogenetics or ecological genetics describes the technique of combined field and laboratory work. Ecological genetics deals with the adjustment and adaptations of populations to their environment, particularly in field of nutritional ecology and infectious diseases. It is study of genetically determined differences in susceptibility to the action of physical, chemical and infectious agents in environment. Such differences in susceptibility may be either unifactorial or multifactorial in causation and some examples are given in Table

The concept of ecogenetics will be particularly important in the identification of individuals at high risk from the effects of mutagens and carcinogens in the environment. The susceptibility to certain common diseases may also reflect genetically determined differences in response to environmental agents. The concept is new but is very likely to develop in next few years as human kind is exposed to more and more pollutants.

The concept of ecogenetics is related to, but different from, evolutionary genetics and population genetics. Evolutionary genetics include laboratory work and development of mathematical theories which do not employ ecology. In evolutionary genetics, the gene and its products are analysed and their evolutionary relationship found out. Ecological genetics does not have a direct

bearing on evolution though some indirect inferences may be drawn. Ecological genetics involves genetic studies of adaptation to different environment by races and populations.

Table : *Ecogenetic variations in susceptibility to environmental agents (After Gardner et. al. 1990)*

Environmental agent	Genetic susceptibility	Disease
UV-Light	Fair complexion	Skin Cancer
Foods		
fats	hypercholesterolaemia	atherosclerosis
fava beans	G6PD defeciency	favism
salt	Na-K pump defective	hypertension
milk	lactase deficiency	lactose intolerance
alcohol	atypical ADH	alcoholism
Inhalants		
dust	α_1-antitrypsin deficiency	emphysema
smoking	AHH inducibility	lung cancer
allergens	Atopy	asthma
Infections	defective immunity	? diabetes mellitus ? spondylitis

Population genetics, on the other hand, is a total laboratory affair. Mathematical formulae are applied to the data and rates of different agents of evolution calculated to explain gene frequency and genotype frequency of a population to measure rate of evolution.

Aim of human genetics is to study human variability through study of existing differences between individuals of a population and between the populations themselves. Genetics can be best studied through studying what is exception to the rule. In the present time human genetics has diversified into multiple branches that makes the aim feasible. There is thus tremendous scope which has been outlined in the previous paragraphs.

Besides the branches mentioned above, there has emerged in recent times still a few other branches. Evolutionary genetics is such a branch. Genetic material and several proteins of man has been compared with genetic material and proteins of other primates and their evolutionary relationship derived on such bases. Such studies are important for they unfold past happenings and future prospects.

GENETIC MATERIAL OF MAN

Human beings, as do other animals, show a programmed development, a definite pattern of growth and development. The blue print for this programmed development is contained in the DNA which is important constituent of chromosomes. DNA functions through mRNA and synthesize protein. This sequence is cardinal point of molecular biology, referred to as central Dogma.

DNA → mRNA → Protien

The first step is referred to as transcription, the second translation (in recent years formation of DNA from mRNA has been shown to occur by reverse transcriptase e.g in retroviruses).

The DNA and RNA, the two master molecules of life are called nucleic acids. The two nucleic acids are each chemically made up of a purine or pyrimidine base, a sugar, and phosphoric acid. On the basis of the kind of sugar (deoxyribose or ribose), the nucleic acids are divided into two main groups : deoxyribonucleic acid (DNA) and ribonucleic acid (RNA). DNA occurs only in the nucleus, where it is the major component of genes; RNA is found throughout the cell, being especially abundant in nucleoli and in the cytoplasm. The nucleic acids may be broken down chemically or enzymatically into nucleotides. Thus a nucleic acid molecule is made up of many nucleotides joined to form long chains. Each nucleotide consists of phosphoric acid, deoxyribose or ribose sugar, and a pyrimidine or purine base. The purine units are adenine and guanine; the pyrimidines are cytosine, thymine, and uracil. Five kinds of nucleotides are recognized on the basis of these purines and pyrimidines: (1) adenine-sugar-phosphate, (2) guanine-sugar-phosphate, (3) cytosine-sugar-phosphate, (4) thymine-sugar-phosphate, and (5) uracil-sugar-phosphate. The DNA molecule has the first four of these nucleotides ; the RNA has the first three and the last one. Although the phosphate-sugar part of the long chain of nucleotides is regular, the base attached to the sugar is not always the same, and the order of these bases is irregular and varies from one section to another of the nucleic acid molecule.

Structure Of Molecule (Watson-Crick Model)

In 1953 J.D. Watson and F.H Crick proposed a model of the structure of the DNA molecule which has been widely accepted. Based on the information then available about the molecule, such

DNA – AGCT
RNA – AGC U

as the x-ray diffraction studies of M.H.F. Wilkins on the spatial arrangement of molecules, the nucleotide composition of various DNA molecule and the ratios of the purine and pyrimidine bases, they constructed a model that suggested plausible answers to such problems as (1) how specific directions are transmitted from one generation to another, (2) how DNA could control protein synthesis, and (3) how the DNA molecule could duplicate itself.

According to this model, the DNA molecule consists of two complementary polynucleotide chains helically wound around a central axis and cross-linked through specific hydrogen bonding between purine and pyrimidine bases. In this arrangement the phosphate and sugar groups are on the outside of the axis; the bases are inside and connected to each other by hydrogen bonds. For each complete turn of the double helix, there are about 10 nucleotides in each chain. The hydrogen bonding is such that, at any level where adenine is found on one chain, thymine appears on the other chain; and wherever guanine is placed on one chain, cytosine is its mate on the other chain. It will be noted also that A and T are joined by two hydrogen bonds and C and G by three bonds. A hydrogen bonding takes place from the sharing of a single hydrogen atom by two atoms. Such bonds are weaker than ordinary chemical bonds. One of the atoms acts as a hydrogen donor and the other as a hydrogen acceptor. Donor atoms and acceptor atoms are found in each of the nitrogenous bases. The DNA molecule has a diameter of about 20 angstrom units (Å) (1Å = 1/10,000,000 mm). DNA chains have various lengths, but some are thought to be at least 200,000 nucleotide pairs long.

2 H2 bonds
A = T
G ≡ C
3 H2 bonds

Semi Conservative Replication

The Watson-Crick model suggests how a DNA molecule can replicate itself. Since each chain of the double helix is complementary to the other, each has the information to direct the synthesis of a partner. The two chains separate or unwind, and each chain then serves as a template to synthesize another chain complementary to it. In the new chain free nucleotides from the surrounding medium are properly assembled and form hydrogen bonds with matching nucleotides of the original chain. That DNA replication occurs this way is indicated by two kinds of experiments. One of these methods is by the use of isotope-labelling, such as phosphorus 32, by which it is possible to distinguish the mother DNA strand from the daughter strand. The second method involves the growing of bacteria on a culture

medium of heavy nitrogen 15. The DNA of such an organism had a molecular weight 1% greater than DNA of bacteria grown on nitrogen 14.

The Composition Of DNA In A Human Cell

There is a remarkable amount of DNA in every cell and it is almost always the same in every cell. Most normal cells are diploid, that is, they contain two sets of DNA, one derived from the maternal egg and one from the paternal sperm: each set (or haploid genome) comprises in humans about 3,000,000,000 base pairs (3000 Mb). All mammals have haploid genomes of about this size. The haploid genome size characteristic of a particular species is sometimes called the C-value. Eggs and sperm are, of course, haploid;some somatic cells have multiples of the diploid amount of DNA, and are polyploid. Our genomes are larger than those of many other organisms. Viral genomes are trivial, some no more than a few thousand base pairs (kb); bacteria have a few million; *Drosophila* 100 Mb. But in size of genome we do not excel other mammals, newts, lungfish or onions.

Experiments have shown that the DNA sequences in all the different types of cell, for a given species, are essentially the same. In hybridization experiments, DNA from human brain cell competes efficiently with DNA from human liver. In principle, this means that the genome of any cell contains the information needed to make the whole organism. In practice, it has indeed been possible to produce entire adults from single cells. With plants, this is easily achieved. Nuclei from rapidly-growing tissues of amphibians can be transplanted into the eggs devoid of nucleus and it develops in adult. Such nuclear transplantation experiment is not feasible with mammals. It has been found that human (and most eukaryote) DNA can be divided into three classes, depending on their abundance in the genome satellite DNA, interspersed repeated DNA and single copy DNA.

Satellite DNA : Some is highly-repetitive DNA, of which one element is satellite DNA, consisting of short sequences repeated many times, often in enormous clusters end to end, (1Mb long), mostly with no known genetic or other function. This makes up about 5% of the human genome; each of the four main human satellite sequences occurs in about 100,000 copies. If the base sequence of such repeated sequence is very different from that of average DNA then the tandem repeat will have a different density from the average and in experiments where DNA is fractionated

according to its density, the repeat appears as a minor fraction distinct from bulk DNA Satellites vary enormously between species. Satellite can be divided into mini and microsatellite. A function can be attributed to the *telomeric minisatellites*, found at the ends of chromosomes, in which a hexanucleotide sequence (mostly TTAGGG) is repeated about a thousand times; these play an important part in DNA synthesis and chromosome integrity. More importantly, from the point of human medical genetics, some of the other satellite elements vary considerably between individuals. These are the *hypervariable minisatellites*, which occur as about a thousand copies of variations on the theme GGGCAGGAXG (x = any base). Almost as variable are the *microsatellite* DNAs, brief lengths of tandem repeats of very short sequences, most frequently CA or CT or just A. A microsatellite occurs, on average, about once every 20 kb; (1 kilo base 1000 nucleotide base pairs) Number of repeats in a satellite vary in every individual. Their variability makes them useful markers in molecular genetics, though most of them have no direct genetic effect. Collectively, they are sometimes known as VNTR elements, short for variable number tandem repeats.

Interspersed Repeated DNA : Another highly repetitive form is interspersed repeated DNA : 300 to few thousand long. This DNA makes up about 20% of the human genome. Some of this is transcribed; some of it, indeed, consists of elements that are present in many genes. One human interspersed element is the *Alu family*, (so called because its members contain cleavage sites for the Alu I restriction enzyme and therefore generate characteristic fragments). Members of the *Alu family* are about 300 bp long, and occur apparently at random in the genome, about one every 6Kb making up about 5% of the whole. Some are transcribed by themselves; most occur inside other transcriptional units, or are silent. Their function, if any, is still obscure. Most human genes contain at least one Alu sequence. In experiments where human DNA is attempted to be transferred to other cells or vectors, Alu sequences are useful markers for the presence of human DNA. Other families of interspersed repeats are rarer, but their elements can be much longer. These long interspersed nuclear elements, or LINEs, occur in various families. In mammals the most common is the LINE1 family, present on average once every 50 Kb, sometimes also known are the Kpn family, because they are cleaved by the restriction enzyme Kpn I. Some small fraction of the genome is moderately repetitive DNA, normal genes

that are present in many copies. Their product is needed in large quantities. They constitute about 10% of DNA.

Single Copy DNA : The remainder of the human genome, about 65% is unique or single copy DNA; this comprises most of the transcribed genes.This DNA also contains much untranscribable materials. The percentage of DNA that transcribe is roughly estimated to be 20% of human genome.

Exons And Introns : Even in 20% of the transcribable genome all are not translated into proteins. Most human genes, as are all eukaryotic genes, split into exons and introns.Exons are translating part of DNA and introns exist functionless between exons. Introns are transcribed in mRNA but are removed during maturation of mRNA. Apparently, it is only exons that are functional part of human genome. All exons can be divided into 2 groups.

Eurkaryotic gene → mRNA before maturation

$Exon_1$ Intron $Exon_2$

∴ Mature mRNA after removal of Intron.

$Exon_1$ $Exon_2$

a. *House Keeping genes which synthesize proteins required by every cell.*

b. *Luxury genes* : which synthesize proteins which are specific to a cell type i.e. cells secreting digestive enzymes, immunoglobulins hormones, etc.

Packaging Of DNA In Human Cell : Nucleosome

All the DNA, except mitochondrial and plastid DNA, are enclosed in nucleus, surrounded by the nuclear membrane. Possession of this membrane, with a consequent division of the cell into nucleus and cytoplasm, is the feature which distinguishes the eukaryotes-animals, plants, fungi and protozoa - from bacteria. The nuclear membrane is really two layers with a space between, the whole being perforated at intervals by complex protein structures, the nuclear pores, which make possible the transport of certain important molecules between the nucleus and the surrounding cytoplasm. Within the inner nuclear membrane there is a network of protein fibers, the lamina. Within this is the DNA, bound to a diversity of proteins mainly histones to form a complex called chromatin, on account of its ability to stain brightly.

Histones are in fact, similar in all eukaryote cells; one type of histone molecule, called H4, differs in only three amino-acids between plants and mammals. This similarity reflects their unvarying structural role. Histones combine with DNA to form a fundamental unit of chromatin, known as the nucleosome, Each nucleosome contains eight histones (two each of H2A, H2B, H3 and H4), which together form a protein core around which DNA is would in two turns, forming nucleosome about 11 nm across and 6 nm deep. The DNA that joins the adjacent nucleosomes is called linker DNA. All the histones are inside the core-protein except Histone - 1 which is present where DNA enters and leaves the core histones.

These nucleosomes are arranged as regular repeating units; in electron microscope pictures of lysed nuclei, the nucleosomes are visible as beads-on-a-string. The string, in this case, is the continuous DNA fibre that links the nucleosomes. This linker DNA, not being protected by tightly bound core histones, is (unlike nucleosomal DNA) selectively vulnerable to DNA digesting enzymes such as micrococcal nuclease.Interactions between H1 histones and nucleosomes allow the formation of higher-order structures. One of these is the *solenoid*, a fiber 30 nm in diameter, consisting of a helical arrangement of nucleosomes. Less compact structures must also exist in regions where DNA is replicated or transcribed. The higher-order structures of chromatin are in part determined by the interactions with a numerous class of proteins, non-histone proteins.

Most of the time, cells and their nuclei are in what is called interphase, the period when they make RNA and (if they are in dividing tissues) replicate their DNA. This period of interphase is conventionally divided into three sections : G1, when the cells have not yet replicated their DNA; S-phase, when they are synthesizing it; and G2 when they have finished replicating their DNA but have not yet divided. Cells may spend a short or a long time in G1 or G2 - hours, days or years. S-phase, once begun, is usually completed in 12-24 hours. The passage between G1, S and G2 must affect chromatin structure considerably, but the differences are hard to visualize. This constitutes what is called a "cell-cycle".

A Highest Order Of Structure : Chromosomes

A cell about to divide must have copied its DNA. Each chromosome, therefore, when it condenses at the start of mitosis, consists of two identical sister chromatids; during mitosis, the

chromatids separate, and are distributed between the daughter cells. Before separation, the chromatids are held closely together at the centromeris regions of great structural importance but no genetic content, often rich in satellite DNA. In human chromosomes, every centromere contains alpha satellite DNA, long tandem repeats of a 171-bp sequence, which may be an important structural feature. The regions outside the centromere, the chromosome arms, are parallel but less closely apposed. They end in telomeres, which contain telomeric satellite DNA but no genes.

Three types of chromosome can be distinguished, on the basis of the position of the centromeres : metacentric where the centromere is situated at or near the middle part of the chromosome; acrocentric where the centromere is closer to one end and telocentric where the centromere is near the end of the chromatids. The whole set of the chromosomes of one cells is known as the karyotype. The normal human karyotype has 46 chromosomes, 23 from each haploid set. Two of these are sex chromosome called X and Y; females have a pair of large X chromosomes, males have one X and one smaller Y.

The remaining 22 pairs are called autosomes. The identification of the chromosomes was at first based simply on size and shape; it has been greatly improved by the techniques of chromosome banding, which distinguish chromosomes. Certain fluorescent dyes, such as quinacrine, stain some regions of chromosomes far more strongly than others, so that with a fluorescence microscope one can see patterns of bands - called Q-bands - that characterise individual chromosomes. Later, several other banding techniques were developed; one of the most popular is G-banding, in which chromosomes are stained with Giemsa dye after trypsin digestion - the resulting pattern can be seen with a normal microscope. G-banding patterns are the reverse of Q-banding patterns; Q-bright bands are G-dark. The number of bands visible on a mitotic chromosome depends upon the degree of condensation of the chromosome. In human cells about 2000 bands can be demonstrated in the least condensed chromosomes; in the most condensed, around 300. Human chromosome number was believed to be 48. It was in 1956 that Tjio and Levans discovered that it is 46. it became possible due to improved techniques of staining it.

At the Paris Conference in 1971, a standard nomenclature was agreed for the human karyotype and its bands. Autosomes are numbered in decreasing order of size, from 1 to 22; X and Y

chromosomes are named separately Arms are denoted by a letter and number : P for the shorter arm of a chromosome (from the French petit, small), q for the longer arm. Bands are numbered outwards from the centromere, using an agreed classification of regions and bands (and sometimes sub-bands), and are denoted by the appropriate chromosome number and arm letter, followed by the band number. Thus 13q 14 1 denotes chromosome 13, long arm, region 1, band 4 sub-band 1. Various structural changes in chromosome is expressed by same method. For example, del(13q14 1) refers the loss of the band defined above: a condition which correlates with the genetic disease retinoblastoma. (del for deletion) A wide range of chromosomal abnormalities has been described. In deletions, a region of chromosome is missing. Such deletions usually have genetic consequences. In translocations, part of one chromosome has been broken off and moved to another. If a gene happens to lie across the region of the break, it will be destroyed. Fusion of telomeres of the same chromosome produces ring chromosomes which have serious topological problems in replication. In isochromosomes centromere divide transversely to produces two long and two short arms of the same chromosome. Another special case, Robertsonian translocation, involves the junction of two telocentric chromosomes, since there are no genes beyond the centromeres of such chromosomes. Robertsonian translocations are often innocuous. In inversions, part of a chromosome has been rotated through 180^0. Inversions are not necessarily harmful, but many cause problems in the pairing of homologous chromosomes in meiosis.

Sometimes chromosomes may undergo unequal pairing resulting addition of an extra segment to one of the chromosomes. In essence, chromosomes often undergo structural changes. In man, some of these structural changes are associated with syndromes which will be described at appropriate places.

In addition to these structural changes, chromosomes often undergo numerical changes, called polyploidy. Increase or decrease can occur in number (Aneuploidy) or by sets (Euploidy). Increase in number of one chromosome make it trisomic; decrease by one number of one chromosome make it monosomic. Such monosomics and trisomics are often produced among human beings and cause syndromes. Such syndromes by chromosomal abnormalities is discussed elsewhere. Euploidy or doubling of whole set of chromosome is common in plants but rare in animals.

non-existent in human being.

Genetic Code

The kinds of proteins in a cell determine the structure and function of that cell. All the different kinds of chemical transformations for biosynthesis and for the utilization of energy are dependent on enzymes. In all cellular organisms there are thousands of enzymes, each being a specific protein. All of them have the same basic structure-large macromolecules consisting of polymers of some 20 amino acids joined to each other. The highly specific nature of enzymes can be traced to the unique sequence of amino acids and to their three dimensional spatial structure that arises from the specific foldings of the amino acid chain and cross-linkages between certain pairs of amino acids in adjacent folds. Genes are made up of deoxyribonucleic acid (DNA). (Certain viruses have RNA in place of DNA.) Earlier it had been demonstrated that genes control enzymes. Since amino acids form enzymes (proteins) there must be some connection between the DNA of the gene and the amino acids of the proteins. How is information in the form of DNA molecules conveyed to sites of protein formation ? In other words how are genetic informations translated ? The coding problem indicated that there must be some relation between the sequence of the four bases of DNA and the sequence of the 20 amino acids of proteins. The coding hypothesis had to account for the way these four bases(adenine, thymine, cytosine, guanine) must arrange themselves so that each permutation is the code for an amino acid. In the coding procedure it is obvious that there cannot be a 1:1 correlation between four bases and 20 amino acids because that will code for only 4 amino acids. If the coding unit consists of 2 bases, only 16 amino acids can be coded for

	A	T	C	G
A	AA	AT	AC	AG
T	TA	TT	TC	TG
C	CA	CT	CC	CG
G	GA	GT	GC	GG

This also falls short of 20 amino acid that needed to be coded for.

Therefore, the protein code must consist of at least three bases because 64 possible words can be formed by four bases when taken as triplets. DNA must then be considered a language written in a 4 letter alphabet. The particular composition or sequence of amino acids in a given protein are thus specified by the particular sequence of nucleotide pairs in a specific DNA molecule. The information is coded in DNA of the nucleus, whereas protein synthesis occurs in the cytoplasm. An intermediary of some kind between the two regions is necessary. This intermediary is special kind of RNA called messenger RNA. Messenger RNA is thought to be transcribed directly from DNA in the nucleus, each of the many messengers RNA being determined by a gene or a particular segment of DNA. (RNA differs from DNA in having a sugar residue of ribose instead of deoxyribose). In this process of making a complementary copy of one strand or gene of DNA in the formation of messenger RNA, an enzyme, RNA polymerase, is needed. The messenger RNA when formed is separated from the DNA and migrates through nuclear pores into the cytoplasm of the cell, where it becomes attached to ribosome, submicroscopic structures of protein, and a nonspecific RNA. Here the messenger RNA molecule serves as a template against which amino acids are lined in a sequence according to the coded instructions in messenger RNA. Amino acids are either obtained in the food supply or synthesized by the organism.

Various amino acids are activated and enzymatically attached to a second type of RNA called transfer RNA. Each transfer RNA is specific for a particular amino acid. More than one kind of transfer RNA is found for certain amino acids, By stepwise addition, the amino acids are guided by the coding sequence on transfer RNA, to which they are attached, and arranged in the correct order along messenger RNA to form a protein molecule. Each gene codes for about 500 amino acids, which is the average of a polypeptide chain, and since the codons are in groups of three mucleotides, there would be 1500 nucleotide pairs in a single gene. These figures naturally will vary with the protein or enzyme being coded for.

Operon Concept

The genetic code does not explain how genes are turned off and on as their products are needed by the cell. It does not explain why certain enzymes are not formed when they are not needed. If an enzyme-forming system lacks control, the whole

economy of the cell would be affected adversely. Cells also require control as they differentiate different amounts of the same enzyme at different times. There must be mechanisms in the cell for repressing the synthesis of enzymes when these are not needed and for inducing them when they are needed.

In 1960 the two French scientists, F. Jacob and Monod, proposed the operon hypothesis, or model, for explaining how repressions and inductions of protein synthesis might occur. Although, the investigators worked with bacteria, it seems highly probable that their hypothesis applies to all living beings. The gist of their hypothesis for which they were awarded the Nobel Prize in 1965, may be stated in the following way :

I. Structural Gene : The structural genes direct synthesis of proteins by forming mRNA.

II. Operator Gene : It is a site that binds repressor or activator elaborated by regulator gene and thereby determines whether a structural gene would form mRNA or not. If a repressor binds to it, RNA polymerase is unable to synthesize mRNA.

III. Regulator Gene : It elaborates regulator proteins such as a repressible protein or an activator protein. Repressible protein inhibits transcription of mRNA by RNA polymerase. Activator protein facilitates transcription of mRNa by RNA polymerase.

IV. Promoter Gene : Promoter is the site of binding of RNA polymerase to DNA for mRNA transcriptions since promotor-operator lie side by side or overlap, binding of repressor to operator physically interfere with binding of RNA polymerase to promotor gene.

Two sites in promotor are highly conserved that facilitate RNA polymerase binding. These are called consensus sequence. The two consensus sequences are :

a-10 TATAAT (Pribnow Box) : Located-10 bp upstream from start of mRNA transcription site. The double stranded DNA open from here for mRNA transcription.

b-35TTGACA : Located-35 bp upstream which is RNA polymerase recognition & binding site.

Such sites allow favourable interaction of DNA and enzyme RNA-polymerase. Most vital activities in cell is due to this protein nucleic acid interactions.

GENETIC PHENOMENA

Genetics has developed its own terminology, understanding of which is essential for present day knowledge. These terms are all important to the student of heredity, because they are essential in understanding the analyses of genetic problems. Whenever a cross involves only one pair of contrasting characters, it is called a monohybrid; when the cross has two pairs, it is a dihybrid; when the cross has three pairs, it is a trihybrid; and when it has more than three pairs, it is a polyhybrid. Characters that show in the F1 are dominant; those that are hidden are recessive. When a dominant always shows up in the phenotype, it is said to have complete dominance; when it sometimes fails to manifest itself it is called incomplete dominance. When two characters form a contrasting pair, they are called alleles or allelomorphs. The term factor that Mendel used so widely is replaced by gene. A zygote is the union of two gametes; whenever the two members of a pair of genes are alike in a zygote, the latter is homozygous for that particular character; when the genes are unlike for a given character, the zygote is heterozygous. A hybrid, for instance, is a heterozygote.

Penetrance refers to the percentage frequency with which a gene manifests phenotypic effect. If a dominant gene or a recessive gene in a homozygous state always produces a detectable effect, it is said to have complete penetrance. If dominant or homozygous recessive genes fail to show phenotypic expression in every case, it is called incomplete or reduced penetrance. Environmental factors may be responsible for the degree of penetrance because some genes may be more sensitive to such influences than are other genes. The genotype responsible for diabetes mellitus, for instance, may be present, but the disease does not always occur because of reduced penetrance.

The phenotypic variation in the expression of a gene is known as expressivity. For instance, a heritable allergy may cause more severe symptoms in one person than in another. Environmental factors may cause different degrees in the appearance of a phenotype. Lower temperatures permit expression of the genes for a black colour in certain regions of the Siamese cat. What is inherited is a certain genotype, but how it is expressed phenotypically is determined by environmental and other factors.

Linkage Is Location Of Genes On A Chromosome

Genes represent the material bases or chemical entities that are responsible for the hereditary pattern of an organism. They belong to cnromosomes and go wherever chromosomes go. By long, patient genetic experiments, their relative positions(loci) on the chromosomes have been mapped in many cases. Evidence indicates that they are arranged in linear order on the chromosome.

Linkage alters the expected mendelian ratios, which are based on free assortment. Linkage was first discovered in 1906 by Bateson and Punnett in sweet peas when it was found that sweet peas with purple flower had elongated pollen grains and those with red flower had round pollen grains. Morgan showed in Drosophila that when a wild type fly with gray body and long wings is crossed with a fly bearing two recessive mutant characters of black body and vestigial wings, the dihybrids (F_1) all have gray bodies and long wings. If a male of one of the F_1's is testcrossed with a female with a black body and vestigial wings, the flies are gary-long and black vestigial. If there had been free assortment, that is if the various characters had been carried on different chromosomes, the expected offspring would have been represented by four types of flies: gary-long, gray-vestigial, black-long and black-vestigial. However, in this case gary-long and black-vestigial had entered the dihybrid cross together and stayed together, or linked.

Crossing Over

Linkage, however, is usually only partial, for it is broken up frequently by what is known as crossing over. In this phenomenon the characters usually separate with a certain frequency. How often two genes break their linkage, or their percentage of crossing over, varies with different genes. In some cases this percentage of crossing-over is only 1% or less;with others it may be nearly 50%.

The greater the distance between any two genes, the more likely they will separate from each other. This crossing-over thus makes possible new combinations of linked genes.

Crossing-over makes possible the construction of chromosome maps and proof that the genes lie in a linear order on the chromosomes. To illustrate how this is done one may take a hypothetical case of three genes(A,B,C) on the same chromosome. In the determination of their comparative linear

position on the chromosome, it will first be necessary to find the crossing-over value between any two of these genes. If A and B have a crossing-over of 2% and B and C of 8%, then the crossing -over percentage between A and C should be either the sum (2 + 8), or the difference (8-2). If it is10% B lies between A and C; if 6%, A is between B and C. By laborious genetic experiments over many years, the famed chromosome maps in *Drosophila* were worked out in this manner.

The Gene And Mutation

Among the variations that appear in the makeup of animals, there are both hereditary and nonhereditary kinds. Nonhereditary variations are due to environmental changes such as nutrition, light, heat, and other factors that operate during the development of the animal. Such fluctuating variations occur in all animals and are not hereditary. The hereditary variations are due to changes in the genes or chromosomes and are referred to as mutations. Ordinarily, genes are very stable, but they are molecules and are subject to change under the influence of many kinds of factors. Some changes arise spontaneously, and other can be induced by artificial agencies. Undoubtedly many more mutations occur than are actually seen, but most of them are recessive and produce visible effects only when they are homozygous. Mutations happen in both somatic and germinal tissue, but only the latter ones are transmitted sexually.

Mutations generally effect a single base-pair of DNA and hence referred to as point mutations. However, more than one base-pair may be affected. In such cases it is known as multisite mutations. Multisite mutations are equivalent to chromosomal mutations.

A mutation involves a change in the chemical arrangement of a gene so that there is a difference in the structure and action of a gene that may result in a new character. In such cases the mutant gene now faithfully reproduces itself just as before. The natural mutation rate, which varies with different animals, is slow but can be speeded up artificially by agents such as radiation, by temperature, by certain chemicals, and by other environmental agents. Mutations are called random because they are unpredictable and because they are unrelated to the needs of the organism, but some mutations are favoured by tissue and environmental conditions. Many mutant genes are actuslly harmful because they may replace adaptive genes that have evolved in the

long evolution of the organism. However, a minority of mutant genes are advantageous and have great significance in evolution. Some mutant genes are dominant genetically, but more are recessive and their effects are masked by normal dominant alleles. Mutation may be a reversible process, and the difference between the mutation of gene in one direction and its mutation rate in the reserve direction is called its mutation pressure. Such reverse mutations indicate that true mutations are not gene losses. Gene mutations may occur in one direction more frequently than in others, and thus certain mutant alleles are far more common that others.

Plasmagenes And Cytoplasmic Inheritance

There is some evidence that some genetic variability is the result of self-duplicating, hereditary units in the cytoplasm. Such units are called plasmagenes and are apparently transmitted only by the cytoplasm. Two examples of this type of cytoplasmic inheritance are offered by plant plastids and mitochondria. Both are known to have their own DNA. It is supposed that during early evolutionary phase of eukaryotes, plastids and mitochondria existed as free living entities. They were trapped by evolving eukaryote cell and thus lost their independent existence (The endosymbiont hypothesis). The view is supported by the fact that DNA of these organelles have only coding region and no non-coding region.We will see later on that eukaryotic genes are split, characterized by exons and intervening introns. Exons code for protein, and introns are apparently functionless part of DNA that separate exons. A gene may have a few exons and a few introns.

Determination Of Sex

Soon after rediscovery of Mendelism in 1902 McClung discovered that in certain bugs males have one chromosome less than the number of chromosomes in females. It was soon found out that chromosomes of a species can be divided into two groups - autosomes controlling metabolic functions and sex-chromosomes primarily determining sex. The sex-chromosome was, in this case, found to be paired in females (XX) and unpaired in males (XO) (the sex chromosomes were largely unknown at that time hence were designated by X, a letter which is often used to denote an unknown factor). Females in this case produced eggs all with one X, whereas males produced two types of sperm - half

with X and half without X. Zygotes with 2x developed in females whereas those with one x developed in males. Such type of sex-determination was called xx-xo mechanism.

Later, other types of sex determination were discovered. In man and many other forms there are the same number of chromosomes in each sex, but the sex chromosomes (XX) are alike in the female but unlike (XY) in the male. Hence the human egg contains 22 autosomes + 1 X chromosome ; the sperm are of two kinds : half will carry 22 autosomes + 1X and half will bear 22 autosomes + 1Y. The Y chromosomes in such cases are diminutive. At fertilization, when 2 X chromosomes come together, the offspring will be a girl; when XY, it will be a boy.

A third type of sex determination is found in birds, months, and butterflies in which the male has 2 X (or sometimes called ZZ) chromosomes and the female an X and Y (or ZW). In this case the male is homogametic sex and the female is heterogametic sex.

Whether or not sex in animals is solely determined by the sex chromosomes may well be doubted, notably in the case of *Drosophila*. In this form certain intersexes have been found that suggest that autosomes may play a part in the development of sex.

In man and the mouse (and perhaps in others), however, the Y chromosomes primarily determines maleness. In man, the abnormal condition of an XXY is a sterile male; the XO is a sterile female. Symptoms produced in such cases are discussed elsewhere.The question as to why presence of Y chromosome results in maleness has been solved recently. It was found out that Y chromosome contains a testes determining gene presence of which will eventually lead to development of testes, irrespective of the number of X chromosomes. Thus all XY, XXY, XXXY, etc. are males, though with certain syndromes.

Barr and Bertram (1949) had found out that all X except one become condensed and largely non-functional. Hence all individuals, XX, XXX, XXXX etc. are essentially female. Condensed X are not entirely functionless, some of its genes are still functional and hence are involved in syndromes produced in conditions where their usual number is increased in a cell.

Sex Linked Inheritance

Soon after discovery of sex-determin ion and sex-chromosomes, it became known that sex-chromosomes carry

genes for characters other than related to sex. Thus Morgan studied inheritance of eye-colour in *Drosopila*.

A few conditions in man such as haemophilia and red-green colour blindness was found to be associated with X-chromosomes and hence its inheritance followed inheritance of X-chromosome. Haemophilia is a condition marked by absence of a blood-clotting factor VIII which results in delayed clotting of blood after injury. In red-green colour blindness, individual is unable to identify red and green colour from other colours. This condition develops due to defects in cone cells of retina which are concerned mainly with colour-vision. Such X-linked characters follow inheritance of X-chromosome. Thus, if father suffers from haemophilia the gene for haemophilia will follow the following course of inheritance:

XX	x	X^hY	————	P
X		X^h Y	————	Gametes
XX^h		XY	————	F_1
Carrier female		*Normal male*		

Thus, if mother is normal all the boys from this marriage will be normal and all the girls carriers. If F_1 matings occurs, the gene for haemophilia will have following course of inheritance.

XX^h		x	XY	——— F_1
X X^h			X Y	——— Gametes
XX	XX^h	XY	X^hY	——— F_2
Normal female	Carrier female	Normal Male	Affected male	

Zebra-fish Genetics

It has been a long journey from Mendel's pea-plant through Morgan's fruitfly, Mcclintock's maize, Beadle and Tatum's Neurospora, Jacob and Monod's *E.coli* to the Zebra-fish ! Zebra-fish, *Danio rerio* is being increasingly utilised in the study of developmental patterns of vertebrates; It is small, beautiful, rapidly multiplying fish. It offers the option of inducing haploid development. Induction and recovery of embryonic lethal mutations has been easy with the Zebra fish which is so essential for the genetic analysis of the embryonic development biology and we shall be learning about genetic control of development through these tiny creatures.

TOOLS OF GENETIC STUDY

Nucleic Acid Hybridization And Co.t Curves

DNA is maintained as a duplex (two stranded) structure by the many hydrogen bonds of the A-T and G-C base pairs. The two strands of the duplexes can be melted(separated) by heating them (usually in a dilute salt solution e.g. 0.01 M NaCl) or by raising the pH to higher than 11. To understand nucleic acid hybridization, take DNA of related species and labell DNA of one species. Mix the two DNA and heat the solution. The two DNA strands will separate. If the temperature is then lowered or if the pH is lowered, the single strands will anneal or reassociate, to reconstitute duplexes. Only complementary strands reassociate and the extent of their reassociation is virtually unaffected by the presence of non-complementary strands. This specific reassociation is termed molecular hybridization. It can take place between complementary strands of either DNA or RNA or between an RNA strand and a DNA strand. The hybrid molecule can be detected under the electron microscope. Single strands of nucleic acid can be distinguished from duplexes. If two single nucleic acid strands that are complementary over only part of their length are allowed to hybridize, the result is a heteroduplex. Homologous (duplex regions) and noncomplementary (single-stranded region) can be distinguished from one another. This technique allows an instant determination of the overall relatedness of two samples of nucleic acid. The techniques is of much importance because if a specific DNA sequence is isolated and lebelled with fluorescent dye or radioactive isotopes, then by hybridization of this lebelled DNA with other DNA the whereabouts of the sequences complementary to the lebelled DNA will be revealed. This technique is called "probing" for a particular sequence, and the lebelled DNA is called a "*Probe*".

The technique is also used to determine complexity of DNA of a species. The rate of hybridization between two complementary single stranded nucleic acids in solution depends on the frequency with which complementary regions collide and nucleate- that is start to form a duplex. This collision frequency, in turn, depends on the concentration of the two strands. Suppose that the DNA fragments of two different organisms say, *E coli* and yeast are incubated in two different test tubes in amounts that yield the same total DNA concentration. The complexity of the DNA (the

number of base pairs in the total genome) is about four times greater for yeast than for *E coli*. A separated strand of *E coli* DNA would therefore encounter its correct partner four times as often as would a strand of yeast DNA and the rate of reassociation of the *E.coli* DNA would be faster.

The reassociation rate of any DNA sample allows the calculation of the relative complexity of the genome. Because experimentally the initial concentration of DNA (Co) and the time(t) are varied to measure reassociation rates, the resulting curves are often called Cot curves (concentration x time)

Southern Blotting And Related Techniques

This technique enables us to identify some region of DNA. DNA is cut into small pieces by restriction endonuclease and are separated by gel electrophoresis. In gel electrophoresis, the differing lengths of DNA is separated in agarose gel, a porous, jelly-like substance across which electric field is applied. DNA, because of phosphates, have net negative charge and hence move to positive pole. The smaller pieces of DNA move faster than longer one because they are less retarded by gel. Once separated in the gel, they are blotted on filters. On the filters, specific DNA regions can be identified by using lebelled "Probes". Southern invented the procedure and , since blotting of DNA was done, the technique was named , Southern blotting. This technique enables us to identify a region of DNA in which we might be interested. For example, if we have isolated insulin gene in humans we can identify the location of same gene in pigs easily because the two genes are very similar and the two DNA immediately hybridize upon coming in contact with each other.

More or less similar techniques can be applied to identify regions of RNA and Protein.

Northern Blotting : This is a technique to identify regions of RNA. RNA is cut with restriction enzymes and separated by gel-electrophoresis, transferred to filters and "probed" with complementary sequences.

Western Blotting : Proteins are separated, transferred to filters and probed with specific antibody.

Far Western Blotting : In this case proteins are probed with other proteins that interact specifically with them in nature.

Dot Blotting : In this case separation of DNA and RNA

restriction fragments is not attempted but they are simply attached to a filter and attempted to be hybridized to a specific probe. This is done to check presence or absence of a particular sequence.

Polymerase Chain Reaction (PCR)

This technique has enormous potential in forensic science : minute traces left by suspects, single cells, can reveal their genetic identity.

1. As little as 20 pg (picogram) of DNA or RNA can be detected by Southern or Northern blotting. Many DNA or RNA sequences within tissues are below this level of detection. The polymerase chain reaction allows massive replication of a target sequence of DNA and allows detection of DNA or RNA sequences that are present as only one or two copies per cell.

2. The target sequence of DNA is extracted from the cell and denatured into its single strands by heating to 90^0C

3. Two oligounucleotide primers complementary to the opposing ends of the single strands are synthesized and annealed.

4. The primed single strand is then extended using DNA polymerase 1.

5. The newly synthesized double stranded sequence is then denatured by heating to 90^0C and new oligonucleotide primers added.

6. This process is then repeated through twenty-five to thirty cycles which results in a ten fold increase in DNA

Originally DNA polymerase from *E. coli* was used but this could not survive the high temperature needed to separate DNA strands and so new enzyme had to be added after each cycle. Now the DNA polymerase known as the Taq-polymerase from the bacteria. *Thermus aquaticus*, which lives in hot springs, is used. This enzyme has an optimum activity at 70-80^0C, and as it retains its activity at 90^0C, it can survive the full thirty cycles of the chain reaction.

Restriction Endonuclease

Restriction endonucleases are named by taking first letter of generic name and first two letters of specific name. The fourth letter is from the name of strain. The Roman numeral is order of its isolation from bacteria. The first restriction endonuclease was isolated from *Escherichia coli* strain RY13 hence it was named

ECO RI

Restriction enzymes or restriction endonucleades, as they are sometimes called, recognize specific part of polynecleotides (from four to six residues long) in DNA and cleave the DNA at all such sites. The name restriction enzyme derives from its function in the bacterium of origin. The enzyme destroys (restricts) incoming foreign DNA by cleaving it at specific sites, which are called restriction sites . When a methyl group is present in host DNA, the restriction endonuclease is prevented from cutting the DNA. Together with the restriction endonuclease, the system protects the host DNA while destroying foreign DNA. Besides, bacterial DNA, restriction enzymes are coded for by plasmids too. Several classes of restriction enzymes are recognised, all of which cut double stranded DNA. Class I restriction enzymes recognise specific sequences but cleave DNA nonspecifically, outside the recognition site eg. Restriction enzyme of bacteriophage P1. Class II restriction enzyme consists of those enzymes that specifically recognise and cut within the recognition site. This results in defined DNA segment. It is used in molecular cloning in genetic engineering. Below is given a list of such enzymes along with their host regions of cut.

Host organism	Enzyme designation	Recognition sequence
1. E.Coli	Eco RI	5' G* A A T T C 3' 3' C T T A A* G S
2. *Hacmophylus haemolyticus*	Hha I	5' G C G* C 3' 3' C* G C G 5'
3. *Brevibacterium-albidum.*	Bal I	5' T G G* C C A 3' 3' A C C * G G T 5'
4. *Haemophylum-aegypticus*	Hae III	5' G G* C C 3' 3' C C* G G 5'

(*The stars show the location of cuts by the restriction enzymes*)

It is found that some enzymes recognise a group of 4 bases whilst others recognise 6 bases. The recognition sequence show a double rotation i.e. a palindreme. The cut DNA can be of following Types :

a. Staggered Cut : In ECORI, single strand ends with four bases are produced that have prejecting Complementary base sequence.

b. Blunt Cut : In Hae III no single stranded regions are produced. Such cuts are called blunt cuts.

Joining Of DNA Fragments : DNA Ligase

This enzyme catalyses repair of the phosphodiester bonds of DNA and thus seals the gaps in the single stranded break. This enzyme is required during replication, recombination and repair of damaged DNA. Replication of one strand is a discontinuous process and takes place in short segments called Okazaki fragments. Polynucleotide Ligase joins these fragments into high molecular weight DNA. In mutants, which produce defective ligase, the joining of Okazaki fragments is greatly impaired. *E Coli* ligase requires nicotinamide adenine ducleotide (NAD) for activity. Ligase is first adenylaed by the AMP moiety of NAD, releasing nicotinamide mononucleotide (NMN).

This adenylated ligase then reacts with DNA having a single stranded break to repair phosphodiester bond and release ligase and AMP.

Cloning Vectors

The procedure of cutting DNA with restriction enzymes and joining it to other fragments with ligase, allows geniticists to create chimaeric molecules (according to mythological belief, chimaera was a beast with lion's head, goat's body and serpents tail). The DNA with which they are joined are called vectors. Vectors are molecular vehicles which are able to carry the introduced DNA fragment into host cells, usually bacterial cells, where they replicate and from enormous number of copies. This is called gene-cloning

Vectors must possess following qualities. It must be capable of replication, thus amplifying the inserted DNA segment in host cell. It must confer resistance to specific antibiotics so that bacteria containing them could be selected for. It should carry many restriction sites so that a wide variety of foreign DNA sequences can be inserted into it.

Three vectors are chiefly in use though others are also around. These are plasmids, bacteriophages and cosmids.

Phage Vectors : Viruses infecting bacteria (bacteriophages or simply phages) contain DNA covered with a protein shell. During infection of bacteria, they inject their DNA into bacterium, where the DNA replicates to form hundreds of copies and this bacteria burst. Thus DNA of viruses can be cut with restriction enzyme, foreign DNA inserted into it, and viruses made to infect bacterium. However, phages have small room inside protein-shell to pack only less than 10 kb amount of DNA. Phage lambda is most commonly used as vector.

Plasmid Vectors : Many bacteria contain extrachromosomal, small, circular, double-stranded molecule of DNA which are not essential for the growth of the cells under normal conditions. If plasmids are removed by UV radiation or other chemical means the bacterial cell grow well in the normal medium. They are generally circular but in some cases, e.g. in streptococci, a straight plasmid has been found.

Plasmids can be transiently integrated into bacterial chromosome and transferred during conjugation or can get transferred to other bacterial cells independently of the bacterial chromosome.

They produce special character on bacterial cell-sexpilli-which make the contact with another bacterium during the conjugation. The sex pilli is coded by plasmid tra genes. It also synthesizes proteins for stability of pairing partners during conjugation and DNA transfer between the conjugants. In some cases, plasmid gene is known to produce a specific pairing signal, or Sex-pheromone, which causes production of adhesive in plasmid donor cells that bring about adhesion of two cell types.Resistance plasmids contain genes which render the host bacterium resistant to antibiotics and heavy metals. Plasmid determined resistance consists of an attack or antibiotic molecule e.g.- production of Penicillinase and hydrolysis of penicillin. Chromosome based resistance involves change in protein synthesizing machinery. (antibiotics attack protein-synthesizing machinery e.g. 30S,50S f ribosomes of bacteria and thus killing it).

Those plasmids that carry genes for catalyzing the degradation of chemical substances are called degradative plasmids. Such substances include Napthalene, Salicylate, Terpene etc. elaborated by various species of *Pseudomonas*.

These plasmids carry genes for complex metabolic reactions such as nitrogen fixation, nodule formation, transport of Sugar etc.

Restriction enzymes and modification enzymes, which are secreted by bacterial DNA, can also be elaborated by plasmids.

Plasmids are used as vector in genetic engineering that serves to carry foreign DNA. Plasmids are cut by special restriction enzymes, foreign DNA is joined and transferred to bacterium *E.Coli* which is specifically treated.

Cosmid Vectors : These are another vectors for gene transfer in genetic engineering. These were developed by Barbara Honns and John Collins (1978). Cosmids are products derived from CoS sites of phage such as lambda and plasmids of bacteria. Thus cosmids are plasmids in which CoS sites of viruses are inserted. It has following advantages.

1. Since CoS sites enable the packaging of DNA in lambda particles, it allows the packaging of cosmids in phage particles, thus permitting their purification.

2. It results in greater packaging of DNA in phages. In phages 23 Kb of DNA is packed whereas in cosmids 46 Kb of DNA is packed.

3. Because it contains antibiotic resistant sites in plasmids it can be isolated in culture medium containing antibiotics resistance.

Other Vectors : A variety of vectors have been engineered to introduce foreign DNA in mammalian cells. They are derivatives of viruses which naturally attack the cells. Important among such viruses are DNA Tumour viruses such as *SV40 or bovine papilloma virus* which replicate as circular DNA molecules in mammalian cells, either independently or after recombining host's DNA; *Adenovirus* which are responsible of many gastric and respiratory infections. In construction of DNA viral vectors, virus signals for DNA replication and transcription is used. They also bear a selectable marker. These vectors can carry foreign DNA upto 20 Kb. Other approaches have used RNA viruses such as retroviruses for transfer of DNA to mammalian cells.

DNA Library

A DNA library is a collection of vectors, grown in bacterial, which has at least one copy of every sequence that occurs in the total DNA of the genome of the given species. The various steps in construction of DNA library include - Digestion of genomic DNA by restriction enzyme and its separation, its ligation to vector which

has been cut by the same restriction enzyme, transfer of vector to bacteria or yeast. The bacteria are cultured in plates or dishes on agar jelly containing nutrients. Bacteria form colonies. All members of a colony will contain the same vector DNA.

Exact copies of the pattern of colonies in a given plate can be made by laying a surface to which bacteria will adhere on top of the agar and then transferring the surface to the agar in another plate. This is called replica technique.

Smaller libraries such as cDNA library is often constructed from mRNA by use of enzyme reverse transcriptase. In recent years chromosomal libraries are also constructed in which the source is DNA contained in a single chromosome.

Searching The Library For Sequences : There are various methods such as genetic, immunologic, molecular hybridization etc. In genetic method, a mutant host for the desired gene is taken and the desired gene can be isolated on the basis of its ability to complement host deficiencies. In immunologic methods, the antibody to the desired gene is reacted with the replica of library and the desired colony is stained by antibody. In molecular hybridization, a lebelled probe is constructed and hybridized with the replica of the library plates. For this technique knowledge of at least a fragment of the desired gene-sequence is necessary to construct a probe.

Restriction Mapping

In order to sequence a DNA, the first thing to do is restriction mapping. The DNA is digested by two restriction enzymes separately and their isolated segments are again digested in reciprocity- Fragments produced by I is digested by II and vice versa. The sets of fragments thus generated are ordered into a restriction map by looking for overlapping pieces.

DNA Sequencing

The ultimate aim of gene cloning is to determine the sequence of nucleotides in DNA. There are two methods, both able to sequence only more than few hundred bases long DNA.

In the method of Maxam and Gilbert, the single stranded DNA molecule is cut by chemicals at specific bases such as C, G, A and T and lebelled at 5' end by enzyme polynucleotide kinase. The reaction is carried out in parallel of four separate samples. The

DNA is then subjected to electrophoresis in gel and separated on the same gel in parallel lanes. The electrophoretic bands can be detected by autoradiography. Bands are created because DNA of different lengths migrate with different rate. Since the label is put at 5' end, only the fragments containing the 5' end will be detected The nucleotide sequence is read off from the sequence of the bands in the four electrophoretic lanes.

The DNA to be sequenced is first incorporated into single stranded DNA viruses. It is because of this reason that restriction mapping is necessary. Restriction mapping provides the information about sites of action of a variety of restriction enzymes. Such restriction enzymes are used to create small, overlapping DNA fragments to be sequenced by Maxum-Gilbert method. The DNA sequencing of humans and different primates are being performed and knowledge thus gained can be utilised for better understanding of interrelationship of man and various other primates.

Genetic Engineering

By using techniques of genetic engineering genes from a donor cell can be implanted into a bacterium. Any kind of cell can be used as donor cell. The technique became available in 1970s. Genetic engineering is a five step procedure consisting of isolation of DNA, identification of DNA, insertion of DNA in plasmid, cloning in bacteria and isolation of bacteria.

1. Isolation Of DNA : Shotgun Experiment : The gene that has to be implanted in bacterium is first isolated from the inner cell. A donor cell can be a bacterium or any cell. the DNA is cut into pieces in one of the 500 or so known restriction enzymes each of which cleaves DNA at a specific DNA base sequence where there is symmetry (such as palindrome sequence). A palindrome sequence can be represented as below :

T G C A A – T T G C A

A C G T T – A A C G T

2. Identification Of DNA : Electrophoresis and southern blot technique Shot gun experiment generates fragments of many sizes. It is necessary to identify the segment of interest. To achieve this the segments are first separated by electrophoresis. Electrophoresis is a technique in which molecules of different sizes are separated on a gel (or paper) with the help of high voltage electric current. Because individual fragments have different

charges, they separate.

Once fragments are separated, deck is cleared for identification of desired segment. This is achieved by southern blot technique. The molecules on the gel is transferred from gel to nitrocellulose filters. The technique is described elsewhere. Some of the DNA is transferred to filter paper. Nitrocellulose contain labelled RNA or DNA of the desired protein which is used as probe. Labeled RNA or DNA hybridises with the complementary sequence. The hybrid region can be detected by autoradiography and the corresponding band in the gel can be located.

3. Insertion Of DNA In Vectors : Once the DNA region of choice is spotted out, it has to be packed in some vehicle which can deliver it to bacterium. The DNA region is inserted into another DNA molecule, generally in the plasmid of bacterium. Plasmid are self replicating circular duplex DNA molecules of bacteria which is present in addition to the nucleoid. When DNA of choice is inserted into plasmid DNA the molecules thus formed is called recombinant DNA or plasmid vector.

To achieve this plasmid from bacteria are taken out purified and cut by the same restriction enzyme which was used to cut the DNA. Thus, the donor fragment has unpaired bases that are complementary to the unpaired bases of plasmid. Thus if two are mixed, hydrogen bond forms between the unpaired bases DNA ligase added to the medium and thus covalent bonds between the sugar and phosphate components of fragment and plasmid.

Plasmid vector are now ready : the circular molecule with donor DNA. Viruses and cosmids are also used as vector.

4. Cloning In Bacteria : The plasmid vectors thus formed are cloned in bacteria. To achieve this, the recipient bacteria treated with calcium chloride that makes membrane of bacteria more permeable. The plasmid vector enters into bacteria. As the bacteria divide, so divides the plasmid vector along with it. The donor gene becomes functional in the bacteria and starts synthesizing its protein.

5. Isolation Of Bacteria : There are three methods to isolate bacteria that have taken up the donor gene. First, the bacterial colony can be tested for the gene product. An enzyme can be detected by its activity; a structural protein by the antibody secondly, a DNA probe can be used in which a lebelled DNA is synthesised on a mRNA transcript by using enzyme reverse transcriptase. This enzyme is obtained from retroviruses. The third

and the most commonly, an additional gene is marked in the plasmid that makes its identity easy. If bacterium shows the trait it becomes certain that the donor gene is also present in the plasmid. Such feature is resistance to antibiotics; a trait conferred by genes in a type of plasmid called the R-plasmid. The donor gene is placed in R-plasmid eg. plasmid carrying resistance to the antibotie ampicillin. After plasmid vector is added to bacteria, the bacterial colony is exposed to antibiotic ampicillin. Bacteria without the plasmid carrying gene for resistance to ampicillin, die leaving only those bacteria that have resistance-gene (along with donor gene).

To be more sure that the bacterium contains the donor DNA, a double resistance plasmid is used- a plasmid that confers resistance to, say ampicillin and Tetracycline. The donor gene is inserted by cleaving the gene for tetracycline. After insertion of vector, all bacteria are treated with ampicillin to remove all untransformed bacteria. Next to it, bacterial population is treated with tetracycline. Those with donor gene has no functional gene for tetracycline resistance hence donot grow well whereas thcse with tetracyclin-resistance gene grow well. Thus bacteria with donor gene is identified.

Gene-gun

Gene guns are guns used to fire genes into target cells. The bullets of the gun include very small particles of gold or tungsten around which the DNA sought to be transferred into a cell is coated, these guns were operated by gun powder. Now a days compressed helium is used for the purpose. It has been successfully used in transferring gene for growth hormone and ulferase into mouse. Recently, in 1994, Gold coated cytokine genes, intereukine, have been successfully fired into mouse tumour cells. The cytokine gene secrete cytokines in the cell. This attracts WBC to attack the tumour. The genes are prepared using cloning techniques and then precipitated into beads of gold about micro metre in diameter. It is fired into target tissue at point blank range by a pulse of compressed helium. The gene gun allows a direct transfer of gene into a cell. The gene gun is better because preparing genes for gene gun is much faster and least hampered by cell's defence mechanisms. The cell repairs the rupture within minutes. Clinical trials of the method will be started in US in late 1995 or early 1996 once researchers get approval from the US food and drug administration. Karol Sikora, leading worker on gene therapy in London, has stated that gene gun is probably a better alternative than viruses in transferring the gene into the cell.

THE CELL AND CELL-DIVISION

A cell is considered to be the minimum unit that manifests the vital phenomena of life. However, the boundary between the living and the nonliving is not as sharply drawn as formerly. Some particles smaller than cells, for example, viruses, are regarded by some as living. Although viruses have the initial genetic mechanism and multiply, they do so at the expense of the host's cells. They are hence considered non-living also.

Many features or aspects of life can be produced in the test tube without cellular organization. Genetic investigations make use of strands of nucleic acid that can synthesize duplications of DNA and proteins. Life must have originated from the nonliving world in much simpler units than the complex cell. Some present cells are simpler than others. Bacterial cells as well as those of blue-green algae lack such organelles as mitochondria, lysosomes, and a definite nucleus. Motile bacteria have a flagellum of a single fibrous protein molecule instead of the ninefold symmetry of higher forms. There must have been many precellular forms in the long evolution of the cell because the properties of life did not arise all at once. Viruses could be treated as an intermediate from between non-living and living and represent a primitive organisation on way to evolution of life. This is, however, controversial and many consider viruses not to be primitive but nucleic acid molecules that escaped from living forms and become specialised.

In the absence of a generally agreed intermediate form between non-living and living, cell is considered as the smallest entity capable of representing a combination of all the vital phenomena.

A technical distinction is made between a unicellular organism and a cell of a metazoan. A cell of a unicellular form may be considered homologous only with be multicellular organism as a whole and not with the individual cells of that organism. On this account, many biologists consider the unicellular organism as acellular. Multicellular condition has many advantages over the unicellular condition. For example, it gives the large development of surfaces on which exchange of material occurs. It also promotes functional differentiation and size increase. This, in turn, enables cellular forms to meet demands of nature.

As stated before prokaryotic cell lacks nucleus, mitochondria, lysosome, centrioles, plastids etc. Bacteria are typical example of prokaryotes. Multicellular forms are called

CELL-DIVISION : It is of two types -

(1) Mitosis - Which occurs in body cells

(2) Meiosis - Which occurs in germ cells

Mitosis is completed in four stages -

(a) Prophase (b) Metaphase (c) Anaphase (d) Telophase. During Prophase, nuclear membrane ruptures and centriole divides and migrate to opposite poles. During metaphase, chromosomes arrange on the equatorial plate and spindle fibres formed by centrioles attach to centromere of chromosomes. During anaphase, centromere of a chromosome divide and two chromatids of a chromosome are pulled toward opposite pole. During telophase, nuclear membrane reappears. Cytoplasm divides and two daughter cells are produced.

Meiosis is completed in two phases -

(a) Reduction divsion (b) Simple mitotic division

Reduction division is completed in four stages : Prophase, Metaphase, Anaphase and telophase but prophase is complex and during this stage homologous chromosomes exchange segments (crossing-over). Two members of a homologous pair are separated and go to opposite poles. The daughter cells thus formed has half the chromosome number of maternal chromosomes. The second phase of meiosis is similar to mitosis wherein two chromatids of a chromosome is separated.

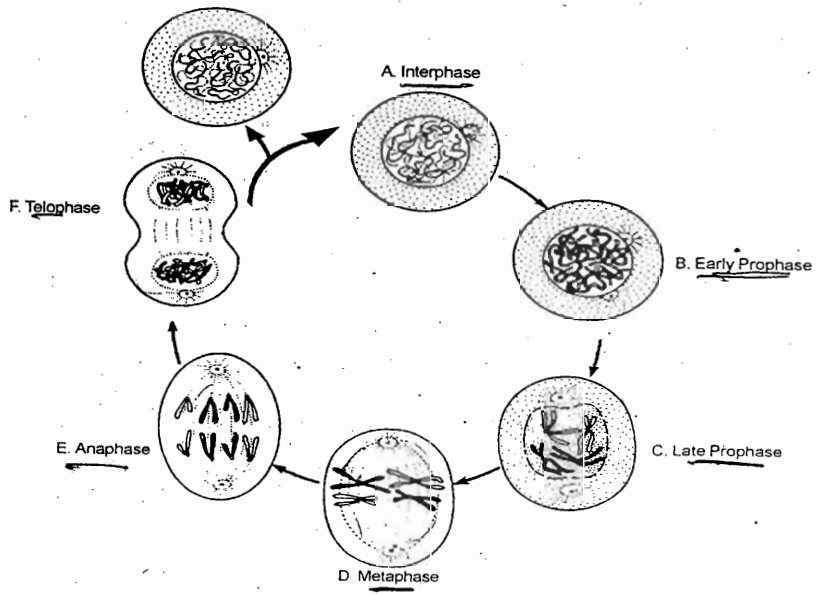


Fig. : Various stages of mitosis in an animal cell.

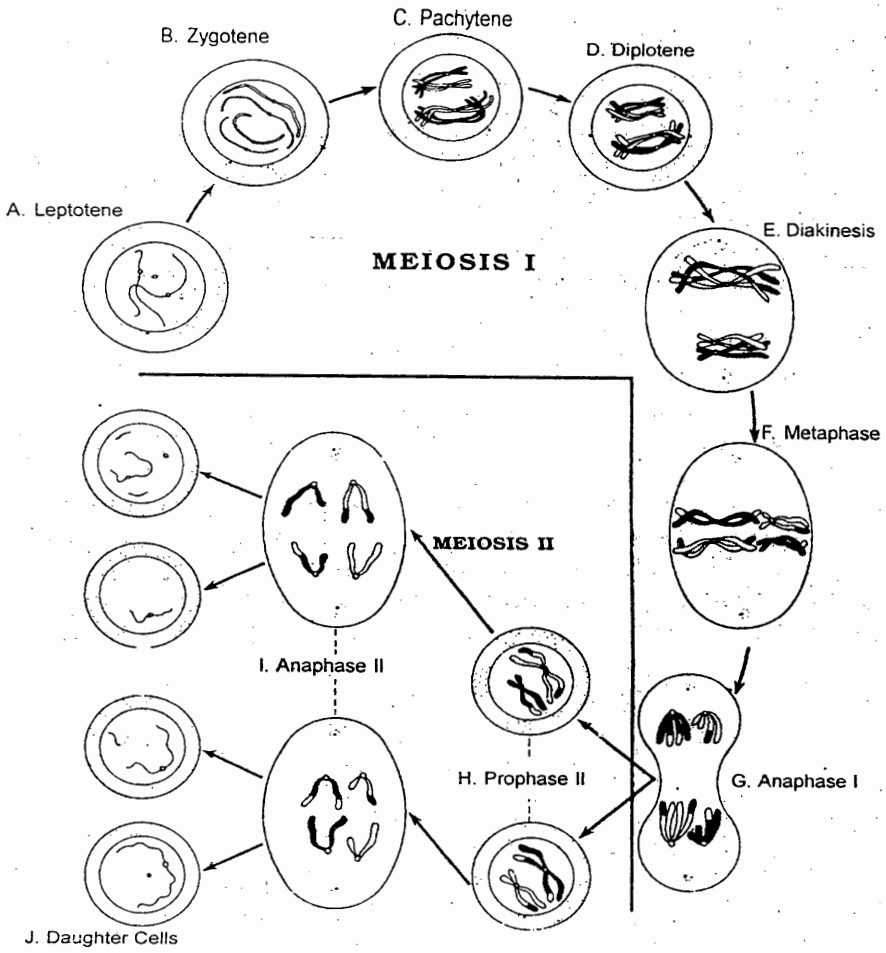


Fig. : Different stages of Meiosis

The Smallest Known Gene

Pastor et. al. (1995) has recently reported that they have discovered the smallest gene. It is present in **Escherichia coli**, the bacteria of our digestive tract. The gene, called microcin A (mcc A) codes for peptide called microcin C7 (mcc C7). The gene is only 21 base pair long!

Such small genes are called open reading frame(ORF) and are generally located close to site on DNA that binds ribosome for protein synthesis, called Ribosomal binding site (RBS).

MENDELISM

Steve Jones (1992), commenting on Mendelism, stated that to discover laws of heredity in a time when nothing was known about nature and location of hereditary material is a feat the type of which was rarely performed in the history of science prior to or after him. Gregor Johann Mendel was connected with Augustinian monastery at Brunn, Moravia, then a part of Austria, later a part of Czechoslovakia. In the small monastery garden he conducted his experiments on hybridization, which resulted in two clear-cut laws that bear his name. His classic observations were made on the garden pea. There were several distinct varieties of these plants that always bred true because gardeners over a long period by careful selection had produced pure strains. For example, some varieties were definitely dwarf and other were tall. A second reason for selecting peas was that they are self-fertilizing, but they are also capable of cross-fertilization as well. He chose single characters and those that were sharply contrasted, avoiding intermediate characters. Mendel selected seven pairs of these contrasting characters, such as tall plants and dwarf plants, smooth seeds and wrinkled seeds, green cotyledons and yellow cotyledons, inflated pods and constricted pods, yellow pods and green pods, axial position of flowers and terminal position of flowers, and transparent seed coats and brown seed coats. Mendel crossed a plant having one of these characters with one having the contrasting character. He removed the stamens from a flower so that self-fertilization could not occur, and then on the stigma of this flower he placed the pollen from the flower of another plant that had the contrasting character. He then prevented the experimental flowers from being pollinated from other sources, such as wind and insects. When the cross-fertilized flower bore seeds, he planted the hybrid. His next step was to cross these hybrids among themselves and to see what happened. He made careful counts of his plants, repeated his experiments, and worked out certain ratios.

Monohybrid Cross And Mendel's First Law

Mendel crossed pure tall plants with pure dwarf plants and found that the hybrids (F_1 or first filial generation) thus produced were all tall, just as tall as the tall parent that was involved in the cross. This result he found was always obtained whether the tall plant furnished the male germ cells or the female germ cells.

Next,he crossed two of these hybrid tall plants together. From this cross he raised several hundred plants and found that both tall plants and dwarf plants were represented among them. He also noted that none of this generation (F_2 or second filial generation) were intermediate in size ; they were either as tall or as short as the parents in the original cross. When he counted the actual number of tall and dwarf plants in the F_2 generation, he found there were three times as many tall plants as dwarf ones, or a ratio of 3:1. His next step was to self-pollinate the plants in the F_2 generation; that is, the stigma of a flower was fertilized by the pollen of the same flower. The results showed that self-pollinated F_2 dwarf plants produced only dwarf plants, whereas one third of the F_2 tall plants produced tall and the other two thirds produced both tall and dwarf in the ratio of 3:1, just as the F_1 plants had done. This experiment showed that the dwarf plants were pure because they at all times gave rise to short plants when self-pollinated; the tall plants contained both pure tall and hybrid tall. It also demonstrated that, although the dwarf character disappeared in the F_1 plants, which were all tall, the character for dwarfness appeared in the F_2 plants.

From the experiment results Mendel formulated certain postulates. He reasoned that the factors for tallness and dwarfness were units that did not blend when they were together. The F_1 generation contained both these units or factors, but when these plants formed their germ cells, the factors separated out so that each germ cell had only one factor. In a pure plant both factors were alike; in a hybrid they were different. He concluded that individual germ cells are always pure with respect to a pair of contrasting factors, even though the germ cells are formed from hybrids in which the contrasting characters were mixed. This idea formed the basis for his first principle, the law of segregation,which states that whenever two factors are brought together in a hybrid, when that hybrid forms its germ cells, the factors segregate into separate gametes and each germ cell is pure with respect to that character. Thus in the gametes of the F_1 plants, half of the germ cells will bear the factor for tallness and half for dwarfness; no germ cell will contain both factors.

Dihybrid Cross And Mendel's Second Law

In a dihybrid cross, plants are selected for two pairs of contrasting characters and crossed to find out their pattern of inheritance. One of the plants was Tall, yellow and another dwarf,

green. Yellow and green was the colour of cotyledons - the part of the seed that surround the embryo. F_1 plants were all tall and yellow. When two F_1 hybrids were crossed, 9 genotypic (and 4 phenotypic) classes were obtained. Of the 4 phenotypic classes, two were parental classes i.e. Tall, yellow and dwarf green, but two were assorted classes i.e. Tall green and dwarf yellow. Mendel postulated that F_1 hybrids must have formed four types of gametes that combined with equal probability to give rise to plants in following ratios Tall,Yellow:9, Tall Green = 3, Dwarf,Yellow : 3, Dwarf Green - 1 (9:3:3:1).

	TY	Ty	tY	ty
TY	TTYY pure tall pure yellow	TTYy pure tall hybrid yellow	TtYY hybrid tall pure yellow	TtYy hybrid tall hybrid yellow
Ty	TTYy pure tall hybrid yellow	TTyy pure tall pure green	TtYy hybrid tall hybrid yellow	Ttyy hybrid tall pure green
tY	TtYY hybrid tall pure yellow	TtYy hybrid tall hybrid yellow	ttYY pure dwarf pure yellow	ttYy pure dwarf hybrid yellow
ty	TtYy hybrid tall hybrid yellow	Ttyy hybrid tall pure green	ttYy pure dwarf hybrid yellow	ttyy pure dwarf pure green

Ratio : 9 tall yellow to 3 tall green; 3 dwarf yellow to 1 dwarf green

Mendel's first law or The law of segregation deals only with one pair of contrasting characters. Mendel also ascertained what would happen when a cross is made between plants differing in two pairs of contrasting characters. Thus when a tall plant with the yellow type of pod was crossed with a dwarf plant bearing green pods, the F_1 generation was all tall and yellow, for these factors are dominant. When the F_1 hybrids were crossed with each other, the result was 9 tall and yellow, 3 tall and green, 3 dwarf and yellow, and 1 dwarf and green. In this experiment each factor separated independently of the other and showed up in new combinations. This is Mendel's second law, or the law of independent as sortment, which states that, whenever two or more pairs of contrasting characters are brought together in a hybrid, the factors of different paired segregate independently of one

Mendelian Inheritance In Man : Monohybrid ratio

In ABO system of blood groups the different alleles are I^A, I^B and I^O. Any of these two can occupy a locus on chromosome 9 of humans making genotype for blood group - I^AI^A or I^AI^O both resulting in group A; I^B I^B or I^B I^O both resulting in group B, I^AI^B resulting in group AB and I^OI^O resulting in group O. Thus persons with blood group A can have two (homozygous) or one doses (heterozygous) of I^A allele. Similarly persons with blood group B can have two doses or one dose of I^B allele.

In short in blood group ABO system, the different genotypes and resulting phenotypes can be expressed thus -

I^AI^A	or	I^A I^O	- group A
I^BI^B	or	I^BI^O	group B
I^AI^B			- group AB
I^OI^O			- group O

Depending upon whether person is homozygous or heterozygous for blood groups A and B, the type of blood groups inherited by progeny with change. Thus, when both parent are homozygous for blood group A and B, all of their progeny will belong to blood group AB

But if parents are heterozygotes for blood group A and B, any of the four blood groups may appear among their progeny.

Thus inheritance of blood group is strictly Mendelian in fashion. Both parents contribute one form of allele to their progeny and when progeny reproduces, its two alleles are segregated and each gamete possesses one allele. However, in this case both the alleles are capable of expression when placed together. Thus when I^A I^B are together, the blood group AB develops. Such alleles are referred to as co-dominant.

Mendelian Inheritance In Man : (Dihybrid Ratio) :
Rollers and Tasters :

The cases listed before are essentially monohybrid crosses in which individuals are crossed for the inheritance of one pair of contrasting characters (presence or absence of Huntington's Disease, presence or absence of cystic fibrosis). Though no experiment can be designed with human beings as subjects like one carried out with laboratory animals, there are certain characters which can be spotted out in the parents and its inheritance traced in their children. Two such conditions are the ability to taste phenylthiocarbamide, PTC (tasters vrs. non tasters) and ability to roll the tongue longitudinally (rollers vrs. non-rollers).

i. Rollers Vrs. Non-Rollers : The ability is inherited as dominant trait hence dominant homozygotes and heterozygotes have ability to roll their tongue longitudinally. In a mating between pure roller and non-roller, all the progeny will be heterozygous roller.

ii. Tasters Vrs. Non Tasters : The gene for PTC tasting occurs in two forms. The allele for tasting is dominant (T) while the allele for nontasting is recessive (t). A person with either TT or Tt genotype will be a taster while tt genotype will be non-taster.

While the tasters and non-tasters cannot be experimented with like laboratory animals couples of certain phenotypes can be located and their children studied.

In a mating between pure taster and non-taster, all the children would be taster, like one in case of mating between pure rollers and non-rollers.

If both of the couple are taster and roller, the state of their genotype can be ascertained by pedigree analysis. If one of their parents were non-taster and non-roller, it is certain they are heterozygotes. Inheritance of their character by their children would be found in the ratio of 9:3:3:1 as predicted by Mendel. It can be demonstrated through checker board diagram as follows :

TtRr X TtRr

Male → / Female ↓	TR	Tr	tR	tr
TR	TTRR taster - roller	TTRr taster-roller	TtRR taster-roller	TtRr taster-roller
Tr	TTRr taster-roller	TTrr taster-non roller	TtRr taster-roller	Ttrr taster-non roller
tR	TtRR taster-roller	TtRr taster-roller	ttRR non-taster roller	ttRr non-taster roller
tr	TtRr taster-roller	Ttrr taster-non roller	ttRr non-taster roller	ttrr non-taster non roller

taster-roller - 9
taster-non roller - 3
non-taster roller - 3
non-taster non-roller - 1

Fig : Checker board showing possible genotypes and phenotypes from a mating between two individuals heterozygous for two traits PTC tasting and tongue rolling.

Other Instances Of Mendelian Inheritance In Humans

1. Anonychia : This is transmitted as dominant trait in which some or all of the nails of the fingers and toes are absent or rudimentary.

2. Chin fissure : Chin fissure is a longitudinal fissure in the middle of the chin. This is due to an autosomal dominant allele. The character finds complete penetrance in males whereas 50% penetrance in females. The trait is both sex- and age- influenced

3. Mid-digital hair : Presence of hair on middle of the fingers is supposed to be caused due to an autosomal dominant allele.

4. Darwin's tubercle : It is thickening of cartilage near the upper rim of the ear and is supposed to be caused due to an autosomal dominant allele.

5. Achondroplasia : Achondroplasia is an abnormal condition characterised by short-limbed dwarfism. Person suffering show minimal proliferation of their growth cartilage of long bones where as other cartilage are normal. Affected individuals are fertile and disease is transmitted as a fully penetrant autosomal dominant trait. Homozygous achondroplasia is usually lethal in the neonatal period and affects 25% of the offspring of mating between heterozygous achondroplasia parents, the gene responsible for the disease has been mapped to chromosome 4P 16.3 (Francis Rousseau, 1994)

6. Free Vrs. Attached ear-lobe :

Free ear-lobe is dominant, attached ear-lobe recessive.

7. Black Vrs. Blond hair :

Black is dominant over blond hair.

8. Straight Vrs. bended little finger :

Straight finger is dominant over bended finger.

9. Widow's Peak :

This is mid forehead hair-line, present in both sexes hence autosomal.

10. Freckling :

Folds or Wrinkles near the skin of mouth is dominant over normal skin.

11. Dimple :

It is autosomal dominant

Difficulties In The Primates Model : It is difficult to analyse human and primates pedigree on the basis of Mendelian inheritance. The determination of genetic basis of human and the primates traits is fraught with difficulties owing to incomplete penetrance, variable age of onset and sex-influence. A genetic trait is modifiable not only by environment but by composition of total genotype which may include several modifier genes for the characters. Sometimes a genetic character is mimicked by environmental character (phenocopy). Various other difficulties are briefly described as below.

1. Environmental Effects : There is no clear-cut association between genotype and phenotype, Phenotype, in a majority cases, depend on environment also. For example, diabetes mellitus and hypertension are genetic diseases but time of onset of the disease and its severity largely depend on such environmental factors as composition of the diet, stress etc.

2. Double Mutant Loci : Sometimes a second gene locus is involved in the expression of phenotype e.g. in case of thalassaemias, a group of related diseases caused by disorders in the haemoglobin synthesis results due to mutant allele at the α-globin locus on chromosome 16 and β-globin locus on chromosome 11. (α-globin form α-polypeptide chains of haemoglobin and β-globin genes form β-polypeptide chains of haemoglobin. They are located on separate chromosomes.

3. Uncertain Dominance : Sickle-cell anaemia illustrates this point. RBC in this disorder become crescent shaped as the result of abnormal haemoglobin molecules that crystallise abnormally when oxygen levels are reduced. The normal gene is designated Hb^A and the gene that determines sickle-cell haemoglobin is designated Hb^S. On microscopic investigation, the trait displays a dominant inheritance pattern because the red blood cells of both the heterozygotes (Hb^A/Hb^S) and the mutant homozygotes (Hb^S Hb^S) are seen to sickle. Thus, 3/4 of the offspring of an Hb^S Hb^A x Hb^S Hb^A mating will display the sickling phenomenon. However, from a clinical viewpoint the inheritance is autosomal recessive because only the individuals homozygous for the Hb^S gene develop serious a symptoms of anaemia. Pedigree analysis indicates that, on average, one in four offspring of carrier parents are affected.

At the molecular level, where the β-globin gene and the haemoglobin protein products can be assessed directly, the Mendelian pattern is co-dominant as all classes of progeny Hb^A/Hb^A, Hb^A/Hb^S, Hb^S/Hb^S can be distinguished.

Application of Mendelism

1. Pedigree Analysis : In Pedigree-analysis transmission of a character is traced from the earliest parent to the most recent progeny along with all blood relatives living or dead, including marital ones. A character is dominant or recessive can be found out by pattern of its distribution in the family. This can lead to the characterisation of the trait and phenotypes associated with it. Invoking laws of Mendel even the likelihood of occurrence of a character in some member of the family can be predicted. Mendelian laws, however, allow pedigree analysis with respect to only those characters that are caused by a single allele pair.

2. Medico-legal Applications : Mendelism can fairly well serve the judgment in the cases of paternity dispute. With the help of the rules of dominance and segregation it can be stated whether a child is the son or daughter of a particular person. This can be proved with the help of ABO-blood group system and MN-System.

Reader is advised to consult the chapter parentage determination page 577.

3. Medical Application : Mendelian principles have helped in the case of many different kinds of histocompatibility and inborn error of metabolism.

The Rh incompatibility between two parents can result in Erythroblastosis foetalis, when mother is Rh -ve and father Rh +ve. Blood group analysis of parents can tell well in advance the probability of Blood group of children and hence a timely measure can be taken to ameliorate the situation.

4. Genetic counselling Hundreds of genetic diseases have been discovered that are inherited as autosomal dominant, autosomal recessive, or are sex-linked. Progression of those diseases in the family can be predicted by finding out whether one or both of the parents are carrier. If both the parents are carriers, geneticcounsellor may advice them not to have a child at all.

5. Hybrid Varieties : A large number of disease resistant, early maturing, high growth varieties of cereals, fruits and vegetables have been produced using mendelian principles of inheritance.

Cytologic Demonstration Of Mendelism In Man

In the old order Amish community of Lancaster Country, pennysylvania, about 10% of persons have a giant satellite on chromosome 14. Individuals heterozygous for the satellite produce two types of gametes - one with satellite and the another without it. When married to a normal person, the individual with satellite will produce two types of offspring in 1:1 ratio.

$$\frac{14+14-S}{\text{Heterozygous person with satellite on chromosome 14}} \times \frac{14+14}{\text{Normal Person}} \quad \text{---P.}$$

(14) (14-S) (14) ------ Gametes of P

$$\frac{14+14}{\text{Normal}} \times \frac{14+14-S}{\text{Person with satellite}} \quad \text{---} F_1.$$

This trait can be combined with Y chromosome to account for second law of Mendel i.e. independent assortment.

$$\frac{14+14 \text{ and } XX}{\text{Normal female}} \qquad \frac{14+14-S \text{ and } XY}{\text{Male with satellite}} \quad \text{---} P_1.$$

(14 + X) (14 + X)(14-S + Y) (14-S + X) (14 + Y) Gametes

14 + X	14 + X	14 + X	14 + X
14 + X	14 - S + Y	14 - S + X	14 + Y
Normal female	Male with satellite	Female with satellite	Male without satellite

F_1

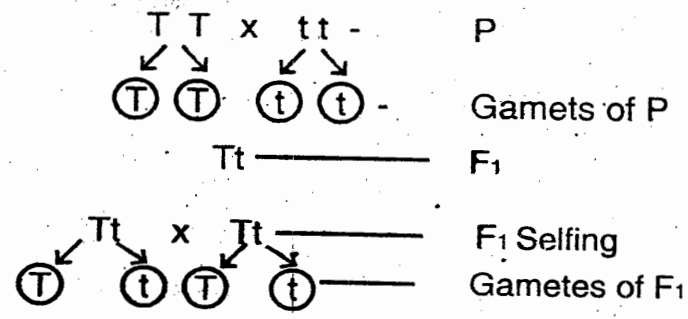
1 : 1 : 1 : 1

To begin with, female parent had no satellite, and male had one. But in F1 females with satellite and male without satellite appear along with normal females and males with satellite in 1:1 ratio. This shows independent assortment of two characters - presence of a satellite and Y-chromosome.

MENDELISM IN RELATION TO MEIOSIS

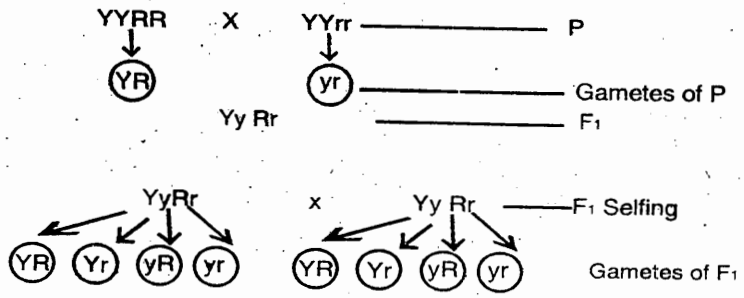
Segregation of characters both in monohybrid cross and dihybrid cross depend on meiotic division in gametes.

(1) In monohybrid Cross : The parental generation forms one type of gamete because it is homozygote and the F_1 generation forms two types of gamete because it is heterozygote.



Because both parents in P-generation produce only one kind of gamete hence progeny is of one type. In F_1 both parents produce two types of gamete hence progeny is of four classes and three genotypic classes.

2. In Dihybrid Cross : The Parental generation forms one type of gemete because each parent is monohybrid and the F_1 generation forms four types of gamete because it is dihybrid.



Because both parents form one type of gamete in P generation hence progeny is of one type. In F_1 both parents form four types of gamete because of independent assortment, hence progeny is of 16 classes and four types.

STUDY OF ANTHROPOGENETIC VARIATIONS

There have been performed a number of studies seeking to determine anthropo-genetic variations and most of the studies have included easily observable Mendelian traits in man viz. ABO blood group, widow peak, mid phalangeal hair, hair whorls, Earlobe attachment, Tongue upfolding, Tongue rolling, PTC tasting, Dimple and relative length of index and ring-finger.

S.P. Sinha and R.K. Singh (1983-85) observed genetic variations in the santals and three Pahariya sub-tribes (the saurias, the Mals and the Kumarbhags) distributed in the various districts of Jharkhand (then in Bihar). The study included 7 different anthropogenetic traits. The frequency of such variations is as follows—

1. Widow's peak: The trait have been found to be distributed in both sexes but more among males, thus indicating sex-bias. The trait is highest in Saurias (54.5%), followed by Santals (50.6%), Kumarbhags (49.5%) and Mals (46.9%).

2. Tongue-rolling : The trait, though present in both sexes, is slightly higher in females, indicating influence of sex. The frequency is highest in santals (54.2%) followed by kumarbhags (49.4%), Saurias (42.8%) and Mals (42.3%).

3. Tongue-folding : This trait is present in low frequency and in both sexes, though slightly higher in females, indicating sex-influence. The frequency is 2.47% in Santals.

4. Ear Lobe attachment : The trait isfairly distributed in both the sexes being highest in frequency among Santals (49.86%) followed by saurias (31.08%), the Mals (28.64%) and Kumarbhags (2538 %).

5. Relative length of the index and ring fingers : The condition showsthe folowing frequency—

a. smaller index-	male	—	Santals 61.4%
	females	—	Sauriyas 74%
	(usually rt hand)		
b. Longer Index-	male	—	Santals 34.3%
	female	—	Sauriyas 23.1%
	(usually lefthand)		

c. Equal condition. male — Kumarbhags 1.3%
female — Santals - 4.8%
(No definite trend)

6. PTC tasting Ability : The frequency of non-taster is about 55% among the Santals, Saurias and Mals, but low (44%) in Kumarbhags.

7. ABO Blod group : In all the four populations, B-blood group is the more frequent, highest among Kumarbhags (40.6%), followed by Santals (37%), the Mals (36.7%) and Sauria (34.2%) . The next common group is 'O' (26% to 35.8%), followed by group A (16% to 26.9%). Group AB is least frequent (7.3 to 9.9%)

When populations were compared for bilogical differences, if was found that the three sub-tribe of Pahariya are indeed closer and different from Santals.

OTHER STUDIES

Other important studies in the field of anthropogenetic variations in India is as follows—

1. Bhatia et. al. (1976)- The study included endogamous groups of Sarswats in western India.

2. Malhotra K.C (1974)- The study includes major models of population-genetics in India.

3. Mukherjee, Malhotra and kate (1979)- The study included incidence of red green colour blindnes in some populations of Delhi, Maharashtra and west Bengal.

4. Naidu and veeraju (1978)- The study inlcluded incidence of colour blindness among the tribal populations of Andhra Pradesh.

5. Pingle, Mukherjee & Das (1981)- The study included blood sample variations in five tribal populations of Andhra Pradesh.

6. Papiha et, al (1980)- The study included anthropogenetic variations among kanet and Koll of Kinnar district of Himachal Pradesh.

7. Sengupta. S (1979)- The study includes ABO blood group variation among Kaibartas of upper Assam.

8. Sengupta S.(1982)- The study includes variation of ABO blood group among three endogamous castes of Assam.

9. Sidhu and sidhu (1980)- The study includes distribution of ABO in Sansis of E. Punjab.

10. Venkateshwara Rao, Verraju, Naidu and Krishna Rao (1981)- The study includes anthropogenetic variation among the waga Vamaan caste of coastal Andhra Pradesh.

Methodology for study of anthropo-genetic variations

1. Morphoscopic- Characters which can be viewed such as widow peak, earlobe attachment, tongue-rolling & folding.

2. Morphometric- Characters which can be measured such as height, IQ etc.

3. Blood group Study- This is performed by using antisera-A and B for ABO system and antisera-D for Rh-system.

4. Red and green colour blindness- It is known by using Ishihara charts.

5. PTC tasting- It is known by serial dilution method of Harris and Kalmus (1940)

Morphometric Characters are polygenic in nature and hence do not follow Mendelian ratio.

Evidences from Gene-sequences

It has been reported in Nature (Feb 18, 2010) that complete genome sequences of Bushman from Namibia's Kalahari desert and of a Bantu from South Africa was obtained. The observati is that the Bushman of Kalahari seem more different from each other in terms of nucleoticle substitutions than typical Asians and Europeans. The observations prove the fact that Bushman with maximum variation probably constitutes the oldest known modern human lineage.

POLYGENE

Most normal human traits that appear to have a genetic base cannot be fitted into a simple. Mendelian mode of inheritance. For example, body size and shape, skin colour and height display continuous variation and cannot easily be attributed to the action of single loci. Such traits are known as polygenic because they are determined by several sets of alleles producing a cumulative effect on the same character. Several characteristics in man are influenced by multiple genes. In such cases the characters, instead of being sharply marked off, show continuous variation between two extremes. This is called quantitative inheritance. In this kind of inheritance the children are more or less intermediate between the two parents. The best illustration of such a type is the degree of pigmentation in crosses between the Negro and the white race. The cumulative genes in such crosses have a quantitative expression. A pure-blooded Negro has two pairs of genes on separate chromosomes for pigmentation though more than two pairs present (AABB). On the other hand, a pure blooded white will have the genes (aabb) for nonblack. In a mating between a homozygous Negro and a homozygous white, the mulatto (AaBb) will have a skin colour intermediate between the black parent and the white. The genes for pigmentation in the cross show incomplete dominance. When such mulattoes are crossed (F_2), the children will show a variety of skin colour, depending on the number of genes for pigmentation they inherit. Their skin colour will range all the way from pure black (AABB) through dark brown (AABb) or (AaBB) half coloured (AAbb or AaBb or aaBB), light brown (Aabb or aaBb) to pure white (aabb).

Table : showing result of mating between two mulatto (AaBb)

AaBb x AaBb — P

Male gametes/ Female gametes	AB	Ab	aB	ab
AB	AABB	AABb	AaBB	AaBb
Ab	AABb	AAbb	AaBb	Aabb
aB	AaBB	AaBb	aaBB	aaBb
ab	AaBb	Aabb	aaBb	aabb

Pure black - AABB, Pure White aabb

The student should realize that when the term "pure white" is used in a cross involving mulattoes, it refers solely to skin colour and not to other characteristic, for other racial characteristic are inherited independently. Thus in such a cross an individual may have pure white colour (no genes for black) but could have other Negro characteristics.

Although skin colour appears to depend on the distribution of two pairs of genes, there are many other traits in human inheritance that involve more than two pairs. These more complicated cases result in more varied ratios than in the simpler cases. When there are so many genes involved in the production of traits, the latter often take the form of distribution curves. One such trait is stature in man, where between a few extremely short and tall individuals, there are many in between these extremes.

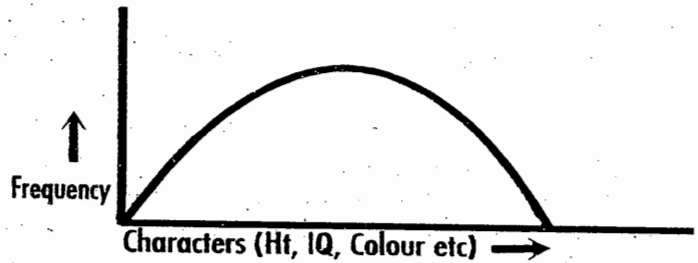


Fig. : Normal distribution curve.

Polygenic characters are normally distributed in population, Those with extreme traits are in lower frequency where as those with mean value are in highest frequency.

Phenotypic threshold Value : Sometimes in the polygenic inheritance is introduced a condition of threshold. A character is not expressed until mutant genes at the polygenic sites don't reach a critical threshold level.

Human eye colour is a polygenic trait that shows threshold effect. It used to be believed that blue is always recessive to brown, but this is not the case. Eye colour varies from pale blue to very dark brown, depending on the concentration of melanin. Two dark-blue-eyed parents can produce brown-eyed offspring. This is presumably because the child inherits from each parent the appropriate combination of alleles at the polygenic loci which enables the child to cross the phenotypic threshold.

LETHAL GENES

Those genes which kill its possessor is called lethal gene. It may be **semi-lethal**, if it kills the possessor after attainment of reproductive age, or **sub-lethal** if death occurs in early infancy or childhood i.e.. before attaining reproductive age. 15% of all infant deaths and 50% of all childhood deaths in US is because of lethal genes. A gene lethal in one environmental condition may not be so in other environmental condition e.g.. mutants of phenylketonuria are normal if reared on phenylalanine-free diet. This is referred to as **conditional lethal**. Some of the semi-lethal gene are conditional lethal.

(A) Dominant lethal : Those lethal genes which kill its possessor even in heterozygous condition are called dominant lethal. It includes both sub-lethal and semi-lethal.

(1) Sub-lethal: For example **epiloia** This is a condition in which there is multiple skin tumours and death is caused in early infancy. The gene always arises by fresh mutations.

(2) Semi-lethal: For example **Huntington disease**, a disease which causes progressive degeneration of nervous system. The age of onset can be 40 years to more than 60 years. Mode of inheritance of this gene is like autosomal dominant (See pedigree Analysis).

(B) Recessive lethal : Those lethal genes which causes death only in homozygous conditions are referred to as recessive lethal.

(1) Sub-lethal: For example, **Thalassaemia, sickle-cell anaemia**. The possessor of the gene often survive to reproductive age and gene is also inherited from affected persons.

(2) Semi-lethal: For example **haemophilia** . Females seldom suffer from this disease because in homozygous condition the gene causes death of zygote or embryo. If females have one gene on another x chromosome, they are carriers and they survive. Males are sufferers.

Lethal genes and human populations: Many necessive lethal genes which are harmful for man are found to be circulating in populations at high frequency and defy rejection by natural selection. Two theories have been proposed to explain this dilemma—

(a) School of Dobjhansky : maintains that recessive lethal genes in heterozygous condition provides heterosis and heterozygotes are superior to both homozygotes. For example, sickle-cell anaemia, thalassaemia etc. It has been found that heterozygotes have resistance against malaria.

(b) School of Muller : believes that there is artificial reduction of natural selection by use from medical sciences and sociocultural practices. Thus a person suffering from phenylketonuria can hope to survive and live a full life if reared on phenylalanine free diet. Such practices ensure circulation of lethal genes in population.

EUGENICS, EUPHENICS AND EUTHENICS

These are the practices which seek for betterment of human races in various ways. **Eugenics** seek to interfere at the inheritance of gene-level whereby either inheritance of better gene is encouraged or, inheritance of lethal gene or deleterious gene discouraged. **Euphenics** seek to interfere after lethal genes or deleterious genes have expressed in an individual and try to minimise its harmful effects. **Euthenics,** on the another hand, seek to enhance quality of the environment so that better genes get chances for its fullest expression.

I Eugenics : The concept of eugenics was given by Francis Galton who sought evolution of human triats through social selection rather than natural selection. The concept will prove harmful if it carry racial connotation since no race is superior in any genetic characteristics such as intelligence. Eugenics can be applied either in positive way or in negative way.

(1) Negative Eugenics: It attempts to decrease the frequency of harmful, deleterious genes by suggesting, for example haemophiliacs and carriers are advised not to reproduce so that harmful genes are not inherited.

(2) Positive eugenics : The concept was championed by Muller. Positive eugenics seek to increase frequency of beneficial genes by any of the following measures—

(a) Selective mating : It carry the connotation that only gifted should marry. There are serious constraints with this view. Firstly, it improves one or few character but lowers overall fitness. Secondly, it is difficult to be practised ie. whom to marry whom.

(b) Sperm-bank or germinal choice ro Eutelegenesis : It provides for keeping sperms from gifted persons in conditions of extreme preservation ie. in liquid nitrogen. The approach is fairly successful in US where 5,000-10,000 babies one born by artificial insemination because of husband's sterility or genetic disease. Sperm-banks are source of sperm in such conditions.

(c) Cloning : This is conversion of somatic tissue into embryos. The nucleus of a desired somatic tissue is implanted in an unfertilized egg of an individual after removing nucleus of the egg and this ransformed cell is reared in a surrogate mother. However, there are serious ethical issues against cloning of human species though some laboratories claim to have achieved it.

(d) Parthenogenesis : Females with desirable characters can be induced to lay "diploid eggs". However, in the absence of Y-chromosome, only girl child is possible. Besides, placenta formation and embryonic development are other serious constraints:

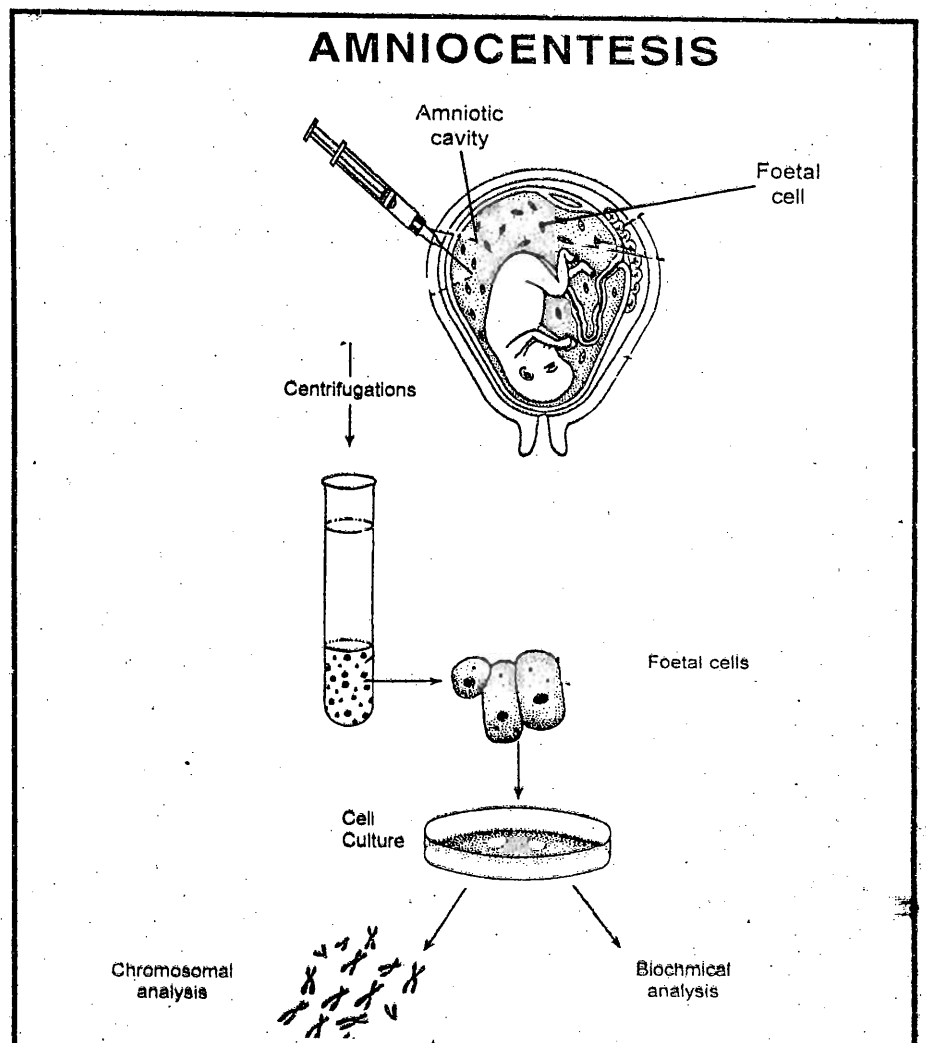
II Euphenics : The concept was given by Lederberg. It largely consists of medical engineering seeking to prolong human life by interfering with the defective phenotype or genotype after birth o an individual. There are a number of heritable heart diseases, heritable anaemias, missing enzymes etc. Which can be treated either at genotype level or phenotype level.

(1) Euphenics at genotype level: It includes gene-therapy where in (a) a missing gene is introduced (b) a defective gene is silenced (c) a defective gene is replaced by a functional gene. Readers one referred to "gene-therapy".

(2) Euphenics at phenotype-level: This includes synthesis of artificial blood to treat heritable anaemia, elaboration of different components of heart to treat heritable heart diseases, genetic engineering and synthesis of enzymes and hormones to treat heritable deficiencies such as haemophilia (factor viii) diabetes mellitus (insulin)

III. Euthenics : This seek improvement of environment to provide fullest expression of positive genotype eg. selection of intelligent students and providing them all facilities for development. Navodaya schools, launched by our government, is based on this concept. It selects intelligent students from the rural set up and provides facilities for their all-round development so

that talents in the rural areas are not wasted. IITs among the engineering colleges are also based on this principle.



The process is used to find out embryonic cells by puncturing into amniotic cavity, draining amniotic fluid, separating embryonic cells, culturing embryonic cells. The process can be used to detect sex of child (xx or xy) by chromosomal analysis and genetic defect (DNA-probing)

GENETIC ANALYSIS OF MAN

1. Chromosomal Analysis

A. Chromosomal Banding

Chromosomes are best visible during metaphase of mitotic cell-division when they arrange at the equator. Thus, for chromosomal analysis, cell are either taken from the tissues that are actively dividing such as bone marrow cells, or are induced to divide in culture. Phytohaemoglutinin, a protein extract from kidney-beans, has been found to induce DNA-synthesis and cell-division in the lymphocyte cells in culture. For analysis of chromosomes, it is necessary to hold the chromosomes at metaphase. It is accomplished by adding Colchicine to the medium which prevents polymerisation of spindle-fibres which is instrumental in cell-division. The cells are then treated with weak salt solution, causing it to swell and disperse the chromosome well. The cells are fixed in this condition by application of suitable fixatives.

After fixation, the cell-suspension is dropped into slides, air-dried, and stained for banding patterns. There are essentially four types of staining procedures -

a. Q- Banding Or Quinacrine Fluorescence Banding : In this technique certain chromosome bands appears fluorescent regions with fluorescent microscopy. The bands are rich in A-T bases, compacted by proteins.

b. G-Banding Or Giemsa Banding : By this method, the same bands appear as dark staining regions. The bands develop due to compaction of chromatin by non-histone proteins.

c. C-Banding Or Centromeric Banding : This method involves harsh pretreatment of chromosomes with dilute acid followed by strong alkali and warm saline treatment prior to giemsa staining.

The harsh pretreatment of chromosomes remove much of the non-histons and histone proteins. Under such condition, centromeric regions, particularly of chromosome 1, 9, 16 and Y-chromosome are intensely stained.

The C-band positive regions are sites of concentration of satellite or repetitive DNA. There has been found individual variations in the pattern of C-banding.

d. R-banding (Reverse banding) : This technique involves saline heat treatment prior to Giemsa staining. This is reverse to G-method. The banding pattern develops because of differential response of chromosomal proteins to denaturation.

The banding patterns of each chromosome is specific and makes it possible to identify each individual chromosome which may differ in different individuals. These structural polymorphisms, called heteromorphism, are inherited in a simple mendelian fashion and therefore can be studied in the transmission of a chromosome from one generation to the next.

B. Flow Cytometry

Fluorescent activated cell sorting or flow cytometry is a recent method of chromosomal analysis. Cells are ruptured, stained with fluorescent dye which selectively stains the chromosome. The chromosomes are then projected as a fine jet through a flow chambers across a laser beam. This causes chromosome to fluoresce which is measured by a detector. Since the amount of fluorescence depends upon the size of chromosome, a rapid Karyotyping is possible.

C. Somatic Cell Hybridization

Hybrids of somatic cells e.g. mouse and human cells can be produced. In such hybrid cells, human chromosomes are eliminated as hybrid cells divide, and some of the human chromosome is retained. Under such condition, it is possible to study specific proteins produced by chromosome retained.

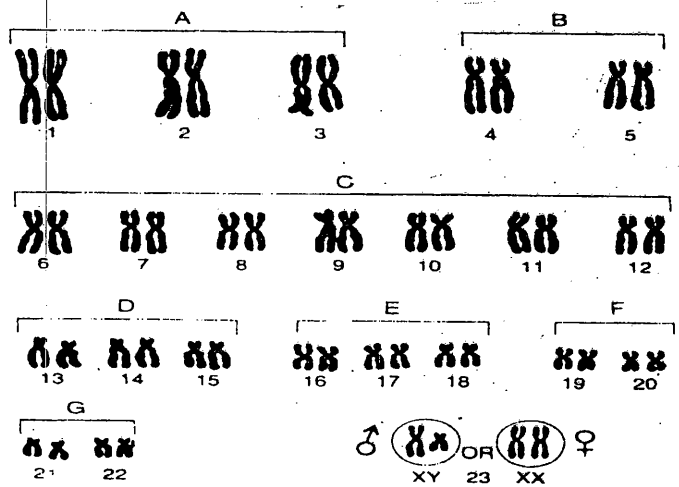


Fig. : Human karyotype

2. Foster Children

The term does not indicate legally adopted children. Foster child method is another method of separating respective influence of heredity and environment in the development of a trait.

In this method various groups of children are selected at random and are placed in different homes classified good, average and poor homes. Since group of children are arbitrarily selected, it is believed that genetic component of a factor, say intelligence, is equally distributed in all of them. After a lapse of time they are tested on different intelligence scales. If intelligence has an environmental component, children placed in good homes should score better than those placed in average and poor homes.

In practice, the experiment is never free of biases and errors. Children selected for placement in different homes are generally not random, and as it generally happens, intelligent children from good families are placed in good families.

However, In Chicago studies the selective placement was greatly minimised. The study revealed that the mean IQ scores of the adopted children were related to the quality of the adoptive homes. The mean scores for the different groups was as follows -

Good homes - 45 adopted children scored on average 112 points.

Average homes - 39 adopted children scored on average 105 points.

Poor homes - 27 adopted children scored on average 96 points.

Such experiments show a noticeable effect of environment on the development of intelligence.

Minnesota graded home study in which children of managerial class were placed in labour class and Vice-Versa. It was found that there is effect of environment on IQ. But, at the same time, it was also found that children of managerial class had more IQ in labour class homes than children of labour class in their own homes. This indicates importance of heredity in determination of IQ.

3. Co-Twins

Twins may be either identical or MZ twins and fraternal or DZ twins. MZ twins develop from the same zygote and hence have almost all their genetic components similar barring mutations. DZ twins, on the other hand, develop from two separate zygotes and are as similar as sibs.

Various experiments have used MZ and DZ twins variously in order to separate the hereditary and environmental components of a character. In co-twin studies, the identical twin along with its co-twin and the fraternal twin along with its co-twin are investigated and compared. The technique has been utilized in many studies, e.g. development of abnormal behaviour such as schizophrenia.

It is necessary to raise two methodological issues which have contributed to disparities in results between early and more recent investigations. In twins investigations, rates of schizophrenia are expressed in terms of concordance, the proportion of twin pairs in which both co-twins are diagnosed as schizophrenic. This is ascertained in practice by identifying a schizophrenic index case and then tracing his or her co-twin for evidence of diagnostic classification.

Earlier investigations determined concordance by *"pairwise"* analysis whereby one simply calculates the proportion of all twin pairs in which both are affected. This analysis did not take into consideration the fact that in any given twin pair either might have been independently registered as an index case and hence both traced for psychopathology.

To illustrate the point, suppose A and B are co-twins. A can be registered and B traced for the psychopathology. Conversely, B can also be registered and A traced for the psychopathology. Thus the co-twins would be counted twice for the concordance rate where as they should have been counted only once.

Recent techniques of co-twin studies is *"probandwise"* in which the twin showing the charater is counted twice. The probandwise analysis, therefore, generates somewhat higher but arguably more realistic concordance rates.

4. Pedigree Analysis

First suggested by Galton, the pedigree analysis is the study of the inheritance of traits which show regular transmission from generation to generation in a family. Since critically informative matings cannot be designed experimentally, pedigree analysis is the best means of study of inheritance of such disorders. The pedigree pattern provides information about Mendelian principles of segregation and independent assortment; furthermore, it may provide information on allelism and linkage.

Study of a particular trait in a family usually begins with an "affected" person who is referred to as the proband, or the propositus (female = proposita), or the index case. The following conventions are useful in the construction of pedigree charts.

i. Males are placed first on the left, represented by square. Females are placed on the right, represented by circle. A marriage is indicated by a horizontal line connecting the two. Double marital lines are used in cases of consanguinity.

ii. Sibs are marked 1,2,3,... in chronological order of birth. If numbers are great, it is customary to write the number inside the square for the boy and inside the circle for the girl offspring. Twins are indicated by joining the sibs with a capping line (^). In case of identical twins, they are joined by a horizontal line also. If zygosity is not confirmed a cap is accompanied by a question mark (?)

iii. Persons affected by the trait under study are indicated by blackening the square or circle. Heterozygous female carriers are indicated by a dot inside the circle to indicate carrier of an X-linked trait.

iv. The heterozygous parents of a person affected by recessive trait is indicated by half-blackening of square and circle.

v. Generation are numbered in Roman numerals, the older one at the upper end of pedigree chart and recent ones at the bottom of the chart.

vi. Within each generation, each individual is identified by Arabic numeral, eg. III 16.

Symbols used in PEDIGREE ANALYSIS

1] Normal male

Normal female

2] Heterozygote male

Heterozygote female

3] Affected male

Affected female

4] Carrier female

5] Mating

Proband

Consanguineous marridge

6] 5 3 Number of sibs

7] DZ Tuins

MZ Tuins

Unknown Zygosity

Dead

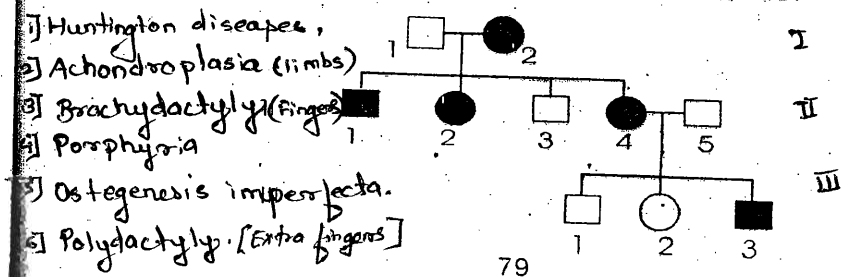
Aborted

Unspecified Sex

Types of Pedigrees : A pedigree depend upon nature of the gene causing the character under study. A gene can be autosomal dominant, autosomal recessive, sex-chromosomal dominant and sex-chromosomal recessive. The nature of inheritance of a gene, therefore, vary.

(a) Autosomal dominant : Several conditions are caused due to autosomal dominant gene. Some of the conditions include Huntington's disease (Progressive degenaration of nervous system) Achondroplasia (short limbed dwarfism), Brachydactyly (short fingers), Porphyria (Skin lesions due to exposure to sunlight), Osteogenesis imperfecta (Brittle bone), Polydactyly (Extra fingers), Creutzfeldt-Jakob disease (Senile dementia, myotonic dystrophy etc.)

Such characters are present almost in all generations, ie. no generation skips with equal frequency in male and female. The character thus shows vertical pattern of inheritance.

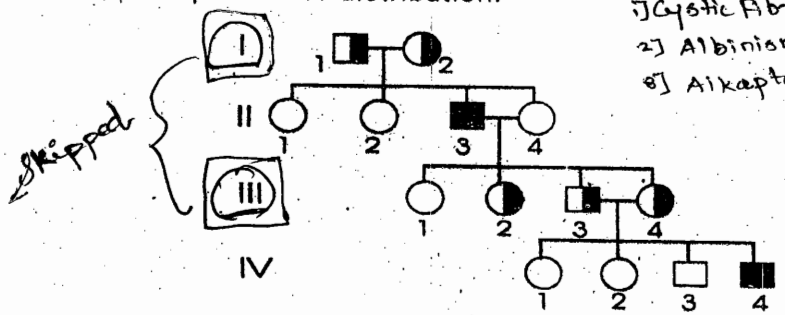


In generation I, mother is affected and in generation II, only 3rd child is unaffected. Affected girl, 4, transmits the character to two of the progeny even if she marries normal person. The character appear in both sexes with equal frequency, without skipping generations.

(b) Autosomal Recessive : Several conditioins result due to autosomal recessive gene. This includes cystic fibrosis (formation of thick mucous in lungs), albinism (absence of melanin), phenylketonuria, Alkaptonuria (Black urine) etc.

Such characters, th ough present in both the sexes with equal frequecy, skip generations. The character, thus shows horizontal pattern of distribution.

1) Cystic Fibrosis–
2) Albinism–
3) Alkaptonuria–

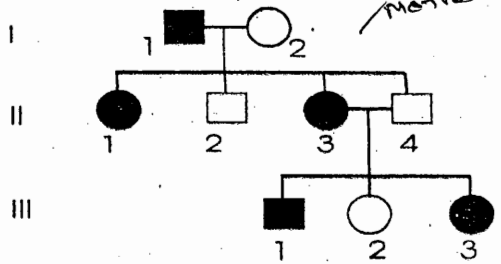


In generation 1, both parents are heterozygotes and unaffected. In generation II, 3 is affected who marries a normal girl. In generation III, 2, 3, 4, are heterozygote but unaffected and the character appear in generatioin IV, 4. Character skips generation I and III.

(C) X-dominant : Some characters such such as vitamin D-resistant rickets, blood group Xg are X-dominant.

The nature of inheritance depend upon whether the gene is inherited from father or mother side. If from father side, the character will be inherited by daughters only because father has one X which is always given only to daughters.

Father → only daughters
Mother → both son & daughters

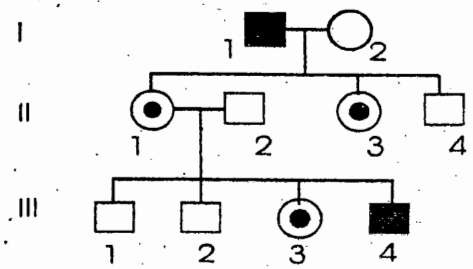


In generation I, father is affected and in generation II both daughters 1 and 3 are also affected. If the gene is inherited from mother side both boys and girls have equal chances to inherit.

The condition, thus, appears in every generation, having sex-bias.

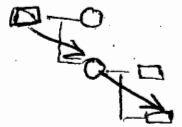
(d) X-recessive : Several conditions such as haemophilia (failure of blood to clot upon bleeding), red and green colour blindness (failure to identify red and green from other colours) etc are X-recessive characters.

Males are often more affected by such conditions than females because of two reasons— since females have two X-chromosome hence for them to be affected it is necessary that the gene is present on both the chromosomes (homozygous) where as males are affected by a single dose of gene since they have only one X-chromosome. In addition, presence of a double dose of such gene in the female zygote is lethal hence they rarely develop.



In generation I, father is affected but in generation II, none is affected but females are carriers. Even if they marry normal male (2) in the generation II carrier females (3) and affected males (4) are born in the III generation. The gene, thus, travelled from father to daughter to son. This is referred to as criss-cross inheritance. The character is inherited from maternal grand father to grandson via his mother.

Sagar



criss-cross.

5. Family Studies

A parent passes half of its genes to an offspring hence a parent and offspring has half of the genes common. This half is known as "coefficient of relationship" between parent and the offspring. Similarly, sibs also have half "coefficient of relationship" because if one sib inherits a gene, there is $\frac{1}{2}$ chance that the same gene will be inherited by another sib. In the next generation, the grand-children also have $\frac{1}{2}$ chance of receiving a gene from parents, hence likelihood of a gene transmitted from grand parent to grand children is $\frac{1}{2} \times \frac{1}{2} = \frac{1}{4}$ This is then" coefficient of relationship between grand parent and grand children. The same ce-efficient of relationship exists between uncle/aunt and nephew/niece. The coefficient of relationship between first cousins is $\frac{1}{2} \times \frac{1}{2} \times \frac{1}{2} = \frac{1}{8}$ (see cousin marriages).

Such coefficient of relationship means that in a totally additive genetic system, an individual is like half of its parent, a quarter like its grand parent, a quarter like his uncle/maternal aunt and an eighth like a first cousin.

Since genetic relationship between different relatives is known, family studies is significant in studying inheritance of factors that have additive genetic basis, environmental component and a dominance factor. For example, in a study of inheritance of blood-pressure, it has been found that 16% of blood pressure variation in the population is because of environmental factors, 48% to additive genetic factors and 36% to dominance.

For family studies, the method adopted is one of calculating coefficient of correlation and the formula is —

Co-efficient of correlation (b) =

$$\frac{\Sigma xy - (\Sigma x \cdot \Sigma y) / N}{\Sigma x^2 - \frac{[(\Sigma x)^2]}{N}}$$

To illustrate, suppose we have to find out heritability of diabetes mellitus. Ten families are studied and average blood sugar

level (fasting) of two parents is compared and constrasted with average blood sugar level (fasting) of their two sons. The operations can be performed as under—

Group	average BS(F) Parents (x)	average BS(F) 2 sons (y)	xy	x^2
1	80	70	5600	6400
2	70	70	4900	4900
3	70	90	6300	4900
4	80	90	7200	6400
5	90	80	7200	8100
6	70	80	5600	4900
7	60	80	4800	3600
8	90	70	6300	8100
9	60	60	3600	3600
10	90	80	7200	8100

$\Sigma x = 760$ $\Sigma y = 770$ Σxy 58,700 $\Sigma x2 = 59,000$

Co-eff.of correlation (b) =

$$\frac{\Sigma xy - \frac{(\Sigma x . \Sigma y)}{N}}{\Sigma x^2 - \frac{[(\Sigma x)^2]}{N}}$$

$$= \frac{58700 - 58520}{59000 - 57760} = \frac{180}{1240} = 0.145$$

Since heritabilty (h^2) = 2b = 2x0.145 = 0.29 or 29%

The condition is approximately 70% environmentally determined.

7. Immunologic Method

Immunologic methods are dependent upon antigen-antibody reaction. While discussing genetic criteria in ethnic determination, we came to know that antibodies are of five types - I_gA, I_gG, I_gD, I_gE, and I_gM, each made up of two heavy protein chains and two method. If protein is treated with phenylisothiocynate and mild acid, the terminal aminoacid (aminoterminal) is separated which can be analysed.

AGDEM

B. Sequencing Of DNA

On the other hand, procedures have become known by which DNA can be sequenced and analysed. Sequencing of DNA can be done by methods such as Maxam-Gilbert method. The DNA is cleaved by four restriction enzymes that cut DNA at different bases. Thus four sets of samples are found, each having differing length of DNA fragments representing position of the bases. The four samples are electrophoresized in four parallel gel which indicate position of the bases.

C. Southern, Northern And Western Blotting

There have been developed techniques to detect the presence of specific DNA, RNA and protein. Since such a method was first described by Southern (for DNA), the tests detecting presence of RNA and protein have been named in a similar way. In Southern blotting, DNA is cleaved by restriction enzyme and fragments separated by gel-electrophoresis. The fragments are then blotted on nitrocellulose filter paper and hybridised with labelled probe. It can give the location of DNA of interest in experimental material.

Northern blotting is performed in the same way for RNA molecules.

For Proteins, they are first separated electrophoretically and blotted on nitrocellulose filter. It is then treated with the antibody. Thus is formed antigen-antibody complex. The complex is then reacted with labelled antibody against the complex. The excess labelled antibody which has not combined with the complex is washed out. Autoradiography can detect presence of such labelled antibody.

9. Recombinant DNA Technique In Study Of Man

Recombinant DNA technique involves the generation of DNA fragments using restriction endonucleases, the incorporation of these fragments into a suitable vector (Plasmid, phage or Cosmid), the introduction of the vector into a host organism (usually bacteria *E-Coli*) and the subsequent selection of clones containing a specific DNA sequence.

The technique has been used for analysing gene structure

& the diagnosis of genetic disorders (either directly or by linkage with restriction fragment length polymorphisms) of both adults and foetus. In case of foetus, the technique has helped in detection of sex of the foetus.

1. Analysis Of Gene Structure

The technique has enabled us to learn a great deal about human genes, particularly the Beta globin gene region. By arranging the fragments generated by various restriction enzymes (restriction mapping), it has been possible to know the genes and their arrangement in this region. There are in total 7 genes in this region - two pseudogenes and E, $G\gamma$, $A\gamma$, δ and β. A similar organisation of five functional gene is found in gorillas, chimpanzees and old world monkeys. Only in the new world monkeys there is an apparent absence of one of the functional genes indicating an early divergence of this groups. During development, the haemoglobin changes from foetal to adult type and the sequence of their formation in human being is similar to the sequence of these genes in β-globin region. Each globin gene is about 1.5 Kb. (kilobase ; 1kb = 1000 base pairs) in length and total length of the complex is about 60 kb, along with non-functional spacer DNA in between them. Using appropriate probes, it has been possible to hybridize the probe in site and find out the location of the gene on a particular region of a specific chromosome. For example, using this technique it has been possible to know that β-globin genes are localised near the centromere of the short arm of chromosome 11.

DNA Probes are important means of study in recombinant DNA technique. For example, if you know structure of protein or mRNA, DNA can be synthesized which is radioactivity labelled by use of 32p : This DNA probe can be used to locate similar DNA in the genome of any organism. The DNA probe will hybridize with similar sequence and its radioactivity can signal its presence. You will learn later on that such DNA probes have many functions - firstly they can identify DNA of any microorganism or virus; Secondly they can identify mutation or changes in any gene by not perfectly hybridizing with it; thirdly, such probes have been used in fingerprinting. DNA of every individual has unique hypervariable regions in which short segments of bases are uniquely repeated. If DNA probe is made on the basis of any DNA pattern available, for example on a crime location, similar sequence can be traced in some individual on the basis of probe.

Diagnosis of Genetic disorders in foetus :

DNA of foetus is extracted from Chorionic villi, cleaved with restriction endonuclease and electrophoresed. One of the DNA fragments, B, contains β -globin gene. A DNA-probe for β -globin gene is obtained from reticulocytes by extracting and separating mRNA of β -globin gene and then obtaining copy DNA (cDNA) of β -globin gene using reverse transcriptase and radioactive Phosphorus, ^{32}P. This cDNA probe hybridizes with B-globin gene of foetus present on fragment B. The probe will not hybridize if foetal β -globin gene is defective.

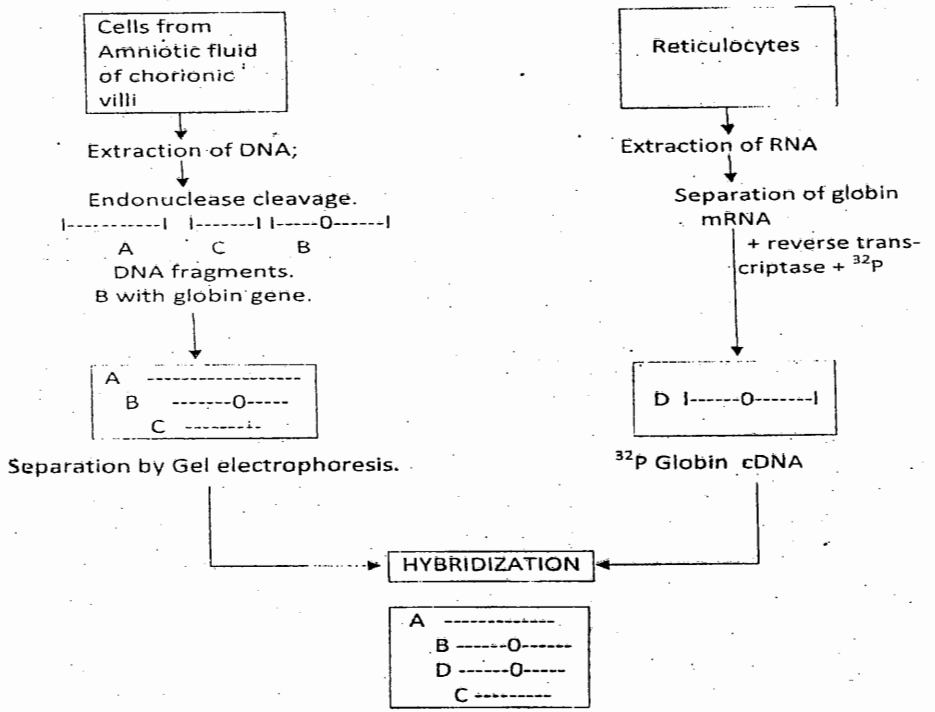


Fig: Use of Recombinant DNA technique to analyze structure of β -globin gene of a foetus.

Similarly, DNA probe for Sickle cell gene and normal gene can be obtained and hybridized with foetal DNA. If foetus contains normal genes, only normal DNA-probe will hybridize; if foetus suffers from sickle-cell anaemia, DNA probe for sickle-cell gene will hybridize; if foetus is a heterozygote, containing both normal and sickle cell gene, both DNA probes will hybridize with the foetal DNA. In this way, recombinant DNA technique is useful for locating not only normal genes but genes causing genetic diseases also.

Dominant Homozygote	Heterozygote	Recessive Homozygote
SS	Ss	ss
↓	↓	↓
Normal Gene	Normal Gene + Sickle – cell Gene	Sickle – cell Gene
(Only normal Probe hybridizes)	*(Both normal & sickle cell probe hybridize)*	*(Only sickle cell probe hybridizes)*

RFLP (Restriction Fragment Length Polymorphism) has been used in study of genetic variation in man. Since different individuals differ in DNA bases every 200 basepairs, it follows that different length of DNA fragments will be produced if cleaved by same restriction endonuclease. It is referred to as RFLP. This can be recognized by the altered mobility of the DNA fragments in the electric field, such as gel electrophoresis, where rate of migration in gel depend on their sizes. Smaller fragments travel longer distance because of less frictional force and become arranged in the gel in the form of smear – from larger to smaller size.

RFLPs can be studied in following four ways:

a. RFLP For Deletion Detection

b. Allele-Linked RFLP

c. Locus-Linked RFLP

d. Mutation-Specific RFLP

a. RFLP For Deletion Detection : It is possible to synthesize DNA from mRNA by using enzyme reverse transcriptase. A special type of blood-cells, reticulocytes, contain mRNA for globin proteins hence globin DNA can be synthesized using it. Such DNA is called copy DNA (cDNA). Such cDNA probes can be used to detect deletion in thalassaemia in case of foetuses. Foetal DNA is extracted, treated with restriction enzyme and restriction fragment separated and probed with cDNA. In case of delta-beta thalassaemia globin gene is deleted hence cDNA probe has no segment to hybridize with.

b. Allele Linked RFLP : In blacks of Afro Caribbean, Hpa I restriction enzyme generates 7.0 or 7-6 kb long fragment containing the β-globin gene, and rarely (3%) 13.0 kb fragment. On the other hand, sickle-cell globin gene is found in the 13.0 kb fragment nearly 90% of times.

This particular type of RFLP is called allele linked RFLP and denotes common origin of the fragment and allele in the population.

C. Locus Linked RFLP : Allele linked RFLP is rare and we have to take recourse to locus-linked RFLP. In such cases, DNA probes are found which reveals a RFLP which has been shown by pedigree studies to be linked to a particular disorder. In order to be useful, a number of RFLP shown to be linked to the disease will have to be found out because all families do not possess all the RFLP linked with disease. Disorders in which linked RFLP have been used are beta thalassaemia, Duchenene muscular dystrophy, Huntington's Chorea, cystic fibrosis etc.

d. Mutation-Specific RFLP : Mutation from one base to another also sometimes changes the restriction site, giving rise to different RFLP.The mutation from GAG to GTG in sickle-cell anaemia eliminates a restriction site for the enzyme Ddel (CTNAG) or the enzyme mst II (CCTNAGG). The mutation can therefore be detected by digesting mutant and normal DNA with the restriction enzyme and performing a Southern-blot hybridization with a cloned β-globin DNA probe. Such an approach is applicable only to those disorders where there is an alteration in a restriction site.

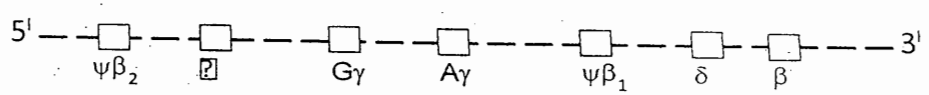


Fig: Map of human β -globin gene (Ψ represents position of pseudogenes)

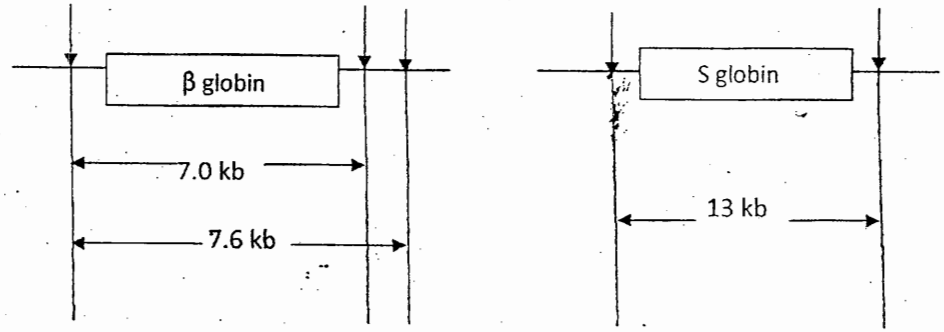


Fig: | represents Hpa I sites which produces 7.0 Kb or 7.6 Kb fragment with DNA from persons with normal β -globin gene whereas 13 Kb fragment with DNA from persons with sickle cell mutation.

VNTR (Variable Number Tandem Repeat): This is also known as hypervariable region in which a core sequence of 10-15 base-pairs is repeated. Such hypervariable regions are distributed throughout the genome, its number and distribution varying in different individuals. Like other genes, VNTRs are also inherited in Mendelian fashion; hence progeny tend to inherit a particular pattern from their parents. If DNA is cleaved, VNTRs go along with fragments of different sizes in different individuals and when probed with complementary regions, give different pattern. Besides being useful in DNA finger printing, VNTRs are also linked to certain allele and presence of a specific size of DNA fragment with VNTR is indicative of presence of that allele.

CA Repeats: Certain VNTRs are small, consisting of repeats of two bases – CA, GT etc. Human Genome contains 50 thousand to 1 lakh blocks of such repeats. The CA repeats have also been found linked to certain disease locus.

Common Genetic disorders of humans

Though there are hundreds of genetic disorders affecting humans, we limit ourselves to a few common ones which, because of its more common presence, is widely discussed.

1. Sickle-cell anaemia : This is probably the commonest of the genetic ailments discussed in anthropology. Our haemoglobin consists of four protein chains Two α -chains and two β chains. The α-chain is made up of 141 amino acid residues where as β-chains are made up of 146 amino acid residues.

In normal β-chain, the aminoacid at the 6th place is glutamic acid which is replaced by valine in sickle cell anaemia. It is because of a point mutation that changes the codon GAG (for glutamic acid) to GTG (valine), adenine being replaced by thymine.

Because of this change in β-chain the solubility of the Hb is reduced that leads to its precipitation and change of shape of RBC from round to sickle-shape. Sickling of RBC has 3 effects—

1. Destruction of RBC by spleen, resulting into anaemia. It leads to enlargement of spleen.
2. Poor vascularization because sickle-shaped RBC is unable to pass through capillaries by squeezing action.
3. Increased viscosity and clumping of RBC is perhaps the most dangerous effect in which thrombosis occurs in various parts of body such as brain (paralysis), heart (heart failure), kidney (kidney failure), gut (abdominal pain), lungs (pneumonia), extremities (limb pain, rheumatism) etc. Such wide and multiple effects resulting from a single basic cause is referred to as **pleiotropic effect**. The genetic picture is recessive homozygosis (ss).

In heterozygotes(Ss), the condition that results is called sicke-cell trait in which there is mild sickling of RBC. The capillary flow is possible though with reduced efficiency and there is no clumping effect. The condition confers resistance against malaria, a mosquito-borne disease endemic in various parts of Africa end south Asia. Because of this selective advantage to the heterozygotes, the gene for sickle cell anaemia continues in the populations.

2. Thalassaemia : It is a genetic disords in which there is no production of Hb chains and hence it can be either α-thalassaemia, or β-thalassaemia.

a. α-thalassaemia - It is of two types - In first type, there is no production of α--chains (β-chains form tetramer), This results in death of foetus in uterus (hydrops foetalis). In another type, there are produced some chains but still β chains outnumber and form tetramer which precipitate on RBC membrane, causing haemolysis of RBC. It has been found that α-thalassaemia results due to deletion in chromosome 16.

b. β-thalassaemia : It is also of two type — B+ thalassaemia in which some β–chains are produced, and Bo thalassaemia in which no β-chain is produced. α–chains precipitate on RBC membrane, causing haemolysis of RBC. Thus, thalassaemia can be major or minor, depending upon severity of the condition. Thalassaemia major requires transfusions from early age and results in death in late teens or early twenties, mostly because of complications of iron overload resulting from repeated transfusions. Thalassaemia minor has milder effect and permits longer longevity.

There is no single genetic reason of β-thalassaemia as it results due to various single base changes, insertions, deletions in β-globin gene on chromosome 11, both inside and in the flanking region. It is supposed that changes may affect splicing of exons, recreating non-sense codons.

3. Phenylketonuria :

It is an autosomal recessive disease in which enzyme phenylalanine hydroxylase, required for metabolism and conversion of phenylalanine to tyrosine, is absent. Phenylalanine accumulates and Impaired features include severe mental retardation, reduction of melanin hence fair skin, eczema and epilepsy. Childre born to phenylketonuric mothers are also mentally retarded because mother are unable to pass sufficient tyrosine to the growing feotus. The condition als results when certain co-factors needed for the function of enzyme phenylalanir hydroxylase is absent.

4. Alkaptonuria : In Alkaptonuria, there is a block in the breakdown of homoge tisic acid, a metabolite of tyrosine. Homogentisic acid accumulates and is e creted in the urine giving it a dark colour upon exposure to air. Deposition black pigment in Joints leads to arthritis in later stages of life. This is also due autosomal recessive mutations.

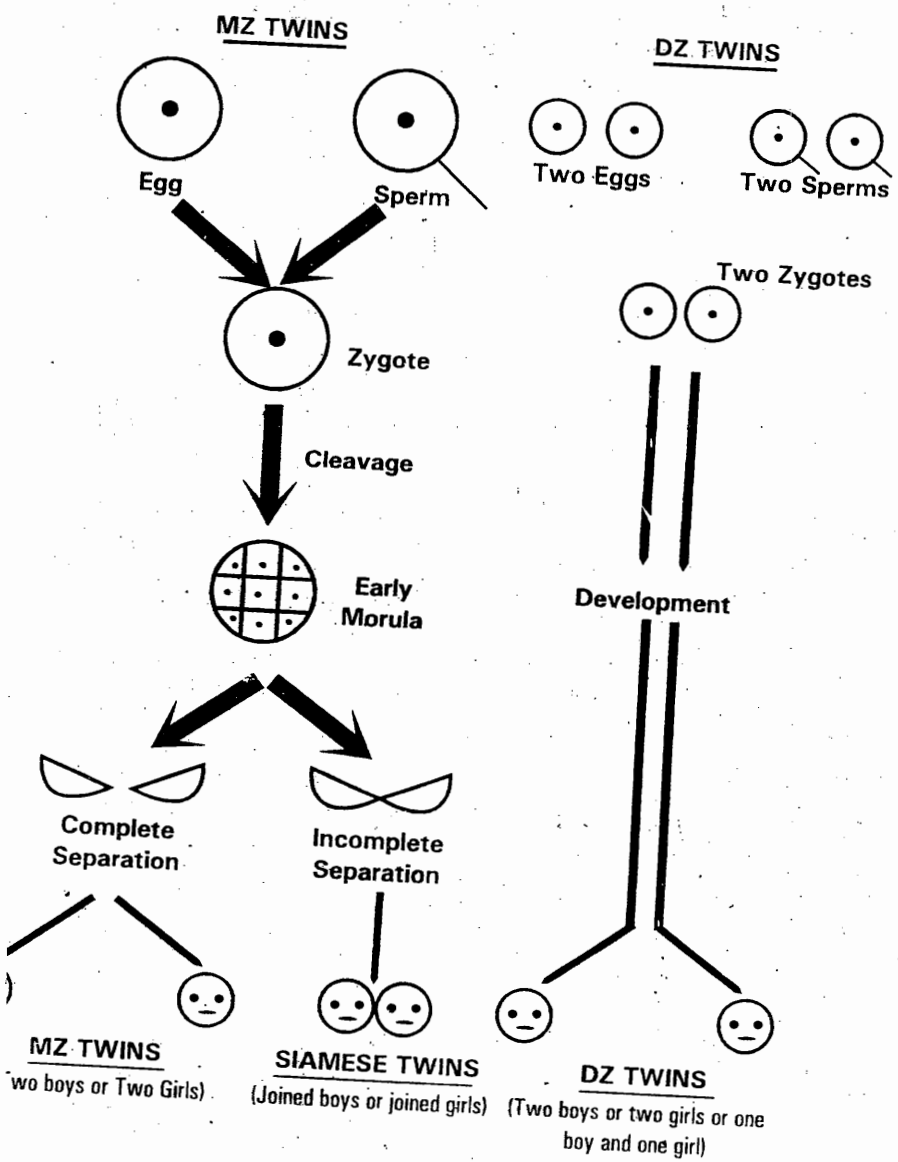
5. Albinism — There is a lack of melanin pigment in the skin, hair, iris etc. T condition results due to absence of tyrosinase which converts tyrosine into me nin. The condition results in poor vision.

6. Galactosaemia : The condition results due to absence of an enzyme to m tabolize a sugar, galactose. The same occurs with lactose, a disaccharide, wh is broken down into galactose. Hence the condition results in lactose intoleran The condition manifests in the early life by failure to digest milk or milk powc Such infants are given lactose-free and galactose- free milk which is comm cially available. This is also an autosomal recessive disorder.

7. Familial hypercholesterolaemia : This is an autosomal dominant disorde which normal metabolism of fat is affected. Elevated cholesterol level leads ischaemic heart disease. In addition, some lipids are deposited under the ski some places, a condition called xanthomata.

8. Cystic fibrosis : This is also an autosomal recessive disorder in which th is formation of thick mucus in lungs and elswhere. The mucus is so thick th blocks the respiratory passage, causing death.

TWINS



Genetics Of Twins: Mz And Dz Twins

Twins are of two types : Dizygotic, two-egg, or fraternal twins result when two ova are produced at about the same time and both are fertilized. Monozygotic, one-egg, or identical twins result from the splitting of the zygote at an early stage. Monozygotic twins are, of course, genetically identical barring somatic mutation. Dizygotic twins are genetically no more similar than ordinary sibs.

Monozygotic twins are either both male or both female. Dizygotic twins are of like sex or of unlike sex in approximately equal frequency. All twins of unlike sex are dizygotic, but twins of like sex may be of either type.

In a population, DZ twins have equal probability of being like sex or unlike sex. If n is the number of twins of unlike sex in a random series, then the same number n of the twins of like sex are also DZ. The remainder of the twins of like sex are MZ.

Monozygotic twinning shows almost no effect from the mother's age. Dizygotic twinning on the other hand, is more frequent in older mothers. The frequency of twinning varies in different ethnic stocks, even when allowance is made for variation in the average age of mothers. In the 1950s, whites in the United States had about 10 twin pregnancies per 1,000 and nonwhites (mainly Negroes) had over 135 twin pregnancies per 1000. Almost all the excess twin pregnancies in the nonwhites were dizygotic. There are quite a few evidences which show that it has a genetic basis. For example, the racial differences in the frequency of dizygotic twinning may be evidence for genetic factors. That twinning shows a familial aggregation is further evidence of genetic factors. According to Mc Cusik the gene for twinning (DZ) is expressed only in females. Males of such families may transmit this propensity to their daughters.

Environmental factors probable also influence the rate of twinning, since the same ethnic stocks in different habitats may show different rates. Furthermore, there was a significant decline in the rate of twinning in white people in the United States in the period from 1922 to 1958. In Sweden there has been a decline in twinning over the last two centuries. Similar fluctuation have been found in other countries.

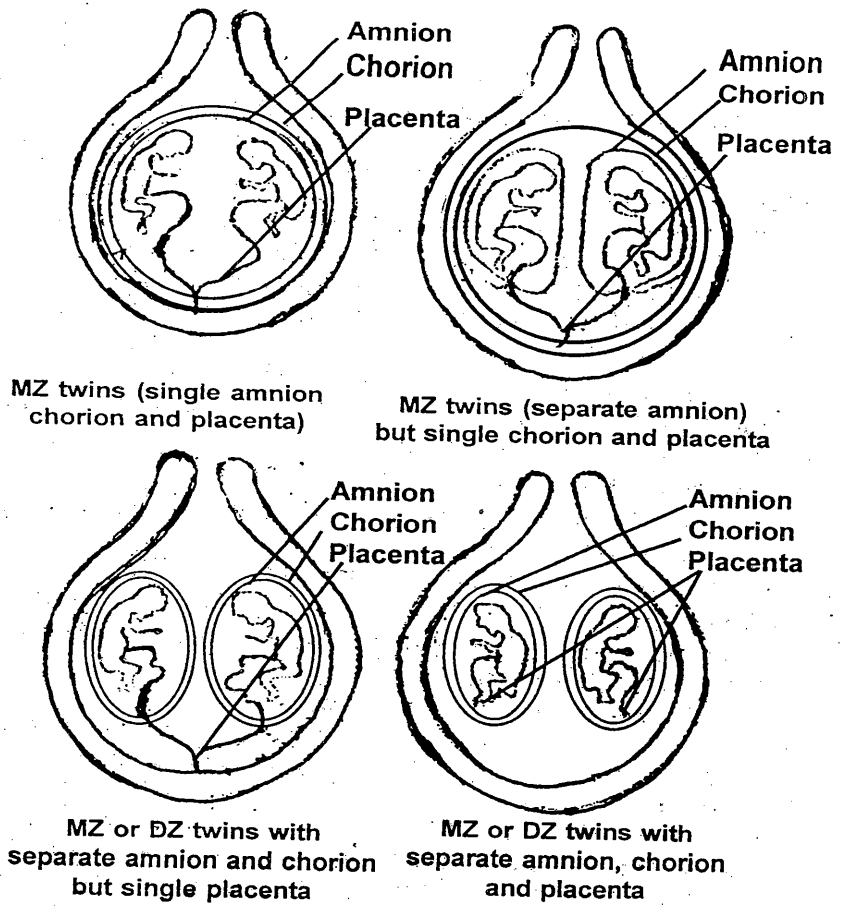


Fig. : Diagnosis of Zygosity on the basis of amnion, chorion and placenta

Chang And Eng - The Siamese Twins.

Chang and Eng were two Siamese twin boys born to a Chinese father and a Siamese mother in Thailand in 1811. Their mother refused to get them separated hence the two survived to maturity, tied by a strip of tissue extending from below their sternum down to the navel. Both displayed variations in temperament: Chang was irritable where as Eng calm. Both married at the age of 42 and Chang had 10 children and Eng 12. Chang was drunkard and it sometimes resulted in exchange of hot words and blows. They set up separate homes and used to spend half of a week at one place and another half at another place. At the age of 63, Chang contracted pneumonia and died. Within a few hours his twin Eng, also died. When postmortem was conducted on them the strip of tissue that joined them was found to contain liver tissue.

Diagnosis of Zygosity

It is, indeed, difficult to diagnose whether the twins of same sex having similar looks are MZ or DZ twins. There exists several methods to diagnose zygosity which can be classified as follows :

1. Placental Method : Distribution of placenta and membrane can help to some extent in the diagnosis of Zygosity though absolute determination is difficult. The developing zygote invests itself in two membranes, an inner(the amnion) and an outer (the chorion). In the case of dizygotic (DZ) twins each twin has completely separate membranes. Their placenta is generally separate but it may get fused.

In case of monozygotic twins (MZ twins) the nature of foetal membranes and extent of placenta vary. Monozygotic twins can be anyone of four types: (1) the zygote may be divided at first cleavage; (2) two inner cell masses may develop; (3) a single cell mass may be formed which subsequently divides; or (4) the division may be particularly late and incomplete, resulting in conjoined twins ("Siamese twin").The placenta in first condition is of type a or type b. If two cell masses develop, the placenta is of type c. If one cell mass undergoes splitting the placenta is of type d. A significant proportion of monozygotic twins also have two chorions and two amnions, and some have two placentas. All monochorionic twins are monozygotic, and about 70 percent of monozygotic twins have one chorion. Only in these cases is an unequivocal diagnosis of monozygosity possible on the basis of placental findings. The four types of placentation shown in Fig. are follows : (a) diamniotic dichorionic separate; (b) diamniotic dichorionic fused; (c) diamniotic monochorionic; and (d) monoamniotic monochorionic.

2. The Similarity Method : Individual variations have been found in many genetic traits e.g.. blood groups, serum proteins, HL-A system, isozymes, ridge counts etc. The twins can be evaluated for these features. MZ (Identical twins) would have the identical features on all the above listed criteria whereas DZ twins may differ. Morphologic features such as eye colour, nose form, ear form etc. are less reliable. For the evaluation of HL-A, skin grafts are to be made. Only MZ twins accept each other's graft.

3. Statistical Approach : If the twins are phenotypically

similar the chances that it is DZ or MZ can be statistically estimated. The chances of occurrence of phenotypic traits for the both DZ and MZ twins can be calculated if genotype of the parents is known. Also, if the frequency of zygosity is known in the population, the probability of DZ and MZ can be worked out.

Example :

Calculate Zygosity of a twin -

(a) Both boys (b) Both MM (c) Parents MM and MN

Prior probability of MZ in population = 3/10

" " DZ " " = 7/10

Conditional Prob of MZ $= \frac{3}{10} \times 1 \times 1 = \frac{3}{10}$

" " DZ $= \frac{7}{10} \times \frac{1}{2} \times \frac{1}{2} = \frac{7}{40}$

(Because DZ can be MM & MN and of opposite sex)

Relative probability of MZ $= \frac{3}{10} : \frac{7}{40} = \frac{120}{70} = \frac{12}{7}$

Posterior probability of MZ $= \frac{\text{Relative probability of MZ}}{\text{Joint probability of both}}$

$= \frac{12}{12+7} = \frac{12}{19} = 0.63$ Approx

Below is given a table which shows parental genotype and the probability of phenotype in DZ and MZ twins. Twins A and B belong to an English family where chance of DZ twins of same sex is 0.35 and MZ 0.30.

Table : Showing parental genotypes and probability of certain characters in MZ and DZ twins.

parental genotypes	Chance of like-sex dizygotic twins 0.35	Chance of monozygotic twins 0.30
$A_2O \times OO$	Chance of dizygotic twins in this family having same	Chance of monozygotic twins in this family having same
Ms/Ns x Ms/Ms	ABO group (A2O) 0.50	ABO group (A_2O) 1.00
$P_1P_2 \times P_1P_2$	MNs groups (Ms/Ms) 0.50	MNs groups (Ms/Ms) 1.00
CDe/cde x CDe/cde	P groups (P_2P_2) 0.25	P groups (P_2P_2) 1.00
Kk x Kk	Rh groups (CDe/cde) 0.25	Rh groups (CDe/cde) 1.00
FybFyb x FybFyb	Kell groups (KK) 0.25	Kell groups (KK) 1.00
JKaJKb x JKb JKb	Duffy groups (F_ybF_yb) 0.50	Duffy groups (F_ybF_yb) 1.00
	Kidd groups (JK^bJK^b) 0.50	Kidd groups (JK^bJK^b) 1.00
	Combined chance = product of separate chances 0.00034	0.30

In England where the family lived, about 35 percent of twins are dizygotic and of like sex. The chance (prior probability) that twin B would be the same sex as A is then 0.35. The mating A_2OxOO will produce 50 percent A_2 and 50 percent O children. The chance (conditional probability) of the second being A_2 like the first, even though they are dizygotic, is 0.50. The mating Kk X Kk will produce 25 percent KK offspring. The chance that the second twin will be KK, even if they are dizygotic, is then 0.25. The other conditional probabilities are worked out in Table. The combined chance (joint probability) is the product of the separate chances : for dizygosity 0.00034 and for monozygosity 0.30. The posterior probability of monozygosity is

$$\frac{0.30}{0.30+0.00034} = 0.9989$$

and the probability of dizygosity is

$$\frac{0.00034}{0.30+0.00034} = 0.0011$$

4. DNA Fingerprinting : We know that restriction endonuclease are very much site-specific and hence by using several types of restriction enzymes distinct RFLPs can be found. The RFLP mapping for the MZ (identical twins) will be exactly similar,though it may differ for DZ twins. Similarly VNTR variations in the hyper-variable region or CA repeats variation can be found out for zygosity diagnosis. Such variations of DNA from person to person can be easily found out, though it is exactly similar for MZ twins.

5. Skin Grafting : MZ twins accept skin graft of one another but DZ twins do not accept

Twins And Heritability Esti .tes

Heritability is never easy to measure, it is particularly difficult to estimate in human populations. There are several reasons for this, the most obvious of which is that people are not experimental animals that can be selectively mated, highly inbred, or raised under strictly controlled conditions. A less obvious reason why heritability is difficult (in fact, impossible) to determine accurately in human populations is that it depends, not only on genes and environment, but on the interaction between the two.

The Formula for calculation of heritability estimate is - $H = \frac{V_G}{V_T} = \frac{V_G}{V_G + V_E}$

Where V_G equals the genetic component, V_E is the environmental component and V_T is total variability due to heredity and environment

There are two methods of heritability-estimate by twins-

(1) Concordance-discordance study

(2) Rearing Studies

(1) Concordance-discordance study: both MZ DZ twins are observed and their extent of concordance known. A high concordance rate for both MZ and DZ indicate environmental determination whereas a high concordance rate only for MZ and a low concordance rate for DZ indicate more genetic determination of a character

The formula used for heritability estimate is —

$$\frac{Conc_{MZ} - Conc_{DZ}}{100 - Conc_{DZ}}$$

Characters	MZ (Conc)	DZ (Conc)
Sitting up	82%	76%
Beginning of walk	68%	31%
Hair colour	89%	22%
Eye colour	99.6%	28%
Blood pressure	63%	36%
Diabetes mellitus	65%	18%

For beginning of walk—

$$\frac{68 - 31}{100 - 31} = \frac{37}{69} = 0.54$$

The concordance rate for sitting up is high for both MZ and DZ which indicate than character is less genetically controlled. But concordance rate for beginning of walk is high in MZ than DZ hence indicate strong genetic basis.

(To find out whether MZ and DZ concordance rate differ significantly, we perform chi-square test. For example,

	MZ	DZ	Total
Conc	82(a)	44(b)	126
Disc	16(c)	22(d)	38
Total	98	66	164

$$\text{Chi-Square} = \frac{[(a.d-b.c)-1/2\ N]^2 \cdot N}{(a+b)\ (a+c)\ (c+d)\ (b+d)}$$

$$= \frac{[(1804-704)-82]^2 \cdot 164}{(126)\ (98)\ (38)\ (66)}$$

$$= 5.4$$

Calculated value 5.4 is much higher than Table value of chi-square at 0.5% level of significance at one degree of freedom hence difference between MZ conc andDZ conc is significant.)

(2) Rearing studies

It should be noted that concordance - discordance study is performed to find out heritability of discrete character. **Rearing studies** are performed to find out heritability of continuous traits such as height, intelligence, etc. Since rearing studies are for continuous traits, pair difference (X) is measured (for example, for IQ 110-102=8) and then mean pair difference (X) is calculated. Variance is calculated by the formula —

$$\text{Variance} = \frac{\sum (X - X)^2}{N}$$

Heritability is known by the formula —

$$\frac{V_G}{V_Q + V_E} = \frac{V_{DZ_{RA}} - V_{MZ_{RA}}}{(V_{DZ_{RA}} - V_{MZ_{RA}}) + V_{MZ_{RA}}} = \frac{V_{DZ_{RA}} - V_{MZ_{RA}}}{V_{DZ_{RA}}}$$

$V_{DZ_{RA}}$ gives total variance, $V_{MZ_{RA}}$ gives enviromental variance and their difference gives genetic variance. If $V_{MZ_{RA}}$ is small, the ratio will be equal to 1 and character more genetic. If it is large, the ratio moves toward zero and character is more environmental.

Is Estimates Of Heritability By Twin Method Justified ? : Twin investigations have played a major role in the analysis of a number of human traits. Many of our behavioural and intelligence data is based on twin studies. It's validity, however, has been questioned.

1. It neither specifies the genetic component nor the environment component. There is no information regarding nature of genes, its location, combination or behaviour. Likewise, there is no recognition of parameters of environment - physical, chemical biological or combined. Heredity and environment is treated as aggregates.

2. Our assumption that MZ twins are exactly identical is fallacious. Evidences show that MZ twins differ in size and vigour, and in many cases, one of the MZ twins dies because of hampered growth either due to decreased placental supply or some other reasons. While estimating heritability such factors must not be forgotten.

3. The heritability estimates cannot be applied in certain cases e.g. in estimating heritability of the tumours. Intrauterine development may be influencing development of some congenital malformations. Studies show low concordance rate in MZ twins. Hence such studies may not reflect a true picture of heritability in such cases.

4. In certain cases there can be mistaken identity of genetic and environmental factors. For example, MZ twins being reared together may attract attention of fellow persons at school or home. This aspect of environment may cause variations in MZ twins which may be presumed to be emanating from the genetic reasons. However such factors of environment will be missing when MZ twins are reared apart.

5. In estimation of heritability it is supposed that total phenotypic effect is the sum total of genetic and environmental effects i.e. $H = \frac{V_g}{V_G + V_E}$

However, it will be accepted that different genotypes react differently to the same environment producing a non-additive or interactive situation. Also, while calculating concordance among MZ twins, they may not be randomly distributed over a range of environmental variations and may seek out certain selected environments.

6. The justifiability of studies conducted on twins and its extrapolation to single persons in the population has been questioned by some.
7. Environment of the twins may not be representative of the environment of the population in general.
8. Such studies do not consider inter-population variation. A character may be more genetic in one population and vice versa.
9. Heritability estimate of complex character such as IQ and behaviour is difficult because of complex interaction of heredity and environment.

Problem : Find out heritability of IQ on the basis of twin-study.

Obs (N)	MZ reared apart (Estimate of IQ)			Mean pair Diff ($\bar{x}$)	$(X-\bar{x})$	$(X-\bar{x})^2$
	MZ_1	MZ_2	Pair Diff (x)			
1	90	95	5	30/10 =3	+2	4
2	94	91	3		0	0
3	102	105	3		0	0
4	98	96	2		-1	1
5	90	94	4		+1	1
6	112	110	2		-1	1
7	108	105	3		0	0
8.	104	102	2		-1	1
9	100	97	3		0	0
10	91	94	3		0	0

ariance = $(X-\bar{X})^2 / N$

$MZ_{RA} = 8/10 = 0.8$

imilarly VDZ_{RA} can be calculated. Suppose it is 2.4. Using the formula or calculation of heritability: $= (VDZ_{RA} - VMZ_{RA}) / VDZ_{RA}$

$= (2.4-0.8) / 2.4 = 1.6 / 2.4 = 0.62$

ince it is nearer to 1 hence IQ has greater genetic component than nvironmental.

f VDZ_{RA} had been a lower value say 1.2 then heritability would be:

1.2-0.8) / 1.2 = 0.4/1.2 = 4/12 = 0.33.

ince it is nearer to zero hence IQ would have greater environmental omponent.

CHROMOSOMAL ABNORMALITIES

Man is inflicted by a certain set of abnormal conditions if he has chromosomal number-and structure (Karyotpye) deviating from he usual 46,xx for females and 46, xy for males. A brief list with primary genetic conditions is as follows :

SYNDROMES	GENETIC PICTURE	LEADING SYMPTOMS
1. Down's Syndrome	3 copies of chromosome 21	Mangolian features, short stubby hands with simian cleft, low blood pressure at birth, mental retardation - SUBLETHAL
2. Patau's Syndrome	3 copies of chormosome 13	Cleft palate and lip, flexed and overlapped fingers - SUBLETHAL
3. Edward's syndrome	3 copies of chromosome 18	small triangular mouth, flexed finger - SUBLETHAL
4. Turner's Syndrome	One x in female instead of two x.	Short stature, sexual infantilism, webbed neck, cubitus valgus, streak gonad, Normal life expectancy
5. Klinefelter's syndrome	two X in male instead of one x	Long legged male with infantile testes (no sperm) Normal life expectancy
6. Cri-du-chat syndrome	Break in the short arm of chromosome 5	Cry like a weak mewing of cat. SUBLETHAL

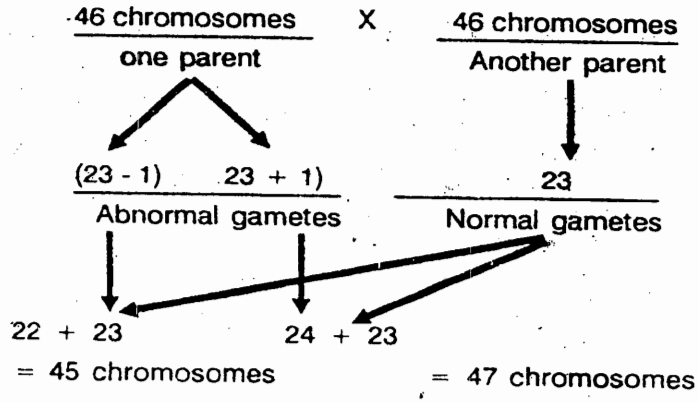
All the six syndromes can be arranged into two groups on the basis of life-expectancy of the patient :

1. **Sub-lethal Group :** Down's, Patau's, Edward's and Cri-du-chat syndrome share a basic similarity in the sense that only these are the four syndromes that are sub-lethal. Children afflicted by the syndromes are often born and survive from a few weeks to one year or, in rare cases, more than this.

2. **Normal Compatible Group :** Persons suffering from Turner's and Klinefelter's syndrome have infantile gonad (ovary and testes in female and males respectively) and thus Sterile. Nevertheless, they have normal life-expectancy.

Polyploidy Is The Cause Of Difference In Chromosome Number : Deviation in the number of chromosomes is called polyploidy. Since the deviation can involve both the autosomes and sex-chromosomes, so the polyploids can be both autosomal polyploid and sex chromosome polyploid. There can be loss of one chromosome, resulting in monosomic; gain of one chromosome resulting in trisomic. Thus, monosomics have all the diploid chromosomes minus one (2n-1) and trisomics have all the diploid chromosomes plus one extra chromosome (2n + 1). In case of humans, thus, a monosomic will have 45 chromosomes and a trisomic will have 47 chromosomes.

Non Disjunction Of Chromosomes Causes Polyploidy : During gamete formation, chromosome number is halved so that both male and female gamete receive half their normal diploid number of chromosomes. For separation of chromosomes, several chromosomal fibres are formed, some push the chromosomes and others pull the chromosomes to opposite poles. Sometimes, it may happen that the two chromosomes fail to separate and one gamete receive both and another gamete none. Thus if in female human being chromosome 21 failed to separate, eggs containing 23 normal number and one extra 21 will be formed (23 + extra 21). If such egg is fertilized by a normal sperm, trisomy for 21 will result.



Non disjunction manifest with increasing maternal age : It is mostly maternal gametes that show abnormality of chromosome number. Though there are some other suggestions, the most acceptable maintains that with increasing maternal age the spindle fibres separating the chromosomes at the time of cell

division are weakening. All the gametes have originated in the ovary by the time a female is born and her gametes are stayed in the suspended meiotic prophase stage. One egg is shed every month, and non of them arise after birth. With increasing maternal age, the spindle fibres separating chromosomes gradually weaken so that likelihood of an abnormality in distribution of chromosome increases. A female ovulating at the age of 20 years has ovum which is only 20 years old; the age of ovum of a female ovulating at the age of 40 is 20 years older than the first. In the latter case, the ovum has stayed in the ovary for extra 20 years. Spindle fibres of the two ova, naturally, cannot be of same strength since these fibres are exposed to a number of chemicals in the egg environment. Males, on the other hand, rarely show disjunction of chromosome because sperms are formed on the regular basis, being formed constantly and replacing older ones. The highest age of sperm formation by males medically certified is 94 years. Since sperms are not stored for any considerable period of time in the testes for means of fertilization, hence disjunction of chromosome is comparatively a rare phenomenon with male gametes. A paradoxical situation exists in actual clinical practice where it is found that many registered cases have mothers of younger ages. It is because fertility is greater in younger mothers and hence more patients with such syndromes are born to them.

Polyploidy Of Autosomes Are More Harmful : *i. Trisomy :* Autosomes carry a number of genes that are expressed in cell. Hence any abnormal conditions related to autosomes are likely to produce many harmful and deleterious conditions. Trisomy of autosomes such as those of chromosome 21, 13 & 18 resulting in Down's syndrome, Patau's syndrome and Edward's syndrome is well documented. Trisomy of 21 is tolerated more but those of 18 and 13 are more harmful and results in death of its possessor soon after birth. It is because chromosome 21 is much smaller than chromosome 18 and 13 and contain lesser number of genes expressed in cell. Trisomy, though does not result in absence of any gene-product, it sure result in their imbalances. Since chromosome 21 is smaller, there is imbalance of lesser number of gene products hence it is tolerated for longer period. Chromosome 13 and 18 are larger hence there is imbalance of large number of gene products hence these are not tolerated resulting in immediate death of its possessor.

ii. Monosomy : Monosomy of autosomes is even less tolerated. As autosomes contain many genes, loss of an autosome

is most likely to result in absence of a number of gene-products without which survival is never a distinct possibility. Hence, foetuses with monosomy of autosomes are aborted during embryonic development. It has been claimed that as high as 40% of all abortions in the initial stages result due to autosomal monosomy.

Polyploidy Of Sex-Chromosomes Is More Tolerated : In Turner's syndrome, there is a monosomy of X, the patients having only one X so that their total number of chromosome is 45 with only one X (45,X). Why is monosomy of X tolerated and monosomy of autosomes not tolerated? Answer to this question lies in the fact that out of the two X-chromosomes in female, one remains inactivated in all the cells of female so that in effect there is only one X chromosome functioning. If females have only one X chromosome, no inactivation of X-chromosome occurs. Hence, in both the cases whether females have one or two X-chromosomes, only one X chromosome is functional. The inactivated X-chromosome is called Barr-body after Barr and Bertram who discovered it. There is, however, a small portion of inactivated X chromosome (Barr body) that functions. This small portion of inactivated X chromosome is essential for normal development of females. Since this small portion of X is absent in females with 45 X, abnormal conditions develop.

Behaviour of Y-chromosome is different from X and autosomes. In males, the sex-chromosomes are XY. Y-chromosome is never in paired condition in normal individuals hence there is always a condition similar to monosomy. Disomy of Y can result if two Y chromosome during gamete formation fail to separate so that one gamete receives both the Y-chromosomes. Disomy of Y, such as XYY, interferes in the growth and development only in a limited way. It is because of the reason that Y-chromosome contains only limited number of genes expressed in cell. Majority of its DNA is non-functional and made up of repetitive sequences.

1. Down Syndrome

a. Clinical Features : The syndrome is also referred to as "Mongolism" or "Mongolian idiocy" because a number of physical traits such as epicanthic fold etc. developing in the syndrome find pseudo resemblances with typical Mongolian features. The syndrome is better named after Langdon Down.

1. The infant with Down's syndrome is usually flaccid, quiet

and does not cry much in the newborn period. The maxilla is reduced with recessed appearance and protrusion of the tongue.

Persons affected have short stature, broad head and round face, epicanthic fold on the eye-lid, and wide nostrils.

Patients have short and stubby hands with a typical simian cleft on the palm. It is a line on the palm of the hand running from one side to the other, found in all great apes. Because of shortened palm, the line intersecting base of the index and little fingers meet to form large angles (large ATD angle). Such angle in normal persons is small.

The palm of the patient shows : (1) the triradius near the centre, (2) absence of pattern in the thenar area, (3) a digital loop between digits III and IV. (4) a radial loop on tip of digit IV and (5) ulnar loops on all other digits. Also, the sole of the patient shows a narrow digital loop or absence of pattern in the hallucal area.

3. Persons affected show various degrees of mental retardation and sub-normal intelligence (hence named Mongolian idiocy earlier)

4. Blood-pressure at the time of birth is severely low.

According to Rasko and Downes (1995) the most consistent traits in the syndrome are various degrees of mental retardation and low blood-pressure.

6. Frequency : Frequency of Down's syndrome is 1/700 live births in humans. However, its frequency among the caucasoid is increased upto 3/200 of all live births. Why the syndrome should have greater frequency in caucasoid is not known. One of the reasons, probably, may be their marriage in advanced stage when such mothers are liable to chromosomal non-disjunctions. Nearly half of liveborn patients are dead by the end of the first year of life. The principal causes of death are respiratory infections and congenital heart malformations. There is a 10 to 20 fold increase in the incidence of leukaemia among children with Down's syndrome when compared with normal infants and children of comparable age. This is, however, not a established case.

C. Genetic Mechanisms Of Causation Of Down's Syndrome: There are two genetic mechanisms of causation of Down's syndrome, though both result in presence of three copies of chromosome - 21. Accordingly, Down's syndrome is divided into nondisjunctional Down's syndrome and translocational Down's Syndrome.

i. Non-Disjunctional Down's Syndrome : It has been discussed earlier in the chapter that chromosomes sometime fail to separate, thus one of the daughter cells get both the chromosomes and the another gets none. In case of Down's syndrome, failure of chromosomal separation occurs at the stage of maternal gamete formation, resulting in eggs with extra 21 chromosome. When such eggs are fertilized with normal sperm, Down's syndrome is caused.

Ovum with 23 + 21st Chromosomes **X** Normal sperm with 23 Chromosomes

↓

Down's Syndrome
46 + Extra 21

Alternatively, Down's syndrome can be caused by non-disjunction of chromosome 21 at the time of early cleavage divisions of zygote. This results in two types of daughter cells-one with only one chromosome 21 and the other with three chromosome 21. The cell with only one chromosome 21 dies.

Normal ovum **X** Normal sperm

↓

Normal Zygote

↓

Cleavage division

↙ ↘

Cell with one chromosome 21 → Dies

Cell with three chromosome 21 → Multiplies

However, evidences are that the non-disjunction of chromosome is more frequent at female gametic stage than the cleavage stage.

ii. Translocational Down's Syndrome : Translocation is a process in which a part or whole of a chromosome is attached with some non-homologous chromosome. (Non-homologous is important because exchange of segments between homologous

chromosomes is referred to as crossing-over).

Translocation involving chromosome 21 and either chromosome 14 or chromosome 15 is another mechanism for Down's syndrome. Such patients are found to have 46 chromosomes with two normal chromosomes 21 one normal 14 (or 15) and a large chromosome resulting due to fusion of 14 (or 15) and a 21. This mechanism of Down's syndrome involves in reality three doses of chromosome - 21 and is virtually indistinguishable phenotypically from more usual trisomy 21. When parents of such translocational Down's syndrome are examined, they reveal a unique chromosomal pattern. They are normal but have 45 chromosomes one 21-chromosome, one normal 14 (or 15) and a large translocated 21 on the 14 (or 15). The parent is normal because the genetic material is present almost in full and certainly not in excess amounts.

It has been found that Down's syndrome occurs in less than one fifth of the children of females who carry the 14-21 translocation. It can be explained by the variable type of gametes produced by the carrier female because of behaviour of translocated chromosomes 14 and 21.

d. Location Of Gene In Down's Syndrome : Much work has been done to locate the genes on the 21st chromosome that produces traits in the Down's Syndrome. Various lengths of chromosome 21 are translocated to different chromosomes and in such cases traits developed can be studied and mapped on the region of 21 chromosome. Several such 21 translocations have been studied and it has been found that the genes causing Down's syndrome lie on the long arm (=q) of the chromosome-21. Most genes are present near the centromere (= the region with which spindle fibres are attached) on q-arm of 21st chromosome. The genes lying at the region of 21 q 22.1 and 21q 22-2 cause mental retardation (21 = the number of chromosome, q = arm, 22.1 and 22.2 the regions). The genes involved in heart problems are lying below the 21q 22.2 region. It is not known, however, that which genes are involved. (Rasko and Downs's 1995)

2. Patau's Syndrome

Patau and colleagues(1960) reported a female infant with multiple congenital defects who showed 47 chromosomes with an extra chromosome 13.

a. Clinical Features : When one first examines a patient with syndrome, the most striking abnormalities are the cleft palate and lip and the flexion and overlapping fingers. Other frequently found changes are eye defects, polydactyly, and congenital heart lesions. The neutrophils show sessile projections in the nuclei, characteristic of syndrome. There is a persistent elevation of HbF and a significant decrease of HbA_2 concentration during the first few months of life. All patients are mentally retarded, with gross malformation of brain.

As with Down's syndrome and trisomy 18 syndrome, the patients with the Patau's syndrome have a markedly shortened life expectancy. The mean survival time is 131.7 days.

b. Frequency and effect of maternal age: Patau's syndrome occurs about 1 in 2,200 live births. The mean maternal age is 32.4 years. This would suggest that there is a moderate maternal age effect in the Patau's syndrome. However, there seems to be no age effect in translocation cases. This condition is in agreement with Down's and Edward's syndrome in which there is no maternal age effect in translocation cases.

3. Edward's Syndrome (Trisomy 18)

Edwards and colleagues (1960) described a female child with multiple congenital abnormalities in whom post mortem cytologic studies revealed an extra chromosome No.18. There are cases of translocation also.

a. Clinical Features : The two most striking and diagnostic findings are small triangular mouths and flexed fingers. Other clinical features include low-set malformed ears, congenital heart defects, abnormal occiput, malrotation of intestines. The fingerprints show arches on six or more fingers. Presence of more than 3 simple arches out of 10 is a rare finding in normal persons.Infants with trisomy 18 syndrome have a shortened life expectancy. The mean survival time is 102 days, with approximately half of the total surviving for 2 months, one third for 3 months, and only 1-2 per cent surviving from birth to 10 years. Females with this syndrome appear to survive much better than males.

b. Frequency And Effect Of Maternal Age : Epidemiological studies show that the frequency of the trisomy 18 syndrome is approximately 1 in 4500 births and is, therefore, somewhat more uncommon than that of Down's syndrome, which

is 1 in 700 live births, and the Patau's syndrome, which is 1 in 2200 live births. The mean maternal age among mothers of trisomy 18 patients is 32.8 years; this indicates that there is a moderate maternal age effect but that it is not as great as in Down's syndrome.

4. Cri-Du-Chat Syndrome

Lejeune (1963)-reported syndrome associated with the deletion of part of the short arm in chromosome - 5. A few families shows balanced translocation : parent who is normal but some of his offspring inherit deleted chromosome and are affected.

a. Clinical Features : Almost all of the patients with this syndrome have a peculiar weak cry which closely resembles the mewing of cat. The three most reliable clinical findings are microcephaly, downward, outward slant to the palpebral fissures of eye and excessively wide-spaced eyes. While almost all patients fail to thrive, a few that survive and live long have severe mental retardation.

Small Head

Genetic Reasons Of Frequent Occurrence Of Down's, Patau's And Edward's Syndrome : Trisomy of 21-chromosome is most frequent of all trisomies, followed by trisomy of 18 and 13. Trisomy of other chromosomes are also found but they are aborted during foetal stage and hence other trisomies are not found in the population. It has been already stated that all trisomics have problems due to the description of their gene-numbers. Why do trisomics of 21,18 and 13 have greater chances of survival them other trisomics ? The answer can be found by staining the human chromosome with Giema stain. It produces a characteristic banding pattern on the chromosome, staining the functional genes engaged in synthetic activity. It can be found out that 13,18 and 21 chromosomes involved in Patau's Edward's and Down's syndrome have the smallest amount of gene rich regions engaged in synthetic activity. Description of normal gene-numbers is, thus, lowest in such cases.

Sex-Chromosome Abnormalities

Human male and female differ in X and Y chromosomes - females have XX and males XY. The Y chromosome contains the important male determinants because testicular differentiation does not occur in its absence. The development of the human reproductive system, therefore, depends first on the sex

chromosome constitution of the fertilized egg. If the father contributes a Y, the undifferentiated embryonic gonad will begin to differentiate into a testis at about $1\frac{1}{2}$ to 2 months. At the end of the third month, the foetal testes elaborate androgenic hormones which masculinize the external genitalia. If the father contributes an X chromosome, the embryonic gonad will remain undifferentiated until about the 4 months when it becomes distinguishable as an ovary. The foetal ovary does not produce hormones which influence the internal genital ducts or external genitalia. The second important stage in sexual differentiation, the development of the internal and external genitalia, is therefore dependent entirely on the presence or absence of a competent foetal testis. The third stage, which is the development of secondary sex characteristics, depends on the internal secretion of the testes and ovaries at puberty. It has been possible to locate the region in the Y chromosome which is at the root of all developments during sex-determination.

In the Y chromosome of males are present 2.1 kb (kb = kilobase = 1000 base pairs) gene, called SRY-gene (Sex-determining Region-Y) which synthesizes a protein called SRY-protein. SRY-protein acts on the promotor of the gene for mullerian inhibiting substance that cause regression of female reproductive system and development of testes in the male embryo. In certain cases, this region of Y-chromosome can be broken and translocated to X-chromosomes. In such circumstance, if one of the two x-chromosomes contain a translocated SRY gene then XX would develop into males. On the other hand, if SRY region breaks off and deleted from Y-chromosome, persons with Xy chromosome would not develop into males ; instead they would develop into females. A curious feature of SRY gene is that it has no introns. It is probable that the gene has been inserted in human genome later in evolution through the action of reverse transcriptase, a viral polymerase enzyme. If this is correct, sexuality in humans may become a fall-out of viral activity.

5. Klinefelter's Syndrome

Human Males typically possess one x and one y chromosome so that their karyotype is 46, xy. However, number of x-chromosomes may vary in them. We know that a portion of heterochromatic x functions. Hence when a male possesses more than one x chromosome, he usually shows a number of

syndromes called Klinefelter's syndrome, after klinefelter. As number of x-chromosome vary, thus klinefelter's syndrome is classified on the basis of number of extra x present - Disomy Klinefelter's syndrome, if there are total two x (47,xxy), Trisomy Klinefelter's syndrome if there are total three x (48, xxxy), and tetrasomy klinefelter's syndrome if there are four x (49,xxxxy). Hence there are recognised 3 classes of Klinefelters Syndrome

1. Klinefelter's syndrome I
2. Klinefelter's syndrome II
3. Klinefelete's syndrome III

Klinefelter's Syndrome I

a. Clinical features : The clinical feature of the syndrome include followings

1. The patient is outwardly male, long-legged
2. Testes is infantile, characterized by azoospermia (= failure to produce sperms) hence infertility.
3. Development of gynaecomastia (= development of breast)
4. Normal external genitalia
5. Urinary output of 17, ketosteroids, a metabolic product of testosterone has subnormal levels, and this shows some correlation with the degree of androgen deficiency as judged clinically by frequency of shaving, distribution of body hair and diminished libido and potency. A common finding is that the height is greater than average with disproportionately long legs. Below average intelligence is usual, and it is rare to find a patient who has had high education.

b. Frequency : Frequency of Klinefeltier's syndrome (47,xxy) is quite high, being 1/700 live births.

c. Genetic determination : The diagnosis of klinefelter's syndrome should be suspected in any male with small testes and otherwise normal external genitalia. Confirmation is obtained by finding X and Y chromatin. The most usual finding is a 47,XXY karotype, but other karotypes are discussed below as variants of Klinefelter's syndrome.

Klinefelter's syndrome seldom occurs more than once in the same sibship, and as sterility is the rule, there is no record of affected individuals in two generations. Most cases are presumably

the result of non disjunctional event occurring during parental meicsis. Investigation of X-linked markers in patients and their parents has shown that non-disjunction of the sex chromosomes can occur during either oogenesis or spermatogenesis. The frequency of the condition increases with maternal age and it has been estimated that in about 60 per cent of XXy cases, both X chromosomes are maternally-derived.

It can also be deducted from the family studies on haemophilia. If mother is suffering from haemophilia and father is normal, it means that father has normal gene for haemophilia on X-chromosome. If non disjunction take place on paternal site, the child would receive normal X, not showing haemophilia. Hence if a boy suffers from Klinefelter's syndrome and inherits condition of haemophilia, it is certain that x is maternally derived.

Klinefelter's Syndrome II (48,XXXY)

Males With XXXY-Show Variant Of Klinefelter's Syndrome : In these cases the associated physical and mental disability increases directly with the number of sex chromosomes (Ferguson-Smith,1966). Thus the xxxy patients characteristically are severely mentally retarded and show prognathism, lower finger ridge counts, and more testicular atrophy.

Klinefelter's Syndrome III (49, XXXXY)

Clinical features produced by this abnormality of chromosome number is similar to those in class II, but are expressed in higher frequency and more marked. Prognathism is thus more marked than in class II, testicular atrophy is of most extreme type and mental retardation is most sub-normal.

47 XYY Males

Old text books mention the class as showing Klinefelter's Syndrome. It is often stated that the present Karyotype predisposes the male toward criminal activity who are often commonly found in mental asylum or behind the bar. The clinical picture as this one is based upon very scanty data and has not been confirmed by any extensive work. Strickburger and others lavel the genotype as normal.

The controversy that has surrounded XYY genotype concerns criminal behaviour. In 1965 it was reported that the genotype XYY was encountered among men in a certain wing of a

"mental-penal institution" (namely, the Carstairs maximum security hospital in Scotland) at much higher rate than among the general population. (To give a more accurate data, Seven out of 197 men were XYYs, which is about 36 times their frequency in the population at large). Since that time, other well-documented studies have been published from around the world. The conclusion is this: Men of sex-chromosome constitution XYY are somewhat more likely to be incarcerated in a "mental-penal institution" than men whose sex chromosomes are XY. (In general, the offenses of XYY men are similar to those of XYs, and contrary to some earlier reports, XYY men do not appear to be concentrated among the most dangerous, aggressive, or violent inmates.)

Nonetheless, the great majority (at least 98 percent) of men in mental-penal institution have XY sex chromosomes, and only a small proportion of the total number of men who have sex-chromosome constitution XYY engage in criminal behaviour. It is estimated that at least 96 percent XYY do not behave in ways that can be labelled 'criminal behaviour'.

The XYY issue is surrounded by so much prejudice that mere discovery of a XYY is sufficient to change behaviour of its possessor and outlook of others to him. It is because of this reason that people in Boston forcibly stopped a programme for XYY screening of population.Criminal behaviour is so widespread that many genetic and environmental factors must be intricately associated in its causation.

The controversy aroused in 1965 by Jacobs et.al on the basis of research at Scottish Prison was tested by various workers (Price and Whatmore, 1967, Witkin 1966, craft 1973, Fox 1971, Shab and Roth 1974; Pyeritz et.al 1977, Theilgaard, 1983; General Survey by Bartol, 1983; Biswas 1989 (in India), Sheley (1991). The quest has ended without implicating in any definite way criminality and XYY. There are significant number of XYY men leading perfectly normal lives, about 0.25 million in the US itself (Shah and Roth,1974). Witkins (1976) reported that XYY men, even if have more likelihood of criminal convictions, it is more due to lesser intelligence, not due to greater aggression.

46, XX MALES

Another rare group of patients with Klinefelter's syndrome and average intelligence have an apparently normal 46, XX karyotype. Evidence has been found which suggests that male

determinants may have been transferred from the short arm of the Y to X during paternal meiosis through accidental crossing over.

Causes Of Klinefelter's Symptoms : When extra X chromosome is present in males, all except one x become inactive, like in females. Syndrome in such cases is due to imbalances between the y genes and the genes contained in the pseudo autosomal region of x-chromosomes that do not become inactive along with the rest of inactive x-chromosomes.

6. Turner's Syndrome (45,X)

This is numerical sex-chromosome syndrome in which the karyotype is usually 45,x though other variants are also possible.

a. Clinical Features : The syndrome was described by Turner in 1938. The important pathological defect is the absence of normal ovaries which are replaced by thin white streaks of ovarian stroma without follicles. Sexual infantilism and short stature are almost common. Other features include shield chest, webbed neck, cubitus valgus, peripheral lymphoedema at birth, short fourth metacarpals, hypoplastic nails and heart malformation. Severe mental retardation is uncommon, but mild forms of mental impairment have been revealed by detailed intelligence testing. By the age of 7 years, affected children are noticeably short in stature and the average final height attained is about 55 inches. The condition presents in adolescence with primary amenorrhea. Therapy with oestrogens allows the adult to develop secondary sex characteristics and live a comparatively satisfactory although sterile, married life.

b. Frequency : 45,X karyotype is found in approximately 1 in 2,500 female births and in 5 percent of spontaneous abortions.

C. Genetic determination : Which of the two parents contribute no sex chromosome to the foetus so that it possesses only one X? In 72% of cases, it has been found that the single X is contributed by the mother and there is no contribution from the father side. The chromosomal disjunction occurs in the male parent so that his both sex chromosomes are passed to one gamete and another gamete receives no sex-chromosome. The ovum is fertilized by the latter type of sperm. The evidences for such an inheritance comes from study of inheritance of X-linked diseases such as haemophilia, colour-blindness etc. If father is colour blind (having mutated gene in his X chromosome) and if he has a daughter suffering from Turner's syndrome, she is not found

to be a carrier of the disease. It is because father is not contributing X-chromosome to her daughter.

Another line of evidence constitute the fact that there is no effect of maternal age on the causation of the syndrome. Inheritance of the blood group studies, Xg, also supports the same conclusion.

Genic Causes Of Abnormalities

We know that out of the two X-chromosomes present in the females, one x is inactivated except for the small region near the lower end (xp 22-32). Thus in Turner's patients, there is only one such functional part of X-chromosome, and only half the required gene product being made. This region is called Pseudo autosomal region. In the inactivated X-chromosome the Pseudo autosomal region is functional. The genes of this region has not been identified upto 1995 hence gene products responsible for Turner syndrome is still unidentified. However, an X-inactivation centre (XIC) has been located in band Xq13. This is a 17 kb gene which produces XIST (x-inactive specific transcripts). XIST gene does not synthesizes protein because its RNA does not leave nucleus. Rather the RNA somehow influences chromatin inactivation. The turner's gene somehow escape this RNA and not inactivated. The gene product in double doses causes differentiation of normal female and in single dose turner's female.

Chromosomal Changes Of Child Can Be Detected Before Birth :

Foetus is surrounded by a membrane, the amnion, which encloses a cavity filled with a fluid,amniotic fluid. In this amniotic fluid are shed foetal cells as foetal formation progresses. A sample of amniotic fluid can be taken out with injection and the cells can be separated in suitable medium. The chromosomes can then be studied after staining it by suitable procedures. The method is called amniocentesis.

Amniocentesis cannot be performed before four months of pregnancy. Premature termination of pregnancy is not possible at such an advance stage of pregnancy if a chromosomal abnormality is detected. There was, thus, a trend towards culture of chorionic villi - the tissues that form placenta. It was, however, felt that chorionic villi sometimes include maternal tissues which gives a wrong projection in the test. Secondly, since tissues of chorionic villi do not enter in formation of foetus, it may not reflect the true chromosomal conditions of the foetus. With this realisation, there is again a trend towards earlier amniocentesis combined with plasma-analysis of mother to discover presence of any abnormal protein resulting due to abnormal chromosomal constitution.

Other sex abnormalities are as follows :

1. Multiple X - Syndrome or Superfemale (47, xxx) :

They are live normal females but show mental retardation. They are also known to produce normal children.

2. Fragile X - Syndrome :

Both males and females may be sufferer but mostly males suffer because they have only one X, There is a satellite on long arm of X. It produces mental retardation, large head and ears, prominent chin and larger testes in males.

3. Mosaics :

Mosaics arise by non-disjunction of chromosomes, usually X and Y during early embryogenesis. Spencer et..al.. (1969) detected a mosaic of the following constitution.

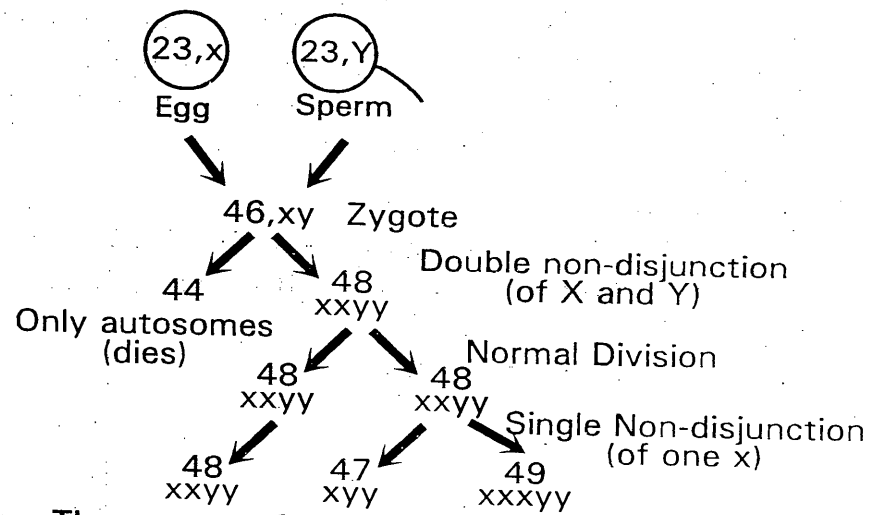


Fig. : Three types of cell-populations in a sex mosaic

(a) Gynandromorph *(Gyn=Female, andro=male, morph=form)* :

As the name suggests, they have both masculine and feminine

characteristics. They are mosaics of male cells and female cells. Whether they will be more masculine or more feminine depend on how many cells of male line and how many of female line constitute the gonadal primordia. If more male cells, testes will be dominant in comparison to ovary. If more female cells, ovary will be dominant in comparison to testes. If equal, ovo-testes results. Both male and female hormones are secreted. In animals, both sperm and ova are formed by ovo-testes and such individuals are called "True hermaphrodites."

(b) Pseudohermaphrodites - In man, and some other mammals, individuals may be partly male and partly female in genitalia and secondary sex characteristics. A male pseudohermaphrodite has undescended testes, a small penis, a rudimentary vagina, no scrotal sacs, breasts and is sterile. In some cases, they have been converted to females by surgical method. A typical female pseudohermaphrodite has underdeveloped ovaries, infantile uterus and vagina, a rudimentary penis, little breast. Some of them have been converted to males by suitable surgery and hormone therapy in early childhood. Presence or absence of barr-body help doctors to decide whether the dominant genotype is XX or XY

4. Chimaera : They are formed by fusion of two zygotes and all the cell populations are derived by two zygotes. There are **dispermic chimaera,** resulting from 2 sperms and 2 ova. There are **blood chimaera,** for example in DZ twins of opposite sex **(Freemartin In cattles).** In such cases, female is masculanized by testosterone secreted by testes of male embryo (Testosterone is secreted twice-during embryonic development and during puberty in males)

5. Testicular feminization and adrenogenital syndrome : Informer, testes is unresponsive to pituitary hormone. In the latter, adrenal andorogen is excess in females causing masculanization of females. They often have moustache and deeper voice.

CONSANGUINEOUS MARRIAGES

Consanguineous marriages are marriages between related individuals who have common ancestors a few generations back. The degree of consanguinity, however, may vary. A marriage between father and daughter, mother and son, brother and sister are highly consanguineous because these involve direct descendants. Such incestuous matings, however, are rare in human populations. Informations about 31 such incestuous marriages is available from England and the United States. Almost all human societies have strict cultural prohibitions against such incestuous marriages. Such prohibitions or incest taboos are outgrowths of social and cultural factors, and not because they disturb the genetics of the population.However, genetics of such marriages show expression of large number of deleterious recessive mutations. In the US and England,where genetics of 31 families has been studied, show only 42% of the children to be normal. We will find out reasons for such a great number of abnormalities resulting in such highly consanguineous marriages when we work out probability of inheritance of such genes.

Many human societies, particularly those of Middle East and Indian subcontinent, allow first cousin marriages. First cousins are offspring of brothers and sisters who were married to unrelated persons. Thus, first cousin marriage is the nearest consanguineous marriage for which there exists no prohibition or incest taboo in many human societies. To differentiate consanguineous marriage and first cousin marriage, it can be said that first cousin marriage is the nearest consanguineous marriage allowed in human society.

Consanguineous Marriages And Inheritance Of A Defective Gene

There can be three types of genetic defects - caused by dominant genes, co-dominant genes and by recessive genes.

Let us find out how consanguineous marriages affect inheritance of all these three types of genetic defects. It will be clear at the outset that consanguinity has no effect on inheritance of first two types of genetic defects. Because defects are caused by dominant genes, they are expressed in individuals possessing them. Related or unrelated individuals can find it out and can be aware of such defects. Marriage to a related or unrelated individual will not make any difference because if gene for such a character is present, it is well-marked before hand. A person suffering from

such a defect will have equal probabilities of having an affected child whether he/she marriages a related or an unrelated person.

For example, brachydactyly (short fingers) is an autosomal dominant mutation. The condition is expressed as soon as mutation is caused. If a person suffering from the mutation marries one from his/her family or to some one else makes no difference. Since the person is carrying a gene for brachydactyly, there is 50 : 50 chance of the trait to be inherited by his offspring. If he carried both the defective genes, all of his offspring will be affected. Thus, Aa individuals will have 50% affected children AA individuals will have 100% affected children.

Consanguineous marriages, however, has different consequences for recessive genes.

Effect Of Consanguineous Marriage On Recessive Inheritance

Numerous examples can be cited which will prove that consanguineous marriages result in expression of large number of recessive autosomal genes in the offspring. A recessive autosomal gene is a gene which is present on the autosome chromosome and is normally not expressed when it is present along with the normal gene which behaves as dominant allele.

At least 600 human traits are known to show an autosomal recessive pattern of inheritance. As discovered by Mendel, heterozygous individuals (Aa) do not manifest autosomal recessive traits because of the masking effect of the dominant allele. Thus, people who manifest autosomal recessive traits are generally homozygous recessive, i.e. their genotype is aa. A few examples can be cited in which it can be shown that consanguinity has resulted in greater number of persons suffering from such recessive traits.

1. Inheritance Of Albinism : Albinism is one of the most common and widespread of genetic disorders present not only in all races of man but in insects, fishes, amphibians, reptiles, birds and mammals. Albinism results due to lack of melanin, the dark pigment of body. Melanin is the principal pigment that imparts colour to human skin, hair and eyes. So human albinos generally have white hair and lightly coloured iris of the eye. Because of lack of pigment, skin is very much sensitive to sunlight. The feature attracts attention of fellow people because of its rarity and thus albinos receive special treatment from their follow persons. The

albinos among the present day San Blaz Indians of Panama are called "Moon Children" because they avoid bright sunlight and are not permitted to marry. Until quite recently it was thought that albinism was the result of a single specific defect in the synthesis of melanin from the amino acid tyrosine. But later on pedigree analysis of some families in England clearly proved that a normal child can occur in marriages between two albinos. The fact clearly establishes that there are more than one loci that cause albinism . In fact, there are at least two, and perhaps as many as six genes that result in albinism depending on which stage of the pathway of melanin synthesis is affected by mutation. All of these defects in melanin synthesis are inherited as autosomal recessive traits. Thus it is possible for two albinos to produce normal children if both are albino due to mutation in gene controlling different stages of melanin synthesis. The proportion of albino persons in general population has been worked out for some populations. In the US, about one white person in 38,000 and one black person in 22,000 are albino. There are, however circumstances in which percentage of albino people in the population is high, for example consanguineous marriages. Although only 0.1 percent of marriages in the US is between first cousins, about 8 % of albino children result from the first cousin marriages.

2. Inheritance Of Six-fingered Dwarfism : Six-fingered dwarfism is an autosomal recessive condition in which person affected is dwarf with six fingers. The condition is frequent among the old order Amish of Lancaster Country, Pennsylvania. Number of Amish people is small and they prefer to marry among themselves. Thus there occurs many marriages between people that have common ancestors one or two generations back. Accordingly, the six fingered dwarfism is rare in other populations but in more than fifty families of Amish people. Apparently, the founding father of the Amish sect in Pennsylvania was the carrier of the defective gene and it has become common due to consanguineous marriages.

3. Retinitis pigmentosa in Tristan da Cunha : The frequency of this allele is very high on this island. It is because this island was inhabited by a handful of persons and there was strong inbreeding among the relatives of the settlers on the island as the island was barren when first inhabited.

Genetic similarity among relatives

Progeny receive half of their genes from father and half from mother. Hence, genetic similarity of progeny with their parents is =½. In the next generation, when progenies marry and produce children, these children also differ genetically from their parents by ½. So, the genetic similarity between grand parents and grand children is = ½ x ½ = ¼.

Likewise, brothers & sisters (kins) are genetically similar to one another by ½. Their children differ from their parents by ½. Hence, first cousins differ from one another by ½ x ½ x ½ = 1/8. Hence there is 1 in 8 chance that first cousins will carry similar genes.

Working Out Ratio Of Heterozygotes In Population

Suppose albinism is present in the population in the ratio 1:10,000 i.e. for every 10,000 persons, there is one albino. Ratio of heterozygotes can be calculated on the basis of Hardy Weinberg equation. In this case,

q^2 = 1/10,000.,
q^2 = .0001,
∴ q = .01

Since P = 1-q (we know p+q=1)
∴ P = 1 - .01 = .99

(in this equation, q represent frequency of allele a causing albinism and P represents frequency of normal alble) Therefore, frequency of heterozygotes 2pq.

= 2 x 0.99 x 0.01

= 0.0198 or, 0.02 or, 2/100 or 1/50.

It is, therefore, clear that if albinism is present in 1:10,000 ratio, it means that approximately 1 person in 50 must be heterozygous for the condition. The chance of a given person being heterozygous is 1/50, and if he marries a random unrelated person, the chance of that person being heterozygous is also 1/50. The frequency of marriages between heterozygotes is therefore 1/50 x 1/50 = 1/2500. One marriage in 2500 is capable of yielding albinos, and as the expectation amongst the offspring is 1 in 4, this

corresponds to a frequency of albinos in the population of 1 in 10,000.

(you will be aware that if two heterozygotes mate, the ratio of recessive homozygotes is 1/4. It can be worked out like this :

Aa X Aa

AA	Aa	Aa	aa
1/4	1/4	1/4	1/4)

Probability Of Heterozygote-marriage And Recessive Homozygote Formation. The chance of a given individual being heterozygous is 1/50, but if he marries a first cousin the chance that she is also heterozygous is 1/8, and 1/50 x 1/8 = 1/400, so that 1 marriage in 400 between first cousins is capable of yielding albinos.

Thus, as we have seen, the probability of heterozygote marriage is 1/2500 in general population where as it is 1/400 in first cousin marriage. Given such a probability of heterozygote marriage in the general population and cousin marriages, we can calculate ratio of albino contributed by the cousin marriage. Supposing that out of 40,000 marriages, 1% is cousin marriage, then out of this 400 marriages are cousin marriages. From these marriages one albino will be produced. Rest of 36,600 has 1/2500 probability hence number of albinos produced by them is about 16. Thus the relative ratio of albino produced by cousin marriages and unrelated marriages is 1:16. Thus about 6% of albino produced in the population is resulting due to cousin marriages though cousin marriage is only 1% in the population.

Cousin-marriages And Rarer Recessive Diseases

It can be shown that rare the disease, greater is the effect of cousin marriages in the recessive homozygote formation.

It is evident that the rarer the trait the more frequent will be consanguineous marriages amongst the parents of affected offspring,for if a trait is extremely rare the chance of a given heterozygote happening to marry another heterozygote in general population is very small, but it remains 1 in 8 if he marries a cousin. For exampl , if the frequency of a defect in the population is 1 in 1 000 000, the frequency of heterozygotes is 1/500 and the chance that an unrelated marriage can yield affected children is 1/500 x 1/500, whereas the figure is 1/500 x 1/8 for first cousin

marriages. If the frequency of first-cousin marriages were I per cent, then the proportion of cousin marriages amongst parents of affected offspring would be about 38 per cent.

If the frequency of first-cousin marriages in the population is *a* and the frequency of a recessive gene is *p*. the proportion of cousin marriages amongst the parents of homozygotes is approximately

$$\frac{a}{a + 6p}$$

for populations where the frequencies of a and p are relatively low.

In assessing the value of this criterion for recognizing recessive inheritance, we need to consider some alternative approximate figures such as those given in the following table (we have worked out for frequency abnormality 1/10,000 and 1/10,00,000 in 1% first cousin marriage)

Frequency of abnormality	Percentage frequency of first cousin marriage		
	0.5	1 .	3
	Percentage of parents who are first cousins		
1/2500	1.5	3	9
1/10000	3	6	16
1/100000	9	16	37
1/1000000	24	38	65

The table clearly shows following features :

1. For a given first cousin marriage rate, say 1%, the proportion of cousin marriages among the parents of affected children increases as the frequency of the gene decreases.

2. The third line of table shows that when the frequency of first cousin marriage is 0.5, the percentage of parents who are first cousin is 9 (an increase by 18 times) whereas when the frequency of first cousin marriage is 3% the percent of parents who are first causins is 37%(an increase by 12 times). Thus, as frequency of first cousin marriages falls, the percentage of parents of affected child who are first cousin has relative increase for a given frequency of the abnormality. We have been discussing the effects of first cousin marriage on the inheritance of albinism. All along we arrived at much lower the ratio of first cousin marriages resulting in

albino. Actually it is found that the parents of albinos are first cousins in about 20 per cent of cases. This rate is much higher than would be expected on the basis of the figures given above. The explanation probably is that there is more than one gene producing albinism, the effect of the different genes being indistinguishable.

First Cousin Marriage And Different Recessive Diseases

We have been discussing all along albinism. It was necessary to theorize various aspects of inheritance in first cousin marriages, and to make it more understandable. Now we take look at some more recessive conditions with reference to first cousin-marriages. Tay-Sachs disease is due to a simple recessive gene and the percentage of first-cousin marriages amongst the parents is about 15. Alkaptonuria is transmitted as a simple recessive. It is very rare, and the proportion of affected persons whose parents are first cousins is no less than something between 30 and 40 per cent. Even higher rates have been reported with some exceedingly rare conditions. The commonest recessive disease in England is cystic fibrosis, which has a frequency of I in 2000 births. It is an abnormality of the mucus-producing cells. With so common a gene very little increase could be expected in the rate of cousin marriage amongst the parents.

Should First Cousin-marriages Be Banned ?

There are several populations with high rates of consanguineous marriage. This is often just a social tradition of that community. In some parts of the Middle East the frequency of first-cousin marriages is 30 percent or even higher, and high levels are also found in some populations in India and the rural areas of Japan. In considering the genetic consequences, it is essential to take account of the length of time that such marriage traditions have existed. Fairly recent isolation of a small section of a population with consequence inbreeding, such as can occur when a group emigrates, will result in a higher incidence of recessive genetic disease than in the original parent population. However, in a population where consanguineous marriages have been a tradition for hundreds of years, the absolute incidence of recessive disease is less. The reason is that because of excessive heterozygote mating in such populations the number of normal and abnormal homozygotes were increased at the expense of

heterozygotes.

The abnormal homozygotes in recessively inherited disease may be severely afflicted and many die at a young age, without reproducing. Thus inbreeding rearranges the recessive genes in the population so that relatively more abnormal homozygotes are produced, who subsequently fail to hand over their genes to the next generation. Thus, consanguineous marriages reduce the proportion of heterozygotes and natural selection eliminates the abnormal homozygotes, leaving just an increase in the proportion of normal homozygotes. Upon their death the frequency of the harmful recessive genes in the population falls, and so does the absolute number of homozygotes manifesting recessive genetic disease in subsequent generations.

In the long run, the net result of consanguineous marriages is similar to those found in population without such marriage, but their genetics differ - one has a low frequency of recessive genes in the face of a high rate of consanguineous marriage, whilst the other has a relatively high frequency of recessive genes, offset by a low rate of consanguineous marriage. The differences in the gene frequencies would become particularly obvious if,for the sake of argument, each population adopted the other's rate of cousin marriage. A fall in the rate in the inbred population would lead to an extremely low incidence of homozygotes manifesting the disease, whilst the change to a high rate of consanguineous marriage in the outbred population would produce a dramatic increase in affected children.

In practical terms, a cousin marriage in a traditionally inbred community is less likely to result in children manifesting recessive disease. The tradition has, however, left a legacy of a low population frequency of recessive genes and, should lower rates of consanguineous marriage occur in the future within their own population, the incidence of recessive disease should fall far below the level found in other populations. Whilst a tradition of cousin marriage does not, in the long run, lead to a high frequency of severe recessive disease. When such affected children do occur, their parents are still blood relatives more often than expected from the general rate of consanguinity in the population. For example, for a defect with a frequency as high as I in 10000 and a rate of cousin marriage of 25 per cent, about 67 percent of the parents of affected children would the first cousins.

INBREEDING STUDIES IN INDIA

Incidence of consanguineous marriages has been found for various states and groups. Basu and Rizvi has reported following percentages of consanguineous marriages in different states and groups in India.

State/Groups	-	% of consanguineous marriages
Tamilnadu	-	37.0 %
Andhra Pradesh	-	33.3 %
Kerala	-	20.0 %
Memon	-	27.1 %
Vohra	-	26.0 %
Khoza	-	13.3 %
Parsi	-	18.0 %
Saiyyad Shia (Lucknow)	-	42.8 %
Shaikh Sunni (Delhi)	-	24.4 %
Mugal Sunni (Delhi)	-	22.1 %
Pathan Sunni (Delhi)	-	23.6 %
Saiyyad Shia (Delhi)	-	27.6 %

Since consanguineous marriages lead to recessive homozygosis (Jones, 1924) hence larger percentage of children born by such marriages suffer from genetic diseases in comparison to children born in general population. Several studies have been performed in India that seek to compare frequency of genetic defects/characteristics in children born out of consanguineous marriages with the frequency of same genetic defect in children born in general population.

The genetic defects/characteristics which have often been selected by various workers as criteria for comparison has been fertility, mortality, IQ, tasting-ability, red-and-green colour blindness, ABO- blood group etc. Sanghvi, L.D. (1966) in his book "Inbreeding in India" has provided a detail account of the phenomenon.

(i) Study of effect of consanguinity on fertility and mortality :

A study demonstrating debilitating effect of consanguinity on fertility and mortality has been by Afzal and S.P. Sinha (1984) on the Ansari Muslims of Bhagalpur (Bihar). The study found out that mortality among inbred child population is about 36% in comparison to 28 % in oubred population. The mean number of live children born to a mother is higher in non-consanguineous mother (7.06) in comparison to 4.66 in consanguineous mothers.

Another study in the same area has been done by P.S. Rao and Imbaraj (1977, 1979, 1980) who selected the Brahmins of Tamilnadu and Maharashtra. Consanguinity is high among these populations. Contrary to the expectation, the study did not find any significant rise in mortality or

fall in fertility due to consanguinity. The paradox can be explained by the fact that South Indian Brahmins have been practising consanguinity for the last two to three thousand years and the period of "inbreeding depression" is over for them. A large number of detrimental genes affecting their reproductive fitness have already been eliminated long ago (Basu, 1975). Ansari Muslims, on the other hand, are neo-convert from local Hindu population who embraced Islam two to three hundred years ago (Ali & Hussain, 1976). The period of "inbreeding depression" is not yet over for them and sufficiently large number of deleterious recessive alleles still circulate in their population. Study of Barua on Muslim population of 24- pargana (WB), however, confirms negative effect of consanguinity on fertility and mortality.

(ii) Study of effect of consanguinity on inhentence of IQ :

A study by Afzal end S.P. Sinha (1984) of Ansari Muslims of Bhagalpur (Bihar) included three populations : Hindu yadava, consanguineous muslims and non-consanguineous muslims. All the subjects belonged to same socioeconomic stata. It was found that IQ value of inbred children is sufficiently lower in comparision to outbred Hindu and Muslim populations.

(iii) Study of effect of consanguinity on inheritance of social profiles :

Another study by the same workers Afzal & S.P. Sinha (1983) studied IQ inheritance and beginning of social profiles in neo-natal children of inbred population of Ansari Muslims in Bhagalpur. It was found that many of the social profiles such as visual fixation, social smile, sound-seizures, oral expression and hand-grasping are significantly delayed in inbred children

(iv) Study of effect of consanguinity on inhentance of blood group, red-&-green colour blindness

The studies include those of Chatterjee & Mukherjee (1979), Ansari & Sinha (1976, 1980), Afzal & Sinha (1984) etc. In all the studies, it was found out that frequency of recessive homozygotes is higher in consanguineous populations.

(v) Study of effect of consanguinity on foetal development

Rao, P.S.S. (1976) found out that rate of foetal development in inbred populations of south India is slower in comparison to that in the general population.

To summarise, studies confirm that those populations which have been practising consanguinity in recent times suffer more from recessive homozygosis whereas those which have been practising it since long do not suffer from handicap and in them recessive homozygosis has been replaced by dominant homozygosis

GENOME IMPRINTING

Principle of Equivalence : While learning Mendelism we have seen that when a pure tall pea plant is crossed with a pure dwarf plant all plants in the next generation are tall

$$\frac{TT}{\text{Tall plant}} \quad \frac{tt}{\text{Dwarf Plant}} \quad \text{---------- } P$$

$$\frac{Tt}{\text{All Tall plants}} \quad \text{---------- } F1$$

It makes no difference here that which of the parents is male or female. The gene for tallness, from whichever parent is derived, expresses in the offspring always the same way. It was Mendel himself who discovered principle of equivalence in reciprocal crosses. First he used a female tall, next he used a male tall. No difference was found and thus reciprocal crosses firmly laid the foundation of principle of equivalence. This was true not only for peas but later on extended to all other classes of plants and animals including fruitfly, mice, humans etc. Principle of equivalence, however, does not apply in case of genomic imprinting. Genomics imprinting is a condition in which males and females stamp their genes with their marking so that a gene for the same character from female behave differently in the offspring from the gene for the same character from male parent. On this basis it can be identified that genes in the offspring are of paternal or maternal origin.

Exceptions To Law Of Equivalence : Genomic imprinting is not the only exception to the law of equivalence. There are three more instances where male and female marking on genes vary -

1. The first instance is those from fungus gnats, gall midges and scale insects in which male chromosomes are eliminated in the egg cytoplasm so that only female genes are contributed to the next generation. This is considered to be special form of meiotic drive under the control of maternal genes.

2. The other instance is in the difference of X and Y where two chromosomes carry different genes in two sexes.

3. The third instance are those of cytoplasmic genes contained in mitochondria of animals and mitochondria, plastid of plants. Inheritance of characters through such organelles is strictly maternal because it is ova of mother that contribute cytoplasm to zygote and with cytoplasm these organelles.

Barring these instances and those of genomic imprinting, law of equivalence in reciprocal crosses apply everywhere. Whatever be the character selected, there will be no difference in its inheritance whether it comes from paternal side or maternal side.

What is Genome Imprinting ? : During its passage from the male and female parents the autosomes and the X chromosomes are stamped differently so that they bear the marking which of the parents they are originating from. Much of the autosomes from the two parents are similar in genic constitution but behaviourally they differ in the manner of expression.

To illustrate the point, Huntington's Chorea is an autosomal dominant disease. Any of the two parents of an offspring can suffer from this disease so that the source of this gene for offspring can be both paternal or maternal. In both the cases, whether it is paternal or maternal, symptoms of the disease will be the same but the time of initiation of different symptoms and severity will be different depending upon whether the gene is paternal or maternal. It seems as if male and female parent stamps a gene differently before it is contributed to the offspring:

Characteristics Of Genome Imprinting

1. Imprinted genomes express variously : Imprinted male and female genes can have different magnitude of expression. There may be difference in time of their expression, one expressing earlier, other late. One imprinted gene may be having enhancing effect on a function but the other a retarding effect. In extreme case, imprinting may turn off a gene in one parent where as left to express in another parent.

2. Genomic Imprints are erasable : Genomic imprinting is done in the gonadal tissues, ovary and testes, of female and male respectively. A offspring receives genes of maternal and paternal marking. However, such marking are erased during gamete formation in the ovary and testes of offspring and he or she stamps his or her marking on the genes contained in his or her gamete. Genomic imprints are, therefore, erasable. Genomic imprinting, thus, is not a permanent modification of the gene.

3. Gene Imprinting is most common in mammals and flowering plants : In both groups, paternal and maternal genes have different phenotypic effects during development of gametes. It has been suggested that this is due to the fact that both groups

directly nourish their embryo (see adaptation theory).

4. Gene Imprinting is species specific : Many mammals have been found to imprint their genes. But imprinting of a gene vary from species to species.; A gene imprinted in one species may not be imprinted in another species. For example, gene for insulin-like growth factor II is imprinted in mice but not in humans.

5. Gene imprinting is implicated in many diseases : Ever since its discovery the phenomenon has been implicated in triggering of many human genetic diseases such as fragile x syndrome, Angelman Syndrome, embryonic tumours, Cancers and several other patterns of inheritance of human disease.

6. Gene imprinting is not a rule : It must be kept in mind that gene imprinting has been discovered only in some male and female genes. Most genes, at present, seem to be unimprinted so that it is difficult to make difference they are maternal or paternal in origin. It has been suggested that they are more involved with genes that ensure nutrition to the embryo.

Nature and Mechanism of Genome Imprinting

The question has been perturbing minds of scientists the world over and quite a good number of them have been engaged in unraveling the mystery. Important among them are James McGrath, Dover Solter, M Azim, C. Sapienza, H Surani, B.M. Cattanach, R.D. Nicholls etc. According to them genome imprinting results due to direct modification of the DNA through DNA methylation achieved differently, quantitatively, in the DNA of two sexes. When a child receives chromosomes from its father and mother, the paternal and maternal chromosomes bore their own imprints. However, in the gonad of the offspring, the parental imprints are erased and new imprints stamped.

It has been found that the DNA (genes) coming from mother, in most of the cases, is more methylated than the one coming from the father. Methylation pattern of the genes change when a gene travels from mother to son. A son will receive highly methylated DNA (genes) from her mother but when he will pass on his genes to his offspring, it will be less methylated. Greater the degree of methylation, lesser is the chances of its earlier expression.

A. Methylation of DNA : DNA Methylation is a usual process to control functioning of genes. This is brought about by enzyme DNA methylase which adds a methyl (CH_3) group at the

Carbon - 5 position of Cytosine. If Cytosine one one stand is methylated, its complementary base, guanine, on the other strand is also methylated. Thus most probable of methylation are

C G
C G

Different cell-types are characterized by activation of different set of genes. Those genes which are being expressed in a particular cell-type will escape methylation; those that are not will not be left naked - they will be methylated and tightly packed in the nucleosome of chromosome. Level of methylation, thus, differ from cell-type to cell-type : those cells that are characterized by activity of large number of genes will have lower levels of methylation and vice-versa. Promotor region holds the key for functioning of entire gene because enzyme RNA polymerase attach at this site for mRNA formation. Methylation is done precisely at this position. To abolish gene activity, it is sufficient to methylate a few C-G sites in the promotor region. It is not our concern here to know in what ways methylation of DNA regulate its function, it is suffice to say that it does so by altering the association between DNA and various proteins that bind to it for gene-functioning.

It would not be out of place to remind readers that DNA methylation has been utilised by bacteria for their advantage in a different way. Bacteria are known to elaborate an enzyme, restriction endonuclease, which is primarily meant to cut DNA of invading viruses. But how is bacteria going to protect and safeguard its own DNA from its own enzyme? It is achieved by methylation of its own DNA when it is not functioning. Restriction enzyme then singles out viral genome for fragmentation and death.

B. Differential Methylation for genome imprinting : What is the mechanism that dictate differential genome imprinting in male and female so that female genes are more methylated in comparison to the male genes? Sapienza and his colleagues, along with a host of other workers, are precisely trying to find out an answer to the same question and a clear cut answer is awaited. A decade of research has yielded some hints but the picture is not entirely clear upto 1995-96.

Methylation is accomplished during DNA replication stage. When ova and sperms are forming in the ovary and testes respectively,there is active division of cells during which DNA replicates. This event of replication is utilised by both males and females in methylating their DNA in their own way. Males and females vary to a great extent in the manner of sperm and ova

production. Females have formed all her ova to be shed for fertilization in its entire life cycle while she is still in the womb of her mother. Her all ova are in a state of suspended meiotic prophase II, and will remain so till, upon reaching adolescence, it has chance to be fertilized by a sperm. The activation of ova by the sperm initiates in it the suspended maturation which is completed and nuclear fusion of sperm and ovam occurs. Males, on the contrary, form sperms regularly and has the capacity to form it well beyond sixty years of age (the highest medically certified age is 94). It is, thus, clear that if methylation of DNA has to occur in the gonad it must occur prior to birth of females and in males while they are forming sperms. Females and males, thus, vary widely in the stage at which methylation of their DNA is accomplished. Such characteristic has been discussed in detail because it holds the key for differential methylation of female and male genes. As female genes has to remain in an inactive state for years, at least for about 15 years for the first ova to be shed, and if female fertility is supposed to last upto age of 45 years, for well about half a century. A cell which is out for such a long Journey must prepare well, and this preparation manifest in the form of greater methylation of its DNA. This ensures that the female genes are less approachable to various chemical fluctuations that may undergo inside and outside it. Ova has formed in the female while she is still in the womb of her mother, and thus equally liable to be affected by the hormones and other constituents of her mother's blood. She has no option but to protect it as meticulously as she can. Higher degree of methylation of female genes, thus, has a selective advantage. After replication, DNA is associated with histone proteins to form nucleosomes and nucleosomes are again folded to form solenoid structure and solenoids are again wound to form chromosomal fibrils. Such windings of chromosome is brought about by various classes of proteins. It is these proteins that carry out methylation process during it is involved in winding of the chromosome. Most workers believe that winding proteins accomplish both winding and methylation. For methylation are selected those C-G pairs that are present in the tight domains of chromosomes. How only C-G pairs sitting in the tight domains of chromosomes are singled out for methylation by winding proteins is not entirely clear.

Mechanism Of Working Of Gene Imprint

Gene imprints work by coordinating growth and

development of the embryo. This conclusion has been arrived at by McGrath and his colleagues working on mice. During fertilization, male and female nuclei remain separate for sometime in zygote before they are finally fused. McGrath took advantage of the event and took out, with the help of a fine glass needle, either male nucleus, or female nucleus in different stages of his experiment. If he took out male nucleus, he put into the zygote a female nucleus, and if he took out a female nucleus he put into zygote a male nucleus so that both the nuclei in the zygote were ultimately derived from female line (developing in gynogenote) or from male line(developing in androgenote). Prior to the experiment all the rats were sufficiently inbred so that there remained little difference in the genes of different individuals except X and Y of two sexes. Under such condition, nuclei of all the male and female mice should be considered similar and hence expected to carry on the growth process.

To their utter surprise, McGrath et.al. found out that gynogenotes and androgenotes did not develop beyond few divisions of the zygote. Theoretically, if there is no difference in the genes of males and females, it should hardly matter which sex they are coming from. But, as Mcgrath noted, this was not to happen. Gynogenote showed a retardation in growth by 50% before it stopped growing; anderogenote showed an enhancement of 50% before it also stopped growing. The results showed that genes in females and males are imprinted and that the two imprints are needed by most mammals. The specific imprinting process in males and females selectively turns off certain genes that would otherwise act during early embryonic development. Genes critical for the formation of placenta and yolksac appeared to be inactive among the maternal genes. Some genes, therefore, are inherited in an active form from only paternally, or only maternally. It is not known how large are these inactivated regions of autosomes of males and females. It is also not known whether there is any specific centre in autosome from where the methylation spreads to some length of chromosome. In x-chromosome inactivation, a region XIC (X-inactivation centre) in the XIST gene has been located which inactivates. No such centre has been located for autosome inactivations. As more cases are being examined, some more results are showing up. Mouse Insulin-like growth factor II has been found to be invariably transcribed from the paternally inherited genes. For its action, it binds to a protein receptor which is invariably derived from the

maternally derived gene. (human insulin like growth factor, however, has not been found to be imprinted at all). In such cases, active genes from male and female parent seem to complement each other and a proper development in absence of any of them would become abnormal.

Evolution Of Genome Imprinting

1. Adaptive Nutrition Theory By Haig And Westoby (1989) : The theory proposes that imprinting has evolved mainly in mammals and angiosperms that directly supply nutrients to their growing embryos. The theory maintains that there are conflicting demands of maternal and paternal genes - paternal genes trying to obtain as much nutrition as it can for the growth of current embryos in which it has contributed, whereas maternal genes trying to save some energy for its future embryos in whose making the present paternal genes may not participate. A mutation in the paternal gene which increase supply of nutrition to the current embryo by way of extra growth of placenta will definitely have selective advantage over the previous established non imprinted allele. The mutant paternal imprinted gene would function. But if a new mutant maternal gene reduces these demands it would be disadvantageous for the current embryos but advantageous for the future embryos. A previously non-imprinted gene thus becomes imprinted. If the genes were concerned with development of placenta, they are still concerned with the same function. The difference is that now paternal gene is active and maternal gene has inactivating or retarding effect. Paternal gene expression enhances the nutrition, maternal gene expression reduces those demands. Paternal genes would express earlier because these would be methylated to lesser degree; maternal genes would express late because these would be methylated to a greater degree.

2. Theory of prevention of Parthenogenesis by Moore and Haig (1991) : Parthenogenesis is a condition in which males are eliminated in reproduction and the ova is stimulated artificially by some physical, chemical or biological means such as infections Parthenogenesis is of short-term benefit for the females because it perpetuates in the population female genes. But it is harmful for the species as a whole because sexual reproduction is prevented and a potent means of genetic variability is lost. Genomic imprinting ensure that both male and female genes participate in growth and development so that uniparental dizygosity is

GENE THERAPY

For man, even the sky is not limit. He doesn't rest with acquisition of a novelty, unravelling of a problem. Milestone reached are used as platform to jump to new greater heights. Ever since the mystery of genetic material was unfolded by Watson and Crick, the DNA is being studied by scientists the world over in its finest detail. In the first two decades that followed its discovery, every aspect of its structure and function was explored. In the 1970s, the technique of restriction endonucleases provided the immense potentiality for manipulation of DNA and, in combination with other enzymes such as ligase and related technology such as vector-technology, stage was set for experimental manipulation of master molecule of life. Thus was born genetic engineering. In the 1980s the chief issue that kept geneticists involved was sequencing of the various genes and determination of its position on the chromosome. Knowing the sequence of the gene was important because it is only by analysing their base sequences can we know the difference between a normal and abnormal gene. By this time geneticists have been able to identify a defect in gene, synthesize a new normal gene or locate it in the DNA of normal individuals, load it into some vehicle DNA, deliver it to some destination, made it to fuse with the new DNA and watch out their function. Higler et.al. (1977) were the first to transfer a cloned gene into an animal tissue culture. By 1980, methods of injecting cloned DNA into animal cell by microinjection developed. Since then a variety of transgenic animals such as mice, pig, fishes, cattles etc. were produced by injecting into fertilized ova the genes for desired character.

With a technology so much sophisticated at his commands, geneticists rightly thought about not to move in a round about way while tackling inherited diseases-they thought of mounting a direct attack on the gene itself. Thus was born "gene therapy".

Initial Steps : Identification of large number of heritable diseases involving defects at the protein level led to the conceptualization of procedures aimed at correcting the molecular defects at the DNA level. The difficulties, however, were many. In addition to the technical difficulties, there were many safety, social ad ethical concerns.

The first step towards gene therapy was taken when gene-marking experiments were performed with human beings in 1989. In this experiment, tumour-infiltrating lymphocytes were taken

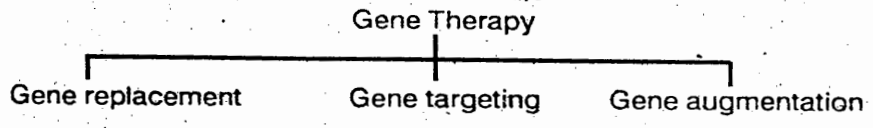
out from patients with advance cancer and a neomycin-resistant gene was introduced in it. The genetically modified lymphocyte cells with neomycin-resistant gene were then injected back into the same patient. According to Rosenberg (1990) such lymphocytes were detected in the patients blood and recovered. The experiment indicated that lymphocyte is dividing and working well. This paved the way for gene therapy.

What Is Gene Therapy ? : Gene-therapy consists of :

i) Removal of a defective gene and its replacement with a normal gene (gene-replacement).

ii) Correction of a defective gene through introduction of a complementary part (gene targeting).

iii) Introduction of a few or more copies of a gene if a gene is not fully functional (gene augumentation) sometimes fewer copies of gene is introduced and steps are taken for its higher level of expression. In short, gene-therapy consists of



I. Gene Replacement

It is important in gene-therapy to know whether the defect is caused by absence of a gene or because of action of a mutated gene. In the former case, integration of a normal gene anywhere in the host DNA is sufficient. For example, in case of a deficiency as long as a fair number of cells carry the gene, the patient will be cured even if all cells donot function.

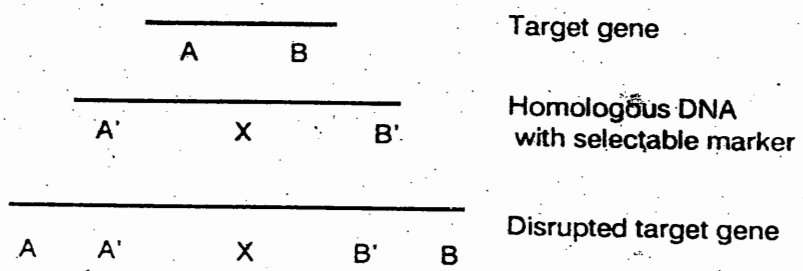
Case with the defective gene is a bit difficult. The disease results due to formation of some harmful substance. Such genes need to be replaced.

No success has thus far achieved in gene-replacement therapy in which it is envisaged to replace the gene. Obviously, therapy cannot be resorted to during adult life because it is almost impossible to replace the defective genes from all the cells of human body. Defective genes can be located. Such genes would need replacement by targeted recombination. This cannot be done with all the cells except in case of blood cells where all the cells can be temporarily withdrawn and altered stem cells injected. If

the cells are inaccessible the situation becomes more problematic eg. in Huntington's disease affecting brain cells. Brain cells are inaccessible and irreplaceable. The dual task i.e. recognising the defective gene and removing it and, at the same time, inserting a normal gene is an uphill task and is presently beyond our reach.

II. Gene-Targeting

The aim of gene-targeting in gene-therapy is disruption of the harmful mutated gene. Some cells of embryo is taken out and cultured on which defective gene is present. A selectable marker is attached to a long stretch of homologous DNA which corresponds to the gene desired to be inactivated. The construct-selectable marker with homologous DNA is inserted into some cell of the embryo. The cells can be selected for presence of the marker. In some of the selected cells, the exogenous construct will be inserted into the host DNA inside the target gene since recombination is favoured between the target gene and the homologous sequences. Such cells with disrupted target gene can be injected into embryo. When embryo grows, it is mosaic, for a proportion of cells are derived from corrected cell. Even in the corrected cells, out of two defective DNA sequences, only one is correct. In the later generation, following typical Mendelian fashion of gamete formation, some of the gametes will be with corrected sequences. Crosses of such individual with normal individuals will lead to birth of normal individuals.

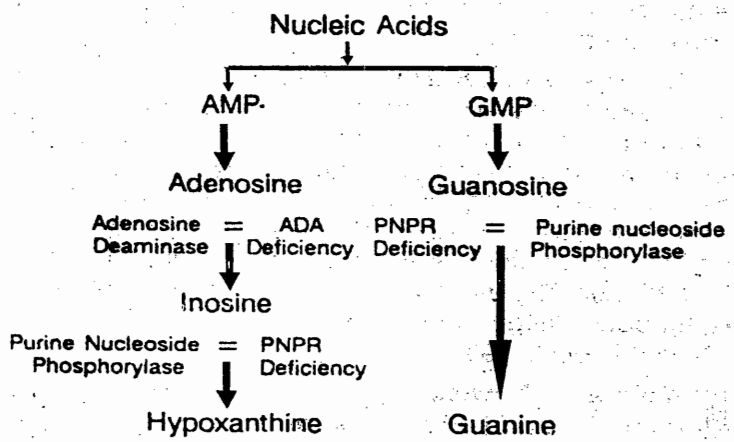


III. Gene-Augmentation

The most successful variant of gene-therapy is gene-augmentation in which patients suffer due to some non-functional gene. In such cases a few copies of gene is inserted in the patient's DNA. In the new location, the normal gene

functions and cures the patient. In the beginning were selected those diseases whose genetics was simple. With success, now diseases with more complex genetics are being undertaken. Genetic diseases like ADA deficiency, hypercholesterolaemia, cancer, cystic fibrosis, sickle cell anaemia, thalassaemia are target diseases for gene therapy, some of which are cured and others are in various stages of experimentation.

ADA-Deficiency Therapy : In the beginning attention was focussed on to a group of diseases collectively called immonodeficiency diseases. In such diseases defects in the gene causes blocks in the metabolism of adenosine and guanosine, the products of nucleic acids. The genes synthesize enzymes Adenosine deaminase (ADA) and Purine nucleoside phosphorylase (PNPR). The simple metabolic defects targets for human gene-therapy is outlined below :



In 1990, the first trial of gene-therapy was conducted in USA on a 4-year girl. She was suffering from ADA-deficiency. Such patients must be kept in sterile chambers otherwise chances of contracting a disease is high resulting in their death. Bone-marrow of the patient was taken out and a normal gene was transfected in the lymphocyte. The lymphocyte was cultured and injected into the patient. ADA-normal cells proliferated in the patient and overgrew the population of ADA-deficient cells.

With the success of first trial in case of ADA-deficiency disease, the same was repeated in the USA with a nine years old

girl in 1991. Both the patients are doing well.

Success in USA led other countries to follow suit. In Italy, a five years old boy was injected with corrected lymphocyte and bone-marrow cells. In Netherlands a protocol concerning ADA-gene therapy was approved in 1992. Since then many European countries have initiated successfully the practice of ADA-gene therapy.

In ADA-gene therapy, the cells of bone marrow are subjected to leukopheresis (a device separating leucocytes, WBC) and mononuclear cells are isolated. These are grown in culture under condition that stimulates activation of T-lymphocytes and its growth. Such lymphocytes are incubated with retroviral vector containing a normal ADA gene as well as the neomycin-resistance gene and then infused into the patient. Selection of neomycine resistant cell confirms integration of gene. Such cells are cultured and infused into patients.

Cancer-gene Therapy : The cancer gene therapy has started and these are extension of earlier gene-marking experiments in which lymphocytes were marked with neomycin-resistant genes and injected back into patients. In the same tumour-infiltrating lymphocytes taken out from the body of patients, in addition to neomycin-resistant gene, a new gene is inserted which synthesizes a protein called tumour necrosis factor (TNF). Although TNF is highly toxic to humans at levels as low as 10 μg/kg body Weight, there is no apparent toxicity resulting from therapy (HWU et.al.1993).

Rasko and Downes (1995) have discussed significance of Interleukin -2 (1L-2) in the gene-therapy in cancer. 1L-2 is lymphocyte activating factor. Hence if tumour cells are transfected with the gene for 1L-2, this would increase lymphocyte activity in the tumour and enhance its immune response. Transfected 1L-2 gene can be put under control of a promotor gene that is greatly activated in the tumour but not elsewhere. Treatment of melanomas is being tried with the 1L-2 gene controlled by melanin promotor.

Familial Hypercholesterolaemia : Familial hypercholesterolaemia is caused by defects in the LDL (Low Density Lipid) receptor gene located on chromosome 19. Plasma cholesterol level is very high because of two reasons-cholesterol is not taken up by the cells as well as genes synthesizing cholesterol is not turned off. The gene encodes a transmembrane protein.

First began the animal trials. The opportunity presented when Watanabe, University of Kobe, found out in one of his rabbits the cholesterol nodules in his feet. The defect was due to hypercholesterolaemia. Animal trial of gene-therapy for the disease started with this WATANABE RABBIT and proved successful.

Gene-therapy for the disease in humans was carried out in Michigan in 1992. A female patient underwent gene-therapy for the disease. A quarter of her liver was removed and it was infected with a modified retrovirus containing the LDL-receptor gene. The transformed liver cells were injected into her blood and these cells re-incorporated themselves in the liver. The patient is doing well (1995-96).

Patient Therapy & Embryo Therapy

Gene therapy can be performed either with the patient (patient therapy) or with the embryo after detecting inheritable abnormality in it. Embryonic cells can be obtained from the amniotic fluid surrounding the embryo (Embryo therapy). There is distinct possibility that both patient therapy and embryo therapy will be performed successfully in large numbers in future.

Patient therapy involves following steps :

1. Identification of defective gene.
2. Isolation or synthesis of normal gene.
3. Isolation of the cells of the tissue where the gene will function.
4. Placement of normal gene on the correct site on the host chromosome so that it can function.
5. Deletion of defective gene, if there is one.
6. Re-introduction of changed cell back into its original tissue.

In general there are faced 3 difficulties :

1. Introduced gene is unable to function in the cell.
2. Introduced cell is unable to function in the tissue.
3. Most of diseases affect variety of tissue hence there is problem in selection of the tissue-system for introduction of normal copies of DNA.

Embryo Therapy

Though used only in case of mouse and rabbits, the

technique can be used for human being also in near future. In such therapy, embryo is not taken out from the womb of mother but an embryo is formed outside her mother. By using technique of In Vitro Fertilization (IVF) or test tube baby, egg is taken out of mother's body and fertilised outside. As soon as zygote starts developing, normal gene is injected either directly by microinjection or attached to a virus and transfected along with it.

Exvivo & Invivo Gene therapy

Patient therapy is performed in two ways- either cells are taken out of the body of the patient, cultured, gene introduced, the modified cell proliferated in a suitable culture medium and transplanted back into patient's body. This is called exvivo gene therapy. Alternatively, a new gene or some construct can be delivered to the cell in the body of the patient. Such a method of gene-therapy is referred to as in vivo gene therapy.

Steps In Gene-therapy

Whatever be the mode of gene-therapy, it is essential to isolate the normal gene which could be used to replace the defective gene. Once the isolation of the normal gene is complete, means and methods are devised to attach it to some vector which would deliver the normal gene into the cell. Hence, following are the necessary steps in gene-therapy-

1) Isolation Of Normal Functional Gene : The sequence of function of the gene is DNA - mRNA - Protein. mRNA of a protein can be located and mRNA can be used to synthesize copy DNA (cDNA). cDNA functions as normal DNA.

2) Direct Transfer Of DNA Into Cell : The DNA thus isolated can either be introduced in the cell needing therapy either directly or through some vector. The methods of direct transfer includes :

a) *By micro manipulation* : The DNA is introduced in the OVA. The OVA is held by a blunt pipette under a microscope and DNA in solution is taken in a micropipette and injected into the cell.

b) *By air-gun biolistic method* : Small microparticles of gold or tungsten is coated with DNA and introduced by helium air-gun. Previous attempts used gun-powder but now high pressure gases are used to operate the gun.

c) *By strong electric current* : A strong electric current is

passed in the solution containing both the cell and the DNA. Due to current, a small hole is formed in the cell through which DNA is taken into the cell and integrated into its genome.

d) *Use of Calcium Phosphate* : When the DNA and the cell is incubated together in presence of calcium phosphate, the DNA is integrated with the nuclear DNA. The process is more useful for transfer of whole chromosomes.

E) *Use of Liposome* : Liposomes are artificial lipid-closed vacuoles. They can be formed by phospholipids extracted from tissues and mixing it with water. They can be filled with DNA. Liposomes carrying DNA is fused with cell in medium containing polyethylene glycol. It is used in gene-therapy of cystic fibrosis.

There are various devices to check whether the exogenous DNA has integrated into cell genome. Southern blotting, Northern blotting, Western blotting can be performed to check DNA, RNA, protein respectively. such techniques are described in the chapter "Tools of molecular genetics".

The integration of the exogenous DNA occurs at random chromosomal positions. The exogenous DNA, if combined with regulatory genes, they function at the new locations. This method, however, does not lead to replacement of defective gene.

3) Transfer Of DNA Through Vectors : A number of vectors are used for transfection of the mammalian cell by DNA. Such vectors include viruses of various kinds, Plasmids, etc.

The viruses that have been found suitable as vectors include retroviruses, vaccinia virus, adeno-associated virus (AAV), herpes viruses and bovine papiloma virus.

Papovaviruses (SV40 and Polyoma) and adenoviruses were initially used but since their capacity for carriage of large DNA segment is limited they can not be used for carrying genes which are large in size. Mashour et.al.(1994) have discussed in vivo adenovirus mediated gene transfer into ocular (eye) tissues.

Retroviuses are useful vectors since they infect several cell-types and can be useful vectors since they infect several cell-types and can be used for transfection of large sized gene. The only difficulty with such vectors is that they are single stranded RNA and they cannot replicate without integrating with the host DNA. Hawley et.al. (1994) have outlined potential use of retroviuses in use of gene-therapy. A brief list of viruses and its genome sizes is being mentioned.

Viral class	Type of Virus	Genome size
1. Adeno	DNA duplex	37 Kb
2. Papova	"	5-6 Kb
3. Herpes	"	160 Kb.
4. Adeno associated	DNA (Single stranded)	5Kb.
5. Retro	RNA (Single Stranded)	6-9 Kb.

RNA viruses such as retrovirus use their mRNA for DNA synthesis which integrate into host chromosome. For gene therapy their genes, that code for protein shell, is removed so that viruses are unable to reassemble protein shell for progeny formation. All the initial experiments have involved defective retroviral vectors, in which the viral genes have been replaced by other; these viruses are obviously incapable of replicating. But retroviruses must be grown in cells, and cannot be purified entirely. If helper viruses are used to help assemble the defective retrovirus, obviously they might be hazardous. This risk has been avoided by the use of PA137 cells, a mouse line containing the necessary retroviral genes in its genome, but unable to assemble their transcripts into a functional virus, as a source of defective retroviruses. Nevertheless, even defective retroviruses might inactivate a functional, important gene by inserting into it; they might even activate cellular proto-oncogenes.

More recently, adenovirus vectors, which do not integrate into the genome and which can (unlike retroviruses) infect non-dividing cells, have become more widely acceptable. Because they do not integrate, they may be lost from dividing cells. But they are being considered even as vectors for gene transfer into brain cells, which are unsuitable for retroviruses.

Adenoviruses, however, induce greater immune response. Commenting upon vector suitability at the Nature's conference on molecular medicine in San Francisco (22-33 Sept, 1994), Inder Verma from Salk Institute, San Diego said that although adenoviruses vectors have many advantages that retroviruses lack (notably growth to high titers and an ability to infect non-dividing cells), host immune responses seem likely to make them virtually unusable in vivo. Modifying cells in culture before returning them to the host (ex vivo) avoids these difficulties and has so far had more promising results with retroviruses.

The viral genetic material is cut with the use of restriction enzymes. The two pieces of the viral vector is attached to the two

ends of the exogenous DNA. Thus are formed viral vectors which are introduced into mammalian cells in culture. Transformed cells are then transplanted back into its original site in the body of host. In addition to virus vector, Caplen et.al. (1994) have suggested use of plasmid vectors also.

According to Rasko and Downes (1995) the safest form of gene therapy would involve HACs (Human artificial chromosomes). Yeast artificial chromosomes (YACs) have been successfully crated by adding telomere, centromere and active replication sites of DNA. The desired gene can be added to HACs. Creation of such a construct is easier but getting them inside desired cell is difficult.

4) Suitable Recipient Somatic Cell : The cells selected for transfection are somatic cells taken out from body. They are stem cells (undifferentiated) capable of being grown in culture and then returned to the patient. The cell-type which is being used in gene-therapy is stem bone-marrow cells from which many blood cells differentiate. A second cell-type is fibroblasts from which various connective tissue cells differentiates. Keratinocytes, the cells of skin, can easily be removed and returned through the procedures of skin grafting, is also being tried. Gene-therapy for haemophilia seems to be comparatively easier through Keratinocytes. Other cell-types such as hepatocytes and myoblasts, the stem muscle cells are also being tested in recent times (Yao et.al.1994). Circulating lymphocytes are easy but since they are not stem cells these donot proliferate in culture media. Somatic cells in their own place in the body (in vivo gene-therapy) can also serve the purpose provided a vector can reach to them along with the normal gene. Gene therapy in the cystic fibrosis is being tackled in the same way.

Deciding gene therapy : Cost Effectiveness

In order to be cost-effective, all alternative ways of therapy must be considered before deciding for a gene-therapy. Many diseases affecting one step of a metabolic pathway can be treated either by removal of a potentially toxic precursor (as in pheylketoneuria where patients receive phenylalanine free diet) or by supplying a missing end-product (as in case of adrenal hyperplasia with the appropriate steroids). Even the missing protein can be supplied directly as in case of haemophilia the missing factor (VIII of plasma clotting factors), or insulin dependent diabetes. In such case, gene-therapy even if possible is not cost-effective.

GENETIC SCREENING AND COUNSELLING

Whenever a problem related to structural or functional aspect of bodily systems afflict and runs in family, there is likelihood of its having a genetic basis. Under such circumstances an expert's advice is needed so that various aspects of the defect could be understood. A person who is seeking advice, the consultant, and the person who is advising, the counsellor, must discuss problem threadbare so that its enormity, its likelihood of occurrence in the progeny of the consultand the remedial measures, if any, that could be undertaken etc become entirely clear. Thus in a broad sense,

1. Genetic counselling aims at Screening of a genetic disorder and explanation to the patients or their parents the genetic and medical implications of the disorder.

2. Calculating likelihood of recurrence of such genetic disorder in a family.

3. To suggest ways & means that constitute best course of action in view of occurrence of a genetic disorder

According to one study, approximately half of the cases prove to involve genetic defects determined by a single gene. Another 20 percent of cases concern chromosomal anomalies and of these more than 80 percent involve trisomy 21. Another 20 percent are congenital defects with a polygenic or unknown genetic cause. On rare occasions, a family may seek advice because of anticipated problems related to consanguinity or to exposure to mutagen.

1. Screening

There are three group of persons who are likely to be screened for a defective gene - the patient himself or herself, their parents and relatives and the intrauterine foetus developing in the womb of her mother. A few years back, medical diagnosis was a problem and was limited to chromosomal examination of the adult patient and his relatives. It is easy to obtain it from their blood. In case of intrauterine foetus, it was taken out from the cells in amniotic fluid of growing foetus. Chromosomes, no doubt, are still taken out by the same procedure except for a few changes. In case of intrauterine foetus, the tissues that used to be taken out was from amniotic fluid of the foetus and its subsequent culturing

(amniocentesis). Since it was not possible to take out fluid before 4th month of gestation, it was too late for an abortion if a genetic defect was diagnosed in the foetus. Thus there started a practice to take out tissues from chorionic villi, the tissues that form placenta. There has been a late realisation that the tissues are composed of both foetal and maternal cells hence involve chances of selecting cells of mother instead of foetus. In case of intrauterine foetal diagnosis the current trend has now again shifted to a somewhat earlier amnio-centesis together with serum test of mothers to detect presence of any abnormal substance in her blood.

Since the development of recombinant DNA technology more than 3000 genetic diseases have been mapped at the DNA level. A very positive development in this field has the use of DNA DIAGNOSTIC PROBES. These are radioactively labelled segments of DNA which have sequence of the bases similar to those present in the genetic disorders. Such diagnostic probe will hybridize with the DNA to be tested if there is a similar sequence present in it. Its hybridisation can be marked due to radioactive labelling. Before application of diagnostic probes it is necessary to enlarge the gene because a gene is small enough for hybridization to be marked. For this, the gene is enlarged by Polymerase chain reaction, PCR(see chapter tools of genetic experiments). With the use of PCR, even a small section of DNA can be highly magnified for hybridization to be visible and detected.

Gene mapping for most of the genetic diseases is complete. Its chromosomal number and position is known. The gene to be tested for a defect is roughly located and probed with a DNA probe.

Currently, ligation chain reaction (LGR) kits are being developed. Diagnosis of genetic defect will then become a routine affair and accomplished with the help of even unspecialized medical personnel. Where such advanced kits are not available, the programme for genetic screening must have a DNA specialist, cytogenetic and biochemical laboratory along with trained paramedical staff who will be responsible for undertaking screening.

Medical diagnosis, together with pedigree analysis, confirms and proves presence of a genetic defect and its nature of inheritance. Pedigree of the person is absolutely essential including his or her all known relatives, with their ages, reproductive history including stillbirths, abortions and deaths. In

some cases, a simple inquiry about the country of origin or the ancestors of the two parents, and their surnames, may give a clue as to the likelihood of consanguinity. Sometimes the pedigree will show unambiguously the method of inheritance and as a result, make a distinction between two similar disorders with different modes of inheritance. However, direct diagnosis of defect by use of diagnostic probes has more or less replaced all those round-about ways used in the past for diagnosis of a disease.

Once the diagnosis establishes the defect, its full implications must be explained to the patient. For this, a counsellor must have access to all informations regarding genetic defects, including all the researches being carried out in this field. Information about mapping of the genes known for defects, their nature of inheritance, the symptoms caused by it, the likely course of remedy, use of drugs etc. are some of the fields the counsellor should be well versed with. There are plenty of medical literature on genetic defects. A catalogue, Mendelian inheritance in Man, issued by DR. V. McKusick, brought up to-date every few year, is useful in providing the basic information about all known genetic disorders. Another useful source is Birth Defects : Original Articles Series, edited by D.Bergsma. Cooper and Schmidt(1986) have also came out with a catalogue of genetic diseases. Rasko and Downes (1995) have discussed in detail mapping of many genes responsible for genetic defects.

2. Calculation Of Risk

Once diagnosis establishes some abnormality in the DNA of an individual, the calculation of risks to their offspring becomes the main task of counsellor. As defects can be due to one pair of allele or several pairs, consequently simple and complex systems exist.

a. Simple Systems : It has been stated in the beginning itself that 50% of cases for which counselling is sought for belong to category of diseases which are determined by a single pair of allele. Such ailments are transmitted in either dominant or recessive fashion, and that their alleles may be located on autosomes or on sex chromosomes. Such genetic ailments have simple Mendelian patterns and hence genotypes of offspring can be predicted on the basis of genotypes of two parents. Estimation of risk is accomplished by application of Bayesian principle. In case, one affected child is born to parents recurrent risk can be calculated.

a. Estimation Of Genotype Status Of Parent : It can be accomplished by application of Bayesian principle. Let us study a case of X-linked recessive gene such as muscular dystrophy. A consultand woman wants to know probability of her being heterozygote.

The consultand (person seeking advice) is marked C. The grandmother of the consultand has two affected sons and is therefore virtually certain to be a carrier. Thus the mother of the consultand has a prior probability of 1/2 of being a carrier. The fact that the mother had two normal sons reduces the likelihood that she is indeed a carrier. However, study the table following the conditional probability is the probability that two sons would be normal under each of the two stated conditions. If the mother is heterozygous this value is 1/2 x 1/2; if the mother is not heterozygous it is, of course, 1.

Table: *Bayesian calculation relevant to the example*

	Consultand's mother heterozygous	Consultand's mother not heterozygous
Prior probability	1/2	1/2
Conditional probability	1/2 x 1/2 = 1/4	1
Joint probability	1/8	1/2
Posterior probability	$\frac{1/8}{1/8 + 1/2} = \frac{1}{5}$	$\frac{1/2}{1/8 + 1/2} = \frac{4}{5}$

The posterior probability that the consultand's mother is heterozygous is 1/5. The probability that the consultand is heterozygous is 1/10 and the probability that a son of hers will inherit muscular dystrophy is 1/20. This is an example of X-linked inheritance, coming from mother's side. For autosomal recessive genes, the probability inheritance of the gene is calculated for both father and mother. *In recent times, because of development of DNA probes, the parents, his relatives etc. can be tested for presence of an abnormal gene.* Amniocentesis and DNA probing of embryo in the recent times directly establishes the presence of defective genes in the embryo.

b. Estimation of risk of recurrence in offspring : However, if an affected child is born to the parents, much of their genotype become clear. Thus, on the basis of statistical data and genetic theory, a recurrence risk of the defect in the offspring can be calculated. Below is given a table showing recurrence risk of a

defect in another child if an affected child is already born to the parents.

MAGNITUDE OF RISK	(%)	GENETIC BASIS	
Total	100	Both parents are homozygous recessives	(aa x aa)
High	75	Both parents are heterozygous for an autosomal dominant with full penetrance	(AaxAa)
	50	One parent is heterozygous for an autosomal dominant	(AAxAa)
	50	For sons, a sex-linked gene carried by the mother	(XXxXY)
Moderate	30	Down's syndrome due to translocation of part of a 21 to another autosome in one parent	chromosomal aberration
	25	Recessives with full penetrance ; both parents heterozygous	(Aa x Aa)
Low	5-	Down's syndrome due to trisomy 21, arising or less from meiotic nondisjunction in one parent, most likely the mother	Chromosomal Aberration

B. Complex Systems : Estimating the risk of monogenic disorders are easier because they follow typical Mendelian pattern of inheritance - if a person with defect marries a person without defect, both the genes will be present in offspring and when the offspring form gametes, the genes will segregate in 1:1 ratio.

Many diseases such as coronary heart disease, high blood pressure, mental disorders, diabetes mellitus, autoimmune diseases such as arthritis, asthma and many hormone related diseases and cancer etc. have genetic basis because in many cases they have been shown to run in families. Such diseases, however do not show Mendelian inheritance. Such diseases are believed to be controlled by polygenes (several genes acting at different loci and controlling same character) with a strong environmental contribution (i.e. with a weak penetrance of a gene). A person with genes for hypertension may not develop it, or develop very late if he is kept away from anxiety. Too much of tension and anxiety predispose him earlier. This has been proved by many experiments, including those of "executive monkeys" in which monkeys who were constantly kept in tension by certain

experimental acts, developed high blood pressure. Studies of monozygotic twins have also confirmed the role of environment in such complex diseases. In such circumstances a counsellor has two options -

1. Cases in which too much of genetic analysis is not possible, it is duty of the counsellor to determine the causative environmental factor(s) so that these may be reduced.

ii. Cases in which at least single genetic factor has been established, such as several psychiatric disorders, the counsellor can screen the potential carrier of the gene. In a few cases, such as atherosclerosis (hardening of arteries because of deposition of cholesterol - hypercholesterolemia), a wide array of genetic factors have been located. The counsellor can screen the patient in probability and advice him accordingly about his dietary and other habits, including his life-style.

Heridibility of complex systems can also, in principle, be calculated for a factor of phenotype i.e. the proportion of a observed variation in co-population which is caused by genetic variation. This calculation, however, will be valid for a population which is exposed to the same degree of environmental variation that applied to the studied population. If genetic factors in psychiatric ailments works out for Bihar to be 60%, the ratio can be applied to only those places which are plagued with the same amount of social tensions of similar nature.

Problems Arising During Screening And Counselling

1. Mistaken Paternity : Situation becomes complicated if patient has mistaken paternity, that is, their mother's husband (and their legal father) is not their biological father, a fact not generally known to either husband or child. It is understandable that the mother might be unwilling to transmit this information during a counselling session, particularly if her husband is present. Mistaken paternity may be revealed if a child is homozygous for an allele that only the mother carries (Tay-Sachs disease or PKU) or if the child carries an allele that neither the mother nor her husband has (sickle cell trait). (It can also be uncovered accidentally in the course of routine blood group testing of the family).

2. The Problem Of Confidentiality : Sometimes during screening process or a pedigree analysis, counsellor may discover a serious genetic ailment afflicting the patient and a similar

probability to patient's relatives. The counsellor or patient has the right to this confidentiality and they may not discuss it with any people.

The point of confidentiality involves patient's socio-economic status also. Genetic discrimination (Rasko and Downes, 1995) has become one of the latest forms of discrimination and screening programmes, if not kept a closely guarded secret, are apt to fan it. Disclosure of a defect would sometime mean loss of a job and chances of insurance.

3. Difficulties In Interpreting The Genetic Analyses : There is less problem in genetic analysis - It can be easily discovered whether patients are carriers or not, or whether their offspring face the risk or not. But these all are matter of probabilities, particularly in autoimmune diseases where a particular type of HLA predisposes to the disease. In addition, in the cases where a dominant disease allele has a low expressivity the nature of advice to be given seems difficult to decide. The question not only is what to advice but also whom to advice (Rasko & Downes,1995)

4. Failure To Differentiate Between Neutral Polymorphism And A Disease State : In both the cases DNA changes are involved. As genetic testing spreads, more and more people will be found to carry small mutations in some gene or other, which are not themselves known to cause diseases, but are not normal. The only way to distinguish a rare neutral polymorphism from a rare disease causing mutation is to wait and see. It is not known how serious is the disease likely to be. Mutations in the CFTR gene presents the same problem (Rasko and Downes, 1995). CFTR (gene for cystic fibrosis transmembrane conductance Regulator) or cystic fibrosis (CF) is located on chromosome 7.

5. Counselling In Late Developing Diseases : It is difficult to counsel a patient or his relative who has a high probability of developing a ailment in several decades. This problem has become acute in the counselling of Huntington's disease patients ; with the recent discovery that the disease (untreatable, dominant but late-developing) correlates with a triplet expansion in the IT15 gene, genetic testing of relatives who are as yet without symptoms has become very easy. A simple PCR test will establish the diagnosis. But it is obvious that an asymptomatic relative should never be tested without their consent. It is generally agreed that the testing of potential Huntington's children should never be done at all.

GENETIC LOAD

It is generally observed that most of the mutations are recessive and harmful. Hence, with increase in number of mutant genes the population will naturally be put to greater loss because many of its individuals will be weak and sterile, or if mutations are lethal, several of them may even die of it.

Genetic load, therefore, has been defined as the extent to which a population departs from a perfect genetic constitution. This is accompanied by the loss of a portion of its individuals through their genetic death which may be expressed through sterility, inability to find a mate, or by any means that reduces reproductive ability relative to the optimum genotype; The optimum genotype is the most fit genotype of the population. The genetic Load (L) of a population is the relative amount by which the fitness (W) of the population is lowered in comparision to the optimum genotype. In a random mating population $L = 1 - W$.

The more the number of mutant loci in the population, greater will be the genetic load. Conversely, fewer the number of mutant loci in a population, lower will be the genetic load. Thus it is evident that load can be increased by high mutation rate, and decreased by low mutation-rate. Selection can only increase or decrease the number of such genes in the population; it has, however, no role in the formation of genetic load.

High selection coefficients will cause the mutant gene to be eliminated more rapidly and low selection coefficients will permit the mutant gene to remain longer in the population. In either case, however, the genetic load is same and the number of genetic deaths remain same. Insofar as deleterious recessives are produced by mutation, any increase in mutation rate will cause a corresponding increase in genetic load and consequent increase in genetic death. Thus, genetic load is increased by deleterious mutations, and selection plays no part in its formation.

Effects Of Genetic Load

Last 20 years of research and consequently the insight gained has completely changed our attitudes. Population geneticists, particularly Haldane, in the years 1930s to 1950s presented several statistical calculations to guess the extent of harm supposed to be caused to human population under varying amounts of genetic load. The situation is just reverse today. Genetic load now a days is not supposed to be a " dreaded

monster " of the earlier geneticists.

To begin with, the optimum genotype is not a stable construct. Environments usually change with time and the advantages of different genotypes change accordingly. It is conceivable that a population so perfectly adjusted to its environment-that is with little or no genetic load-may become extinct within a short period because of a rapid environmental change. On the other hand a population with a relatively large genetic load may be successful when subjected to a new environment in which formerly deleterious genes now enable it to survive. The absence of genetic load may; therefore be more detrimental to a population than its presence. Therefore, although the genetic load can be measured in terms of departure from the optimum genotype the evolutionary value of a particular optimum genotype may be a very limited one: the optimum genotype may change from place to place, or may even differ in the same place.

There has been a different angle too. For survival of a species, it is necessary that the population size matches with the carrying capacity of the environment. Too many seeds in a small field, or too many deer in a small stretch of forest ma, y cause death and extinction of the entire species. It is necessary that self-thinning of the population must occur in order to match with the carrying-capacity of the environment. To this end, phenotypic load with or without genetic load is essential because some individuals must be weak and die out in order to secure survival of the rest. Consequently, to the extent the genetic load expedites self-thinning of the natural population, it increases the probability of population avoiding extinction i.e it increases persistence of the population. Thus, contrary to the earlier beliefs, genetic load increases population fitness by bringing about thinning of the population through phenotypic load.

Overcrowding and carrying-capacity of an environment are important factors for a population fitness. If there are too many uniform seedlings in a small area, all are destined to be destroyed; if some are more vigorous than others, the chances are that those more vigorous will establish dominance and grow normally. Sacrifice of weaker individuals is necessary for the growth of stronger ones. Mutant alleles may decrease fitness of an individual, but increase those of populations.

GENETICS - LAW AND ETHICS

Genetic manipulation of human are fraught with dangers and involves several ethical aspects too. The first and foremost is the rights of the people to be individuals and no one should be allowed to deny, abridge or harm in any way this right of the people. In UK, USA and many developed countries there are national legislation which prevents genetic manipulations except under lecense. It took ten years in USA to get clearance for the first somatic gene therapy and variable times in UK, France, Japan etc for the same purpose.

The guiding force in the sphere of genetic manipulation to the different countries is the US National Institue of Health's Recombinant Advisory Committee (NIH-RAC). Many countries have suitably modified their existing drug laws to suit the purpose.

Intellectual Property rights

Another area of genetics where various laws are involved are intellectual property rights. Trade-related biotechnical processes and its products are known as intellectual property and its protection and rights are guaranteed by the state. As stated earlier, in the field of genetics the most important intellectual property is the processes and products which results from genetic engineering techniques through the use of restriction enzymes to create recombinant DNA. This is important because those who spent money on research and development must be rewarded with a license of limited term for the exploitation of their inventions. This is guaranteed under a patent.

Patents

A patent means grant of "right to exclude others from making, using or selling" an invention. Patents are usually allowed for a specified period, e.g. for 17 years in USA. The Indian patent Act of 1970 allows process patents but no product patent in the field of food, chemicals, drugs etc for five years or seven years from the filing of the application, whichever is the less. In case of a dispute, the aggrieved party has to prove that his patent has been improperly used by others.

Patentable subject matter should meet following requirements.

1. Novelty : The invention must be new.

2. Utility : It must have some utility.

3. Inventive : the process Must represent a real advance made through the insight of the inventor.

4. Disclosure : It must be disclosed in a way that a person with normal skill could reproduce it.

5. Patentable : It must relate to a technology where patents are permitted.

The patent application, with its accompanying description and the deposited material, is published after sometime during which deposited material is also available to the public in UK. In USA and other countries, the deposited material is available to the public only after some enforceable right has been granted to the applicant.

Patenting Genetically Altered Live-Forms : First patent of live-form was granted in US to a multinational corporation for a oil eating bacteria, *Pseudomonas*, discovered by a non-resident Indian Dr. Chakraborty. It was made more effective by genetic manipulation. These are used for cleaning up oil-spills. Genetically - engineered *E-coli* for production of human Insulin, human growth hormone and various other protein and hormones have been patented, such as Factor VIII for blood clotting in haemophilia, Erythropoietin for stimulatory action for RBC formation, tissue plasminogen activator for thrombolytic activity etc.

Such patenting was done is case of transgenic animals and plants also. The first animal patented was an 'oncomouse' that contained an oncogene. The oncomouse is referred to as nude mouse because of its loss of hair. The mouse is kept in a completely sterile environment because of its hampered immune system. Initially, the patent was refused by European patent office (EPO) on grounds of ethics.

Among transgenic plants, herbicide resistant cotton, insect resistant tobacco and virus resistant potato have been patented and several are in various stages of clearance.

Patenting Genes And DNA-Sequences : There is no difficulty in the patenting of artificially synthesized genes, its products proteins and the organism in which such genes function because such organisms are genetically altered.

Most hotly debated are the patenting of naturally occurring useful genes because they are not invented. There are arguments both in favour and against. Protagonists maintain that companies

must be rewarded for its expenses on isolating and utilizing hitherto unexploited gene present in nature. Opponents, mostly from developing countries, maintain that multinationals would utilise genes of their flora in making of some commercial products and then sell it to them on exorbitant prices. However, patents have been granted for genes isolated from nature and cloned. For example, patent has been granted for a mutated gene in a bacteria that confers resistance to herbicide glyphosate. The gene, when transferred to plants, would confer glyphosate resistance to it.

Patents have also been issued for gene-fragments, the 300 to 500 base gene-fragments, called **expressed sequence tags (ESTs)**. It represents only 10 to 30% of cDNA which is itself 10-20 times smaller than genomic DNA. In several cases even the full sequence chromosomal locations and biological function of the full gene were unknown. This sparked controversy and US Patent and Trademark office (US PTO) has issued a guideline (2001) stating that unless usefulness of the gene-fragment, specifically how its product functions in the nature is not explained, the gene fragments would not be considered patentable.

Critics maintain that patenting EST is inappropriate because the effort to find any given EST is small in comparison to isolating and characterizing a gene and gene product. Beneficiary of such patent will have undue control over commercial fruits of genome study. Also, allowing multiple patents on different parts of the same genome sequence would add undue cost to the researcher. He would have also to pay to his own staff for researching the different patents to determine which are applicable to the area of genome he wants to study.

Single Nucleotide Polymorphism (SNPs) — SNPs occur if there is a single base change in DNA e.g. from a sequence AAGGTT to CAGGTT. SNPs occur regularly in human genome also, both in coding and non-coding regions. Many SNPs have no effect on cell function, particularly if they occur in non-coding region but some SNPs occurring in coding region of the gene can predispose people to disease or influence their response to a drug. Many diseases of complex genetic origin eg. cancer, diabetes, vascular diseases, many forms of mental illness donot involve a single gene and single gene-hunting is not profitable in such cases. SNP maps may provide a clue to such forms of genetic diseases. It was for this purpose that, in 1999, ten large pharmaceutical companies and UK wellcome Trust Philanthropy established a consortium to map 300,000 common human SNPs and patented it.

Procedural precautions for human gene patenting

Patents in human DNA is granted only when inventor mentions that the DNA sequences proposed to get patented is "Isolated" or "purified" or "consists essentially of " DNA sequence encoding a certain protein. The phrase can be found used in the patent applications filed by different institutions/organisations who were awarded patents such as—

1) ARCH Development has patented (2001) "Isolated and purified" DNA encoding calpain 10 that can be useful in diagnosis and treatment of type 2 diabetes.

2) Oncormed obtained a patent (1988) for coding sequence of BRCA 1 gene. The sequence can be used for screening individuals with an increased genetic susce-

tibility to breast and ovarian cancer.

3) University Technologies obtained a patent (2001) for a tumour suppressor gene, designated ING1.

4) Human genome science Inc. obtained a patent (2001) for DNA encoding tr 10 receptor, a member of Tumour Necrosis factor (TNF) receptor family.

More similar instances can be cited where applicants, in order to get patent of a DNA sequence, used the aforesaid words. The words *isolated* and *purified* means the sequence is excluded from the way the particular DNA occurs in nature.

Similarly, inorder for the patent to be of any use to the patent holder, the patent must be a broader one and not just for the DNA sequence applied for. Because of degenaracy of the genetic code the natural bases can be replaced by a copyist by non-natural base. Also, some of the aminoacids can be replaced or removed without altering the protein structure and function. By such practices infringement on the patent by a copyist can be avoided. That is why patenting in DNA sequences is a broader one that seeks to minimise such tendencies which may deprive the patent holder its genuine reward.

Gene-tests : As diseased gene is found, complementary gene tests are developed to screen the populations so that individuals at risk may be found out. These tests are generally patented and licensed by the owner of the disease gene patent. Each time such tests are conducted, royalties become due to the patent holder.

Proteins : Genes function via protein. Whenever a gene is changed, protein structure changes and the function is paralysed. It is, thus, important to study protein structure especially in order to design drugs. Pharmaceutical companies have to pay rayalties if they use protein structure for drug designing.

Stem Cells :

Stem cells are undifferentiated cells of our body. These are totipotent and can be converted into any desired cell-type. It is because of this reason stem cells have become important in biomedical research. Stem cells are rare in born individuals but abound in embryos. It is because of this reason the embryo cloning is practised so that largescale harvesting of stem cells become possible. The intention is not to create a human clone but to use stem cells for treating diseases. Patents for stem cells from monkeys and other organisms have already been issued. Stem cells of human, therefore, is technically patentable. But a host of social and legal controversies and debates have originated against potential patentability of human stem cell. The concern is that such patents violate principle of ownership of human beings which says that embryos have a right over its organs and has a right to survive. Patenting has not been influenced by ethical concerns but for stem cell patenting is difficult because of such reasons.

Advantages :

1. A patent is a reward to inventor and money gained is used in pursuing research.
2. There is no wasteful duplication of effort.
3. It stimulates research in unexplored areas.
4. Secrecy is reduced and there is access for the all researchers to the new invention.

Disadvantages :

1. Patent filings are replacing journal articles, reducing the body of knowledge in literature.
2. Private biotech companies can monopolise certain gene-test markets.
3. Patent holders are allowed to own a part of the Nature — a basic constituent of life. This allows one organism to own all or part of another organism.
4. A single genomic sequence can be patented in various ways such as EST, SNP, cDNA and as a gene. This "patent-stacking" discourage product development because of high royalty costs owed to all patent owners of that sequence. These costs are ultimately passed to the consumer.
5. Patents of partial and uncharacterized EST and cDNA reward non-serious workers whereas penalise those who are serious workers engaged in determining either the complete sequence of a gene or its functions and applications. This is virtually an inappropriate reward given for the easiest step in the process.

International Co-operation

Paris convention of 1988 is guideline in making patent laws by about 100 countries who are members of this convention. The main instrument of international collaboration for intellectual properly is the world intellectual properly organisation (WIPO) based in Geneva. It doesnot enforces law but administers Paris and subsequent conventions. Member states are asked by WIPO to introduce agreed principles in their national law. Most DNA related patents are issued by the US Patent and Trademark office (USPTO), The European Patent office (EPO) and the Japanese Patent office (JPO). In India, patent cases are under the ministry of Law and Justice and governed by the Patents Act (1970) and the Patent (Amendment) Act, 2005.

Ethics of Gene-patenting

A patent is an incentive for conducting extensive research, providing monetary support and intellectual property protection. It increases creativity and allows the researchers to release their ideas freely. Income from patents allow companies to invest in expensive research towards new drugs. It takes about one billion dollars and ten years to discover, produce and market a formula. Thus, granting a patent for the novel acquisition is not out of place.

On the contrary, holding of patents, at the same time, may discourage other individuals and institutions from pursuing advanced study in that sphere of knowledge because they are supposed to pay out a huge chunk of money as patent fee. Thus majority of workers detach from it and , with only one organisation working with the research problem, the result could take a longer time than if several laboratories collaborated to study the gene.

Though patent benefits patent holders, it sometimes inhibits research in other laboratories. In a study by Cho (2005), it was found that when the pharmaceutical company Glaxo Smithcline patented a gene for haemochromatosis, a common genetic disorder in the US characterized by excess iron deposits, 25 out of 100 laboratories decided never to use this gene, and five laboratoreis discontinued

their research on the gene. The stimulation of research that patent bring to some laboratories inhibits research in other laboratories.

Gene-patents are allowed for a period of about 7 years. In this period, the laboratory is free to develop drug against the diseased gene and makeup all the expenses that it incurred on the research work. After 7 years, it is free for all laboratories to pursue their own work and the original laboratory no longer reaps all of the profits from the original drug though it may remain the leader drug by virtue of being the pioneer drug. Thus, so far development of drug is concerned, a patent for the gene seems justified.

In 2002, the Nuffield council of Bioethics proposed a compromise gene patenting. The council, which had Barton as its member, supported certain forms of gene patenting and dicouragement of others. "I am not unhappy with the patents which cover the genes involved in pharmaceutical products (such as Insulin) but I am much less happy with patents that cover diagnostic sequences and use of patent as a way to restrict research or use of informations" thus reacted Barton.

Thus, Barton argues that patents that regulate molecules still prime for research should not be granted whereas patenting of molecules that are pharmaceutically produced as drugs are appropriate.

Eliminating patents altogether is not a realistic solution. Nuffield council of ethics upheld patenting of products that compensates for the deficient body proteins arising from genetic mutations. "To get the drug, to provide incentive for (making) the drug. there you need the patent" explains Barton." The main opposition to gene patenting appears to be the academics, since in Europe and the US the public has not yet generated a strong response to gene-patenting" thus opines Stanford Emeritus law professor John Barton.

Though patents are granted for genes, it can be terminated either by the patent office or suitable court of appeal. If, anytime in future, it appears that patenting of a gene is in someway or the other preventing a noble cause the patenting can be challenged. Patenting of breast cancer gene BRCAI, and BRCA2 is case in point. Though the discovery of the gene was possible wth the collaboration of international women volunteers and British laboratories, American Pharmaceutical Myriad Genetics claimed seven patents over two breast cancer genes. With these patents, Myriad Genetics controlled all therapeutic products, lab-testing services, and diagnostic tests that use these two genes for breast cancer diagnosis which they provided for $ 2500, while French biotech companies had developed kits for the same for $ 680. The Myriad kit remained the dominant diagnostic test. In 2004, cases were filed against Myriad Genetics in Belgium, Netherland and France which led European patent office to revoke Myriad Genetics patent for BRCA 1 and BRCA2. The patent was later given to a cancer research institute that announced free use of the gene by all labs. The objection to gene patenting can be made and patent can be terminated.

But the BRCA controversy is not over. Globe Newswire via COMTE News Network posted a news on March 30, 2010 that Myriad Genetics lost the BRCA

case in the Federal District court of Newyork with the Judge Robert W. Sweet ruling that certain claims covering isolated DNA sequences in 7 of the 23 patents covering BRCA analysis are invalid. Myriad is going to appeal against the decision in the court of Appeals for the Federal circuit. Myriad Genetics believes that it has lost the battle but would try to win the war for BRCA analysis.

There is another angle to the gene patenting and its utility. With widely diverse flora and fauna, India is considered a huge gene-bank. There are many herbs of medicinal value which are being used to treat a variety of ailments in our country since time immemorial. Vedic literature (1000-2000 BC) cites 248 botanical drugs many of which find regular uses in a number of tribes for curing a variety of ailments. There have been attempts to patent these plants of medicinal value. After neem plant, there was a sinister design to patent turmeric and Kalmegh which was disallowed by active interference by government of India. Similar was the case with Basmati Rice. In India, there are thousand varieties of rice and mango which must not be allowed to be patented. We must protect our gene-bank vigorously and foil any attemp to patent them.

In a nutshell, so far law and ethics is concerned with the gene-patenting, it can be said that it is an exercise of maintaining a delicate balance between allowing continuance of wider academic pursuits and, at the same time, seeking recourse for resource generation to find ways and means for alleviating human sufferings.

Social utility of gene patenting

Consider the case of patenting of human Tissue Plasminogen Activator (TPA) gene by Genentech (1988). The drug is used in myocardial infarction throughout the world. Largescale production of pure TPA, obtaining FDA approval, conducting clinical research and bringing it to the market in the remotest part of the world needs money. The patent on the isolated TPA gene cannot be used to stop basic research on DNA whereas refusing patent to Genentech can stop it from producing TPA and supplying it to different parts of world. Who else, if not humanity, is the ultimate sufferer? Patent on TPA gene does not encompass TPA gene in any one's body. It can be argued that such patents should be awarded to the academics alone and not to corporates. In that case, it is entirely possible that there would have not been TPA in the pharmacies of the world had the discovery been made at a university and published without patent protection. However, Whether it is an academics of a corporate who "isolates and purifies" a human gene it needs to be privatised so that its fruits accrue to the society.

To conclude, whether it is academics or corporates, privatising isolated and purified human genes promotes commercialization and risk-taking. These are beneficial to society. Even the receptor protein genes, whose patenting is confusing, can be used as a drug discovery tool, or as antigen for generation of therapeutic antibodies.

GENETIC POLYMORPHISM AND SELECTION

Different individuals of a population, and different populations in themselves, differ from one another on different counts. All these differences can be broadly categorized in three groups : those differences that are purely environmental (non-genetic) such as a person's language; those differences that are purely genetic such as blood-type of a person, and, those differences that result due both to environment and heredity such as intelligence.

Genetic Polymorphism Versus Phenotypic Polymorphisms : The genetic variations far outnumber phenotypic variations. Phenotypic variations are only the proverbial tip of the Iceberg of the genetic variation. Many genetic variations are concealed at the DNA, chromosomal and cellular-levels and are not expressed for us to see. Darwin was amazed to see the extent of phenotypic variations of different populations though he could not get to the roots of these phenotypic variations. With the growth of biology and consequent improvement in the techniques for study of DNA chromosome and cell it is now clear that phenotypic variations are negligible in comparison to vast accumulation of genetic variations displayed at cellular and sub-cellular levels.

Polymorphic Vrs. Monomorphic Population : Many of the genetic polymorphism is expressed at the phenotypic levels that is why we come to know about existence of genetic variations. Those characters that are present in continuous, graded series of phenotypic trait such as skin colour, height in man are not polymorphic traits. Polymorphic traits are discrete, discontinuous genetic characters such as ability to taste phenylthiocarbamide (PTC), or ability to roll the tongue longitudinally. Individuals fall into discrete classes - taster or no -taster, tongue rollers or no-rollers - The graded or continuous variations are controlled by many genes (polygenes) and are strongly modified by environment. The discrete, discontinuous traits are controlled by single genes or closely linked genes (=super genes) acting together as unit and are less modified by environment. By examining discrete, discontinuous variations, genetic polymorphism existing in the population can be deduced without recourse to examining their DNA, chromosome and cell.

Populations composed of individuals with discrete, discontinuous genetic traits are said to be polymorphic whereas

those lacking such individuals are monomorphic. A population which includes individuals some of whom are taster and some non-taster; some of whom are roller and some non-roller is a poly morphic population. Populations with only tasters, or with only non- tasters etc. are, naturally monomorphic.The term polymorphic and monomorphic are applicable to both phenotype as well as genotype.

Definition and Sources of Polymorphism : Polymorphism is defined as "Occurrence of more than one morph (or gene loci or supergene) in a population in such a way that the rarest of them cannot be maintained by recurrent mutation". Though mutation is the ultimate source of all genetic polymorphisms, in order to be classified as genetically polymorphic trait a character must be present in a frequency greater than about 1 percent. If it is present in frequency below this, it is supposed that it is arising due to mutation and selection is not operating on it. It is only above 1% ratio of its presence in the population that we are sure that some selection is involved in its maintenance in the population and it is not because of recurrent mutations.

Though mutation is the ultimate source of all new genes in the population, a population is not dependent entirely on mutations for genetic poly morphism to develop. Mutation rate is very slow, a mutation appearing in a locus at the rate of 1 per 1,00,000 loci per generation. Such a small rate of mutation cannot maintain the observed genetic polymorphism in the population. The supply of genetic polymorphism upon which selection acts is provided by a variety of genetic combinations built up over many generations by the flow of genetic information from neighbouring population (migration) and genetic recombination and product of mutation and selection. Evolution is never dependent solely upon mutation.

Genetic Polymorphism At Cell-surface

Various types of cells are characterized by presence on their surfaces certain antigenic molecules (Antigens are complex bio-molecules of high molecular weight capable of inducing formation of antibodies. It includes such bio-molecules as proteins, polysaccharides, lipids etc). Human blood has antigens A,B,AB,O on the surface of their RBC. These antigens are glycoproteins in which certain sugars are linked with protein. The genes present on chromosome - 9 elaborate enzymes called transferases which add a particular sugar to the protein - in group A, a particular sugar, acetyl galactoseamine is added to the parent substance. In group

B, the sugar galactose is added to the parent substance. In group O neither substance is added to the parent substance. Thus a bio chemical substance present on the surface of RBC vary in different individuals of a population. The extent of variation with ABO system differ in non human primates chimpanzees have A and O blood groups, and Gorillas have only B.

This is not the only antigenic variations at RBC surface. Antigens of different chemical nature determined by different gene loci are known such as Rh-antigen by genes on chromosome 1, MNS antigen by gene on chromosome 9, Duffy antigen by gene on chromosome 1, kidd antigens by gene on chromosome 2, Lutheran and Lewis antigen by genes on chromosome 22, Xg by gene on chromosome X and so on. Many of these antigens are present in great majority of populations the world over, others are limited to a few families. Some of these antigens have been identified in the non-human primates also. Rh-antigens are shared by man and rhesus monkeys. Kell and Lutheran antigens are also indicated in some non-human primates.

Only RBC do not specialise in possessing polymorphic traits. Other tissues also possess significant amount of genetic polymorphism. In graft or transplantation experiment the graft is rejected by the host organ. The reason is that tissues from different individuals possess different antigens, called histo compatibility antigen or HL-A (Human leucocyte antigens because these antigens are best expressed on leucocytes). The genes involved in the elaboration of these antigens are complex and known as major histo compatibility System (MHS), located on chromosome 6. The system has extraordinary levels of polymorphism so that no two individuals, except identical twins, possess the same HLA - system.

Genetic Polymorphism at Chromosomal Level

Chromosomes often undergo various rearrangements. Many of such rearrangements have been studied in prokaryotes and eukaryotes, including mammalian systems. These include insertional elements (IS elements), deletions, transposons, amplified and converted regions of chromosomes. Besides, chromosomal aberrations such as inversions and translocations are often present in the chromosomes. (Chromosomal rearrangernent or sequence rearrangements differ from chromosomal aberrations arrangements are usual process of chromosomal behaviour where as aberrations are unusual distortions of chromosomal structures

Both can be present in the population if they confer adaptive advantage to its possessor).

Insertional elements (IS elements) are stretch of nucleotides averaging more than 1000 base-pairs that are removed from a chromosome and moved to another chromosome. Such a feature affect function of genes present in both of the chromosomes depending upon where the segments are removed from and where attached to - making a functional gene non-functional or vice-versa, Deletions are removal of a portion of chromosome; deletion of a functional part of chromosome can be detrimental, but removal of a non-functional part may bring two functional parts close together thus modifying each other's functions. Transposons are mobile genetic elements which are copied from one chromosome in the form of DNA (prokaryotes) or in the form of RNA and then back to DNA (eukaryotes). Such mobile elements move on to another chromosomes and inserted there. Enzyme transposase makes such events possible. This enzyme is synthesized by transposons themselves.

Several such transposons have been described in maize by Barbara Mclintock for which she was awarded Nobel Prize. Later on its presence in *Drosophila* was also reported and it included Copia elements, P-element and Fold Back (FB) element. Mammalian systems are not exception to this rule. The details of such systems should not concern us here.

Amplified Chromosomal Regions are characteristic of lampbrush chromosome of amphibian Oocyte and polytene chromosome of many insect larvae. In many circumstances chromosomal portions are amplified so that many copies of the DNA are present to synthesize larger amounts of RNA. This is a developmental feature and any change in such regions is sure to have major consequences for the developmental patterns.

In the converted regions, there occurs a loss of original part of chromosome and its replacement with part of another chromosome so that there occurs triple copies of the same region of chromosome.

Chromosomal inversions and chromosomal translocations are described in many eukaryotic systems, including man. In many cases these are involved with syndromes but nevertheless express polymorphism at the chromosomal levels.

Chromosomal fusions often occur. Chromosome-2 of man seems to be produced from fusions of two shorter chromosomes

of its ancestors because chromosome-2 pair in apes Chimpanzee, Gorilla and Orang-utan is represented by two smaller chromosomal pairs, making total chromosome number in them 48. Upto 1956, it was believed that human chromosome number is also 48 but Tjio and Levans, because of improved techniques of staining, showed that the number is 46. Similar is condition with Indian and Chinese deer muntjac. Both are closely related but Chinese deer has 46 smaller chromosomes but Indian variety has only 6 in females and 7 in males, but their chromosomes are much larger than the Chinese variety. Such features point out that in course of evolution chromosomes may undergo fusion exhibiting polymorphism at the chromosomal level.

Different types of chromosomal rearrangements, aberrations and fusion described as above may involve drastic shifts in the character manifested, thus providing opportunities to agents of selection to act and effect major evolutionary consequences leading to macro evolution (evolution of taxa higher than species level). Though such a consequence has not been witnessed in the evolutionary history of man in recent times, it might have had occurred during periods of upheavals when human ancestors evolved from one lower taxa to higher one. Such drastic changes in chromosomes are pronounced during periods of shock and result in the origin of new chromosomes that are acted upon by agents of natural selection.

Polymorphism at the level of Gene Products

Two sorts of tools enable us to identify polymorphism at the level of gene product (the proteins). These are electrophoresis and amino acid sequencing. Proteins are charged molecules, and genetic changes in their structure may involve a change in electric charge, which in turn can alter their shape. Proteins with quite small differences in charge or shape can be separated by gel electrophoresis. The method was first used in a survey of human molecular polymorphism in the 1960s, and the results were unexpected. Instead of most people being alike in most of their genes products as had previously been assumed, about a third of the enzymes surveyed showed differences in electrophoretic mobility between two randomly chosen Englishmen. Diversity was the rule with these gene products .

We now know that some proteins, such as proteins of the eye lens and muscle scarcely vary at all, whereas others have much more variation that can be seen from simple electrophoresis.

Other primates are almost as variable as are humans, and share many of their protein polymorphisms with ourselves. Several human proteins (such as haemoglobin) have been sequenced. In haemoglobin, sequencing has revealed hundreds of hidden variants. Some involve changes in single amino acids, or duplication or deficiencies of sections of the protein. Occasionally, different protein chains are fused together, or there may be changes in the time when the protein is produced. Effects of such changes can range from those of neutral to beneficial to harmful. Thus haemoglobin Hikari from a few families of Japan is a neutral change, haemoglobin Chesapeake is a beneficial change that loads Oxygen more efficiently, and haemoglobin M such as Hb-M Boston, Hb-M Iwait, Hb-M Hyde park and Hb-M Milwaukee I are harmful. Such polymorphisms at the gene product level is sure to provide a much varied assemblage of raw materials upon which selection can have opportunity to act upon to produce adaptive types. A much studied Hb- variant, sickle cell haemoglobin, that results due to a single aminoacid change at 6th position in B-chain (aspartic acid replaced by valine) is a case in point. The change definitely lowers the capacity of haemoglobin to load oxygen, nevertheless it is useful because it provides resistance against malaria. Polymorphism at the level of gene product thus will be maintained by selection so that population will always show up polymorphism with this feature of Hb. Another protein which show considerable polymorphism is isozymes or isoenzymes. These are various forms of an enzyme so that enzymes are functionally similar but structurally different. One such enzyme is lactic dehydrogenase(LDH). The enzyme shows up 5 forms in a single individual - AABB, AAAA, BBBB, AAAB, ABBB, A and B are different protien chains.

Polymorphism at the level of DNA

All inherited differences whether in height, colour, blood group or proteins represent changes in the structure of DNA. Molecular biology using techniques such as restriction enzyme analysis and DNA sequencing is beginning to give us an insight into the extent of variation into all our DNA. Nature and action of restriction enzyme (restriction endonuclease) and method of DNA sequencing has been discussed in the chapter dealing molecular techniques. It is suffice to say here that these enzymes cut DNA at specific points determined by definite sequence of bases; by DNA sequencing we analyse the sequence in which different bases are

arranged in the DNA.

In the chapter dealing with nature of hereditary material of man redears were informed various types of DNA present. It was pointed out that a vast majority of the DNA is non-functional among which various types of satellites predominate. Satellites are short sequence of few bases which are repeated several times. B-globin gene family has been thoroughly analysed. It is found that when DNA of different individuals are cut with restriction endonucleases, we find different restriction fragment lengths of DNA in different individuals, meaning thereby that sequence of bases is differing in different individuals. Such polymorphism at DNA level is called Restriction fragment length polymorphism (RFLP). At the hypervariable minisatellite, several fragments are generated which contain variable number of tandem repeat (VNTR). The extent to which human DNA can be variable is amply proved by RFLP and VNTR.

Role Of Selection In DNA Polymorphisms : How is selection applied to such an enormous extent of polymorphism shown at the level of DNA? Answer to this question lies in another question : To what extent the enormous polymorphisms at DNA level are useful to us? There is no universally accepted answer. Some reject all such DNA as "genetic garbage" or "Selfish gene". Others see in such sequences a storehouse of genetic information which can be utilised in various ways to work out novelties whenever the species is in need for its survival in periods of threatened existence. We can safely reject both the extreme views with the conclusion that all such polymorphisms at DNA level may not be important for selection to act upon to effect Darwinian fitness either in the short term or long term. To say the same thing in another way, these are not genetic variations which Darwin would have been interested in even if he had come to know about it for he was interested in those genetic variations which provided Natural Selection opportunity to act upon and produce adaptive types. A number of genetic polymorphisms may not be adaptive in the true sense of the word. All persons differ with respect to Major Histocompatibility Complex (MHC) genes when they do not differ much in life span and offspring born to them.

Theory Of Genetic Load : The issue has been a point of hot debate among the biologists. Population geneticists had earlier concluded that the total amount of genetic variation maintained in natural populations could not be large. It was because too much variation in a population would lead to serious departure from

overall fitness because variants would have differing gene-frequencies from the gene-frequencies producing overall fitness, the optimal average population fitness. Thus maintenance of too much of genetic variation would mean increase in genetic load, affecting overall average population fitness and the population would be driven to extinction. Two things are now recognised : genetic load is not deterimental to population (see genetic load) but essential for thinning of population ; and secondly, fitness has a threshold effect, capable of abosrbing a great amount of genetic variation.

Neutral Theory Of Kimura : Contrary to the earlier beliefs of population geneticists, the amount of genetic variability has turned out to be immense. It is, however, not indicated that how these polymorphisms at genetic level is reflected at the function level. Kimura advocated the theory that vast genetic polymorphisms at the gene and protein level involve only alteration of structure, being equivalent at functional level. Such variants, being functionally equivalent, would respond similarly to selective forces. Such polymorphisms are referred to as "selectively neutral" by Kimura.

Many object to Neutral theory of Kimura. Notable among them are Ewens, Johnson etc. They maintain that these polymorphisms have selective basis and might be useful in some way for different shades of environment, including its biological and physico chemical aspect such as nutrition, infectious disease, parasites, predators, physical features of environment. Alternatively, it might be useful in limiting inbreeding so that gradually building up over a period of time sufficient genotypic differences for species divergence. There are still more arguments but no argument is universally accepted. Operation of selective agents clearly manifest when genetic polymorphism provide definite advantage to the population. Studies of distribution of ABO blood group, Sickle Cell anaemia etc. clearly prove the point. (see selection)

Monomorphism And Stablizing Selection

Several characters in the population are more or less permanently polymorphic. Sex is one such polymorphic feature. Stable polymorphic features are maintained in the population by stabilizing selection. Stabilizing selection removes from the population those individuals that deviate from the population mean. Thus individuals not perfectly male or female are removed from the population so that population shows only two discrete individuals

with reference to sex - male and female.

Transient Polymorphism And Directional Selection

Polymorphism may be a transitory phase in the sense that certain populations, with shifting environmental demands, shift their population mean for some character in the direction of environmental change. This has been shown experimentally by Kettlewell in case of industrial melanism in a moth, Biston betularia. When environment got polluted, a mutation for black colouration spread in the population of white moths that protected it from being sighted by predator. At a time, when one form has not replaced the other, a polymorphic population may exist. But gradually over the time transient polymorphism is replaced by monomorphism.

Balanced Polymorphism And Superiority Of Heterozygotes

When, in a polymorphic population, heterozygotes are superior to both homozygotes, it is favoured by selection.

An outstanding example is the selective control of sickle-cell gene. Recessive homozygotes ss develop sickle-cell anaemia which is characterized by gross distortion of RBC. The condition is mostly fatal. Heterozygotes, Ss develop sickle cell trait showing sickling effect under low 0_2-tension. Dominant homozygotes SS, are normal. With regard to this gene, thus, individuals are Normal (SS), showing sickle-cell trait (Ss) and sickle cell anaemic (ss).

The gene for sickle cell anaemia, though largely disadvantageous, has continued to exist in many African populations because the condition of sickle cell trait provides resistance against malaria. The advantage is responsible for maintaining a balanced polymorphism at sickle-cell locus-(0.2).

Superiority of heterozygotes have been found in some more cases of haemoglobin :

1. In West Africa variant of haemoglobin occurs called Hb-c. It has been found that heterozygotes of the Hb A/Hb-c are at advantage in comparison to both homozygotes because heterozygosity results in resistance against many blood parasites, not against malaria only.

2. Similarly, in thalassaemia, production of α and β chain is abnormal and can result in two states - thalassaemia minor if only

one chain is affected (heterozygous) or thalassaemia major if both chains are affected (homozygous). The former provides protection against malaria in several African tribes, but the latter is fatal.

Polymorphism, thus, provides a population with alternative set of traits of a character. In a stable environment it may be of little significance. But under conditions when an environment comes under flux of changes, populations with different polymorphic traits can explore for an adaptive success. The different polymorphic traits, thus, are not only suitable for the present environment but also a potential solution for the future environment. DNA polymorphism has only beginning to show : Only future can assess the potentialities of these vast polymorphisms.

ORIGIN OF LIFE (BIOPOIESIS)

Since the conditions under which life originated no longer exist and the initial products of biopoiesis not available to us in the from of fossils, the various steps through which life could have originated is largely a matter of conjecture. Many theories about the origin of life, such as special creation, origin on other planets, or sudden creation from inorganic materials, either lack experimental investigation or are so improbable that they receive little consideration. Serious and sincere theories are known to us only since the time of Darwin and we owe it to Darwin, Haldane, Oparin, Miller-Urey, Fox , Orgel, Crick, Woese, Eigen, Cairns-Smith, Dyson(1985) and a few others for our knowledge about biopoiesis.

Origin Of Earth And Primeval Atmosphere : There are two main theories that explain origin of the earth- the planetesimal theory that supposes earth to be a broken part of the sun, and the nebular theory that supposes creation of the sun and the planets together from a spherical cloud of cosmic dust, the latter theory has generally been accepted. The cosmic dust, because of rotation and gravitation, developed a sun at the centre with halo of gas around it. The halo, later on, broke off into smaller clouds, condensed by gravity and formed planets.

a. Sorting Of Atoms : While the earth was in a more or less gaseous condition, the various atoms became sorted out according to weight, with the lighter elements (H, O, C and N) in the surface gas, and the heavier ones (Silicon, Aluminum, Nickel and Iron) towards the centre. At first, many gases such as hydrogen, Helium, Methane, Water Vapour and Ammonia escaped from the earth, but when the gaseous materials became dense enough, the gravitational field tended to prevent these gases from escaping into outer space.

b. Cooling Of Earth : As the initial temperature of the earth was very high (5000-6000^{0}C) no formation of molecules could take place because heat disrupted the bonds that held the atoms together. However, the earth cooled rapidly due to convection and radiation. As temperature dropped, water vapour condensed and poured as rains, further cooling down the earth. As the hydrogen, carbon, oxygen and nitrogen were at the surface they cooled first, and accordingly, formed molecules first.

The rain-water, in repeated cycles over millions of years, formed large bodies of hot sea-water to which simple molecules thus formed were washed out. The flowing rain water carried along

with it minerals and salts dissolved from the rocks that it found in its way.

c. The Primeval Atmosphere : The primeval atmosphere was a reducing one in which most of the oxygen was bound in water or metallic oxides. The four elements viz C,H,N and O combined to form ammonia, methane, hydrogen, and water. The oxidising atmosphere at present day evolved later on with the evolution of photosynthesis and release of oxygen in the process. Formation of CO_2, an oxidised product of carbon, also occurred later on together with release of oxygen. Origin of photosynthesis is thus primary mechanism that changed original reducing atmosphere into present day oxidising atmosphere (with the release of oxygen and formation of carbon dioxide).

d. Problem Of Biocatalyst And Energy : Organic compounds are synthesized in the body of organisms only because every step of the synthesis is dependent upon some biocatalyst, called enzymes. These are proteins. When there was no organism, how would one account for these enzymes? Moreover, enzymes themselves are protein, a complex macromolecule. Hence they must have evolved only after evolution of simple organic compounds. The dilemma has been solved by recognising the fact that chemical reaction for synthesis of simple organic compounds can occur in the absence of enzymes, though slowly. Enzymes only hasten the reaction rate.

In present times, the source of all energy is the sun; the energy fixed by green plants by photosynthesis. How would one account for sources of energy in the absence of green plants which must have evolved much later. Therefore, other sources of free energy must have been used. It has been demonstrated by a series of experiments that UV-light from the sun, electric discharges such as lightening from clouds, heat from volcanoes supplied energy. This is evidenced by following experiments :

i. Miller's Experiment (1953): S.L.Miller circulated a mixture of water vapour methane, ammonia and hydrogen continuously for week over an electric spark and he was able to get certain amino acids.

ii. Calvin's Experiment (1964) : M.Calvin and others subjected a mixture of methane, ammonia and water to a bombardment of electrons from the Berkeley cyclotron, and after an hour got adenine, one of the four bases of the DNA molecule.

iii. Fox's Experiment (1964) : S.W.Fox propose that heat

may have played an important part in the synthesis of organic compounds. He heated a mixture of methane, ammonia and water to 1800^{0}F and found a series of amino acids.

iv. Bahadur's Experiment : Bahadur obtained almost all the possible amino acids by subjecting a mixture of paraformaldehyde, ammonia and ferric chloride to strong sunlight.

V. Synthesis Of ATP : Experiments similar to this have been performed by different workers. In one experiment when hydrocyanic acid (HCN), adenine, ribose, ethyl metaphosphate etc were exposed to UV-radiations, several aldehydes, purines, pyrimidines, fatty acids, RNA nucleotides and ATP were formed. Thus it was proved that ATP could have formed in the primeval ocean. ATP is the great energy molecule of living systems and is immediate source of all energy.

It is thus concluded that several sources of energy such as lightening, UV-radiations, heat of volcanoes and strong sunlight was utilized in the synthesis of simple and complex organic compounds including ATP that acted as immediate source of energy for the living entity as and when it arose.

Traditional Views : It was Darwin who suggested for the first time that amino acid could have survived as aggregates because of absence of microorganisms, and might have linked together to form protein under the impact of light, heat and other substances. Such organic aggregates can no longer exist today because it is sure to be devoured by microorganisms.

JBS Haldane the British biologist, recognised the importance of four elements (C,H,O and N) and hypothesized that primeval gaseous atmosphere consisted of water, CO_2 and ammonia. When UV-rays shone on these gaseous mixtures, many organic substances such as sugars and amino acids were formed. He further stressed that because of no free Oxygen (from plants), and consequently no ozone and ozone-layer that filters UV-light from coming down to the earth, the UV-light must have been intense in those days.

Modern Theories Of Origin Of Life

There are three groups of theories about origin of life - Oparin's, Eigen's and Cairns-Smith's.

Oparin's View : Oparin (1924) supposed that the orders of events in the origin of life was : cells first, enzymes second genes

third. He put forth the idea of coacervates-small droplets of fat suspended in medium of water, analogous to biological membranes of living cells. Oparin proposed that life began by successive accumulation of more and more complicated molecules within the coacervates. Enzymes and genes arose within it later on. The theory ruled the scientific world for fifty years because it was the only alternative to Biblical creationism.

Eigen's View : Eigen et.al. (1981), however, consider the entire event in opposite direction - genes first, enzymes second and cells third. It has now more supporters because structure of RNA is simpler than protein and they are the primary molecules, proteins being the secondary.

Cairns-Smith's View : Cairns-Smith's theory (1982) of the origin of life has clay first, enzymes second, cells third and genes fourth- a natural clay crystal directed origin of life which finds no supporter.

Dyson's Theory Of Double Origin Of Life : Dyson (1985), in his book "Origins of life" discusses that there are two logical possibilities for life's origin. Either life began only once, with the function of replication and metabolism already present in rudimentary form and linked together from the beginning, or life began twice, with two separate kinds of creatures, one kind capable of metabolism without exact replication, the other kind capable of replication without metabolism.He further stresses that if life began twice, the protein beginning must have been the first, nucleic acids the second. The protein creatures might have existed independently for a long time , eating and growing and gradually evolving more and more efficient metabolic apparatus. The nucleic acid creatures must have been obligatory parasites from the start, preying upon the protein creatures and using their product for their own replication.

There are many other theories, but they all revolve somewhere round these three. Any of the three may be true because there is no compelling reason to accept any of them. But evidences are in favour of theory of Eigen et.al. (1981) Origin of life.

Based on such informations an integrated theory of origin of life, called biochemical origin of life, has been proposed in recent years. Newer discoveries constantly enrich our knowledge regarding finer details of biopoiesis.

Modern theory of origin of life, called biochemical origin of

life, considers three steps in the origin of life-

Step I - **Pre-Biotic Stage** - During which several organic molecules and macromolecules are formed.

Step II - **Precellular Stage** - During which self-duplicating, transcribing and translating system were present.

Step III - **Cellular Stage** - During which pre-cellular, self duplicating system gets status of a cell and acquires several cell-organelles

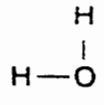
Step I - Prebiotic Stage

1. Formation Of Molecules : In biological systems there exist two types of molecules called biomolecules-

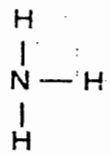
a. Simple molecules such as sugars, neutral fats, phospholipids, amino acids and nucleotids.

b. Macromolecules such as proteins, nucleic acids, nucleoproteins and viruses. In the first step, simple organic molecules were formed.

Since the primeval atmosphere was reducing one characterized by presence of a lot of hydrogen, the high-energy radiations resulted in formation of following molecules by H,C,N and O atoms.



Water (H_2O)



Ammonia (NH_3)

Hydrogen (H_2)

Carbon formed dicarbon (C_2), cyanogen (CN), some carbon monoxide (CO) with little CO_2. CO, because of its reactivity, is supposed to have been formed in primeval atmosphere and CO_2, the main oxidised form of carbon, appeared later on because there was little molecular oxygen initially.

2. Formation Of Hydrocarbons : Since the primeval atmosphere was reducing with plenty of hydrogen and ammonia as first molecules, carbon appeared first in reduced form as hydrocarbons. They first appeared as highly reactive free radicals, CH and CH_2 and formed various hydrocarbons as shown below :

$CH + CH \longrightarrow HC \equiv CH$ (Acetylene)

$CH_2 + CH_2 \longrightarrow H_2C = CH_2$ (Ethylene)

$CH_2 + CH_2 \longrightarrow CH_4 + C$ (Methane)

$2CH_4 \longrightarrow HC \equiv CH + 3H_2$ (Acetylene)

Such hydrocarbons were also formed when metal carbides reacted with steam (such as calcium carbide)

$CaC_2 + H_2O \longrightarrow HC \equiv CH + CaO$ (Acetylene)

3. Formation Of Derivatives Of Hydrocarbons : The hydrocarbons thus formed reacted with superheated steam to form oxy- and hydroxy- derivatives such as aldehydes, Ketones etc.

$HC \equiv CH + H_2O \longrightarrow CH_3CHO$ (Acetaldehyde)
(acetylene)

$HC \equiv CH + 2H_2O \longrightarrow 2HCHO + H_2$ (Formaldehyde)

4. Formation Of Carbohydrates : The derivatives of hydrocarbons underwent condensation, polymerisation, and oxido-reduction reactions to form simple carbohydrates such as glucose and fructose. They further underwent condensation to form di- and polysaccharides.

i. $2CH_3CHO \xrightarrow[+H_2O]{\text{oxido-reduction}} CH_3COOH + CH_3CH_2OH$
(Acetaldehyde) (Acetic acid) (Ethyl a/c)

ii. $CH_3COOH + CH_3CH_2OH \xrightarrow{\text{Polymerisation}} CH_3COOCH_2CH_3 + H_2O$
(Acetic acid) (Ethyl Alc.) (Ethyl Acetate)

iii) $CH_3CHO + CH_3CHO \xrightarrow{\text{Condensation}} CH_3CHOH.CH_2CHO$
(Aldol)

5. Formation Of Amino Acids : Likewise, amino acids were also produced by formaldehyde or hydrocyanic acid (HCN).

a) *By formaldehyde-*

$2HCHO \xrightarrow{\text{Polymerisation}} CH_2OHCHO$
(Formaldehyde) (Glycol aldehyde)

$$2CH_2OHCHO \xrightarrow{\text{Oxido- redtion}} \underset{\text{or}}{2CH_2OHCH_2OH \text{ (Glycol)}} \quad 2CH_2OHCOOH \text{ (Glycolic acid)}$$

(Glycol aldehyde)

$$CH_2OHCOOH + NH_3 \longrightarrow CH_2NH_2COOH + H_2O$$

(Glycolic acid) (Glycine)

b) *By hydrocyanic acid-*

When a mixture of Nitrogen, hydrogen, CO, and CO_2 is subjected to radiant energy, hydrocyanic acid (HCN) is produced. This theory supposes presence of some CO_2 in the primeval atmosphere to drive the reaction. When hydrocyanic acid is irradiated with UV-light, amino acids are produced in abundance.

$$N_2 + H_2 + CO + CO_2 \xrightarrow{\text{Radiant energy}} HCN$$

$$HCN \xrightarrow{\text{irradiation}} \text{Aminoacids.}$$

6. Formation Of Fatty Acids And Glycerol : Long chain of hydrocarbon may have formed due to condensation reaction finally resulting in the formation of fatty acids. These fatty acid might have combined with glycerol to form fats.

7. Formation of Nucleotides : Formaldehyde (CH_2O) and hydrocyanic acid (HCN), which might have contributed in the formation of amino acids, seems to have formed nucleotides too. When formaldehyde and Hydrocyanic acid is mixed with water and subjected to UV-light, adenine, guanine and urea is formed.

Nucleotides could have arisen in a different way too. Methane and ammonia by electric discharge form ammonium cyanide from which nitrogenous bases can be derived. Formaldehyde and water could be made to form ribose and deoxyribose (the sugars of RNA and DNA).

8. Formation Of Proteins : Formation of aminoacids is easy to demonstrate but formation of protein, the macromolecules, is a bit difficult. Fox, who had earlier demonstrated formation of aminoacids by using Berkeley cyclotron again demonstrated that if these amino acids are treated together at modest heat ranges (150-180^{0}C), these could unite to form chains of polypeptide, easily digestible by enzymes. By adding Polyphosphate, he demonstrated that proteins could be formed at lower temperatures (70-80^{0}C).

9. Formation of polynucleotides of RNA : Polymerisation of nucleotides could have resulted into formation of polynucleotides. This could have been affected by mineral surfaces. These associated, in some stage, with proteins to form nucleic acids.

Origin of nucleic acids in itself should not be considered equivalent to origin of life unless it acquired the characteristic of self-propagation, the basic property of "life". This property was acquired in the next-stage when "hot dilute soup" of Haldane-Oparin, containing a number of organic molecules and acromolecules combined and behaved in such a way that self-duplicating property of organic macromolecules descended on the earth.

10. Origin Of RNA-Duplication : It is supposed that a RNA molecule acquired the property of self-duplicating. This could have happened by lining up of activated nucleotides on a template RNA and later on their separation. RNA is considered primitive to DNA in the origin because of simplicity of its structure and the central role played by it in translation of protein as rRNA, tRNA and mRNA. Presence of many RNA viruses also supports the point that RNA can act as genetic material. Viruses themselves are at the boundary of living and non-living.

11. Origin Of RNA-Splicing : It is believed that primitive RNA was capable of "cutting" and "splicing" (joining) itself. In present day, such reactions are performed by proteins. There are evidences that splicing reaction can take place in the absence of protein. Cutting and splicing of RNA is necessary because RNA may be containing sequences of non-translating regions (called introns) or regions of no significance. A group of biologists believe that genome with introns (like eukaryotic genome) is primitive from which genome without introns (like prokaryotes) evolved. Thus it is necessary to conceive splicing.

12. Origin Of Genetic Code And Translation : A particular sequence of nucleotides in RNA might have resulted in protein that conferred greater selective advantage to the RNA molecule. Thus, selection is supposed to have started at the very beginning of life. Thus was established the primitive code. The primitive code might have been different from modern code as in evidenced by code of mitochondria. (Mitochondria is supposed to be an eubacteria fused with eukaryotic cell).

Ribosomes are most primitive of all cell-organells. A

comparison of rRNA of several organisms indicate that its two subuit character is very ancient and universal and it's secondary structure (stem-loop) is extremely similar in all organisms studied so far.

Tnis RNA-genetic system, capable of splicing, transcription (formation of RNA from RNA at this stage) and translation with the evolution of genetic code possibly entered into next stage of origin of life.

Step II - Precellular Stage

This step is characterized by two important developments-

i. *Origin of DNA*

ii. *Origin of membranes*

i. Origin Of DNA : It is supposed that DNA arose from RNA by the action of reverse transcriptase like activity. Reverse transcriptase like activity is present in viruses and many eukaryotic groups, including ancient one, hence it is supposed that this type of enzymatic activity is fairly primitive. Reverse transcriptase is an enzyme which forms DNA in presence of RNA.

$$\text{RNA} \xrightarrow{\text{Reverse transcriptase}} \text{DNA}$$

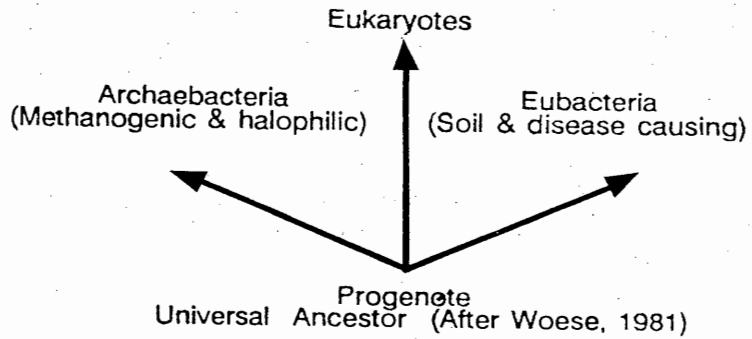
DNA of Prokaryotes (bacteria) and Eukaryotes (plants and animals) differ- In prokaryotes the DNA is functional in continuous stretch; in Eukaryotes functional DNA is punctuated by non-functional DNA (called introns). The functional DNA is called exons.

ii. Origin Of Membrane : Origin of membrane could have happened before the origin of DNA. But if not, they are supposed to have definitely formed at this stage to pack highly labile DNA molecules and protect it from fluctuating environment. DNA with membranes got selective advantage over those without membranes.

Ourisson and Nakatani (1994) claim that they have been able to infer, from the constituent of the membrane of the extant cells, that terpenoids were plentiful among the constituents of the first cell membranes. Molecules such as Ropanoids, related to terpenoids, occur extensively in sediments and petroleum. Such terpenoid could have been formed from isopentenol (units which are simple alcohols) by polymerization. The polymerization was brought about on a catalytic solid surface.

Step III - Cellular Stage

With the origin of membrane and DNA the first ancestral cell is supposed to have had come in existence. The nature of first cell as well as its genetic system is controversial. It is not known wether it was like prokaryote or eukaryote. Living being are divided into two groups- Prokaryotes and Eukaryotes. Prokaryotes, such as bacteria, have no definite nucleus whereas Eukaryotes, such as animals and plants, have definite nucleus. On the basis of sequence comparisons of ribosomal RNA, C.R.Woese (1981) has proposed that both prokaryotes and eukaryotes had a common cellular ancestor, called PROGENOTE. From it diverged 3 groups- two groups of bacteria (archaebacteria and Eubacteria) and Eukaryotes.



(After Woese, 1981)

Till sometime back, a prokaryotic genetic system, in which DNA has no introns, was considered ancestral to eukaryotic genetic systems (i.e. DNA with Introns). This view seemed logical because evolution always proceeds from simpler to complex one and prokaryotic genetic system was simpler in design.

In recent years, several evidences are forthcoming which show that the three lineages are completely separate and none of them is likely progenitor of the other two. Rather all may have descended from the same ancestor. Woese (1981) hypothesized that such an ancestor be called Progenote. Both prokaryotes and eukaryotes supposed to have independently arisen from progenote. There is probability that the genetic system of progenote was similar to eukaryotes i.e.genes with introns. From this progenote genome evolved both prokaryotic and eukaryotic genomes.

i. Evolution Of Prokaryotic Genome : The progenote

seems to have had introns in their genetic system, a feature of present day eukaryotes. When environment placed premium on fast, rapid growth, introns were lost and thus were formed prokaryotes. In the primordial ocean, when organisms that showed rapid synthetic activity were naturally got selective advantage and multiplied rapidly. It is because of this reason that prokaryotic microfossils are abundant in the earliest geologic records.

ii. Evolution Of Eukaryotic Genome : When supply of nutrients dwindled, slow developing forms were favoured in comparison to fast developing bacteria and thus arose single celled eukaryotes from progenote. The assumption that eukaryoteic genetic system is very ancient one is supported by following lines of evidences.

a. Position and number of introns in globin gene family is similar. In globin gene family, there are three exons separated by two introns. Position of introns is highly conserved in globin gene family- the first intron is present in DNA after it codes for 30 or 31 or 32 amino acids.

The only difference among the globin genes is that introns of myoglobin are longer, and there is an extra intron in exon-2 of leghaemoglobin. Leghaemoglobin is found in roots of legume plants that binds oxygen.

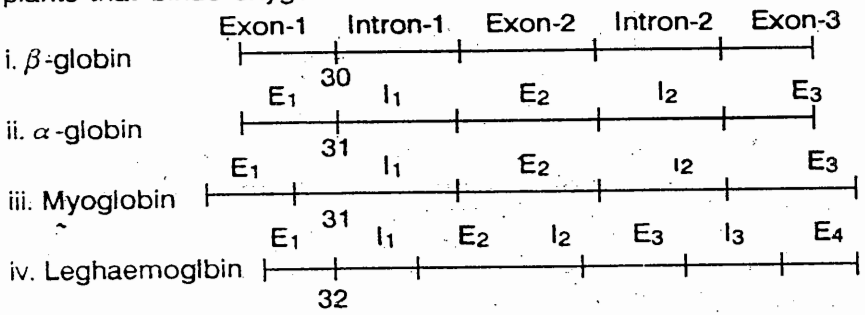


Fig : Position and number of introns in globin gene family. The first exon ends with 30, 31, 31, 32 aminoacid in the four groups respectively. E and I are short form for exons and introns. (After Liss and Jenson 1981).

b. *Loss, and not gain, of introns during evolution-* Evolutionary studies of eukaryotic genome shows that during the course of evolution eukaryotes have lost the introns; none of them

have gained an intron. Comparison of insulin-gene in Hag-fish, chicken, and man shows that in each of them there are two introns. Thus basic number of introns in insulin gene is 2. But in rats is present only one intron and two exons have become contiguous. Thus, it is hypothesized by Baltimore and others (1986) that rat insulin gene evolved because of loss of intron. Such loss of intron is prevalent in the evolution of animals. Thus it is supposed that first living being had genetic system with introns. Prokaryotes evolved by loss of it.

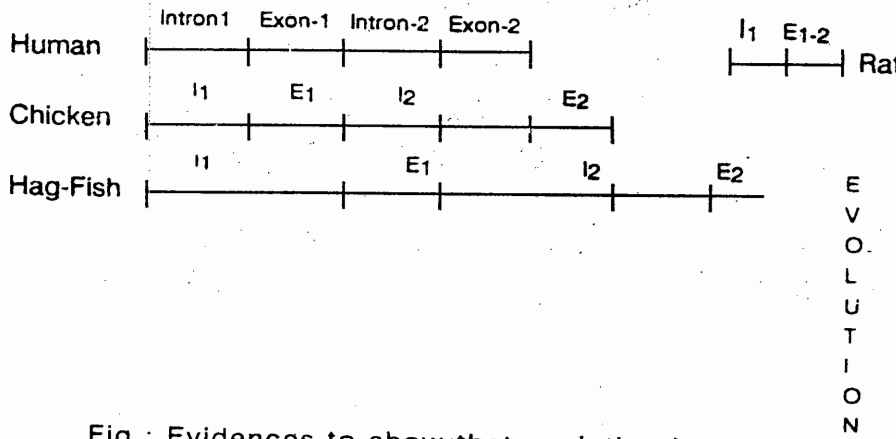


Fig : Evidences to show that evolution involves loss of introns,not its gain. The point in case is insulin gene. I and E represent introns and exons. (From Baltimore, 1986)

c. *Eurkaryotes have Reverse transcriptase activity.* Recent evidences indicate that the first living thing was a RNA and that this RNA formed DNA by the action of reverse transcriptase. The Enzyme is present in all eukaryotic cells also. Because aminoacid sequences of the enzyme is more or less similar throughout, the enzymatic activity is considered an ancient one. The evidence support the contention that eukaryotes is an ancient group having originated from a common ancestor along with prokaryotes.

The first functional cells were probably heterotophs and anaerobes. Heterotrophism might have involved chemosynthesis in the initial stages and later giving rise to saprophytism, animalism, parasitism etc. Photosynthesis might have developed later on with origin of chlorophyll.

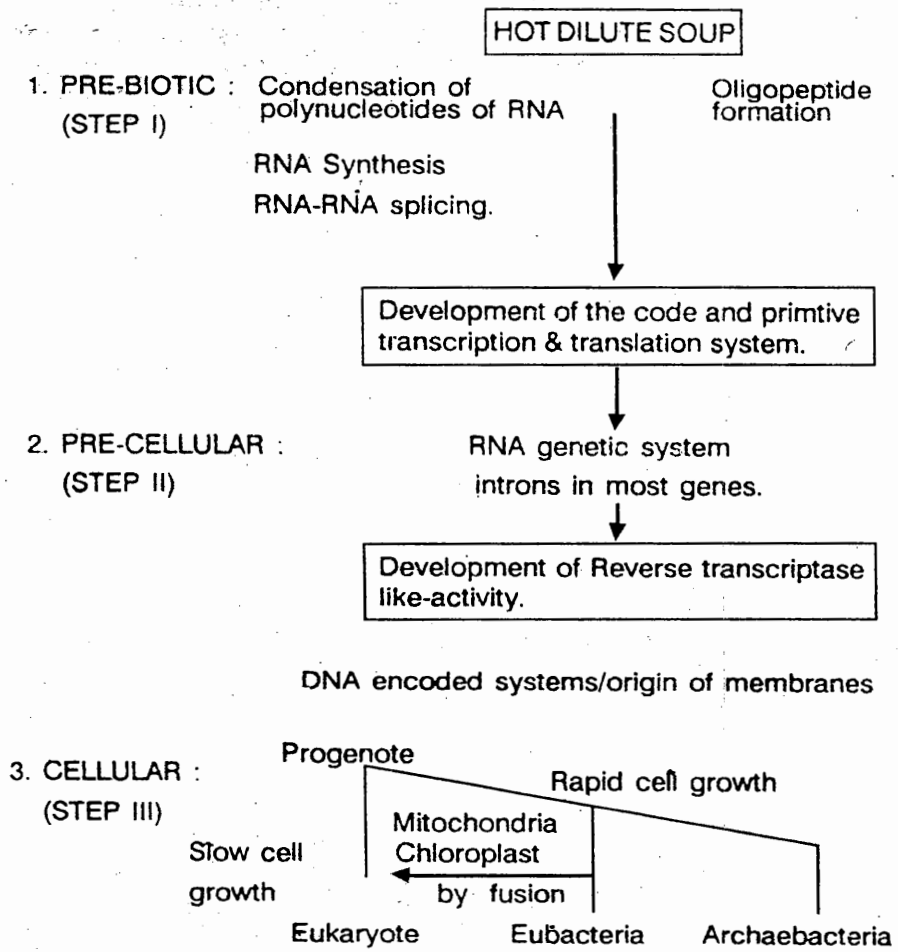


Fig. A possible course of early origin & evolution of life. The pre-biotic era ends with evolution of RNA encoded genetic system capable of primitive transcription & translation as suggested by Crick, Woese & Orget. First genome is RNA. Pre cellular era ends with origin of DNA encoded genetic system. Origin of membrane is hypothesized at this stage. The progenote differentiated into fast growing bacterial lineages (autotrophic) and slow growing single celled eukaryotes (heterotophic) with multiple introns. Cell organelles of eukaryotes is supposed to be derived from fusion of bacterial cells that become symbiont in eukaryotic cell

From earliest cell-type evolved three lines of cells :

1. Archaebacteria (*3 - 2.5 billion years ago*) : These are primarily chemosynthetic bacteria that shows unique energy utilisation. Hydrogen in them is used to reduce CO_2 to CH_4. These developed along three lines- Methanogens (producing marsh gas); Halophiles (Living in concentrated sea water) and Thermoacidophiles (living in hot and acidic environment).

2. Eubacteria (*3 - 2.5 billion years ago*) : These included soil and disease causing bacteria and cyanobacteria (previously known as blue-green algae because of possession of chlorophyll). Cyanobacteria are, however, different from plants in having prokaryotic organisation of cell, cell wall of peptidoglycan, and chemosynthesis in addition to photosynthesis. They are capable of fixing atmospheric nitrogen directly into NH_3 and utilising it in synthesis of protein. Mycoplasmas are smallest bacteria living in soil and sewage.

The various bacteria are included in group monera, the prokaryotic group. Chemosynthesis could not succeed as efficient energy-utilisation system because of limited resources. With the evolution of chlorophyll the door opened for trapping of unending solar energy. The oxygen that evolved combined with CH_4 (to form CO_2) and NH_3 (to form N_2) and thus "Reducing atmosphere" was charged into oxidising atmosphere.

3. Single-Celled Eukaryotes (*1.5 billion years ago*) : The third group to evolve from the progenotes were the ancestral flagellated eukaryotes from which different protistans (single celled animals and plants) evolved. Evolution of ancestral eukaryotes involved various symbiotic events in which bacteria fused with ancestral eukaryotes to form several cell-organelles. Chloroplast have rRNA sequences that are similar to the rRNA sequences of the cyanobacteria. It is supposed that union between the eukaryotic cell precursor and cyanobacterium resulted in choloroplast of eukaryotes. Likewise, rRNA sequences of plant mitochondria is similar to rRNA sequences of purple sulfur bacteria. Hence it is considered that union between the eukaryotic cell precursor and sulfur bacteria resulted in mitochondria (endosymbiont hypothesis).

4. Evolution Of Multicellular Organisms (*1 billion year ago*) : Protistans gave rise to fungi, plant and animals. The fossil record of subsequent periods of evolutionary change begins about 600 mya (million years ago).

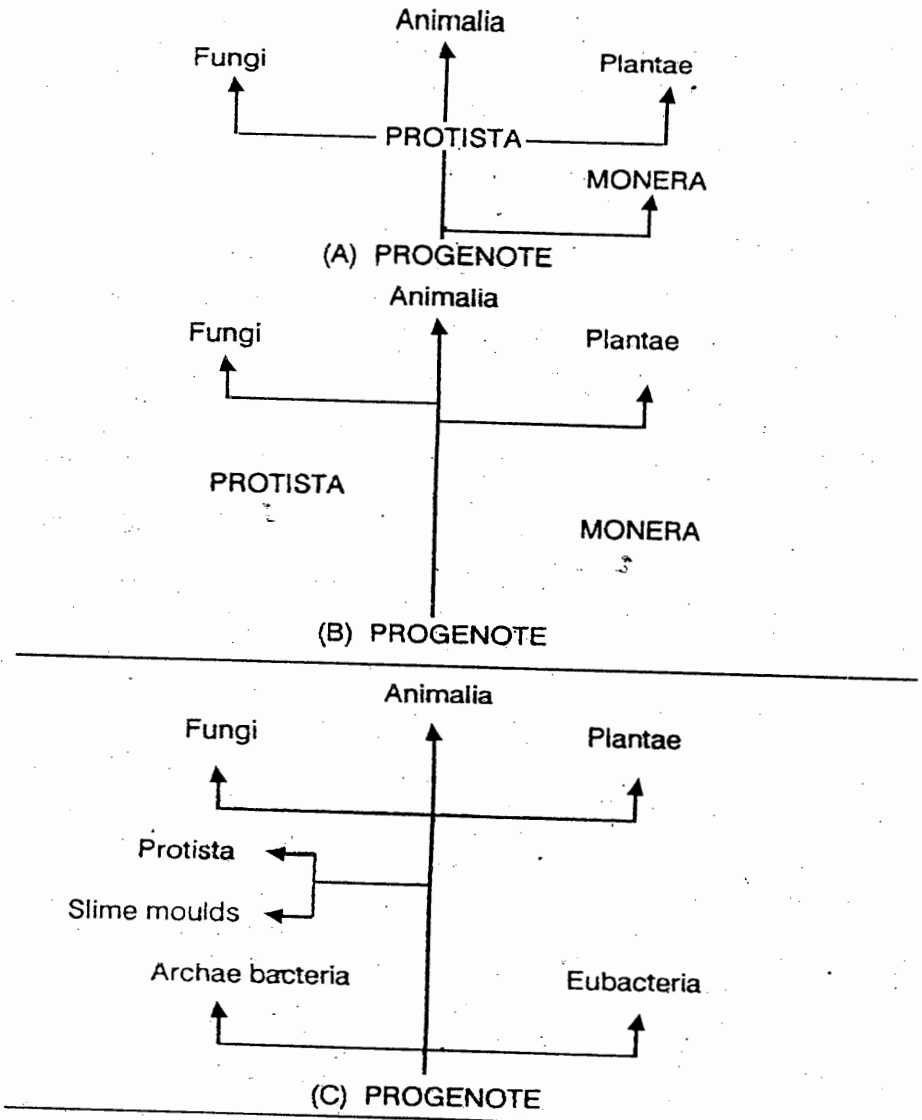


Fig. : The view of evolution of progenote (A) and (B) considers prokaryotes acting as ancestral to Eucaryotes, (B) considers protistan as separate evolutionary line from monerans. (C) considers separation of three lineages from begining with slime moulds separated from protistan

Controversial Position Of Viruses : Virus is not a cell. They consist of a single nucleic acid molecule enclosed in a protein shell called a capsid. The nucleic acid can be either DNA or RNA. They are unable to synthesize proteins or conduct energy metabolism. Viruses are a set of genetic instructions that can make copies of themselves only by invading into animal, plant or bacteria. The viral proteins are synthesized by the protein-synthesizing machinery of the host. The dependence of viruses on cells for reproduction make them non-alive.

It was thought that viruses represent an earlier stage of evolution of life, or are degenerate cells. It is now thought that they represent "escaped genomes" from bacterial, plant or animal system. The fact that they are not primitive is supported by the evidence that they need some cell to initiate their duplication. Bacteria, on the other hand are truly living creature.

Extra Terrestrial Origin Of Life : *i. Exobiology :* Study of life on places other than the planet earth (exobiology) has been a constant thought of the biologists, more so in this space-era. It has also been postulated that life originated somewhere else and was "transported" to earth.

Condition of different planets of the solar system is hardly conductive for origin of life. In most of the cases they are either extremely hot (mercury and Venus) or extremely cold (Jupiter, Saturn, Uranus, Neptune and Pluto) to support life. It is only on the Mars where condition are conducive- normal temperature range (30-60^{0}C) with- N_2, CO_2 and water vapour. All attempts by different space-missions to Mars have thus far failed to discover life on this planet.

ii. Study Of Meteorites : A variety of hydrocarbons have been found in several meteorites, especially in those belonging to a large family of stony meteorites knows as chondrites. One of these, the cold Bokkeveld meteorite from South Africa was studied in 1953 by G.Mueller. By use of organic solvents such as benzene and alcohol, he was able to extract an organic substance with following composition-

Oxygen 49%, Carbon 24%, Hydrogen 17%, Sulphur 9%, Nitrogen 4%, Chlorine 5%, ash of iron oxide etc. The extract contained no optically active compounds so characteristic of living organism. Presence of such compounds may be interpreted as life on places where these meteorites came from. But Mueller believed that meteorite's organic material consisted of organic acids that

originated abiogenetically by polymerisation in a gaseous medium of N_2, Cl, and S.

Another group of scientists working with orgueil meteorite in US reported that the hydrocarbons of the meteorite resembled the biogenetic hydrocarbons of the earth. By means of physico-chemical test these investigators have found that the extracts contained amino, carbonyl and other groups and their spectral wavelengths comparable to the extracts of terrestrial oils. Some staining evidence even points to the possible presence of nucleic acid. In explanation of the evidence, there is possibility of terrestrial contamination. Several claims of the same nature have been made since then, keeping the issue open. Scientists, however, believe that study of these materials may throw some light on primordial material of solar system and early origin of the earth.

In the recent years there have been found evidences of certain hydrocarbons believed to be synthesized at the begining of origin of life. Besides some common hydrocarbons synthesized at the beginning of origin of life, a few rare hydrocarbons were also present. Keefe et.al. (Nature, vol 373, No.6516, Feb 1995) have shown that one of such compounds was coenzyme - A. CoA is involved in many enzymatic reactions, including peptide synthesis suggesting that it might have played a part in the early development of life on earth. Keefe et.al. (1995) provides evidence by demonstrating that pantetheine, a precursor to CoA can be synthesized at temperatures as low as 40^0c from a mixture of pantoyl lactone, β-alanine and cysteamine. Such chemicals and conditions is believed to have existed on the prebiotic earth.

EVIDENCES OF EVOLUTION

1. Evidences From Comparative Anatomy : several fossils of primates and ancestors of humans have been discovered. It includes cranial and post-cranial specimens . These are basically similar so that their primates nature can be identified. However, each group has its specific variation from adaptation to its specific habitat. Underlying such variation is the fundamental similarity of plan which indicate common descent with modification (see fossil history of hominids).

2. Evidences From Biochemistry And Physiology : All animals, including primates, are made up of similar elements and biochemical substances such as carbohydrate, protein, fat, nucleic acid and a host of other organic substances. A unique similarity among all living group is presence of enzyme system that drive metabolic reactions. In all organisms, such substances are proteins. There is fundamental similarity among different groups of animals so far digestive, circulatory, respiratory, expiratory and reproductive physiology are concerned.

3. Embryological Evidences : Such evidences are clear from studies of embryos in different group of animals, including primates. It is found that the embryonic stages of evolved group shows the embryonic stages of its ancestors (Biogenetic law or recapitulation theory). The embryos of primates and other mammals are identical and similar even to fish embryo for a few weeks initially. This shows that all groups have descended from a fish-like creature.

4. Evidences From Taxonomy : In taxonomic classification, organisms are grouped together on the basis of common characters. Such grouping together of the organisms show similarity in the underlying plan of the structure. Thus all mammals have a diaphragm, separating thoracic form abdominal cavity. This is fundamental underlying similarity hence all individuals possessing this characteristic are included in class mammalia. Australopithecus and Neandertal man are included in different genera. Neandertal man had large brain, used fire and symbols. On the other hand australopithecus had small brain and did not use fire and symbols. But because both had two cups on their premolars and both walked erect hence both are included in a single family - Hominidae. Similarly, apes and man differ on several counts, hence both are included in different family - apes in pongidae and humans in hominidae. But beacuse both have several common

features of structure and behavour hence both are included in a single super family - hominoidea. Such features indicate descent with modification from a common ancestor. Taxonomy shows that organisms have fundamental similarity that allows higher grouping. Thus, they must have descended from a common ancestor.

5. Evidences from Geographical Distribution : One finds presence of similar or related forms of fossil or living organisms in the same geographical region. After evolution, the different forms generally inhabit the same geographical region and thus are characteristically distributed. Thus Chimpanzee and gorilla are limited to Africa where its earlier forms can be found out. similarly, orangutan is distributed in Asia where its earlier forms, *Sivapithecus* is found. However related animals can be widely distributed because of formation of land-bridges and human introduction.

6. Cyto-genetic Evidences Of Evolution : Eukaryotic chromosomes, including those of mammals, bear a typical structure of nucleosome that indicate a fundamental similarity in their genetic design and provides strong evidence of evolution.

In primates, there has occurred certain changes in the chromosomes which can be found in more than groups, suggesting evolution of the groups from the same ancestor. Take the number of chromosomes itself. Its number varies in humans and apes, being 46 in former and 48 in latter group. G-bands of ape chromosomes 12 and 13 perfectly match with G-bands of short and long arm of human chromosome 2 respectively indicating that human chromosome 2 is fusion product of ape chromosome 12 and 13..

G-banding (see chromosomal analysis) has indicated that a small part of chromosome 12 is inverted. This inversion is shared by chimpanzee and gorilla. This indicated that they have descended from ancestor that possessed inversion in a segment of chromosome 12.

C-banding of chromosomes of great apes and man indicate that in all of them there are regions of small C-bands near centromere (Centomeric, or C-bands). Though there are ambiguous data for human-chimpanzee-gorilla relationships, these data clearly show that three are most closely related.

7. Immunologic Evidences Of Evolution : Immunologic evidences is dependent upon antigen antibody reaction. Antigens are those bio-molecules which are capable of eliciting formation of

antibodies. Antigens includes mainly molecules of proteins and complex carbohydrates whose molecular weight is too great as well as their ability to form diverse structures is immense. DNA and lipids on the contrary have high molecular weight but they are incapable of structural variability.

For immunologic analysis, a protein is injected into an experimental animal, say rabbit or horse, that can elaborate antibodies against the protein injected which behaves as antigen. The blood of experimental animal is taken out and its serum separated. Serum is blood minus its cells and fibrinogen, the protein necessary for blood clotting. Serum thus separated has antibodies elicited against the antigen injected. Such serum is called anti-serum.

The anti-serum that we now possess has antibodies against a type of antigen. Thus anti-serum can be utilized to test the presence of the antigen against which it has been prepared.

For example, take the case of human albumin protein present in blood. It is called serum albumin and is made up single polypeptide made up of 584 amino acid. It can be separated (see biochemical analysis of man) and injected into an experimental animal and antisera against it can be obtained. This antisera can be used to detect presence of such albumin in different groups of animals and amount of precipitate can be measured. For example, human antisera gives 95% reaction with chimpanzee and gorilla serum, 85% with orangutan; 82% with gibbon, 73% with old-world monkeys; 60% with new world monkeys; 35% with prosimians, 25% with dogs and 8% with Kangaroos. The extent of reaction of human antisera with these group of animals reflect the degree of their relationship. In general, 1% of differences mean changes in 2 amino acids. Between apes and humans, there is difference of 5% only hence 10% amino acid changes. Thus out of 584 amino acid present in human albumin, 574 is present in chimpanzee and gorilla. and 530 in old world monkeys. This clearly shows that in evolution human chimpanzee and gorilla shared a common ancestor with exclusion of others.

LAMARCKISM

Lamarck shares with Darwin the distinction of having offered a complete theory to account for evolution. Lamarck had a chequered career working as french soldier, a doctor, a bankman, a botanist, a zoologist and an evolutionist but was shot into prominence, or rather disrepute, for his ideas about evolution which he summarised in his book entitled 'philosophic zoologique' published in 1809. In its nutshell, Lamarckian theory supposes that changes in environment brings about bodily changes in individuals energized by their inner urge. Such changes are developed by use and are handed over to the next generation.

Lmarckian Postulates And Criticism

Though Lamarck himself proposed no postulate or law, all his discussions in the book centre round four ideas which, for our convenience, can be given status of postulate or law-

Postulate I : Theory of "elan vital" or growth : The internal forces of life (elan vital or besoin or pourior de la vie of Lamarck) tend to increase the size of an organism by growth in organs and systems. Thus, the internal forces of life are capable of of forming organs and systems.

It is a fact. A seed, in course of time, becomes a tall tree; a zygote, after development becomes a giant creature. All the forces of growth, indeed, remain hidden in the seed and zygote. But why did Lamarck cite a common and accepted principle of life as one of his postulates? Perhaps he wanted us to swallow a bitter pill coated with gelatin of "growth principle".

Postulate II : Theory of environmental pressure & spontaneous formation of organs : New organs and systems are formed because of need or want which has arisen due to environmental pressure and continue to be felt by the organism. In other words, changes in environment initiates need or want in the individual and its "internal forces" direct formation of new organs to meet the changes in environment.

This postulate has three components - Environmental pressure - feeling of need by organism - Spontaneous acquisition of new characters. First two can be agreed with. Environment is a dynamic concept always getting moulded and modified by various agents and phenomena. An organism living in such a everchanging environment will naturally feel need of structures that adapts it to

such an environment. But feeling of need and formation of organs accordingly is a sort of dream which is not a horse which one can ride upon. In totality, the two postulates hold that if inner urge (elan vital) can form organs, it can form one if need arises under some environmental pressure. This is against all known facts of biology.

Postulate III : Theory of use & disuse : The development of organ is directly proportional to its use; continuous use strengthening the organ while disuse having reverse effect.

Lamarck cited many examples to drive home the point that continuous use, or disuse, has caused organs concerned to develop, or atrophy, respectively such as.

a. Development of strong biceps muscles in blacksmith

b. Elongated body and loss of limbs in snakes due to continuous creeping through the holes and crevices

c. Migration of both the eyes towards the upper side in flat-fishes which are lying on the bottom of sea.

d. Development of strong leg-bones, muscles and tendons for fast running and thickened enamel in teeth for chewing in horses during a shift from forest-life to savannah life.

e. Lenghtening of neck in giraffe due to its continuous use in reaching to the leaves and fruits of high rise trees.

f. Development of opposable digits, claw and muscular system to facilitate perching in birds.

g. Occurrence of vestigeal organs such as Pinna, similunar membran, vermiform appendix etc in man due to its constant disuse.

h. Development of web in between the digits in water birds to facilitate swimming.

Postulate IV : Theory of inheritance of acquired characters : All changes that organism acquire during the life-time are transmitted to the next generation.

Publication of Darwin's work in 1859 and rediscovery of Mendelian inheritance in 1900 saw rise of genetic theory of evolution since 1920 and this divided the scientists the world over into two sharply differing camps : Pro-Lamarckians maintained that acquired characters are transmitted where as Pro-Darwinians believed that it is the nature that selects the fittest among the existing variables and that acquired characters, unless they are

genetic in origin, can not be transmitted. Battleline was thus clear : If it is proved that environment brings about changes in body (soma cells) and these bodily changes somehow affects genetic component (germ cell) to make it hereditary, lamarckism will be proved. Unfortunately, there has remained misconceptions in the minds of some workers and the question has not been tackled in the right perspective.

Several experiments have been performed either in support or against the postulate.Unfortunately, several experiments performed to prove it are not accurate and seem to have lost the track.

Evidences And Experiments Against Lamarckism

1. Mutilation experiment : Weismann was the main opponent of Lamarckian theory. He mutilated (cut) the tails of white rats and mated them but found no loss of tail in succeeding generation.

2. Artifical Parthenogenesis Loeb produced artificial parthenogenesis in the Sea-Urchins egg with the help of chemical stimuli. However adults developing from such parthenogenesis need normal fertilization by sperm for development.

3. Boring of ears and nose- It is common practice in many socities. Many primitive societis mark their members with cuts on head, body and limbs. But such alterations in body is not transmitted.

4. Wearing of iron shoes by females in china : It is a practice to reduce size of their feet but their female child encounters the same problem when they grow up.

Such practices and experiments prove that acquired characters are not inherited.

Experiments In Favour Of Lamarckism

Herbert spencer, Hackel, Gadow, Hyatt, Cope, Lysenko etc

are some of the prominent supporters of lamarckian theory (NEO-LAMARCKISTS). Lysenko, a powerful scientist in the uppermost hierarchy of communist Russia in early 1950s, was such a vehement supporter of lamarckian theory that he put all its finances in jeopardy by undertaking large-scale wheat development programmes based on the theory of inheritance of acquired characters only to be discredited and sacrificed later on. Following experiments in support of inheritance of acquired characters are worth mentioning.

1. F.B.Sumner's Experiment : He reared white rats at 20^0c to 30^0c and found that rats develop larger bodies, long tail and hind feet and the acquired chracters were transmitted. However, high temprature may have affected germ cells along with soma cells.

2. Lindsey's Experiment : He experimented with a number of different animals and plants subjecting them to diverse parameters of unusual environmental conditions and found inheritance of several deviating characters. However, the experiment suffers from the same flaw.

3. Tower's Experiment : He put potato in experimental harsh conditions and found altered structures which was transmitted. The experiment suffers with the same flaw.

4. Kammerer's Experiment : Kammerer reared larva of Salamander in yellow & black boxes and tried to show that animal acquires such colourful features and transmit it to the next generation. When Kingsley Nobel, the famous American biologist, visited laboratory of Kammerer, it was found out that he had fraudulently painted the adults with China-ink to prove his point. The disrepute was so overbearing that Kammerer had to commit suicide.

5. Griffith's Experiment : He put white rats in cage and rotated it on a wheel in such a ways that rats developed dizziness. The dizziness was shown to be inherited in various degrees by the offspring. It has not been confirmed by others.

6. McDougall's Experiment : He trained white rats to come out through a maze fitted with electrical wiring so that when a rat committed mistake it got a shock. Such trained rats were

mated and later genefations were raised which were again put to a maze-learning experiment. It was claimed that number of mistake committed decreased in succeeding generations indicating inheritance of learning, an acquired character. However, Agar et al (1954) who performed similar experiment with utmost precautions, found no such inheritance of learning.

7. Brown-Sequard mentions inheritance of exopthalmia in the progeny of individuals in whom restiform body (in brain) was damaged leading to development of exopthalmia in them. The disease, however, can develop by abnormalities in brain-pituitary-thyroid axis.

8. Experiment by Guyer and Smith (1918-24)

They prepared anti-bodies against the lens-protein of rabbit. This was done by injecting lens-protein in fowl. In the blood of fawl, the antibodies developed and it was separated from the blood.

Antibodies were injected into pregnant rabbits. It was found that some progeny of rabbits had deformed eyes. The character was transmitted by the females as well as by the males. Had this transmission been by the females only, it would have been argued that there had occured a direct transference of anti-bodies from the blood of a mother to the blood of her offspring since the two blood are in close contact during embryonic development. However, one possibility still remained that the anti-bodies acted on the eyes of the embryos and along with it, on the genes of those embryos directly and thus donot constitute change in the germ cells conditioned by the soma cells.

They performed another experiment. Eye-lens is not in direct contact with blood. and if blood comes in contact, the individual will form antibody against it supposing it to be a foreign protein.

They damaged areas surrounding the lens so that blood came in direct contact with the lens substance. Such a male was subsquentely mated to a female. Seven young were born to this pair of parents; four of the young had defective eyes. Unfortunately, the experiments could not be continued because of an epidemic.

The experiment clearly demonstrated the fact that if changes in body parts lead to anti-body production then the anti-body might interfere with the gene controlling the character and cause mutation in it making the lamarckian theory come true.

Current Controversy

The 'Central dogma' was the rule of molecular biology which meant that DNA bring about formation of specific RNA and these specific RNA synthesize specific proteins. Somatic or bodily features of organisms depend upon type of protein synthesized.

DNA ———> RNA ———> Protein.

The experiment by the Guyer and smith showed that bodily changes can bring about formation of new RNA and this new RNA to the formation new DNA.

A part of this assumption has been proved true. An enzyme, reverse transcriptase (r.t.) has been isolated from a variety of organisms that bring about formation of DNA from RNA (RNA—>DNA). Thus one step in sequence Protein-RNA-DNA has been proved feasible. This leaves only first step (Protein-RNA) to be proved feasible.

if the first step in the sequence protein-RNA-DNA is proved feasible then there will be no difficulty in showing that environment effects produces distinct antibodies (protein) which can bring about changes in RNA, and RNA can direct synthesis of new variety of DNA. Somatic changes involve formation of new antibodies. Thus the only step that remains to be proved is Protein-RNA. The entire sequence with a part of it being hypothetical, can be represented as below

Somatic Changes-->Antibody-->RNA-->DNA (inhertance)
(Protien)

Support to Lamarckian theory of evolution has been coming in the recent years that negates Darwinian theory of evolution. One such worker is Ted Steele of Australian National University, Canberra, whose works appeared in 1980 and 1994. An immunologist, he caused a furore 15 years ago when he claimed that traits acquired during a lifetime can be passed on to offspring. He has presented (1994) data which he claims support his controversial theory. If the work of Ted Steele and his colleagues at the Australian National University in Canberra is correct, then the immune system is violating one of the central tenets of modern Darwinian evolutionary theory - that mutations acquired by normal body cells are not passed on to the next generation.

Darwinists believe that evolutionary progress arises from random genetic mutations in the germ cells, the sperm and ova. Natural selection means that mutations that help an organism to

survive will tend to be passed to offspring. But Steele says that in the immune system, another factor is also at work. Mutations in circulating cells of the immune system, he claims, can be transferred back to the germ cells, perhaps by jumping genes - genetic sequences that behave like retroviruses and can copy themselves from one position on the genome to another.

In 1980, Steele stunned evolutionists by claiming that mice whose immune systems had been made to tolerate cells grafted from another strain of mice could pass this acquired tolerance to their offspring. This seemed to support the ideas of the 18th century French biologist Jean Baptiste Lamarck, who argued that acquired characteristics could be inherited. Other researchers were unable to repeat Steele's work.

Steele's new results are based on the DNA sequences of a family of mouse genes involved in the production of antibodies by white blood cells. The sequences came from coding regions where the DNA is used as a template to make an antibody, and adjacent regions which do not code for any protein. If the two regions had evolved together, says Steele, they should show a similar pattern of mutation. But the researchers consistently found more mutations in the coding regions. Steele's explanation for these findings is that beneficial mutations arising in circulating B cells are being transferred back to the germ cells. Thus, somatic mutations are transferred to germinal cells. Other researchers, however, remain unconvinced.

Ian Tomlinson of the Medical Research Council's Centre for Protein Engineering in Cambridge, who has studied the equivalent genes in the human immune system, adds that the DNA sequences in these genes do not support Steele's explanation. These genes contain three regions which code for the parts of an antibody. One of these regions mutates extremely rapidly in B cells, but these genetic changes are not reflected in the corresponding sequences in germ cells.

Misunderstanding About Lamarckism : Experiments with bacteria donot prove Lamarckism. Bacteria, being a prokaryote has its DNA dispersed in the cytoplasm and hence any change that affects bacteria might affect the DNA also making the change genetic. Hence, one must differentiate between change of germ cells and soma cells together, and change of germ cells conditioned by soma cells, the latter aspect being the essence of Lamarckism.

In addition, following instances donot prove lamarckism—

a) Bacterial transduction in which a virus, while infecting a bacterium, attaches with its DNA and takes away a part of bacterial DNA when detaches from it and carries it to the next bacterium infected.

b) Eukaryotic induction in which shade, high temperature, antibiotic kill plastids and its DNA and colourless condition inherited.

c) Alcohol poisoning because it affects somatic and germinal tissues at the same time.

d) Transmission of infection because it reaches germ cells.

e) Temporary effects of environment because this is phenotypic plasticity produced by allelic "norm of reaction" or "reaction-range".

Latest evidences for Lamarckism from EPIGENOMICS : Lamarckism may lack genetic support but epigenetic evidences are now beginning to accumulate in its favour. This has been found in inheritance of food-controlled coat colour in mice and environmentally induced heritable epigenetic change involving alterations in HSP 90.

Duke university reported in 2003 that agouti coloured mice when fed upon methyl- rich diets (folic acid, Vit B_{12}) developed brown fur whereas those not fed upon these diets developed yellow fur which was inherited by their offspring. Agouti is a mixture of two colours. The trait is under control of a transposon which is highly methylated. Methyl rich diets methylate the region and render it inactive which is inherited by the offspring.

HSP90 is a heat-shock protein which regulates folding of over 1000 proteins (and thus decides its function) and also causes chromatin remodeling and epigenetic modifications thus regulating gene-expression. Thus, if environmental influences suppress HSP90 activity epigenetic variations are released and inherited. One such example has been found in fruit fly in which HSP90 alterations cause changes in eye-morphology (appendage-like protrusion) which is heritable. However, the evidences may become doubtful if it is found that methylation and HSP90 like substances affect simultaneously both somatic and germinal tissues.

Criticism :

1. The theory places much weight on 'inner urge'.
2. The theory considers environment as a docite force, whereas modern theory of evolution

considers environment as a dynamic force that selects the adaptive types from a range of variation. In the lamarckian scheme of things, variation theory is the end-product of evolution; in modern theory variation provides raw-material for evolution on which natural selection and other forces act.

3. Developement and atrophy of organs can be explained on the grounds of accepted modern theory of evolution. Thus lenghtening of neck of giraffe occurred not because of its constant use but because of presence of individuals of variable length of neck in the giraffe's population out of which those with longest neck were selected for. They were at greatest advantage and thus fittest type in an environment that had high-rise trees. Thus snakes with more slender body forms, aquatic birds with webs in feet, flat fishes with both eyes on one side, horses with capacity to run fast & browse, birds with perching ability would be favoured by natural selection in their respective habitat. All these arose as differing variations and perpetuated by differential reproduction because those with favourable variations had greater chances of survival and reproduction, thus leaving more offspring in the next generation i.e.contributing significantly to the gene pool of next generation.

4. Most of the experiment devised in support of lamarckism were either biased, or lacked confirmation, and a few were even forged. Thus to show that a salamandra reared in yellow or black environment develops more yellow or black pigment respectively in their body, Kammerer coloured salamanders with China-ink. Maze-learning experiments by McDougall and others when repeated with precaution by Agar et.al., were found to be lacking in truth. Experiment by Guyer and Smith, that reaches upto the maximum in meeting the conditions laid down by the theory, has not been confirmed.

In conclusion, rise and growth of Darwinism and Mendelism provided a scientific base for explaining process of evolution and Lamarckism was put in the background because it had no scientific base and its propositions were mostly make-believe. On the other hand, mutation, recombination, hybridization, polyploidy, structural changes which produce variations are all scientificaliy testable. Natural selection, isolation, gene-flow, genetic-drift that shape variations into adaptive types and effect evolution are all corroborated by evidences and experiments. All these scientific theorems have such an overbearing weights that Lamarckism, crushed under these, has been gasping for fresh air since long.

DARWIN'S THEORY OF EVOLUTION

(Human examples discussed in chapter "change in gene frequency").

I. Darwin's Theory Of Natural Selection

Theory of natural selection was conceived by Darwin during a voyage for five years (1831-1836) on board the HMS Beagle, a vessel that had been commissioned to make oceanographic charts for the British admiralty. The vessel spent much time around South America and Darwin had ample collections of flora and fauna of these regions. The fauna of regions that intrigued him most were fauna of Galapagos island.

Factors Influencing Darwin : a. *Industrial revolution* of England clearly emphasized the point that those industries that produce good and cheap goods flourished, and those that did not, perished. From this fact Darwin concluded that in order to survive and evolve organism must be possessed with favourable variations.

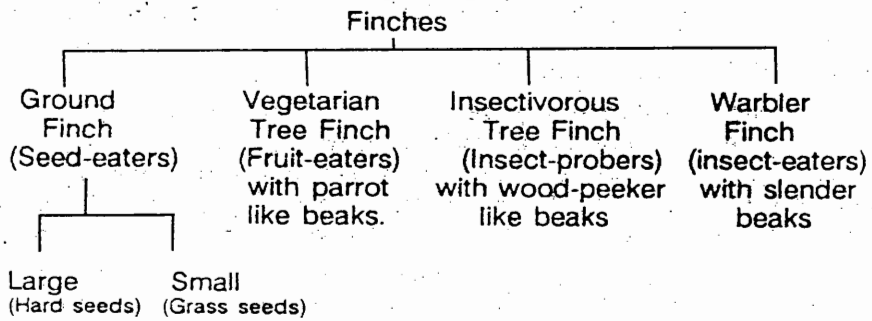
b. *Malthusian essay on population* which indicated that population increase by geometric ratio whereas food production increase by arithmetical ratio.

c. *Theory of uniformitarianism by sir Charles Lyell.* In earlier times theory of catastrophism explained the presence of fossils and contained the idea that animal life is destroyed when there is large-scale changes in the environment periodically. Lyell (1797-1875) in his book principles of Geology (1830) emphasized the point that catastrophes are not the reason of environmental changes but it continuously operates, including at present time. Darwin could know that environment has been constantly moulding and modifying the earth and its inhabitants since its formation.

d. *Alfred Russel Wallace* who wrote a manuscript "on the tendency of variations to depart from the original type" after his voyage to malayan Archipelago and sent it to Darwin to be forwarded to Sir Charles Lyell. Both Darwin and Wallace had same view about process of evolution and thus both presented a joint paper to Linnean society of London in 1858. In 1859, Darwin wrote "on the origin of species by means of natural selection " in which he dealt in length about various facets of evolution.

e. *Fauna of Galapagos island*- Galapagos is an archipelago consisting of five large islands , located on the equator 600 miles west of S.America. The fauna in the whole shows affinity to central American fauna, though differing from it in various details. There

are no fishes and amphibians. Reptiles are represented by giant land tortoises and giant guana lizard. Native mammals are one species of rat and bat. In absence of mammals, reptiles represent virtually the last vestiges of their Mesozoic superiority. Darwin was struck most by the bird population, notably finches (Geospiza) belonging to family fringillidae, and popularly called Darwin's finches. Finches display great modification of beak for different food habits that form basis of their speciation. They can be broadly classified into following categories :



Darwin emphasized t[illegible] originated in Galapagos, and in the event of stiff [illegible] for existence, migrated to adjoining lands where they developed differently. When they returned they had become sufficiently different, occupied a different ecological niche and become different species.

The theory of natural selection as put by Darwin can be summed up in following observation and deductions.

A. Over Production : This is matter of common observation that organisms lay eggs or give birth to young ones in much greater number than actually survive because a great number of eggs, immature stages are destroyed in one of the following ways-

1. By predation : Eggs and larvae constitute food for many species of animals and since they are defenseless, they fall easy prey.

2. Delicate & Low viability : The eggs and larvae are immature stages of organisms, are delicate, tender with low viability and very few of then reach adulthood.

3. Low Susceptibility Against Biotic & Abiotic Vicissitudes :

Since eggs and immature stages are delicate & generally without defense-system,they are easily parasitized and killed. Besides even normal environmental factors are unbearable to them.

B. Struggle For Existence : Since population in crease by geometrical ratio and food production by arithmetical ratio it is thus natural that there ensues a struggle among them for existence. The struggle for existence can exist at intraspecific or interspecific level and also against environment.

1. Intraspecific Struggle : The occurs among individuals of the same species eg. Paramoecium aurelia and Paramoecium caudatum competing for food and space. Since members of the same species occupy the same ecological niche the competition among then is more fierce. (origin of species P, 87).

2. Inter specific struggle : Actually there exists a complex relation of struggle among plants and animals. Darwin cites example of Paraguay fly that lays its eggs in the navel of cattle, These flies is controlled by birds. If population of birds increase, number of parasitic insects decrease, causing an increase in number of Paraguay flies hence afflicting more cattles causing a surge in vegetation. This in turn will support more insects. The inter-specific struggle is a complex vicious circle in which changes in one compartment affect another compartment.

3. Struggle Against Environment : The climate, particularly the periodical seasons of extreme cold & drought is the most effective of all checks. Extreme climates have effects chiefly through scarcity of food during these periods when struggle among individuals be come severe (Origin of species p.81)

C. Variation : Darwin had no accurate idea of variation. He mentioned four types of variations :

1. Individual Variations : Darwin considers then to be of highest importance. These are the slight differences which appear in the offspring of the same parents of a species. Now it is known that such differences arise due to recombination of genes in the parents and plays only secondary role in evolution. (origin of species,p 50, 67,).

2. Sport Or Sudden Variations : Darwin was aware of sudden appearance of new characters not present in either of the parents and called them "sports". Darwin considered them to be of minor importance, certainly "subordinate" to individual variations. The sport of Darwin is mutation and considered today as the main and original source of variation (origin of species p,32).

3. Variations Due To Use And Disuse : Darwin was a critic of Lamarck. Yet he leaned towards lamarck's idea of use and disuse as the source for origin of variation. Darwin mentions that udders in cows and goats became developed because of frequent milking and wing-muscles of domestic duck atrophied due to infrequent flying (origin on species p,33)

4. Hybrid Variations : Darwin emphasized that individual variation is often strengthened by a cross between distinct varieties and strains, mostly in plants and occasionally in animals, resulting into greater vigour and positive variation. A cross between related strains or varieties result in negative variation (origin of species p106-109). Even in modern times, hybridization is considered significant source of gene flow.

D. Survival Of The Fittest : Thus in the struggle for existence only fittest survive. Fitness of a group of population is decided on two criteria-

1. Capacity Of Adaptation & Preadaptation : Individuals, in order to survive, should possess not only those characters that are essential for living in that particular environment but , at the same time must possess sufficient variations as a measure of preadaptations that would enable the group to cope up with the circumstances when environment is no longer friendly. Only those species have future that are adapted to the present environment and at the same time preadapted for a uncertain future environment

2. Differential Reproduction : In order to be fittest, individuals must have capacity to leave more offspring forming the next generation. In current terms it can be said that they must contribute a proportion of genes to the gene-pool of next generation. If a highly adapted and preadapted group of individual is unable to contribute to the gene-pool of next generation, they are dead from evolution point of view. With them all their favourable genotypes are destined and evolutionary death (However, in stable environment, organisms employ K-strategy i.e. carrying capacity instead of R-strategy i.e reproduction strategy. In K-strategy, number of offspring is kept at minimum so that food suplply does not dwindle rapidly.

II. Darwin's Theory Of Artificial Selection

According to Darwin, the commonest method of producing new race of individuals is that of selection under human control.

The man select only useful variety of plants and animals and breeds them together expecting that offspring will have beneficial characters. Thus various new races of plants and animals are produced which are more useful, viable and of domestic value to common man. Darwin conceived about this selection to act at two levels :

a. *At the unconscious-level (Unconscious selection)*

b. *At the conscious-level (Conscious selection)*

a. Unconscious Selection : The artificial selection operates at the unconscious level when man has no intention of permanently altering the breed of animal or variety of plants. As an example, Darwin cites the instances of origin and evolution of spaniel and pointer breed of dogs.

b. Conscious Selection : Conscious selection differ from unconscious selection in the fact that the selection applied are methodical and quick, fast with an intention to alter the breed and variety of animals and plants respectively. Darwin cites the example of origin and evolution of race-horses, cattles, Sheep, Pigeons among animals & Rose, Pelargonium, dahlia, Pear etc. among the plants.(origin of species, P.50-57)

III. Darwin's Theory Of Sexual Selection

According to this theory, there is always a contest among males for possession of beautiful female. During this contest, inferior males are eliminated (due to their less courageous nature or ill-equipped with weapons of combat) and superior males dominate. Thus sexual dimorphism becomes marked in highly developed individuals.

Darwin put forth several examples to explain competition among males for possession of females such as : A stag with beautiful horns, A cock with heavy spur and strength in the wings, Fighting among the male alligators for the possession of females, Fighting among the male salmons etc.

Darwin concludes that the differences in structure, colour, ornamentations between males and females are product of sexual selection. Individual males, in successive generation, has slight advantage over other males in their weapons, means of defence, or charms which they transmit to their male offspring. Thus dimorphic differences has more a basis of sexual selection than natural selection. (Origin of species, P 99)

IV. Darwin's Theory of common descent :

The theory supposses that related group of individual have common ancestors, for example : Man & Apes. This theory, like theory of natural selection has also been found to be correct.

V. Darwin's Theory Of Pangenesis

As laws of inheritance were not known in the times of Darwin, he proposed theory of Pangenesis to explain the same. The theory is absolute, incorrect and hence abandoned and has only historical significance. According to this theory :

All somatic cells of organism produce minute particles, called Pangenes, which are included in the germ cells.

Growth Of Darwinism

Soon after publication of rediscovery of Mendelism in 1900, there were many who announced "death of darwinism". Thus in the first quarter of 20th century, scientists began to believe more in neo-lamarckism, saltationism and other theories. However, this was the period when foundation of Darwinism was laid.

There were two groups of workers; the one consisting of experimental geneticists and the another consisting of naturalist-systematists working with populations. However, the two groups were non-communicating and hence synthesis of their works was delayed to 1930 and 1940.

The experimental geneticists were concerned with nature and origin of genetic variation that is necessary for natural selection to be successful. The question had eluded Darwin all his times. The group worked for vertical evolution.

The naturalists systematists were working to explain horizontal evolution and believed that divergence of population (micro-evolution) and of species (macro-evolution) were major component of evolution. They believed that these phenomena cannot be explained at the level of genes. Thus Huxley, Simpson, Mayr, Stebbins agreed that evolutionary phenomena can be explained by natural selection. Thus in 1950 it was return to purer Darwinism. They saw that the individual and not the gene is target of selection.

Darwinism And Lamarckism

Commemorating hundred years of Darwin's death (1882-1982), Biological journal of the linnaean society of London in 1982 brought out a special issue on Darwin. Ernst Mayr has summarised in an article published in this journal the various contemporary ideas that Darwinism had to face, the oppositions to the Darwin's view, and, the current evaluation of the Darwinian theory of evolution.

The Darwinian theory of evolution is a complete and comprehensive theory of organic evolution dealing with both its vertical and horizontal aspect. Organic evolution is change in the adaptation and in the diversity of populations of organisms. Thus the theory deals with both "vertical" phenomenon of adaptive change and with the "horizontal" phenomenon of the diversity of populations, incipient species and new species.

The origin of adaptation and the origin of diversity are two entirely separate problems. Lamarck concentrated more on vertical aspect of evolution whereas Darwin, though explaining both in his theory, concentrated more in horizontal evolution. Ernst Mayr (1982) has divided Darwinian theory of evolution into five major sub-theories-

1. Evolution As Such : Like Lamarck, Darwin challenged the traditional well-entrenched view that the world is a constant one and not undergoing any change. He also denied that the world has been created in a day or a few days and has not undergone changes since then. Darwin provided such an overwhelming documentation that within a few years after 1859, evolution was no longer denied by any serious student.

2. Evolution By Common Descent : This component of evolution was missing in the Lamarck's theory.

3. The Origin of Diversity In Lamarckian scheme, higher-taxa results due to intrinsic perfecting force (= elan vital). In Dariwinian scheme, higher taxa results due to struggle for existence and favourable variations. The competing species thus are forced to search out different niche in nature.

4. Gradualness : Both Lamarck and Darwin believed in the gradualness of evolution and discarded essentialism. Essentialism claim that all living nature consists of constant and discontinuously separated types (typological thinking). Darwin maintained that organisms consists of populations, individuals of which show continuous range of variation (population thinking). The shift in the thinking from that of typological to that of population thinking was a great contribution of Darwinism. Speciation was no longer a problem, since a population can gradually change whereas a type can change only by mutation or saltation.

Criticism of darwinism

By Physical Scientists : They were strongly inclined to atomistic reductionism and considered experimentation to be the only true scientific method. They had great prestige and authority. Darwinism suffered a great deal at their hands because of their demands that evolutionary biology should be a science like physical science, with its set of absolute laws and an ability to supply 'proofs. Such a demand overlook that evolutionary events are unique historical events that could never have been predicted. Most biological systems are large and extremely complex where chance plays a large role. Hence existence of a such a law in evolutionary biology, in the sense of physicists law, is never a possibility.

By Non-Darwinian Biologists : There were two classes of such biologists - a radical minority denied that natural selection played any role in evolution, while the majority did not deny the existence of selection but denied, as had Darwin himself, that selection alone could account for all adaptations and evolutionary changes

1. Since mechanism of inheritance was unknown to Darwin, he believed in "pangenesis" and "blending inheritance". Blending inheritance believed that blood of mother & father got mixed up in offspring not to be separated again. Now we know that inheritance is particulate i.e. genes for characters from parents do not mixup but remain pure and segregate again.

2. Regarding variation, Darwin laid emphasis on individual differences. Now we know that individuals differences are caused by recombination which plays a secondary role in causing variation.

3. Darwin referred to mutations as "sports" and did not assign it primary importance in causing variation. Today mutation is known to be only means by which new genes arise.

4. Though he criticized Lamarckism yet used his use and disuse theorem to explain origin of certain variations.

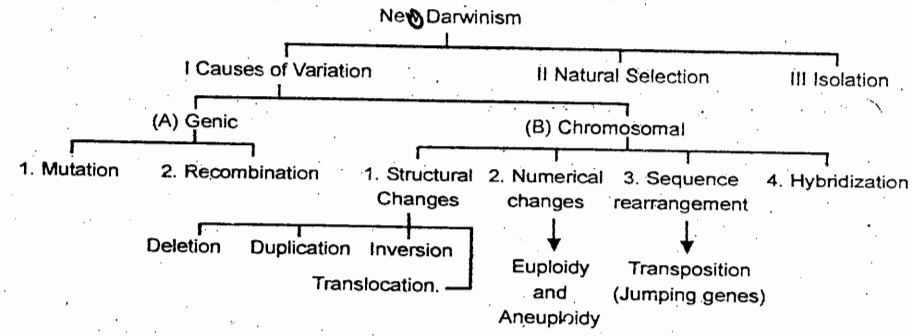
5. Why does natural selection permit in the first place development of overspecialized features such as horns of extinct Irish deer that ultimately cause the extinction of its possessor?

6. The theory of sexual selection portrays females to be selective agents selecting for positive features of males which are themselves passive fellow. In recent time active participation of males in selection process is recognised.

It is needless to say that Darwin was severly criticisized by orthodox christians, natural theologians, lay-persons & most of the philosophers. Mayr (1981) says that it is embarrassing to read them.

NEO-DARWINISM

One of the main weaknesses of Darwin was his inability to explain causes of variation. Present day biologists now know a host of causes. In addition, Darwin considered natural selection as a force that only favours positive variations and eliminates unfavourable variations. Modern biologists find many shades of natural selection. All biologists who explain evolution in terms of natural selections are called neo-Darwinians and their theory the neo-Darwinism. No factor other than the natural selection is used to explain the evolution. Such biologists, therefore, are referred to as pure selectionist (Synthetic theorists as partial Selectionist).



I. CAUSES OF VARIATION

1. Mutations : are sudden changes in genetic material and, if germinal, is heritable. It arises by **deletion** of a base, **addition** of a base, **Transition** (substitution of a purine base by another purine base or a pyrimidine base by another pyrimidine (i.e. A⇄G, C⇄T) and **transversion :** Substitution of a purine by a pyrimidine or vice-versa (Pu⇄Py). The effects can be of four types—

a. Silent— When changed codon code for the same aminoacid hence there is no change in protein. Changes occur only in DNA. This is caused by Transition and Transversion.

b. Missense— This is also Transition and Transversion. When changed codon code for a different aminoacid. protein is changed. It can be acceptable, partially acceptable or unacceptable missense. **An acceptable missense** mutation doesnot cause any change in protein functions e.g. Hb-Hitkari in 2% population of Japan.

A Partially acceptable missense mutation causes slight changes in protein function (eg. Sickle cell haemoglobin in which glutamic acid is replaced by valine at 6th position of β-chain). The condition in homozygous state causes sickle cell anaemia which is fatal, and in heterozygous condition causes sickle cell Trait in which protein is partially functional. Since haemoglobin becomes polymerized near surface of RBC it is difficult for the malarial parasite to invade the RBC. If RBC is invaded, its shape becomes so deformed that it is picked up by spleen and destroyed. Sicklecell Trait, therefore, provides immunity against malaria. In **unacceptable missense**, the protein is so deformed that it is unable to function (eg. in Methemoglobin in which there is permanent binding of O_2 with Iron, a condition resulting in ferric state of Iron)

c. Nonsense— In such mutations a termination codon (UAA, UAG, UGA) is generated, halting and releasing a protein which is dwarf.

d. Reading-frame shift— This is produced by deletions and additions and cause changes in the all subsequent codons. Such mutations affect many codons and change many aminoacids of a protein, hence deadliest of all .

A mutation is generally recessive and hence must occur in both sexes to cause its appearance in progeny. Effects, from species point of view, can be of three types–

a) Neutral effect— This is produced by silent and acceptable missense. Such mutations, however, effectively alter physical characteristics of genetic material (DNA) which accumulate in the gene pool. Natural selection is not operative on such mutations hence it brings about large scale changes in genetic material over long period of time. Kimura (1969) holds such factors as major force of evolution.

b) Beneficial effects— Thus we have advantageous mutations that change fragile barley stem into thick stem, fragile pea-nut shell into heavy shell, a large number of improved varieties of cereals, friuts and vegetables, drought resistant and rust-resistant varieties of plants etc. Such mutations confer positive advantage and are immediately included in gene-pool. It is such mutations that cause changes in gene-frequency without selection having acted upon them.

c. Harmful Effects: it is often said that most of the mutations are harmful. At the same time, we also say that only

mutations can create new genes and that it is main source of variation and thus evolution. The paradox is resolved when we consider that all species existing today are product of evolutionary history of long duration during which they might have gathered most of the beneficial mutations so that when a mutation occurs now there is possibility of disturbance of its equilibrium with the environment. In addition, significance of mutation is judged in relation to environment. It may be harmful in one environment but beneficial in another environment. A case to this point is sickle cell anaemia. It is definitely harmful in malaria-free environment because individuals suffer. But in malaria-infested environment, it provides resistent against it. So is the case with thalassaemia. In thalassaemia, there is less synthesis of either α-chain (α-thalassaemia) or β-chain (β-thalassaemia) of haemoglobin. If homozygous, thalassaemia major (fatal) results. But if heterozygous, thalassaemia minor (non-fatal) results. Thalassaemia minor also provides resistance against malaria.

To conclude, a population in order to survive, must contain sufficient number of mutational variability so that it is not found wanting if demands are placed by future environment. At the same time it should not possess too many of it became in that case too many of its individual will be crippled.

2. Recombination: mutations creat new genes. Recombination takes old and new genes and creat new combinations of genes. Since such combinations are different in different gametes hence sibs differ. The process is thus important for sib-variation. There is no long-term advantage from such combinations because such combinations are broken down when sibs themselves reproduce.

(B) CHROMOSOMAL VARIATIONS

(i) Structural changes: This includes deletion, duplication, inversion and translocation. **Deletion** is loss of a segment of chromosome which can be terminal or intercalary. Loss of a portion of genetic material is never advantageous. If loss removes a dominat gene from a homologous member the recessive gene may become functional (**Pseudo dominance**). It is the only way in which deletion can be useful. **Duplication** is repetition of a segment which may occur due to unequal crossing-over. One homologous member gets duplicated region, other member suffers a deletion. It leads to **dosage-effect** whereby doubling of gene-products occur. In inversion a broken part of

chromosome, when recombines, is inverted. There is no loss or gain of chromosomal region, only the sequence of genes altered. This leads to **position-effect** because functioning of a gene is influenced by genes in its vicinity. It can be pericentric (involving centromare) or paracentric (away from centromere). **Translocations** are exchange of segments between non-homologous chromosomes. It can be one way exchange or mutual exchange (reciprocal translocation). In Robertsonian translocation, two acrocentric chromosomes fuse

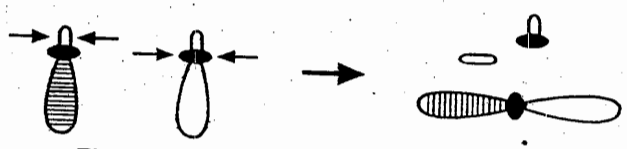
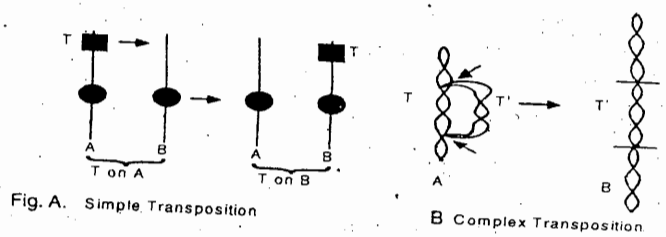


Fig. : Batesonian translocation

It has been found that human chromosome-2 has evolved because of fusions of 12 and 13th ape-chromosomes. This feature seems to be one of the main genetic reasons leading to separation of human and ape-lineage. Man has 46 and apes 48 chromosomes.

(ii) Numerical changes: Chromosom-number changes sometimes by number (aneuploidy) and sometimes by sets (euploidy eg triploid, tetraploid). Aneuploidy can be trisomy (3 copies of a chromosme), Monosomy (one copy of a chromosome) Nullisomy (both copies of a chromosome lost) double monosomy (loss of two different chromosome) etc. **(Refer to syndromes due to chromosomal changes)**

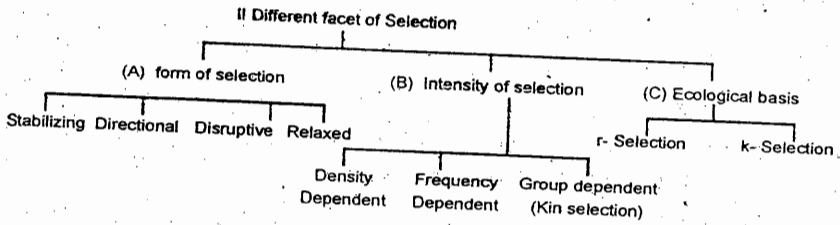
(iii) Sequence-rearrangement: This is different from structural changes hecause it is not product of chance accidents of chromosome but regularly occur as normal process in the cell. Transposons are regions of chromosome which contain gene for an enzyme, transposase. The enzyme cuts the DNA from its place and pastes it on another chromosome. The same enzyme makes cut at another site also. It results in loss of DNA from a site and gain for another site, essentially involving position-effect. The type described above is simple type. In complex transposition, the gene, before transposition, is replicated and one copy stays back in the original chromosome. This requires presence of another gene which produces enzyme resolvase.



T=Transposon; A and B = Two Chromosomes

(iv) Hybridization: Hybrids suffer from two main debilities- They are misfit in the parental environments and they are sterile. Thus nature prevents hybridization by way of species recognition (pheromone, courtship dance), vaginal reaction, abortion, hybrid enviability, hybrid sterility and hybrid breakdown. However, one form of hybridization can cause variation retaining fertility— introgressive hybridization. In such cases, hybrids are fetile in F_1 generation and mate with similar parents. F_1 crossing-over exchanges segment between chromosomes of two species. Thus small portion of sp A circulates in B and vice-versa causing **variation.**

II. Role of Selection in Evolution



(A) FORMS OF SELECTION

Selection takes one of the following forms

(1) Stabilizing Selection: It was found after a stormy night that a large number of birds were killed. Body-parameters of dead birds were taken. It was found that majority of birds that had died had body parameters fluctuating much from the average parameters of a population. The selection removes from the population the extreme forms and conserve intermediate form of a character. Such selection can hardly be imagined to cause evolution because if eliminates variation from the population so that population is homogenous.

The phenomenon has been found to be true with humans also. In a survey it was found that of the neonatal mortality most belonged to those individuals who had extremes of weight, less than or more than average 4 kg. Those with average 4kg showed maximum survival.

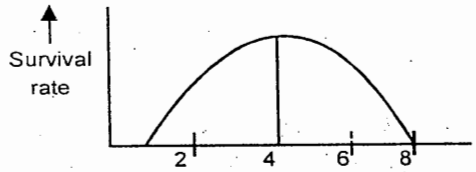


Fig. : Rate of survival in newborns

(2) Directional Selection: Kettlewell found in the state of Birmingham, UK that natural colour of a moth, *Biston betularia* is white (white peppered moth).It gets survival benefit in the sense that the white background of snow hides the moth who escapes predator. But as pollution became prevalent in this industrial city the white form was at disadvantage. A mutation arose in the population that changed the colour to black (carbonaria form). This form got selective advantage and its ratio in the population increased progressively.

Thus, in directional selection, selection favours one extreme form over another extreme form and the change is in the direction of change in the environment.

Several instances of such selection can be found in human being too.

(a) Selection of colour: Those in the temperate regions have white skin wheras black in the tropical areas. It is because there is low sunshine in temperate area hence white skin allows some sun rays to penetrate deep into skin for Vit D synthesis. Black skin prevents rays from penetrating too deep to prevent denaturation of Vit D.

(b) **Selection of B blood group in oriental region:** As we progress from western hemisphere to eastern hemisphere, the ratio of blood group B increases. Blood group A has been

associated with high physiological activity but group B is associated with resistance against infectitious diseases. Conditions in tropical regions is conducive for growth of infection hence selection of B genes.

(c) Selection of lactase gene: Those populations which donot use fresh milk donot show selection of lactase gene which forms enzyme lactase for breakdown of milk sugar.

(d) Selection of fast allele of alcohol metabolism in Oriental region: Alcohol is metabolized in the following way in the liver—

Alcohol
↓ alcohol dehydrogenase (ADH)
Acetaldehyde
↓ acetaldehyde dehydrogenase
CO_2+H_2O

There are two alleles of ADH— slow and fast. Acetaldehyde produces intoxicating effect on synapse. If acetaldehyde is produced rapidly, as with the fast allele, it is irritating to the nervous system. Oriental people live in hot climates and they donot require warming effect of alcohol. Slow allele in temperate region fulfil the requirement.

(e) Selection of wide nose in hot, humid regions: This allows fast exit of warm air of lungs and prevents excessive heating of interior. Narrow nose in cold climates warm up cold air going in the lungs.

(f) Selection of long extremities (limbs) in hot, humid climates: This increases surface area of body and allows thermal radiation which is the only source of heat loss (sweating is ineffective in hot humid climates) But this is not so in hot, dry climates because hot dry air can caue heat stroke. Hot dry conditioins favour shorter individuals. (They also have higher surface area than volume favouring thermal radiation. In addition, they present less net surface area to avoid contracting heat).

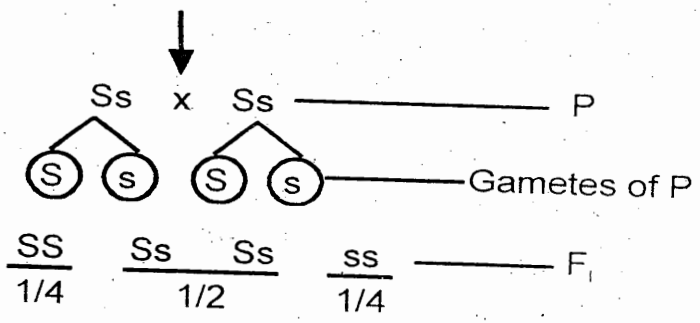
(3) Disruptive Selection : It has been fond in african

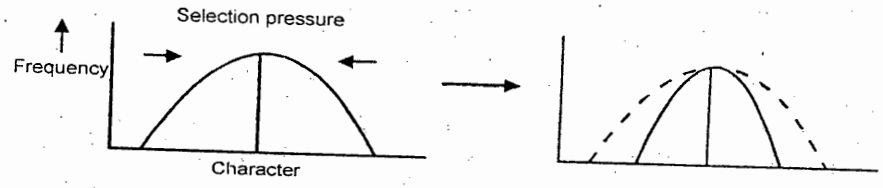
swallow tail butterfy, *Papilio dardanus* that individuals mimic some distasteful species (**Batesonian mimicry**) which delp them excape predators. Intermediate forms are removed and a population splits into two original population and mimetic populations. Such selection, therefore favours extreme forms and intermediate forms are at disadvantage.

(4) Relaxed Selection and heterozygote advantage: Such selection allows the detrimental and harmful alleles to circulate in the population because, when in heterozygous state, it provide some advantage to the population, This is a case of heterozygote-advantage, different from heterosis or superiority of heterozygotes because in heterosis, heterozygotes are superior to both homozygotes. Here, heterozygotes are not superior to normal parent but get conditional advantage.

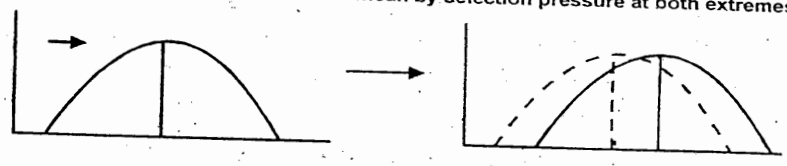
A case in point is sickle cell anaemia and thalassaemia. With respect to sickle cell anaemia, individuals can be normals (SS), having sickle-cell Trait (Ss) and sickle cell anaemics (ss). In SS individuals, RBC is normal but they fall easy prey to malaria in malaria infested environments. In Ss individuals there is slight sickling of RBC which is able to cross capillary beds. ss- individuals are at a loss because sickled RBC are unable to cross capillary beds. Heterozygotes have maximum survival hence they are the individuals that form next generation, causing birth of sickle cell anaemic in every generation.The deleterious lethal gene escapes from clutches of natural selection. Similar is the case with thalassaemia, a condition in which there is low formation of either β chain or α-chain. This also provides resistance against falciparum malaria in heterozygote form.

SS	Ss	ss	— Three types of individuals
↓	↓	↓	
Less Survival	Maximum Survival	Least survival	

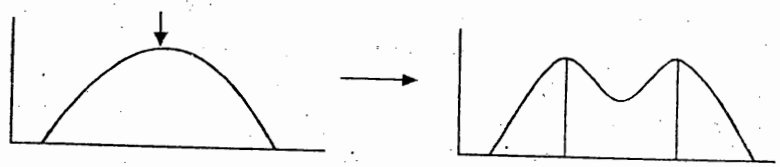




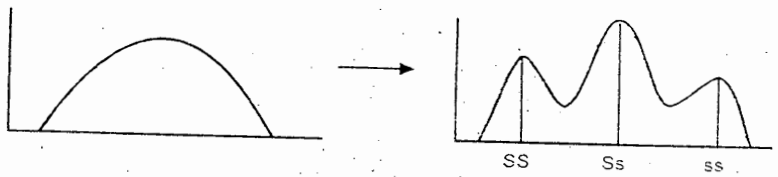
Stabilizing Selection (Conservation of mean by selection pressure at both extremes)



Directional Selection (shifting of mean by selection pressure at one extreme)



Disruptive Selection (Two means by selection pressure at intermediate forms)



Relaxed Selection (heterozygote advantage)

(B) MAGNITUDE OF SELECTION

Selection can have any of the magnitudes—

(a) Density- dependent selection

(b) Frequency dependent selection

(d) Group- selecton.

(a) Density dependent selection: Refer to the case of disruptive selection in which mimetic forms get selective advantage. But this depends on their density. If their density is greater than that of distasteful model, there is more likelihood that a predator will first encounter the mimic. In such condition the advantage which was accruing to it will stop and its number will fall quickly. The model is also at disadvantage.

(b) Frequency dependent selection: Bird-predators have search image for their prey and the prey which is most distributed becomes the target of heavy attack by birds because the 'search image' is that of most frequent type (Ehrlich et al, 1974). Dolinger et.al. have cited another example of plant alkaloid. The most often distributed plant alkaloid becomes the target of heavy attack of insect pests because pests are most likely to develop resistance against most frequent alkaloid.

(c) Group selection: Kin selection, or altruistic gene. In Baboons, dominant males lead the troupe and challenge predator enemy. The leader is often killed in encounter. The question arises as to why the leader, in possession of best genotype, is first among all to be eliminated. The answer is that selection operates here not on an individual but on group. Leader is eliminated so that "his genes or ""genes like his" can survive. Most of the children of a troupe is fathered by dominent male.

(C) Ecological basis of selection:

(a) r-Selection— 'r' refers to how rapidly a population can establish itself by high reproductive eficiency. There is no constraints on the food supply hence there is high genesis. Individuation in such cases tend to be lower. Thus, in the plentiful environment, selection tends to favour individuals with high

generation potentiality and low individuality.

(b) k- Selection : 'k' refers to "carrying capacity" of the environment. There is constraints on the food-supply hence genesis is low. Individuation in such cases is high. Thus, in scarce-environment, selection tends to favour individuals with low generation potentiality and high individuality.

CATASTROPHIC SELECTION Lewis et. al. have described chromosomal patterning of three species of *clarkia*, a self-pollinated plant of San Francisco— *C.franciscana, C-rubicunda* and *C-amoena*. They have noticed that the main difference among them is number of inversions and translocations and there is fast re-pattering of such inversions and translocations. The resulting groups, if separated to a different environment, may develop a population at a place where original population failed to develop. Lewis has termed it 'Catastrophic Selection'

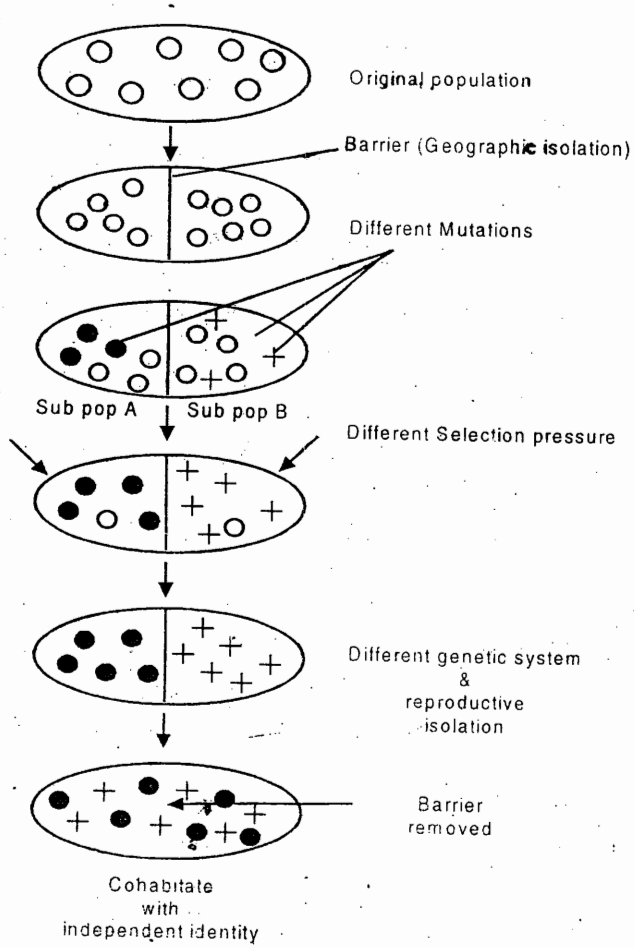
Darwinian fitness and Selection-Coefficient relative contribution of a genotype to the gene-pool of next generation is **fitness.** It ranges from 0 to 1. If there are 1000 black and 1000 white moth in Ist generation, and 1000 black and 500 white in 2nd. generation, fitness of black is 1 and that of white is 0.5. **Selection Co-efficient** is the difference in the contribution of most fit genotype and most inferior genotype to the gene-pool of next generation. The selection-Coefficient in the above case is 1-0.5=0.5. Selection co-efficient in lethal gene is 1.0 because most inferior genotype die (1-0 =1)

III. ISOLATION

The significance of Isolation in formation of species was accepted by the Darwin himself. Isolation prevents gene-exchanges and this allows formation of unique genotypes, resulting into speciation.

Isolation operates through everal prezygotic and post-zygotic mechanisms. Impo tant pre-zygotic mechanisms are geographic, sheer distance, ecological, behavioural, etc, finally leading to reproductive isolation. Once reproductive isolation is achieved, populations become different species. Geographic

isolation has to come first. Genetic differences arise in populations once they are geographically isolated. They gather different mutations; are under different environmental conditions hence different selection pressure which constantly moulds and modify gene-pool of two populations so that they become two different species in due course of time. Once new species, they can co-habitate, maintaining their genetic differences.



MICRO-EVOLUTION

Goldschmidt (1940) introduced the concept of micro-evolution to emphasize the fact that small mutations accumulate in a population to bring about small changes in it and account for evolution of races and sub-species. Large mutations accumulate in a population to bring about large changes in the population and account for evolution of species and higher levels of taxa (Macro-evolution) There are four main factors and three subsidiary factors that account for micro-evolution :

1. Mutation : Micro-evolutionary changes involve changes in phenotypic characters of small magnitude hence micro-evolution is produced by mutations of small magnitude .

The changes introduced by these mutatios are such that they do not completely jeopardise the age-old adaptations. Idea of such little mutations can be invoked to explain heat and cold adaptation in Eskimos, Peruvian, Nepalese and Africans.

2. Natural Selection : Action of Natural selection in micro-evolution is evidenced by three lines of studies - molecular genetics, trait distribution and single population studies.

Studies in molecular genetics clearly bring out the fact that mutations in the vital areas of gene-functioning is not tolerated and such regions are highly conserved, while allowing for the small mutations to accumulate outside the domain of DNA for critical functioning. For example, mutations in the haemoglobin genes that are concerned with association of the four polypeptide chains crucial for its functioning is weeded out whereas mutations in the other areas of haemoglobin gene is allowed to accumulate by natural selection. Similarly, histone proteins are crucial for formation of nucleosome and chromosomes. Mutations in histones are lest favoured by natural selection. Natural selection, thus, selectively incorporates or weeds out mutations and is thus main agent of evolution.

Trait distribution studies also confirm role of natural selection in micro-evolution. Sickle-cell-trait, resulting due to heterozygous state of gene for sickle-cell is favoured over homozygotes because it confers resistance against malaria which is prevalent in African & Asian environment. It shows that an allele, even if it is disadvantageous in one way, can be selected by agents of natural selection if it confers an overall advantage to the population.

Single population studies have clearly indicated that certain genotypes are especially more preferred or less preferred than other genotypes. e.g. A & AB Blood group is related with high incidence of small pox in rural India, thus there is higher frequency of group B. Another study involving Peruvians and Nepalese (inhabiting high altitudes) show that low 0_2 tension at such places cause several physiological and structural changes such as greater lung capacity, greater marrow capacity of long bones and ability to deliver a large amount of O_2 to tissue. Several of the adaptations in response to high altitude may be due to acclimatization but with Gorkhā people such changes are shown to be genetic.

Natural selection, can act in three ways - stabilising, directional and disruptive way. Stabilising selection removes individuals that deviate from population mean of a trait. Such form of selection does not bring about micro-evolutionary changes. The two other types of selections, directional and disruptive, are able to produce micro-evolutionary changes. Those individuals who show adaptive changes in the direction of environmental changes are favoured by natural selection (Directional Selection). When a population is split into two or more sub-groups so that intermediate types are not favoured, such form of selection is known as disruptive selection.

Sexual Selection operates when there is selection of mates on the basis of certain preferred standard of beauty or other desirable quality. This leads to formation of two distinct group because non-preferred type mate only with non-preferred type e.g. in group in which kinky hair is preferred over straight hair, the gene for straight hair would become rare in course of time. Negro males prefer women with light shades of skin hence phenotypic variability is present in Negro-skin.

Social Selection operates when there is artificial barriers of caste, religion etc. in the mating of individuals. Such selection divides population into several sub-populations that are partially isolated from each other. Selection in such instances have a stabilizing form, eliminating individuals that differ from social norms.

3. Gene Flow : Gene-flow is the movement of genes across the population boundaries. If number of people immigrating is large and degree of difference in gene frequencies between the recipient and immigrating population is large, the effect of gene-flow can be drastic. In several societies marriage with outside group promote gene flow and results in changes in head shape and height. e.g. Swisscantn of ticino (See changes in gene frequency)

4. Genetic Drift : Genetic drift is random changes in gene frequencies associated with small population size in which a gene is fixed in the population irrespective of its adaptive value. In small populations the number of children is small and chances of some

genes not inherited is large (See genetic drift)

5. Isolation And Hybridisation : Isolation plays a significant role in micro-evolution because isolated populations are exposed to different mutation and selection pressure as well as prone to different migration and drift trends. Occasional hybridisation between them prevent emergence of reproductive isolation and restrict the evolution upto the geographical races or sub-species level. Most of the hybrids are at disadvantage because of the developmental and segregational disturbances and non availability of a separate habitat to establish itself. If the abovesaid conditions are not met with, hybrids distinguish themselves from the two parental populations.

Large populations, when geographically isolated accumulate different mutations and are exposed to different selection pressure that adapt it to environment. Comparatively smaller populations are prone to drift that lead to possession of non adaptive genes.

There has been numerous studies of different populations from micro-evolution point of view. One of the recently concluded study is that by Das (1981) who studied Khasi, Bodo and Chutiya populations of N.E. India. There are various sections of each tribe, each characterized by differing facial features. Das has concluded that neither mutation nor drift seems to have played role in the micro-evolution of these populations because the group is a large one. Selection, combined with gene flow, seems to have caused micro-evolutionary changes in this group (Das, 1981).

Microevolution has not ceased : The following examples amply justify that micro-evolution has nor ceased.

1. The wisdom teeth in man which generally appears at the age of 16-18 years does not appear even in the early or late 20's. It means that the man does not need the wisdom teeth anymore

2. Menarche in Female The average age of menarche is decreasing in all societies.

3. Increase in height Children of all ages of all societies are attaining greater height.

4. Blunting of canines The sharpening of canines in man is decreasing day-by-day.

Such changes are occurring because genes are having better expression in the modern environment.

MACRO-EVOLUTION

There is controversy whether the forces that cause microevolutionary changes are sufficient to cause macro-evolutionary changes. Some vote in favour, others against. Those who vote in favour believe in gradualism; others that vote against believe in punctualism. Gradualism and punctualism are different.

There are basic differences between theory of punctuated equilibrium proposed by Gould, S.M. Stanley (1979,1982) and E.S Vrba (1980) and theory of gradualism. The model of punctuated equilibrium proposed that morphological evolution happened in bursts, with most phenotypic change occurring during speciation events, so that new species are morphologically quite distinct from their ancestors, but do not hereafter change substantially in phenotype over a period that may encompass many millions of years. The punctuational model is contrasted with the gradualistic model, which sees morphological change as a more or less gradual process, not strongly associated with speciation events.

Whether phenotypic changes in the macro-evolution occurs in bursts or is more or less gradual, is a question to be decided empirically. Examples of rapid phenotypic evolution followed by long periods of morphological stasis are known in the fossil record. But there are instances as well in which phenotypic evolution appears to occur gradually within a lineage. The question is the relative frequency of one or the other mode ; and palaeonologists disagree in their interpretation of the fossil record (Eldredge 1971), Eldredge & Gould(1972), Hallam (1978), Raup (1978), Stanley (1979), Gould (1980) and Vrba (1980) are among those who favour punctualism; whereas Kellogg (1975), Gingerich (1976), Levinton & Simon (1980), Schopf (1979,1981), Cronin, Boaz, Stringer & Rak (1981) and Douglas & Avise (1982) favour phyletic gradualism.

Theory Of Punctuated Equilibrium

The notion that small microevolutionary forces are unable to cause major macro-evolutionary changes was held by Goldschmidt (1940)

a. Systematic Mutation Of Goldschmidt : Goldschmidt (1940 p. 183) argued long ago that the decisive step in evolution, *the first step towards macro-evolution, the step from one species to another, requires another evolutionary method than that of sheer accumulation of micromutations.*

Large changes seem usually to have arisen rather suddenly, in terms of geologic time. This fact has been one of the reasons why a special type of large mutation, "systemic mutation", has been postulated by Goldschmidt (1940) to account for the large changes observed in evolution. By "systemic mutation" Goldschmidt meant a complete repatterning of the chromosomes - "the arrangement of the serial chemical constituents of the chromosomes into a new, spatially different order, i.e. a new chromosomal pattern." Chromosomal aberrations qualify as systemic mutations under this definition. The arrangement of the genes present usually makes less difference than does the nature of the genes present, whatever their arrangement in the chromosomes. Gene mutations are of more importance to evolution than are these "systemic mutations" known to us (i.e. chromosomal aberrations). His theory, therefore, is less acceptable.

b. Homeotic Mutations : Single gene or chromosome mutations are known that have large effects on the phenotype because they act early in the embryo and their effects become magnified through development. Examples of such 'macro mutations' carefully analysed in *Drosophila* are 'bithorax' and the homeotic mutants that transform one body structure e.g.antennae, into another body structure (e.g. legs). Such homeotic mutations are known in the mammalian systems also. Supporters of the theory of punctuated equilibrium hold that generation of morphological novelties in the evolution of new species results due to alterations in developmental programmes. The genes regulating the developmental programmes are highly conserved and molecular mechanism of macro-evolution involves changes in such regulatory genes.

A series of papers appearing in last few years is testimony to the fact. N.H. Patel (1994), Carroll (1994 and 1995), Burke and Nelson (1995) have established clear cut relationship between these regulatory genes and gross morphological features of arthropod appendages and segmentation as well as vertebrate axial Skeleton. Sordino et.al. (Nature Vol. 375, June 1995) as well as a series of workers such as Dolle et.al.(1989, 1993), Davis and Capecchi (1994), small and Porter (1993), Fawier et.al (1995) have shown that one such regulatory gene, called Hox genes, are essential for growth and patterning of the tetrapod limb Skeleton. A *mutation in this gene causes important delay in morphogenesis* and reduced proliferation. It is suggested by Sordino et.al (1995) that Hox-gene regulation may have been a source of

morphological variation during the evolution of tetrapod limbs. Dolle (1993) and Duboule (1994) holds the same opinion. Sordino et.al (1995) cloned Zebrafish (*Danio Rerio*) HOX D and HOX A complex genes and analysed their expression during fin development. They have suggested that the gene might have had a regulatory role in creation of macro-evolutionary group. tetrapoda. The relative importance for Hox-genes for primates is not established as yet but it does indicate that mutation of regulatory gene holds the key to macro-evolution.

2. Theory of Gradualism

Another group of workers have supported the gradualistic mode of macro-evolution. They hold the belief that small mutations accumulated over long period of time is sufficient to account for the macro-evolutionary changes. Whether the kinds of morphological differences that characterize different taxa are due to 'macromutations' or to the accumulation of several mutations with small effect, has been examined particularly in plants where fertile interspecific, and even intergeneric, hybrids can be obtained. The results do not support the hypothesis that the establishment of macromutations is necessary for divergence at the macro-evolutionary level. Major morphological changes, such as in the number of digits or limbs, can occur in a geologically rapid fashion through the accumulation of mutations with a small effect. The analysis of progenies from crosses between races or species that differ greatly (by as much as 30 phenotypic standard deviations) in a quantitative trait indicates that these extreme differences can be caused by the cumulative effects of no more than 5 to 10 independently segregating genes.

Interpreted in terms of the punctualist hypothesis, human phylogeny would have occurred as a succession of jumps, or geologically instantaneous saltations, interspersed by long periods without morphological change. Could these bursts of phenotypic evolution be due to the gradual accumulation of small changes ? Consider cranial capacity, the character undergoing the greatest relative amount of change. The faster rate of net change occurred between *H.erectus* (1mya or more) and Neanderthal man (75 thousands years ago) when cranial capacity evolved from about 900 cc in Peking man to about 1400 cc in Neanderthal people. The change from 900 cc to 1400cc in the intervening period can be explained by micro evolution.

According to Charlesworth et al.(1982). Explanation for

macro-evolution based on forces producing microevolutionary changes is as follows :

1. Rapid change may be expected to occur when an organism faces the demands of a new environmental niche radically different from the one formerly occupied. Under such conditions the severity of natural selection will be greatly increased. Organisms faced with radically new conditions of life will adapt rapidly to those conditions under the stimulus of a severe natural selection operating upon the raw materials provided in the form of mutations and other types of genetic variability. During such periods evolutionary rates are accelerated. This has been termed quantum evolution by Simpson.

2. Even during this phase there is no sudden or abrupt change from one taxa to another. The change is gradual. There is sometimes no connecting-link because there has not been discovered one.

3. This accelerated rate of evolution can occur in an isolated group of population. Evolutionary potentialities of a group increases if it is divided into sub populations. In such cases, mutations can spread rapidly through genetic drift. If altered characters enable the species to adapt to changed environment, it will be favoured by natural selection.

4. The small population might have lived under conditions that might have had not favoured fossilization, or if some that might have formed, have not yet been discovered. Thus, lack of fossils or transitional stages in many groups of animals do not imply that there has occurred a sudden change from one taxa to another.

In the conclusion, supporters of the gradualistic theory hold that macro-evolutionary changes occurred when a small population entered a new niche so that it was faced with a very strong selection pressure. Once it conquered the niche the selection pressure eased and perfection of the adaptation proceeded at slower rate. It is during this phase of perfection that adaptive and non-adaptive changes are included and the original population eventually divides and sub-divides into sub-species, varieties, geographical races etc.

POPULATION GENETICS & HARDY-WEINBERG LAW

All the aggregates of interbreeding individuals constitute mendelian populations. The mendelian population is not restricted by absolute size - it may include individuals living in a village, a town or a country if individuals within it mate at random (Panmixis). In such population, every individual has equal chances of mating with all the other individuals of the population. However individuals may tend to mate with each other on the basis of caste and other factors. In such cases an element of inbreeding is added to the genetic picture.

Gene-pool and Gene Frequency

Gene Pool : Consider a hypothetical population in which all individuals are heterozygotes containing Aa genes at a locus. In such a population, mating will be between Aa x Aa. According to probability law, the composition of population in next generation can be deduced by a checker board diagram :

	1/2 A	1/2 a
1/2 A	1/4 AA	1/4 Aa
1/2 a	1/4 Aa	1/4 aa

Assembling the results from the chart we find that the offspring occur in the proportions 1/4 AA, 2/4 Aa, 1/4 aa, all derived from A and a sperm & Ova.

Grouping the two together we have a gene-pool in which half the genes (regardless of whether they are in sperms or ova) are recessive, half are dominant. In such a gene pool the equilibrium 1/4 AA, 2/4 Aa, 1/4aa will be maintained as long as random mating occur (i.e., as long as choice of mates is entirely a matter of chance and hence obeys the mathematical laws of probability)

A model of such a gene pool is afforded by a box containing red and blue beads (corresponding to gene A and gene a respectively) in equal numbers. If without looking you pick up two beads at a time, you may pick up two red ones (AA), a red and a blue one (Aa), or two blue ones (aa). If you do this enough

times you will obtain a good approximation of the ratio: 1/4 both red, 2/4 one red and one blue, 1/4 both beads blue.

A gene pool, thus, is described as total genetic information possessed by a population which is available to the next generation. If the gene pool could be described completely, one would know not only what kinds of information were present but also the frequencies of the different kinds.

Gene Frequency : One of the basic ideas of population genetics is that of gene frequency. If it is assumed that there are only two alleles at the locus (A, a) under consideration, and N diploid individuals of which D are homozygous for one allele (AA), H are heterozygous (Aa), and R are homozygous for the another allele (aa). The D + H + R = N. The N individuals have 2 N genes at this locus. Since each AA individual has two A genes and each Aa individual has one A gene, the total number of A genes in the population is 2D + H. The proportion of A Genes in the population is

$$p = \frac{2D + H}{2N} = \frac{D + \frac{1}{2}H}{N}$$

The quantity p, the proportion of A genes in the population, is known as the gene frequency of A. By convention, the gene frequency of the other allele (a) is q. Since these are the only two alleles at the locus, p+q = 1 and q= 1- p.

Gene frequency and Zygotic frequency

If gene frequency of certain genes are known, the zygotic frequency (the type of individuals, also called genotype frequency) of the next generation can be calculated because of gametes have equal chances of combination in a random mating (mating without choice) in a population.

Consider the same example we described while discussing gene-pool in which all individuals of a population were heterozygous for A and a allele.

If p stands for percentage of A alleles in the gene pool and q stands for the percentage of a alleles, the checkerboard of both alleles may predict possible chance combinations of A and a gametes as follows:

Male gametes ———	p (A)	q (a)
Female gametes		
p(A)	(AA) p^2	(Aa) pq
q(a)	(Aa) pq	(aa) q^2

or, $(p+q)^2 = p^2 + 2pq + q^2$

Thus, p^2 is the fraction of the next generation expected to be homozygous (AA), 2pq is the fraction expected to be heterozygous (Aa) and q^2 is the fraction expected to be recessive (aa).

The zygotic combinations predicted in a randomly mating population may be represented by $p^2 : 2pq : q^2$ where p^2 represent the AA genotype, 2pq the Aa, and q^2 the aa genotype; or in the form of equation, $p^2 + 2pq + q^2 = 1$. When only two alleles are involved, and therefore p and q represent the frequencies of all of the alleles concerned $p + q = 1$.

Hardy-Weinberg Law

The formula $(p+q)^2 = p^2 + 2pq + q^2$ is expressing the genotypic expectation of progeny of the parental gene pool. It was formulated by a British mathematician Hardy and a German physician Weinberg (1908). According to them both gene frequencies and genotype frequencies will remain constant from generation to generation in an infinitely large interbreeding population in which mating is at random and no selection, migration or mutation occur. Should a population initially be in disequilibrium, one generation of random mating is sufficient to bring it into genetic equilibrium and thereafter the population will remain in equilibrium (unchanged in gametic and zygotic frequencies) as long as Hardy-Weinberg condition persist. Following condition, thus, must be met with for genetic equilibrium to occur.

1. The population should be infinitely large and mate at random.

2. No selection is operative.

3. The population is closed, i.e., no immigration or emigration occur.

4. No mutation is operative in alleles.

Mating between Aa x Aa individuals in our example produced 1AA : 2Aa : 1aa individual in the first generation, and genotype-frequency in the first generation was $p^2 + 2pq + q^2$. It can be shown, both from probability and mathematical point of view, that the genotype frequency in F_1 will remain constant in F_2 generation.

Table : *Matings and Offspring in a population in Hardy-Weinberg Equilibrium*

Type of mating	Frequency of mating	Proportions of offspring		
		AA	Aa	aa
AA x AA (p^2 x q^2)	p^4	p^4		
AA x Aa (p^2 x 2pq)	$2p^3q$	p^3q	p^3q	
Aa x AA (2pq x p^2)	$2p^3q$	p^3q	p^3q	
Aa x Aa (2pq x 2pq)	$4p^2q^2$	p^2q^2	$2p^2q^2$	p^2q^2
AA x aa (p^2xp^2)	p^2q^2		p^2q^2	
aa x AA (p^2 x q^2)	p^2q^2		p^2q^2	
Aa x aa (2pq x q^2)	$2pq^3$		pq^3	pq^3
aa x Aa (2pq x q^2)	$2pq^3$		pq^3	pq^3
aa x aa (q^2 x q^2)	q^4			q^4
Totals	1.00*1	p^2 *2	2pq *3	q^2 *4

Now let us consider a hypothetical example again. In a population consisting of AA, Aa and aa individuals, percentage of AA = 50, those of Aa = 30 and aa = 20. Hence frequency of A

* The frequency of type of both males and females given by the terms of the expression $p^2 + 2pq + q^2$. there is with random mating the frequencies of the different mating are $(p^2 + 2pq + q^2)(p^2 + 2pq + q^2) = p^4 + 4p^3q + 6p^2q^2 + 4pq^3 + q^4$

*1 The sum of this column $p^4 + 4p^3q + 6p^2q^2 + 4pq^3 + q^4 = (p^2 + 2pq + q^2)^2 = \{(p+q)^2\}^2 = (1^2)^2 = 1.0$

*2 The sum of this columns $p^4 + 2p^3q + p^2q^2 = p^2(p^2 + 2pq + q^2) = p^2(1) = p^2$

*3 The sum of this columns $2p^3q + 4p^2q^2 + 2pq^3 = 2pq(p^2 + 2pq + q^2) = 2pq(1) = 2pq$

*4 The sum of this columns $p^2q^2 + 2pq^3 + q^4 = q^2(p^2 + 2pq + q^2) = q^2(1) = q^2$

and a genes in the population is

$$\text{Frequency of A } (=p) = \frac{50+15}{100} = \frac{65}{100} = 0.65$$

$$\text{frequency of a } (=q) = \frac{20+15}{100} = \frac{35}{100} = 0.35$$

According to Hardy-Weinberg equation the frequency of A and a should not change over generations if conditions of Hardy-Weinberg is met with.

If all the individuals are mating at random then all gametes have equal chances of combination. Hence, in the next generation, genotype will appear in the following proportions-

$$p^2 + 2pq + q^2$$
$$= (0.65)^2 + 2x(0.65)x(0.35) + (0.35)^2$$
$$= 0.4225 + 0.4550 + 0.1225$$
$$= 1$$

In the second generation, the genotype frequency has changed so that, we have 42 AA individuals, 46 Aa individuals and 12 aa individua's per hundred. Though the genotype frequency has changed but, if we calculate, we will find out that frequency of A and a has not changed. Thus in the second generation -

$$\text{Frequency of A } (=p) = \frac{42+23}{100} = \frac{65}{100} = 0.65$$

$$\text{Frequency of a } (=q) = \frac{12+23}{100} = \frac{35}{100} = 0.35$$

In the first generation, genotype frequency was AA = 0.5, Aa = 0.3 and aa = 0.2. But in the 2nd generation it stabilized on AA = 0.42, Aa = 0.46 and aa = 0.12. Gene-frequency has stabilised on p = 0.65 and q = 0.35.

The two will remain the same in the successive generations. It can be represented in tabular form like this :

Generation	Genotype frequency			Gene frequency	
	AA	Aa	aa		
1	0.5	0.3	0.2	p = 0.65	q = 0.35
2	0.42	0.46	0.12	p = 0.65	q = 0.35
3	0.42	0.46	0.12	p = 0.65	q = 0.35
4	0.42	0.46	0.12	p = 0.65	q = 0.35

Unless changes in the mating pattern, or a drop in population size disturbs the equilibrium, there is no change in the genetic structure of population. Overcoming this inertia (especially changing the gene frequency) is what is described as evolution.

Although populations in equilibrium are rare (or nonexistent) in nature, the law is of great value in describing a situation in which there is no evolution at a single locus, as it provides a base line for measuring evolutionary change. Some of the ways in which populations deviate from Hardy-Weinberg equilibrium are considered in next chapter.

Significance of Genetic Equilibrium for Evolution

Laws of chance or probability operate upon gene distribution in ways tending to preserve the status quo-to maintain an unchanging equilibrium as generation pass.

If the equilibrium is upset there is a tendency to establish quickly a new equilibrium. Evidently this tendency to equilibrium forms a sort of inertia which must be overcome if evolutionary change is to occur. This may give us the impression that equilibrium is entirely detrimental, and obstructive of progress. The equilibrium tendency is conservative. It tends to conserve gains which have been made in the past and to prevent too rapid change.

It helps to insure that a species will not gamble in undergoing evolutionary change. "Radical change, may lead to progress; it may also hustle a species down a blind alley to speedy extinction". Thus observed Moody.

A further conservative function of the gene equilibrium is to maintain a good proportion of recessive genes in the population. They may or may not be useful in the present day environment but may assume significance in a future environment.

SYNTHETIC THEORY OF EVOLUTION

(CHANGES IN GENE FREQUENCY)

Migration : Mutation : Genetic Drift:Inbreeding : Selection

If Hardy-Weinberg conditions are met with, there will be no changes in the gene frequency. But we know that there exists practically no population that meets all the conditions set by Hardy-Weinberg Law. Nevertheless, the law is important from the point of view that it sets a base-line from where magnitude of evolution can be compared.

To interpret evolution in terms of changes in gene-frequency is characteristic of population-geneticists. In such theories of evolution the relative contribution of natural selection is underplayed and many factors are brought into action to explain causes of evolution. Population geneticists, in this sense, seem to have outdarwined Darwin.We have seen earlier that genetic equilibrium is a sort of conservative force which does not allow too much experimentation because there is involved question of survival of the species. At times, however, when the tides of certain factors are mounted up, the genetic equilibrium downs its defences and allows the gene-frequency to attain a level different from its earlier value.

1. Migration And Change In Gene Frequency

Immigration When Local Population Is Large : Immigration to a local population when it is large in size does not produce a marked change in the gene frequency of local population. In such a condition the migrant or straggler genes coming from the another population has one of the two facts :

A

i. The migrant or straggler gene is swamped and eliminated by the local genes because local gene complexes are balanced to fit their own local environment, where as many of the straggler genes would be adapted to the environment where they came from. The hybrid between local and straggler would not be favoured as it is very unlikely to be properly adjusted. (similar is the case when two large population extend their range and meet but do not merge and remain distinct because hybrids between them are not adjusted to the either environment).

ii. The straggler gene can be introduced in the local population by introgression i.e., the hybrids that it produce

resemble one of the two parents. Those like the adjusted local population may breed successfully enough to introduce into it a few new useful genes & super-genes, thus causing a change in gene-frequency.

B

Immigration When Local Population Is Small : Immigration to a local population when it is small in size may or may not produce a marked change in the gene-frequency of local population depending upon stability of the environment.

I. when Environment Is Stable : Under such conditions the local population, though small, is perfectly adjusted to the local environment and hybrids between them and the stragglers would be at disadvantage and would not result in change in gene frequency.

Ii. when Environment Is Unstable : This is the condition when immigration is most effective because local population is not perfectly adjusted to the environment. Under such conditions, hybrids between local population and stragglers may find the environment suitable enough to survive. If stragglers possess genes which are of survival value in the new environment, selection would operate to incorporate these in the gene pool of next generation.

To conclude, immigration do not produce a marked effect on local population when the latter is large or small in stable environment. It produces change in gene frequency when local population is small in unstable environment.

Migration causes change in gene frequency can be proved algebrically. Below is given effect of migration on the gene-frequency differences between the recipient (Hybrid) population and the donor (Migrant) population.

Gen.	Gene-frequency		Gene-frequency Diff
	Recipient	Migrant	
0	qo	Q	qo-Q
1	qo (1-m)+mQ = qo-qo.m+mQ	Q	q_1-Q=qo-mqo+mQ-Q = (1-m) (qo-Q)
2	=qo-mqo+mQ (1-m)+mQ	Q	q_2-Q=qo-2mqo+m^2qo+2mQ -m^2Q-Q = $(1-m)^2$ (qo-Q)
n	(qn-1) (1-m)+mQ	Q	qn-Q = $(1-m)^n$ (qo-Q)

In every generation 1-m alleles of recipient population is replaced by mQ alleles of migrants hence in every generation recipient gene-frequency is multiplied by (1-m)+mQ.

2. MUTATION AND CHANGE IN GENE FREQUENCY
(Refer to Neo-darwinism for detailed account on mutation.)

Forward And Reverse Mutation Pressure : Mutations are the raw material of evolution. They are changes in genes and are inherited in accordance with the Mendelian principles. The Dutch botanist, Hugo De Vries, first emphasized the importance of mutations in evolution. Indeed, he proposed a 'mutation theory' of evolution intended not only to supplement but in large measure to supplant the Darwinian theory of natural selection. Occurrence of mutations does have a tendency to disturb any equilibrium which may exist. But mutation pressure is observed to be of low order of magnitude. Accurate data on this point are difficult to obtain. In the *Drosophila*, it is estimated that mutations of one kind or another are present in from 1 to 10 percent of the germ cells produced in every generation. Individual genes, however, vary greatly in frequency of mutation. Some kinds of genes may be so stable that only one in a billion will mutate. Accordingly, there must be great variation in the efficacy of mutation pressure in disturbing genetic equilibrium. Some genes may mutate so frequently that the constitution of the gene pool is considerably altered from the equilibrium in a short span of time.

The mutation pressure is opposed by what is known as reverse mutation. This would also occur at a rather constant rate, although, judging by evidence available, at a lower rate . Thus there are two opposed mutation rates 1. The rate at which wild gene changes into mutant gene, 2. the opposite rate. The combined action of the two rates is to change the gene frequency until a point is reached at which the both forward and reverse mutation pressure balance each other. At this point an equilibrium is established. Thus, while mutation pressures may alter genetic equilibriums, their ultimate net effect is to establish equilibrium, even though it is a different equilibrium from that which would otherwise prevail.

Mutation causes changes in gene frequency can be proved algebrically

A mutation introduces new genes into population causing shift in gene-frequency. If gene A continuously mutates to gene a and reverse mutation never happens frequency of a will increase and frequency of A will decrease. In due course of time a will replace A. if

Po = Initial frequency of A

u = mutation rate of A ⟶ a

The frequency of a after first generation of mutation

= uxpo The frequency of A is reduced by a factor of

Po-upo = Po (1-u)

In the next generation a will arise in frequency

= u [Po (1-u)] = Po (u-u²)

The frequency of A in this generation will be

[Po (1-u)] - [Po - (u-u)²]

= Po - 2 Pou + 2 Pou² = Po (1-u)²

As the number of generation increases to n, the frequency of A will become equal to Po [1-u]ⁿ. Thus even if rate of mutation (u) is small, after several generation it will approach 1 and Po will be equal to zero.

If the mutant gene A' is a dominant, the character is immediately expressed in the phenotype; if it is recessive, the character will not appear in the phenotype until two heterozygous individuals mate to give rise to the homozygous recessive A'A'.

Measuring Mutation Rate In Humans : Measuring forward mutation and reverse mutation in order to measure mutation rate is comparatively easier for microorganisms and fruit fly because they are fast breeders. Measuring such a factor in case of man who is much slow breeder in their comparison is a bit difficult. Also, humans are diploid but microorganisms haploid. A mutation in microorganisms, as soon as it arises, is identified. Since most mutations are recessive and there are two copies of a gene in every individual a mutation in human being, as it arise, will be suppressed by normal gene. For a mutation to express and identified, it must occur in two copies, hence one copy must be contributed by each parent. A mutation must have arisen long before in parents before it is actually shown up by some offspring.

However,some of the commonest genetic abnormalities such as achondroplastic dwarfism and myotonic dystrophy - are inherited as dominant alleles. If the disease is severe enough to prevent its carriers from surviving or reproducing, then in principle every new patient must represent a new mutation. The mutation rate should hence be the same as the incidence of the disease. This direct method has also some difficulties. For example, a new mutation might be recognised by its producing congenital deafness; but as there are many genes and conditions involved in normal hearing and a change at any one can lead to its loss, the

direct method will overestimate the rate per gene. These problems explain why most estimates of human mutation rates are higher than those in other creatures. In recent times mutation rate is calculated by comparing electrophoretic rate of proteins of parent and offspring. The largest survey was conducted in Japan where 3 new mutations were detected in half a million genes.Although rate of mutation per gene is low, rate of mutation per generation is high. A moderate guess work has it that half of all sperms and eggs carry on altered gene not present in parent. Thus each of us has three in four chance of carrying a new mutation in a functional gene. Thus, there are 3 billion new mutation in the human population of present generation, not present in the previous generation.

3. GENETIC DRIFT

Also known as drift, or sewall wright effect, or chance, genetic drift is a phenomenon in which certain genes, without being advantageous to the population increase in frequency and may be fixed (frequency becoming 1.0). This generally happens in small, isolated population. If population is large, it will be illogical to suppose disappearance of majority of persons. If population is small, disappearance of majority of persons can be assumed. If a population is not isolated some advantageous allele of the gene can be introduced in the population by migration which will hamper spread of disadvantageous allele. A population experiencing drift, therefore, has to be small and isolated.

We can consider a simple example. An isolated population of 100 individuals has 25 healthy male in reproductive age group and all of them vanish in a storm. The population will continue with residual males and their genes, howsoever deleterious, will circulate in the population.

Examples:-

1. Six-Fingered dwarfism in old order Amish : Old order Amish is a highly endogamous sect of Pennsylvania, US. The members of this sect number a few hundred who migrated from Europe in last century. The gene for six fingered dwarfism circulates in this population at a very high frequency in comparison to those in general population. The cause of drift here is migration and inbreeding.

2. Retinitis Pigmentosa in Tristan Da Cunha— Tristan is a small island near St Helena, in the Pacific. A small garrison was placed at Tristan to watch over Napoleon who was exiled at St.

Helena. After Napoleon's death, the garrison returned but two related families decided to stay and majority of the individuals at st. Helena are their descendants. The gene for retinitis pigmentosa, a gene for spotted retina, is in high frequency. The cause here is founder-effect and inbreeding.

3. Spread of ITD gene in US — Neil Risch (1995) has reported that US population is expanding in current years, with some populations expanding faster and there is rise in frequency of gene for idiopathic Torsion Dystonia (ITD).

4. Spread of Glycogen storage related diseases in S.E. Asian island- Sharp (1969) is of the opinion that this has probably occurred because of bottlenecks-death of individuals due to oceanic storms.

5. Drift in Dunker community, Pennsylvania — Glass et. al. have reported deviating gene-freqencies for many alleles which has occurred due to bottlenecks and inbreeding.

6. Drift in Parma highland, Italy - Ehrlich (1974) has reported deviating gene-frequencies for many traits. including blood groups, in this area.

7. Drift in Pit cairn Island, Pacific - The island was inhabitated by the descendants of 6 of the mutineers of the British ship Bounty and a few polynesian women. The is also characterized by deviating gene-frequencies for blood-groups.

8. Drift in Bass Strait Island, Australia - It started with 21 individuals and is characterized by drifi in gene-frequencies for blood groups.

9. Island of Saint Barthelemy, Carribean - It was colonised by 30 men in 1659. The island is known for deviating gene frequencies for many traits, including blood group.

CAUSES OF DRIFT

Natural calamities and migration & inbreeding are the major causes. In **addition, other causes may be.**

IV. All The Individuals May Not Be Reproducing : It may be that some of the individuals may not reproduce at all. Because population is small, each individual may be in possession of genes not available to the other members of the population. With the death of the individual, the gene is lost for ever to the population causing a shift in the gene-frequency.

(v) All Individuals May Not Be Leaving Large Number Of Offspring : The population must be heterozygous for many genes. There is thus 50% probability of one member of a allelic pair to enter a gamete and, thus, if one child is born, there is 50% chances of one allele to be handed down to next generation.

For example, Blood group B is determined by both homozygous allele I^BI^B and hereto zygous alleles I^BI^O. If an individual is heterozygous for the allele, I^BI^O then chances of inheritance of allele I^B increases with the number of offspring born.

Type B Blood : Genotype I^BI^O

No. Of Children	Chances than allele I^B will not be inherited
1	1 x 1/2 = 1/2
2	1/2 x 1/2 = 1/4
3	1/2 x 1/2 x 1/2 = 1/8
4	1/2 x 1/2 x 1/2 x 1/2 = 1/16

Table : showing that as number of children born increases, the chances of non-inheritance of an allele decreases.

Thus, if individuals do not leave large number of offspring, there are chances that some of the alleles may not be inherited by the offspring causing a change in the gene frequency. For smaller populations, this is a precarious situation.

Effects of Drift

There are two effects of drift—

(a) Bottleneck-effect (b) Founder-effect

(a) Bottleneck effect: This effect of drift comes into play when a natural calamity removes a good proportion of population so that the population again grows with residual population. Glycogen- storage related diseases in S.E. Asian islands is an example. Spread of ITD gene in some population of US is also of this type because a small population with deleterious gene is growing fast.

glycogen storage - S.E Asia
ITD - US

b) Founder effect : This effect of drift comes into play when a population either migrates to a barren land or migrate to populated land but practises endogamy eg. six fingered dwarfism in old order Amish, retinitis pigmentosa in Tristan Da Cunha.

Selection Versus Drift :— Drift, along with selection, acts on the gene-pool of populations to bring gene-frequency changes. A classic example to this effect is distribution of ABO blood group world wide. The ABO blood group is so distributed that frequency of 'A' allele is 0-55% B allete 0-35%, and O allele > 50%. It has been claimed that the selection agents for the blood groups are various diseases. Livingstone (1969 a) believes that plague, cholera, smallpox, pneumonia, diptheria or other infectitious diseases have been responsible for selection of blood group B hence frequency of B gene increases as one travels eastward from Europe to Asia (See genetic criteria of Race).

However, in some situations the role of random factors are also indicated. In the wellesley islands off the coast of Australia the aborigines of one island have highest frequency of B and for one of the Rh allele but no A. On another island, A and B is the same but Rh allele is different.

It is hard to believe that any factor but drift could account for such differences. Such marked differences in blood group among people of neighbouring villages has also been marked in New Guinea populations. New Guinea is a highly variable terrain, split into hills and valleys where adjacent populations stay isolated.

On the basis of blood group and haptoglobin, Neel (1970) has reported that in seven neighbouring villages of South American tribes, the differences in the gene frequencies is as great as 85.7 and 95.5% respectively, similar to between twelve different Indian tribes scattered throughout south America. This intervillage variability is explained on the basis of founder effect, which involves fission and fusion i.e. new villages are split from old (fission) by a group of related (similar) individuals (fusion)

Drift and increase in population size :— If small, isolated groups develop unique gene-constellations through drift, these unique gene-constellations have potentiality to spread far and wide with the increase in population-size which often occur in such cases. Population on the Bass strait island, Tristan da Cunha multiplied 10-fold by 1960; old order Amish increased from 91 to more than 15,000 within 70 years; a few thousands French settlers in canada became over six million by 1970 and replaced American Indian in vast areas of Quebec and other provinces. Many factors contribute to this expansion in population — early marriage, no birth control, better medical facility and low infant death-rate etc. Once an isolated population reach an optinum, the spread of a population is dependent upon "machine and weapons" i.e. its technology and not on biological difference. "The enormous increase in the world frequency of blondness, light-skin colour and blood group A_2 which occurred during European expansion can be understood more easily in terms of development of machines and weapons by Europeans than by biology of pigmentation and blood" thus writes Laskar. Though number of isolates of human populations may be large, history is testimony to the fact that expansion of only a small fraction of them account for subsequent racial distribution. "Recent out of Africa model" of human evolution & distribution maintains that a small fraction of Africans left Africa and subsequently populated the whole world in 50-60 thousand years.

Role Of Genetic-Drift In Evolution

1. Formation Of Different Gene Combinations

Given itself, random genetic drift may not bring any major evolutionary change but it can change adaptive characters of a population by dividing it into several sub populations of differing gene-frequency. This leads to competing sub-populations in a similar environment with different gene-frequency. It leads to species divergence. The picture that now emerges is that of a population, broken into several sub-populations, each with different sets of genes trying to explore the best means of exploitation of a given environment. The advantage here is of trying a whole combination of genes, rather than a single gene.

2. Success Of Disadvantageous Genes : A gene which, in a large population, had a net disadvantage may prove to be advantageous in a different combination of genes and thus get a foothold in the population which it was earlier denied in a large population. Formation of such a combination of genes is not possible under circumstances when selection is acting on a population.

Genes, thus, are enabled locally to pass through the combinations in which it would have never been allowed to pass through in the original, large population. In this way, observed Sewall Wright, the proponent of this theory, a gene through some unique gene-combinations traverses through Valleys and arrives at peaks of advantage. Then, in intergroup competitions, such novel combination of genes can prove advantageous over other combination of genes The evolution in this way can occur through leaps and bounds rather than plodding along a conservative mode of progress of the large random mating species

4. INBREEDING

Inbreeding usually refers to mating of two closely related parents Brothers and sisters matings and matings with the first cousin is very close inbreeding. Beginning with these extreme cases there is series of possible mating showing everdecreasing degree of relationship which finally merges with outbreeding. The dividing line between inbreeding and outbreeding is thus not very hard and fast.

Inbreeding tend to eliminate hybrids from the population and to replace them by pure breeds of homozygous type It does this by simple process of segregation according to Mendel's first law of segregation Thus the proportion of homozygotes in the population is increased Under such circumstances if a recessive gene is comparatively rare in the general population, inbreeding often

allows two such genes to come together and express themselves Autosomal recessive disease, that number about 600, are rare. Heterozygous unaffected persons are hence more common than the clinically affected homozygotes. For example, many more people carry the cystic fibrosis gene than have the disease. Similarly, phenyl Ketonuria (PKU) in which there is defect in metabolism of the aminoacid phenylalanine in the blood and severe mental retardation - affects about one in every 10,000 newborn Caucasians in Europe and North America.

The percentage of heterozygotes is, thus, definitely much larger than the homozygotes. With inbreeding, the percentage of homozygotes showing up the disease will increase.

Inbreeding increases homozygosity but it does not alter the gene-frequency. This can be shown by comparing crosses in two families. Two families are selected, each having two children. The two children of one family are heterozygous for idiocy (Aa) and two children of other family is pure normals (AA). Let the children of each family cross between themselves. Total number of dominant and recessive genes present inbreeding and outbreeding will be as follows (offspring restricted to 4).

Inbreeding	
Parent	Offspring
Family a - Aa x Aa Family b - AA x AA	gives 1AA : 2Aa : 1aa gives 4AA
Total recessive 2 out of 8 or 25%.	Total recessive 4 out of 16 or 25%.
Outbreeding	
Family a - Aa x AA Family b - Aa x AA	gives 2AA + 2Aa gives 2AA + 2Aa
Total recessive 2 out of 8 or 25%	Total recessive 4 out of 16 or 25%.

Thus we see that in both the cases, the recessive is present in the same percentage They are in existence in outbreeding too, but simply under cover.

We may, therefore, conclude that inbreeding in itself is not detrimental It is hazardous only to the extent when undesirable recessive genes are present in the original stock. If lethal genes are present in the heterozygous state inbreeding can bring the two recessive genes in one individual and causing its death.

Thus, if recessive gene is lethal, formation of recessive homozygote will lead to its elimination. For a self-fertilizing species, the recessive gene can be theoretically eliminated from the population in 9th generation. For example, if alleles of a gene are A and a and all individuals are heterozygote in the population, the

genotype-frequency will change in the generation in following way

Gen 0 Aax Aa (A=0.5, a=0.5)

Gen	A	Aa	aa
1	0.25	0.5	0.25
2	0.125	0.25	0.125
3	0.061	0.125	0.061
4	0.03	0.061	0.03
5	0.015	0.03	0.015
6	0.005	0.015	0.005
7	0.002	0.005	0.002
8	0.001	0.002	0.001
9	0.0005	0.001	0.0005

Thus after 9th generations, the frequency of heterozygote is almost nil and hence frequency of recessive allele is almost nil.

5. SELECTION

(Refer to Neo-darwinism for detailed account on selection,) Selection is variety of mechanisms that modify the gene-pool for reproductive success of a genotype.

Population Geneticists' Concept : Population geneticists donot contradict this aspect of selection. As they are statistician, they are more interested in figures. How many offspring a particular genotype left for the next generation ? This is the question they ask while looking for an aspect of selection. They are naturally interested more in fertility and fecundity of the population than merely agents of natural selection and its benevolent, holier-than-thou actions.

Gene-Frequency Approach Of Selection : The difference in their outlook is but natural. Darwin was a naturalist. He observed organisms in nature and focussed his attention on agents of natural selection that acted either to remove a harmful variation or to perpetuate a useful variation. Population geneticists want to record changes from generation to generation and find out whether there is any change in the relative distribution of different genotypes in the population on the basis of the changes in the genotype, the gene-frequency for any gene can be calculated. If there has occurred any change in the gene-frequency then it is considered that the population is evolving. To explain the changes in gene-frequency, various factors such as chance or genetic drift, migration etc are invoked. If such factors fail to explain the nature of gene-frequency, it is supposed that selection has acted.

Selection Not The Sole Agent : Selection thus, for population geneticists, is not the only means of evolution. It is one of the causative factors of evolution along with migration, drift, hybridization etc.

Selection can bring about changes in gene-frequency. It can be proved algebrically.

For example , posible genotype for a single gene difference is AA, Aa and aa. If there is complete dominance, and a is lethal then aa individuals are removed from the population but a circulates in population in heterozygote, shielded by A.

Frequency of a can be calculated algebrically as follows :

	Genotype AA	Aa	aa	Total	Freq. of a
Initial freq.	p^2	$2pq$	q^2	1	q
adptive value	1	1	1-s=0		
after selection	p^2	$2pq$	0	$p^2+2pq = p(p+2q)$ $= p[(p+q)+q] = p(1+q)$	
Relative freq.	$\frac{p^2}{p(1+q)}$	$\frac{2pq}{p(1+q)}$	0		$\frac{1}{2}\left[\frac{2pq}{p(1+q)}\right]$
	$\frac{p}{1+q}$	$\frac{2q}{1+q}$		$= \frac{pq}{p(1+q)}$	$= \frac{q}{1+q}$

$$\triangle q = \frac{q}{1+q} - q = \frac{q}{1+q} - \frac{q(1+q)}{1+q} = \frac{q}{1+q} - \frac{q+q^2}{1+q} = -\frac{q^2}{1+q}$$

It can be calculated by algebric calculation that gene-frequency change after one generation is $-\frac{q^2}{1+q}$. If q is initially large, its value will decrease rapidly. As q becomes small the change is approximately equal to q^2 because denominator 1+q=1, Thus if q=.01 the change per generation $(.01)^2 = .0001$ or loss of 1 out of 10,000 a genes.
Thus selection against recessive lethal gene is quite inefficient

Tristan Da Cunha

The island of Tristan da Cunha in the South Atlantic was uninhabited until a garrison (to watch over Napoleon in exile on St Helena, thousands of miles away) was placed there in 1817. When this was withdrawn, one William Glass and Thomas Swain decided to stay. A few other immigrants arrived during the next century. By 1960, there were 260 people on the island. 60 percent of the genes in the population could be traced back to two sisters and their husbands. Genetic drift has acted in establishing a degenerative eye disease, retinitis pigmentosa. Its frequency in most of the world is less than 1:4000, but on Tristan persistent inbreeding has produced an unusually high frequency of sufferers from this disease.

RACE - CONCEPT

Dobzhansky defined race as 'a group of population which are reproductively isolated to the extent that the exchange of genes between them is absent or so slow that the genetic differences are not diminished or swamped'. This definition of race underlines following ingredients for a group to be called races -

1. Group Of Population : All populations have their own genepool with differing gene frequencies. If race is defined in term of gene frequencies, all populations would qualify to be called a race. Race is higher in hierarchy than populations, and consists of many populations that have gene frequencies related to one another.

2. Genetic Differences : The group of populations forming a race have some genes in very high frequency and some in very low frequency and these genetic differences characterize a race. Such differences in gene-frequency arise partly as a result of selection and partly as a result of chance.

3. Reproductively Isolated : The group of populations forming races are reproductively isolated. This reproductive isolation, in fact, maintains the genetic differences between the races. The reproductive isolation, however, is not complete. Whenever races expand their range and come into contact of other races, they potentially hybridize and a now gene-frequency is set up.

4. Biological Concept : Race is different from national, religious, and cultural groups. Indians or Germans are not racial groups, they are national groups. Buddhists and Protestants are religious groups. Aryans and Dravidians are linguistic groups. Race is a biological concept and there is no race except biological races. Such races are identified because of differing gene frequencies resulting from isolation, hybridization, selection, small mutations and chance.

Major Races of the World

1. Caucasoid : This includes large number of ethnic groups that includes Mediterranean (distributed in Portugal, Spain, France Italy, Greece, Turkey, parts of North Africa, Arabia, Iran, Afghanistan, Pakistan and India), Nordic (Scandinavia, Baltic region, North Germany, North France, Belgium, British Island, US etc.) Alpine (Central Europe, Denmark, Norway, North Italy etc.)

East Baltic (Poland, Russia, Finland etc.) Armenoid (Turkey, Syria, Palestine, Iraq, Iran etc). Keltic (Scotland, Wales) Lapp (Sweden, North Finland, Norway etc); Polynesian (Polynesian island of pacific. Such as New Zealand, Samoa, Hawaii etc) Ainu (North Japan) etc.

They are characterized by all shades of skin ranging from white to dark brown; Hair vary from flat wavy to different degrees of curliness : Hair texture is usually medium to fine ; body and face hair is usually moderate to abundant; Head form ranges from dolicocephalic to brachycephalic; Nose ranges from leptorrhine to mesorrhine, never platyrrhine, with high nasal bridge; No prognathism of face; Cheek bones are usually not prominent; lips usually thin ; chin is pronounced or medium; forehead high and colour of the eye is of lighter shades.

2. Australoid Or Archaic Caucasoid : They resemble caucasoid and form two main groups - The Australian aborigines and pre-Dravidian or Veddoid, the former distributed in Australia and the latter in South and Central India (Bhil, Gond, Kadir, Oraon etc.) and Sri Lanka (Veddoid). These people suggest an admix of an archaic caucasoid with Negroid. It is, however, controversial

3. Mongoloids : They also include diverse ethnic groups represented by classic Mongoloid (Siberia, North China, Mongolia, Tibet); the arctic or Eskimoids (arctic coast of North America, Greenland, Alaska etc); Indonesian - Malay (South China, Burma Thailand, Malay Peninsula, Philippines, Japan, Indonesia etc.) American Indian or Ameriindian (North, middle South America)

Mongoloids are characterized by black, straight, coarse head hair; skin colour is yellow or yellow brown; Hair is scanty on face and body; broad flat face has prominent check bones; epicanthic fold on the eye lid

4. Negroid : They are basically comprised of African Negro and Oceanic Negro. The African Negro includes true Negros, Nilotic Negros, Bantu, Bushman-Hottentot and Negrillo. True Negros are found in West Africa, the Nilotic Negro in the upper Nile Valley, Bantu in Central and South Africa, Bushman in Kalahari desert of South West Africa, hottentot in South West Africa and Negrillo in equatorial forest of Congo region. Negrillos are African Pygmy. Pygmies are very short people, also distributed in oceanic and Asiatic regions. Such Pygmies are called Negrito.

The Oceanic Negros include Negritos and Melanesian Papuans. The Andamanese, Semang, Aeta, Tapiro are the

important representatives of Negritos, distributed in Andamans, East Sumatra, Philippine island and New Guinea respectively. Melanesians papuans are distributed in New Guinea, Fiji and neighbouring Island.

Negroids are characterized by woolly or frizzly black hair, colour of the skin is dark brown or black; nose is broad and flat; lips are thick and everted, eyes are black, ears are with little or no lobe; facial prograthism is well-marked; the head is predominantly long etc.

Racial Classification On The Basis Of Geographical Distribution - Garn has classified human races into three groups : Geographic races, Local races, Micro races.

1. Geographic Races are those group of Mendelian populations which are separated from each other by major geographical barriers. Following geographic races are recognised.

S.No.	RACES	GEOGRAPHICAL RANGE
1.	AMERINDIAN	From Alaska, Northern Canada, and Labrador through all of the America to the tip of South America.
2.	POLYNESIAN	Pacific Island, from New Zealand to Hawaii and Eastern Island.
3.	MICRONESIAN	Pacific Islands, limited to area from Ulithi, Palau and Tobi to Marshall and Gilbert Islands.
4.	MELANESIAN-PAPUAN	New Guinea and neighbouring islands.
5.	AUSTRALIAN	Australia.
6.	ASIATIC	Eastern Continental Asia, Japan, Philippine Islands, Sumatra, Borneo, Celebes, Formosa.
7.	INDIAN	India, from the Himalayas to the tip of Indian Peninsula.
8.	EUROPEAN	Europe and Western Asia, the Middle East and Africa north of the Sahara.
9.	AFRICAN	Africa south of the Sahara.

2. Local Races : If the population is small or isolated, it is easier to identify and define a local race. A local race may be isolated geographically (for example, the Eskimos of North America or the Ainu of Japan) or culturally (for example, Gypsies or the Yemenite Jews).

Major Local Races Of Homo Sapiens

S.No.	LOCAL RACES	S.No.	LOCAL RACES
1.	Eskimo	16.	Hindu
2.	North American Indian	17.	Dravidian
3.	Central American Indian	18.	Early European
4.	Fuegian	19.	Northwest European
5.	Ladino	20.	Northeast European
6.	Neo-Hawaiia	21.	Lapp
7.	Murrayian Australian	22.	Alpine
8.	Carpentarian Australian	23.	Mediterranean
9.	Turkic	24.	North American coloured
10.	Tibe	25.	South African coloured
11.	Irani	26.	East African
12.	Nori	27.	Sudanese
13.	Classic Mongoloid	28.	Forest Negro
14.	Southeast Asiatic	29.	Bantu
15.	Ainu	30.	Bushman and Hottentot
		31.	African Pygmy

3. Microraces : Microraces are Mendelian populations which differ from each other in few genetic loci. Their boundary cannot be defined and their number range to infinity.

BASES OF RACIAL CLASSIFICATION

Races may be defined as group of population that share a common gene pool and is differentiated from other groups in gene-frequencies.

The characters upon which races are distinguished-

i) must be non-adaptive hence least influenced by environmental factors.

ii) must be hereditary hence genetic in origin.

Morphological Bases : A. Morphoscopic

This include morphological features that cannot be measured but can only be visually discriminated. This includes skin, shape and colour of eye

1. Skin Colour : Skin colour depends upon two factors- smaller vessels of dermis and concentration of melanin, a pigment in the outer layer of skin, formed in special pigment cells called melanocytes located in the deeper layer of skin. When there is little

melanin, skin colour depends upon amount of blood vessels and state of oxygenation of the haemoglobin reflected in the white to pink colour of the skin. In dark skin concentration of melanin increases. Melanin absorbs the harmful solar radiation and thus protects skin from likely damage. In white skinned people, there is minimum of melanin on the outer surface thus allowing even slightest of sun-shine reach to the deeper layer of skin for protection against cold and synthesis of Vitamin D. The skin colour has developed as adaptation to the moist heat of equator, at least in the northern regions of the old world. However, any generalization is freit with dangerous and misleading conclusions as people with different shades of skin in somewhat similar geographical conditions such those of congobasin (black), Borneo (Pale yellow) and Amazon Valley (Cinnamon) exist. Skin colour is Polygenic and multiple allelic not following simple Mendelian inheritance. It is believed to be determined by small number of genes, most probably 3 or 4 gene loci.

There are three distinct categories of people based on the skin colour :

1. Leucoderm : Various shades of white e.g. caucasoid.
2. Xanthoderm : Various shades of yellow e.g.Mongoloid
3. Melanoderm : Skin colour dark eg.Negroid.

2. Hair Colour, Texture & Form : Hair of different races is differentiated on the basis of colour, texture and form. The colour varies from light blonde to brown (Caucasoid), brown to brown black (Mongoloid) and brown black (Negroid). The difference in the hair colour is due to difference in the same pigment - melanin. In the lighter shades of the hair melanin granules are less and less completely packed with melanin than in darker ones. In most parts of the world hair colour are dark, being mainly blonde and red in N.W.Europe. Even in dark-haired populations there are considerable variation in the actual amount of pigment in the hair, but it is not easy to detect differences by eye or even by reflectometry when the shade is black Apart from it, there is considerable regional variation. In Italy there is gradient of increasing blondness from South to North. Similar increase is found in North U.K. Genetically red hair seems to be produced by single pair of recessive genes. Dominant genes are involved in production of black hair. Texture varies from fine (-56μ) to medium (57-84μ) to coarse (85bμ +) in the above races respectively excepting Chinese and Japanese among mongoloid who have coarse hair. The hair form is generally

classified into 3 groups :

a) Cymotrichous or wavy of caucasoid and can be classified as broad wavy, narrow wavy and curly wavy.

b) Leiotrichous or smooth of mongoloids and can be differentiated as stretched smooth, flat smooth.

c) Ulotrichous or woolly or kinky of Negroids and can be differentiated as frizzly, filfil or pepper corn. Filfil is characteristic of Bushmen who have small knots of thick rolled hair separated by bare spaces.

Races can also be differentiated on the basis of hair-whorls, clockwise, or anticlockwise, though the former is common. Two whorls also sometimes appear.

There appears to be no relationship between hair form and climatic conditions because Mongoloids and caucasoid inhabiting tropical regions like Negroids don't possess hair-form similar to Negroids.

3. Body Build : Racial differences can be perceived depending upon the body-build in following way-

CAUCASOID	MONGOLOID	NEGROID
Linear to lateral Slender to rugged	More lateral than linear	Lateral with traces of linear

4. Eye-Shape And Colour : On the basis of shape of the eye, races can be divided into mongoloid and Non-mongoloid. Mongoloid-eye is characterized by (a) Oblique paplebral fissure, the outer angle being higher than the lower angle (b) a narrow slit (c) inner or complete epicanthic fold in various degree of development. Epicanthic fold is fold of skin hanging over the free edge of upper eye-lid, and is of four types :

a) Inner epicanthic fold : at the inner edge of upper eye-lid, most pronounced in infants and women.

b) Complete epicanthic fold : at the complete edge of upper eye-lid.

c) External epicanthic fold : at the outer edge of upper eye-lid, most pronounced at advanced age.

d) Median epicanthic fold : at the middle part of edge of upper eye-lid, at advanced age.

Colour of the eye varies from light blue to brown black and is due to the pigments on both back and front side of Iris If

pigments are only on back side, blue eye-colour results. When it is on both sides, brown-black eye-colour results. Colour appears due to the different refractive indices of the deposited pigment and there is no blue, or green pigment. In lighter colours, there is no pigment on front side and light passes through this layer. Some of the rays are absorbed by the back side of the iris while a majority is selectively reflected. The reflected beam is of shorter wavelength hence blue colour predominates. It is thus varying amount of pigment melanin in iris that determines nature of the reflected beam, the latter determining colour of the eye. There is no difference in the pigment of the eye in different eye-colour. The dark eye colour restricts the entry of light into the eye to the pupil and help to protect retina against damaging uv-radiations. People belonging to areas of great sunshine tend to have dark brown to brown black eyes. The dark eye-colour is dominant to light eye-colour is probably determined by several genes. Eye-colour varies in the following manner in the different races -

CAUCASOID	MONGOLOID	NEGROID
Light Blue	Light Brown	Dark Brown
to	to	to
Light Brown	Dark Brown	Brown Black.

Morphological Bases : B. Morphometric

5. Cephalic Index (C.I.) and Cranial Index (C.I.) : Shape of the head is largely genetic though environment also has some role to play eg.European immigrants in US have somewhat altered shape of the head, though out crossing with different racial groups may have led to altered shape. Nutrition also influences shape of the head to some extent. Cephalic Index is expressed as percentage of the breadth of head in relation to the length of the head. ie.

$$\frac{Breadth \times 100}{Length} \quad *1$$

In case cranial Index, the figure is 2 units lower. Following types of head is recognized :

*1 Length is calculated from mid forehead to back of head, the occiput, and the breadth as distance between two parietal elevations at the side of head.

Type	Cephalic Index	Example
Dolicocepahlic (long or narrow)	< 76	Negroid-Caucasoid
Mesocephalic (Medium)	< 81	Mongo-Neg-Caucasoid
Brachycephalic (Broad)	> 81	Mongoloid-Caucasoid

Only Length and breadth don't give a complete idea of the shape of the head, hence head-height is also considered. However, less data is available because of difficulty in measuring height of the head in living condition. It is from tip of the fronto-parietal junction to tip of the chin and expressed as :

$$\frac{Head\ height \times 100}{Head\ Length} \quad \text{and} \quad \frac{Head\ height \times 100}{Head\ Breadth}$$

6. Facial Index : Shape of the head (or cranium) may match with the shape of the face ie. a long cranium going with a long face, or a broad cranium going with a broad face (harmonic condition), Sometimes, however, the two may not match (disharmonic condition) eg.Armenoids who have narrow face with broad cranium, and cromagnon and Eskimos who have broad face with narrow Cranium.

Face may show prognathism (Protrusion of jaw) or Orthognathism (no protrusion). Prognathism may result due to projection of alveolar margins of upper and lower jaw (alveolar prognathism), or projection of the complete jaw . facial prognathism)

Facial Index show sex-based differences because females have shorter and broader faces.

The facial Index is described as percentage of length in relation to breadth

$$\frac{length\ of\ face \times 100}{Breadth}$$

*1 Breadth of face is measured across Zygomatic arch, the two upper cheek bones, and length of the face measured from nasion (the forehead nasal joint) to gnathion (the tip of the chin).

Following types of faces are recognized :

Type	Facial Index	Race
Euryproscopic (Broad)	< 84	Caucasoid
Mesoproscopic (Medium)	< 88	Mongoloid
Leptoproscopic	> 88	Negroid

7. Nasal Index : The nasal index is calculated as percentage of breadth of the nose in relation to its length.

$$\frac{\textit{Nasal Breadth} \times 100}{\textit{Nasal Length}} \quad *1$$

The nasal index is as high as 104 in Ituri Pygmies and values above 90 are found in many African Negro peoples, in Melanesia and in Australia Aborigines. The noses of the Eskimos are unusually narrow. In India, the index shows a general, but irregular correspondence with status in the Caste-hierarchy. It is lowest in the Brahmins and highest in the lower castes and highest of all in some of the tribal people.

The shape of the nose seems to be an adaptive feature because platyrrhine condition seems to be heat-adaptation because the broad nostrils permit exit of greater quantity of warm air from lungs thus providing a cooling effect. Leptorrhine condition seems to be a cold-adaption because the narrow elongated nostrils provide enough surface area for the incoming air to be warmed. Besides, it is influenced by age and sex because children and females show platyrrhine condition.

Stature : Stature is dependent upon both paratypical (environmental) and diatypical (hereditary) factors. Paratypic factors for stunted stature include forest and mountain living, excessive cold, low nutrition etc whereas for tallness in included open wandering habit, free air and excess sunshine, regular life and high nutrition. Among the diatypical factors besides genetic blue-print, secretions from pituitary, thymus and gonad are included. Between the two, the paratypical forces seem to play secondary role because in the same place people of different stature may live side

*1 Length of the nose is measured from nasion, (the noso-fronal joint) to subnasale. In skull, the same is measured from nasion to the mid-point formed by tangent lines cutting across inner margins of nostrils. The breadth is the distance between the outer ends of two nostrils.

by side such as tall Norwegian and the short Lapps living together in the North of Scandivania. In Africa we find extreme contrast of stature, from the very tall Tutsi and Nilotic tribes such as the Nuer and Dinka to the miniature Pygmies and Bushmen. In both the latter cases, however, there is again considerable variation from one group to another. the Bushmen of southern Kalahari appear to be shortest (1.45-1.50m) but to farther north the average rises to 1.55 or more.

Though the stature shows even wide intra populational variation, it is commonly used as criterion for classifying primary races. Among the three scales of height viz.Topinard's, Haddon's and Martin's, it is last which is mostly followed. Martin's scale is reproduced below with some modifications.

Stature	Height	Main races
1. Tall (Tall, Very Tall, Giant)	> 170cm	Caucasoid, Nilotic Negro (Including Sikh Rajput of India)
2 Medium (Below Medium, Medium, Above Medium)	170-160 cm	Mediterranean, Eskimo, Dravidian
3. Short (Pigmy, Very Short, Short)	< 160 cm	Andamanese, Negrillos.

Genetic Criteria Of Races

A. Serological B. Non-Serological c. DNA variation

A. Serological Criteria

1. Blood - Groups

ABO Systems : Of the four blood-groups A, B, AB and O, as classified by Landsteiner, O is the commonest one. Its gene frequency in worldWide average is about 0.623.It is followed by A gene (0.215) and then by B gene (0.162).

Simplest condition exists in American Indians who exclusively possess I^O with almost negligible I^A or I^B and Eskimos with sufficiently high I^O with little I^A & I^B. I^A gene occurs in very high frequencies in some regions of Europe and Asia and also among certain Australian tribes. Most of the caucasoids show prevalence of I^A.

The highest frequency of I^B gene is observed in North India and central Asia. 'B' gene is absent is most of the Australian tribes. It appears that frequency of 'B' gene decreases and that of A gene increases as one proceeds westward from the pacific coast of Asia to the Atlantic coast of Europe.

Such geographic concentration of different blood groups can be explained on the basis of origin of mutation leading to I^A in Europe and I^B in central Asia. whereas I^o as wild gene continues in the Amerindians.

MNS System : In 1927, Landsteiner and Levine found two human antigens, which they called M & N. These two antigens have no natural antibodies and as such these have no effect in transfusion of blood. When M antigen is present in red cells the blood type is called 'M' where N is present it is called N and when both M & N are present it is termed as MN. M & N are co-dominant. The frequency of M is lowest in Australia (20%) and highest in US (90%) and a few other areas such as S.E. Asia, Arabia etc. In Europe, it averages 50%.

In 1947, Sanger and Race discovered another antigen called S. This antigen 'S' differs from the M & N. It occurs among individuals of all three MN blood types. There are two antigens- S and s. Persons can be MSMS, NSNS, MSNS, MSMs, NSNs, MSNs, MsMs, NsNs, MsNs, MsNS. Frequency of S is highest in India and middle East (40%) where it is mostly associated as MS. In Europe, its frequency is 30-35% and lowest in East Asia (5-20%).

Rh-System : Landsteiner and Weiner (1940) discovered the Rh-system in rhesus monkey first and then in humans hence it was named so (rh from rhesus). It was originally thought that there are only one pair of allele, D/d determining three genotypes D/D, D/d and dd, the first two being Rh-positive and the last Rh-negative. Later on, fisher proposed six alleles C, D, E, c, d, e, three of which are located on single chromosome (eg. one genotype can be CDe/cde). Weiner proposed 8 alleles - Rz, R1, R2, Ro, r, r', r'' and ry. Landsteiner and Weiner (1940) discovered another system (LW - system, based on first letter of their names) closely associated with Rh-system. Most people are LW^+. 85% of population is Rh^+ and 15% Rh^-. The situation is complicated when a Rh^- mother gives birth to Rh^+ child. Since she has no Rh antigens, the same of foetus may leak into her blood circulation and her blood cells build up antibodies against Rh antigens. During next pregnancy, if she conceives a Rh^+ baby, it's RBC will be lysed (Haemotytic Disease of Newborn, HDN).

Among mongoloids, Rh-negative is very rare (0.5 to 1.5%) but is high in caucasoids (upto 15%). Among Negros, Rh^- occurs in 5-8% of population

Duffy System : it was discovered in one Mr. Duffy and has been named after him. Allele Fya and Fyb control Duffy positive and Duffy negative blood types. Fya is dominant over Fyb. Three possible combination of these two alleles are :

i. Fya / Fya
ii. Fya /Fyb } Duffy Positive
iii. Fyb / Fyb Duffy negative.

In England Duffy positive are 65%. In Pakistan and India the frequency of Fya is even higher. Lower frequency of Fya (0.14) occurs in American coloured population.

Diego System : Two alleles Dia and Dib determine blood types Diego +ve and Diego -ve. Dia is dominant and responsible for Diego antigen (+ve group).

Diego +ve individuals are Asiatic (mongoloids) and the New World people who descended from mongoloids. It has been postulated that the mongoloids are of fairly recent origin and that the Diego antigen is one of the characteristics of this group.

Dia is absent in Europe and Africa, Australia, Micronesia, Polynesia and Eskimos.

Kidd : Two alleles Jk^a (dominant and cause phenotype Kidd +ve) and Jk^b (recessive; expressed as Kidd - ve) govern Kidd positive and Kidd negative blood types. It is most common in West Africa and American coloured people. It is least common in Chinese people.

2. The Histocompatibility (HL-A) System

HL-A or Human leucocyte antigen is present on the surface of most organs and is responsible for graft rejection. The antigens are determined by five closely linked loci A, B, C, D and Dr on short arm of chromosome 6. There are 19, 27, 7, 11, 7 alleles on each A, B, C, D and Dr loci generating enormous number of haplotypes. The alleles broadly fall into 3 groups - those that are frequently high in all populations such as A_2; those that are present in all but high in certain such as A_1 in Africans ; and those that are confined to some population such as Bw 42 in Africans.

3. Haemoglobin

Haemoglobin is made up of four protein chains α α β β

each of which contain a haem group (with iron). The α chain is coded for by the gene α-globin on chromosome 16 and β chain by the gene β-globin on chromosome 11. The α and β chain have 141 and 146 amino acids respectively.

The adult haemoglobin has two α and two β chains ($\alpha\ \alpha\ \beta\ \beta$). This is Hb-A. About 2% of adult's blood have different Hb-(Hb-A2) with $\alpha\ \alpha\ \delta\ \delta$ chains. δ chain differ from β chain in 10 positions. Foetal haemoglobin (Hb-F) has $\alpha\ \alpha\ \gamma\ \gamma$ chains, γ-chain differing from β in 39 positions. All these haemoglobins are normal coded for by genes α-globin and β-globin on chromosome 16 and 11 respectively.

Over 100 variants of haemoglobin are know, over 70 for α-chain and 35 for β-chain. Majority result in single amino acid substitution. A few of the variants reach polymorphic proportions in some population such as Hbs, Hbc HbE, HbD Punjab (β-chain variants) and Hbj Tongariki (α-chain variant).

Hbs : This results due to mutation that causes replacement of glutamic acid by valine at position 6 in both β-chains. The variant is well distributed in Africa because it provides resistance to malaria. It is also found in South India.

Hbc : This results due to β6 Lysine ⟶ glutamic acid. It is well distributed in Eastern Africa.

HbE : This results due to β26 glutamic acid ⟶ Lysine. It is well distributed in S.E.Asia.

Hb-D Punjab : It has been found in various parts of the world and is highest (1-5%) in Sikhs and Gujaratis. It is β121 glutamic acid ⟶ Glyc. Three other forms of Hb-D are known : Hb-D Ibadan (β87 Threonine ⟶ Lysine), Hb-D Bushman (β16 glycine ⟶ Arginine) and Hb-D Baltimore (α68 Asparagine ⟶ Lysine). Haemoglobin J Tongariki is α115 Aspartic acid ⟶ alanine. In addition, a number of variations in the haemoglobin is found, some of which is mentioned below (see table next page).

Such a wide variation in the structure of haemoglobin is puzzling. However, in many cases, such variations have been shown to occur in malaria prone regions, conferring especially in case with Hb-S. It occurs in high frequency in Africa and other tropical countries, including India.

Thalassaemia : During development, the type of haemoglobin chains change from embryonic to foetal to adult

being types, the normal adult type being $\alpha\ \alpha\ \beta\ \beta$ chains. In thalassaemia there is defect in the synthesis of α or β chains so that adult haemoglobin is not normal. A defect in α-chain is called α-thalassaemia and a defect in β-chain is called β-thalassaemia.

β-thalassaemia can be major if there is no β-chain at all. This results due to homozygous condition. In β-thalassaemia minor there is some production of β-chains. Unused α-chains are deposited on red cell membrane and causes rupture of RBC leading to anaemia (Cooley's anaemia).

α-thalassaemia occur mainly due to α-genes which may involve loss of one to all α-genes (Hydrops foetalis).

α- and β-thalassaemia is prevalent in most tropical and subtropical countries including India, S.E.Asia, New Guinea, some pacific islands etc.

Table : Showing variable forms of haemoglobin

Hb-I reiburg - β23 deletion

Hb-Constantspring - α (addition of 31 aminoacids)

Hb-Lepore - mixed $\delta-\beta$ chains

Kenya haemoglobin - Mixed β and γ chains

M Boston	α58	His	⟶ Tyr
M Iwate	α87	His	⟶ Tyr
M Saskatoon	β63	His	⟶ Tyr
M Hyde Park	β92	His	⟶ Tyr
Torino	α43	Phe	⟶ Val
Hammersmith	β42	Phe	⟶ Ser
Sydney	β67	His	⟶ Tyr
Chesapeake	α92	Arg	⟶ Leu
J Capetown	α92	Arg	⟶ Gln
Yakima	β99	Asp	⟶ His
Kempsey	β99	Asp	⟶ Asn
Wien	β130	Tyr	⟶ Asp
Genova	β28	Leu	⟶ Pro
Gun Hill	β92-96 deleted		

4. Isoenzymes And G6PD

There are many enzymes whose function is same but they differ structurally. Such enzymes are called isoenzymes or isozymes and a typical example is glucose-6-phosphate dehydrogenase which is found in many tissues including RBC. The enzyme catalyzes conversion of glucose-6-phosphate into 6-phosphogluconate, an intermediate step in the formation of pentose 5-phosphate.

G6P ——G6PD——> 6 Phosphogluconate ——PGD——> Pentose 5-phosphate

In certain cases, there is deficiency of G6PD, leading to destruction of RBC in certain condition eg. upon intake of bean, *Vicia fava* (Favism) and malarial drug, primaquine.

The variability in the enzyme G6PD is reflected in rate of migration of the enzyme in an electric field and severity of RBC destruction during intake of certain substances. The normal form is designated [Gd(B+)] and variants are [Gd(B-)], [Gd(A+)] and [Gd(A-)], each differing from normal in one or few amino acids B(-) from is prevalent in Mediterranean, Middle East, Greece, India in about 20% population, reaching a level of 50-60% in a Jewish isolate. It has same rate of migration but severity of RBC lysis is great. A(+) and A(-) forms are present in 20% African population, both characterized by slow rate of movement : A(-) slower than A(+) and having a half life of only 13 days in comparison to 62 days for normal enzymes.

Other variants of G6PD deficiency includes GD Canton in 5% population of Southern china, and, GD Markham, a common variant in lowland New Guinea. The deficiency state is found to be resistant against *P. falciparum* infections.

5. Serum Proteins

This includes haptoglobins, transferrins, albumins, anti-trypsins, C3 component of complement, the GC-component, pseudocholineterase etc.

Haptoglobin : Haptoglobin is a serum protein which is concerned with transport of free haemoglobin to liver for breakdown of haem and ultimate production of bile salt, biliverdin. Haptoglobin gives three bands in electophoretic studies.

Type 1-1 (Single strong band), Type 2-2 (a seriers of slowly moving bands) and Type 2-1 (a weak band like 1-1 along with a

number of slow moving band). Two alleles, Hp^1 and Hp^2 are implicated with the following genotype and phenotype-

Hp^1/Hp^1 – resulting in phenotype band 1-1
Hp^2/Hp^2 – resulting in phenotype band 2-2
Hp^2/Hp^1 – resulting in phenotype band 2-1

Studies indicate that the frequency of Hp^1 gene is around 40 percent in Western Europe. However, its incidence is much higher (60-70%) in tropical Africa. In some African populations a fairly high proportion of people (about 30%) show no haptoglobins. In areas of Asia (India,China) Hp^1 is found in lower frequencies ranging from 10-20 percent. The selective factors at work are not precisely known. In a variety of infection, increased concentrations of haptoglobins have been noted.

Transferrin (Tf) : Transferrin transports iron from sites of red-cell destruction and from the intestine to the bone marrow, where Hb is synthesized. Each molecule can bind two atoms of iron.

About 20 variants have been distinguished by differences of electophoretic mobility. A slow (cathodal) variant, TfD_1 is quite common in Africa, Australia, New Guinea, and adjacent islands. Another variant, TfD_{chi} with an electophoretic mobility very much like that of TfD_1 was first described in Chinese, and has been found in various populations of south-east and East Asia, in the Veddahs of Ceylon and in some Indian tribes.

Serum Albumin (A1) : A fast (anodal) variant has been remarkably frequent (gene frequency 9-14 per cent) in Naskapi and Montagnais Indians of Labrador. ($A1^{Naskapi}$, now re-named $A1^{Algonkin}$). Though the distribution of this gene is mainly in northern USA and Canada, it also occurs in the Navajo and Apache of the south-west.

More than a dozen rare albumin variants have been reported from various parts of the world including Malaysia, India, Africa, Europe, and New Guinea.

α1 Anti-Trypsin (Pi System) : This protein inhibits trypsin and certain other proteolytic enzymes. Its physiological role may be to block the proteolytic enzymes released from white cells at sites of inflammation. In Norwegians four alleles were present at appreciable frequencies: Pi^m (95 per cent) Pi^s (2.3 percent), Pi^z (2.0 per cent) and Pi^f (1.3 per cent) and two other rare alleles were also found. Little is known at present about the world distribution

of these alleles, but in Lapps, finns, and some Asiatic samples Pi^s was not found. Pi^z homozygotes are unusually susceptible to chronic obstructive lung disease. This implies some selection against these genes.

The C_3 Component Of Complement : Complement is a factor of fresh serum that is needed for the destruction of foreign cells that have been coated with antibody. It is very complex system of 11 proteins that interact in sequence when the first in the series becomes attached to antibody molecules that have combined with the invading antigen. Polymorphism of one of the complement components, C_3 can be detected by electophoresis. Two common alleles, C_31 and C_32 and about 10 rare alleles are known. C_31 has a frequency of 15-25 per cent in most European populations.

The Gc (Group Specific) Component : The Gc locus is closely linked to those of serum albumin and seems to have originated by duplication. Three phenotypic patterns, due to two common alleles, Gc^1 and Gc^2 are found in all populations. Gc^2 frequencies vary around 25 per cent in Europe, but are lower in Africans and Australian Aborigines. Another allele $Gc^{chippewa}$ in certain North American Indians and yet another, $Gc^{Aborigine}$ in Australia and New Guinea. It has been shown that the Gc protein is involved in the transport of vitamin D, and Gc^2 frequencies tend to be low in regions of low sunshine

Serum Pseudocholinesterase : Pseudocholinesterase hydrolyses certain organic esters and is present in various tissues, but not in red cells. It is distinct from acetylcholine esterase which is active in splitting the neurotransmitter substance, acetylcholine, at neuromuscular junctions, and which also occurs in red cells. It was noticed that some individuals develop prolonged paralysis and breathing difficulties when given muscle-relaxant suxamethonium prior to surgery.

Individuals homozygous for the allele show weak enzyme activity and heterzygotes show intermediate activity levels. The recessive gene has high frequency in Europeans.

6. Immunoglobins

The immunoglobins are the humoral antibodies formed primarily by B-lymphocytes in response to the presence of foreign substances in the body and represent one of the main defensive mechanisms against infection by pathogens. IgG, IgA, IgM, IgD,

and IgE are the 5 types of immunoglobins

Immunoglobulins (antibodies) are formed against antigens. Immunoglobulins are glycoproteins consisting of four polypeptide chains- two identical light chains and two identical heavy chains. Chains are held together by disulphide bonds. Two types of light chains are recognised: k (kappa) and λ (lambda); both occur in all classes of immunoglobulin. A given antibody molecule always contain two kappa or two lambda light chains; never a mixture of two. The heavy chains, on the other hand, are specific for each class of immunoglobulin: γ (Gamma) for IgG, μ (Mu) for IgM, α (alpha) for IgA, δ (delta) for IgD and ϵ (epsilon) for IgE.

It would not be out of place to introduce readers to the classes of immunoglobulins.

There are five classes - IgM, IgG, IgA, IgD, and IgE.

a. IgM : The structure of IgM is unique in that it consists of five units linked together by a small polypeptide known as J-chain. Primary response antibodies are of IgM class because of their less specificity with ten combining sites (each IgM has two combining sites, $2 \times 5 = 10$). It results in precipitation or agglutination of the antigens. Clumped antigens are susceptible to phagocytosis.

b. IgG : Majority of the secondary response antibodies belong to this class. Antibodies are found throughout the tissue spaces and are directed against a large variety of antigens. Most virus antibodies and antitoxins belong to this class of immunoglobulin which is the only one that crosses the human placenta. It is the most abundant immunoglobulin in mammals.

c. IgA : The principal role of IgA is at mucous membrane, e.g, of respiratory and digestive tract. It is the chief antibody secreted in milk after childbirth and protect gastro-intestinal tract of newborn against microbial infection. It is only type of antibody found in sweat, tears, saliva, nasal fluid, genito-urinary and intestinal secretions where it performs a highly specialized role in maintaining barrier against infection entering the tissue through mouth, gut, or excretory system. It sterilises skin and gums.

d. IgD : IgD has little or no antibody activity but may be important in early life as an antigen-trapping determinant on the surface of some B-lymphocytes. This antibody appears on the surface of B-lymphocytes during early life.

e. IgE : IgE is involved in hypersensitivity reaction such as asthma. In combination with antigen, it causes release of histamine

from mast cells. It is also supposed to have a role in the defence against intestinal parasites such as roundworm and tape-worms.

Antibodies are elicited by the antigens and one type of cell produces one type of antibody. An individual is capable of producing million types of antibodies because of permutations and combinations in the genes for immunoglobulins. An antigen selects a type of antibody and that type of cell is multiplied. The variability of the antigens results due to changes in the variable regions, not in the constant regions of the light and heavy chains.

There are, however, present variations in the constant region of the antibody between individuals, and this is best known for IgG. If IgG is different in the constant region it will be treated as antigen. This variation is called GM factor. If mother has a GM-factor not possessed by her baby, mother's antibody will be attacked upon when baby grows and forms its own antibody. Mother's antibody which the baby has gained through placenta or milk, tend to disappear, however, after first few years of life.

Several GM types have been discovered, such as GM(1)+ and GM(1)- which has there different amino acids at positions 356-358 : aspartic acid, glutamic acid and leucine in GM(1)+ and glutamic acid, glutamic acid and methionine in GM(1)-. These two are produced by one locus. There have been found many such loci in different individuals. It has been found that different populations are characterized by different GM characteristics.

B. Non-Serological Criteria

a. Secretor Status : It has been noted that various body secretions viz. sweet, tear, semen etc, certain a substance called "blood group-like substance". It is found that the secretor gene(s) is dominant over non-secretor gene(s) thus a person with SS or Ss will be secretor and with ss non-secretor.

It has been found that a high frequency of S is found in Caucasoids and s in Negroids, and Mongoloids are placed in between

b. Tasting Ability : Individuals may have ability to taste phenylthiocarbamide (PTC) or not hence they can be classified as taster or non-taster. The gene for tasting, T is dominant over t(non-tasting). Thus the faster will be either TT or Tt and non-taster tt.

If has been noted that a very high frequency of T is found

caucasoids and t in Negroids with Mongoloids lying in between the two.

C. Human Chromosome And DNA Polymorphism

Chromosomal Variation : The most striking variation is in the length of the Y-chromosome which can be as large as a member of the G(13-15) group or as small as a short acrocentric chromosome. This difference has been shown to be due to the amount of Q-staining heterochromatin in the distal region of the long arm of the Y which may be massive or virtually absent A long Y is relatively common among Japanese and a very short one in Australian Aborigines. Q-band variations are also noticed particularly in chromosome 3 and some other chromosomes.

Methods have been devised that stain heterochromatin around the centromere (C-banding); particularly large C-bands are seen in chromosomes 1,9, and 16 and these also show polymorphic variation. Significance of variable C-bands is not clear at present.

Variations in DNA : Several types of variation in the DNA has been found with the use of restriction enzymes. These are RFLPs, VNTR, CA-repeat etc.

a. RFLPs : Restriction endonuclease enzyme has been involved to demonstrate variation at the DNA level itself. DNA of most people vary once every Zoo bp, there are present different sites of cleavage for restriction enzymes(which are very much site-specific). Enzyme Hpal recognises sequence of GTTAAC present in B globin gene and produces fragments of 7 6 Kb (kilobase; 1kb = 1000 basepair). A mutation from GTTAAC to GCTAAC looses the cut site so that the fragment generated now is 13 0 kb length. Another mutation has been found to introduce extra cut sites in the globin gene and fragment generated is 7kb long.

7.6kb fragment is associated with sickle gene in Kenya, Saudi Arabia and India, but in Ghana, Nigeria and around Mediterranean sickle gene is associated with 13kb fragment In ivory coast and Sierra Leone, both associations are common. Enzyme Bam H also generate different RFLPs.

Various estimates have been made of the number of RFLPs which range from 1 restriction enzyme-site in 85 nucleotides to 1 in 500 However, it has also become evident that they do not occur randomly over the genome, but are more common in the

non-coding sequences. Thus of 12 RFLPs found in the B-globin gene cluster, seven are in flanking DNA, three in introns, one in the pseudogene and only one in a coding sequence.

b. VNTR (Variable Number Tandem Repeat): There appear to be certain hotspots of hypervariability which are particularly to be found in minisatellite DNA- regions of repeat sequence DNA which, unlike satellite DNA, consist only of short lengths of common base pairs. In hypervariable regions, there is essentially no homozygosity.In one family, a DNA probe for one of the patterns, 29 repeats of 16 base core sequence, was found in none of the 54 members of the pedigree. Populations are being compared on this basis.

Mitochondiral DNA : Mitochondria are organelles within living cells which contain its own DNA. It occurs as closed circles of about 16.5kb. Heterogeneity from individual to individual is detected by restriction endonucleases, the radioactive labelling of restriction fragments and separation by electrophoresis. With 12 restriction endonucleases, 163 polymorphisms have been detected in 112 people. Estimation of population variation on this count in also going on.

Dermatoglyphic :

Dermatoglyphics is the study of the ridge patterns on skin of the fingers, palms, toes and soles, Dermatoglyphic patterns are permanent and does not change with age.

Thus it is clear that maximum whorls occur in mongoloids, loops in caucasoid and Arches in Negroid.

Of the Palmer main line formulae, 11, 9, 7 is found in caucasoids. 7, 5, 5, in Negroids while 9, 7, 5 is found in mongoloids.

Population	Whorls	loops	Arches
Mongoloid	40-50	50-60	1-2
Caucasoid	20-30	60-70	4-7
Negroid	30	50-60	6-7

Dermatoglyphics has added advantage that, being polygenic in nature it is rather more difficult for mutation to affect the characteristi pattern but, at the same time, its inheritance is complicated

RACISM - A TOTAL MYTH

What is Racism ? Several wrong notions and unscientific beliefs have been existing since long about Racism. This has led to the existence of numerous thinkings amongst the different races so much so that some of the races have begun treating themselves as superior and more pure in comparison to others. Such wrong thinkings have given birth to several social injustices and many tyrannical activities and have strengthened the feeling of high and low amongst several races. This has come to be known as 'Racism'.

In short, Racism is that bitter thinking which gives birth to the growth of feeling of 'high' and 'low' amongst the races. They are wrongfully based on the unscientific differences regarding physical and mental qualities, creativeness and other factors pertaining to the races.

Exponents of Racism hold the belief that every human group have some hereditary specialities regarding their physique and mental capabilities and they get influenced by their social, educational and other environmental factors. They further hold that races are high or low by birth and that hereditary factors regulate every aspect of their cultural life. The acceptance of such unscientific beliefs have led to numerous discourteous, dividing and senseless behaviours by such persons. Racism gets manifested in its extreme form when one race starts treating itself superior in comparison to the other race or races. Such so called superior races not only nurse several economic, political and social narrowness against so called 'low' races, rather they perpetrate several injustices, atrocities and other such crimes upon them.

Bases Of Racism : There are four main bases of Racism. These are 1) Base of the purity and superiority of blood. 2) Base of fine colour, 3) Base of mental and physical ability, 4) Base of cultural superiority.

Anthropological and other studies of mankind has accumulated various datas concerning variations in humans at different levels. These evidences can be utilised to show that all the four pillars on which Racism rests is hollow and hold no reason for a race to be declared higher. We shall analyse all the four bases of Racism one by one finally blasting the support on which concept of racial superiority is based.

The race differs from species in two ways (1) absence of

there productive isolation and (2) smaller amount of genetic difference. Both these attributes are complex variables, since there are degrees of reproductive isolation as well as degrees of genetic difference. As noted above, it is largely because of the absence of reproductive isolation that we conclude that the races of man are races and not species, despite the genetic differences between them.

The differences between races are of the same kind as the differences between groups of people within races. Much of our deplorable race prejudice would disappear if people generally could come to understand that fact, with all its implications.In recent years a great volume of evidences has been amassed on this point.

1. Base Of Purity And Superiority Of Blood

One of the main bases on which blood differ are the blood groups the genetics of which has been well worked out and its distribution in various racial groups and geographic regions thoroughly serveyed. The point that cannot escape conclusion is that differences in the blood groups between the races is in reality to the same extent as there are chances of variation in populations of a race..

Most American Indians, for example, exhibit a high percentage of individuals belonging to group O. Yet the Blackfoot and Blood tribes in Montana have an unusually high proportion of members belonging to group A. Contrariwise, groups of people usually considered to belong to different races may be quite similar in their blood group distributions. Thus while a high proportion of group B characterizes Asiatic peoples, it is also characteristic of Abyssinians and of Pygmies in the Congo. Eskimos, Portuguese, and Australian aborigines resemble one another in blood group distributions. Similar differences and diversity exist in the distribution of the other blood cell substances (M.N. Rh, etc). A point of great importance for us is the fact that there is no correlation between the distributions of these various substances - they vary in frequency independently of each other, and of such characteristics as skin colour.

Increasing knowledge of early and prehistoric men affords no evidence of "pure races . In fact, quite the opposite is the case . The more we learn of our predecessors on this planet the more we understand that they were always a highly diversified lot of

people. We have seen that racial differences in the Pleistocene period were at least as great as they are today. Furthermore, the genes possessed by modern races were undoubtedly derived from a mixed ancestry of Pleistocene peoples.

Haemoglobin is the another element of blood. Its level and structural variations have been thoroughly worked out. Structural changes in haemoglobin has nothing to do with the race, rather they are reflection of the environment. The underlying structure of haemoglobin is the same in all the races and differences have developed to environmental selection against malarial infections. It would be seen that gene -frequency changes within a race is as much prevalent as between the races. Take for example sickle cell gene. The frequency of this gene changes from race to race. Within a race, the frequency of the gene changes according to the populations, depending upon their environmental conditions.

Studies on sickle cell haemoglobin have been conducted in India by several people. In the latest, Sri devi and Veeraju(1994) have studied these variations among malas of Vishakhapatnam, Andhra Pradesh (India). The studies, along with others, confirm the fact that there is gradual increase in the range of frequency of sickle cell gene from advanced caste population to primitive tribal population via socially depressed scheduled class population. Thus differences in gene-frequency between two races is as great as within a race.

2. Base Of Fine Colour

Most persons think first of skin colour when they think of racial differences. But here also there is great variability in amount of skin pigment present in different members of a single racial group. There is also great similarity in this respect among members of some diverse racial groups. Some inhabitants of India, for example, have darker skins that do some inhabitants of Africa. And again, variability in skin colour occurs independently of variability in blood groups, tasting ability, and so on. Even hair form (straight, wavy, curly, kinky) is independent of skin colour in inheritance, and most importantly, there is no correlation between any of these characteristics and such attributes as mental ability.

It is not difficult to visualise how changes in skin colour could have come about. Initially number of men evolving must have been less. As their number increased they must have migrated and diversified into different geographical regions. As

groups of people became separated from each other, opportunity was presented for gradual development of genetic diversity. Certain mutations would have occurred in some isolated groups but not in others. By chance some mutations would have been lost in some of the groups in which they occurred and would have become established in some other isolated groups. Mutations which conferred some advantage on their possessors would have been favoured by natural selection. For example, if some groups entered regions characterized by high intensity of sunlight, mutations increasing the amount of pigment in the skin might have been of advantage (protection from harmful concentrations of ultraviolet rays). It hence might have been favoured by natural selection. Thus in such a region the population might eventually have become quite dark in colour. If, conversely, other groups entered environments having sunlight of low intensity, mutations decreasing pigmentation of the skin might have been favoured by natural selection, since maintenance of a certain level of ultraviolet irradiation of the skin is important in providing the body with vitamin D. Consequently in this region a lightly pigmented population might have evolved.

Of all the genetic characteristics by which individuals differ from one another, why should skin colour be the one about which we become emotional ? it would be just as sensible for blood group A people to develop "race prejudice" against blood group B people The principal difference is that one characteristic is exposed on the surface for everyone to see, while the other is hidden away, detectable only by serological tests. It is sensible, as observes Moody, for a Rh -ve woman to develop 'prejudice" against Rh +ve man because some of her children might become affected with haemolytic disease of newborn. But to develop "prejudice" against colour is beyond the all known boundaries of human rationality.

3. Base Of Superior Mental And Physical Abilities

Superior mental ability can be judged either by comparisons of the brain features between the so-called high and low races, or by mental ability tests, and the concept of racism fails on both the counts. Weight of the frontal lobe of brain which is seat of ability, averages 44% of the total weight of the whole brain and it is constant in both male and female, and black and white. Differences in the total weight of brain between two race is as much as among the individuals of a race. Marked differences in brain features and

weight can be found in the individuals of the same race. Moreover, weight of brain has nothing to do with the level of intelligence.

Similarly, intelligence involves both genetic and environmental components, though their relative contribution is controversial. Experiments with twins have indicated that MZ twins reared apart differ on intelligence scale where as DZ twins reared together show closer approximating on intelligence scale, than when they are reared apart.

In body proportions, variability within racial groups resembles variability between racial groups, and there is no correlation of this with blood groups, skin colour, hair form, tasting ability, and so on. Thus we think of Scandinavians as tall and long-headed (dolichocephalic) although not all of them are so, by any means. Exceptionally tall and long-headed are the Watusi tribe in eastern Africa, while their "next-door neighbours", the Pygmies, form a marked contrast in both respects.

4. Cultural Superiority

It also does not serve as base historically. It can be proved that human civilization, culture or scientific achievement is not the monopoly or contribution of any particular race. It is, infact, a collective achievement of all. It is thus quite evident that all the bases of Racism is nothing but imaginary and unscientific. There is no Divine or spiritual speciality in any race. Each race, as we have noted earlier, developed as an isolate with different mutation, selection and migration pressures, together with the different "chances" or drifts. Hence each race is characterized by a different gene frequency of head form, hair, nose form, ear, tasting ability, secretor status, blood group, serum proteins etc. A race, then can be considered as " constellation of characters" to use Boyd's phrase (1950), in which there is no intercorrelation between different characters. As Dobzhansky (1950) stated, "It is most important to realize that the differences between the 'major' human races are fundamentally of the same nature as the relatively minute differences between the inhabitants of adjacent towns and villages".

Accordingly, we can say that races are populations characterized by certain frequencies of genes. Contrary to older ideas, there is no such thing as a racial "type" which all members of a race tend to approximate.

Frequency of the genes in a population, as we have noted above is determined by certain adaptive or chance factors

because such racial characteristics as are not adaptive may have become established in isolated populations by chance. The net result of these processes was development of diversity among geographically isolated peoples - the production of geographic races. When these diverse peoples came into contact with each other (migration, conquest) they exchanged genes. Some of the combinations of characteristics thus arising may have proved superior to the characteristic of one or both of the parental populations. If so, natural selection would have favoured the new combinations at the expense of the old.

If our interpretation is correct, the modern races are descendants of ancient races, but probably no one modern race is the descendant of any one ancient race alone. Our inability to draw any clear-cut lines between races gives added confidence that such is the case. The genes have been continually "reshuffled" as time, in geologic copiousness, has gone by (Moody, 1971).

UNESCO Declarations (1952) About Races

1. All human being on this hemisphere belong to only one species which is *Homo sapiens*.

2. There is no doubt some differences in the physiological anatomy either because of hereditary trait or environment but generally both affect it.

3. The change in hereditary trait is because of mutation and cross marriage.

4. The race cannot be grouped on the basis of nationality, religion, geographical, cultural, and linguistical factors.

5. The present day classification of mankind as caucasoid, Mongoloid and Negroid are nither because of any anatomical signs nor it gives rise to any notion of superiority or inferiority.

6. Intelligence do not play any part in the classification of Races.

7. Culture differences are not the cause of Racial differences.

8. The so-called 'pure' race are nowhere to be found either these days nor they were found in the distant past. There have been intermingling of Races going on since time immemorial without any adverse effect.

9. The human beings are equal and they deserve equal treatment.

People have used the term Racism indiscriminately and without any proper understanding in a scientific manner resulting in gross misrepresentation of the term. Huxley and Haddon have rightly approved that the term Racisms is quite unfit to be used in the present day world.

Many authors have advocated that the term Racism should be completely banned and instead the term Ethnic group should be used which is more appropriate and helpful. The use of the term Racism has infact done incalculable harm to the cause of world peace and the imagination of world brotherhood and it is desirable and proper to avoid it.

Negrito Elements in India

Negrito are very short statured, Woolly haired people. The Negrito controversy in Indian context started with observation in 1877 of De quatrefages who observed that such elements form the basic ethnic substratum of the Dravidians and some tribes of India. His observation was based on presence of Woolly hair. He was, however, opposed by such distinguished scholars as Ball, Callamand, Jagor, Koerbin etc. Keane initially supported the view of quatrefages, but later on he was also doubtful about presence of such elements in Indian population. Such conclusion was arrived at by various studies, especially by Sarasin brothers who studied Vedda in 1893, Lapicque who studied Kadar in 1905, Turner who studied Vedda in 1905.

The main proponents of Negrito elements in India were Hutton and Guha. Hutton, on the basis of his studies of Angami Naga, and Guha on the basis of his studies of Kadars of South India put forth the idea of presence of Negrito elements in Indian population.

Hutton's View : Hutton studied Angami Nagas and observed sporadic occurrence of Negrito hair among them. He also put several cultural evidence to show that Angami nagas are related to Negritos. Hutton has been, however, criticized by Sarkar and Majumdar.

To support Hutton's view, Guha and Basu collected skull remains from Naga hill. Guha, on the basis of his finding of woolly hair in Kadar, as well as the Negrito traits found in skull collected from Naga hills, has been the main supporter of the notion of presence of Negrito element in Indian population.

Guha's View : Guha has been main proponent of presence

of Negrito element in Indian population. He found presence of not only woolly and frizzly hair among 16 Kadar individuals, but has also put forth evidences from skulls collected from two different regions of Naga hills. The cranial materials collected by him and Basu from Naga hills have been divided into two groups - one groups is Mongoloid whereas the second group, as claimed by them, shows Tasmanian and Malanesian affinities in having low forehead and deep nasal root. Basu and Guha maintain that these elements were one time present from north east to South West of India but later on, under migration pressure from other groups these people were driven to Oceania, leaving sporadic traces of their presence in India.

Guha's view has been criticised by many on many grounds. Though form or texture of hair is one of the racial criteria, it seems that Guha overplayed the evidence by putting too much emphasis on a single criterion.

The sporadic occurrence of so called Negrito hair in Indian population does not indicate presence of a negrito element in Indian population. As has been pointed out by Fisher, Woolly hair has developed from Wavy hair from mutation and such mutations can occur in the Indian population.

Sarkar (1959) made extensive studies of Kadars of South India that included anthropometry, somatotyping, blood group studies and other relevant studies. He came to conclusion that in no way a negrito trait is demonstrated. He concluded that Kadars of South India are very much similar to australoids of South India in manner of skull construction and other features.

View Of Eickstedt : Eickstedt classified Indian people in 1933. He has stated that Negrito element was never distributed in Indian population. Confusion has arisen because most people failed to differentiate between woolly hair and spiral or frizzly hair. According to him, Negrito element is present in Andamanese but they have not shared in the making of Indian population. Andamanese are different from aboriginal tribes of India. Andamanese were confined to a particular area and there are no fossil evidence from anywhere in the ancient or modern India supporting distribution of the Negrito trait in the mainland of India

Skeletal remains unearthed from different sites of India ranging from Neolithic to Iron Age, there is no evidence to indicate presence of Negrito element in India during those times. According to Majumdar, had there been an assimilation of the Negrito race

by the Indian population, the characteristic Negro traits, such as woolly hair and broad heat associated with flat nose and dark complexion would have been met frequently in Northern India as well. Admittedly, there has been some Negroid settlements in the Coastal regions of India, particularly Gujarat coast, and penetration of some Negrito element in the Indian population, but such things occurred comparatively in later times that in no way influenced the ethnic make up of Indian population.

Earliest Settlers Of India

Different workers hold different views as regards earliest settlers of India. Guha suggests they were Negritos; Risby suggests they were Dravidian ; Sarkar and Majumdar suggest they were Autstraloids. When every theory is considered relatively, it is Sarkar's view that seems to be more logical and accepted by most anthropologists.

Distribution : We can identify such people in different parts of India and outside. In South India they are Urali, Kannokar, and Muthivan of Travancore; panyan of Malabar, Chenchu of Hyderabad; Kadar of Cochin. In Central India, tribes like oraon, Gond, Khond are also Australoid.

Outside India, such people are to be found in the west, east and south of India. In the West of India, such people are present in South Arabia and Persia. In the east, they are found in Great Nicobar. Sakai of Malay. Lubu and U/u of Sumatra and some other places of South East Asia. In the South, tney are found in Sri Lanka and North Australia. Veddas of Sri Lanka are Australoids and they resemble tribes of South India.

Distribution pattern of Autstraloids suggest that they have had made Indian subcontinent their homes in very earlier times from where they migrated far and wide to the different Islands and mainlands.

Primitiveness : Australoids are short statured, dark coloured people with long head and dark hair. Bhagawata Purana describes people called Nishada by the same features : black like crow, very low statured, short armed, with high check bones, low tipped nose, red-eyes and copper coloured hair".

Between the Negrito and Australoids, the latter are considered to be more primitive and descendants of Neanderthal whereas negrito is considered to have originated later than Autstraloid. Australoid traits can be seen in Neanderthal man

whereas Negrito trait appeared first in Grimaldi Man, which is considered later to Neanderthal. Woolly hair, one of the sallent features of Negrito, can be derived from wavy hair of Australoid. Thus wavy haired Australoid evolved first from Neanderthals where as wolly-haired negrito later on. Australoids are definitely more primitive than negrito.

Presence of Negrito elements in India is very much disputed. Hutton and Guha are the main supporter of presence of Negrito elements in India, though it has been conclusively proved by Sarkar and others that such elements never existed as basic ethnic characteristics. Even if we accept presence of Negrito element in India, they have been shown to be later outcomes. This leaves Australoids who are supposed to be the earliest settlers of India.

Evidences : There are consistent evidences of Australoids from prehistoric India. Some skulls from Mohenjodaro (3250-2750 BC) are definitely of Australoid elements in Sindh, Baluchistan and Punjab. Australoids seem to have represented the basal population of Indus Valley Civilization.

Similar is the case with finds in South India. The iron age fossils of Addittanallur and Neolithic fossils of Brahmagin (Mysore) indicate presence of Australoid elements. On the basis of such widespread distribution of Australoids in prehistoric times in India as well as in present day times. Sarkar has concluded that they were the original settlers of India.

GROWTH AND DEVELOPMENT-CONCEPT

After fertilization, the zygote is implanted in uterus where placenta is formed and the embryo derive nutrition from maternal body for its growth and development. Almost all the internal organs are well laid down at the end of 2 months when the embryo is 1 inch long. The characteristic external features are established, and subsequent growth merely modifies existing proportions without adding new structures. Internal organs undergo tissue specialisations.

During the third month, the young foetus resembles a human being, although its head is disproportionately large. Intestinal loops are concentrated away from umbilical cord into abdomen. The ears rise to eye level; ossification centres appear in most of the future bones and external genitalia becomes reconizable.

At four months facial features become distinguishalbe. Eyes move more close together. At five months, down hair (lanugo) cover the body, and some head hair appear. At six months eyebrows and eyelashes are clearly present. At seven months, the eyelids reopen and wrinkled skin is smeared with a greasy substance. At 8 months subcutaneous fat deposit starts and testes descend to scrotum. At 9 months, the body and limbs become well rounded. After 266 days of pregnancy (38 weeks or 9 months) the foetus is delivered.

The two terms, growth and development, are sometimes mistakenly used as synonyms. In reality, the two terms, growth and development, represent two different facets of the dynamic of change, i.e., those of quantity and quality. Growth and development usually proceed concurrently, but may not always be interrelated

The term growth denotes a net increase in the size or mass of tissues. It is largely attributed to multiplication of cells. Expansion of cell size contributes to a lesser extent to the process of growth.

Development, on the other hand, involves expansion of cells and is related to the maturation and myelination of the nervous system and indicates acquisition of a variety of skills for optimal functioning of the individual.

Periods Of Growth : The entire life-span of man beginning

from embryo to death is characterized by some form of positive or negative growth and development. These changes are accelerated at some point of time hence there are recognised periods of growth

Prenatal period

Ovum	0 to 14 days
Embryo	14 days to 9 weeks
Foetus	9 weeks to birth

Postnatal period

New born	First 4 weeks after birth
Infancy	First year
Toddler	1 to 3 years
Preschool child	3 to 6 years

(In some studies children under 5 years are classified as preschool children)

School age child	6 to 10 years (girls)
	6 to 12 years (boys)

Adolescence

Prepubescent	10 to 12 years (girls)
	12 to 14 years (boys)
Pubescent	12 to 14 year (girls)
	14 to 16 years (boys)
Postpubescent	14 to 18 years (girls)
	16 to 20 years (boys)
Adulthood	20 to 40 years
Mature	40 to 60 years
Senescent	60 years onward

LONGITUDINAL GROWTH STUDY

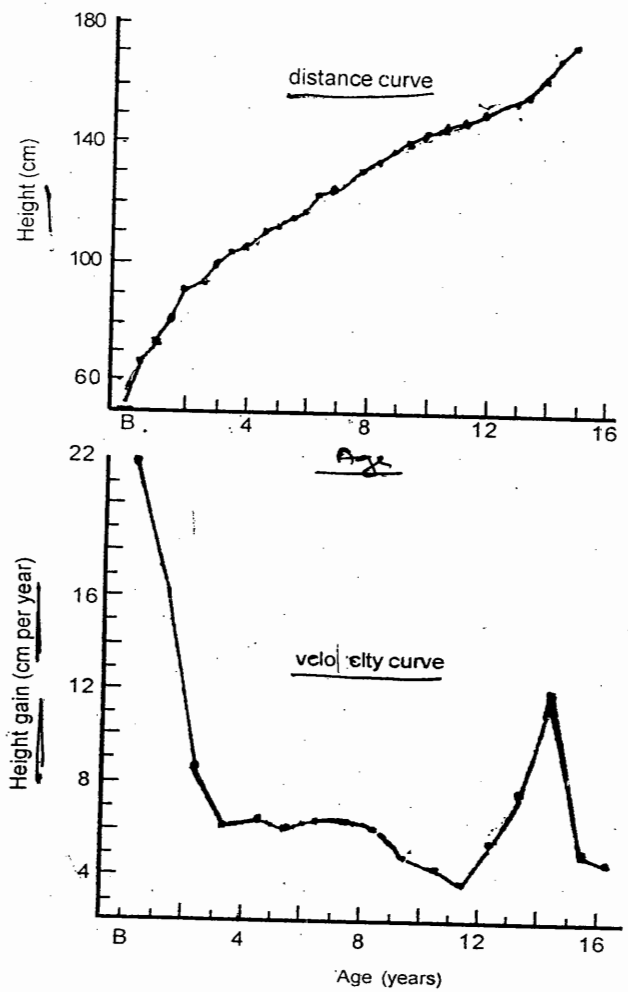
It is perfomed on the same individual at different point of time.

A-Linear or Distance Growth

It is overall growth at some point of time. Gradually, with time, there occurs increase in height and weight of a child which can be revealed by measuring at some point of time.

B - Growth Velocity

It is increment in growth in a unit of time. The comparison of child's height and weight with the growth-chart helps to determine if the particular child is within the expected normal range for his sex and socio-economic stratum. It does not show whether the child's growth was normal in the recent past.



Growth in height

— development → expansion of cells.

maturation + mylination of nerve fiber acquisition of variety of skills optimal functioning of individuals.

Measurement of velocity of growth is more fruitful. It helps in early assessment of retarding factors of growth as well as prediction of ultimate growth. ★

Laws Of Growth

A. Orderliness : Growth follows a sigma shaped curve. There are specific periods in a child's life, when the rate of growth accelerates, decelerates or there is a steady build up of body tissues. The foetus grows fast in the first half of gestation. Thereafter, the rate of growth is slowed down till the baby is born. In the early postnatal period the velocity of growth is high during the first few months. There is a steady rate of growth during mid childhood. A second phase of accelerated growth happens during puberty. Growth decelerates for some time after that and then ceases altogether. ★

B. Growth Gradient : Order of growth in human beings is cephalocaudal and distal to proximal. During the foetal life, growth of head antedates that of neck while arms grow before legs. Distal parts of the body such as hands increase in size before upper arms. In the postnatal life, growth of head slows down but limbs continue to grow rapidly. At all ages the foot is nearer its adult status than the calf, and the calf nearer than the thigh. A maturity gradient is said to exist in the leg, running from advanced maturity distally to delayed maturity proximally. The same gradient is illustrated in the upper limb. Girls are more advanced in maturity at all ages than boys without this affecting in any way the distal-proximal gradient. ★

C. Growth - Curves

i. General Body Growth : The general body growth is rapid during the foetal life, first one or two years of postnatal life and also during puberty. In the intervening years of mid-childhood, the somatic growth velocity is relatively slowed down (sigma-shaped).

ii. The Brain Growth : The brain enlarges rapidly during the latter months of foetal life and early months of postnatal life. At birth, the head size is about 65 to 70 percent of the expected head size in adults. It reaches 90 percent of the adult head size by the age of two years. The curve is stepped up initially and then flattens.

iii. The Growth Of Gonads : Gonadal growth is dormant during childhood. It becomes conspicuous during pubescence. The curve is flattened initially and later stepped up. ★

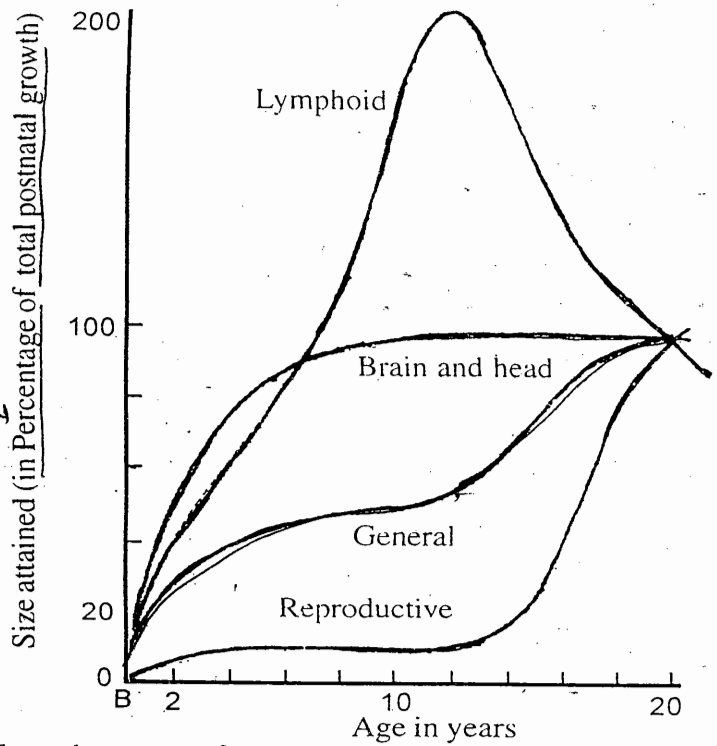


Fig. : Growth curve of parts and tissues of body on the Vertical axis is plotted percentage of total gain from birth to 20 years.

CROSS-SECTIONAL GROWTH STUDY :

Longitudinal growth is studied on an individual over long period of time. For rapid study, we perform cross-sectional growth study. In such a study, individuals of different ages are selected randomly from a population and their growth measurements are obtained. It is believed that individual of this population will show the same growth norm over period of time. ★

SEMILONGITUDINAL GROWTH STUDY

It combines the longitudinal method and cross-sectional method. In this method, two measurements are performed on the same individual and other measurements can be performed on other individuals of the same age-group in that population. Growth rate is calculated by the formula-

$$\text{Growth Rate} = \frac{b - a}{b} \cdot c$$

Where a = measurement at a time
b = measurement after a
c = interval of time between a & b

iv. Lymphoid growth : The growth of lymphoid tissue is most notable during mid-childhood. During this period, the lymphoid tissue is overgrown and its mass may appear to be larger than that in the fully mature adult. Children between four and eight years of age often have hypertrophied tonsils and large lymph nodes, which is in fact a sign of lymphoid hyperplasia. Thus, it reaches its maximum amount before adolescence and during the adult phase it regresses to some extent due probably to influence of sex-hormones. The curve is more or less bell-shaped. ★

v. Sub-cutaneous fat : It has a different curve. Subcutaneous fat begins to be laid down in the foetus at about 34 weeks until about 9 months after which it decreases until age 7 years, when it begins to increase once again. The decrease is less in girls than boys, so that after age 1 year girls come to have more fat than boys.

The increase from age 7 years occurs in both sexes, in both limb- and body-fat. At adolescence, however, the limb-fat in boys decreases and is not gained back until the age of about 20 years. In girls there is a slight halting of the limb-fat increase, but no loss and the trunk-fat shows steady rise. ★

D. Growth Patterns : Differences in the growth velocity of different organs establish a characteristic pattern of growth for every species. How are these growth patterns established? Understanding of this phenomenon holds the key to understanding of all the later phenomena. ★

A zygote, formed from union of sperm and ovum, can be said to be the starting stage for all the later growth and development. The ovum or egg of every species has its own characteristic genome and distribution of cytoplasm. There are certain changes in the egg after it is activated by the sperm. Nature of distribution of chemical substances in the egg makes certain genes active. The substances synthesized under action of these specific genes have their own specific distribution pattern, ★ thus activating again a specific set of genes. In individuals belonging to different species, there are different genome and their differential activation. Individuals of the same species differ somewhat in growth patterns because of some genetic differences. At the same time the amount and nature of cytoplasm cannot be exactly identical in two individuals even if their genetic component is exactly similar as in Monozygotic twins (Monozygotic twins or MZ twins are formed by division of same zygote hence have identical genetic makeup). This differential distribution of cytoplasm

can set up different growth pattern even in MZ twins. To conclude, every species has its own genomic characteristics and distribution pattern of egg cytoplasm that results in characteristic growth pattern of the species.

Catch-up Growth

After illness or starvation which is a period characterized by slow growth, there has been found tendency in the younger subjects to bridge the deficit as soon as possible and catch up with the original growth-curve. This is known as catch-up growth.

The velocity during initial period of catch-up may reach three times the normal for age. The term compensatory growth is sometimes used by nutritionists to describe a similar phenomenon; however, that term was first applied to the quite different phenomenon of the replacement growth of organs or parts. Thus, showing compensatory growth. Catch-up may be complete or incomplete; if the stress has been severe, and particularly if it has been applied early in the animal's life, then even though a catch-up velocity may be established for a while it may be insufficient to return the animal completely to its normal curve of growth.

Growth Charts

Growth charts show progressive changes in height and weight of a child with age. The growth chart depict average and permissible range of variation for the particular age or attribute. If the growth measurements are recorded in a child over a period of time and are plotted on a graph paper, the deviation in the growth profile of the child from the normal pattern of growth for that age can be interpreted visually. ★

If the height measurements in a large population of normal children of the same age are arranged in regular order starting from the lowest, going to the highest, a bell shaped curve is formed. Most of the measurements fall around the middle of the curve, which taper off on either side, since there are fewer observation towards the end of the curve. If the selection and distribution of the sampled group is properly stratified and represents the group as a whole, the curve should be symmetrical, with nearly half of the observations lying above and half below the median or the 50th percentile. This is called Gaussian distribution (bell shaped curve).

PRENATAL GROWTH

1. During early embryonic period of life, an increase in the number of dividing cells occurs. The number of cells increases from about 0.2×10^{12} at 60 days of foetal life to 2×10^{12} at birth and 6×10^{13} in a fully grown adult. This is evidenced by an increase in the DNA content of tissues. In the latter half of pregnancy and early childhood, there is also an increase in the cell size. This manifests as increase in the Protein : DNA ratio. The cell size continues to enlarge till about 10 to 11 years of age. After that, increase in cell size occurs more slowly. The body cells remain in a state of dynamic equilibrium, so that the old cells are continuously being replaced by new cells. ★

2. The velocity of growth in length is not very great during the first 2 months of foetal life. This is the period of the embryo. During this period, differentiation of the originally homogeneous whole into regions, such as head, arm, and so forth, occurs ('regionalization'), and also the differentiation of cells into specialized tissues such as muscle or nerve (histogenesis). At the same time each region is moulded by differential growth of cells or by cell migration into a definite shape. This process, known as morphogenesis, continues right up to adulthood. But the major part of it is completed by the eighth post-menstrual week. ★

3. The peak-velocity of length is reached at about 18 weeks post-menstrual age, and that of weight in 34th post-menstrual week.

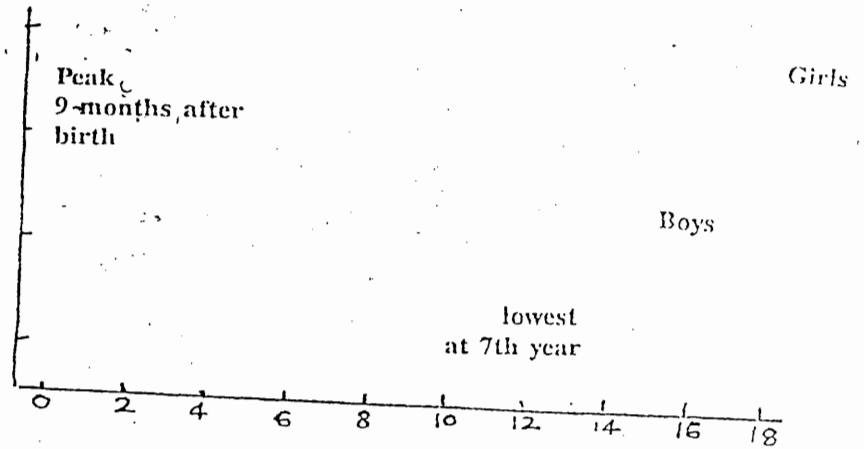
4. From about 36 weeks to birth (at 40 weeks), the rate of growth of the foetus slows down due to the influence of the maternal uterus, which is by then becoming fully occupied. Birth weight, and birth size in general, reflect the maternal environment more than the genotype of the child. After birth, the growth rate increases again, particularly in genetically large children, and in weight reaches its peak approximately 2 months after birth. ★

5. The proportion of cells undergoing mitosis in any tissue becomes progressively less as the foetus gets older, and no new muscles- or nerve-cells (apart from neuroglia) appear after 6 foetal months.

6. The muscle and nerve-cells of the foetus have very little cytoplasm around the nucleus. In the muscle there is a great amount of intercellular substance and water than in mature muscle. The later foetal and postnatal growth of muscle consists of building

up the cytoplasm of the muscle-cells: salts are incorporated and proteins formed. The cells become bigger; the intercellular substance largely disappears, and the concentration of water decreases. This continues up to about 3 years of age and slowly thereafter; at adolescence it briefly speeds up again, particularly in boys, more substances being incorporated into the fibres under the influence of androgenic hormones. ★

7. Thus postnatal growth is, for at least some tissues, a period of development and enlargement of existing cells rather than the formation of new ones. Adipose tissue is perhaps an exception to this rule; the number of countable fat cells continues to increase till about the beginning of puberty; the rate of increase, however, gets continuously less. At any event, even in this tissue, the quantitatively more important change during postnatal growth is an increase in the size of each cell. ★



INFANCY AND CHILDHOOD

1. Infants and children are characterized by physical and behavioural development. The physical development is gauged by changes in weight, length or height, head circumference, circumference of chest and stem stature index.

2. During the first few days after birth, the newborn loses extracellular fluid equivalent to about 10 percent of the body weight. Most full term infants regain their birth weight by the age of 10 days. Subsequently, they gain weight at a rate of approximately 25 to 30g per day for the first three months of life. Thereafter they gain about 400g in weight every month, for the remaining part of the first year.

An infant usually doubles his birth weight by the age of five months. The birth weight trebles at the end of fist year and is four times at two years of age. The weight of a child at the age of three year is usually five-times that of birth weight. On an average a child gains about two kg every year between the ages of three and seven per years and three kg per year after that till the pubertal growth spurt begins.

3. The baby measures 50 cm at birth, 60 cm at three months, 70 cm at nine months and 73 to 75 cm at one year of age. Average height of a two years old child is 90cm. The Indian child is 100cm tall at the age of four and a half years. Thereafter, the child gains about 5cm in height every year, until the age of ten years.

4. The circumference of chest is about three cm less than the head circumference at birth. The circumference of head and chest are almost equal by the end of first year. Thereafter, chest circumference exceeds the head circumference. In undernourished children, the chest circumference remains less than the head circumference even by the age of two or thee years.

5. With age, the stem stature index decreases. The stem stature index is obtained by the equation:

$$\frac{\text{Stem length (Sitting height)}}{\text{Standing height}} \times 100$$

The mean stem stature index at different ages during childhood is as follows :

At birth – 67%; 6 month – 66%; 1 year – 64%; 2 years – 61%; 3 years – 58%; 5 years – 55%; 10 years – 52%.

6. The new born infant has disorganised behaviour. But as age advances he or she reacts to his/her environment in a wilful manner.

7. Infancy and childhood is characterized by motor clave component :

a. Within a few days of birth the head can be turned to one side. At 1 month the baby lifts the chin up momentarily in the midline. At 3 months, the infant lifts his head and front part of his chest up, supporting his weight on the stretched hands or forearms. By 6 months, he can lift his head and greater part of his chest while supporting weight on extended arms. Between the age of 5 and 8 months, he learns to roll in bed at first from back to side then from back to stomach. By the age of 8 months he crawls in bed and by 10 months creeps, keeping his abdomen off the ground.

b. The infant learns to control his body in the sitting position from the age of 5 months onwards. Initially, he needs several pillow support. By the age of 8 months he can maintain steady sitting position with straight back. By the age of 10 months, he can pull himself up from the supine to sitting position.

c. From the age of 9 months he makes early stepping movements. However, he cannot support the body in a coordinated manner. By 10 months or so the infants starts cruising around. By the fist birthday, the child can stand without support for 10 seconds or more and can usually take a steps in walking. At the age of 15 months, most toddlers can take several steps. A child learns to walk on tip toes by the age of two and a half years.

d. The child can climb up the stairs by the age of two years. In the process he brings both his feet up on one step before he climbs to the next step. At three years, he climbs up the stairs in a coordinated manner, keeping only one foot on each step.

8. The period is also marked by fine motor control. This include coordination of eyes, hand-eye coordination, hand-mouth coordination and skills for manipulation with hands.

a. Eye coordination starts developing between 2-4 weeks and by 3-4 months infant follows the objects with steady movement of the eyes.

b. Hand to mouth coordination develops slightly later, the baby is able to feed himself only after 18 months.

c. Hand-skills begin to develop from 2 years when he can

perform crude skills. It is perfected by 4-5 years when he is capable of drawing a triangle.

9. The childhood is also marked by Racio-cultural development. The child is capable of social smile (smiling back) by 2 months. He recognises mother by 3 months and shows anxiety meeting strangers by 6 months. By one year, the child repeats any performance that evokes appreciative laughter and mimics the action of mother.

Language development is crucial for infants and children. By one month, the infant attends to curious sounds. by nine months, he produces monosyllable sounds (ma-ma, da-da) without attaching any meaning to it. By ten months, he understands speech and responds to it. True speech develops between 1-2 years when he is able to make simple sentences of 2-3 nouns.

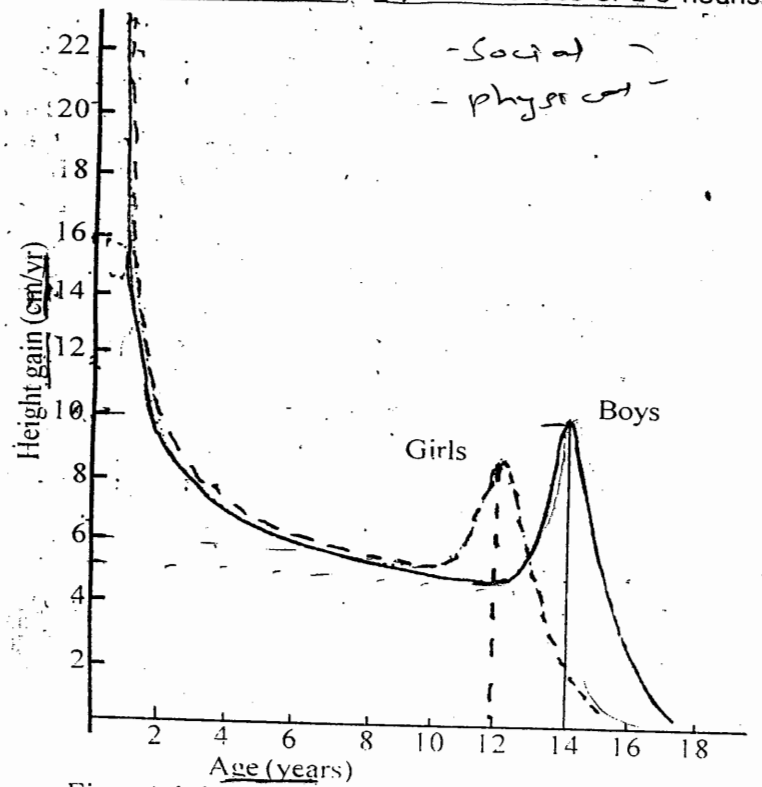
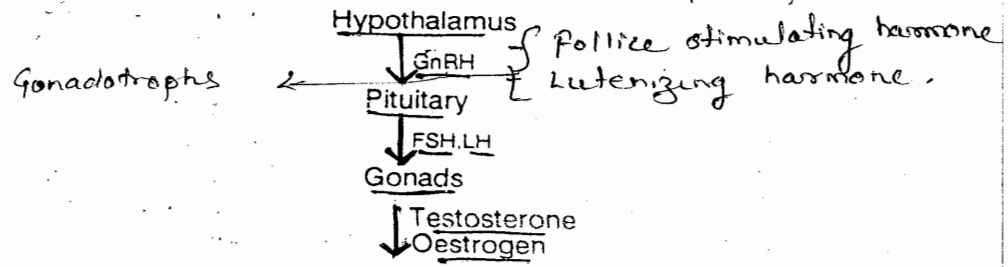


Fig : Adolescent growth spurt in boys and girls (Girls' spurt 10 to 14 years: boys' spurt 12 to 16 years)

ADOLESCENCE

After childhood comes adolescent period. Adolescent period extends from the onset of puberty till the time sexual maturation is completed. The ages of onset of puberty and sexual maturation vary widely in different individuals, depending on the genetic and environmental factors. The puberty usually begins in girls around the age of 12 years. In boys, puberty begins at 14 years, two years later than girls though the range is variable.

Hormonal Basis Of Adolescence : Adolescence is intimately linked to the secretion of sex-hormones in boys and girls. The male sex-hormone is testosterone secreted by the gonad, testes. The female sex-hormone is oestrogen secreted by ovary. The gonads, ovary and testis, are simulated by pituitary hormones, called Follicle-stimulating hormone (FSH) and Luteinizing hormone (LH). Together, these are called gonadotrophins (or gonadotropins). The pituitary hormones, FSH AND LH, in turn, are controlled by hormones of specialised region of brain, called hypothalamus Hypothalamus secrets gonadotrophin-releasing hormone (GnRH). Under appropriate internal and external signals, GnRH is released from hypothalamus that has effect on pituitary causing release of ganadotropins. Gonadotropins act on gonads and effect release of testosterone and oestorgen in males and females respectively.



Secondary Sexual Characters during adolescence

Bodily Changes During Adolescence : During adolescence there occurs a spurt in both height and weight along with certain changes in external genitalia of both males & females. In males, testes, scrotum & penis enlarge. In females, there is gradual enlargement of breast, labia majora, labia minora and clitoris. A clear whitish fluid is secreted from Bartholin's glands a few months before menarche. Size of the uterus and ovaries enlarge, graafian

follicles mature and ovulation sets in. Pubie hair and axillary hair also make their appearance.

At birth, boys are about 4 weeks behind girls in skeletal age, and from then till adulthood they remain about 80 per cent of the skeletal age of girls of the same chronological age. It is for this reason that girls reach adolescence and their final mature size some 2 years before boys. The percentage difference in dental age is not so great, the boys being about 95 per cent of the dental age of girls of the same chronological age.

The sex difference in maturity is not confined to man; it occurs in apes, monkeys, and rats. Its full biological significance is not at present obvious.

Changes In Reproductive System (Boys) : The first sign of puberty in boys is an accelerated growth in testes and penis. The testicular growth is mainly due to increase in size of the seminal tubules; the androgen-producing Leydig cells appear to develop more or less simultaneously. One year after testicular acceleration, pubic hair also grows fast along with height and penis acceleration.

Axillary hair and facial hair in boys, appears about 2 years after the beginning of pubic hair growth, though there is sufficient individual variability. The growth of body hair starts at about the time of axilliary hair but continues for considerable time after puberty. The ultimate amount of body-hair an individual develops seems to depend largely on heredity.

The enlargement of the larynx (voice-change) in boys occurs at about the time the penis growth is nearing completion. There are some changes seen in the breast; the areola enlarges in diameter and darkens. In some boys - about a third of most groups - there is a distinct enlargement with projection of the areola and the presence of firm subareolar mammary tissue.

Sperm begin to appear in early morning urine samples on average a few months after peak height velocity; but in some boys sperm appear somewhat earlier than this. Whether they are fully functional during the first year or two after their appearance is doubtful.

Studies on appearance of puberty signs of the adolescent boys in India are limited (ICMR 1984; Prabhakar et.al.1972; Agrawal.1974, Kant et.al.1980; Kant et.al.1982). It was pointed out by Kant et.al.(1980) that puberty appears to set in early among the Indian boys but full maturation seems to take longer time than the

boys of the Western countries. Their study was based on Jabalpur boys.

For Indian boys (urban and rural) median age for development of pubertal signs is 14 years. The onset of puberty is found to be late in tribal boys. Below is given a comparative puberty development in Indian boys.

Puberty signs	Jabalpur boys (Kaul et al. 1950)	Gaddi boys (Himalayan range - Singh & Sidhu)	Orissa urban boys ICMR 1984	Indian urban (pooled) ICMR 81	India rural (pooled) boys 1984	Koraput (Orissa) boys Choudhary et.al. (1994)
Penis (G)	9.83	-	-	-	-	13.40
Pubic hair (PH)	10.96	13.45	14.60	14.00	13.82	13.44
Change of Voice (V)	12.75	14.17	15.14	14.24	14.30	14.41
Axillary Hair (AH)	13.41	15.83	14.59	14.59	14.25	15.77

Based upon their studies and those of others, Choudhary et.al.(1994) have concluded that there are found considerable regional and populational variations in the median and mean age of appearance of different pubertal signs among the adolescent boys in India.

Changes In Reproductive System (Girls) : In girls, as in boys, there is a large variation in the time at which the spurt begins, though the sequence of events is fairly constant. The appearance of the breast-bud is as a rule the first sign of puberty, though the appearance of pubic hair may sometimes precede it. The uterus and vagina develop simultaneously with the breast. Menarche (the first menstrual period) occurs almost invariably after the peak of the height spurt has been passed. But the early menstrual cycles frequently occur without an ovum being shed; during the first year or two after menarche there is a period of relative infertility, characteristic of apes and monkeys as well as the human. It is not before 5-6 years after menarche that 75% ovulation is achieved.

The age of menarche varies considerably in different parts of the world and it is influenced by socio-economic status, nutritional status, besides genetic component.

Age of menarche of girls of different countries, population and different states of our country has been surveyed.

Age of Menarche in different world Population

	High status	poor status
South Africa	13.40	13.90
Slovenians	13.28	14.20
Guatemala	12.80	14.50
Singapore	12.40	14.45
India	12.85	13.89

In all the countries surveyed, it is clear that nutrition has significant effect on age of menarche.

A.M. Tripathi (1987) has released the data of age of menarche of girls of various Indian states, surveyed from 1951-1985. The lowest age of menarche has been found to be in the girls of Delhi (11.20) followed by Calcutta (12.50) and U.P. (12.80). The highest age of menarche was found to be in Gujrat (14.80) and Lucknow (14.50). Median age of menarche in Indian girls is around 13 years.

Age of menarche in different Indian population

Delhi	11.20
Calcutta	12.50
U.P.	12.80
Gujrat	14.80
Lucknow	13.50
Madras	14.16 (Rural)
	12.76 (Urban)

The survey also shows that girls belonging to urban group of high society experience their menarche earlier than the rural groups. Factors pertaining to the nutrition and health care have profound effect on onset of menarche. Shukla et.al. (1994) have found similar situation in rural and urban sports women.

Physiological Changes : Changes in physiological function occur during adolescent spurt. They are much more marked in boys than girls and serve to confer on the male his greater strength and physical endurance. Before adolescence boys are on average a little stronger than girls. After adolescence boys are much stronger, chiefly by virtue of having larger muscles. Boys

have larger hearts and lungs relative to their size, a greater capacity for carrying oxygen in the blood, and a greater power for neutralizing the chemical products of muscular exercise. In short, the male becomes at adolescence more adapted for the tasks of hunting, fighting, and manipulating all sorts of heavy objects, as is necessary in some forms of food-gathering.

There occurs in the boys an increase in the number of red blood cells at puberty. and consequently in the amount of haemoglobin in the blood. No sex difference exists before adolescence. The systolic blood-pressure rises throughout childhood, but this process accelerates in boys at adolescence; the heart-rate falls. The alveolar carbon-dioxide tension increases in boys and not in girls, giving rise to a sex difference in the partial pressure of carbon dioxide in arterial blood. Coincidentally, the alkali reserve rises in boys. Thus, the blood of an adult man can absorb during muscular exercise, without change of pH, greater quantities of lactic acid and other substances produced by the muscles than that of a woman - a necessity in view of greater relative development of muscular bulk in the male.

As a direct result of these anatomical and physiological changes the athletic ability of boys increases greatly at adolescence.

Adolescent Growth Spurt : The adolescent growth spurt occurs in both boys and girls; in girls between 12 and 13 years and in boys between 14 and 15 years of age. Before adolescent spurt, males are longer than females by only 2%, but after the spurt the difference comes to about 8%. The difference party comes about because of the later occurrence of the male spurt, allowing an extra period for growth and partly because of the greater intensity of the spurt itself. In absolute terms the adult sex difference is around 13 cm, of which 2 cm are due to prepubertal growth, 7 cm to the later occurrence of the male spurt, and 4 cm to the greater intensity of the spurt.

Most of the spurt in height is due to trunk growth rather than growth of tne legs. The muscles appear to have their spurt about 3 months after the height peak; and the weight peak velocity occurs about 6 months after the height peak.

Though there occurs a spurt in size of the heart and to some extent in the eyes, it is not clear whether a spurt occurs in brain-growth. In the bones of the face there is a spurt, though a relatively slight one. The jaw become longer, thicker and more

projecting. The incisors of both jaws become more upright, and the nose more projecting. All these changes are greater in boys than in girls.

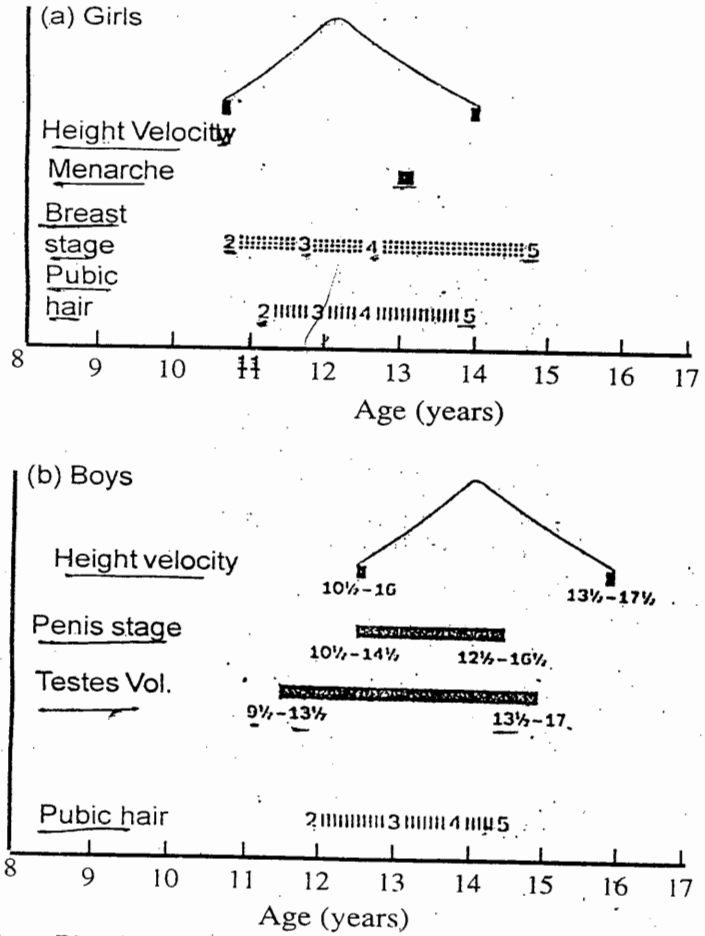


Fig. : Physical development in adolescent girls & boys.

– Jaw – thick. long pr
– cani – upr
– nose pr.

POST-ADOLESCENT GROWTH

Growth of the skeleton does not entirely cease at the end of the adolescent period. In man the epiphyses of the long bones close completely and cannot afterwards be stimulated to grow again. However, the vertebral column continues to grow from age 20 to 30 years by apposition of bone to the tops and bottoms of the vertebral bodies. Thus, height increases by a small amount, on average 3-5 mm, during these years. From the age of 30 to 45 or 50 years it remains stationary, and then begins to decline.

The chronological age does not indicate maturity hence there have been found biological criteria for maturity. There are three such criteria

1. Skeletal Maturity, 2. Dental Maturity, 3. The Shape Age

1. The Skeletal Maturity : Bones show gradual development in its histologic structure. There appears first a main ossification centre and gradually, with time, there appear many subsidiary centres that fuse with the main ossification centre. Such centres are easily diagnosed in X-rays because ossification centres, because of its high calcium content, make it opaque. The bone-age is calculated by the number of ossification centres as well as stage of its development.

The X-rays of hand-bones is matched with the atlas specifying the changes with increasing age and found out to which of the sample in the atlas the radiograph matches. In recent times, there can be found developmental age of each bone. Hence each bone is matched separately and given a score. The total scores thus gained is matched with the range of score of the standard group.

2. Dental Maturity : It is calculated on the basis of stages of calcification as seen in the Jaw X-rays in just the same way a the skeletal maturity assessment through radiograph. For details see forensic anthropology.

3. Shape Age : Shape age is difficult to derive and is a research problem. Mere calculating height or weight or 1Q do not give any indication of age. In shape-age, a combination of body measurements are taken into account, all of which change with ages but independent of final size and shape. It should not concern us here because, as already stated, it is a research problem. Individuals are characterized by several maturational characteristic.

SENESCENCE

There are many bodily and physiological changes that occur with the passage of time. In some individuals such changes are fast; in others slow. Individuals are characterized by several senescent characteristics such as greying of hair, loss of strength, reduction in sensory capabilities, poor homeostatic mechanisms, reduced resistance of body against the diseases, cardiovascular irregularity and several other criteria. Like maturity characteristics, the sensescent characteristics also appear at different chronological ages. A person at 35 years of age may suffer from greying of his/her hair, loss of homeostatic mechanism and a cardiovascular irregularity. In such cases, chronological age of the person is low, but his/her biological age is much advanced. For late maturers, however, biological age is generally lower than chronological age.

Ageing Changes In Man : One of the most obvious signs of human ageing is the greying of hair. with increasing age more and more people have some grey hair. Greying begins before age of 30 and steadily increases.

Skin elasticity changes with age. This measurable change in skin properties is probably associated with one of the obvious visible signs of ageing, namely changes in skin texture and appearance. In both sexes there is a gradual rise in the modulus of elasticity, but this is more marked in women than in men, in spite of the fact that women have longer life-span. The age-related change in skin elasticity is probably caused in part by changes in the collagen molecules which form a high proportion of the protein in skin.

One of the most familiar signs of biological ageing is a general loss of strength. Several different methods have been used to measure this change e.g. from measuring hand-grip strength. The values plotted are the averages for each decade of life, and they show that after an initial rise there is decline in grip strength for men and women. Blood pressure and the vital capacity of the lungs show marked changes after the age of 40. Hearing, visual acuity, vibration perception, manual dexterity and mental reaction time show deterioration, particularly beyond the age of forty.

Some of the most striking age-related changes are revealed by studying the responses of the body to a physiological chalienge. The pH, ion concentration, temperature, levels of metabolites etc in the internal environment of mammals are

normally maintained within very narrow limits. Numerous feedback mechanisms tend to restore the composition of the internal environment to normal if a natural or artificially applied stress causes it to change. It is clear, however, that these homeostatic control of mechanisms become less efficient as age increases. For example, normally the glucose level in blood, shows very little change with age, but if glucose is injected into blood, the rate of restoration to the normal level shows a marked dependence on age: it is far slower in old people than in young. This decline in the efficiency and effectiveness of the homeostatic regulatory mechanisms could be due to deficiencies in one or all of a number of interdependent tissues and cells. In the case of glucose, the muscles and liver are important for its storage, the pancreas is involved in the production of insulin, which regulates storage and mobilization, and the kidneys are involved in getting rid of excess amounts.

Nathan Shock has made extensive studies of ageing changes in man and other mammals, and has concluded that the functions which show the greatest change are those which involve the co-ordinated activity of a number of organ systems. Those which show little or no change usually involve only a single organ or system. For example, nerve conduction velocity changes by only about 10% between the ages of 20 and 90, whereas the maximum breathing capacity decreases by 50%. The former is a measurement of the performance of nerves only, the latter depends on the efficiency and co-ordination of both the nervous and muscular systems. Shock (1974) has suggested that from a physiological point of view, ageing involves primarily an impairment or breakdown of control mechanisms. The more complex a task is in biological terms, the more likely it is to show an age-related deterioration.

Almost every system which has been studied shows some change. There is no difficulty in finding measurable age-related changes. The problem is deciding what these changes mean in relation to probability of dying. One of the best indicators of age is hair-greying; yet it is difficult to believe that this has much to do with the increased likelihood of dying as age increases. Skin elasticity is good indicator of age; yet, if judged only by skin elasticity, a woman of 30 has the same biological age as a man of 80. Perhaps changes in the neural system and cardiovascular system are the most deleterious changes that increase the probability of dying.

GENETIC CONTROL OF DEVELOPMENT

Right from the stage of egg an individual is exposed to genetic control of development. There are relative distribution of some substances in the egg-cytoplasm that activate maternal genes that control growth and development upto blastula stage. There are evidences that upto blastula stage no genetic control is exercised by paternal chromosome. During gastrulation, substances formed by the maternal genes activate paternal as well as other maternal genes and their product induce different cell types.

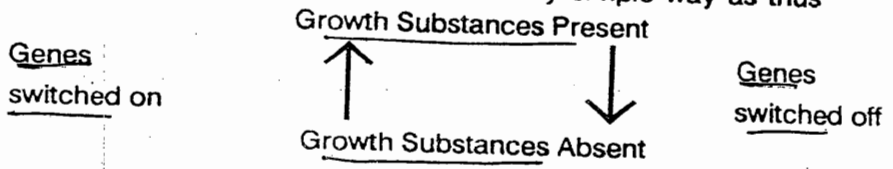
Induction : For a coordinated growth and development it is necessary that genes for different characters are activated in a definite sequence - it has been found that a regulated chain reaction is found during growth and development. This regulated chain reaction of growth is termed induction. The term implies that when one part of the embryo is differentiated, it releases substance or inducer for differentiation of another part of the embryo. When a cell at higher order functions, it releases inducer substance that becomes stimulatory for the cells of lower order. The different regions of embryo can thus be arranged into a hierarchy in which a lower order function is dependent on a higher order function. Factors generated at a higher order becomes stimulatory for several lower order functions. The organisation of the embryo thus becomes very fast. The nature of the inducting substance is proteinous. These proteinous substances are supported to act upon the membrane of the cells being organised so that there occurs a permeability change in the cell. This leads to accumulation of different substances and change in their relative concentration in the cell, activating certain genes. In this manner, growth of the embryo becomes coordinated. The gastrula stage is the first stage of cellular differentiation in higher organisms. Up until this time, every cell has been essentially totipotent with expression of only maternal genes. In chordates, the mesoderm/mesenchyme component (chorda mesoderm) which proliferates cranially from the dorsal lip of the blastopore represents the first definite embryonic inductor. Dorsal lip of blastopore is the first inductor of the embryo present in blastula. Thus dorsal lip of blastopore induces chrodamesoderm, chorda mesoderm the neural plate, neural plate the optic cups, optic cups the lens and so on. Cells of different regions are thus

differentiated leading to formation of distinct regions in the embryo.

Cell Differentiation : Though all the cells contain the same genome, different genes are activated in different parts of the body. On this ground, all the genes of an organism is divided into housekeeping genes and luxury genes. Housekeeping genes are those that synthesize protein required by all the cells such as protein for cell-membrane. Hence, such genes are activated in all the cells. Luxury genes are related with protein of specific function and they are activated only in certain cells. The control is exercised at the transcriptional level (when DNA is forming mRNA). Cells synthesizing insulin receive substances from surrounding for activation of insulin gene; cells synthesizing bile receive substances for activation of bile genes.

Operon Control Of Differentiation In Prokaryotes

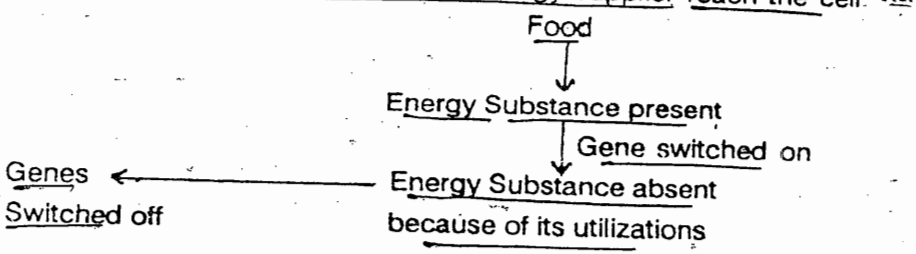
There are two regulatory pathways - repressible and inducible. Repressible Pathway is involved in elaboration of substances to be used in growth. When level of these substances reach optimum level, such gene control mechanisms are inactivated. Once the substances are used up in growth, the genetic mechanism is switched on again. As soon as the substance is synthesized and available to the cell for its use in growth ,the control mechanism is switched off or repressed again. The sequence can be described in a very simple way as thus



Since growth substances are being used continuously in the growth and development, the cell always experiences lack of such substances hence the control system remains switched on for most of the time. Control in such cases depend on repressing or switching gene off hence the name of the control system "repressible".

Inducible Path Way : Energy is needed for growth and development hence some substances must be broken down to release its energy content. When substances potential for energy release reach the cell, control mechanisms are activated to break it

down. Genes remain switched off for most of the time and switched on only when a potential energy supplier reach the cell.



The difference between the repressible and the inducible system of gene control is simple : repressible system is switched on most of the time and switched off occasionally. It is characteristic of synthetic or anabolic pathways. Inducible system is switched off most of the time, switched on only occasionally when potential energy supplier reaches the cell. It is characteristic of catabolic pathways.

This is a control by genetic mechanism in prokaryotes. All available evidences indicate however, that such a narrow genetic control mechanism in growth and development does not exist in eukaryotes, the higher plants and animals except in a nematode worm in which the system of genetic control of growth has been recently discovered and being thoroughly investigated in 1994-95.

Genetic Control In Eukaryotes

Genetic control of growth in Eukaryotes, including mammalian system, is very much different from those discovered in prokaryotes. You will be aware that for any growth to occur duplications of DNA for cell division and synthesis of mRNA and protein is the first requirement. Without it, cells can increase neither in number nor in size. DNA polymerase is an enzyme (protein) which is essential for DNA duplication. Without it, DNA strands would not duplicate. Similarly, for synthesis of protein, formation of mRNA is needed. Formation of mRNA is also dependent on an enzyme, RNA polymerase. Both the events, duplication of DNA and formation of mRNA, thus, are dependent on action of some proteins on DNA. If these proteins are not allowed to interact, or favourably allowed to interact with the DNA, growth processes can be controlled.

Control Of Cell Division : Various events associated with

replication (= duplication) of DNA and division of a cell is known. But the question as to what genetic control are exercised to regulate cell division is largely unanswered. The ratio of cell surface to volume is important. There is a critical surface area that will support a volume. If volume exceeds that limit, the surface area will multiply in the form of cell division to provide additional surface area to increased volume. Increased supply of nutrients to the cell thus seems to induce duplication of DNA and cell-division with resultant increase in cell-number. Since many cells such as neurons and muscle cells do not divide after birth, hence nutritional state of mother is important for controlling growth of embryo.

At the molecular level, events are all the more unclear. It has been hypothesized that increased nutrition means increased level of proteins, including DNA polymerase and other ingredients of DNA molecules hence duplication of DNA. This is gross simplification of the probable reactions that might be occurring but nutrition surely plays a dominant role in the duplication of DNA.

Control At Transcription Level : The main genetic control in the growth and development is exercised at the level of mRNA synthesis because it is the substance which is translated into enzymes and proteins which are the root cause of all growth related changes. The formation of mRNA is called transcription and transcription occurs with the help of enzyme RNA polymerase.

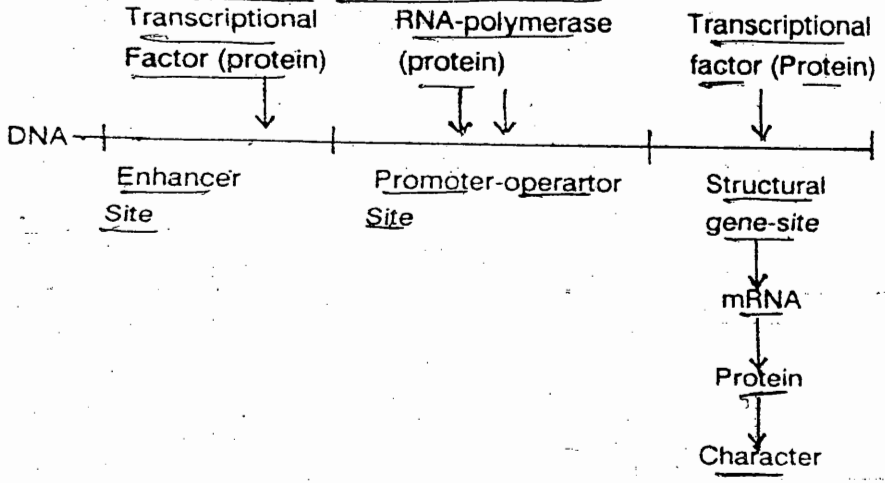
RNA-polymerase attaches to DNA for synthesis of mRN There are certain regions of DNA which facilitate this attachmer namely the promoter site. But transcription needs presence o certain TRANSCRIPTIONAL FACTORS without which transcription would not occur.

Transcriptional Factors : There are certain sequence of bases in the DNA that promote RNA polymerase binding to DNA. This include TATAAT sequence TTGACA sequence in prokaryotes and TATA, CAAT sequence in eukaryotes.

While there is no transcriptional factors required for the attachment of the enzyme to DNA in prokaryotes, eukaryotes are charactrised by requirements of a number of transcriptional factors without which gene would not function. These transcriptional factors are themselves proteins thus must have been formed by earlier activity of some gene These factors, attached at promoter sites, are proteins that interact with enzyme RNA polymerase. Thus protein - protein interaction controls the genetic mechanism

of growth.

Transcriptional Factors At Enhancer Site : Controlling factors can attach to promoter gene located close to genes synthesizing proteins. It can, however, be located far from the gene synthesizing protein called enhancer sites. Such a transcriptional factor attaches with the DNA and DNA forms a loop to make a contact between proteins attached to the enhancer site and RNA-polymarase protein at promotor site. The protein - protein interaction for control of genetic function thus can occur between proteins located close together at transcriptional site and also located farther from each other at enhancer site and transcriptional site. These two types of protein interactions are main controlling mechanisms of gene-function.



Homeotic Genes And Homeobox : In the zygote, and prior to it in egg itself, various substances are distributed differentially, which may be protein or certain neurohumors (serotonin, acetyl choline, adrenalin etc. ions etc;) that activate the highest order genes so that axes of the embryo is demarcated. Later on, these activated genes give out products that activate genes of lower order. The higher order genes form axes and major segments such as head, trunk, leg etc. Lower order genes gives identity to these segment. These lower order genes are homeotic genes. The homeotic genes of different regions do not vary much so that once a major landmarking has been done in embryo, the finer

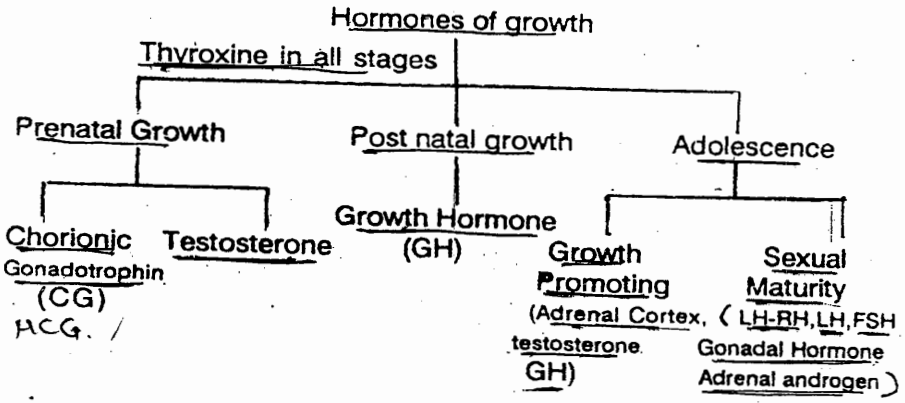
differentiation of a part can be carried on by similar transcription factors in different regions. The homeotic genes have been found to contain an identical sequences of about 180 nucleotides. This sequence is involved in formation of proteins that interact with DNA. It is supposed that transcriptional factors are the product of these homeotic genes. Protein from these genes have DNA binding regions and hence capable of regulating transcription by interacting with RNA polymerase. This ensures differential activity of genes both in time and space for coordinated growth.

Hox Genes : Dolle (1989), Favier et.al.(1995) and many group of workers have pointed out importance of Hox genes in growth and patterning of the tetrapod limb skeleton. Mice mutant for Hox D-13 gene have delayed morphogenesis of the limb. It had earlier been suggested that modification of Hox gene regulation may have been a source of morphological variation during evolution of tetrapod limb (Duboule, 1994). Sordino et al(1995) working on cloned genes of Zebrafish (Daniorerio) Hox D and Hox A have arrived at the same conclusion.

- Transcriptional factors
  - TATA } promote site.
  - CAAT }
- protein

BIOCHEMICAL FACTORS OF GROWTH

Human growth and development is largely an interplay of hormones secreted by various endocrine glands. Though some or all are needed during most of the periods of growth and development, one or a few definitely become crucial at some stage of development, and any fluctuation in its normal level in blood is sure to reflect serious imbalances in growth and development. A broad classification of hormones can be suggested depending upon its cruciality for the inauguration and maintenance of definite stages of growth and development. Hormone thyroxine, from thyroid gland, is not included in the classification because it is needed for different periods of growth and development.



Thyroxine

Human foetus secretes thyroxine from the 12th week of gestation under the influence of thyroid stimulating hormone (TSH) from pituitary. All pervasive effect of thyroxine on growth and development is because of its three fold action on body - firstly, it acts on cell-membrane causing increase in permeability so that uptake of substances by the cell is increased. Cell shall need these substances for synthetic purposes causing growth. Secondly, it acts on mitochondria, increasing its size and number. Mitochondria is called "Power House" of the cell and elevated levels of energy supplied by it shall be utilized during synthetic reactions. Thirdly, it acts on DNA in nucleus, activating it for synthesis of RNA which is needed in protein synthesis. Also, thyroxine increases

responsiveness of tissue to other hormones.

Prenatal Growth

1. Chorionic Gonadotropin (CG) : Foetus is attached to uterine wall of mother through placenta. Placenta is also an endocrine organ and secretes hormones that stimulate gonads. The hormone, chorionic gonadotropin, reaches its peak in the 12th week of postmenstrual age. The CG is supposed to cause appearance and stimulation of leydig cells or interstitial cells in testes to secrete testosterone.

2. Testosterone : Testis determining gene (Tdg) on Y-chromosome of male humans completes its task of differentiation of testis by 9th week of foetal age (post-menstrual). Whether this is the result of hormonal action is at present uncertain. At the eleventh post-menstrual week leydig cells appear in the testis and by the twelfth week they secrete testosterone under the influence of chorionic gonadotrophin. The hormone causes the undifferentiated external genitalia to form a penis and scrotum. In the female, it seems that differentiation of the ovary and external genitalia proceeds more passively. In the absence of the Y-chromosome, nothing happens at the ninth week and at about the tenth post-menstrual week the gonad turns into an ovary. The external genitalia of female develop around the fourteenth week, apparently without hormonal intervention.

In many mammals, it is found that testosterone has a determining effect on hypothalamus - the region of the brain that controls pituitary. If pituitary is master gland, hypothalamus is master of master glands. All secretions of pituitary are regulated by hormones secreted by hypothalamus. It is hypothalamus which decides a pituitary has to function as male pituitary or a female pituitary. Determination of hypothalamus by testosterone is thus crucial. This determination must occur within fixed period, 2 or 3 days after birth in rats. The role of testosterone in the development of sex-organs has been investigated. The genital primordia, from which ovary and testes develop is divided into cortex and medulla - medulla develops in testes and cortex in ovary - a feature determined by genotype. In case of male determination medulla differentiates into testes. The embryonic testes secrete testosterone that causes differentiation of vas deferens, seminal veside, epididymis, glans penis, shaft of penis and scrotum. Testes also secrete a substance, called Mullerian inhibiting substance (MIS) that suppresses growth of ovary from cortex.

In females, absence of testosterone is sufficient to cause development of ovary. The prenatal role of other hormones is uncertain. Maternal oestrogen passes across the placenta and cause the uterus of newborn girls to be temporarily enlarged at birth. The adrenal glands has a special zone which is well developed at birth and regresses soon afterword; its significance and its cause is uncertain. Insulin is found to stimulate foetal growth and it is secreted by foetal gland. Insulin-like growth factor I & II (somatomedins) are also needed for normal growth of foetus. (Somatomedins are plasma proteins)

Postnatal Growth

1. Growth Hormone (GH) or Somatotrophic hormone (STH) or Somatotrophin : GH is secreted by the foetal pituitary gland but it is not essential for growth during prenatal period. However, after birth upto attainment of adolescence. GH is needed for growth. It is very species-specific and GH of only monkeys is known to have stimulatory effect on humans.

GH causes growth by stimulating bone formation at the epiphyseal cartilaginous joints of long bones. The action is mediated through somatomedin A and C. Somatomedins are proteinous growth factors released from plasma proteins of blood by the action of GH. Actually there are three somatomedins released - A, B and C A and C causing cartilaginous growth and B causing increased synthesis of DNA by increased uptake of thymidine. This is needed for cell-division. Somatomedins A & C have structure very much similar to insulin hormone from islet of langerhans (Pancreas), hence are also referred to as insulin-like growth factors I and II. There are indications that GH cannot cause growth alone, rather a definite level of thyroxine is needed. The effect of thyroxine on growth is, however, supposed to be a peripheral one. It increases responsiveness of the target tissues of GH. Maximum growth is attained when both thyroxine and GH have their optimum levels. ★

Thus, mechanism of action of GH consists of proliferation of cartilaginous tissues at the epiphyseal ends via somatomedins A and C of plasma. These become sites of bone-formation later on. Cartilaginous cells respond only when they are primed by thyroxine. Later on, GH act on liver also to produce somatomedin C. ★

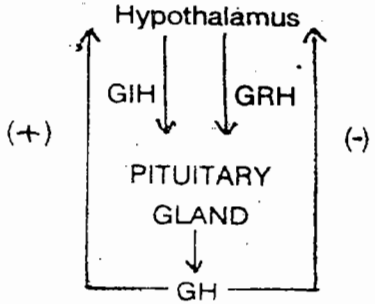
GH causes a concomitant increase in the muscles because

of increased protein synthesis. GH is known to increase incorporation of amino-acids in protein. It is because of this reason that GH is also known as protein anabolic hormone. Growth includes both bone and muscle growth and GH is capable of causing both the phenomena. GH causes utilisation of fat in the adipose tissues, shifting balance from fat synthesis to protein-synthesis. It is because of this reason that children with low GH are small as well as fat. ★

During post-natal period, the levels of GH is highest during 2-17 years of age but a daily rhythm is established only from 4th years of age. Growth hormone is secreted in pulses, not continuously. Exercise, anxiety, and sleep regularly cause secretion. Under normal circumstances some six or eight pulses occur each 24 hours. The amplitude and the frequency of pulses increases at puberty, contributing to the adolescent growth spurt.

GH is regulated by two hormones from hypothalamus- GH-RH (Growth Hormone Releasing Hormone or GRH) causes an increase in GH secretion and GH-IH (Growth Hormone-Inhibiting Hormone or GIH) causes decrease in GH secretion by pituitary gland. The two hormones of hypothalamus are controlled, in turn, by the levels of GH itself - higher levels of GH is stimulatory to the GIH secreting neurosecretory cells of hypothalamus and lower levels of GH is stimulatory to the GRH secreting cells of hypothalamus,

The circuit of control of GH shows that higher level of GH (indicated by (+) sign on the left side) increases GIH secretion, whereas lower levels of GH (indicated by (-) sign on the right side) increases GRH secretion. An interplay of these hormones ensure an optimum level of GH.



Adolescence and Puberty

The hormones controlling growth at puberty can be divided into two groups- growth promoting (GH, adrenal cortex hormones and testosterone) and sex-characters differentiating hormones (LH-RH from hypothalamus, FSH and LH from pituitary and oestrogen from female gonad and testosterone from male gonad.

1. Growth-promoting Hormones : In addition to GH from pituitary, three groups of hormones from adrenal cortex control growth - mineralocorticoids (eg.aldosterone), glucocorticoids (eg.cortisone) and cortical androgen (e.g. 7,dihydroxyepiandrosterone). Mineralocorticoids regulate mineral-metabolism and chiefly enhances rate of Na-uptake by the kidney cells. Actually, aldosterone acts on DNA and enhances synthesis of RNA which cause synthesis of specific proteins (aldosterone-induced proteins). These proteins cause uptake of Na in a manner not completely understood (Norris, 1985). This is necessary for maintenance of proper osmotic-balance of body and an optimum blood pressure for all organs to perform well. The second group of adrenal cortical hormone is glucocorticoids which is responsible for regulation of food-metabolism (not digestion). It causes increase in level of blood-glucose by :

a) Decreasing use of glucose by peripheral tissues such as skin, adipose cells. *

b) Increasing conversion of protein into glucose. *

c) Increasing breakdown of fat. *

The increase in level of blood glucose enables the body for its redistribution, particularly to those tissues which are under stress such as high metabolism, trauma, cut, injury, operation, stress etc. An optimum level of glucose is needed by most of the tissues so that they are responsive to the action of other hormones. In cases of absence or low-level of glucocorticoids the tissues are not responsive to other hormones. *

The third group of adrenal hormones, the adrenal the optimum level at that it is androgens, appears at the time of mid-growth spurt. Androgens increase gradually from about age 7 until puberty begins, during which their rate of increase doubles. It seems likely that it is concerned with muscular function. However, testosterone is the major cause of the increase in size and strength of the male muscles at adolescence. *

7 → muscular functions

arcuate
Ventromedial
neurosecretory

2. Reproduction promoting hormones :

i) *LH-RH from hypothalamus* : At the root of all changes leading to sexual maturity lies the small area in the hypothalamus - the arcuate and ventromedial Neurosecretory neuclei. The cells of these areas contain receptor proteins which bind certain brain chemicals such as dopamine. Level of dopamine reaches an optimum level at puberty during which time it triggers the neurosecretory cells of arcuate and ventromedial nuclei. Though there are evidences of FSH-RH also but LH-RH is potent for release of both LH and FSH. *

ii) *LH & FSH from pituitary* : Once the arcuate and ventromedial nuclei is activated, the cells of these nuclei (= group) secrete a hormone called Luteinizing-Hormone-Releasing Hormone (LH-RH or LRH). LH-RH has effect on pituitary gland causing release of gonadotrophins (LH and FSH) from pituitary gland. FSH (Follicle-Stimulating Hormone) in females causes growth of ovarian follicles which induces secretion of female sex-hormone oestrogen. Oestrogen is responsible for development of secondary sexual characters in females. FSH in males helps in the spermatogenesis and maturation of sperms.

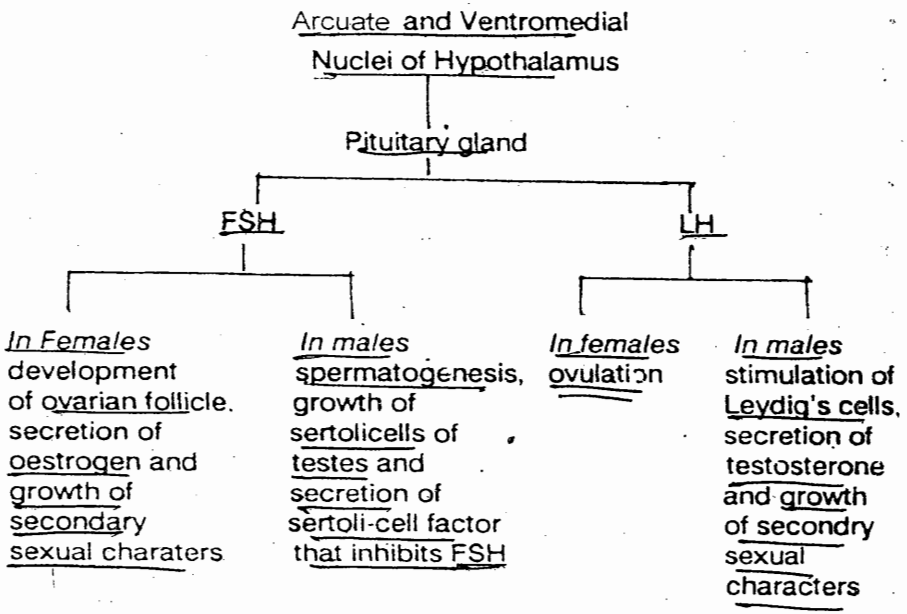
LH, in combination with FSH, is required for ovulation (release of ovum from ovary) for fertilization. LH in males is called interstitial cell stimulating hormone (ICSH) which stimulates interstitial or Leydig's cell for secretion of testosterone. * Testosterone causes development of secondary sexual character in males. *

Secretion of gonadotrophins (FSH & LH) is delayed till onset of puberty because of another reason too. During neonatal period there has occurred secretions of testosterone in boys and oestrogen in girls and high level of these sex-hormones have negative feed-back mechanisms on hypothalamus, inhibiting release of LH-RH. During adulthood, too, high levels of sex-hormones from ovary and testes regulate hypothalamus.

iii) *Sex-Hormones from Gonads* : Oestrogen from ovary and testosterone from testes are the hormones from gonads that cause development of secondary sexual characters of females and males respectively. Gonadal hormones are steroids which have effect on the DNA. This cause synthesis of mRNA which, in turn, results in increased synthesis of protein. In skeletal muscles, gonadal hormones have anabolic response, causing burst in protein synthetic activity thereby effecting growth. *

Certain aspects of hormonal control remains unsolved. Biochemical sophistication of analysis at our disposal have been late. A number of longitudinal studies have been undertaken with the more sensitive biochemical methods that have recently become available.

The circuit for sexual development in males and females can be represented as follows :



FSH — Sertoli cells of testes.
↓
Sertoli Factor

HEREDITY AND ENVIRONMENTAL CONTROL

Heredity is the dominant, if not absolute, component of growth and development. The controversy of nature and nurture also revolve round the theme whether heredity is absolute or not. There are people holding the extereme view, but all evidences indicate that neither is correct. Growth and development occurs according to a genetic blue-print which in certain characteristics and certain circumstances is liable to environmental influence. Hence a few, cardinal points regarded heredity and environment need to be mentioned at the outset :

1. Hereditary Factors include all the genes contained. Their norm of reaction or reaction-range vary. Some genes have narrow reaction-range and least modified by environmental factors. Pattern of teeth, bone has narrow reaction range. some genes have wide reaction range and its action is modified by environment. ★

2. Environmental Factors include factors of interior of the organism created by all other genes (internal environment) as well as external environment which can be everything except genes. The external environment can be in the form of microenvironment as when the organism exist as embryo in the womb of mother.

3. The Interaction Between Heredity And Environment may not be additive. Good nutrition can cause an increase of 10cm in Negros but only 5 cm in Japanese. There is nothing such thing as increase in 5000 calories causing increase in growth by 10cm in all races. The effect of heredity and environment is multiplicative, not additive.

4. In general, the relative importance of heredity and environment in controlling growth and development cannot be specified except in some cases. For many characters it is difficult to say how much of it is because of hereditary reasons and how much because of environmental. However, when environmental conditions are optimum, genes express maximally.

5. The organism's receptiveness to environmental factors is set by genetic influences. This is known as ecosensitivity. Following periods of growth or conditions of genotype are eco-sensitive-

a. Developmental Period : Some body traits such as breadth of nose, face and head, which develop predominantly in

the prenatal period are less susceptible to environmental factors in the postnatal life.

b. Degree Of Heterozygosity : Heterozygous individuals are influenced by environmental factors to a greater extent than the homozygous persons. Thus if children receive proper nourishment, a heterozygous child is more likely to grow taller than his predicted height, as compared to a homozygous child.

c. Concept Of Sensitive Period : There is a particular sensitive period for learning a skill or sensation in human beings. Young children learn a foreign language fluently with proper accent compared with adults who may never do so.

Role Of Heredity

While discussing nature-nurture significance let us first see characters whose heritability is less influenced by environment; Later on, we would see whether heredity is so strict as to allow no environmental influence in development of characters or does it allow enough morphological plasticity. Our discussion takes this form because the controversy consisted of all heredity and no environment vrs. both heredity and environment. Evidences in support of heredity first :

1. Phenotype : The parental traits are usually transmitted to the offspring. Thus, tall parents have tall children, and children of short statured parents tend to be short in height. The size of the head is more closely related to that of parents than are the size and shape of hands and feet. Similarly, the structure of the chest and fatty tissue has better genetic association than other somatic characteristics.

2. Characteristics Of Parents : Parents with high intelligence quotient (IQ) are more likely to have children with higher level of inherent intelligence. This is further enhanced because of greater degree of environmental stimulation in such homes. Children of certified mentally subnormal mothers have lower IQ than the average but the outlook is not as gloomy as it was once thought.

③ Studies Of Twins : Identical twins develop from one Zygote hence their genic constituent is almost similar. A number of studies involving twins have been performed and in most of the cases identical twins have been found to resemble showing influence of heredity on development.

a. The genetical control of growth is manifested in the inheritance of age at menarche. Identical twin sisters reach menarche an average of 2 months apart; non-identical twin sisters an average of 10 months apart. The correlation coefficient between age at menarche of mother and daughter is about 0.4 similar to correlations for height. The inheritance of age at menarche is probably transmitted as much by the father as by the mother, and is due not to a single gene, but to many showing same pattern of inheritance as shown by height and other body measurements.

b) Skeletal maturity shows a close correspondence at all ages in identical twins. A maturing bone has a primary centre of formation (ossification) along with one or more epiphyses where independent ossification goes on. The number and stages of development of these ossification areas is similar in identical twins.

c) The twin studies on intelligene-test behaviour shows greater similarity of scores by identical twins whether reared together or in different homes than that of the non-identical twins reared in the same home. The differences of IQ scores of non-identical twins, however, may also result due to earlier differences in their respective environments.

d) Most authentic evidence of influence of heredity on growth and development comes from correlational studies of identical twins for diverse anatomical and physiological characteristics.

Various studies involving identical twins and fraternal twins show high concordance rate for certain characters in identical twins indicating a greater genetic component in such characters. Below is given a comparative concordance rate for some characters in MZ and DZ twins.

Concordance rates for MZ and DZ twins (Data modified from strickberger)

Traits	MZ twins (% concordance)	DZ twins (% concordance
Eye colour	99.6	28
Feeble Mindedness	94	47
Hair Colour	89	22
Rickets	88	22
Schizophrenia	80	13
Diabetes mellitus	84	37
Manic depressive psychosis	77	19
Epilepsy, Idiopathic	72	15

no develop

Such correlational studies always fall short of 100% even in MZ twins meaning that they are very much similar but no exact replica of each other. This difference between them can be explained on the basis of environmental differences they are exposed to since their implantation in the womb of mother. As embryo, the two identical twins in the womb of mother might have been exposed to different pressure. Variation in the environment to which the two identical twins are liable to exposed to continue throughout their life-tune. No wonder, therefore, that these identical twins donot show a 100% positive correlation on different counts.

4. **Sex** : Boys are generally longer and heavier than girls at the time of birth. At the age of one year, there is no perceptible difference in their length and weight as related to sex. Although the pubertal growth spurt occurs earlier in girls, their mean height and weight are usually less than those in boys of corresponding ages at the time of full maturity. This is possibly due to differences in the sex-chromosomes. Girls posses 2 X chromosomes whereas boys possess one X and a Y. This difference in the chromosomal complement reflect not only in their sexes but in the rate of their respective growth which is a constant feature, not altered by the environment. So far expression of this characteristic of genes is concerned it is least influenced by the environment.

5. **Pattern Of Growth** : is clearly manifested in the growth potential of children of different racial groups. A typical Negro of Africa and US is advance of whites in all spheres of growth and development right from the birth. Upto 3 years of age, no environmental factor can affect this greater tempo of growth, though it is modifiable by different environmental factors, chiefly nutritional, in later stages of growth and development. Japanese children reach their growth peak and mature earlier than Negros and whites and their this feature is least affected by any environmental factors. ★

An endless examples can be cited to drive home the point that different racial groups have their characteristic growth pattern and rate of growth. ★

Rate of growth is modified by the nutritional factors as we shall see later on. But pattern of growth is more rigid genetic character least or not modified by environmental influences. A Negro can be stunted if kept on poor diet but its Negroid pattern of skeletal and other features are hard to vanish. A white boy kept on rich diet can be ahead of Negros in rate of growth but its skeletal pattern and other feature will remain different from the

Negros. A Japanese boy kept on very good diet can be made a bit longer but its trunk will remain shorter and its sitting height would not increase. Nutritional differences easily influence rate of growth of children of different racial groups but pattern of their growth has indellible marking of their heredity which are very hard to be removed.

6. **Biorhythm** : Daughters often reach menarche at a similar age as their mother. They may have a similar length of menstrual cycle. Menarche is the first menstrual cycle of girls. The similarity of age of menarche between mother and girl show that the character has greater influence of heredity. Moreover, female individuals belonging to a particular community all have similar age of menarche, provided all are equally well-fed. Thus Assamese girls have it at around 13.2 years, similar to the European girls though the two inhabit completely different environment, Assamese belonging to more hot and with plentiful rainfall. The age of menarche is decided by the genes which allows little influence from environment. ★

7. **Dental Eruption And Maturity** : One feature which has strong genetic basis is the time of eruption of the teeth, both deciduous and permanent and also the sequence in which teeth calcify and erupt. Deciduous teeth erupt between 6 months to 2 years of age and permanent teeth between 6 to 13 years of age. The events between 2 to 6 years and beyond 13 years are little informative about dental pattern of eruption except calcification studies in jaw X-ray. But studies of events before 2 years and between 6-13 years are testimony to the fact that dental characteristic is perhaps the most rigid hereditary character least modified by environmental influences. ★

8. **Skeletal Maturity** : Bones have indellible marking of the heredity not only in its pattern of maturity and shape but also in its growth requirements. An immature limb bone removed from a foetal or new born mouse and implanted under the skin of the back of an adult mouse of the same inbred strain (which therefore produces no antibodies to it) will continue to develop until its closely resembles a normal adult bone. Furthermore, the cartilage scaffolding of the bone, removed at the stage preceding actual bone formation, will do the same. Hereditary factors clearly are of immense importance. ★

Sex
Pattern of
Biorhythm

Phen
Pace
I

age of menarche - gene

Environmental Interaction

Organisms always develop according to the basic pattern determined by heredity, but this pattern to some extent depends upon the environmental factors. Thus we can say that the environment provides the opportunities for the development of some innate potentialities of heredity. Environmental influences on growth is seen in following circumstances :

1. Migrant Population : When a section of homogeneous population migrates to another land and continue to maintain their group identity, such a population provides an opportunity to evaluate the role of the changed environment. The subsequent generations of such a population can then be compared with their counterparts in the original home land. The differences observed in the migrant population will thus be attributable to the effects of the environment. Japanese migration to Hawaii demonstrated that in new environment of the United States of America, the migrant population showed increase in height and weight and some other somatic measurements.

2. Twin studies. The twin studies, which supported heredity as the main component of development, also yielded data that support environment component. Thus, there are several characters in which concordance rate is low in both MZ and DZ twins. Such traits show minimal gentic component. In other characters the concordance rate is not so high in MZ twins but fairly high for DZ twins. such characters also show a greater environment component

Table : concordance rates for MZ and DZ twins. (Data Modified from Strickberger)

Traits	MZ twins (% concordance)	DZ twins (% concordance)
Pulse Rate	56	34
Blood Pressure	63	36
Age when walking begins	68	31
Criminality	68	28
Stomach Cancer	27	04
Mammary Cancer	06	03
Uterine Cancer	06	00

3. Effects Of Malnutrition On Racial Differences : Comparative influences of genes and environment on the rate and

pattern of growth of races show that some of its features are not altered by environment whereas others can be. Two such characters are shape and size of body.

Different races differ in the shape of their bodies. There is no denying the fact that this difference among them is genetical. In each of the major populations of the world the shape of its members have been adjusted, by means of selection to the environmental condition in which they evolved. The differences are genetical in origin. Genes produce in them a characteristic shape which can be seen in native populations in its entirety and at least in vestiges in the populations that have moved out of its original habitat. Shape is characteristic feature of race which is little altered by the nutrition or climate. A white boy, if starved, can remain smaller but shape of his skeleton would not change.

Size of an individual however, is easily influenced by the nutrition. Negros of East Africa, West Africa, US are advance of whites in skeletal maturity and such aspects of postnatal growth as sitting, crawling. But in Africa this difference in rate of growth disappears by 3rd year of age due to poor nutrition. Such aspects of growth which are not affected by malnutrition such as dental eruption, however are not affected. Those Negros who are comparatively well off and can afford good nutrition remain ahead of whites in skeletal maturity and other aspects of growth. Thus, nutrition directly affects rate of growth.

Malnutrition causes deficiency of protein and essential minerals and vitamins and thus retards growth. Such children suffer nutritional stress and are prone to several deficiency diseases also.

The evidence that malnutrition can affect growth comes from a study of height and weight of children in Stuttgart from 1911 to 1953. It was shown that height and weight of children was normal from 1920-1940 but was below normal in both post world war I and II.

Children have great recuperative powers, provided the adverse conditions are not carried too far or continued for too long. During a short period of malnutrition, growth is halted. Growth takes place unusually fast with the arrival of favourable period until genetically determined growth is reached or approached once more and subsequently followed. During this 'catch-up' phase, weight and height and skeletal development seem to catch up at approximately the same rate. The 'catch-up'

growth is slowed down once genetically determined growth-rate is obtained.

Many features of growth and development are genetical in origin but are influenced by environment such as nutrition. Once the environmental constraint is removed, growth occurs according to the genetical plan. Nevertheless, it proves the point that genetical characters can be modified by environmental conditions.

4. Climatic Factors : Rate of growth, however, is less affected by the climatic factors. It has been found that both Nigerian school girls and Eskimo girl have average age of menarche 14.3 and 14.4 years respectively, a very minor difference. The two inhabit completely different the climates. Burmese and Assamese girls, under excellent nutritional conditions, have age of menarche of about 13.2 years, a age very much similar to European girls though former lives in excessive hot conditions in comparison to the latter. Between the two factors nutritional and climatic, the former can alter rate of growth, but the latter seems to be less or not effective.

It is, therefore, concluded that in some sphere genetical characters are non-modifiable; in others they are easily influenced by such environmental characters as nutrition. Climate plays a little or no role in the modification of the genetic characters.

Thus, contrary to the popular belief, climatic factors have little effect on rate of growth. However a higher velocity of growth has been claimed in spring and lower in summer months. Datas claiming such an influence are mostly older from European countries.

But Tanner (1992) contradicts such a belief. He categorically mention that there is considerable individual variation and different children reach their peak-velocity during different periods of year. This may be due to their individual differences in the endocrine reactivity.

5. Emotional Factors : Besides nutritional factors, a factor that influences rate of growth and development is emotional factor. Children from broken homes and orphanages do not grow and develop at an optimal rate. Anxiety, insecurity, lack of emotional support and love from the family prejudice the neurochemical regulation of the growth hormone.

In certain children under emotional stress the GH Secretion is inhibited and they come closely to resemble cases of idiopathic growth-hormone deficiency. However, when taken out of the

stressful conditions they begin to secrete GH again and have the usual rapid catch-up growth. Widdowson has provided evidence to the effect more or less similar to this in 1948 in Germany.

In studying the effect of increased rations on orphan children living on the poor diet, Widdowson observed the change brought about by replacement of one sister-in-charge by another. The design of the experiment was to give orphanage B a food supplement and to compare the growth of the children there with those in orphanage A, which was not to be supplemented. The result was just the reverse of that expected; the B children actually gained more weight than the A children during the first, unsupplemented, control period. The reason appeared to be that at precisely the 6-months mark a certain sister had been transferred from A to B. She ruled the children of B harshly and frequently chose mealtimes to administer rebukes, which upset all present. An exception was the group of eight favourites whom she brought with her from orphanage A. These eight children didn't receive all those rebukes and gained more weight than others.

- genetic character can be modified by environmental condition

I. Tanner — individual variation

P

- Migrat →
- Twin - concordance High → env.
- Malnutrition ← Size → & env + nutrit
  shape → genetic.
- & Climate - Eskim - Nig., Ta
- Emotion

SOCIO-ECONOMIC AND CULTURAL FACTORS OF GROWTH

Socio-economic conditions is well reflected in the growth and development of children. Tanner (1972), citing Goldstein data, indicated that the difference between the height of children of unskilled labourers and those of managerial classes is about 2 c.m. at the age of 3 years and rises to 5 c.m. at adolescence. A study of height in British people in 1980 showed that social class difference in height is about 3 c.m. in males and 2 c.m. in females. There is also a difference of 2-3 months in menarche (onset of menstruation) of daughters of unskilled labourers and managerial classes. Children from well-off families are always taller than their less fortunate brethren. Causes of such differences are not far to seek and can be listed as follows : (After Tanner,1992).

1. Nutritional Deficiency : Nutritional deficiency in the children of weaker sections can start right before birth and continue till adolescent. A child may be born nutritionally deprived because of deficient food-intake by the mother and poor health during pregnancy. During infancy, inadequate lactation or lack of desire to breast-feed the child may be other causes of nutritional deficiency. A poor state of economy of the weaker sections deprives the child of a balanced diet. Parents may be unaware of the child's nutritional needs and may adopt inappropriate feeding techniques.

2. Home Conditions : Tanner (1992) places more emphasis on home-conditions as a causative factor for growth retardation in weaker sections than the economic conditions. Home conditions reflect intelligence and personality of the parent and provide social and emotional needs for normal growth and development of children. Depression and excessive grieving on the part of parents will only cause social and emotional deprivation of the child affecting his normal development.

3. Economic Deprivations And Faulty Family Budgeting: Economic conditions are one of the main causes of socio-economic differential of growth and development. A low economic condition of the weaker section is the fountain-head of all deprivations they suffer from-from nutritional deficiency to the emotional deficiency. Family budgeting never shows child-centredness in such families and their diet is no better than diet of old peoples of the family.

4. Minor Illnesses : Children of the weaker sections are generally poorly nourished and are unable to bear the brunt of even minor illnesses. Minor illnesses such as measles, influenza, antibiotic-treated middle ear infections, pneumonia etc.cause no apparent growth retardation in well-nourished children but have quite discernible effect on children of weaker sections of society. It is supposed to reduce their growth rate.

5. Habit Of Smoking : In mothers, smoking is quite prevalent in women of weaker sections of society. Tanner(1992) states that smoking causes birth of children who are 100 gm. less in weight and 1 c.m. smaller in height on an average. The more distressing aspect of the situation is that the difference is maintained throughout the life.

6. Depressive And Grieving Parents : An intelligent parent can create a good home-conditions for proper emotional and social development of child. He can even arrange for nutritional needs of the child at much cheaper costs. Parent's positive attitude towards life provides the child necessary emotional and social security needed for proper growth.

7. Social Mobility : A few studies have shown that the abnormalities of growth resulting due to poor socio-economic conditions acts as both cause and effect. It has been found that, in general, intelligent boys are taller on an average than the average boys. Being intelligent such taller boys show greater social mobility towards the upper strata. Average boys, being less intelligent are pushed to the all more lower social strata. The association represents a complex mixture of genetic and environmental effects, the one reinforcing the other.

Latest Secular Trend

a. Increase In Height & Weight : Overall economic conditions of world has improved in last 100 years and there is found tendency for children to become progressively larger at all ages. The trend has been operating since last many years and in some well-off industrialised nations the trend has virtually stopped indicating that children of these societies have attained their full genetic potential. Data of heights and weights of school-children of Sweden is available for the years 1883.1938 and 1965-71. It is found that all the children groups from age seven and above in 1938 were larger than the groups of same age in 1883, and those of 1965-71 larger than those in 1938.

b. Extent Of Increase : Similar increase in heights and weights of children throughout the world has been registered. It is indicated that there is average increase of 1 c.m. in height and 0.5 kg. in weight per decade between 1880-1950 in the 5-7 years age group. For adolescent group, the same data increases to 2.5 cm. and 7 kg. per decade. It is, however, indicated that maximum average increase occurred in 2-5 years age group though there is only scanty data to prove the point.

c. Fate Of Increase : This trend of increase in size is still continuing in many parts of the world such as many European and Asian countries. In Japan, this increase has taken a peculiar form. There is average increase in the leg-length, though trunk length has remained the same. Thus trunk to leg length is similar in both Japanese and Europeans, though the former mature earlier and are slightly short.

d. Origin Of Trend : It is not known when such a trend originated. Norwegian data is the oldest one, registering adult height growth from 1741. Danish data is slightly younger, registering growth from 1815 and English data is from 1833 to present. These data confirm lack of an increase in the height upto around 1845 and gain of 0.3 to 0.6 cm. per decade thereafter.

A comparison of these older data with the present data of height and growth of children indicate that average growth of present day boy, irrespective of socio-economic class, is greater than even upper class boys of 100 years ago. This increase in height and weight shows a very secular trend that has overridden all the boundaries of class.

e. Earlier Age Of Menarche : There has been rather a fast reduction in the age of menarche. Western European data indicate that it occurred earlier by about 4 months per decade between 1830-1960. The trend shows that the reduction in the age of menarche in most European countries since 1970, and the age of onset of menarche has stopped in most European countries and USA. Like increase in height, the decrease in the age of menarche also seems to have attained its fullest genetic potentialities.

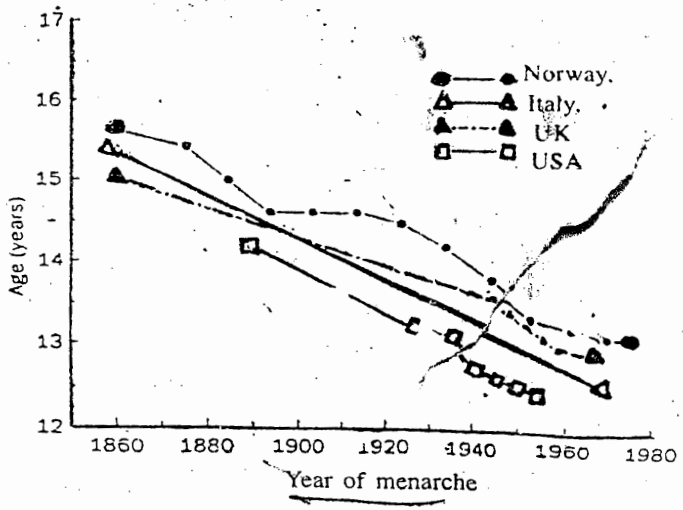


Fig : Secular trend in faster growth rate among girls in the last hundred years as revealed by decreasing age of menarche.

Causes Of Secular Trend

1. Improved Nutrition : It has been suggested by Tanner (1992) that the improved nutrition involves a better balanced diet and intake of certain essential factors than simply ingestion of more calories.

2. Improved Environmental Circumstances : A better medical facility and overall concern for the human health through improved hygienic conditions resulted in removal of many pathogenic diseases and its debilitating effects on the human growth and development.

3. Out Marriages : Industrialisation, urbanisation with concomitant development of transport facilities has brought in high mobility and broken down the boundary of genetical isolates by increasing degree of out marriages. There has occurred a considerable hybridisation of height genes. The postulate, however, considers that gene for greater height and gene for shorter height when placed together do not produce a height midway between the two but a height towards tallness. Though a conclusive proof is lacking, initial experiments do show that it is, indeed, so.

ABNORMAL DEVELOPMENT WITH SPECIAL REFERENCES TO AGE, SEX AND WEAKER SECTIONS

There are many factors that control development, hence disturbance in any of them acts as limiting factor in growth and development giving rise to disorders of development. Such abnormal development is reflected in both structural and behavioural development. The most usual indication of abnormal physical development is short stature which can result due to various reasons. Similarly, abnormal behaviour takes different forms and it results, like short stature, due to various reasons.

Age, sex and socio-economic conditions of individuals often determine or influence occurrence of such abnormalities. Growth takes place from the intrauterine stage of the foetus to the end of adolescence. However, intrauterine growth of foetus and few initial years of infancy are crucial for normal development. Most of the etiological factors for abnormal development strike during this period. Such factors hence can be prenatal or postnatal.

Sex of the child often determines or influences certain abnormal developments. Short stature in females can result due to Turner's syndrome which is largest contributor in the abnormal development of girl child. Tall stature in males can result due to hypersecretion of GH from pituitary but often it is a function of abnormal karyotype 47, XXY and 47, XYY, known as klinefilters syndrome and XYY-syndrome respectively. Barring these few cases of enhanced growth, abnormalities of growth generally result in short stature.

Since weaker sections of society are faced with nutritional deprivation, higher incidence of infectious diseases and a pathological psychosocial environment in general, they are more affected by abnormalities of growth.

Height of 95 percent of normal children lies between the 3rd and 97th percentiles of height or within two standard deviations above or below the mean height for the age. If the height of the child is below the 3rd percentile or less than two S.D. from the mean, he or she is considered to be short in stature.

There are various causes of abnormal growth that results in short stature. Some of these factors can be summarised as follow:

Pre-natal causes : 1. Intrauterine growth retardation; 2. Genetic disorders (chromosomal and metabolic disorders)

Post-natal Causes : 1. Nutritional dwarfism; 2. Chronic visceral disease (Renal, cardiopulmonary, malabsorption, chronic infections and anaemias); 3. Endocrine Disorders; 4. Psychosocial short stature (Emotional deprivation).

Pre-natal Causes

1. Intrauterine Growth Retardation : Environmental factors affecting growing embryo in the womb of mother include maternal malnutrition, maternal illness, maternal medications and maternal infections. In addition, mother contributes only half the number of her chromosomes to the child. Genes contained in the rest of the chromosome i.e that part of the genome of the mother which is not transmitted to the foetus, but which, nevertheless, is present in the maternal tissues (where the embryo is growing) influence the foetal growth. Maternal malnutrition is identified with intrauterine growth retardation and consequently small size of the foetus. Medical illness of mother and infections also result in poor growth of the foetus. Average birth weight of infants born to mothers receiving nutrition supplements during pregnancy is higher than that of babies of mothers who did not receive nutritional support in the antenatal period.

Administration of some drugs, to the mother during the first trimester of pregnancy adversely affects the differentiation of those organs which are developing and differentiating at that phase of pregnancy. These drugs or agents are termed teratogenic.

Maternal infections, e.g. syphilis, viral hepatitis, toxoplasmosis, etc. may be transmitted to the foetus and thus may arrest or retard the foetal development.

Arrest of the foetal growth during early embryonic life causes reduction in the total number of cells with subsequent diminished growth potential in the postnatal life. These children are physically slender and have sharp fine facial features. Craniofacial disproportion is usually present. The height is generally three standard deviation less than the mean height for age. The velocity of growth is not markedly altered. The bone age is normal or moderately delayed. Children with intrauterine growth retardation often exhibit learning disabilities in school.

2. Genetic Disorders :

a. Genetic short stature : In these children the height is between one and two S.D. below the mean. The parents are of short stature and the height can be related to the mean parental height. The velocity of growth, bone age and body proportions are normal.

b. Inborn errors of metabolism : Certain inherited metabolic disorders e.g. galactosemia, mucopolysaccharidosis, achondroplasia, glycogenosis, aminoaciduria and renal tubular acidosis are associated with short stature.

c. Chromosomal disorders : Turner's syndrome (XO) must always be considered in differential diagnosis of short stature in girls. They have gonadal dysgenesis, widely placed nipples, short webbed neck.

Post-Natal Causes

1. Nutritional Dwarfism : Protein energy malnutrition deficiency of certain minerals such as zinc, iron deficiency anaemia are common causes of nutritional dwarfism. In gross nutritional deficit, the weight gain is slow and the muscles are wasted. Longstanding malnutrition results in stunting of the height. If the weight and height of the child are affected concurrently, the child looks smaller for his age.

2. Chronic Visceral Disease : Several chronic disease of viscera such as heart, lungs, liver and gastrointestinal system are associated with stunting of growth. Serial record of weight and height of the child on growth charts may unmask the existence of associated chronic disease.

a. *Chronic infections* : Tuberculosis, malaria, leishmaniasis etc. are important causes. The growth retardation is attributed to impaired appetite, diminished food intake, increased catabolism, poor utilisation of food, vomiting and diarrhea, which are often associated with these illnesses.

b. *Malabsorption syndromes* : These include chronic recurrent infective diarrhea, lactose intolerance etc.

c. *Birth defects* : Growth retardation is seen frequently in congenital heart disease. Anomalies of urinary tract and nervous system are also important causes of stunting of growth.

d. *Metabolic disorders.*: Several inborn errors of metabolism.

e. *Hematologic disorders* : Such as thalassemia and sickle cell disease also results in dwarfism.

f. *Miscellaneous causes* : Cirrhosis of liver, bronchial asthma, cardiomyopathies, renal disorders and chronic renal failure.

Nutritional dwarfism and chronic infections are the two main reasons for the short stature of children of weaker sections. Their diet generally lacks minerals, vitamins and proteins which are so essential for bone-growth. As their living conditions are very unhygienic, incidence of infectious diseases is high. Nutritional deficiency and chronic infections start a vicious circle in them - these factors make them weak also, hence they are unable to earn a good livelihood which in turn make them more weak.

3. Endocrine Disorders :

a. Human Growth Hormone Deficiency : These children appear normal in height and weight at birth. Delay in growth is observed usually after the age of one year. Growth is regular but slow. Bone age is significantly delayed. Gonadal development is infantile or retarded with delay in the appearance of secondary sexual characters. The condition results either due to diminished secretion of GRH from hypothalamus or GH from pituitary.

b. Hypothyroidism : The child appears short and stocky. Bone age is delayed. Sexual development is usually infantile. The abdomen is often protuberant. The face appears puffy and crentinoid. The skin and subcutaneous tissue are thickened. The child appears lethargic and reaction time is increased. The facial expression is dull and these children are unusually susceptible to cold. The diagnosis is confirmed by low T_4 levels.

c. Gonadal Disorders : Children with precocious puberty grow rapidly initially but their epiphyseal centres prematurely fuse with the diaphysis, resulting in a marked stunting of growth.

d. Cushing's Syndrome : In [illegible] me, the growth retardation is an early feature [illegible] excess[illegible]ve secretion of glucocorticoids by the adrenal c[illegible]. Other features of cushing syndrome are obesity, moon sh[illegible]d facies, abdominal striae, hypertension and diminished glucose tolerance.

e. Diabetes Mellitus : Juvenile diabetes mellitus is associated with significant growth retardation.

f. Diabetes Insipidus : This is caused due to insufficiency of pituitary hormone ADH which results in poor water reabsorption in

kidney and hence frequent and voluminous urination.

4. Psychosocial Short Stature

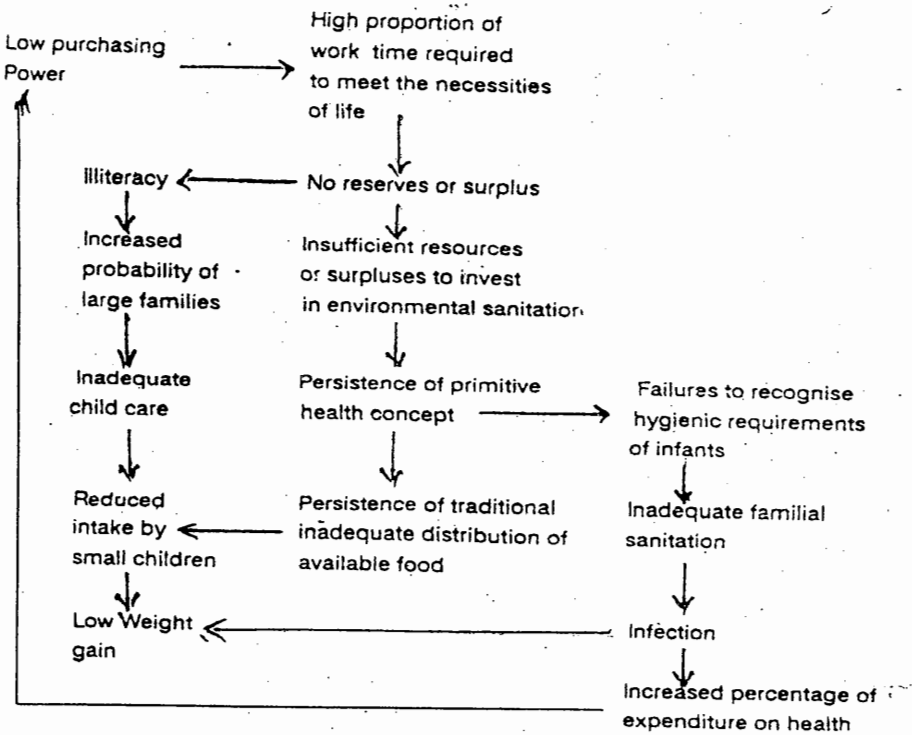
Social and emotional deprivation may result from (i) early frequent separation of mother from the infant so that there is lack of opportunity for adequate mother-infant bonding (ii) depression in parents (iii) a family disaster such as death or anticipated death in the family, excessive grieving and devoting less time for interaction with the infant (iv) unwanted child and parental rejection of the child, (v) single parent, (vi) young mother who is unable to care for the child or (vii) psychopathic personality of the mother.

Almost all psychosocial factors that predispose infants to abnormal growth can be traced in weaker sections, though some of these can be present in affluent sections of society for different reasons. A mother in affluent section of society may spend less time with child because of her social and other obligations but a mother in weaker section has to earn livelihood due to which early frequent separation from the infant is inevitable leading to a poor mother infant bonding. Parents in weaker sections are always preoccupied with ways to keep somehow their body and soul together. They have little or no savings for any recreation in life hence remain depressed most of the time. Such parental depression has telling effect on child's development. In order to make life a little easier, parents in weaker sections engage themselves in all sorts of economic activities even if it is a trivial one and find no time to interact with the child.

There is a very low rate of literacy among weaker sections hence they are less aware of such concept as a small family. Little income and too many children put them from "frying pan" into the fire. Most of the infants weather parental rejection and feel unwanted in the family. In weaker sections there is virtually a condition of single parent. Adult males most often leave their homes and migrate to faraway industrial or metropolitan city to earn a fair livelihood. A child thus has to satisfy his or her childhood with single parent though both parents may be alive.

Parents in the weaker sections of society are unable to invest in the education of girl child who are generally married off at much lower age with the result that they are blessed with motherhood at the age when they are still mentally immature. They are just unable to understand the physical and psychological requirements of the infant which results in their abnormal development.

Though both of the parents of weaker section have to weather adverse conditions of life, the main brunt comes in the share of females. Denied an honourable place in the family hierarchy, she is expected to play roles at the social and economic levels without a buzz. This often make them an unique case of psychopathology and mother with psychopathic personality is least expected to care for growth requirements of her infants. children of weaker sections are more prone to "failure to thrive" characterized by low weight gain. According to Cravioto et.al. (1967) the reasons are the same as that of short stature



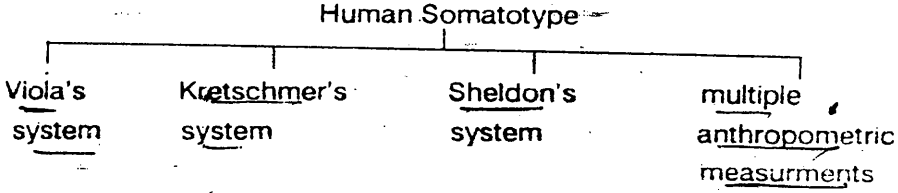
HUMAN PHYSIQUE AND SOMATO-TYPES

Human Constitution Is Consistent : Human beings are characterized by different constitutions. Human constitution is consistent in the sense that various aspects of its structure, function, or behaviour is almost permanent and do not show change in an individual from day to day, or even from a year to year. Human beings with different constitution have traits for which the variation in a single individual is less in comparison to its variation between individuals of different constitution. Thus persons with a constitution can be recognised with certain sets of morphological, physiological and behavioural characteristics some of which show little variation, others a bit more. Stature is a morphological trait that shows little variation ; Blood group and ability to test PTC are physiological traits comparatively stable; reacting to circumstances is behavioural trait showing less change. Persons with different constitution can be shown to possess different set of traits of characters like one mentioned that will show little variation in an individual.

Human Constitution Is Largely A Reflection Of Genetics : Study of human constitution is much older than the science of genetic study. Thus, it inevitably included several non-genetical explanations such as effects of early experiences etc. With the growth of science of genetics, particularly human genetics, the intricate relationship between genetics and constitutional types is being gradually discovered and its role in development of specific human constitution recognised.

Morphology Is The Most Attempted Basis For Constitutional Classification : Though physiological and behavioural characterisation of a constitutional type also exist, in practice morphology has provided the main basis for classification of human constitution. In such studies, humans are divided into certain classes according to their physique or built. Such classification also combine various aspects of growth, physiology, evolution, disease and behavioural traits to various degrees hence different schemes of classification of human physique have been proposed by different worker. Three are associated with those of the names of their originators : Viola, an Italian physician; Kretschmer, a German psychiatrist; Sheldon, an American psychologist; and the fourth results from the application of the statistical technique known as factor analysis to multiple

anthropometric measurements.



1. Viola's System : Viola's system recognised four somato-types - longitype, brachitype, normotype and mixed type. For general purposes, ten measurements were used. These were combined together in a rather empirical way to give four indexes. In each of the indexes the position of the individual relative to the standard group of the same age and sex was recorded and the person classified as 'longitype', 'brachitype', 'normotype', or 'mixed-type'. The longitypes had long limbs relative to their trunk volume, a large thorax relative to their abdomen, and large transverse diameters relative to antero-posterior ones. Brachitypes were the reverse, normotypes in between and mixed types those whose four indexes failed to agree amongst themselves, one placing the individual in one category and another elsewhere.

Viola's system has fallen into disuse Though hundred of papers have been published linking viola's system with disease susceptibility, physiological and behavioural impacts but most of it stands unjustifiably neglected now a days.

Kretschmer's System : His system was based on anthroposcopic inspection and lacked in detail in comparison to the viola's system. The system is now a days entirely outmoded. Kretschmer described and illustrated three types, the 'pyknic', the 'leptosome' and the athletic. The pyknic was broad, round and fat, sturdy and stocky; the leptosome long, thin, and linear; and the athletic heavily muscled with large throax and shoulders, and narrow hips. Both viola's and Kretschmer's system had to face very rough weather because both classified human beings into fixed, discrete classes though intermediary between these are easily recognised.

Sheldon's System And Somatotyping : Though Sheldon's system has some relation to Kretschmer's, being a three-way rather than a two-way classification, it suffers from the same idea that there are no discrete 'types'.

There were three components in Sheldon's system

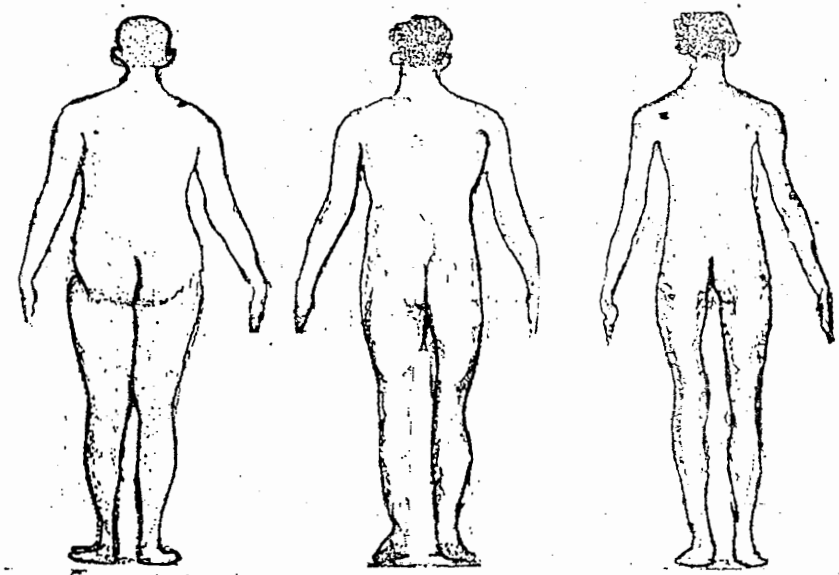
endomorphy, mesomorphy and ectomorphy and each person was evaluated on a scale for each of the components and rated. The rating scale was 1 to 7, 7 being the highest and 1 being the lowest. A man getting a rating of 4 for example, was twice in the character from the person who was allotted 3 and similarly 3 was more than 2. The first extreme example was rated 7-1-1 (extreme endomorphy), the second extreme 1-7-1 (extreme mesomorphy) and third 1-1-7 (extreme ectomorphy). The whole system is known as "somatotyping", a word reserved for Sheldon's classification and used nowhere else. The extreme in endomorphy (7-1-1) approaches spherical; he has a round head, a large fat abdomen predominating over his thorax, and weak, floppy arms and legs, with much fat in the upper arm and thigh, but slender wrists and ankles. Relative to his general size he has a large liver, spleen, and gut; large lungs and a heart shaped differently from those of the other extreme physiques. He has a great deal of subcutaneous fat and his thoracic and pelvic skeleton is greater in the antero-posterior than in transverse direction. Fatness is related to this build, and the amount of weight put on as a person gets older is fairly directly related to his rating in endomorphy, though it can be delayed by dieting and exercise. It may be that persons high in endomorphy have more fat cells than persons low in this component, just as those high in mesomorphy have, presumably, more muscle-cells. There is no quantitative estimation of fat cells and muscles cells in endomorphs and mesomorph respectively hence such observations can best be taken simply as hypothesis.

The extreme in mesomorphy is represented by Hercules in whom muscle and bone predominate. He has a cubical, massive head, broad shoulders and chest, and heavily muscled arms and legs. Relative to his size his heart muscle is large. He has a minimal amount of subcutaneous fat.

The extreme in ectomorphy is the linear man; he has a thin face with a receding chin and high forehead, a thin, narrow chest and abdomen, a narrow heart, and thin arms and legs. He has neither much muscle nor much subcutaneous fat, but , a large skin area and a large nervous system.

The vast majority of people are not extremes but have a moderate amount of each component. Thus, the common somato-types are the 3-4-4, 4-3-3, or 3-5-2 of endomorphs, mesomorphs and ectomorph and method of plotting somatotyping is presented in diagram following

HUMAN PHYSIQUE AND SOMATO-YPES



Somatotyping is carried out anthroposcopically, by inspection of photographs, with the subject standing in a rigidly standardized pose. There is a rotating table on which subject is made to stand, his photograph taken in various angles. The technique has been much developed, and pictures are now taken from which bodily dimensions can be accurately measured with special apparatus, a technique known as photogrammetric anthropometry.

The somato-type is assigned by inspection of the photograph, but its comparison, if necessary, with photographs of known somato-types, and by reference to tables published in Sheldon's Atlas can be made. There are few criticisms against Sheldon's system of somatotyping such as -

a. The components used in Sheldon's system are not independent and negatively intercorrelated so that a high rating in one precludes high rating in other.

b. There must be compensatory allowances for age, disease, muscular exercise. Recent publication of Tanner and whitehouses's Atlas of children's growth (1982) gives many serial pictures of children of different somato-types. In general, best time for somatotyping a person is at age 20-25 years when he/she is in normal nutrition.

c. Somatotyping woman is difficult because there is no published atlas. There have been a number of variations of somatotyping suggested since Sheldon's work.

4. Factor Analysis Of Physique : The factor analysis classification results from measuremental approach to human physique. Factor analysis is a branch of multivariate statistical technique used for reducing a large number of measurements, all of which are intercorrelated, to a smaller number of factors, which account for most of the variability defined by the original measurements. The starting point is a table of correlation coefficients for a group of body measurtements. The finish is a series of few factors. In such method, no body part is measured twice. The most used factor analysed is that of gross size which are divided and subdivided into smaller groups.

The Analysis Of Physique By Tissue Components

X-rays are used to measure the widths of fat, muscle and bone: a special caliper is used to measure thickness of the subcutaneous fat.The sites most simply X-rayed are the upper arm, calf and thigh.

a. Fat : Data, however, show that there is a subsidiary factor for fat on the trunk versus fat on the limbs. This means that one person may have a particularly large fat layer over the calves, another a particularly large over the upper arms. It is trunk versus limb factor and the specific local factor which give characteristic shape of fat to an individual whether fat or lean.

b. Muscle : The muscle factor is easily estimated by adding three measurements of limb muscles. There is little evidence of important regional factors.

c. Skeleton : Factor analysis of Skeleton is most complicated because different factors do not correlate. Limb bone width is unrelated to width of the vertebral bodies so that slenderness of limb bone is independent of slenderness of spine. Trunk length may be split into several independent component such as head and neck length. Thorax length (top of sternum to umbilicus) and pelvic length (umbilicus to is ischial tuberosity).

With the help of tissue component analysis we can reconstruct the major elements of individuals physique in terms of scores. Such elements of physique can be skeletal frame size, limb bone width, limb-bone length muscle width, fat thickness.

Relevance / Importance of Somatotyping :

1. Function :

Literature is full of claims about involvement of physique with different states of function, disease and behaviour, most of them untested and thus has no scientific basis. There is a belief that ectomorphic individuals have higher habitual rates of thyroid secretion than others, but no studies with modern methods have been reported. A number of studies have shown that systolic and diastolic blood-pressure, as measured by the cuff method, are higher in broadly built persons than in linear ones. Blood-volume has been shown to be higher, relative to body-weight, in persons high in mesomorphy and lower in either ectomorphs or endomorphs. It is almost a certainty that different body build must be interrelated. But little is known about relationships between body-build and physiological function. It seems fairly certain that such relationships must exist, at least in endocrine function and in metabolism physique may indeed relate to endocrine activity, or it may relate to amounts of the tissue receptors which translate the endocrine message into information regulating the cells. Only physiological functions which are relatively stable from week to week or year to year can be expected to relate to build. By using a suitable statistical design involving measuring the individuals twice or more over a period of time, it is possible to separate the stable and the fluctuating components and to calculate the relationship between the stable values for each individual and various indexes of his build. There is one study which has provided evidence for relation between physique and hormonal activity.

Adrenal cortex secretes three hormones-mineralocorticoid, glucocorticoids and adrenal androgens. Mineralocorticoid and gluco corticoid is excreted as 17 - ketogenic steroid and adrenal androgen is excreted, along with testes androgen, as 17 - Ketosteroid. Both groups of steroids have constant rate of excretion over the time. Creatinine, the excretory substance from muscle breakdown, is also excreted at a constant rate.

The 17-ketosteroid excretion is significantly related to the amount of muscle in the body. The 17-ketogenic excretion is related to the width of the shafts of the bones, or more precisely to the width of the marrow cavities. It is also related, much more than is 17-ketosteroid excretion, to the overall size of the body.

Creatinine excretion relates closely to muscle bulk.

These results are still a long way from revealing differences in rates of secretion of hormones by the adrenal itself. Research along these general lines will reveal the true manner in which each physique is dependent on hormonal agents and their receptors.

2. Disease

a. Pulmonary Tuberculosis has been claimed to be a disease of ectomorphic builds, or at least of persons with a low weight for their height. In one study it has been shown that the initial infection occurs irrespective of physique, but a spread of the germ to cause clinical disease several years later occur much more frequently in tall people of relatively low weight than in others, unfortunately all studies fail to differentiate fat from muscle and heavy from light bones. Consequently, all chance of a physiological analysis of the situation is lost.

b. Coronary Thrombosis is also certainly related to physique, the incidence being higher in persons of high weight for height. It seems that both above-average fat and above-average muscle contribute to the susceptibility. It may be that mesomorphic men put themselves more than others into positions where they are at increased risk of developing coronary thrombosis, perhaps because of increased stress.

c. Diabetes is another disease related to build. Clinically, two forms are distinguished. One appears early in life and requires much insulin for its control; the other appears in middle age and requires little insulin : juvenile onset diabetes (JOD), and maturity onset diabetes (MOD). Sufferers from the MOD are more endomorphic than sufferers from the JOD and have a fat pattern in which trunk fat predominates over limb fat.

d. Most Cancer are said to occur more frequently in the brachitype than the longitype; and modern studies by Damon et al. tend to bear this out, at least for breast cancer.

e. Mental Disorders There is a marked affinity with physique.

Anxiety neurosis - ectomorphic
schizophrenia - ectomorphic
manic - depressive - Low ectomorphic
Paranoids - mesomorphic
Hysteria, depression - Mesomorphic.

3. Behaviour

Of all the behaviours, temperament is most closely related to build. Kreschmer described originally two types of temperament, the 'cyclothyme' and the 'schizothyme', which corresponded more or less to Jung's 'extrovert' and 'introvert'; he related these closely to the types of build, the cyclothyme being pyknic, the schizothyme leptosomic, (long, thin). Sheldon produced three components of temperament, each defined by 20 traits. Each trait is rated on a 7 point scale, and the average of the 20 ratings gives the score in each component. For example, there are 7 points for the trait number 2, Individuals getting any point for every component from 1-7. Twenty such traits would be evaluated. A selection of 7 traits is given in Table. Sheldon found correlations of the order of 0.8 between viscerotonia and endomorphy, somatotonia and mesomorphy, and cerebrotonia and ectomorphy.

Table : *A Selection of traits from Sheldon's scale of temperament*

Trait no.	Viscerotonia	Somatotonia	Cerebrotonia
1.	Relaxation	Assertiveness	Restraint
2.	Love of Physical comfort	Love of Physical adventures	Inhibited social address
3.	Greed for affection and approval	Psychological callousness	Secretiveness of feeling, emotional restraint
4.	Easy, communication of feeling; extraversion of viscerotonia	Horizontal mental cleavage; extraversion of somatotonia	Vertical mental cleavage; introversion
5.	Relaxation under alcohal	Aggression under alcohal	Resistance to alcohal
6.	Need of people when troubled	Need of action when troubled	Need of solitude when troubled
7.	Orientation toward childhood and family relationship	Orientation toward goals and activities of youth	Orientation toward later periods of life

There are two main difficulties with the Sheldon's temperamental trait-rating scale.

1. The precise age at which rating is to be done and the extent of time to which it should continue so as to capture all the subjects necessary temperamental traits is uncertain.

2. Prior contact of the subject with the rater may colour his ratings. Thus a rater must not "see" the subject while rating him on Sheldon's scale.

There are two main theories to explain the nature of relationship between physique and behaviour.

1. Genetic Theory : It considers that genes for physique and behaviour are either pleitropic or closely linked. A pleitropic gene is one whose action is a fundamental one a change in which can be traced in different systems. A gene forming membrane-protein of cell is a pleitropic gene. If a mutation occurs in it, all the systems e.g. digestive, respiratory, excretory etc which are derived from the cell shall have defects in the membrane of its cell affecting system's functioning. Linked gene are located on a single chromosome, often located close together forming a linkage group and inherited together.

2. The Theory Of Conditioned Behaviour states that mesomorphic, once among the boys of his age knocks down a boy and wins, his behaviour is positively reinforced by his success and gradually reflects his temperament. The two theories are not mutually exclusive, the condition may be supporting and reinforcing the earlier genetic determination. We have in our minds certain stereotypes that has persisted since long and have become almost a cultural fantasy. "It may be a collective cultured fantasy" thus observed Tanner, but it seems more likely to spring from the firm ground of human biology.

SENESCENCE AND AGEING THEORIES

The term senescence is used when talking about the changes which occur during the period of obvious functional decline in the later years of life-span. Some people use the term ageing for the same processes and period. Others use it in a much general way, with ageing meaning simply growing older, and ageing changes being any changes related to age, regardless of when in the life-span they occur. Thus the onset of puberty might be described as an ageing change, but not as a senescent change.

However, there have been many formal definitions of ageing processes and senescence. "According to Sir Peter Medawar (1952) first transplant surgeon in mice, senescence is that change of bodily faculties and sensibilities and energies which accompanies ageing, and which renders the individual progressively more likely to die from accidental causes of random incidence. Strictly speaking, the word "accidental" is redundant, for all deaths are in some degree accidental. No death is wholly "natural"; no one dies merely of the burden of the years.

According to Strechler (1962) "Senescence is the changes which occur generally in the post-reproductive period and which result in a decreased survival capacity on the part of the individual organism.

"According to Maynard Smith (1962) ageing processes are those which render individuals more susceptible as they grow older to various factors, intrinsic or extrinsic, which may cause death".

According to Comfort (1960) "ageing is an increased liability to die, or an increasing loss of vigour, with increasing chronological age, with the passage of the life cycle".

It is evident from definitions that senescence has at least three cardinal characteristics - Firstly, the changes that occur during ageing are deleterious; they increase the chances that an animal will die. Ageing, therefore, involves a decrease in the ability of an animal to cope with its environment. Secondly, the deleterious age-related changes are cumulative. Death, the ultimate result of ageing, is sudden, but the process of ageing involves a progressive increase in the probability of dying. A third characteristic of ageing and senescence, which is implicit in most of the definitions which have been given, is that the processes involved are common to all members of a species and are

inescapable consequences of getting older. That is to say, ageing and senescence are fundamental intrinsic properties of living organisms.

Rapid advances in medical sciences have reduced infant mortality, controlled infectious diseases, and increased the average life span of humans though the maximum life-span of human of 90 years ± 10 or 20 years appears to be fixed in all societies. The eternal fear of old age and consequent death haunts man's mind since eternal. Aim of Gerontology, the science of ageing, is, however, not to prolong total life-span, but the youth period so that onset of some of the old-age diseases such as arthritis, rheumatism, arteriosclerosis and cancer can be postponed, and man can enjoy physical fitness and can have psychological satisfaction of being young and active. The motto of gerontology is to "add life into years and not years into life".

All individuals of any species follow the same course - growth, maturity & reproduction, senescence(ageing), and death. After reproductive functions are performed there sets in decline in activity and death occurs at some point during this decline not because all functions reach zero level, but because of the onset of one or more diseases or the dysfunction of some organs. Thus, ageing is the post maturation period, when the adaptability to the environment decreases, or the susceptibility to the diseases increases.

Senescence is, in general, a gradual process which is initiated at the molecular level much advance in time before its external symptoms appear. It is generally recognised as six-step process.

1. Organisms, ever since it is conceived as zygote, has accumulation of a large number of substances within the cell. The accumulated substances, gradually with time, causes much damage to the biomolecules, particularly DNA in the cell and to different elements outside the cell.

2. End result of such damages to the DNA and other biomolecules would be impaired sub-cellular functions eg. many enzymes synthesized by the genes will be missing. Extracellular changes may involve collagen and matrix. (e.g. cross-linkages in elastin and collagen may affect tissue flexibility ; changes in the extracellular matrix may lead to diffusion barriers).

3a. Decreased efficiency of subcellular functions will lead to a reduction in cell efficiency (e.g. inability to transcribe mRNA

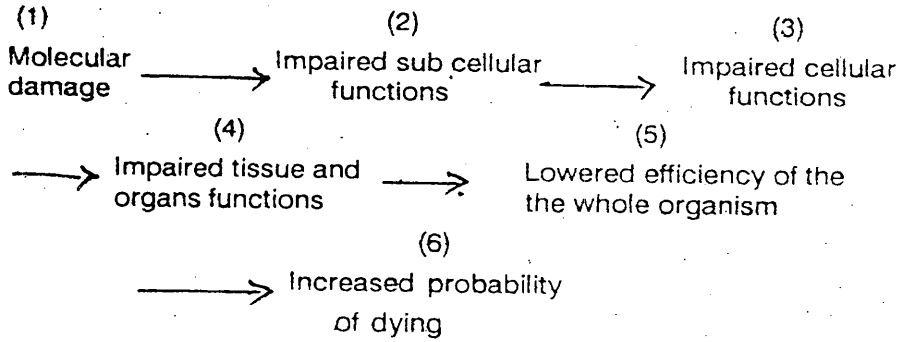
might prevent secretory cells from producing their products; mitochondrial defects are likely to affect all energy requiring processes; nuclear changes may affect the ability of lymphocytes to proliferate in response to antigenic stimulation.

b. In some cases the decreased efficiency of subcellular functions will lead to cell death because the cell will no longer be able to maintain itself.

4. As a result of the decline in cell efficiency, cell death, andchanges in the extracellular environment, the functional capacities of tissue, organs and organ systems will deteriorate (e.g. changes in nerve cells will affect brain function; changes in lymphocytes will make the immune system less efficient.)

5. Deterioration in tissues and organs leads to deterioration of the whole organism (e.g. declining efficiency of the immune system will make animals less resistant to infectious diseases; deterioration of the neuromuscular system will reduce an animal's ability to get sufficient food and to escape predators).

6. Deterioration of the organism results in an increased probability of dying.



Effects Of Genotype And Environment On Senescence : Though there exists a genetic blue print to life span, ageing and longevity are also influenced by environmental factors. It will affect the probability of dying because, in an environment in which there is plenty of food, few predators, and little competition, an old "inefficient" animal may survive, whereas in a harsher environment it could not. Environmental factors will also have effects at the tissue and organ level For example, some diets may lead to more rapid wear or decay of mammalian teeth, and this might lead to

malnutrition.

At the molecular level, the environment will affect the type and frequency of molecular accidents. High temperatures may increase the level of metabolic errors in poikilotherms because they increase metabolic rate; ionizing radiation will increase the damage in some types of molecule; a diet deficient in antioxidant may increase the damage caused by free radicals.

The life-span of mammals can be prolonged by restricting the intake of calories. Cutler (1972) has suggested that restricted diets lower specific metabolic rate and slightly lower the temperature of the extremities. This lower metabolic rate will, he suggested, decrease the rate of production of damage, and thus relatively more time will be available for the repair of the damage that is produced.

The Influence Of Genotype : All living systems depend ultimately on the genetic programme hence senescence can be said to be programmed. However, it is probably better to regard senescence as the result of a positive programme for death. At the cellular level, however, it is probable that death of some cell types is programmed and has been selected during evolution. Selection may not favour immortality of cell lineages because an indefinite capacity for cell division would mean that cells which escape from their normal sites would be likely to form tumours capable of growing indefinitely. It has also been suggested that the accuracy of DNA replication and repair will not be allowed to become too good, because too efficient repair and replication enzymes would reduce the rate of production of new genetic variation within a species (Burnet, 1974).

Theories Of Ageing

Over the years, numerous theories have been proposed to explain cause(s) of ageing, some of which have declined in favour of others, others totally abandoned, and still others stimulating further research to establish its authenticity.

The simplest theory of ageing states that it is governed in a major way by an organism's genetic inheritance or 'genetic time-table' or "genetic clock". It is because of this genetic clock that different sp. of animals have different maximum life-span - *Drosophila* of 40 days, Dogs of 20 years, humans of 90±10 years, and giant tortoises 180 years. Many research workers believe that every organism has "ageing genes" that control its rate of ageing

and thus its maximum life-span, though no one has identified such genes. Nevertheless, a question remains to be solved whether such genes reside in all the cells or is it present in certain organs which initiate process of ageing. In answering this question, theories are broadly divided in following categories :

1. Cellular Theories Of Ageing

Theories that attempt to explain the ageing process as result of defective intracellular processes are based upon several assumptions. The underlying assumption is that there is limited frequency of error in the biochemical operation of every cell. Over a period of time these errors might accumulate to produce a cell with defective function or they might result in the death of the cell. Genetic blueprint, theory of free-radical and error theories are main theories.

1. Genetic Blueprint & Hayflick Limit

The best evidence that individual cells undergo deterioration has been obtained with cells growing in culture. In 1965, it was reported by Leonard Hayflick that when human lung fibroblasts are followed in tissue culture, the number of divisions these cells can undergo is limited. Hayflick found that the number of cell divisions is roughly related to the age and life span of the animal from which tissue is taken. Fibroblasts from human divided 50± times, cells taken after birth divided only 20 to 30 times. Human foetal cells frozen after a certain number of cell-divisions went on to complete the normal (about 50) number of cell divisions when they were revived even years later. Also, the longer the life-span of a species, the greater was the number of divisions of fibroblast cells. And, when cultured cells did proliferate indefinitely, they were found to be abnormal or cancer cells.

In vivo studies have also been performed to substantiate contentions of in vitro studies that species-dependent cell divisions has finite numbers. Daniel & his colleagues (1968) at University of California (USA) used mouse mammary epithelial cells that they transplanted serially into mammary fat pads of other female mice. The recipient had the same genetic make up as the donors, and the fat pad is the site where these cells normally grow. The investigators found that even in this highly physiological conditions the cells showed a characteristic decline in proliferative capacity even with repeated transplantation. This was done to remove possibility that senescene of surrounding tissue may not be able to affect the transplanted cell. From results of tissue

culture and cell transplantation studies, Hayflick concluded that senescence is due to the loss of cell functions that occurs before cells reach their maximum division point. Such conclusions are substantiated by both in vitro and in vivo studies as discussed earlier.

The results obtained so far from this study of cells in culture & transplantation have led several workers to suggest that there is a built in biological clock which decides the cell's capacity to divide (Hayflick limit) as well as the average life span of a species. If this is so, two questions arise - firstly, where is the clock located in the cell, and, secondly, is it located in all the cells of the body? From results of studies based on the fusion of cytoplasm from young cells with old nucleus and vice versa, and by determining the number of cell divisions that follow Hayflick & his colleagues think that the "clock" is located in the nucleus of the cell. Regarding answer to the second question, it is believed that senescence sets in tissues that are more sensitive and it then secondarily affect the other tissues of the body in destructive way. The potential victim in this case may be one or more of the endocrine glands whose effects on the function of whole body is well-known. Another potential victim may be lymphoid system which has received a great deal of attention in recent years.

2. Theory Of Free Radical Reactions

Such theories propose that free radicals produced in the cells, particularly those of oxygen, cause much damage to cell and bring about death of the cell. In aerobic cells, certain enzymatic reactions are responsible for generating a superoxide radical (O_2) as a free intermediate. In the presence of water, this species is converted into highly reactive hydroperoxyl radical (HO_2). These radicals react primarily with unsaturated lipids to produce 'age-pigments' lipofuscin. It is established that the concentration of lipofuscin increases in the cells as a person grows older. But how these pigments are involved in the damaging processes is yet to be worked out in detail. The free radicals may be specially harmful when they attack unsaturated lipids in the cell membrane. The resulting altered lipids may seriously impede the diffusion of nutrients into the cell and extrusion of waste products out of the cell. This might be associated with cell-senescence or cell-death.

Lester Packer and James R.Smith have provided evidence in support of "free-radical' theory. Vit E is a natural antioxidant, and its addition to the human embryonic cells in culture doubled the number of times of divisions of cells. It is well known that vit E is

fully capable of interfering with reactions mediated by free radical. Packer has pointed out that the results of his study do not necessarily conflict with the idea that the cells have a built in 'biological clock' that determines the number of cell-doublings. He contends that they may have such a programmed potential but that it is not always attained. Addition of anti-oxidant such as vit E to the environment may allow the cells to reach their full potential for dividing and thus achieve an apparently lenthened life-span.

3. The "Error" Theories

Cell generally functions in normal ways but errors do take place. Such errors might occur at the plane of DNA, RNA protein synthesizing mechanisms and enzymatic reactions.

A. Errors At The Level Of DNA : Though DNA replicates very accurately, it may commit errors which pile up in the DNA as individual ages. If the damage to DNA is too subtle for the DNA-repair system to detect or if it accumulates faster than the repair system functions, the cells will gradually be defective in essential control systems or enzymes. Thus senescence steps in.

If mutations in the somatic cells are involved in senescence, then the efficiency of DNA-repair mechanism may help determine susceptibility to ageing. There is evidence that the efficacy of DNA-repair correlates with longevity. Greater the efficacy of DNA-repair mechanism, longer is the life-span of animal.

Ronald Hart & Richard Setlow have measured the extent of DNA- repair in culture fibroblast from seven species. The cells were first exposed to the radiation,a known inducer of DNA damage. Human, elephant and bovine fibroblasts were almost five times more active in repairing their DNA than were fibroblast from rats, mice and shrews.

B. The "Error Catastrophe" Theory : Accumulation of simple random somatic mutations may not prove as fatal to the cell as "error catastrophe" -- a concept proposed by Leslie Orgel. In this theory it is pointed out that certain types of errors are likely to produce a great numbers of subsequent errors. DNA polymerase enzyme synthesizes new DNA during replication of DNA. A mutation in the DNA polymerase gene will give rise to an enzyme that will make further mistakes during replication. Thus error in the replication would be "error catastrophe" Such defective enzymes will soon fill the entire cell with a spectrum of defective proteins.

Robin Holliday and his associates have provided evidence for the theory. They could shorten the life-span of adult fruit flies

by feeding them a variety of amino acid analogues eg. P-fluorophenylalanine and methionine to the larvae. These amino acid analogues substitute phenylalanine & methionine respectively in the proteins and interfere with the functions of proteins. Holliday has also detected abnormal forms of enzymes in ageing fibroblast, others have observed reduced specific activities (activity per unit of enzyme protein) of some enzymes isolated from aged organisms. Some workers postulate that error catastrophe are intentionally planned by "ageing genes" that limit the lifespan. Still it is a speculation.

C. Theory Of Missing Factors : Dr. M.S. Kanungo of B.H.U (India), a leading gerontologist of India and Some other workers hold the mechanism to operate in different ways. According to them, the reproductive phase of an individual deplete certain factors essential for maintenance of adulthood and reproductive phase, and result in senescence and ageing. Thus ageing may not be due to any specific gene(s) for ageing but rather may be due to non functioning of genes necessary for the maintenance of adulthood that may be brought about by several endogenous factors produced during adulthood. Exogenous factors like malnutrition and stress may advance the onset of ageing and also accelerate the rate of ageing. ★

II. Extra Cellular And Pace-maker Theories

Important theories in this group are - Collagen theory, Immunological theory and Brain theory

1. Collagen Theory : A significant part of individual's body is composed of extracellular substances that chiefly include mucopolysaccharides and fibrous protiens, chiefly Collagen and Clastin. Collagen is estimated to account for upto 40 % of the body protiens, is present in extracellular spaces of virtually all tissues, and has been suggested as the primary site for age-related changes. ★

Collagen is made up of three polypeptide chains wound into a superhelix. The three chains are stabilised by noncovalent bonds. As age advances, the three chains are further stabilised by covalent bonds making them practically insoluble. Collagen surrounds the tissue and is virtually in between cell and its environment. Because of changes in properties of Collagen, a healthy intracellular composition is difficult to maintain as the cell receives O_2, nutrition, ions, hormones etc from its environment and

release Co_2 and other waste products in it and Collagen is the substance that stands in between the cell and its environment.

2. Immunological Theory : Body fights foreign agents or antigens, like microorganisms, by means of two types of lymphocytes - B-lymphocytes (Bone marrow - dependent) and T-lymphcytes (Thymus-depedent). Antibodies by B-lymphocytes bind with antigens and inactive them and T-lymphocytes directly attack them and destroy them. The immune system include spleen, lymph nodes, bone marrow and thymus. Several workers, including Burnet of Australia & Walford of USA, have shown that efficiency of immune system deacreses after attainment of adulthood. Amount of B-antibodies produced in response to certain antigens in old rats is one fifth to that produced in the young rats. A similar decrease in the functional ability has also been observed for T-lymphocytes. T-lymphocytes help in B-lymphocyte's differentiation and any retrogressive changes in T-lymphocytes has profound effects on the B-lymphocytes : a fact that seems to be responsible for age-related decline in immunological system. Since T-lymphocyte is thymus-dependent for its differentiation, it seems that thymus gland is Pace-maker for the whole body, and its atrophy seems to be programmed event that leads to ageing of the animal. It is well-known that thymus begins to atrophy shortly after puberty in humans ★

The another way in which immunity can determine ageing is through "autoimmune" response. As age advances several somatic mutations seem to occur in antibody and body's immune system is unable to identify self from foreign and produces antibodies against body's own tissues. Several old age diseases such as arthritis, Addison's disease etc are believed to be due to autoimmune reactions. However, how and why decay occurs in the immune system is not yet completely known ▲

3. Brain As The Pace-maker : Since the endocrine and the nervous systems act often together to enable an organism to adapt to environmental changes, these systems are also being examined as possible sites of ageing pace-maker. It has been observed by Finch, Merites and a host of other workers that if ovary of a old rat is transplanted into young one it starts secreting oestrogens and begin to function normally. The same result can be obtained by stimulating the old rat's brain electrically or pharmacologically by administering drugs like L-dopa. L-dopa is known to build up levels of substances that are called neurotransmitters (Catecholamines in this case). According to

current models, Catecholamines are released at nerve-endings in the hypothalamic section of the brain that trigger the discharge of hypothalamic-releasing factors, which, in turn, act on the pituitary to secrete its hormones. The fact that the electrical or pharmacological stimulation of the brain can reawaken the ovaries of female rats at least indicates that the brain is a key locus of ageing in reproductive senescence. ★

It has been found that the rate of catecholamine synthesis is reduced in old mice. In humans, Parkinson's disease, which is associated with 50-80% losses of dopamine, a precursor of catecholamine, is inflicted after age of 40 years. ★

There is evidence that a number of other phenomena of ageing, too, may derive from altered catecholamines metabolism in the brain, for the hypothalamus controls body-temperature, water balance, blood-pressure, heart-rate. Besides, it influences pituitary hormones, which in turn, influence thyroid & adrenal cortex through TSH & ACTH. This is in addition to influence of pituitary on gonads. In older men, these hormones are progressively secreted in small quantities, affecting a series of functions including mental & physical growith and immune system. ★

The brain contains receptors (proteins) that bind specific adrenal and gonadal steroids and transport them to the cell-nucleus. There occurs a reduced receptor content during ageing, resulting in decreased cellular responsiveness to hormones. It is this reason that probably explains altered hormonal functions of brain & hypothalamus. Thus sets in vicious circle - reduced responsiveness of brain - reduced brain chemicals - reduced pituitary hormones - reduced thyroids and adrenal hormones - reduced responsiveness of brain.

III. Combined Theory

In a recent symposium sponsered by the American Association for the advancement of science, Bernard L.Strehler reconciled many theories by postulating ageing as a process programmed by the action of 'on-off switches' that reside in the genetic machinery. The effect is that one set of genes after another are swithced on to produce special products (enzymes, hormones, antibodies, structural proteins etc) as individual matures. Such gene-coded information is not available for use once the "off switch" genes have been activated. The specific off-switch that appears to be central is that which prevents the very body cells

H
P.
G.

on-off switches — genetic machinery

found in the thymus, brain, endocrine glands and heart from dividing. ★

Influence Of Diet

It has been shown by McCay that a high protein diet early in life followed later by low protein diet prolonged life at least in rats. ★★

Later on, it has been shown by Ros & Brass that low intake of calorie in first half of life increases life-span. It is theorized that a restricted diet in early life suppresses imuune-system. This probably delays the onset of autoimmune diseases in later life. Intake of Vit E, the natural lipid anti-oxidant, reduces chances of free-radical reactions and has been claimed to enhance life-span. ★

B13K - AKT - mTOR Cascade

There is a Kinase enzyme TOR which is related to regulation of protein translation, cell growth and autophagy. It is part of a trigger cascade. B13K-AKT-mTOR. Reducing TOR functions is known to extend life of yeast, worms and flies. It is now proved with the rats also. In several experiments. TOR functioning was reduced by anti-cancer drug Rapamycin which enhanced life span of rat by 14%.

CONCEPT OF AGEING GENES

A gene, called **daf-2,** has been identified in *coenorhabditis elegance* mutation of which increases life-span of the worm by 33% Similarly, a gene called **methuselah** has been discovered in *Drosophila* with same effect. It is considered that such ageing genes become active at appropriate time, releases hormone and cause senescence to appear all over the body.

Somapalli rediscovered

It has been reported in August 2010 that Somapalli, the wonder drug for enhancing life-expectancy, supposed to have become extinct, has been rediscovered in Riwa forest, Rajasthan and efforts for its largescale production has been initiated by department of forest, Rajasthan. Scientists will try to find out mechanism of action of this wonder vedic drug against ageing.

Comb

→ — process

PHYSIOLOGICAL VARIATIONS

1. Hb-Level : Haemoglobin is present in RBC of Blood. It is made up of haem group (containing iron) and 4 protein chains. RBC concentrate haemoglobin in the cell-fluid upto approximately 34 gm/dl. The level of Hb never rises above this because it is the metabolic limit of the RBC. In normal persons, there is always a maximum level of Hb in the RBC. Hb level varies with sex, being slightly higher in males than in females. When there is normal level of RBC, the amount of haemoglobin contained in the blood of adult male contains 16 grams of haemoglobin per deciletre of blood whereas those of adult female contains 14 gms/dl. Such a level of Hb may not be achieved and in many studies of Indian populations, it has been found to be 12 gm/dl. for adult mates and 10 gm/dl for females. The difference may be attributed to monthly blood loss due to menstruation in females (Hurkat & Mathur,1976 Talwar,1989) In addition females have lesser number of RBC in comparison to males. According to Allan and Girdwood (1982) the haemoglobin level of 12 gm/dl is to be regarded as anaemic in adult male but normal in adult female.

Pearson et.al.(1971). Owen et.al.(1973), Owen and Owen Yanochick (1977), Garn et.al. (1977) Verma(1976,1989), Chattopadhyay (1992), Pandey et.al. (1994) etc have studied Hb level in different populations. In fact there has been growing interest in the study of ethnographical diversities in Hb-level because Hb-level is correlated to the activity-level of the population. Those cultures that demand higher activity levels have selective influence on the Hb-level. At the same time, Hb-level is an indicator of nutritional state of the individuals of a population. Pearson et.al. (1971) Owen (1977) and others have found in a survey of Quebec (Canada) that Hb-level of 15.3 gm/dl is achieved by the male at the age of 20 and it is maintained upto 60 years of age. In females, the highest level of Hb-level is 13.5 gm/dl which is attained at the age of 10-14 when it is similar to Hb-level of boys. Hence, there is no much difference in the Hb-level in pre-pubescent boys and girls. After the age of 14, however, boys improve and attain a level of 15.3 gm/dl, where as females remain stagnant more or less at 13.5 gm/dl. This difference of about 2 gm/dl. in Canadian males and females is due probably to menstrual losses in females. There is American data too for the Missouri. USA. It shows the same trend - upto 10-14 years, both males and females are similar in Hb-level, being 13.9 and 13.8 gm/dl. for males and females. After puberty, it increases to 15

gm/dl. for boys and decreases to 13.3 gm/dl. for girls. There have been quite a few studies of Hb-level in our country too. Verma (1976) conducted survey of great Andamanese in which both males and females were found to be anaemic, and proportion of such anaemics in both males and females exceeded 30%. In a recent survey by Chattopadhyay (1992) it has been found that 50% females are anaemic with haemoglobin level less that 8.4 gm/dl blood. No case of anaemia among the adult male population has been reported. However, among children 57% male and 62.5% female children were anaemic (Chattopadhyay 1992). In a study of oraon tribe, Pandey et.al. (1994) have found that Hb-level in them varies between 60.83% to 74.25%.

There has been found in most ethnic groups gradual rise in the Hb-level with age upto about 30 years. In Americans, a high value is maintained throughout life and there is a gentle fall only in the old age.

The distribution of average haemoglobin percentage in the Indian sample agrees with the hypothesis of a secular trend of increase. According to the hypothesis, the rise in Hb-level currently even in the primitive societies is greater than the level prevalent in advanced societies several years ago, and this trend in increase is true for all ethnic groups.

2. Blood-Pressure : The blood pumped by heart into blood vessels for its distribution to different parts of the body must leave the heart at some pressure because it has to overcome the resistance offered by frictional and other forces. The pressure at which blood leaves heart is called systolic blood pressure (SBP) and it gives an estimate of contractility of the heart. As heart expands or relaxes, this pressure drops, which gives a measure of diastolic blood pressure (DBP). It is at this pressure that heart receives blood. A rise in the SBP indicate increased contraction whereas a rise in the DBP indicates decreased relaxation of the heart, both being harmful if cross optimum levels. Blood-pressure is indicated in fraction : the upper number indicating SBP and the lower number indicating DBP. Though a pressure of 120/80 is considered an average for the adults, values as low as 115/70 is also considered normal. For the SBP, 100 plus age is also considered normal. Researches show positive correlation between blood-pressure and age (Reddy et.al.1991), Sex (Celine and Mathur, 1979), heredity (Nirmala and Chengal Reddy.1992), body composition (Sambhasiva Rao,1983) and social status (Srivastava et.al.1977)

Knowledge about blood-pressure at the population level is of utmost importance in the assessment of health status, particularly in the detection of cardiovascular diseases. The variations in blood pressure according to age is high during growth and development upto adolescent, thereafter it shows a rhythmic variations on the daily basis. The blood pressure in the neonates during first day averages 70/50. There occurs increase in blood pressure during the next several months to approximately 90/60. The rate of increase is higher during this period. Thereafter, there is increase in blood pressure with decreased rate until the adult blood pressure of 115/70 is attained at adolescence. Thereafter, it remains more or less same throughout the adult period.

Using family studies, it has been possible to underline factors for blood pressure variation in a population. it has been estimated that 16% of blood pressure variation is due to environmental factors, 48 percent to additive genetic factors, and 36 percent to dominance. Heredity is indicated in causation of blood-pressure because, it has been shown to run in families, though environement seems to be the precipitating agent.

According to Kaplan (1978), the populations can be arranged into three groups on the basis of variation of the blood pressure :

a. Hypertensives : Systolic blood pressure > 160 mm Hg
Diastolic blood pressure > 95 mm Hg

b. Borderline cases : S.B.P 140 - 160 mm Hg
D.B.P. 90 - 95 mm Hg

c. Normotensives : S.B.P <140 mm Hg
D.B.P < 90 mm Hg

In majority of the rural Indian population surveyed, the percentage of the normotensives have been almost always found to be more that 95%. In many cases, percentage of normo fensives and hypertensives has been found to be higher than borderline. This indicates that in majority of the populations persons either are normotensives or hypertensives. The cardiovascular system perhaps has the ability, because of homeostatic mechanisms, to sustain changes due to stress and strain of environment. This seems to have a threshold limit. Once it is crossed there is no scope of return and a normotensive becomes hypertensive. This may be reason for low percentage of borderline compared to hypertensive.

① Rural India → normotensives Low % of borderline
② Industrial popl" → Hypertensives.

Such conclusions have been arrived at in many studies. V.Rami Reddi et.al. (1995) in their populational studies of blood pressure variation in rural Andhra Pradesh have arrived at the same conclusion. The proportion of normotensives, borderline and hypertensive was 96:2:2 for systolic blood pressure and 97:0.3:2.7 for diastolic blood pressure.

On the contrary, studies conducted by Reddy et.al. (1992) indicate that in industrialised population, the proportion of normotensive in comparison to hypertensive is not so high Hypertensives are around 5% subjects showing increase in both SBP and diastolic blood pressure. Another feature of the industrialised society is that there can be found in such population a small but significant group of borderline. According to Reddy (1992) this is probably because of homeostatic mechanisms are disturbed in such societies due to nutritional and life style reasons. Among the nutritional reasons, absence of green vegetables and fruits, and inclusion of fat to a great extent in the diet has been the most glaring reasons for the increase in percentage of border-line cases and hypertensive.

In cases of both rural and urban populations, it has been found by Reddy et.al. (1990) and V.Rami Reddy et.al. (1995) that the variations of the blood pressure tends to be lower in the household samples than that of hospital. According to them, it is probably due to natural settings of the house, free from anxiety and tension. Blood pressure, as it is a multifactoral condition, may tend to recover in situations of normal, tension-free, emotions.

Scientists associated with such populational studies of blood pressure variation outside India are Boyce Attenborough, Harrison, Thornabrook and Sinneff. The group has been involved in recording populational variation in blood pressure since 1970. They have analysed populations of New Guinea etc. and have reached to the same conclusions that, in addition to heredity, diet and stress and strain of life are the two most important causative environmental factors of high blood-pressure.

3. Sensory Variation : There has been some populational studies of physiological variations that include survey of different sensory mechanisms. Among the various sensory mechanisms, the most thoroughly surveyed are ability to taste phenythiocarbamide and red and green colourblindness. The ability to taste PTC is an autosomal polymorphic trait (Vogel and Motulsky,198(Tasters with genotypes TT, Tt have the ability to taste the substance while non tasters are homozygous for the recessive allele 't'.

The defective colour vision has long been used as a genetic marker in th study of human variation. Red-green colour blindness is an x-linked trait in which individuals fail to distinguish red and green from other colours. Various populations inside and outside our country have been surveyed, for in Turkey (Bokesoy and Togan,1987) Balkans (Ibraimov and Khimov, 1979) Nigeria (Scott Emuakpor et.al.1975), Myanmar (Sint and Maya-Tu,1979) etc. In India, such studies have mainly been conducted in South India by Veerraju (1973), Rao and Reddy (1973), Naidu (1977), Naidu et.al.(1988), Shanthi Devi et.al. (1995) etc.

Most of the studies related to PTC tasting have found sex-differences in the trait : females are found to be more sensitive to the taste of PTC than males and the difference is statistically significance. In Balkan, Burmese and Nigerian population though females are more sensitive than males, the difference does not appear to be significant one. Muslims of India also do not show sex differences in ability to PTC tasting.

4. Fat Level : Recent studies have indicated that fat, particularly sub-cutaneous fat, is uniquely distributed over the body. Both genetics and environment play significant role in establishing fat level. Fat level of body, especially sub cutaneous fat, has unique role in heat and cold-tolerance. Sub cutaneous fat is a sort of covering that conserves core-heat. Thus, in warm climates the sub cutaneous fat layer seems to be thin allowing loss of heat. Studies indicated that core temperature of larger men is not higher than smaller men if both have similar amount of sub cutaneous fat. The sub cutaneous fat is more important in cold climates than body-size. It has been found in a study that minimum rectal temperature elicited by nude adults depend significantly upon the measure of their body fat (Daniels and Baker.1961). In another study by Hanna (1976) of Amerindians, it was found that women elicit higher-rectal temperature than children or males because of their higher fat level when they were made to sleep at below freezing temperature. Measurements of sub cutaneous fat is accomplished by a special caliper. Skin along with fat is pinched away from underlying muscle and caliper is applied to it. This gives an estimate of sub cutaneous fat.

There are age-related changes in the sub cutaneous fat layer. Sub-cutaneous fat begins to be laid down in the foetus at about 34 weeks and increases from then on until the birth, and from birth until 9 months of age when a peak of neonatal is reached. This peak value of fat level can be attained earlier (in six

months) or later (13 to 15 months)

From 9 months, the fat level show negative velocity which continues upto the age of 6 or 8 years when the child attains maximum of prepubescent increase in height. It has been proposed that this decrease in fat-level is due to the action of Growth hormone which brings about breakdown of fat and causes growth. The fact is corroborated by the evidence that those children that show lower GH-level show higher level of fat deposition. This decrease in fat level consists of both fat-width and cross-sectional areas. As bone and muscles enlarge in cross-sectional areas with age, there is thus reduction in the cross-sectional areas of the fat which is present as a ring around bone and muscles.

There is sex-differences also in this negative velocity of fat-level during childhood. While both boys and girls show reduction in fat-level upto the age of 8, the decrease is less in girls than in boys so that by 8 years of age girls come to have more sub cutaneous fat than the boys.

The period between 8 years upto puberty is marked by increase in fat level in both the sexes and a difference in the sexes with respect to the fat level is marked only about at the time of adolescence. At adolescence, there is temporary halt or slight reduction in trunk fat and significant reduction in limb fat in case of boys. Such reductions are not gained back until 20 years of age.

In case of girls, however, there is slight halting of limb-fat increase, but no loss and the trunk fat shows constant increase. The deposition of the sub cutaneous fat in the females result in erotic figures and may influence selection.

The sub cutaneous fat, deposited in the adipose tissue, is not haphazard but shows a definite pattern on the body. Thus fat-level shows high saturations in subscapular, abdominal region in trunk, and arm, thigh and buttocks, calf in the limbs. Fat-level of an individual depend upon the total number of fat-cells present in the region and the degree to which these cells are filled up with fat. There are indications that the first factor depend on genetics of an individual and the second on the environmental factors. it is unnecessary to mention that in absence of the first factor, the second factor is constrained. That the fat deposition has some genetic element is proved by the study of fat-distribution in Bushman and Hottentots. It has been found that a significant amount of fat is deposited in their thighs and buttocks. There are

many ethnic groups that inhabit similar environment but do not show presence of such fat depots. Hence, it can be concluded that genetics not only determines the number of fat cells but their characteristic distribution over the body.

Role of Adiposity in blood pressure variation has been studied for many populations. Blair et.al. (1984) from their study and by reviewing other studies reported that total body fat appears to be a less important indicator of health than the pattern of fat distribution. Moreover, upper body fat is more closely associated with high blood pressure compared to lower body fat. Blair et.al. (1988) have reported that regardless of age and the total amount of body fat, sub-cutaneous fat on the trunk is more highly related to coronary risk factors than sub cutaneous fat on the extremities. Abraham (1971) has reported that hypertension and cardiovascular, renal disease are more common in those persons who became overweight in adulthood. Tyroler et.al.(1975) has also reported the close association of weight change in adulthood and a change in blood-pressure. There are no dearth of research papers indicating significant association between high fat level and blood pressure (Blair et.al.1984 Weinsier et.al. 1985, white et.al.1986; Baumgarther et.al.1987; Shear et.al.1987; Selby et.al.1989; Adams et.al.1990).

Nirmala et.al.(1993) have studied relationship between different measures of adiposity and blood pressure to ascertain the relationship between blood pressure and fat-level in a single population with different life style in Andhra Pradesh (India). It has been found that

" Centripetal fat distribution involves increase in deep, intraabdominal adipose tissues which are more active metabolically than subcutaneous adipose tissue "

Brown fat and obesity

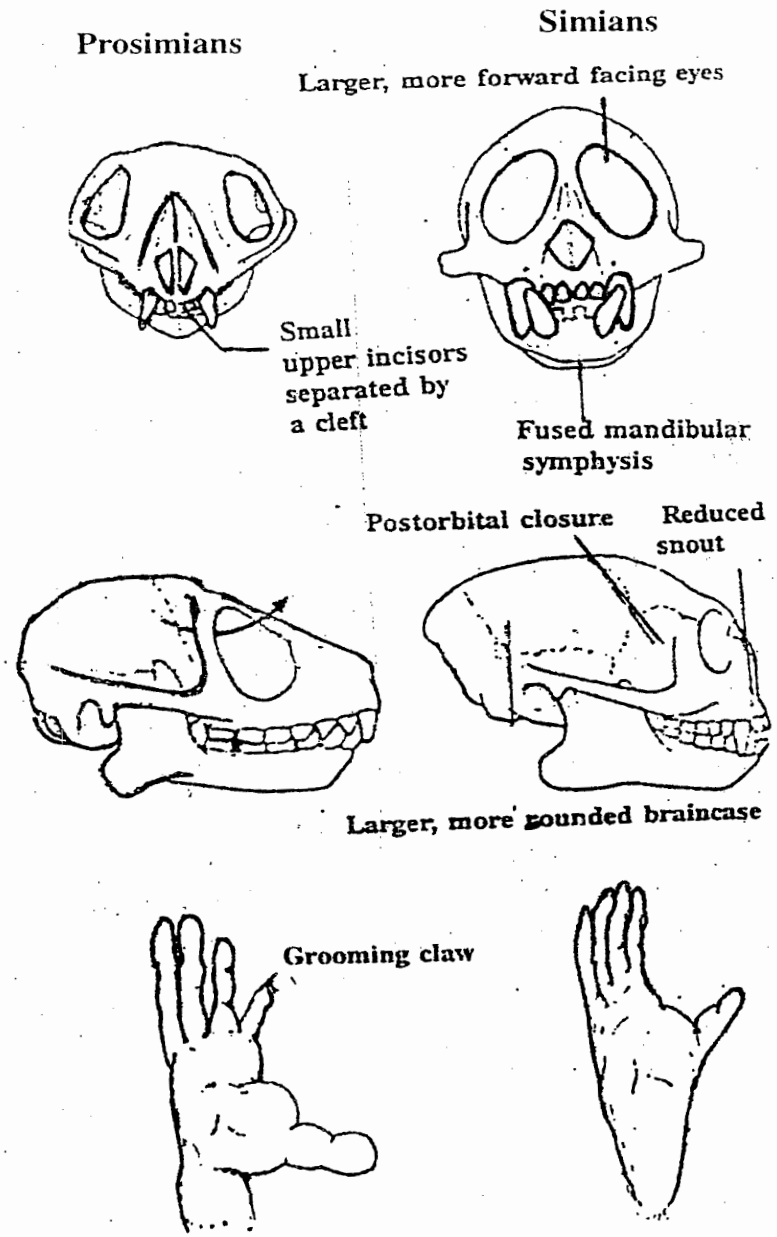
Scientists at the Harvard medical school, Boston have reported in nature (August 21, 2008) that brown fat, which is burnt to generate body heat, is different from the common white fat. Brown fat cells share a developmental pathway with muscle cells. Presence of a protein factor Bone morphogenetic protein 7 (BMP7), promotes brown fat development. Similarly, in presence of a transcriptional factor PRDM16, brown fat is produced from fat precursor cells. In its absence muscle cells are formed. It is possible to treat obesity by mimicking these pathway.

CLASSIFICATION OF PRIMATES

SUBORDER	INFRAORDER	SUPERFAMILY	FAMILY	SUBFAMILY
PROSIMII (prosimians)	PLESIADAPIFORMES (archaic primates)		Plesiadapidae	
			Paromomyidae	
			Carpolestidae	
			Picrodontidae	
			Microsyopidae	
			Saxonellidae	
	LEMURIFORMES (lemuriforms)	ADAPOIDEA	Adapidae (lemur-like prmates)	Adapinae
				Notharctinae
		LEMUROIDEA (lemurs)	Cheirogaleidae (mouse and dwarf lemurs)	
			Lemuriade	Lemurinae (true lemurs)
			Indridae (indri group)	
			Daubentoniidae (aye-aye)	
			Megaladapidae	
	LORISIFORMES (lorisiforms)	LORISOIDEA (loris group)	Lorisidae	Lorisinae (lorises)
				Galaginae (bushbabies)
	TARSIIFORMES (tarsiers)	TARSIOIDEA	Omomyidae (tarsier-like primates)	Omomyinae
				Microchoerinae
				Anaptomorphinae
			Tarsiidae (tarsiers)	

CLASSIFICATION OF PRIMATES

SUBORDER	INFRAORDER	SUPERFAMILY	FAMILY	SUBFAMILY
ANTHROPOIDEA (simians or anthropoids)	PLATYRRHINI (New World Simians)	CEBOIDEA (New World monkeys)	Cebidae (true monkeys)	Cebinae (capuchins etc)
				Aotinae (Owl monkeys etc.)
				Atelinae (spider monkeys etc.)
				Alouattinae (howler monkeys)
				Pitheciinae (sakis etc)
				Cebupithecinae (Goeldi's monkey)
			Callitrichidae (marmosets and tamarins)	
	CATARRHINI (Old World Simians)	CERCOPITHECOIDEA (Old World monkeys)	Cercopithecidae	Parapithecinae
				Victoriapithecinae
				Cercopithecinae (check-pouched monkey)
				Colobinae (leaf monkeys)
		HOMINOIDEA (apes and humans)	Oreopithecidae	
			Hylobatidae (gibbons)	Pliopithecinae
				Hylobatinae
			Pongidae (great apes)	Dryopithecinae
				Ponginae
			Hominidae (hominids)	Australopithecinae
				Homininae



The main distinctions between prosimians and simians (anthropoids).

Primates, one of the orders of class mammalia, is characterized by following features-

1. A generalized structure of the limbs with a primitive pentadactyle plan and retention of the clavicle which is reduced or disappeared in some groups.

2. Free mobility of the digits, especially the thumb and the big toe, which are used for grasping purposes.

3. Replacement of sharp, compressed claws by flattened nails which are provided with highly sensitive tactile pads.

4. Short snout or muzzle.

5. Elaboration and perfection of visual apparatus and development of varying degrees of binocular vision.

6. Reduction in the sense of smell and consequent morphological changes.

7. Loss of certain elements of primitive mammalian dentition and preservation of a simple cusp pattern of molar teeth.

8. Progressive expansion and elaboration of the brain and development of cerebral cortex.

9. Progressive and increasingly efficient development of gestational processes particularly those concerned with foetal nourishment.

10. Prolongation of post-natal life-span.

Grade Based Classification (Gradualistic Classification): Classification of Primates has been a bit controversial. Simpson (1945) classified the primates into two sub-orders - Prosimii and Anthropoidea. The system, modified by Simons (1972), and Robert Martin (1990), has been adopted by many physical anthropologists on the ground that it is time-honoured. The system is grade-based because it considers evolutionary-rate as the main basis of classification.

All workers today agree that there are three phyletic groups in primates-lemurs (along with lorises), tarsiers and anthropoids. System of Simpson lumps lemurs and tarsiers together in prosimii and place it against anthropoidea (new world monkeys, old world monkeys, apes and man).

Gradualistic classification by Simpson (1945), modified by Simons (1972), Robert Martin (1990) is as follows :

Sub-order I.prosimii

They have their distribution in the tropical forests of the old world from Africa to Madagascar, South and South-East Asia and Philippines.

1. Arboreal with vertical clinging and leaping movements.
2. Insectivorous or Frugivorous.
3. Muzzle faced.
4. Small brained primates.
5. Naked moist rhinarium in the nose.
6. Upper lip attached to the gums, the facial muscle mobile.
7. Multiple breast pairs.
8. Greater dependence on olfaction.
9. Presence of a toilet claw.

1. **Infraorder Plesiadpiformes** : The infraorder consists entirely of extinct forms and has been discussed with origin & evolution of prosimians.

2. **Infraorder Lemuriformes** : i. They are found in the tropical forests of Africa and the island of Madagascar. Some members inhabit the Indonesian islands and Phillipines.

ii. Lemurs are small animals of the size of cat or mouse, arboreal insectivorous or frugivorous, coated with furry covering and a large bushy tails which are not prehensile but help in balancing.

iii. All digits of the hand and feet with nails except the second digits of hind limb which bear claw (Toilet claw). It is modified nail.

iv. Typical dental formula is 2133/2133. It is divided into five families-

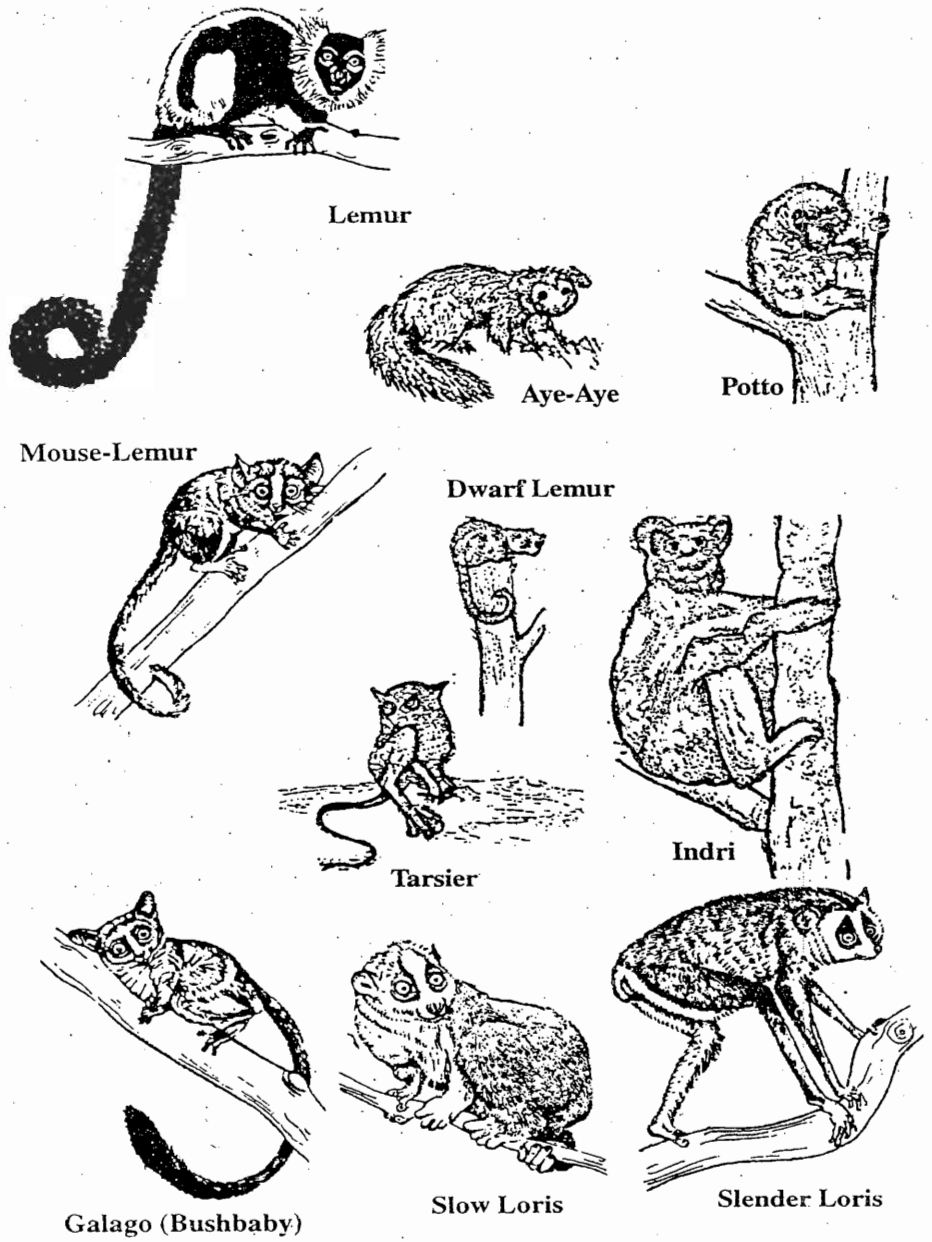
a. Cheirogaleidae : Anterior carotid artery present, upper incisors not reduced, elongated calcaneum and navicular eg. *Phaner, Mirza*. Cheirogaleus (dwarf lemur), Microcebus (mouse lemur).

b. Lemuridae : Full set of dental complement use reserve food of tail eg. *Lemur*.

c. Indriidae : Marked by numerical reduction in dentition, hind limbs are relatively strong. eg. *Propithecus, Indra*.

d. *Daubentonidae* : Large and rodent like incisor teeth & gross reduction of the rest teeth. eg. Aye-Aye (*Daubentonia*)

e. *Megaladapidae* : Specialised mandibular condyle near



SOME PROSIMIANS

jaw, eg. *Lepilemur, Megalada.*

3. **Infraorder Lorisiformes** : The group is differentiated from Lemurs on one ground - Less pneumatization of tympanic floor. It has two sub families

a. **Lorisinae** : Tail is either greatly reduced or absent; limbs are of equal length; slow climbers eg *Loris*, Nycticebus in South Asia; *Perodictus, Arctocebus* in tropical Africa.

b. **Galaginae** : Hind limb modified and elongated for jumping *Galago*, Euoticus..

4. Infraorder Tarsiiformes : 1. It comprises only a single family which has single genus *Tarsius* and are confined to Malayan island eg Sumatra, Sara, Bornee, Celebes, Phillipines. etc.

2. They are small nocturnal and completely arboreal. It can rotate its head 180^0. Another important feature is its salfatory or frog like leaping movement.

3. The second and third digits of the feet bear toilet claws while other digits are provided with flat nails. The claws are not modified nails as is case in Lemurs.

4 The post orbital wall is present. lachrymal foramen is outside the orbit, orbits are large and completely directed forward.

5. Dental formula 2133/2133.

it is divided into two families :

a.Omomyidae (Tarsier-like primates) - It is an extinct group with Sub families Omomyinae, microchoerinae and Anaptomorphinae.

b.Tarsiidae - It includes Tarsiers.

Sub-order II.anthropoidea

1. Arboreal with branchiation or bipedal locomotion or quadrupedalism.

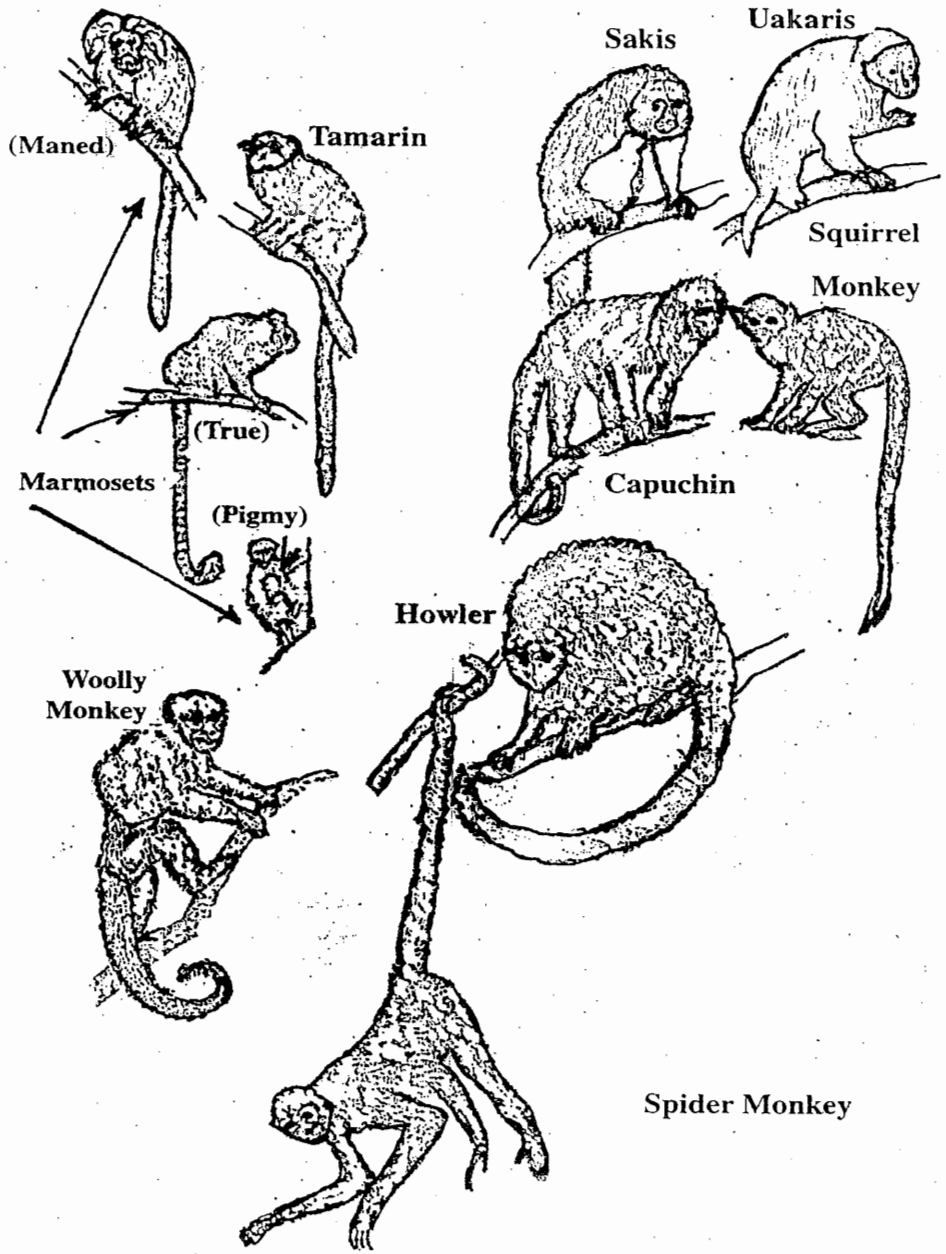
2 Frugivorous or omnivorous.

3 Short-Snouted, forward eyed.

4 Complex brained.

5. Upper lip not cleft and not attached to upper gums.

6 Rhinarium dry and hairy



New World Monkeys

Intra Order - Platyrrhini (New World Simians)

1. Tympanic ring not elongated into tube.
2. Premolars three in number.
3. No Canine-premolar sectorial system.

I Super Family Ceboidea(Or New World Monkeys)

1. They are characterized by their distinct nose shape. They have wise nasal septum separating the outwardly directed nostrile
2. Thumb non-opposable or absent.
3. Tail often prehensile. living in families & groups.
4. Cheek pouches absent.
5. Dental Formula - 2132/2132 or 2133/2133.
6. Retain yolksac in embryo.
7) Tail is modified, sparsely haired below with rat like scale.
8. Enlarged eyes without cones
9. Ear is enlarged and mobile.

It consists of two families

a. Callitrichidae • They are of small size with long prehensile tail. Their body is covered with soft fur. All digits have sharp laterally compressed claws with the exception of the big toe which has flattened nail. Thumb is not opposable, ischial callpsites are present. No third molars. Dental Formula 2132/2132 eg.Marmosets and Tamarins.

b. Cebidae : Members are larger in size. They have prehensile tail, all digits have flat nails and thumb is more opposable. Ischial callosities are absent. Third molars present, but may be reduced. Dental Formula 2133/2133. The family has 6 sub-families -

i. Cebinae - eg. *Cebus*, the Capuchin Monkey.
ii. Aotinae- eg. *Aotus*, the Owl Monkey.
iii. Alouattinae - Spider, Wolly & the howler monkey.
iv. Pithecinae - the Sakis (*Pithecia*)
v. Callimiconinae - eg. *Callimico* (Goeldis' monkey)
vi. Cebupithecinae - the extinct group.

II Infraorder - Catarrhini (Old World Simians)

1. Elongation of tympanic ring into a tube

1. Absence of tail.
2. Interstitial placentation.
3. Presence of vermiform appendix.
4. Sperm mitochondria with few gyres.
5. Very large complex brain.
6. Locomotion by brachiation. quadrupedalism, bipedalism.

a. Family - Hylobatidae

1. Commonly called "lesser apes", they are represented by gibbon and siamang, distributed in the forests of S.E.Asia.

2. Predominantly tree dweller, frugivorous.

3. Both males and females have canine/premolar sectorial complex.

4. Orbits encircled by peculiar thickened rims.

5. Very short faces and reduced jaw cheek teeth.

6. Both arms and legs elongated beyond allometric trends.

7. Live in small family groups. When a juvenile male or female in a family group reaches sexual maturity, the parent of the same sex drives it out. New family groups formed when the ousted gibbon meets another of the opposite sex who has also been driven out. Thus family size is kept small.

8. No sexual dimorphism or behavioural dominance of either sex.

9. Gibbons vocalize beautifully while swinging. This is also a territorial signal that helps to space the family groups.

10. *Symphalangus* (Siamang) differ from gibbons in having larger body weight, Shorter trunk, broader chest, presence of throat pouches etc.

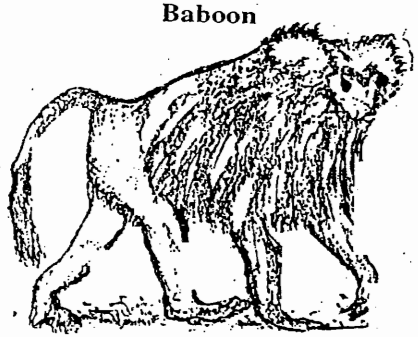
11. Lesser apes are characterised by presence of ischial callosities (also occasionally present in the Ponginae).

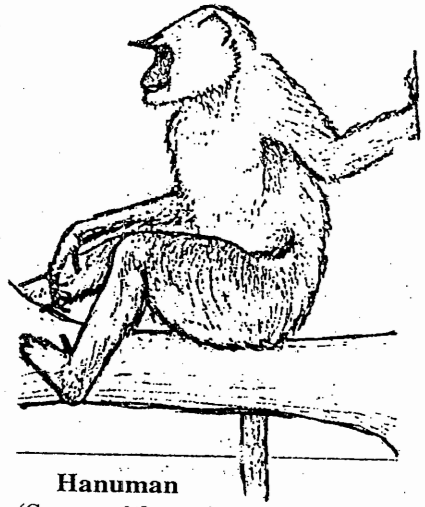
12. It contains two genera : *Hylobates* or common gibbon, with six species : (*H. concolon, H. Lar, H. agilis, H. moloch, H. hoolock and H. klozii)*; and *Symphalangus* or siamang, a genus with a single species, *S.syndactylus* The Hylobatinae inhabit Southeastern Asia. Sumatra, Java Borneo, Hainan, and Formosa.

b. Family Pongidae : The pongids are the apes and comprise the orangutan, gorillas and chimpanzees, referred to as "great apes". They are predominantly quadrupedal (Knuckle walker).

Gelada (male)

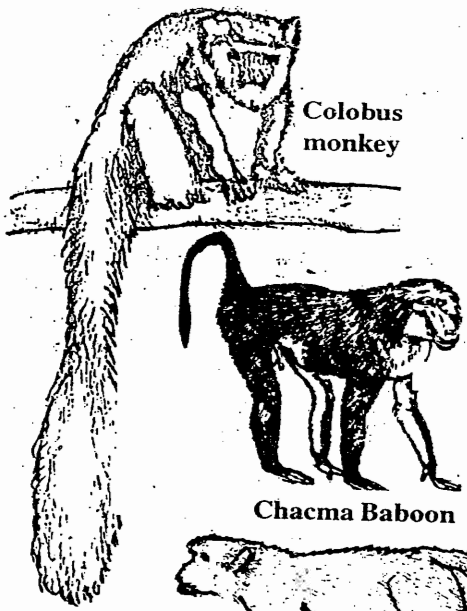
Hamadryas Baboon



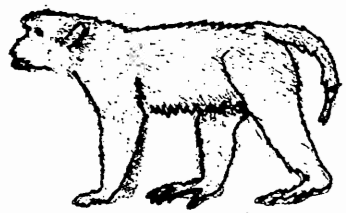


Hanuman (Semnopithecus)

Colobus monkey



Chacma Baboon



Rhesus Monkey

Old World Monkeys

1. Absence of tail.
2. Interstitial placentation.
3. Presence of vermiform appendix.
4. Sperm mitochondria with few gyres
5. Very large complex brain.
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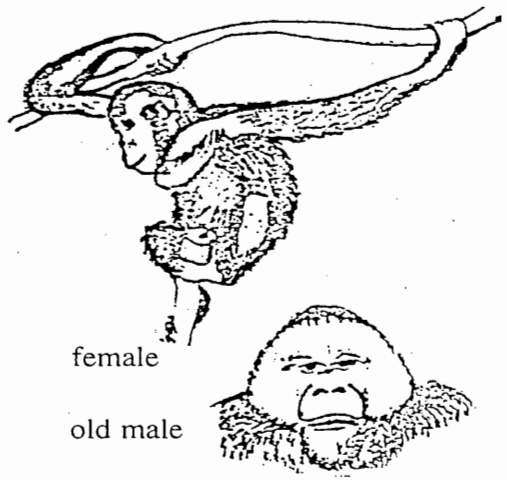
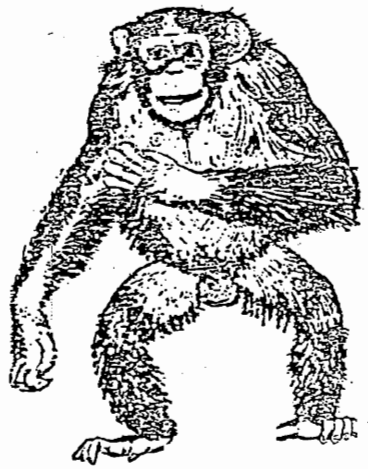
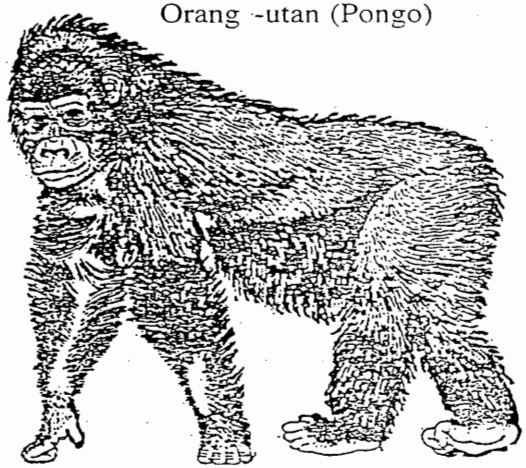
Gibbon (Hylobates)



Orang -utan (Pongo)



Chimpanzee (Pan)



Gorilla (Gorilla)

Fig : Some Apes

on land, capable of brachiation on the trees, males with canine/premolar sectorial complex. The different groups are differentiated more on behaviour.

Pongo Or Orangutan

The Orang-utan (*Pongo pygmaeus*) has a heavy body, short and curved legs, narrow hands and rudimentry thumbs; in the male, height reaches 1.50m with an average weight of 60 to 80 kg. Its present habitat is restricted to Sumatra and Borneo but during the Pleistocene it was found in southern China, Indochina and Java. In Borneo, they are found in rain forests and in Sumatra in mountainous regions. They are arboreal and predominantly frugivorous. They are found at all levels of forests and their night nest is found at 6-24 metres. Sexual dimorphism is well marked in orangs: males are 37" long and weigh 77 kg. Whereas females are 30.5" long and weigh 37 kg. Bornean male resemble Budha where as Sumatran males, with its moustache and beard, resemble Chinese. Brow-ridges are weak with a projecting muzzle. Adult males have throat pouch that houses laryngeal air-sacs which extend under arm and over the shoulders. Orbits are long, narrow and closely set with small, separate brow-ridges.

Their large size precludes brachiation and all the four limbs are used on branches. A quadrupedal gait is used on land and bipedalism is marked in captivity. It has long arms and short lets (Intermembral Index 145). Thumb and big toe are reduced.

Orangs are relatively unsocial, the common group being an adult female and one or two young male. The adult male is the patriarch of a territorial domain that overlaps the ranges of several females. The males use loud calls for spacing mechanisms. Life-span is about 50 years.

Gorilla

The Gorilla (*Gorilla gorilla*) is the largest of all the Primates, sometimes reaching a height of 1.80 m, with an average weight of 200 kg. The forelimbs are considerably longer than the hind and the hands have short fingers and small thumbs. The hind limbs are relatively short and habitually bent at the knees. Gorillas are not entirely terrestrial in their habits, for the smaller ones occasionally climb trees in which they progress by brachiation and by walking erect while grasping the branches above them with their hands. The two subspecies are (a) *G.g. gorilla* in the West African lowlands or coastal gorilla which inhabits Gabon, cameroons and the French Congo; (b) *G.g. beringei*, or mountain gorilla which

lives in the wooded high lands or the eastern Congo, along the boundary with Uganda and Tanganyika. An eastern low land gorilla, *G.g. graueri* is also recognised from Zaire. Male Gorillas are almost wholly terrestrial though females and younger ones are arboreal. They are basically frugivorous though they often eat leaves, bark and insects etc. Adult females are half the weight of males. The western gorilla has an overhaging tip to its nose which is lacking in eastern gorilla. Unlike Chimpanzee, the ears are small and set close to the head.

In nature males develop a saddle of grey hair across the back hence the term silver back for an adult male.

Most informations about social behaviours of Gorilla comes from studies of the mountain gorilla by Schaller (1963) and Dian Fossey (1970, 1981). The group consists of 5-30 individuals with a single silverback male who acts as leader. young males become silver backed by 10-12 years and driven out by the leader and the young gorilla, after kidnapping a young female from another group, starts his own group.

Chest beating is a behaviour to express anger and frustration. Schaller has suggested that chest-beating in gorilla is innate. The life-span is between 40-50 years.

According to Annette Lanjouw of the International Gorilla conservation Programme in Nairobi, Kenya, only 600 mountain gorillas remain in the dense mountain forests at the junction of Uganda, Zaire and Rwanda (June, 1995). There has been some poaching of mountain gorillas. Several poachers want to capture infant gorillas but poachers would have to kill several adult gorillas before they could capture an infant gorilla.

Attempts to breed gorillas in captivity have failed and with such a small population left, wildlife biologists feel it is too risky to try again. That is why no breeding programme for gorillas is presently on.

Chimpanzee (Pan)

There are two species of Chimpanzee (Pan)- *P. troglodytes* or common chimpanzee and *PPaniscus* or Bonobo or Pygmy Chimpanzee. *P. troglodytes* is found in west, central and East Africa whereas *P. paniscus* is found in tropical rain forest of River Zaire and Lualaba in Zaire. Both are partly arboreal and partly terrestrial.

In body it is slimmer than that of orangutan with

proportionately shorter arms. The thumbs and great toe are well developed.

In their social behaviour, chimpanzees are extroverted compared with dignified gorilla and lethargic orangutan. They live in variable, everchanging bands of 30 to 80 individuals. They are characterized by dominance hierarchy among the adult males; and social grooming. Communication calls are pant-hoots- a series of hoots interrupted by audible intakes of breath. These are perhaps contact calls. A loud (Wraah bark), which is long and high-pitched, spreads the news that something unusual has happened. Greeting after a period of separation is an integral part of chimpanzee's way of life.

Chimpanzees are capable of wide range of cultural behaviour. They hunt, make simple tools and throw sticks and stones as weapons. Life span is 50 years.

According to Craig B.Stanford (American scientist, Vol 83, may-June 1995), it has been found after 30 years of research that meat is a natural part of chimpanzees' diet. They are found hunting in all the places across central Africa. They are capable of hunting alone but can form large hunting parties consisting of 10 adult males plus females and juveniles. They hunt monkeys and other small animals. According to Stanford (1995), male chimpanzee uses meat as a tool to gain access to the sexually receptive females. McGrew (1995) has shown that those female chimpanzee that receives plenty of meat produce more offspring that survive.

Nishida has shown that meat is offered to the friends but withhold from foes, thus meat being used as a political tool in a chimpanzee society. A hunter chimpanzee thus gets social, political and reproductive benefits.

John Mitani, University of Michigan, East Africa has spent past 15 years recording the vocal communications of apes and trying to make sense of them. Most recently he has found evidence of regional dialects, or accents, in male chimpanzees Pant hoot, a loud call by chimpanzees was previously thought to be group cohesion call for a food source. But in 1989, the primatologist Adam Clark (US) who was working in Kibale Forest of Uganda, found that it was neither group cohesion or food call. He could not understand what it was all about

Mitani recorded chimpanzee calls in 1990 and 1992 at Mahale mountains National [illegible] Tanzania. He observed that the hoots seemed to indicate a male-male bond. Comparing physical

attributes of sound waves of mahale chimpanzee and gombe chimpanzee (Gombe national park, Tanzania), Mitani discovered distinct differences in the build up and climax phases of the pant-hoot in the two populations.

Clutton Brock and parker (1995) have summarised primates social behaviour with particular reference to establishment and maintenance of dominance relationship, establishment of mating bonds, the enforcement of cooperative behaviour, parent-offspring conflict etc. and have analysed behaviour change in condition of punishment. Females of gorillas, chimpanzees, rhesus monkeys etc have been shown to be ready to mate to more aggressive males. In chimpanzee, it has been found that not only rivals challenging the dominant males are punished but their supporters are also punished. Though higher non-human primates often show co-operative behaviour, particularly during hunting or play times, there are proofs that they attack their allies that fail to support them in competitive interaction with third parties.

c. Family-hominidae : 1. Bipedal walk with erect posture.

2. Complex brain eg. *Australopithecus Paranthropus, Homo.*

Homo Sapien Sapiens

External Character : 1. Density of hair, except-scalp, is reduced.

2. Tactile hair completely absent.

3. The nose is prominent. The elevated bridge is formed by the nasal bones and the fleshy tip is supported by osteo-cartilaginous framework.

4. A median furraw or philtrum is present on the upper lip.

5. Mucous membrane of upper lip out rolled.

7. Margin of ears rolled.

8. Legs much longer than the arms.

9. The great toe is not opposable.

10. Hands capable of power and precision grip.

Skeletal Character : 1. Cranium enlarged and face reduced.

2. Mastoid and styloid processes are well developed.

3. Foramen magnum is placed for antoriority at the base of the skull so that the head is well balanced on the spinal cord. Lumbar curve present

4. Chin is present.

5. No sexual differentiation in teeths. Upper molars are single or double rooted. Canines are small and at the same level of other teeth.

6. Diastema is absent.

7. Linea aspera in the femur is well marked.

In Favour Of Gradualistic Classification : This kind of classification is relatively stable because it is compatible with a variety of different phylogenetic trees and need not reflect any particular interpretation of evolutionary relationships. The system provides some solution to controversial plesiadapiformes. There is a little connection between plesiadapiformes (archaic primates) and other primates (primates of modern aspect or euprimates). There has thus been tendency to separate these two main groups more clearly. One solution is to raise the Plesiadapiformes to the rank of a separate suborder, placing the group at par with Prosimii and Anthropoidea. A more extreme solution is a classification with a primary division between Plesiadapiformes and Euprimates. The most radical solution of all would be to exclude the Plesiadapiformes from the primates altogether.

1. The division between the two main groups Prosimii(prosimians) and Anthropoidea(Simians or anthropoids) is based on the notion that prosimians are generally more primitive than simians. This view has the advantage that all early fossil primates can be classified as prosimians. It is difficult to derive relationship of such forms.

2. Modern tarsiers are more closely related to simians than to other prosimians. Many authorities thus favour an alternative division between the suborder strepsirhini (lemurs and lorises) and the suborder Haplorhini (tarsiers and simians). However, the degree of relationship between fossil tarsier-like primates and modern tarsiers is still not certain, so that the place of fossil forms in such a scheme remains unclear.

3. There exist quite different conclusions about the phylogenetic tree of the New World monkeys and the basic principles of cladistic classification lead to markedly different classifications. A grade-based classification is not prone to such fluctuation.

4. The classification of the Old World monkeys is relatively straightforward, as they form a well-characterised group with a fairly clear division between two subfamilies: leaf monkeys with a complex stomach (Colobinae) and monkeys with cheek pouches

(Cercopithecinae).

5. There has been controversy over the extinct family oreopithecidae, which is linked by some with the Old World Monkeys and by others with the apes. Because there is now good evidence that *Oreopithecus* is related to the apes, and because Old World monkeys are well defined by a dental specialisation called bilophodonty lacking in *Oreopithecus*, it seems appropriate to include the Oreopithecidae within the Hominoidea.

6. Great apes (orang-utan, gorillas and chimpanzees) were classified in the family Pongidae and the family Hominidae was reserved for humans and their fossil relatives. Because it is now widely accepted that the African apes (gorillas and chimpanzees) are more closely related to humans than are orang-utans, there have been numerous attempts to reflect this in new classifications. If chimpanzee and gorilla are included in hominidae, the term would lose its earlier essence. A gradualistic classification, therefore, donot favour the idea of including chimpanzee and gorilla in the hominidae.

Clade Based Classification

There is an alternative system of classification that considers lemurs (strepsirhini) against tarsiers and anthropoids (Haplorhini). In this system tarsiers and anthropoids are lumped together and placed against lemurs. Thus the system bifurcates prosimii and considers tarsiers with anthropoids. The system was originally proposed by Pocock (1918) and Hill (1953). The system has been accepted by most of the present day physical anthropologists including Eaglen (1983), Heads (1985), Corrucini and Ciochon (1987), Grover (1992) etc. The system is based upon cladistic analysis.

In cladistic analysis, there is no extra emphasis on evolutionary rate or phylogeny but totality of characters of living forms are taken into consideration. In this system of strepsirhini/Haplorhini scheme, different aspect of anatomy has been considered along with varying characters of foetal membranes (membranes surrounding the foetus during gestation period) and nature of placentation, eye-structure etc. For characterisation of fossils, in which such aspects of soft anatomy and embryology is missing, hard structure of living forms are taken account of and then these are detected in fossils.

There are two new ranks in the cladistic classification -

incertae sedis(i.s.) and plesion. An incertae sedis is a controversial taxa for which it is hoped that future discoveries would clarify the matter. A plesion (Patterson & Rosen 1977) is an unraked catagory to be inserted at appropriate level so as not to disturb a pre-existing classification.

The Cladistic classification divides primates in three sub or de:s-Paromomyiformes, Strepsirhini and haplorhini. Paromomyiformes are characterized by Small brain; Marked post orbital constriction of skull; No post orbital wall; Laterally facing orbits; Claws on all digits.

The suborders strepsirhini and haplorhini can be distinguished on following characters:

Strepsirhini	Haplorhini
1.Nose not hairy, with rhinarium.	1.Nose hairy, without rhinarium
2.Upper lip not free from gum.	2.Upper lip free from gum.
3.Upper central incisors not medially opposed but with gap between them.	3.Upper central incisors medially opposed, with no gap between them.
4.Palcenta not haemochorial.	4.Placenta haemochorial
5.Retina without fovea centralis and macula lutea.	5.Retina with fovea centralis and macula lutea
6.Tapetum lucidum present.	6.No tapetum lucidum (reflecting layer due to which eyes glow in the dark) behind retina.
7.No post orbital plate.	7.Post orbital plate developed.
8.Synthesize Vit C.	8.Failure to synthesize Vitamin C (Pollock and Mullin, 1987).
9.Dental Comb in lower jaw of many.	9.No dental comb.
10.Nails not on all digits. on the second pedal digit claw is enlarged forming toilet claw.	10.Nails on all digits

EVOLUTION AND RADIATION OF PRIMATES

What features differentiate human being from all other animals? An erect bipedalism that has freed his hands from locomotion and provided opportunity for greater manipulative works ? Opposability of the thumb in the hands that has made his hands more dexterous ? A unique dental pattern that has made him omnivorous ? Development of higher faculties of brain that has made possible higher degree of wisdom and thought and its articulation through gestures and speech ? A complex set of behaviour patterns that regulate various activities of the human groups ? Yes, of course, in all such features humans are different from all other animals.

Humans didnot originate overnight with these set of characters. If one studied fossil records, it would become apparent that in the past various evolutionary forces had been operating and man is a product of such forces. The order primates, to which humans belong, is broadly divided into two groups - lower primates or prosimians and higher primates or anthropoids. Majority of the primatologists believe that order primates evolved from order insectivora. After its origin, the members of the order experienced evolution in different directions and today we find lemurs, lorises, tarsiers among the prosimians and new world monkeys, old world monkeys, apes and man among the anthropoids.

Linnaeus grouped lemurs, monkeys, apes and man together and named the group primates which literally means chieftains. Linnaeus had kept, no doubt, the intellectual superiority of human being in mind while naming this order, though a number of primate groups are far from this intellectual attainment. Later evolutionists considered primate evolution to be governed by a series of evolutionary trends that culminated in the human being. Human being with big brains, reduced ability to smell, increased manual dexterity, upright posture etc was considered to be the climax of primate evolution and any group deviating from attainment of such features was labelled aberrant, less evolved and backward.

This outlook about primates evolution is being questioned by recent workers. The fallacious situation has arisen because the primates as a group has been evaluated against the backdrop of human attainments. Recent workers prefer to study primate

evolution by not comparing the group with human being but with other animals that have adapted to similar environments.

Arboreal Theory : Arboreal features are common in many of the primate groups. The most striking of these are in the anatomy of hands and feet, possession of nails, eyes and developed sense of vision etc.

1. Hand, Feet And Nails : In most primate groups, the thumb is opposable to the rest of fingers. Likewise, in many non-human primates, the big toe is opposed to the rest four. This is used for grasping tree branches. Various non-primate animals also have grasping feet. Hind feet of many primitive marsupials, opossums, South American porcupines etc is grasping and has opposable big toe. All such animals have similar arboreal feature and that the primates ancestor must have been an arboreal creature. Possession of flat nails in place of claws has also been explained on the basis of arboreality. Flat nails allow fingertips to be more pliable in operating on the bark of the trees.

2. Eyes And Sense Of Vision : Most primates have their eyes located close together and look in the same direction that allows three dimensional vision. Also, most primates have reduced olfaction. Reduction in olfaction and enhanced visual sense are supposed to be direct outcome of arboreal habit. For a creature that sneaks through branches of a tree, often by way of jumping, olfaction may not be a necessary feature; on the contrary its visual sense can be compromised only on its own peril. Thus, it is explained, that snout was gradually reduced along with the sense of olfaction and more location of eye was made forward.

The theory of arboreality dominated for quite a long time. But the theory fails to account for some of the characters that many successful arboreal groups of mammal other than primates possess. These include-

i. Squirrels are successful arboreal creatures but have sideways-facing eyes, large snouts, non-opposable digits with sharp claws.

ii. Most non-primate arboreal animals have claws. Even some arboreal primates such as the aye-aye, Goeldi's monkey, marmosets and tamarins have redeveloped claw-like structure from ancestral nails.

iii. Forward location of the eyes increases depth perception but reduces the distance over which depth perception can operate.

iv. Many arboreal non-primates have developed sense of smell such as squirrels.

v. Many arboreal mammals donot show any enlargement of brain.

On the basis of such arguments it can be safely concluded that arboreality is not the only aspect that explains primate evolution because arboreality has produced many mammalian groups that possess characters quite contrary to that of primate groups.

Visual Predation Theory : The theory supposes that evolution in primates has not occurred along the lines of arborealism but for visual predation. Forwardly located, close-set eyes are the feature of predators that rely on vision in hunting especially those that hunt by night, for example Owl, Cat etc. The theory supposes that the last common ancestor of primates was a small, big-eyed nocturnal insect-eating creature.

Fossil records show that ancestors of primates were, indeed, insectivorous. Earliest ancestors of primates are lemur-like and tarsier-like prosimians of Eocene, some 50 million years ago. The earliest animals of this group possessed teeth that resemble those of modern insect-eating primates. The fact supports visual predation theory of primate evolution.

To summarise, the primates evolution took the following course :

Palaeocene proto-primates split in prosimians and anthropoids in Eocene. If tree-shrews are considered with prosimians, they also must have split from ancestral line during this period. Of *Tarsier, Lemur* and *Loris, Tarsier* split first during late Eocene. Early oligocene and Loris-Lemur splitting afterwards during oligocene. Among anthropoids, New World monkeys separated first in oligocene. The ancestral line then split into old world monkeys and apes during late oligocene. Thus by miocene all monkeys and apes had arrived. Man separated from ape-line during pliocene and developed into *H.sapiens* in pleistocene. Present form *H.sapiens sapiens* was acquired 10,000 years ago.

Evolution and radiation of primates can be studied under two seperate heads :

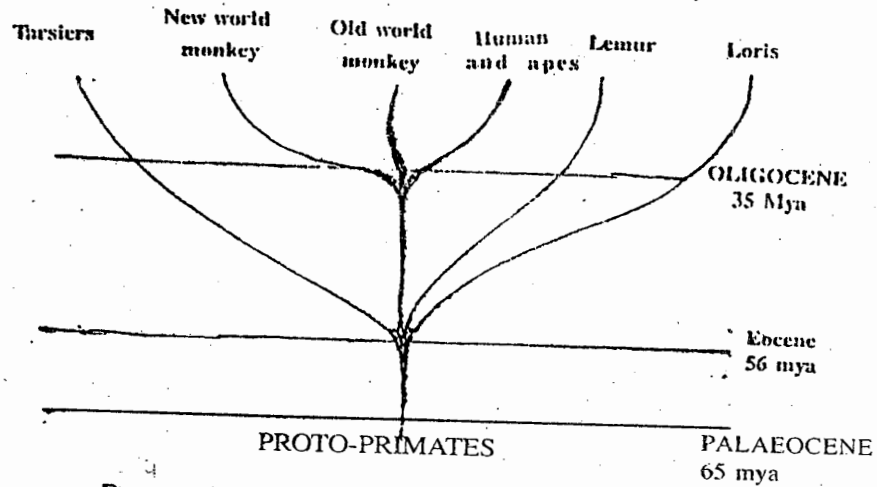
1 Evolution and Radiation of Prosimians

2 Evolution and Radiation of Anthropoids

1. Evolution And Radiation Of Prosimians

Earliest fragmentary remains of insectivore ancestors of primates are available from the beds of palaeocene, 65 million years ago. Since these fossils are fragmentary, a model of such ancestor is represented by present day tree shrews, Tupaia, *Ptilocercus* of the oriental region. These animals so much resemble both insectivora and primates that their position is controversial - some authorities place them with insectivora, while others prefer to keep them with primates.

There seems to have occurred two radiations in primates - first during palaeocene-Eocene (56 mya) when primitive primates or stem primates or proto-primates diverged into lemurs and lorises on one hand and tarsiers on the another. A second radiation seems to have occurred during eocene-oligocene time (35 mya) when later primates, supposed to have been derived from lemuroid ancestors, split into lines leading to new world monkeys, old world monkeys, apes and man.



Purgatorius (Montana, USA) regarded as oldest Primates

Fig. Two radiations in primates evolution. First radiation is supposed to have occurred during palaeocene-eocene times (56 mya) into lemurs, lorises and tarsiers and the second radiation seems to have occurred during Eocene-oligocene times (35 mya) into new world monkeys, old world monkey and man.

the earliest primates traced is *Purgatorius* from early palaeocene. During this time existed proto-primates that can be divided into four groups. Plesiadapidae, Carpolestidae, Paromomyidae and Picrodontidae. During Eocene the two major families of primates were Adapidae and omomyidae. Adapidae was represented by *adapis* of Europe and *Notharctus* and *smilodectes* of N.America. It is believed that *Notharctus* developed into Lemur during miocene and *smilodectes* is ancestral to Loris, also developing in miocene. Another family of Eocene, Omomyidae represented by genera such as *Neorolemur* and *Tetonius* of which *Tetonius* is supposed to be ancestral to present day *Tarsius* which developed in Oligocene itself. Because it has originated in distant past and has retained more or less past form, it is also referred to as living fossil.

The group Paromomyidae was probably ancestral to all monkey, apes & man. The group is supposed to have split into paromomyinae and Phaenacolemurinae in eocene of which the latter is supposed to have evolved into monkey, apes & man.

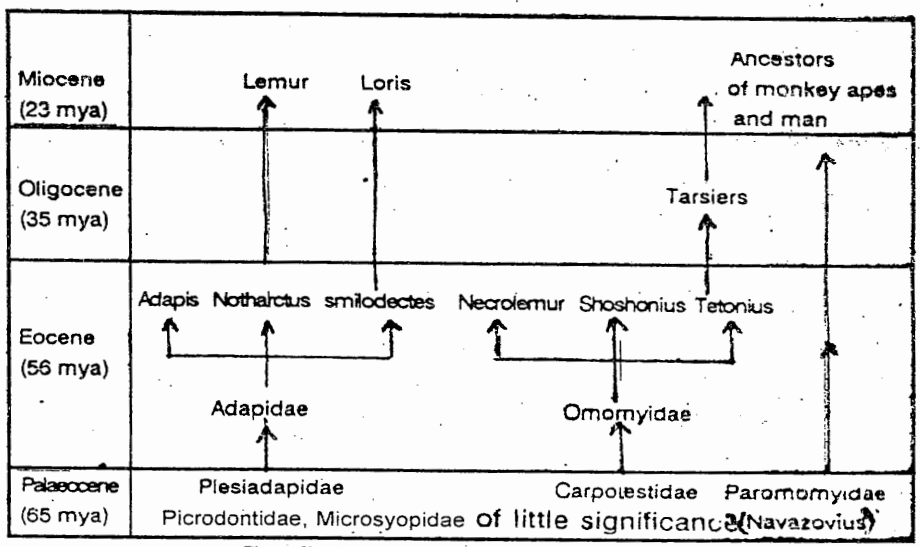


Fig. : Evolution of prosimians

monkey, apes & man. The group is supposed to have split into paromomyinae and Phaenacolemurinae in eocene of which the latter is supposed to have evolved into monkey, apes & man.

2. Evolution And Adaptive Radiation Of Anthropoids

Anthropoids may have evolved either from Adapids or omomyids. No anthropoid fossil has been recovered from Eocene except *pondaungia* form late eocene of Burma.

Presence of ancestors of anthropoids is indicated in Africa. From Fayum deposits of Egypt come oligocene fossils (23-35 mya) Several genera and species have been recovered, including *Aegyptopithecus* and *Propliopithecus*, representing an early catarrhine stock from which the Old World monkeys as well as the apes and man are thought to have evolved.

A. Evolution And Radiation Of New World Monkeys

There are three broad divisions of modern primates- platyrrhines, Catarrhines and Prosimians. New world monkeys are included in platyrrhines - so called because of the wide gap between the two nostrils. Among the three primates group, platyrrhines are the only group which are confined to South America and a part of Central America. That is why they are also called new world monkeys. Monkeys of Africa, Asia & Europe are called old world monkeys. The new world monkeys are different from old world monkeys in several aspects of morphology, ecology and behaviour and mere use of the term monkey does not bring them any closer. The old world monkeys and new world monkeys were separated 40 MYA and the two groups have adapted to their different mode of life. A major difference between the two groups is that the new world monkeys have adapted for life in trees, the thick forests of Amazon Valley, whereas old world monkeys have invaded grassland and adapted for terrestrial life as well. Though staying back in the forests, the new world monkeys have produced more varieties than has produced old world monkeys. They have broader range of feeding and locomotor adaptions in the trees and greater variety of social systems and mating strategies. Rosenberger (1992) has stated that it is probably the internecine, continuous stretch of closed evergreen forest that has made it possible.

It is difficult, however, to reconstruct the evolutionary past of new world monkeys because of paucity of their fossil remains :

barely hundred or so of their fossil remains have been discovered till date and that too a fragmentary one. The molecular evidence offers only limited help and only confirms results obtained by morphological studies. Thus a great many problems lie unresolved concerning their origin and evolution.

New world monkeys are characterized by widely separated nostrils by broad, flat septum, absence of cheek pouches and ischial callosities, prehensile tail in many groups, non-opposable thumb, nails (except in marmosets and Tamarins in which a nail is present on big toe only).

Though taxonomy of new world monkeys is disputed, there are five groups of them which are universally recognised-

1. Marmosets and Tamarins plus Goeldi's monkey (Sub family Callitrichinae)
2. Sakis and Uakaris (tribe Pitheciini)
3. Spider, Woolly and howler monkeys (Sub family Atelinae)
4. Squirrel and Capuchin monkeys (Sub family Cebinae)
5. Titi and Owl monkeys (tribe Homunculini)

1. Marmosets & Tamarins : They are small with smooth (unconvoluted) brains, simple grasping hands, claws on fingers and toes (apart from great toe), uncomplicated molar teeth, and a genetically fixed pattern of non-identical twinning; they also rely heavily on the sense of smell.

The features of marmosets and tamarins result from selection for small size, a reversion to an insectivorous diet and high reproductive output. For example, locomotor specialisations make possible their unique ability to range freely through the tropical forest, especially just below the canopy. When searching there for insects and especially when collecting tree saps and gums, their small arms and hands act like grappling irons. The delivery of twins rather than singletons and the unconvoluted brains may also be an outcome of reduction in body size.

Only two fossil species, *Micodon kiotensis* and *Mohanamico hershkovitizi*, from the middle Miocene site of Colombia, may be related to modern callitrichines. Apart from these fossils, circumstantial evidence indicates that callitrichines already existed during the Miocene epoch (between 23 and 5 million years ago). Various lineages of their nearest living relatives, the cebines, are represented as fossils during that period.

2. Titi And Owl Monkeys : It includes *Aotus* (Owl monkey) and *Callicebus* (Titi monkey). These are sometimes included in separate groups, Aotidae and callicebidae. Both have extreme karyotypic diversity and diverse hair-banding patterns on neck and limbs.

3. Squirrel & Capuchin Monkeys : Although squirrel monkeys saimiri and capuchins (*Cebus*) are superficially quite different, in part because of their difference in size, they share many derived features that indicate a common ancestry. Among these are a high ratio of brain to body weight, a shortened face, close-set orbits, a rounded braincase, marked sexual dimorphism and a capacity to alter their diet greatly during lean periods. *Cebus* shows other interesting traits that parallel those of early hominids. such as augmented manual dexterity and thick-enamelled molar teeth.

A new set of fossils from La Venta- represented by a talus (ankle bone) and a well-preserved lower jaw with nearly all its teeth - is intermediate in morphology between squirrel monkeys and callitrichines. It suggests that callitrichines and cebines are closely related and that the La Ventan *Saimiri fieldsi* may be a direct ancestor of modern squirrel monkeys.

4. The Sakis & Uakaris : The pitheciin - the sakis and uakaris - are confined to the deepest region of Amazonia. Their habitats are inundated for many months of the year by the Amazon. Many plants have fruits and seeds with thick coatings (which may waterproof them) and foliage with toxic secondary compounds that repel browsers. Primate numbers are accordingly low.

Sakis and Uakaris are adapted to cope with these conditions. They have powerful incisors and canines for husking fruit and flat postcanine teeth powered by strong muscles for crushing and grinding seeds.

We donot yet understand the evolutionary or ecological position of sakis and uakaris They are merely an isolated genealogical side branch, as the living titi and owl monkeys.

5. Spider, Woolly And Howler Monkeys : The fourth sub-family. the atelinae, includes the spider, woolly and howler monkeys. They are the largest platyrrhines. Howler monkey (Alouatta) has most primitive dentition, skull and brain. Hyoid is enlarged and hollow that gives it the loudest voice in animal kingdom. Climbing quadrupedalism is their typical locomotor style.

However, spider monkeys (*Ateles*) and the woolly spider monkey (*Brachyteles arachnoides*) are fast and acrobatic suspensory locomotors, and can brachiate like gibbons. All have prehensile tails used in posture, locomotion and grasping. Their shoulders, hind limbs and feet are also adapted for hanging. By contrast, the tail of *cebus* lacks the elongation, flexibility, neural circuitry and gripping pad shared by all atelines. Cebines also lack long limbs and flexible joints essential for climbing. They have semi-prehensile *tails* which evolved convergently.

In their diets, atelines range from leaves-eating (Howler monkeys) to fruit eating (Spider monkeys), and in their locomotor habits from sluggish quadrupedal climbing to acrobatics. The woolly monkey (*Lagothrix*) is intermediate in this respect.

The fossil record of atelines is provocative. Teeth from two species have been found at La Venta. Both are allocated to the genus *Stirtonia*. They are morphologically and functionally similar to *Alouatta* and some question the need to place them in a separate genus from living howlers. However, a highly distinctive Pleistocene form (*Paralouatta Varonai*) has recently been found in Cuba. Its large, uptilted face resembles a howler monkey. but its braincase is more primitive. The teeth of *paralouatta* are also relatively smaller than in living howlers, so the fossil form could not have been as extremely adapted for leaf-eating as the modern howler.

The remains of *Paralouatta* are much more primitive than those of *Stirtonia* but are far younger. Even more surprisingly, they were found outside South America. Proto-howlers dispersed from South America earlier in the Miocene, leaving behind an ancestral stock that also gave rise to the *Stirtonia-Alouatta* group. *Paralouatta* may be a recently extinct descendant of the proto-howler group. This is most satisfactory explanation.

Origin of new world monkeys in South America is completely obscure. Forms resembling primitive monkeys are found from Miocene beds. Beyond this, little is known about their origin in the continent.

Two theories have been put forward to explain their presence in South America.

a. They came to South America from Africa. There is impressive records of early Anthropoids from the Fayum deposit of Egypt dating over 30 MYA. They reached from Africa to North America and then to South America.

b. Another theory explain the origin in North America itself where no early Anthropoids but more archaic adapid and Omomyids lived at least 56 mya. There is no record of early Anthropoid from North America. Both theories require crossing a sizable span of sea-water most probably on floating logs. Fossils remains are meagre and thus a definite conclusion is lacking.

The Fossils from South America offer only two small clues to platyrrhines origins : The earliest *Branisella boliviana*, from Salla in Bolivia, and a new genus, *Szalatavus attricuspis* from the same area. The Branisella Zone locality has a late Oligocene age of 27 million years. It sets the upper limit on the date of their appearance. The recognition of a new genus "*Szalatavus*" in the late Oligocene of Bolivia suggest that more will be discovered as explorations continue. Study of Platyrrhine origins will make little progress until more South and Central American fossils are discovered.

The platyrrhine invasion of south America is even more problematical. For many years, while the continents were considered to have held fixed positions on the face of the earth, it was assumed that the ancestral platyrrhines evolved from a prosimian, probably omomyid stock, which entered South America from North America, migrating via a chain of islands following the line of the present-day isthmus of Panama. The earliest evidence that a platyrrhine had indeed reached South America is the fossil *Branisella* of the early Oligocene of Bolivia. *Branisella* was about the size of the titi (*Callicebus*), approximately midway between the smallest and largest living platyrrhines - the pygmy marmoset and the spider monkey. In recent years, following the general acceptance of the theory of continental drift, the origin of the platyrrhines has had to be re-appraised. Studies of rock palaeomagnetism and sea-floor spreading shows South America as an island, in eocene times the gulf between North and South America was considerably larger that between South America and Africa. The surface currents and winds, probably the most important factors in successful rafting, are also thought to favour the trans-Atlantic route. Large volcanic island that could have provided stepping stones for the ancestral platyrrhines are known to have existed both in the Caribbean and the South Atlantic. In the latter, distances between islands could have been as little as 200km. Current opinion favours Africa as the source of origin of the New World monkeys on geographical grounds (Ciochon & Chiarelli, 1980). This has been reinforced recently by some primate

fossil teeth from the late Oligocene of Argentina which are described as being very similar to the Oligocene catarrhine, *Aegyptopithecus*, from the Fayum of Egypt, This suggests a common anthropoid origin for both groups with Africa as its source (Fleagle & Bown, 1983). Nevertheless, as with the lemurs, some kind of sea voyage must have been involved, whether from North America or Africa.

By whatever route the ancestral platyrrhines reached the New World, once there they radiated rapidly in tropical forest - a relatively unexploited ecological niche. Since that time, the forest is thought to have remained virtually unchanged except in the south where, after the elevation of the Andes in the late Miocene, the grasslands of the pampas took over. Later the forest may have contracted and expanded in response to the marked climatic changes of the Pleistocene, but this probably did not significantly affect the primates which are all exclusively arboreal both in structure and habit. The sparse fossil record of eight genera, ranging form the early Oligocene *Branisella* (about 31 MYA) to the subfossil *Xenothrix* from Jamaica (25000 years ago) confirms their homogeneity (Rosenberger, 1977).

B. Evolution And Radiation Old World Monkeys

Old world monkeys are much more variable, ranging from the completely arboreal to the completely terrestrial.

The story of the diversification begins in the Fayum Depression of Egypt about 35 mya. The earliest, *Oligopithecus* (30-35 mya) has the same dental formula as modern catarrhines, but was much smaller. The later *Propliopithecus* (28-30 mya) and *Aegyptopithecus* (28 mya) were dentally ape-like and are considered broadly ancestral to all living catarrhines.

Two other fayum primates. *Parapithecus* and *Apidium*. are doubtful cercopithecoids. *Parapithecus* and *Apidium* retained three premolars like the prosimians and New World monkeys, though they had clearly reached the monkey grade of organization.

Undoubted members of the cercopithecoidea are not found until the early Miocene about 18 mya. *Prohylobates tandyi* from Wadi Moghara in Egypt and *Psimonsi* from Gebel Zelten in Libya have almost completely bilophodont teeth (four cusps linked by two transverse crests. the pattern typical of the cercopithecoid.

1. Colobine Radiation : In the middle Miocene about 15 mya, the division of the Cercopithec into two subfamilies is foreshadowed by the discovery of two species from Moboko Island

in Lake Victoria in Kenya - *Victoriapithecus macinnesi* and *V. leakeyi*. The former shows resemblances to the leaf-eating colobines and the latter to the omnivorous cercopithecines. By the late Miocene, about 10 mya, the colobines are clearly distinct, their teeth showing the characteristic high cusps and deep notches of present-day leaf-eaters. *Mesopithecus*, a large colobine from Pikermi near Athens (about 9.5 mya) must have invaded Europe from Africa. The later *Dolichopithecus* of Perpignan in southern France (4.5 mya) was more macaque-like in its adaptations. European colobines of the Miocene may have given rise to the Asian colobine monkeys of today though the time of such a dispersal cannot be surmised. The first evidence of colobines in Asia comes from the siwalik Hills where a small colobine monkey has been recovered from Dhok Pathan (about 7 mya). There are no further finds of colobines in Asia until the middle and late Pleistocene, and these are clearly related to modern forms.

African colobines are represented by *paracolobus* from Pliocene deposits of South and East Africa. Several other species have been found from Ethiopia and Kenya, and it may be from among these that the modern genera, *colobus* and *Procolobus* evolved.

2. Cercopithecine Radiation : The cercopithecines also reached Europe from Africa; but probably later than the colobines. From the late Miocene (about 6 mya), fossils similar to the macaque have been recovered from throughout Europe. Later, about 2 mya, a larger more baboon-like genus, *Paradolichopithecus*, is found in southern Europe. The cercopithecine invasion of Asia may also have taken place rather later than the colobines. It is not until 3 mya that a macaque-like fossil ? *Macaca palaeindica*, is found in the siwalik Hills. From a later formation of siwaliks (about 2 mya), another larger genus, *Procynocephalus*, has been recovered.

In Africa, three main evolutionary lines developed during the Pliocene, one leading to the gelada (*Theropithecus*), the second to the baboons, mandrills and mangabeys, and a third to the guenons. The first evidence of the gelada is a single tooth from Lothagam in Kenya (about 4 mya) which is indistinguishable from those of living geladas. During the Pleistocene, geladas spread widely in Africa from Algeria to the Cape. The history of the baboon stock also begins at Lothagam but earlier in time (about 5 mya) with the genus *parapapio* which was a medium-sized monkey. Later in the Pliocene, the baboon stock spread to South

Africa and Ethiopia, becoming larger and more diversified, with three further genera, *Dinopithecus, Gorgopithecus* and *Papio* itself, which first appears in the fossil record in the late Pliocene (about 3 mya) in the Omo Valley, Ethiopia.

Both lines continued to flourish until about 50000 years ago when the spread of human populations with improved hunting techniques began to disturb the ecological balance. Fossil *Theropithecus* fed on grasses and seeds as they do today. Man's preference for such sites put him in direct competition with the gelada which also provided him with valuable food. Unable to adapt to other environments, the geladas vanished from their lowland habitats. Today only a small relict population survives in the highest mountains of Ethiopia. *Papio* on the other hand survived competition and predation by man, by spreading into the widest possible range of habitats from tropical rain forest to semi-desert.

The third branch of the African cercopithecines, not closely related to the baboons and gelada, is that leading to the mainly forest-living guenons (*Cercopithecus* and their allies, the talapoin (*Miopithecus*), the patas monkey (*Erythrocebus*) and Allen's) swamp monkey (*Allenopithecus*). Very few fossils have been found; the earliest dated to the late Pliocene of Kenya (about 3.25 mya), and all are attributed to the living genus Cercopithecus.

C. The Apes And Man (Hominoidea)

Evidence of the evolution of the hominoids is first found in the early Miocene, Between 15-23 mya, three genera (*Proconsul, Limnopithecus* and *Rangwapithecus*) are found in Kenya and Uganda, of which one species, *Proconsul major*, was about the size of a female gorilla. Later still, in the middle Miocene, from about 10-13.5 mya, *Dryopithecus*, the "wood ape", is found in Europe. From the middle Miocene between 9-15 mya - rougmy contemporaneous with *Dryopithecus* in Europe- two genera were evolving both in Africa and Asia, *Sivapithecus* and *Ramapithecus*. They also had lower molars with the Y-5 cusp pattern, showing their close relationship, but differed from the dryopithecines in having small incisors and canines and relatively large molars with thick enamel on the biting surfaces. It was probably from the Asian branch of this stock that the orang-utan (with fairly thick molar enamel) is descended. Orang teeth are found in caves in south and central China as well as Borneo, Sumatra and Java, from the early Plaistocene onwards (1.5 mya), indicating that orangs were once present on the mainland of Asia. The last record of

Proconsul (P. nyanzae) is dated to 15 mya. and of *Ramapithecus (R.wickeri)* to 14 mya. Apart from fragmentary evidence from Ngorora (c. 11 mya) and Lukeino (c. 6 mya) the next evidence of hominoids in Africa comes from the fossils of *Australopithecus ramidus* from Aramis, Ethiopia, 4.4 mya in age, discovered by Tim white et.al.(1994). There is no record of the stem leading to the living chimpanzee and gorilla.

The smaller members of the Hominoidea, the lesser apes, the gibbon and siamang (Hylobates)- are thought to have diverged from the ancestral stock even earlier (16-20 mya). Small gibbon-like fossils, *Dendropithecus* and *Micropithecus*, are found in the early, Miocene of Kenya (18 mya), and *Pliopithecus* in the middle Miocene of Europe (12.5-16.5 mya). An isolated gibbon tooth from the Siwalik Hills dated at 8-10 mya is the only connection between them and the modern family Hylobatidae of south-east Asia, until the middle Pleistocene of China.

Proconsul is beleived to be common ancestor of apes and man. The split between African ape and human lineage is much speculated and estimated from 15 to 6 mya. The earliest fossil of hominid affinites is that of *A.ramidus* from Aramis, Ethiopia, (4.4 mya), *A.anamensis* from Kanapoi (4.2 mya) and *A.afarensis* from Laetoli, Tanzania (3.77 mya). Later in pleistocene *H-erectus*, *H-sapiens neandertalensis* and *H.sapiens* appear in different parts of globe which indicated world wide radiations of modern humans.

Modern Hominoids : Hominoids of present day are broadly divided into two families-pongidae and hominidae.

1. Pongidae : The pongidae is a subsidiary radiation of the Hominoidea distinguished from the hominidae by the following evolutionary trends : progressive skeletal modifications in adaptation to arboreal brachiation; lengthening of the upper extremity as a whole; limb bones for increased mobility and for the muscular developments related to brachiation; Thumb strong and opposable; great toe reduced; pelvis retaining the main proportions characteristic of quadrupedal mammals; marked prognathism ; massive jaws associated with strong muscular ridges on the skull; nuchal area of occiput becoming extensive, occipital condyles retaining a backward position; cranial capacity showing no marked tendency to expansion; formation of simian shelf; enlargement of strong conical canines with interlocking in diastema; sectorialization of first lower premolar U-shaped Jaw etc.

2. Family Hominidae : P. 367

HUMAN SKELETON

Human skeleton may be subdivided into axial skeleton and appendicular skeleton. Axial skeleton forms axis of the body and include skull and vertebral column. Appendicular skeleton is comprised of bones in shoulders, hips, arms, and legs which are attached to axial skeleton.

Skull : The skull is divided into the brain box (that houses the brain), and the facial part. The brain box consist of 8 bones and the facial part of 14 bones, together accounting for 22 bones in the skull.

A. Bones And Features Seen From The Front

Following are the parts of our head seen from the front and the bones that enter in its formation :-

1. Fore-head : Our fore-head is made up of a pair of bones called frontal. Its upper part is smooth and orbits convex but lower part irregular and interrupted by nasal.

2. Nose : Our nose is made up of a pair of nasal bones which is situated just below the frontal that make the fore-head. The left and right nasals from bridge of the nose.

3. Eyes : A pair of eyes lie in the two depression, called orbits, on the two sides of the nose, just below the fore-head. The orbits are made up from contributions by the three surrounding bones - maxilla with which are attached upper row of teeth, Zygomatic which is bone of our cheek, and third the frontal that make our fore-head.

4. Cheek prominences : These are made up of Zygomatic bones. This bone gives out a prominence, called Zygomatic arch, in the formation of which another bone, called temporal bone, also enters. Temporal bones are located on the sides of our skull. Zygomatic arch is supported from the skull by a gap.

5. Upper Jaw : Upper Jaw is made up of a pair of maxillae bones. The maxillae bones bears sockets for upper row of teeth. Above, maxillae form boundaries of orbits and nasal opening and meet with the Zygomatic bones of cheek and frontal of fore-head.

6. Lower Jaw : Lower jaw is made up of a pair of bones called mandibles. The two mandibles are attached to the cranium and bear sockets for lower row of teeth.

Besides, there are some other features of the skull that can be seen from the front side : 1. The Superciliary arch : Just above each orbit there are present superciliary arch formed by the frontal

bones. It is the site of eyebrows and better developped in males than in females. 2. The glabella : It is the median elevation that connects the two superciliary arches. 3. The Nasion : It is the point where the internasal suture meets the frontal bones. 4. The frontal tuber : It is a pair of small, rounded elevations of frontal bone just above the superciliary arches.

B. Bones And Features Seen From Above

1. If seen from above, the main bone of the skull visible are a pair of parietals bounded anteriorly by a pair of frontals and posteriorly by occipital.

2. The meeting point between frontal and parietal bones is called Coronal suture, that between the two parietals is called sagittal suture, and between parietal and occipital bones is called Lambdoid suture.

3. The points where two sutures meet have been given specific names. Thus Bregma is the meeting point between coronoid and sagittal sutures. If you touch this place in new borns,

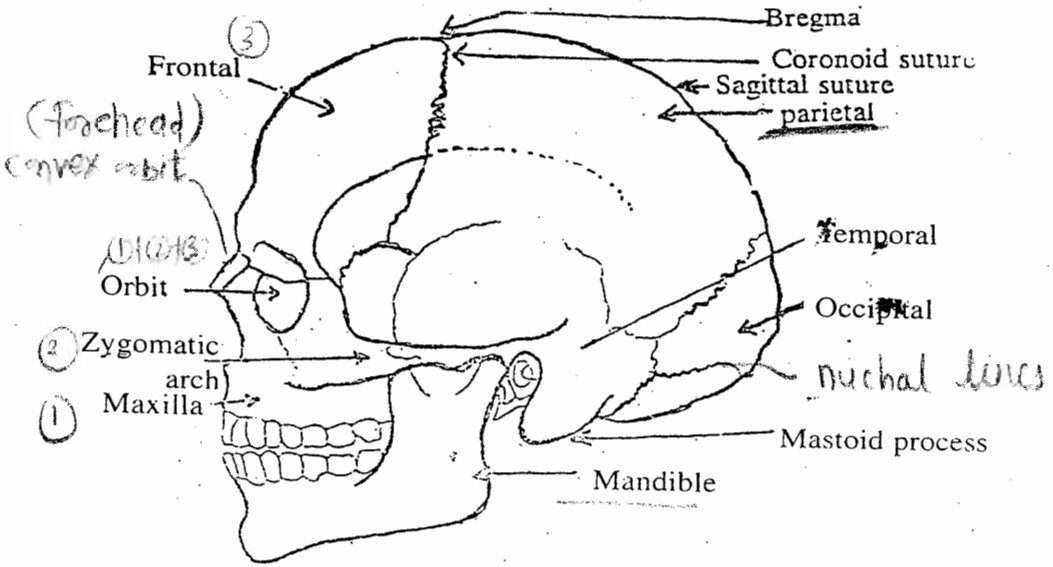


Fig. : Human Skull (side view)

you will feel soft. It is the site of a membranous gap that does not fill up before $1\frac{1}{2}$ years of age. The Lambda is the meeting point between sagittal and lambdoid sutures. A gap similar to bregma does also exist here but it closes at 2 to 3 months of age.

4. The vertex and the vault are other terms associated with skull. The Vertex is the highest point on the sagittal suture. The vault of the skull is the arched roof of the skull.

C. Bones And Features Seen From Behind

1. The main bones visible from behind is the occipital which is bounded anteriorly by parietals and postero-laterally by mastoid part of the temporal.

2. The most prominent feature on occipital is the external occipital prominence that marks the junction of head and neck. The Inion is the most prominent point on this prominence. Also present on the occipital are several bony ridges, called nuchal lines.

D. Bones And Features Seen From The Lateral Side

1. The bones visible from lateral side include frontal, parietal, occipital, temporal, sphenoid, Zygomatic, maxilla, nasal and mandible. Out of these all have been described except temporal and sphenoid.

2. Temporal bone is roughly present in the region surrounding our ears. We have already known that it gives out a process called Zygomatic process of temporal that joins with the temporal process of Zygomatic, making Zygomatic arch, the prominence of the cheeks. At its posterior margin is located external acoustic meatus, the opening leading to middle and internal ear.

3. The temporal bone gives out two prominent out growths- the mastoid process and the styloid process. The mastoid process lies just behind the opening of the ears and articulates with the posterior part of parietal bone which makes roof of the skull. The styloid process is a thin, long projection located below mastoid process.

4. The point where parieto-mastoid, occipito-mastoid and lambdoid sutures meet is called asterion.

5. The H-shaped point where frontal, parietal, temporal and sphenoid bones meet is called pterion. Location of both asterion and pterion is of evolutionary significance.

Foramen magnum is the foramina in the skull through which spinal cord comes out of the skull and continues through vertebral column.

Vertebral Column

1. The vertebral column consists of 33 irregular bones, the vertebrae, so connected to one another as to allow forward, backward, and sideways movement. Some region of the column are more flexible than others. In man the verbetral column is curved, a characteristic associated with greater carrying strength and balance in the upright animal.

2. The vertebrae differ in size and shape at different sites along the backbone, but they share certain common structural features. The main portion of a typical vertebra is called the centrum. A small pad of tough cartilage called a disk lies between centra of the vertebrae. Pairs of small openings occur between the vertebrae from which the spinal nerves emerge.

3. The first 7 so called cervical vertebrae make up the skeletal framework of the neck. These are followed by 12 thoracic vertebrae, 5 lumbar vertebrae, and below these the sacrum and coccyx region of the backbone. In man, the 5 sacral vertebrae are fused into a single solid bone. It is joined to one of the bones the pelvic girdle which attaches the legs to the (Ilium) column. The coccyx in man is also a single bone which has resulted from the fusion of 4 tiny bones. In many vertebrates it give support to the tail, but in man the coccyx is a useless vestigial structure.

4. In our chest region, you find a bony cage which is formed of ribs. The ribs are connected to the vertebrae dorsally and to sternum ventrally. Thus, the bony chest cage consist of the 12 thoracic vertebrae, the 12 pairs of ribs, which are joined dorsally to the thoracic vertebrae, and the ventrally located breastbone or sternum. Ten of the 12 rib pairs are directly fused or indirectly attached by means of cartilage to the breastbone. The eleventh and twelfth pairs of ribs are attached only to the backbone and for this reason are called the "floating ribs".

Appendicular Skeleton

1. The appendicular skeleton consists of 126 bones, organized into the appendages (arms and legs), and the bones composing the pectoral and pelvic girdles which attach these appendages to the axial skeleton.

a. Pectoral Girdles & Fore-Limb :

1. Each of the 2 pectoral girdles is made up of a collar bone (clavicle) and a shoulder blade (scapula). Each clavicle forms a joint to the breastbone at one end, whereas at its other end it articulates with a scapula. The scapula connects to the ribs by muscles and ligaments, which accounts for the flexibility and freedom of movement of the shoulders and arms.

2. The socket (glenoid cavity) formed by the union of clavicle and scapula is the site to which the arm is attached. The bone of the upper arm is called the humerus and articulates with the shoulder sockets by means of ligaments. The 2 bones of the forearm are the radius and the ulna. The 8 small bones composing the wrist are called the carpals and the hand consists of 5 slender metacarpals of the palm and the 14 finger bones or phalanges - 3 phalanges for each finger except for the thumb which has only 2.

b. Pelvic Girdle & Hind Limb :

1. The pelvic girdle consists of 2 hip bones.

2. Each hip bone in reality is made up of 3 separate bones which have fused together. These are Ilium, Ischium and Pubis. The pelvic girdle in the female is broader with a wider central opening in contrast to the narrower corresponding structure in the male, thus facilitating the child-bearing function.

3. The bone of the upper leg or thigh is called the femur and is the longest and the heaviest bone in the body. Its on end fits into a deep socket (acetabulum) in on the hip bones of the pelvic girdle. The lower leg or shank comprises 2 bones, the tibia or shin bone and the narrower and smaller fibula. The tibia is articulated to the femur by a hinge-like attachment, the knee joint. The knee-joint is protected from front by a triangular bone with rounded margins, the patella. The upper end of tibia is much longer than the lower end.

4. Tibio-fibula is followed by bones of the foot. It consists of three sets of bones. a. The Tarsus : It is made up of 7 bones, arranged in 2 rows. They are talus and Calcaneum in first row & the three cuneiform, and the cuboid on the distal row. The 7th, navicular, is placed between the talus and the three cuneiforms. b. The metatarsals : are 5 in number. Each bone has a head, a shaft & a base. c Phalanges : As in the hand, they are 3 in each toe except the big toe in which there are only 2 phalanges.

EVOLUTION OF PRIMATE HAND

Most mammals are capable of only two types of movements of their digits - Divergence & Convergence. Divergence is brought about by extension of the digits and is helpful in load-bearing acts. Convergence is brought about by flexion of digits and is helpful in holding food for eating.

To the above two types of movement of digits in mammals is added the third type - prehensility in the primates. This results due to wrapping of the fingers round an object. Side by side, thumb also acquires various degree of movements. Prehensility & opposability of the thumb has given rise to the development of power grip and precision grip to a greater degree in human which helped him in tool-making & tool-using.

Primates are basically tree dwelling animals. They came into existence in the trees and developed and prospered there. It was wrapping their fingers and toes around branch (prehensility) instead of simply by driving their claws into it (as almost all tree-dwelling mammals do) that the primates were able to make themselves the undisputed masters of the trees.

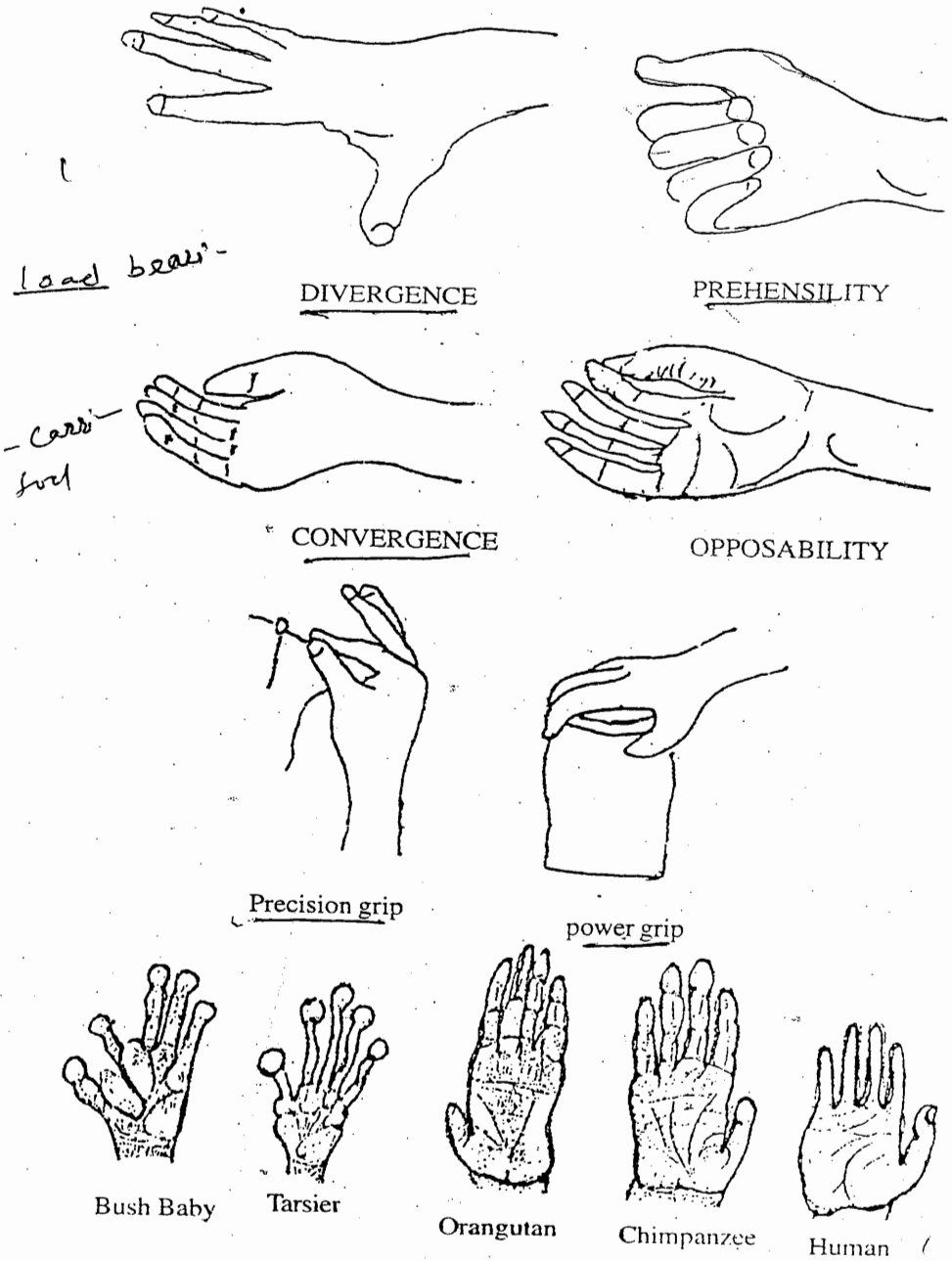
Beginning of change in the hands can be marked right from the stage of the tree shrews that appeared on the earth some 60 million years ago. From then on the story of the primate evolution is largely a story of how each successive group improved its ability to move about in the forest canopy. A good grasp decreased the dangers of falling down and increased the range of feeding. Wrapping of the fingers and toes round the branch also enabled them to increase their size. If it had depended on its claw, such increase in their bodies could not have been effected.

1. Tree-Shrews : i. Tree shrews show beginning of thumb formation.

ii. They have only what is called "Whole-hand control" while they can move their fingers & toes freely, they can only move them together, not individually. when they reach out to grasp a branch, all five of their digits close over it together. All their fingers & toes open up and close together.

iii. In whole hand control, tree shrews are capable of only divergence and convergence.

iv. While moving on the branches, tree-shrews drive their claws into branches and thus get stability. Thus they lack prehensility.



2. Tarsier : Dependence on claws for grasping is absent in tarsiers, instead terminal part of its digits are knobbed that provide strong grasp. Another significant change has occurred in the thumb of Tarsiers. In tarsiers, the thumb evolved an stage ahead of the tree shrews - It can be rotated at the joint of digit and palm. This is known as pseudo opposability because thumb moves at the level of digit palm joint only. ★★

3. New World Monkeys : The third stage of hand-evolution can be traced in new-world monkeys. Complete prehensility of the digits appear for the first time in new world monkeys. It is in them that all claws are finally replaced by flat nails that also aid in prehensility of the fingers. New world monkeys are also one stage ahead in the thumb evolution - It is found that one more joint of the thumb is movable : at the base of the palm. The thumb is also set at greater angle. However, this is also pseudo opposability because thumb don't show all round movement. ★

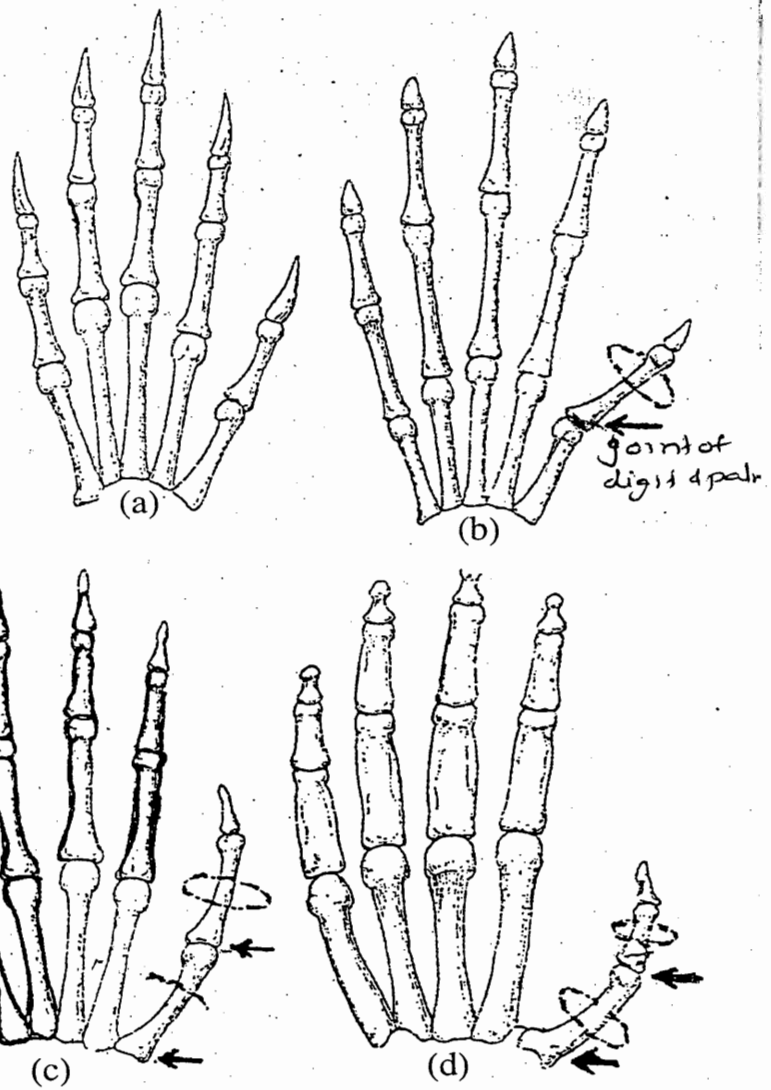
4. Old World Monkeys & Apes : True opposability of thumb developed for the first time in old world monkeys when thumb acquired the ability to rotate all round at the base. Old world monkeys and apes, therefore, are able to hold things in a manner very much similar to ours. ★

The overall structure of hands of monkeys, apes and man differ. In monkeys, hands are used in locomotion and metacarpals (palm bones) in them are shorter than digits and finger tip bones are narrow. In apes, hands are used in swinging or br: tion hence both metacarpals & digits elongated. It is also used in Knuckle-Walking in gorilla and chimpanzee hence terminal port of fingers in them is thickly padded. The hand in apes therefore is utilised in locomotion both in the trees or on the land. Facilitated by prehensility and knuckle-walking respectively.

In apes thumb is opposable but feebly developed and a specialized one. Thus, though it is capable of precision grip, it can't derive any benefit from it. Human thumb, which is highly dexterous, cannot be derived from ape's thumb. ★

Both human thumb and apes thumb can be derived from thumb of the old world monkey-in apes it got reduced due to development of brachiation; In humans it developed because of tool-using and tool making ★

5. Modern Man : In humans, hand is capable of all types of movements-convergence, divergence, prehensility and opposability. Both the components of prehensility - namely power grip and



Evolution of thumb (a) tree shrew (b) Tarsier (c) New world monkey (d) old world monkey & apes.

precision grip have reached highest degree of development. To facilitate such an unique development of precision grip, the phalanges of the hand have undergone following changes-

i) Phalanges decrease in curvature from monkey & apes to man.

ii) Terminal phalanx of thumb increase in length and in breadth.

iii) The length of thumb and the angle between thumb and index finger also increases.

There are present strong muscles in the hand, adductor pollicis and abductor pollicis. Adductor pollicis bring the thumb in alignment with other fingers, particularly with index finger and palm. Abductor pollicis take it away from fingers and palm. A saddle joint between the trapezium (a bone of wrist, one of the carpals) and the metacarpals of thumb is such that it allows movement of the thumb by 45^0.

Saddle joint - Trapezium & metacarpal 45°

Hand In Human Ancestors

1. Australopithecines : They show earliest evidence of human manipulative abilities. Hand and arm bones of *A.afarensis* is known and they are indistinguishable from those of *A.Africanus*, *P.robustus*, and *P.boisei*. Fingers in them had reached their relative lengths. thumb was set opposite and had the ability to rotate the second finger towards the thumb. Thumb and little finger, however, were capable of only little rotation, middle finger had a transverse flat articulation with palm and finger tips were small. Finger bones were, however, curved allowing prehensility and finger and wrist flex or muscle were powerfully developed as is found in apes for suspensory locomotion.

Australopithcine hands, therefore, were used more for locomotor purposes than manipulative functions. It was capable of, of course, for pounding with large hammer stone or throwing. It also shows that *A.afarensis*, though bipedal, spent much time in trees.

2. Homo Habilis : *Homo habilis* show a human pattern of joint mobility of fingers. Though there was less curvature of the digits indicating less prehensility, the muscles were greatly developed. *Homo habilis* is held as first manufacturer of stone tools. The stone tools, known as Oldowan industry, was based on idea of knocking a flake off a cobble, producing sharp edge. The

tools revolutionised their dietary habits and provided the selection pressure that began the anatomical modification of hand.

3. Homo Erectus To Archaic Sapiens : Between the period of H.erectus and Archaic Sapiens, hands changed only gradually. The stone tool technology included flakes as well as stone handaxes. One of the major advancement of the technology (the A Cheulean industry) over oldowan industry was manufacture of tools on flakes. All such advancements must have demanded manual dexterity. But, as shown by a few neck vertebrae, there had occurred no expansion of spinal cord and hence fine control of manipulation must have been missing.

4. Neandertal Man : Though neandertal hands were basically like ours, a few characteristics clearly stand out-

i) There were great development of muscle of shoulder, arm and hand which were used in bringing hands down with a force as in "throwing" or striking a blow.

ii) Joints were large that resisted the force generated in action.

iii) Large fingertips for holding.

iv) The two finger bones of thumb was of equal length rather than first being larger than the second as in our case. This increased their power grip.

v) Differences in the shape of their shoulder joints and elbow joints show that they used their hands more in flexed positions.

The structure of neck vertebrae show that they had enlarged spinal cord and hence fine neurological control of hand than his predecessors.

The middle palaeolithic industry associated with them show flaking and its retouching with soft hammers to produce evenly curved, notched or saw toothed edged implements.

Modern Skills : Manipulative skills, similar to ours, developed in our ancestors 0.1 MYA, proof of which can be discerned in "upper palaeolithic" industry based on long prismatic blades struck off specially prepared stone cores. These blades were used in manufacture of points, Knives etc. All these served to reduce load on human frame. Development of brain facilitated precision grip. During past 40,000 years it has become important aspect of our biological and cultural evolution.

EVOLUTION OF PRIMATES' FOOT & LOCOMOTION

Primates show four types of locomotion 1. Vertical clinging and leaping 2. Quadrupedalism 3. Brachiation 4. Bipedalism. In addition various forms of intermediate locomotor patterns are also evidenced.

1. Vertical Clinging And Leaping

This type of locomotion is present mainly among prosimians. Prosimians developed during palaeocene in the thick forest canopy around 60 mya. Napier and Walker consider this mode of locomotion to be of basic type from which all different primate patterns of locomotion evolved. The animal keeps its trunk erect and grasps the branch of the tree with its both limbs. The hind limb is long and the fore-limb is short. The hind limb is used to propel the body and the animal leaps on the branches.

Tarsiers & Lemurs of present day are typical example of this pattern of locomotion. The tarsal bones of foot which is very small in us, is extremely long in tarsiers. The tarsier uses the bones for extra leverage, giving itself an added spring. Though of the size of a squirrel, tarsiers can cover a distance of 6 feet in a single leap. For holding the branch with foot while leaping, the big toe diverge to some extent from rest of the toes.

2. Quadrupedalism

Monkeys and apes show quadrupedalism :

a. In Monkeys : Monkeys perfected vertical clinging and leaping to their advantage in a different way. With vertical clinging and leaping, there was great constraints in increase of the body size as it would have been difficult for heavy-bodied animals to perform vertical clinging & leaping. The big toe of monkey's foot is set at greater angle than that of prosimians and is prehensile.

Both the thumb and the big toe diverge from rest of the toes, thus both hands and legs of monkeys are prehensile. This makes monkeys very much agile on the trees. They can run on the branches very fast covering great distances quickly and jumping from one branch to another separated wide apart.

b. In Apes : Apes perform quadrupedalism on land. Two forms of quadrupedalism have been practiced by the apes. These are :

i. Palm And Fist Walking : Such quadrupedalism is

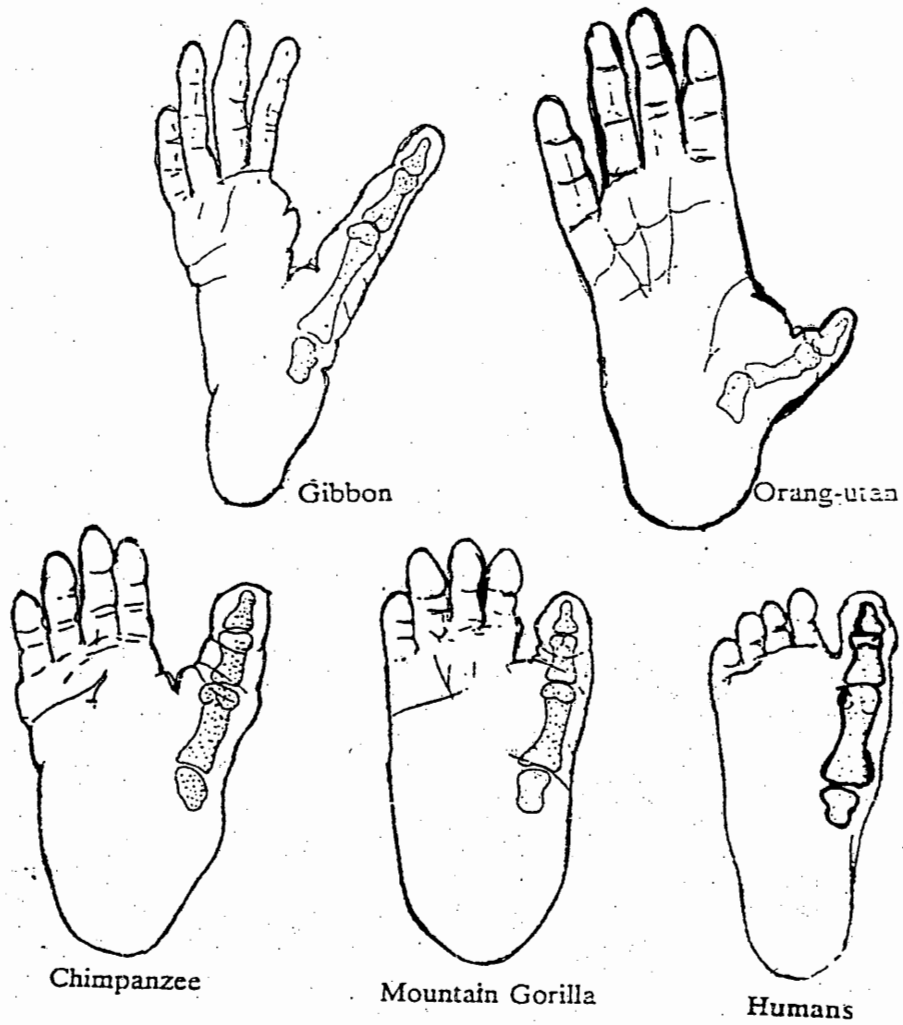


Figure : Feet of modern hominoids compared, showing some skeletal parts in relation to foot form. Note difference in arboreal specializations of gibbon and orangutan, and the degrees of specializations for terrestrialism in chimpanzee, gorilla, and Human.

performed by orangutans on the land. Orangs on the land look awkward and use their whole palm and fist of hand, with legs, in quadrupedalism.

ii. Knuckle-Walking : Chimpanzee and gorilla on the land perform knuckle-walking. Their fingers are thickly padded. When apes perform quadrupedalism their fingers are bent and touch the ground. To effect quadrupedalism in apes, the bones of pelvis and hind limb and muscles associated with these regions, show following characteristics-

1. The pelvis is elongated because both of constituent bones, Ilium and Ischium, are elongated.

2. The head of the femur does not form great obtuse angle with the shaft hence movement of the foot is limited in direction.

3. The knee is habitually bent.

4. The whole foot makes contact with the surface.

5. Gluteus medius and gluteus minimus, which connect pelvis to upper part of femur, and the hamstring muscle (biceps femoris) that connects the femur with the lower leg are the principal extensiors of hip.

3. Brachiation

There are two types of brachiation - Primitive brachiation and True brachiation. In primitive brachiation the animal uses both hands alternately and turns 180^0 while progressing through a branch. in true brachiation there is flight in the air and the animal jumps from a branch to another branch of the tree. In such cases both hands are used at the same time.

It is the chief locomotor pattern of apes though all apes are not equally efficient in brachiation. Gibbons and Chimpanzees are particularly efficient in brachiation because of their small body sizes. They may be found up to 100 feet high on the trees. Large bodied apes, such as gorillas, take to the trees for food and sleeping and that too in the lower strata of forest canopy, seldom exceeding 10 feet of height. Hands are the main organs in brachiation. The four fingers, other than the thumb, form a sort of hook and the animal swings around it. Foot, however, also has some role to play. Foot is also prehensile in the apes, the big toe deviating at an angle of about 45^0 from rest of the toes. Gibbons are the most efficient brachiators of all apes because of its very small body size as well as extremely long fore-limbs in comparison to its hind limb. The shortening of the posterior part of the body

converts the body into a compact mass consisting mainly of trunk which can rotate more easily due to increased centrifugal force.

The clavicle and the nature of attachment of head of humerus with scapula facilitate free rotation of the arm in the overhead position. As a matter of fact, this is the main difference between movement of arms in monkeys & apes - In monkeys, arms can perform only forward & backward movement, with slight sideward movement; In apes, arm is capable of all round movement.

4. Bipedalism :

Types Of Bipedalism : There are various grades of bipedalism such as bipedal hopping, bipedal running, bipedal walking and bipedal standing and striding. While the first three modes of bipedal locomotion is occasionally performed by all higher primates, bipedal standing and striding is performed only by us. For true bipedalism, an erect posture is must, and only we have complete erect posture.

Origin Of Bipedalism : Human bipedalism, according to Napier, developed from vertical clinging and leaping through quadrupedalism. Ape's brachiation and Knuckle-walking is a highly specialized locomotion from which human bipedalism can not be derived.

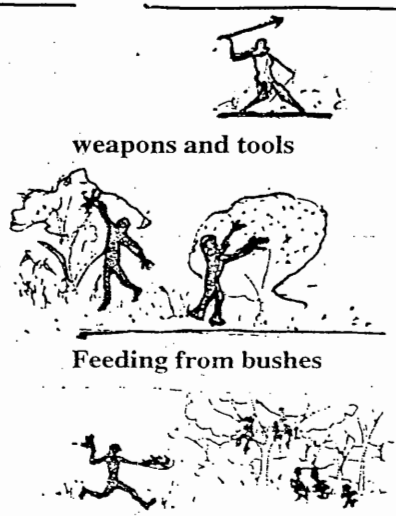


Fig. : Some theories of the origin of bipedal locomotion

intermediate between forest & grassland - sparse trees in which shelter and some food is available.

There are two contrasting views regarding origin of bipedalism. Washburn points out that bipedal gait demands lesser energy in covering greater distances in comparison to other gaits. Man's ancestors at the close of miocene had no option but to venture out to long distances for hunting. Gordon Hewes, on the contrary, proposes that bipedal gait was acquired to free the hand from locomotion. It then can be used in feeding from bushes and grasses, carrying food for provisioning the family, or for future use, use of weapons and tools etc.

Anatomical Changes : According to Napier, human bipedalism has evolved due to following anatomical changes-

a. A shortening and broadening of the pelvis.

b. Elongation of the hind limb with respect to the fore-limb.

c. Adjustment of musculature of hip in order to stabilize the trunk, during erect bipedalism.

d. Reshaping of the foot.

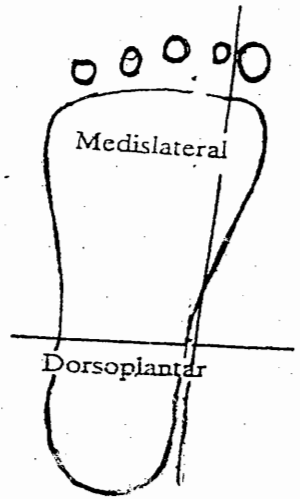
a. Changes In The Pelvis : The short, broad pelvis has moved higher and formed a basin type structure to support the viscera from below against gravitational pull. It has changed its position and has come to lie in the axis of hind limb bone, thus transferring the head and trunk's load directly to legs. The ilium of pelvis has a number of spines that serves to provide attachment surfaces for the muscle such as sartorius, Rectus femoris etc that help in thigh movements and bipedal locomotion. The Ischium of the pelvis has flattened allowing human to sit comfortably.

b. Changes In Hind Limb : Both the bones of leg, femur & tibio-fibula is elongated. Especially femur shows some positive changes for bipedal locomotion. The head of femur has undergone shifting and forms 120^0 angle with the femoral shaft. The femur head, after its attachment with the pelvis, is capable of all round movement. Linea aspera, an attachment surface for muscles on femur, is particularly developed in humans that keep hind limbs straight during bipedal walking.

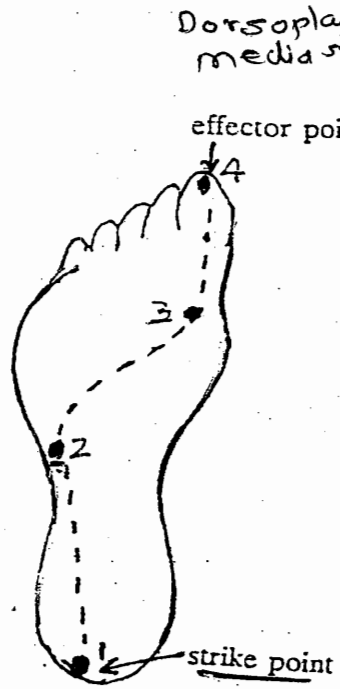
c. Changes In Muscle : Leg, thigh and hip musculature have developed to facilitate upright standing, walking, running and climbing. Gluteus medius, Gluteus minimus and Gluteus maximus stabilize pelvis during walk. Sartorius and Rectus femoris of thigh, biceps femoris and Gastrocnemias of legs are also well developed.

d. Reshaping of The Foot : The axis of the human foot lies between the big toe and the second toe. For this reason, the big toe has become non-opposable to bear maximum load transmitted upon the foot. In addition, foot has developed two arches- the dorsoplanter and the medislateral arches. The two arches support the weight of the body.

When standing, the load is distributed equally on each side of the axis of the two arches; while in motion the load is dynamically distributed from point of contact (heel) through the fifth metatarsal to the big toe that provides propulsive thrust.

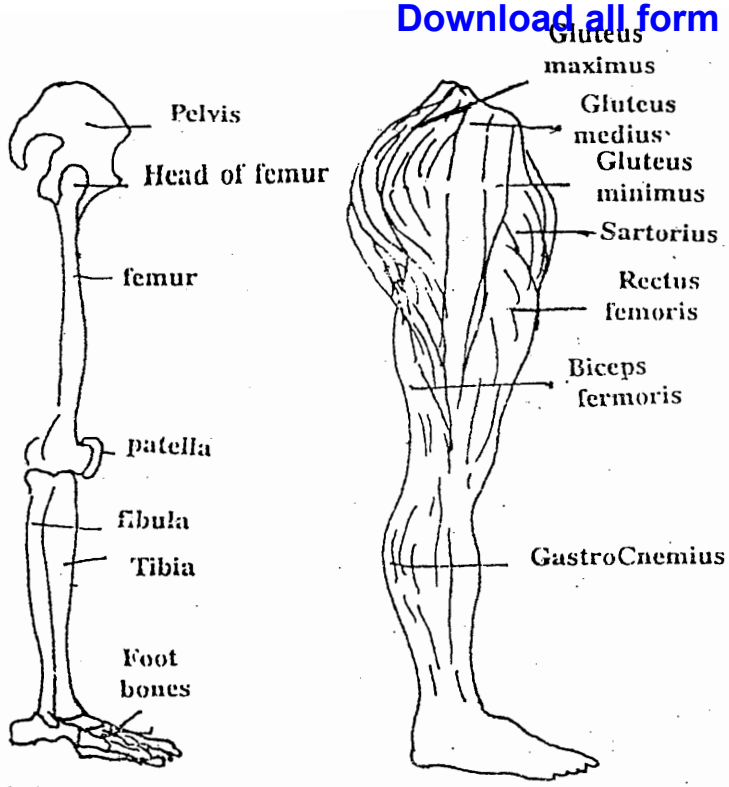


(a) Distribution of load along two arches while standing.



(b) distribution of load, & thrust during walking

Fig : Human foot axis (a) during standing (b) during walking



(A) skeleton (B) muscles of hind lumb of man

Associated Changes Due To Bipedalism : Changes in locomotion pattern from quadrupedalism to bipedalism initiated changes in many parts of the body, chiefly vertebral column and skull, including thoracic cage. The various changes can be outlined as follows-

i. Formation Of Four Spinal Curves : There has developed four curves in the spinal cord- cervical, thoracis, lumbar & sacral of the four curves, thoracic and sacralare are congenital whereas cervical & lumber develop during childhood. The four alternative curves of the spine allow erectness of the trunk.

ii. Modification In Sacrum : The vertebrae of sacral region unite with ilium of pelvis, the latter in turn to femur. In man, the sacral - pelvis joint is nearest to the pelvis-femur joint so as to transfer the load directly to femur.

iii. Progressive Increase In The Vertebral Dimension : The vertebrae increase in size downward thus forming a cone-shaped spine which is more stable in load-bearing function.

iv. Shifting Of Foramen Magnum Of Skull : In quadrupeds, foramen magnum is situated more dorsally & posteriorly. In humans due to bipedalism, it has shifted forward and downward.

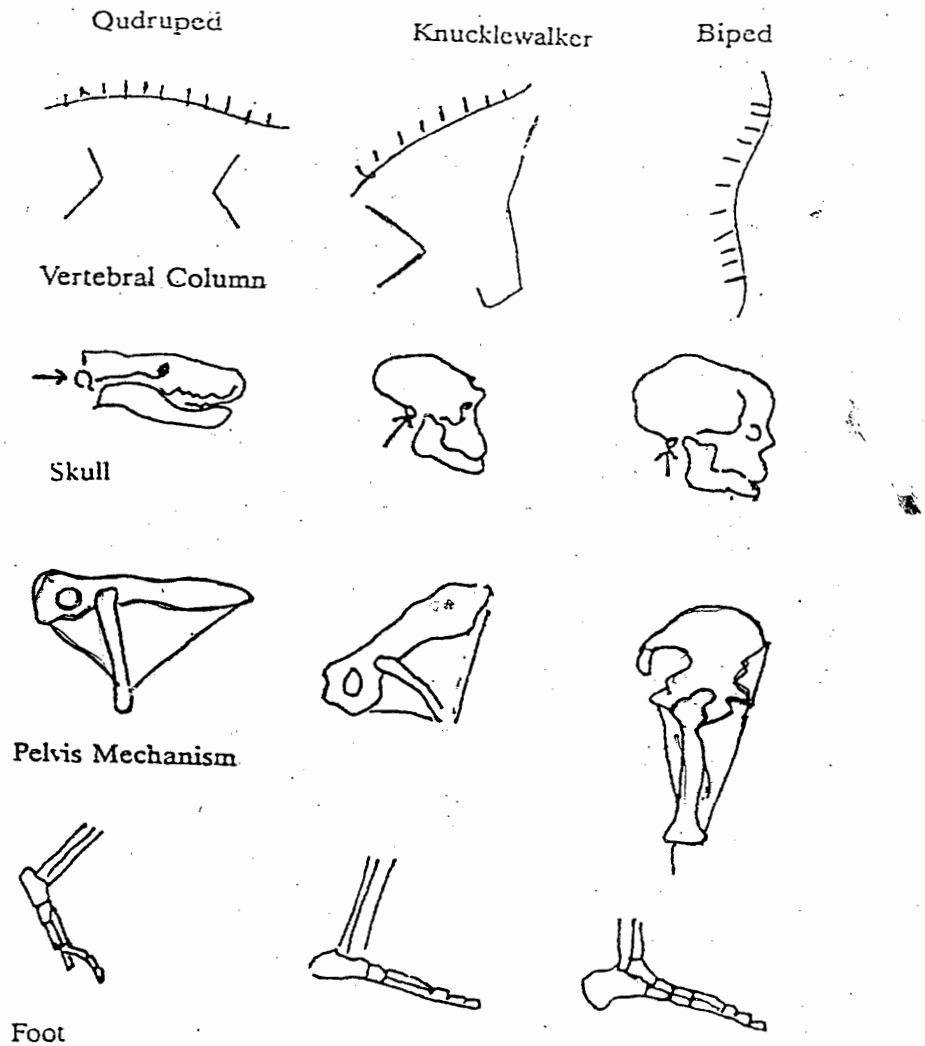


Fig : Changes in body due to bipedalism

EVOLUTION OF JAW & DENTITION

Dentition is an important feature useful in deciphering evolutionary relationships because

1. Dental characters are heritable and unchangeable over the years.

2. Teeth are durable & hence ideal for fossilization.

3. It is indicative of the nature of the ecological habitat in which the animal survived. All mammalian teeth can be derived from insectivore's teeth. Most mammalian groups, with exception of primates, is basically carnivorous. Primates had a basal stock of animals from insectivores that was predominantly frugivorous and only occasionally and opportunistically carnivorous. This dual dietary habit is reflected in the structure of teeth of primates.

Structure Of Tooth Of Primates : Primates teeth, like other mammalian teeth, is made up of hollow core, the pulp, containing blood vessels & nerves. Surrounding the hollow core is the dentine. The crown of the teeth, projecting above the gums, is the outermost layer which is ectodermal and the hardest of all parts of the body. This is enamel. It is made up entirely of calcium phosphate crystals.

The pattern of enamel vary in living and fossil primates - In gorilla and Chimpanzee enamel is not as thick as is found in fossil apes, hominids and modern humans. It is only slightly thicker in orangutans. The thin enamel allows underlying dentine to be exposed earlier so that foliage can be cut more effectively by Chimpanzee and Gorilla. Thicker enamel probably evolved in fossil apes and hominids to combat the effects of tough food.

Nature Of Dentition : Primates, like most mammals, show diphyodonty - i.e. replacement of milk-teeth by adult teeth. Molars develop only once in the adult life. Since there are 12 molars altogether, number of milk teeth is 20.

Enamel preserves growth lines and by cutting sections of teeth it is possible to calibrate the time of such event as eruption of permanent teeth. It is 6 years in modern humans and 3-5 Yrs. in great apes. In several young hominid fossils such as Taung baby (Australopithecus) from south Africa, it is estimated to be around 3 years. Fossil hominid thus resemble extant great apes in this

Dental Formula : The four types of teeth present in mammals are incisor, canine, premolar and molar, designated in dental formula by symbols ICPM, and number of each teeth written for upper and lower half. Thus, to get the full number of teeth; the dental formula has to multiplied with 2 and added together.

Dental formula of primitive mammals = $\frac{3143}{3143}$

Dental formulae of primates : The following are the dental formulae of different primates group-

a) Prosimians :

Tree Shrews : $\frac{2133}{3133}[\times 2] = 38$

Lorises & Lemurs : $\frac{2133}{2133}[\times 2] = 36$

Tarsius : $\frac{2133}{1133}[\times 2] = 34$

b) Anthropoidea :

New world monkeys : $\frac{2133}{2133}[\times 2] = 36$

Marmosets and Tamarins : $\frac{2132}{2132}[\times 2] = 32$

Old world monkeys, apes & man : $\frac{2123}{2123}[\times 2] = 32$

Types Of Teeth : The types of teeth in primates is similar to those in other mammals. These are from front to back- incisors, canine, premolars and molars. Incisors and canines are meant for biting of the food - incisors more helpful in frugivorous biting and canine in carnivorous biting. Premolars and molars have variable surface cusps meant for grinding of the food. These are also called "cheek teeth".

1. Incisors : During the course of primate evolution, there has been a trend towards reduction in the size of incisors. this may have been possible because of ever increasing use of hands in manipulative works for preparation of food, thereby decreasing gradually incisor's role in such activities. In prosimians incisors form comb-like structures for grooming hair.

2. Canines : Canines play two roles in primates- Shearing of tough food and agonistic display. In monkeys and apes, the upper canine bites against first lower premolar which is sectorial and thus helps in shearing activities. Enlarged canines of monkeys

and apes, particularly males, is used in agonistic display during combat, or while disciplining erring members of their own species. In modern sapiens canines don't project beyond the level of other teeth and never used in agonistic display. Large canines were lost because it must have lost selective advantage to the use of tools and the small canines must have gained some selective advantage. Through time, frequency of large canine gradually decreased. Mutation and natural selection must have played dominant roles though drift and associative mating also seem to have aided such forces.

3. Premolars : Apes, monkeys and some of the earliest hominids such as *A.afarensis* has lower first premolar which is sectorial (A cutting surface against which upper canine bites). In all the later fossil hominids and modern sapiens, the first premolar is a bicuspid tooth, with two cusps on the biting surface.

All the remaining premolars in monkeys, apes and hominids are bicuspid. In many fossil hominids, premolars have become molariform by acquiring extra cusps and expanded to deal with tough food. Such is the case with *Australopithecus africanus, Paranthropus robustus* and *P.boisei*.

The number of premolars were 4 in primitive mammals. Its number has decreased to 3 in prosimians & new world monkey and to 2 in old world monkeys, apes and man. It is supposed that 2 premolars nearest the canines are lost hence in old world monkeys, apes and man are named P3 and P4 indicating loss of P1 and P2.

4. Molars : Though number of molars have remained constant (3 in a quadrant) throughout primate evolution, except marmosets and tamarins, its shape has considerably changed in different groups.

Monkeys always have four cusps on the molars which are joined in pairs to form two ridges or lophs (bilophodont), one at the front and one at the back. The molars of lower and upper jaw slice past each other and crush plant materials.

In apes and man, the upper molars has four cusps whereas lower molars have five cusps. The pattern of grooves between the cusps in the lower molars form a modified 'Y'- shaped fissure.

Nature of cusps has also changed during the course of hominid evolution. Earlier hominid fossils show up large molars with expanded biting surfaces with pointed cusps.

In later hominids. molar sturcture has changed. Molars are adapted to deal with both kind of food. In human, it has short, low crowns (Brachyodont) with rounded cusps (Bunodont). The reduction of size of teeth may be related to the development of tool-use & a meat oriented diet. The large canines are used by the apes in breaking open hard fruits. Humans use a chopping tool. As for agonistic displays, canines lost its importance because humans used weapons for defence and depended upon co-operative hunting society.

The molar teeth of ancestral placental mammals had a basically triangular pattern. The upper molars were simple triangles with only three main cusps. The lower molars were similarly shaped with three main cusps but the distal side also had a small talon bearing two or three extra cusps. The basic pattern is still recognisable in modern tarsiers. In other living primates, however, there has been a trend to add a fourth cusp on the upper molar and to lose the leading cusp on the main triangle of the lower molar, leaving only four or five cusps. This arrangement has been developed in various ways. The most striking change is found in old world simians. Both upper and lower molars of old world monkeys have four cusps linked in pairs by transverse ridges (Bilophodonty). By contrast, the lower molars of great apes have five well developed cusps, a Y-5 pattern.

Brachydonta – Bunodont Bilophodonty

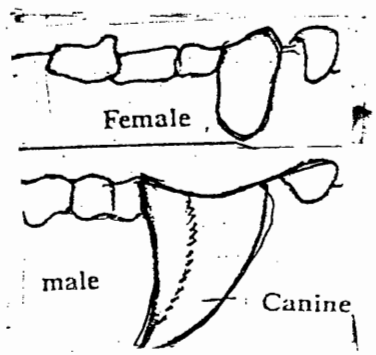


Fig. : Sexual dimorphism in Canine tooth in Primates

Evolution of molar and premolar teeth has influenced shape of the jaw and size of the front teeth. Hominid fossils with greater sizes of cheek teeth had smallest incisors and canine (*Paranthropus boisei*)(Nut cracker man). The jaw in them is also massive for resisting strain of masticatory muscle. On the contrary, fossils with smaller sizes of cheek teeth had greater size of incisors and canines eg. *A.afarensis, A.af ricanus, H.habilis* etc. The jaw in them is also slender.

A. In Prosimians :

1. In prosimians except tarsiers, the teeth are present in the form of dental comb which is used to clean the body. Lower incisors make the main part of this dental comb. There is, however, reduction in the number of incisors of the lower jaw progressively. The number of lower incisors in tree shrew is 6; in lorises and lemurs 4; and in tarsiers 2. The number of other teeth remain the same in all the groups hence total number of teeth decreases in them by factor of 2; 38 in tree shrews, 36 in lorises and lemurs and 34 in tarsiers.

2. In Aye-Aye insicors grow throughout life as in rodents. The cheek-teeth (premolars and molars) are not specialized and conform to basic mammalian pattern with 3 cusps (Tribosphenic).

3. In some prosimians, such as lemurs, the lower canine is also incorporated with comb.

4. Lemurs and Lorises have a central diastema on the upper jaw.

In tree shrews lorises and lemurs the upper lip is fused with the jaw and has a median cleft. In Tarsiers, however, lips are not fused with the jaw and development of some facial muscles have enabled them to experiment with some facial expression.

B. In Anthropoids :

Premolars show reduction in number. The number of premolars vary in different anthropoid groups - In new world monkeys, the number of premolars in both upper and lower jaw is 3 + 3 whereas in world old monkeys, apes and man the number is 2 + 2. Thus, the number of teeth in new world monkeys is 36 and rest of the anthropoids 32. Marmosets and Tamarins among the new world monkeys is exception. They have lost a molar or on each side of jaw.

1. **New World Monkeys** : Molar tooth of monkeys differ from those of apes and man in the number of cusps and its

arrangement. In monkeys first lower molars have four cusps which are arranged in two transverse crests forming a pattern of plus (+). Marmosets and tamarins are exception who show three cusps.

2. Old World Monkeys : In some old world monkeys such as baboons, the canines are large and are larger in males than in females. By rolling back lips, these creatures present a fierce aggressive look. The molars in them bear the same number and pattern of cusps as is found in new world monkeys, except differing in minor details.

3. Pongid Dentition : i. Incisors are broad, spatulate.

ii. Canines projecting and fitting into a diastema. Such diastma (simian gap) is present on both upper and lower jaws - in between incisor and canine in the upper jaw and between the canines and first premolar on the lower jaw. Thus jaws cannot be moved in rotary motion like in hominids. Canine is larger in males hence display sexual dimorphism.

iii. The first lower premolar is specialized, the upper canine shears directly in front of it. The 1st lower premolar is larger than the other teeth and presents a cutting edge for the canines. This is known as sectorial premolar.

iv. Molars are in parallel rows and the number and arrangement of cusps in lower molars resemble the Y-5 pattern.

In Y-5 pattern of lower molar, three cusps (1,3,5) are arranged along cheek side and two cusps (2,4) along the tongue side. The five cusps are separated by the grooves. Cusp 3 is separated from 1 and 5 by forked part of a Y. Y is completed by a groove between cusp 2 and 4.

v. The dental arch of apes is U-shaped and lower jaw shows presence of a bony-ridge called simian shelf. It extends backward from the symphysis of the jaw and supports enlarged incisors and canines of the lower jaw.

vi. Because of longer tooth rows the face of apes p... into a sort of muzzle - prognathous. In humans, the face does not project in this manner; it is more nearly vertical, or orthognathous.

4. Hominid Dentition : The hominid dentition can be differentiated from ape-dentition in following :

a) All teeth are at the same level. Incisors are chisel shaped

b) Canines are not projecting.

c. First lower premolar is not sectorial. Premolars have 2 cusps.

d. Lower molars have 5 cusps with modified Y-5 pattern in which there is present a deflecting wrinkle on cusp 2 and a lobe on cusp 3. The number of cusps may be reduced to four in 2nd & 3rd lower molars. Each lower molar possesses 3 roots.

The number of cusps on upper molar is always less- 4, 4 or 3, and 3 in first, second and third upper molar, respectively.

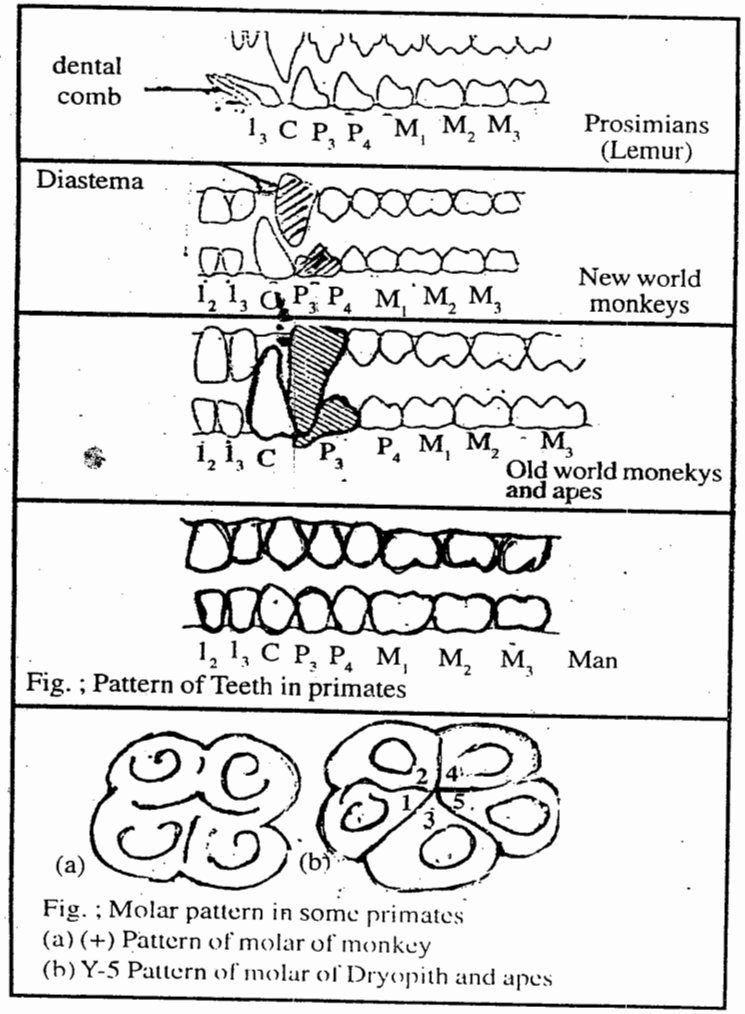


Fig. ; Pattern of Teeth in primates

Fig. ; Molar pattern in some primates
(a) (+) Pattern of molar of monkey
(b) Y-5 Pattern of molar of Dryopith and apes

EVOLUTION OF BRAIN

In this chapter we shall try to understand the general organisation and function of human brain and compare it with those of apes and monkeys, the other groups of primates. The adult human brain, a most complex and highly developed organ, has five main regions : the medulla oblongata, cerebellum, midbrain, thalamus and cerebrum. The Medulla oblongata and midbrain are often collectively referred to as the brain stem due to their general location and shape.

The lower anatomical regions of the brain deal with automatic functions (e.g., heart rate and respiration), whereas successive higher region of the brain are concerned with correspondingly more integrative and advanced activities, such as coordinated muscular activity and reasoning or abstract thought.

The lower regions of the brain, which are similar in most mammals, are the most primitive brain portions. The evolution of higher mammals has been accompanied by an increased development in size and function of the anterior portion of the brain, the cerebrum. Although, the brain stem still carry out their original functions, in man they are subject to various degrees of control and regulation by the higher centres.

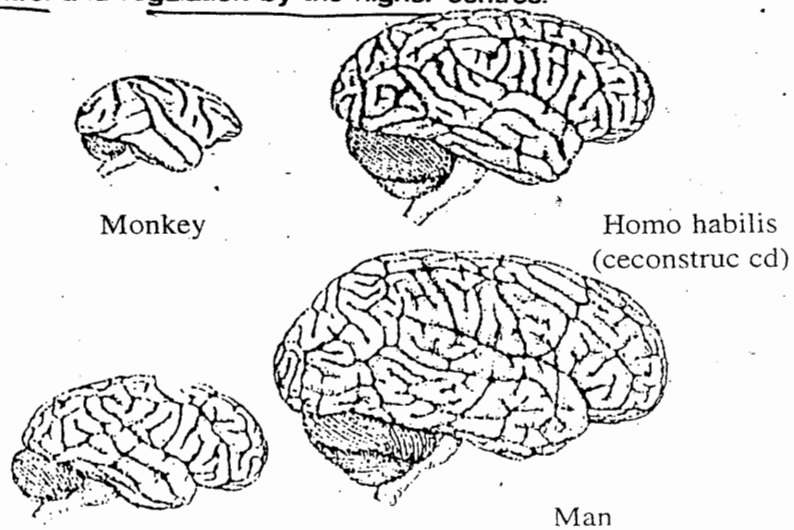


Fig. : anthropoid brains :

cortex as a whole.

i. The Frontal Lobe : It is the centre for the control of motor behaviour and complex aspects of adaptive behaviour such as motivation. The centre imparts man the capacity to concentrate on his work. In the left frontal lobe there is specialized area called Broca's area. It is concerned with structure of speech, the grammar, and with the mechanics of muscle movement in face, lips, tongue and larynx and hence important for vocalization. This area is feebly developed in monkeys and apes.

ii. Parietal Lobe : The parietal lobe contains both sensory and motor areas. Its' sensory area assess the sensory inputs from the sensory channels and organise appropriate motor responses.

iii. The Temporal Lobes : It is the house of memory. In

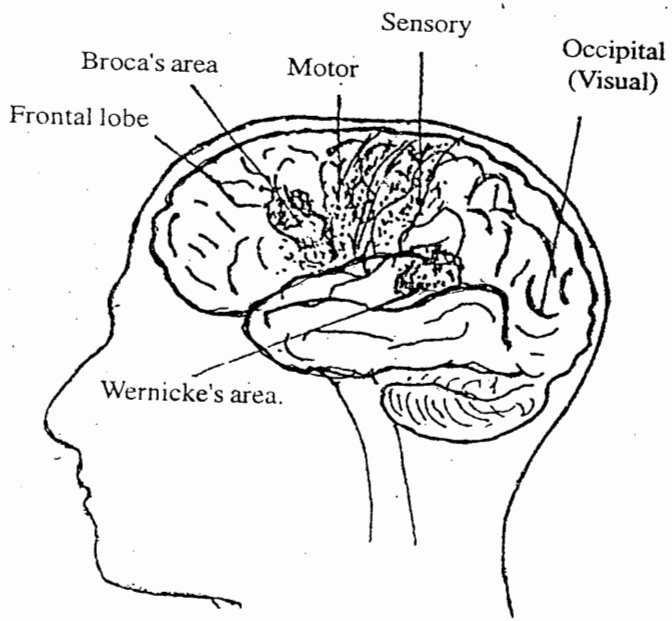


Fig. : Localization of function in the cerebral cortex of man.

Since cerebrum presents the main difference among various groups of primates it will be discussed first, followed by other regions of brain, namely thalamus and hypothalamus, mid brain, cerebellum and medulla oblongata.

1. Cerebrum

The cerebrum, the largest part of the human brain, consists of more than half the 10 billion neurons of the entire nervous system. It is also the largest brain region of apes and monkeys but is a less prominent structure in the brains of lower vetebrates. It is the unique organ of the human species, for its various activities account for the basic differences between man and all the other existing animals as well as those that preceded him in the evolutionary sequence. Within the cerebrum reside the most advanced functions of the nervous system including memory, intelligence, insight, personality, and judgment and the most highly developed centres for various sensations including sight, hearing, smell, taste, and so on.

Structure : The surface or cortex of the cerebrum in man covers and overlaps most of the other structures, covering an area of about 400 square inches. It is composed of some 2 billion cell bodies in a vast interconnection mass arranged in folds or convolutions. The cerebrum is divided by a deep longitudinal groove into two halves called hemisphe es which are not completely separated from each other but are connected together by the underlying white matter. This white matter is composed for the most part of nerve tracts connecting different parts of the cortex to each other, as well as to other parts of the brain and spinal cord.

Function : Cerebral functions can be known in a variety of ways. These have included examining the effects of removing or destroying different cerebral areas in experimental animals, observing the reactions evoked by stimulating exposed cerebral regions in human and animals, studying the symptoms of patients with known brain damage, and using a relatively recent technique for measuring electrical changes called brain action potentials in the brain of intact, living individuals. Microscopic investigations have contributed important information establishing that there are more than 100 different structural areas in the cortex concerning several functions. Although we know that certain areas of the cerebral cortex are responsible for specific roles, it seems highly likely that many other functions are completely dependent on the

the left lobe is situated a specialised area, called wernicke's area. It is the major storehouse for visual, auditory and verbal memory. It enables man to find out appropriate words based on his memory. The Wernicke's area is connected with Broaca's area which is concerned with structure and mechanics of speech. Together, the Broca's area of frontal lobe and Wernicke's area of temporal lobe enable man a meaningful articulation with use of appropriate words. The areas are well developed in man; feebly developed in monkeys and apes.

iv. The Occipital Lobe : It is concerned with visual perception. The size of the occipital lobe in monkeys and apes is larger than that of man. Thus situation is reversed in case of occipital lobe; other lobes, namely frontal, parietal and temporal are smaller in monkeys and apes. Large occipital lobe of Chimpanzee is characterized by Lunate Sulcus or Furrow. Occipital lobe, which is concerned with visual sense is of greater importance for predominantly tree-dwelling monkeys and apes than the terrestrial man.

2. Thalamus and Hypothalamus

The thalamus (and hypothalamus) lie above the midbrai: and below the cerebrum and serves as a relay station, receiving nearly all the impulses arriving from the different sensory areas of the body before passing them on to the cerebrum where they give rise to conscious sensations.

The hypothalamus possesses the visceral reflex centres for controlling and integrating the metabolism and functions of the internal organs and tissues. It regulates body temperature, smooth muscle activity, water balance, appetite, blood pressure, and possibly carbohydrate and fat metabolism. For example, reflex centres in the forward part of the hypothalamus act to prevent overheating by increasing blood circulation to the skin, thus accelerating heat loss by perspiring and by a faster rate of breathing. The mechanisms of fever production are thought to be associated with release from damaged body cells of a substance that affects the temperature regulating centres of the hypothalamus

The hypothalamus apparently also participates in producing sleep and maintaining the waking state. It determines the sexual drive, and develops such basic sensation as hunger, thirst, fear, and rage. Finally, the hypothalamus is also centre of control for

anterior pituitary function and the producer of certain hormones.

3. Midbrain

Immediately below the lower part of the cerebrum is the midbrain, a mass of projection tracts made up mostly of white matter surrounding a central cavity. The tracts serve largely as conduction pathways between the spinal cord and other parts of the brain. The dorsal portion of the midbrain also possesses a prominent mass of gray matter which collaborates with the cerebellum in controlling muscular coordination. In addition, the dorsal surface of the midbrain displays four rounded protuberances in which lie certain auditory and visual reflex centres. These areas mediate such reflexes as constriction of the pupil of the eye (when exposed to strong light) and the pricking up of an animal's ear (in response to sound)

4. Cerebellum

Above the medulla and extending laterally from it is the cerebellum which is made up of two large masses. Each hemisphere of the cerebellum is compos d of an interior of white tracts, which link the cerebellum with other parts of the brain and spinal cord, and an exterior of gray matter (mainly neuron cell bodies) arranged in numerous folds and convolutions. The cerebellum does not itself directly control body activities. Instead the impulses from its gray matter somehow operate to coordinate the activities of several other brain centres regulating and integrating certain body functions, particularly skeletal muscle activity. It is responsible for normal movements that are smooth, timed, steady, precise and graded in terms of force, extent, and rate (coordinated muscular activity).

Injury, disease, or experimental removal of the cerebellum in an animal result in a disorder characterized by movements which are jerky, shaky, and poorly regulated. More recent evidence indicates that the cerebellum is also concerned in the integration of the sensation of touch, hearing, and sight.

5. Medulla Oblongata

The medulla oblongata is the lowermost part of the brain, which connects to the spinal cord. it measures about an inch in length and consists mostly of ascending and descending tracts of white matter, with some gray matter in its interior. The enlarged

cavity within the medulla oblongata is called a ventride, one of four which occur in brain. The gray matter scattered within the interior of the medulla contains several vital reflex centres including those that control the rate of heartbeat, breathing, and constriction and dilation of blood vessels. Other reflex centres include those responsible for vomiting, coughing, sneezing, hiccuping, and swallowing.

Evolutionary Features Of Human Brain : Besides decrease in size of olfactory lobe, the human brain is differentiated from other primates brain by its several functional uniqueness. Several theories have been extended to explain the uniqueness (After Deacon, 1992)

a. Expansion of the brain to increase intelligence and memory, enabling humans to learn complicated skills such as tool-making and language.

b. Addition of new brain structures to provide new functions such as specialized language abilities.

c. Reorganisation of the connections of existing brain structures to allow them to serve novel functions such as the analysis of grammar.

d. Changes in the relative sizes of different brain areas, expanding certain structures to augment particular abilities.

Brain Size : The absolute size of the brain is not important; it is relative size of the brain with respect to body-size which is important. In humans, this ratio is higher than many other animals and primates. Intelligence, however, does not depend even on this ratio; intelligence depends on how much neurons of brain are extra, not associated to essential bodily functions. Brain possesses "extra neurons" when there is allometric differences in growth between brain and rest of the body; rate of growth in brain being faster than the overall growth of the body (encephalisation quotient). The encephalisation quotient is higher in the humans and three times greater than the chimpanzee and gorilla with our body-size.

This difference in the encephalisation quotient in human and apes is not marked during gestation period. Brain is approximately 12% of the body weight and grow at the same rate. In apes, brain slows growing after birth whereas in humans this slowing of growth doesn't occur until more than a year after birth. As a result, the shape of the curve described by human brain and body growth differs from that of other primates

APES AND MAN - DIFFERENCES

Ancestors of man and apes started following different evolutionary pathways since miocene when large scale mountain building activities and resulting aridity had destroyed miocene forests, limiting forest niche. The increased competition for forest niche may have compelled a group of dryopithecus (the miocene ancestor of ape and man) to leave the forest and opt for savannah living where competition may have been less intense. Ancestor of apes stayed back in forests and thus developed as apes; ancestors of man took a risk in opting for a savannah living and developed as man. The difference in apes and man is, basically, due to difference in their habitats they were exposed to since long. The differences between apes and man can be seen in following areas of their structure and function :

a. Differences due to locomotor pattern.
b. Differences due to dietary habits.
c. Differences in hand-structure.
d. Differences in skull
e. Differences in brain
f. Cultural differences.

a. Differences Due To Locomotor Pattern

1. Man is erect bipedal whereas apes are basically tree dwellers with brachiation as the main locomotor pattern. Larger apes, such as male gorilla. take to trees for food and sleeping and seldom takes to brachiation. On the ground, Orang-utan performs palm and fist walking and gorilla and chimpanzee perform knuckle-walking - both patterns being variants of quadrupedalism.

2. In man are present four curves in spinal column, cervical, thoracic, lumbar and sacral - the first and the third being acquired in the childhood whereas the second and the fourth being congenital. Apes lack such curves of spinal column. Man, thus, can stand erect habitually, apes not.

3. In man, vertebrae of the spinal column show progressive increase in the size so that it is conical in outline. A conical spinal column can bear load of head much efficiently. Not so in apes.

4. Thoracic basket in apes is expanded hence centre of gravity lies much away from the long axis of the body. In man, the thoracic basket is compressed so that centre of gravity of human

pass through their foot.

5. In man, forearms is shorter than legs, the latter support the body. In apes, forearms are larger than legs which, together with forearms, supports the body.

6. Ilium of pectoral girdle is basin type in man to support internal organs against gravitational pull. In apes, Ilium is elongated. Anthropoidal plate and extension of Ilium is shorter in apes but extended in man.

7. The spinal column-pelvis axis is closer to pelvis-femur axis for smooth transference of the weight of body in man. Not so in apes.

8. In man, neck of femur makes large angle with the axis of shaft so that it articulates with the pelvis laterally and allows all round movement of the leg. In apes, femur is short, thick, and its neck doesn't make great angle with its shaft. Thus an ape lacks perfect erectness and bipedality.

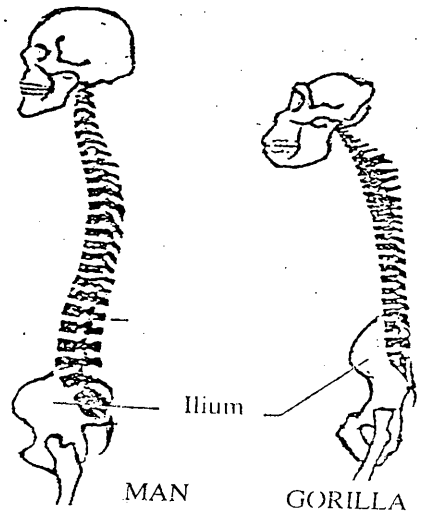


Fig. : Comparison of skull, vertebral column and pelvis of man & gorilla

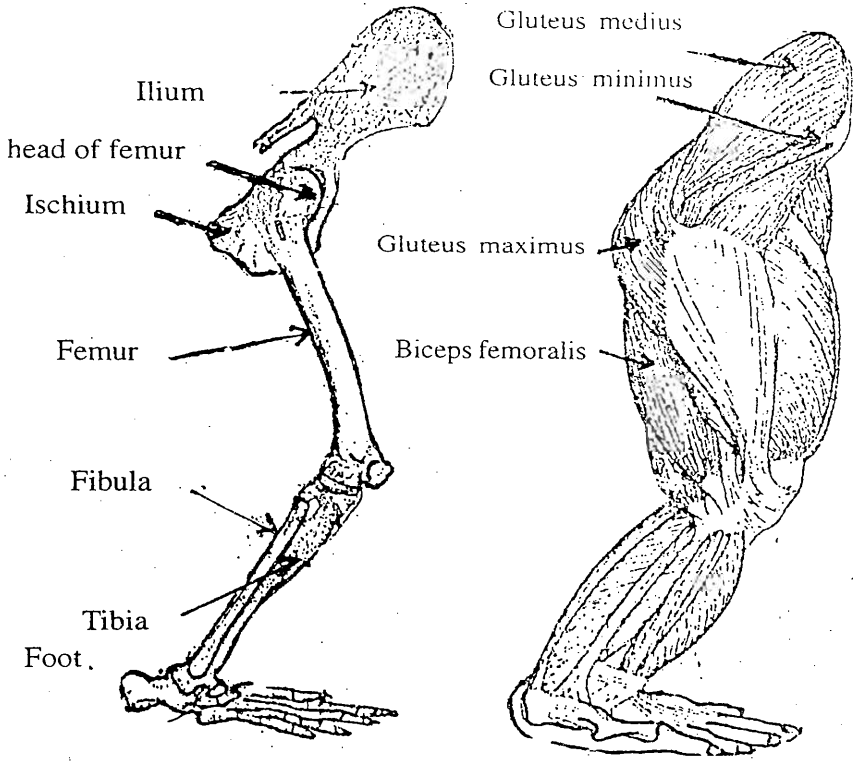


Fig. : Apes' petvis and hind limb bones (A); Its associated muscles (B).

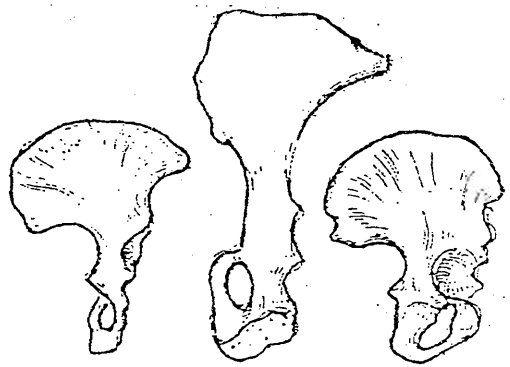


Fig. : The right pelvic bones of : A, Australopithecus; B, chimpanzee: C. Homo sapien

9. In man, linea aspera is greatly developed, but not so in apes. Linea aspera, at the back of femur provides attachment surface for the muscle that helps in erect posture.

10. In man, foot with adaptation for erect posture. Calcaneum formingheel, metatarsals held closely by transverse ligaments, hallux or great toe or big-toe non opposable and doubly arched foot are some of the adaptation of human foot for bipedalism. Apes have their heels poorly developed and foot without arches. Their toes are longer than man's and load-line is in the centre.

11. Development of leg, thigh and hip musculature in man has reached a stage that facilitates upright standing, striding walk and running. Hip muscles, gluteus maximus, gluteus medius and gluteus minimus are well developed for stabilizing pelvis during walk. Sartorius and rectus femoris of thigh and biceps femoris and Gastrocnemius of legs are also well developed.

b. Differences Due To Dietary Habits

Apes are predominantly frugivorous while man is largely omnivorous with greater dental and alimentary adaptation for vegetarian diets. This difference in diet has caused many dissimilarities in the masticatory apparatus of the two.

1. In apes incisors are broad spatula-like that makes the jaw broad U-shaped. In man, small incisors make the dental arcade smooth rounded parabola.

2. In apes, canines are large, projecting above the level of other teeth, the lower canines fitting into a gap, simian gap or diastema, between lateral incisors and canines of upper jaw. The canine-interlocking in apes, thus, allows only vertical motion of the jaws where as the motion is rotatory in man.

3. In apes, the first lower premolar is sectorial.

4. In apes, molars have conical cusps (5 in lower molar) separated by characteristic arrangement of intervening grooves (Y-5). Human molars have low, blunt cusps adapted for crushing by rotatory motion (a variable of Y-5).

5. Simian shelf is present in apes but absent in man.

6. In apes, face is prognathous without chin. In man, face is Orthognathous with chin.

7. Sagittal crest and supra orbital ridges in the skull well

developed in apes for attachment of jaw muscles.

c. Differences In Hand Structure

1. In apes, hand is utilized for locomotor purposes. In brachiation the fingers form a hook. Thumb, though opposable, is not well developed. In man, however, hand is free from locomotor purposes and utilized for handling objects. This has been facilitated by several anatomical changes in hands.

2. Thumb of man is more elongated then that of apes, though both have opposable thumb.

3. Terminal phalanges in man wider; it is narrower in apes. Man is thus capable of precision grip to the greatest extent.

4. Phalanges are curved in apes; straight in man.

5. The angle between thumb and index finger is greater in man than in apes.

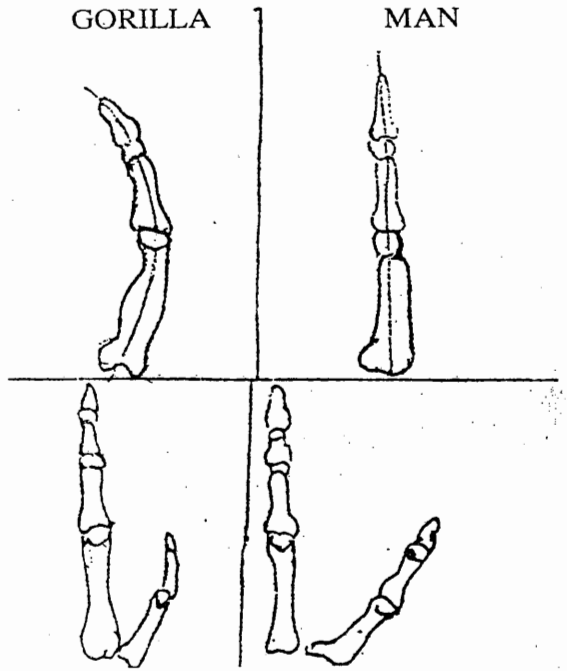


Fig : Showing (a) Reduction in curvature of phalanges
(b) Increase in length of thumb & its angle with index finger from gorilla to man

6. Hand muscles in association with thumb i.e. adductor pollicis and abductor pollicis are better developed in man.

d. Differences In Skull

1. Nuchal crest, present at the back of skull, is lesser developed in man than the apes. The crest serves to attach nuchal muscles of neck that balance the head in quadrupeds. Skulls is well balanced in man hence nuchal muscles are also reduced resulting in slender neck in man. Slender neck can perform maximum rotation.

2. Sagittal crest is not much developed in man, whereas in

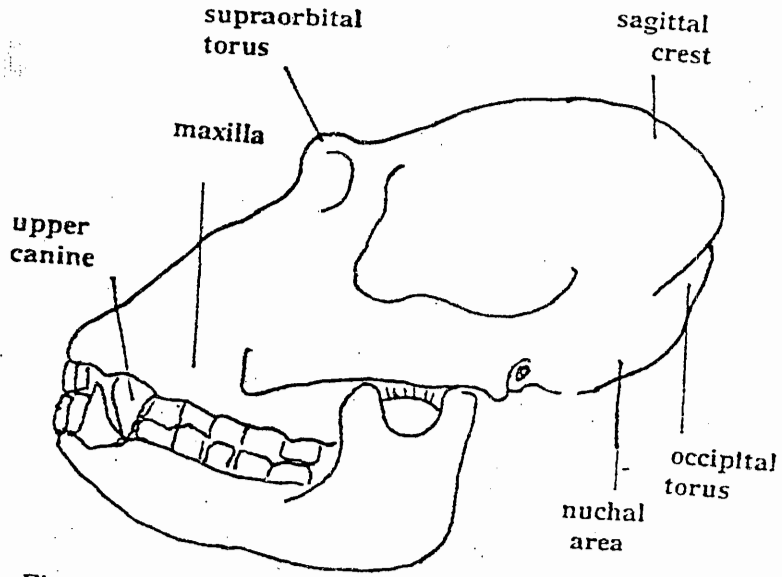


Fig. : Skull of a male gorilla

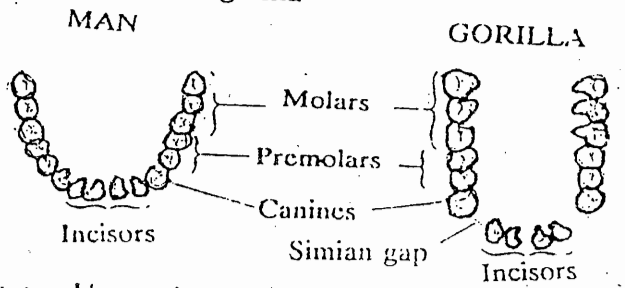


Fig. : Upper dental arches of man and gorilla.

apes it is developed. The crest serves to attach jaw muscles which are heavy in apes.

3. In man, cranial part of the skull is large than the facial part whereas reverse is true for the apes.

4. Cranial capacity of man average 1400cc whereas those of apes between 500-600cc, lowest in chimpanzee and highest in gorilla.

5. In man, both frontals and parietals are well arched and have tuberosities. In apes, they are not well arched and tuberosities are not well marked.

6. In man, premaxilla is not well-marked off from maxilla. In apes, it is well marked off (Premaxilla lodges incisor teeth in upper jaw).

7. Supraorbital ridges are not much developed in man. In apes, it is generally well developed and may be continuous or separated.

8. Occipital region bulges out in man, in apes, it is flat and receding.

9. Foramen magnum is placed anteriorly at the base of the skull. In apes, it is placed posteriorly towards dorsal side.

e. Differences In Brain

1. Association-areas, the seat of memory, intelligence, reasoning learning etc constitute large areas in frontal lobe. This seat of higher intellectual faculties are particularly well-developed in man.

2. Greater chunk of somatosensory areas and motor areas are devoted to hands, lips and mouth because the selective advantage it confers through flexible hands and vocal communication, and the size of the chunk increases from monkeys to apes to man (Campbell, 1974).

3. Visual cortex in occipital lobe more developed and olfactory lobes less developed in man than apes.

4. Nerve-fibre connection between cerebellum and cortex is maximum in man hence man has maximum conscious control of co-ordinated muscular movement.

5. The limbic-system*[1] of brain is brought more under conscious control in man because of interconnections of the system with cortex. (*[1] The system translates sensory stimuli into

states of arousal, caring for offspring, finding food, mating, fighting etc.)

f. Cultural And Other Differences

1. Great development of association areas in frontal lobe of brain has gifted manpower to concentrate. The ability to concentrate has developed in response to hunting. High intelligence and ability to concentrate has played a great role in development of culture.

2. Acquisition of languages and script has led to complex social life, sophisticated artform and accelerated technical progression that has further enhanced the dichotomy between man and all animals, including apes.

3. In man, lips in association with tongue, palate and pharynx, play a great role in vocalization hence it is well developed, thicker and reddish. In apes, lips are stretched over margin of jaw without median furrow in upper lip. Lip has little quantity of fat in apes.

4. In man, there has developed many muscles in the face that aids in facial expression. Some facial expression can be practiced by chimpanzee, though at a much lower scale, whereas in other apes such facial muscles are at very low level of development.

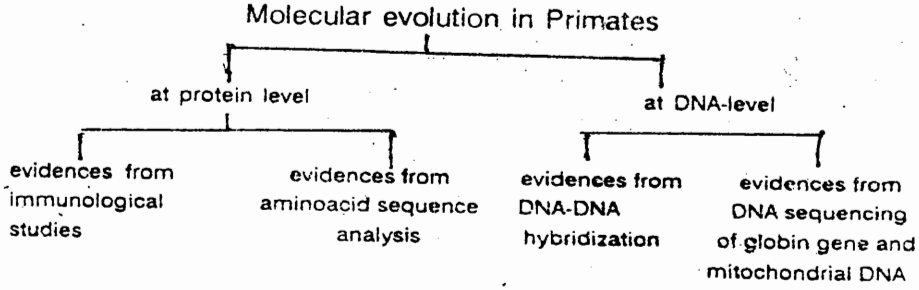
5. Hearing is vital for vocalization hence pinna has rolled margins in man for echo-location.

6. More prolonged period of gestation, infancy and childhood and slowness of skeletal maturation mark human beings. Prolonged infancy and childhood aids in social-learning and intellectual growth and hence contributes to the growth of culture.

7. Man differs from apes in the pattern of hair distribution, body-form and morphology partly due probably to socio-cultural practice of use of clothing to keep itself warm or some other yet unexplained reasons. Man has reduced and definite tracts of hair on the body which has different form in comparison to apes. This difference in the body-form is all the more different in female of humans which are characterized by sharp and erotic curves. Such features may aid in assortative matings perpetuating the difference further. Man, though seemed to have had shared an ancestor with apes only 5-7 mya, has the satisfaction of being much different from these forest beasts.

MOLECULAR EVOLUTION IN PRIMATES

1. Several molecules of life such as proteins, DNA etc have undergone considerable evolution and their present day structure is considerably different from the one from which they can be traced to their present form. Tracing their evolution is valuable because data obtained through such studies can be extrapolated to speculate phylogeny of the groups in which such molecules are studied. Studies of proteins through amino acid analysis & immunological studies, and studies of DNA through DNA-DNA hybridisation, sequence-analysis etc have contributed to the understanding of evolution of organisms in general and primates in particular.



2. In order to understand the kind of evolutionary relationship among primates that these studies suggest, let us have a brief look at the various proposals put forth to indicate their inter-relationship. So far evolution of prosimians and its general relationship vis-a-vis anthropoids is concerned, molecular data confirm the conclusions derived on the basis of comparative anatomy. Hominoids, however, remain problem areas. At least five different branching patterns for the phylogeny of the hominoids have been proposed. There is general agreement that the gibbons (Hylobates) are the descendants of the oldest hominoid branch and that the orang-utan (Pongo) lineage is the next-oldest branch. The principal controversies concern the branching pattern of the lineages leading to the African apes-the gorilla (Gorilla) and the two chimpanzees (Pan) - and humans (Homo). Some methods of analysis produce a simultaneous triple branching for gorillas, chimpanzees and human. This is unlikely and probably indicates only that the methods being used cannot resolve two branches

close together in time.

3. There is no denying the fact that amino acid sequence analysis and three dimensional studies of protein have provided with a unique opportunity in discovering various aspects of molecular evolution and reconstruction of various phylogenetic relationships. Elaboration of protein is the main function of DNA and it is through studies of protein that changes in DNA can easily be understood. But in recent years the fact has dawned to us that in eukaryotes (all organisms except bacteria) the DNA consists of two regions-coding and non-coding regions. Coding regions of DNA is involved with synthesis of protein and non-coding region not. It is also known that a great majority of DNA is non-coding and such regions may constitute over 90% of all DNA present in cell. These non-coding regions of DNA has been termed "Selfish genes" by Richard Dawkins.

There is controversy regarding significance of such non-coding regions but non-coding DNA can be very informative in revealing closer patterns of relatedness such as those between gorillas, chimpanzees and humans. The fraction of DNA that codes for proteins doesnot accept mutations freely, as they are likely to upset delicate balance of the species with environment and hence have to face adverse selection. Such a mutation, as and when it arises in the individual, is weeded out and hence DNA and proteins remains the same. Such an adverse selection will never be operative on non-coding DNA and all mutations occurring in them must be preserved. Amino acid sequences, hence, evolve more slowly and is indicative of more distant evolutionary relationship. Non-coding DNA evolves faster and is indicative of recent evolutionary relationships.

4. Selection and molecular evolution : Molecular evolution of primates clearly brings out the fact that, like other animals, primates too are product of fast selection and slow selection. Fast selection occurred during the times of encounter with new environment, and slow selection occurred when most of the demands of new environments were fulfilled and species existed, in a broader way, at harmony with it. Natural selection thus first acted as creative force and then as conservative force. A striking example of speed-up in protein evolution followed by a slow-down occurred in primates when advantageous mutations transformed an embryonic haemoglobin of earlier primates into a foetal haemoglobin that helped extend the period of foetal life. This provided with the chance of longer gestational period and larger

prenatal brain enlargement in the higher primates.

As discussed above, all changes occurring in protein must not have been accepted since it may have compromised the delicate balance of the species with the environment. However, during the times of radiations into new physical and ecological environment, new mutatations that gave rise to new proteins may have been selected. Natural selection must have favoured these novelties in proteins and must have protected these improved arrays of molecular sites from further change till a new radiation again occurred in a new environment.

1. Evidences From Immunological Studies

It has already been mentioned that antigens elicit antibodies with which they react and form antigen-antibody complex. The complex is sometimes large enough to precipitate which can be measured.

For example, serum albumin of humans is made up of a single polypeptide chain with 584 aminoacids. It can be separated from human serum and injected into experimental animals for antibody production. Such antibody against human albumin can be separated. This is known as anti-sera.

The anti-sera contains in this case antibody against human albumin. If it is mixed with human serum, a 100% reaction will occur. In similar way, serum albumin of different primates can be mixed with anti-sera against human albumin and percent reaction can be obtained by measuring antigen-antibody complex precipitated. Wilson and Sarich have been on fore-front since 1970s in carrying out such experiments. They have noticed following percent reaction of human antisera -

with human's	- 100%	with Baboon's	- 73%
with chimpanzee's	- 95%	with spider monkeys	- 60%
with Gorilla's	- 95%	with lemur's	- 35%
with Orangutan's	- 85%	with Dog's	- 25%
with gibbon's	- 82%	with Kangaroo's	- 8%

The extent of differentiation between two groups is easy to comprehend. The difference between human and ape antisera percent reaction is 5. It has been calculated that there are 2 aminoacid changes for every 1% difference in percent reaction. Hence, the difference between human and great apes is of 10

aminoacids in albumin protein. Percent reaction between human and Baboon is 73% - a difference of 27% hence aminoacid difference between the two is 54. Great apes, naturally, are closer to humans than Baboons are. The information can be utilised to understand branching order of the phylogeny. For example, both chimpanzee and Gorilla show 5% reaction. When Chimpanzee and Gorilla are compared between themselves the percentage difference is 10 (5% in each lineage). Chimpanzee and Gorilla, thus are more closely related to us than they are with each other. Many such studies have been conducted from which evolutionary relationship of different primates groups can be inferred.

2. Evidences From Aminoacid Sequence Analysis

Protein molecules are the primary products of gene expression and their structures have, therefore, long been studied for evidence of evolutionary mechanisms and relationships. By the present time the structures of more than one hundred globular proteins have been determined in atomic detail and relationships between them are emerging which provide intimations of evolutionary mechanisms.

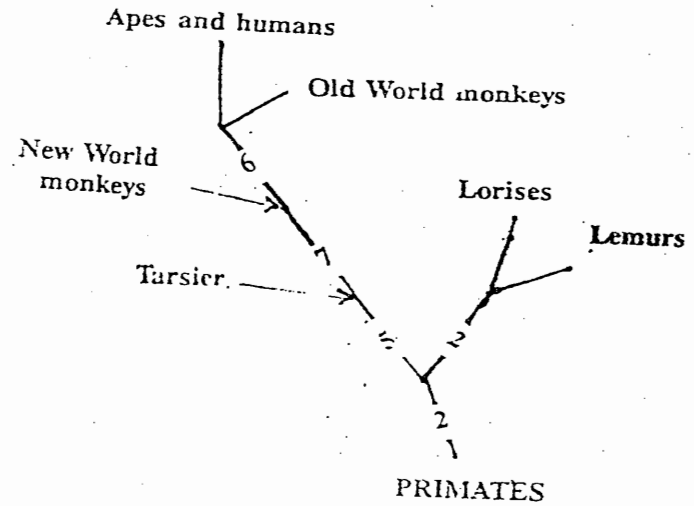


Fig : Relationships of the main primate groups from combined protein sequences. The number on the stems are the minimum number of nucleotide replacements (After Friday 1992)

1. Fibrinopeptides : are small peptides- 15 to 30 amino acids long and thus were one of the earliest proteins sequenced. By 1972, their sequences were available from more than 40 mammals. Including 12 primates.

Fibrinogen is protein that forms fibrin (blood clot.) Fibrinopeptides A and B are portions of fibrinogen. When they are removed from the fibrinogen by the enzyme thrombin, fibrinogen start forming a mesh of fibrin fibres - blood clot. As the only function of fibrinopeptides is to sheild the polymerisation site of fibrinogen, they do not require a highly conserved amino acid sequence. They have evolved rapidly and the fibrinopeptides of different mammalian orders and even of closely related mammals aery greatly.

The fibrinopeptide sequences of humans, chimpanzees and gorillas are identical and differ from those of orang-utans in only two of their 30 positions and from those of the gibbons in two further positions.

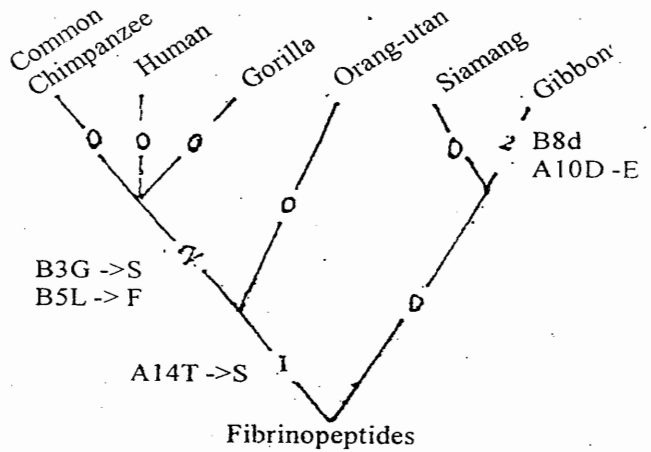


Fig : l Evolutionary tree for humans and apes based on fibrinopeptides A and B. The nature of the changes are recorded along the side of the links. For example, A14T- >S, which is placed alongside the link between the hominoid root and the branch point for divergence of the orang-utan from the gorilla/human/common chimpanzee clade, means that at fibrinopeptide A sequence position 14 the ancestral amino acid residue threonine (T) changes to descendant amino acid residue serine (S). There are two ancestral to descendant changes on the link to gibbon and the small d of the change designated b8d stands for a deletion (i.e. the amino acid residue at fibrinopetide B sequence position 8 was deleted.)

2. Haemoglobin And Myoglobin : Haemoglobin, the oxygen-transporting protein of red blood cells, is made up of four chains - two identical α chains and two identical β chains. Each α chain is 141 residues long and each β chain has 146 residues. Myoglobin, on the other hand, is present in the muscles and serves to store oxygen in muscle. It is made up of a single chain of protein, consisting of 153 amino acid residues.

It has been found that among the hominoids the amino acids in the α and β chains of haemoglobin differ in four positions in all. It has been found that in humans and chimpanzee haemoglobin there is one amino acid replacement in α chain at 23rd position, but not in gorilla and Asiatic apes. Humans, chimpanzee and gorilla share two amino acid replacements in haemoglobin at position 87 and 125. These studies places Homo, Chimpanzee, gorilla closer together away from orangutan and gibbon. Gibbon and orang-utan are removed from other hominoids by one replacement at position 12 in α chain.

Similarly, sequence analysis of myoglobin indicates that human, **Pan** and **Gorilla** share one amino acid replacement at position 23, and gibbon and orangutan are removed by one replacement at position 110.

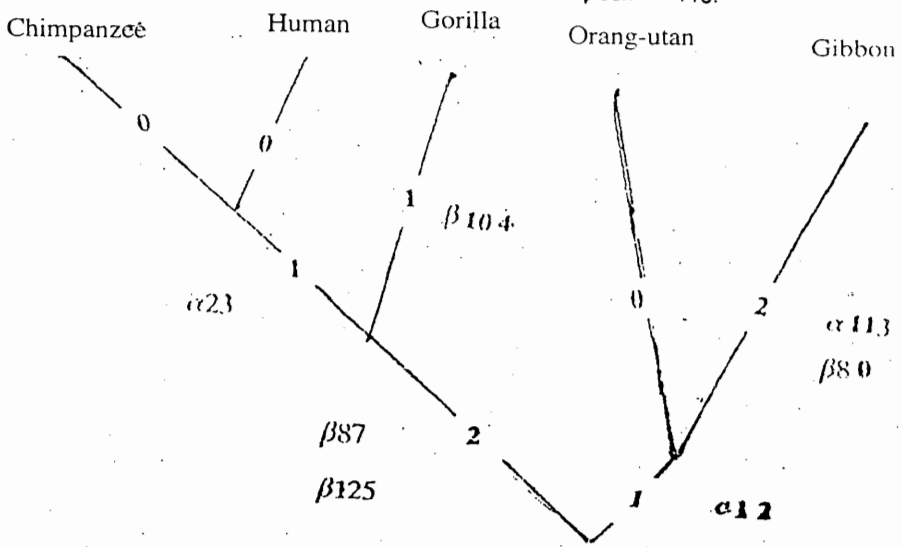


Fig. : Evolutionary tree for apes ... man based on haemoglobin. α and β indicate the chain and numbers indicate the position of aminoacid Human and chimpanzee share one replacement (α23) and chimpanzee, human and gorilla share two replacements (β87, β125). Orangutan and gibbons are removed from African apes and humans by one replacement at position α12. One replacement (β104) is unique for gorilla and two (α113 β80) for gibbons. There are seven replacements in all.

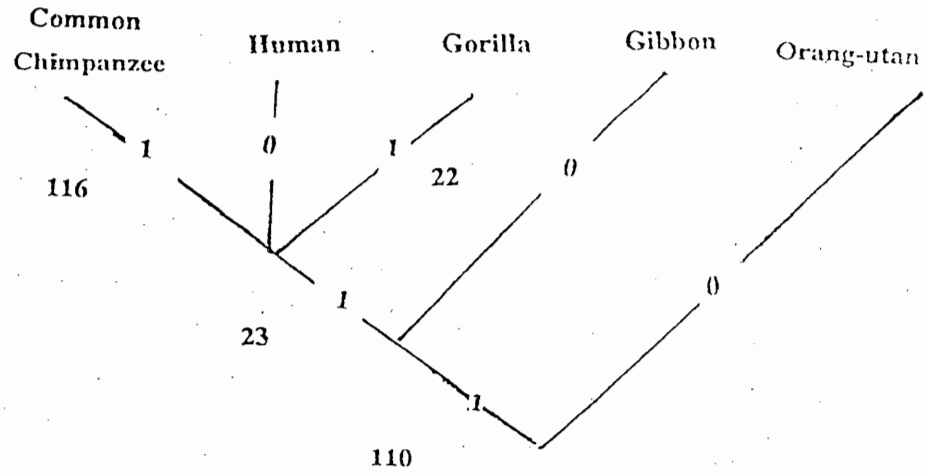


Fig. : Evolutionary tree fro apes and man based on myoglobin. Underlined number indicates position of replaced aminoacid. chimpanzee, human and gorilla share one aminoacid replacement at position 23, Gibbon shares with them one replacement at position 110. On this basis orang-utan is brought closer to gibbon but all other molecular evolutions point to orange-utans closer affinity with African apes and humans.

3. Evidences From DNA-DNA Hybridization

When two lineages diverging from a common ancestor is assessed in terms of genetic information the extent of their divergence is reflected in the amount of genetic change that has occurred over the time. More is the amount of genetic change, greater will be the evolutionary divergence. By measuring amount of genetic change, phylogenetic trees of related taxa can be reconstructed that would indicate sequence of their divergence.

The two helices of DNA are held by hydrogen bonds which are disrupted by heat. Heating DNA in solution would then result in separation of its two strands. When the solution is cooled, the two strands reassociate forming double helix again.

If DNA of two related species are taken together and then heated, each of the DNA will be denatured and become single stranded. If the solution is cooled, the single strands will

reassociate. Greater the similarity between the two DNA, faster will be the reassociation because each single strand will find its complementary mate faster. During reassociation both homoduplex (= DNA strands of the same species) and heteroduplex (= DNA strands of different species) will form. If a suitable isotope eg 125_I is used, heteroduplex can be identified from homoduplex.

Heteroduplex will have large areas of complementary base-pairs. However, it will have some mismatched regions also. Such heteroduplex will have lower melting point because all its bases are not hydrogen-bonded. The melting temperature is calculated as the temperature at which half the DNA sequence are double stranded and half single stranded. This is known as T_{50H} (the temperature at 50 percent hybridisation). Thus T_{50H} of homoduplex as well heteroduplex is calculated. The difference in the melting temperature (ΔT_{50H}) is indicative of their evolutionary divergence. Lesser the ΔT_{50H} value, closer the lineages on the phylogenetic scale. Conversely, larger the ΔT_{50H} value the farther the lineages on the phylogenetic scale. Such evidences have indicated that human Chimpanzee and gorilla have lesser Δ. T_{50H} value than Orangutan and gibbon.

4. Evidences From DNA Sequencing And Mitochondrial DNA

In the study of sequence of bases in DNA a tool that has been very crucial is the enzyme restriction endonuclease or simply restriction enzymes. These enzymes occur in bacteria where it serves the purpose of destroying any foreign DNA of viruses that penetrate into bacteria. Hundreds of such enzymes are available that recognises and cuts a particular four- or six-base sequence of DNA. The more frequent that sequence- for example, GGCC or GAATTC along the DNA molecule, the smaller the ensuing pieces will be.

Evolution Of β-globin Genes : Analysis of DNA sequences has proven vexingly ambiguous in attempting to discern the two closest relatives among humans, gorillas and chimpanzees. A few regions of nuclear DNA have been analysed and results are difficult to interpret. For example, in the β-globin gene cluster on chromosome 11, the $\psi\eta$ sequence links humans to chimpanzees, γ^1 links gorillas to chimpanzees, γ^2 links gorillas to humans, and β-globin itself has linked chimpanzees to gorillas and to humans in different studies.

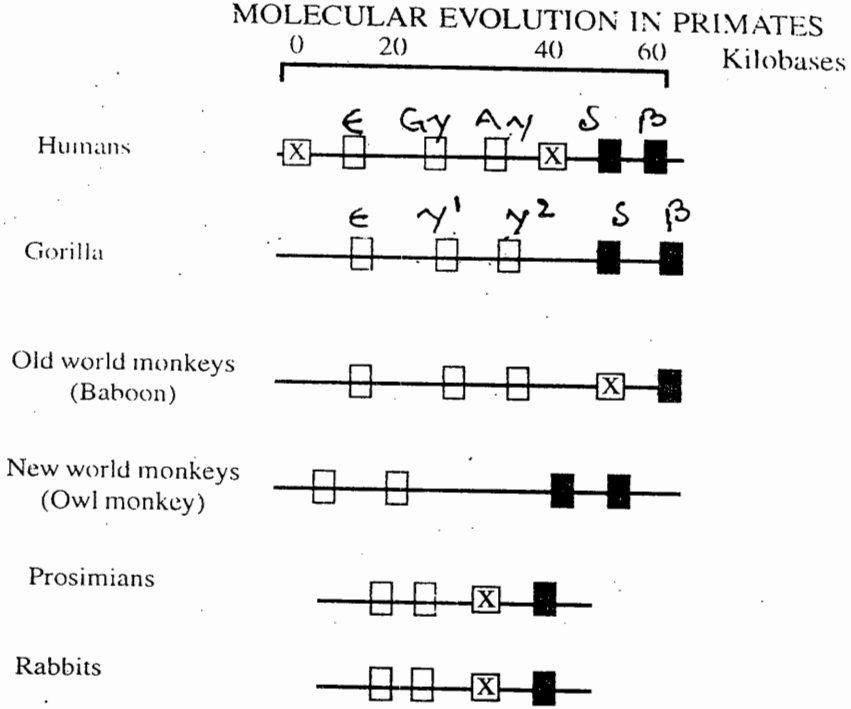


Fig. : Chromosomal organistion of β-globin gene clusters in humans, apes, old world monkeys, new world monkeys, prosimians and rabbits as revealed by recombinant. DNA technique. Each gene, denoted by a small rectangle is transcribed from left to right Light coloured genes are responsible for embryonic and foetal development, the dark coloured gene for adult β globins. Each of these genes have 3 exons and 2 introns. The presence of psendogenes are indicated by crosses.

Evolution of immunoglobulin genes : The organisation of the heavy chain constant (CH) region genes of human immunoglobin (Ig) is $5' - Ce^1 - Ce^2 - Cy^3 - Ce^3 - C^3 - C\alpha 1 - \psi - Cy - Cy^4 - Cx - 3'$ located on chromosome 14. In addition to this gene cluster. human genome contains a processed Ce pseudogene (Ce^3) on chromosome 9. The human Ig Ce gene family consists of three members : the Ce^1 gene (active). the Ce^2 gene (truncated pseudogene) and Ce^3 (processed pseudogene). S.Ueda et.al. (1986) studied these three Ce genes comparatively in gorilla. chimpanzee and human by the Southern hybridization technique using Ce gene fragments as probes. Their results show that only human and gorilla genomes

contain the three Ce genes (Ce1 Ce2 and Ce3). The chimpanzee has lost the Ce2 gene. Sequences of Ce3 gene, however, show that the three-human, Chimpanzee and gorilla are intimately related.

Mitochondrial DNA :— Ferris et.al. (1981), Garner et.al. (1996) and a host of workers have studied mitochondrial DNA variation among apes and have compared it with that of humans. All the studies indicated that mitochondrial DNA variation in great apes was two to ten times higher than in humans.

Mitochondrial RFLP variations indicate a closer relationship between human and chimpanzee than gorillas and orang utans. (It has been claimed that humans and chimpanzee have exchanged their mitochondrial DNA via viral infections and this is the reason of their greater similarities in the mitochondrial DNA).

Xq 13.3 Studies

Kaesmann and Paabo (2002) sequenced 10,000 bp of Xq 13.3 in higher primates and constructed phylogenetic tree. The tree shows that humans form a clade together with chimpanzee (including bonobo) to the exclusion of gorillas and orang-utan. Chimpanzees differ from humans by 0.9% nucleotides whereas gorillas and orang-utans differ from humans by 1.4 and 2.9 % respectively. Thus, the results obtained from xq13.3 concur with the majority of studies in placing chimpanzees closer to humans.

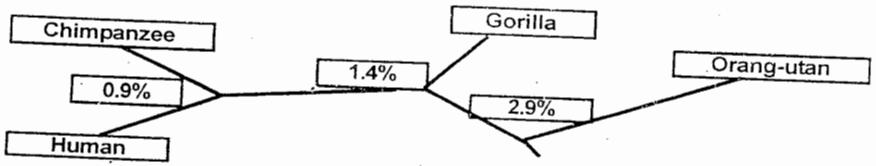


Fig. Phylogenetic tree on the basis of xq 13.3 region in human and higher primates. A gibbon sequence was used as an outgroup. (After Kaesmann and Paabo, 2002).

Molecular Clock Hypothesis

Almost five decades have elapsed since hypothesis about molecular clock was proposed by Zuckerkandl and Pauling (1962) who studied time of divergence of four members of the haemoglobin gene family (α, β, γ & δ) and estimated time of divergence of human and gorilla. Since then, the hypothesis has been tested time and again not only in different protein molecules but also with diverse DNA molecules and has become an invaluable tool for building evolutionary time-scale. The clock functions on the premise that rate of protein and DNA variation has ocurred at the same rate in the different lineages and if some reference point exists as anchorage e.g. in the form of fossil or a global event, the approximate time of divergence can be calculated.

Protein Molecular Clock

ZuckerKandl and Pauling, while calculating the time of divergence between human and gorilla calibrated the molecular clock on the basis of human-horse divergence time which is known on the basis of horse fossils, which is as old as 100-160 mya. There are 18 aminoacid substitutions in α chains of human and horse. While calculating time for one amino acid substitution, the formula used is 2T/D (because distance, D, is equal to the sum of divergence time from common ancestor to two descendants). Thus time for one aminoacid substitution between man and horse comes to 200/18=11 (if T = 100 mya) and 320/18 =18 million years (if T = 160 mya). In such cases, the average is used which is 14.5 mya. Thus, 14.5my./per aminoacid sustitution was the calibration for molecular clock.

Human and gorilla α chain differ by two aminoacid substitutions and β chain by one. Hence for α chain, divergence time is t x ½D = 14.5 x ½ x 2 = 14.5 my and for β chain = 14.5 x ½ x 1 = 7.5 my and the average is 14.5 + 7.5 = 22/2 = 11 my. Thus average divergence time between human & *Gorilla* will be 11 mya from analysis of two protein chains (The expression 1/2 D is used here because D is equal to the sum of divergence from common ancestor to two descendants.) Zuckerkandl and Pauling believed that accuracy of the molecular clocks will improve by using many proteins of different types. The example also shows that α chain diverged much earlier than β chain.

DNA molecular clock

For this we need to calculate the number of base-pair differences that have accrued among pair of species since their common ancestor. Goodman et. at (1989) plotted these nucleotide base pair differences in globin gene in higher primates as follows (see figure ahead)

From common ancestor of *Homo*, *Pan* and *Gorilla*, there has been 76 autapomorphic+14 synapomorphic changes=90 leading to *Homo*, 14 Synapomorphic+92 autapomorphic changes = 106 leading to Pan, and 94 changes leading to *Gorilla*.

From more remote common ancestor of these and *Pongo* (orang-utan), there have been 160 change to Homo, 176 to *Pan*, 178 to *Gorilla* and 199 to *Pongo*. The observation clearly indicated that humans are closely related to chimpanzee and gorilla than it is related to orang-utan.

The average rate of base-pair substitution in any lineage can be calculated if we have an estimate of absolute time of divergence. For example, oldest old world or cercopithecoid monkey e.g. *Macaca* is 25 mya. Thus, the divergence time between *Macaca* and hominoid (man and apes) is at least this old (It can be more old if more ancient fossil of *Macaca* is discovered).

On these data, the number of substitution/base pair/million year for *Macaca* is 457/10,000 bp sequenced/25mya.

= 0.0457/25 my

= 1.83 x 10^{-3}/my
or 1.83 x 10^{-9}/year
For *Homo*, 310/10,000/25 my = 0.0310/25 my = 1.24 x 10^{-3}/my
or 1.24 x 10^{-9}/year

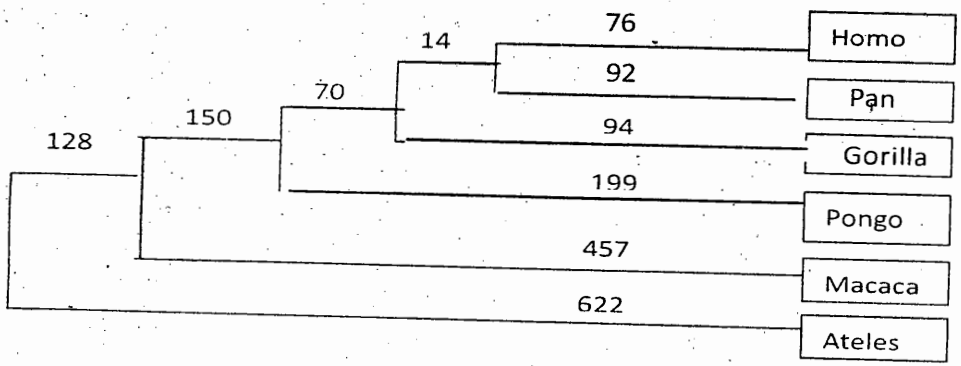


Fig : Phylogenetic relationship among higher primates, based on globin region, using Ateles as the outgroup (based upon sequencing of 10,000 base-pairs)

Calculating divergence time on the basis of DNA sequences. Conflicting evidences for clock- hypothesis.

The divergence time calculated on the basis of DNA substitutions has been very much conflicting and many times in complete disagreement with the fossil data. The molecular data gives much higher estimates in comparison to the fossil data. Divergence time calculated on molecular data is more than double of that calculated on the basis of fossil evidences . Even if it is assumed that fossil dates are always conservative estimates, still the difference is too much.

It is because of these reasons that concept of 'relaxed clocks' and 'local clocks' have beeb proposed. A'relaxed clock' doesnot require relative rate-test. It has been suggested that molecular clocks should be allowed totick at different rates in different groups of species in a plylogenetic tree (local clocks) rather than follow a global molecular clock. In the absence of a global molecular clock there is no necessity for rate tests.

Supportive evidences for clock hypothesis from Ig genes and x q 13.3

Not that all the DNA datas are conflicting with the fossil data. Take for the example immunoglobin genes and xq13.3 discussed earlier. In the first, the difference between human-chimpanzee is .0205 and between human-gorilla is .0295. Considering the evolutionary divergence rate estimated for the primate immunoglobulin pseudogene to be 1.55 x 10^{-9} nucleotide difference per site per year, the divergence dates for chimpanzee and gorilla from human line comes to 6.8 million and 9.6 million years, respectively, the dates which donot differ much from the fossil dates. Likewise, 'clock-test' was also performed with xq 13.3 region for

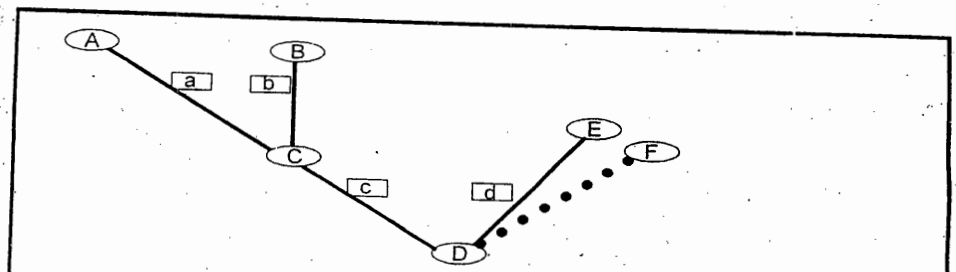


Fig : Hypothetical model for relative rate-test for constancy of the rate of molecular divergence,. (C) and (D) are common ancestor. (A) & (B) are living species and (E) & (F) are outgroup species. a, b, c, d are genetic distances in terms of nucleotide substitutions.

In the above hypothetical model, the genetic distance between A and E is D_{AE} = a+c+d and that of B and E is D_{BE}= b+c+d. It the rate of nucleotide substitution is constant,

a = b so D_{AE} = D_{BE}. If rate constancy holds throughout the tree, the distance between any pair of species that has D as a common ancestor will equal any such pair of species D_{AE}=D_{BF}.

human, Chimpanzee and gorilla (Kaesmann and Paabo, 2002). Chimpanzee differ from humans by 0.9% of their nucleotides at xq 13.3 whereas gorillas and orang utans differ from human by 1.4 and 2.9%, respectively. The test places chimpanzee as the closest relative of human. When put to clock-test, results coincided with those obtained from fossil studies and thus the results failed to reject the clock-hypothesis.

Current Approach :

Kumar and subramanian (2002) have characterized mutation-rate differences within and among different group of mammals including humans and old world monkey. Because generation time, physiological attributes and other life history traits are different in different groups, hence the same molecule can experience different rates of change in different groups. Within the group, level of DNA methylation, recombination, and, DNA-repair mechanisms have greater role as sources of mutation. In summary, it can be said that mutation rates in different mammals (and primates) are not identical. As a result emphasis of current research has changed from testing the existence of a global DNA clock in mammals to quantifying the extent to which there are rate-differences among species and determining their causes.

MULTI DISCIPLINARY APPROACH IN STUDY OF FOSSIL TYPES

Study of fossil types in order to differentiate one type from others is the hallmark of all activities of palaeoanthropologists. Once a fossil is discovered, it becomes necessary to determina its precise traits and relationship vis-a-vis other group of animals. Fossils, by their very definitions, can be remains or impressions of the past and can be in the nature of preserved hard-parts such as bones and teeth, impressions of foot-prints, an object of culture such as tools or product of life activities.

A. Comparative Anatomy : Until quite recently palaeoanthropologists relied almost exclusively on readily quantifiable overt morphological features, combined with essentially qualitative interpretations of what these characteristic implied, derived from broader understanding of comparative anatomy. This is still the starting point of most fossil though it has become much sophisticated. There has been attempts to reconstruct the gross anatomy and even the appearance on the basis of very limited samples of skeletal material. From appearance, the reconstruction of behaviour is an easy step. Study of a mere fossil tooth can lead to the estimation of the fossil species life style. At the root of all such comparisons is comparative anatomy which is the oldest approach in the study of fossil types and remains. In addition to the study of comparative anatomy of fossil bone and tooth, some newer methods are being employed to understand a fossil.

B. Morphometrics And Cladometrics : Morphometrics is the use of advanced statistical technique to analyse morphological measurements. Cladometrics is concerned with use of morphometric data for analysing the degree of similarity between the different species. Such cladometric analyses have become possible due to modern computing techniques which can handle far greater number of variables than what was traditionally possible. This reveals covert patterns of correlation which would have earlier remained unspotted.

Cladistic methods analyse, then, overall level of similarity between species rather than tracing lineages via particular inherited feature as a basis for classification and an index of affinity. Such practices can provide measures of mutual affinity or distance among fossil specimens both to identify number of species present and compare them. Though the cladistic system is opposite to the traditional phylogenetic system of evolutionary taxonomy, the

system has been useful in testing hypotheses about fossil species affinities. Waddle is the leading contribution in this field.

C. Wear-Analysis : Nature of the tooth wear provide much information about the nutrition ecology of the fossil species. Alan Walker and Al Ryan, the two prominent workers in this field, are convinced that by analysing wear pattern of tooth under microscope, one can deduce the different types of tool uses. The various methods adopted in analysis of tooth wearing are polishing, pitting, scratching and microflaking. Wear analysis of tools is still another area of fossil study. The principal worker in this field has been L.H. Keeley. Such studies are on sound basis because usage of fascimile tools on different materials can be undertaken extensively in order to establish a clear picture of the typical wear pattern produced by eg. meat cutting, wood working, bone-working or skinning.

D. Gait - Analysis : Anatomical studies of knee-joint morphology has been important in the study of locomotor patterns. Discovery of certain footprints have also been important in the analysis of fossils. Discovery of laetoli foot prints have been impetus to such studies. Day and Wickens (1980) have compared the contours of modern human foot-prints with those found at Laetoli and have concluded that makers of the Laetoli footprints transmitted their body weight and the forces of propulsion on the ground in a manner very similar to modern man. Stern and Susman (1983) have been more cautious, finding these foot prints to lack the characteristic human "ball" below the big toe. This branch of study of palaeoanthropology is well-flourishing, Russell Tuttle of University of Chicago being the leading authority on primate gait. Traditional studies of fossil bones, combined with foot-print analysis might clarify many of the enigmas of hominid.

Three types of studies, namely configurational analysis, stress analysis and bio-chemical analysis are important for deciphering locomotor pattern of fossil specimen. Configurational analysis demonstrate configuration of the hip, knee, ankle joint and foot. **Stress analysis** consider interrelationship between bone joint and muscles. **Biomechanical analysis** analyses bone / joint / muscle relationship in terms of adaptation.

E. Endocast Analysis : Columbia University's Ralph Holloway has been leading in such type of studies. Natural casts of crania are sometimes obtained, such as those of first Taung fossil discovered by Dart. Study of the cranium and estimation of the cranial capacity provides important information about

encephalisation quotient score (E Q score). It, however, sheds no light on changes in the organisation or structure of the brain. Endocasts provide us with information about the surface feature of the brain.

Brain In Human Ancestors : Apart from the size of the brain, the fossil skull of human ancestors do sometimes show up certain features of brain. Brain is enveloped by a tough fibrous membrane (dura mater) below the inner surface of brain case. Many surface feature of the brain leave impressions on the inner surface of the brain case which can be known by making plaster cast of the inside of skull (endocranial cast or endocast).

Through preparations of such endocasts of several human ancestors we are in possession of several revealing aspects of brain structure and function. The important features that show up in such casts are : Lunate sulcus; Central sulcus; Sylvian fissure; Broca's area.

i. Lunate Sulcus : Lunate sulcus divides the primary and secondary areas of brain and its localisation to the more posterior position denotes advancement of mental abilities. Hominid bipedal locomotion seem also to have affected this structure. An upright position would mean greater vertical disposition of the brain stem than in quadrupeds, and together with it repositioning of cerebellum, occipital lobe and visual cortex. We know, through endocranial casts, that such was the lower position of lunate sulcus in Australopithecines.

ii. Central Sulcus : The central sulcus divides the somatic from motor cortex and has made appearance from monkey to apes and man. Presence of central sulcus thus guarantees anthropoid affinity and distinguish it from prosimians. The central sulcus is present in *Aegyptopithecus*, the Oligoncene (65 mya) fossil The central sulcus is marked in the Australopithecines also.

iii. Sylvian Fissure : The sylvian fissure divides the frontal, parietal and temporal regions of brain. It is lower and longer on the left side than on the right side of the brain. This is associated in modern humans with Broca's area of language. The asymmetry in Sylvian fissure is found in the archaic *H.sapiens* also (Asymmetry in the sylvian fissure, however, does not indicate a superior status for human being- it is also indicated in many monkey and ape brains).

iv. Brocas's Area : In the left lobe of cerebrum there is a specialized area called Broca's area which is important for

vocalization. Broca's area also show up faintly in the endocasts of *Homo habilis* and *H.erectus* but fail to show up in australopithecine. Deacon (1992) cautions against making anygeneralisation about origin of vocalization in *Homo* on the basis of this meagre evidence but nevertheless accepts that between the australopithecines and *Homo*, the latter definitely displays a greater possibility of development of language. with the use of endocranial casts, the timing of hominid brain expansion is fairly well established. The brains of australopithecine hominids fall within the range of modern great apes, with a mean weight of approximately 450 grams (assuming that 1 cubic centimetre of brain weighs 1 gram). It is not clear whether the slightly higher brain to body ratio of australopithecines is a significant departure from that of apes. Encephalisation probably first exceeded the ape range at least 2 million years ago, with the appearance of the first member of our genus, *Homo habilis*. The fossil KNM-ER 1470 from Koobi Fora in Kenya is a highly encephalised specimen of *H.habilis*, with a brain weight of approximately 750 grams.

By 1.5 million years ago, the brains of *Homo erectus* weighed almost 1000 grams. Brain size continued to increase without a corresponding increase in body size until the appearance of first Homo sapiens perhaps 0.4 mya. The brain of early sapiens or archaic sapiens was large as ours and so was that of Neanderthals though in case of latter it was enlarged at wrong places. There is some dispute regarding language capability of neandertals.

Language And Speech : The areas of the brain specialised for language are in the region surrounding the sylvian fissure of left hemisphere. This also contains centres for auditory perception, tactile perception and motor control of the face, mouth and larynx. Broca's area (immediately in front of the motor areas) and Wernicke's area (immediately behind and to the side of auditory area) are most directly involved in language. Broca's area and Wernicke's area are large on the left side in most human brains. Similar asymmetries are present in other primate brains and hominid fossils. Thus it is likely that lateralisation of language may have developed from earlier forms of brain asymmetry. Endocast studies, thus, have completely revolutionized our knowledge regarding human ancestors.

F. Artefacts : Artefacts associated with fossils do possess a wealth of information. In some respects, they are more directly relevant to psychological evolution than most anatomical data

since they embody actual behaviour. In this category are included chiefly the stone implements which has survived for the most part of human evolution though horns, shell, wood, cave- art, paintings, carvings appear on the later part of evolution.

G. Fossil DNA : Ancient DNA research was born in 1984,when Allan Wilson and Russell Higuchi, biologists at the University of California, Berkeley, extracted fragments of DNA from museum specimens of the quagga, a zebra-like animal that became extinct more than a century ago. The announcement was a great surprise, because biologists knew that when an organism dies its tissues quickly decompose.

A year later molecular biologist Svante Paabo, (University of Munich) extracted human DNA from an Egyptian mummy almost 2500 years old. It was Paabo again who began to expand the limits of the field when, in 1989, he reported extracting DNA from a specimen of the extinct ground sloth, some 13 000 years old. He did the same with a 40 000 year old woolly mammoth, preserved in Siberia.

Early in 1990 Edward Golenberg and his colleagues, at the University of California, Riverside, announced the recovery of DNA fragments from 17-million year old magnolia leaves, from an unusual fossil deposit in Idaho. This was followed in 1992 and 1993 by reports of 25 million year old DNA from a bee and a termite and 120 million year old DNA from a weevil. Each specimen had been entombed in amber since its death.

In all studies of ancient DNA so far, the recovered genetic material has been limited to fragments no longer than about 800 base pairs, and more typically 200. By comparison, DNA in living tissues exists as strings of tens of thousands of base pairs. A vital factor in the recent surge in ancient DNA research is the Polymerase Chain Reaction (PCR). Developed in 1985, this biochemical method permits vanishingly small quantities of DNA to be multiplied, producing sufficient material for analysis. In principle, PCR can produce millions of copies from a single DNA molecule. But this power is also a curse, because PCR doesnot discriminate between DNA from the specimen and infected DNA. This might come from bacteria or fungi that infected the specimen during the life or death, or from the sweat of curators who handled specimens over the years, or other sorces of modern contamination. Study of fossil DNA can lead to wrong interpretations if this happens.

THE HOMINIZATION PROCESS

The hominization process consists of evolutionary transformation of hominoids into hominids. It is a process that has occurred in the hominid-line since its divergence from the last common hominoid ancestor shared with any living ape. Initially, the term had a restricted meaning and implied emergence of modern man, different from all other forms. Currently, however, the term is broadened and includes all those aspects of structural and behavioural changes that occurred in the hominid line finally leading to man. All such changes can be broadly grouped into following heads.

1. Bipedalism; 2. Hand manipulation and tool use.
3. Modification of jaw and teeth.; 4. Enlargement of brain.
5. Changes in vocal tracts and language and speech.

1. Bipedalism

Analysis of postcranial elements of *A.africanus*, *A.afarensis*, *A.ramidus* (Tim white et.al. 1994) and *A.anamensis* (Leakey et.al.1995) clearly establishes bipedalism to be one of the oldest of all hominid characteristics. The age of most primitive australopithecines, *A. ramidus* is estimated to be 4.4 mya, perhaps one million years after separation of ancestral lines leading to great apes and man. The branch- point between ape and human ancestors is estimated to be 5-6 mya. According to Craig B. Stanford (1995), *A. ramidus* was a biped; its lower body was clearly adapted for walking on the ground, though they may have continued to use trees for gathering fruits and for shelter at night. Postcranial elements of *A. afarensis* is well-documented. The kind limb and pelvis show many bipedal adaptations. Iliac blades were short and broad; ischium was short; anatomy of hand and ankle joints were favourable; big toe was parallel. In all such features afarensis was more human-like than ape-like.

In addition to post-cranial elements, the Laetoli (Tanzania) foot prints of *A. afarensis*, austratopithecine to have existed around 3.77 mya, is another proof of bipedalism. It shows a convergent big toe, heel strikes, arches etc similar to humans in many aspects.

There are, however, certain features possessed by afarensis such as shorter hind limbs, longer foot, longer toes etc. which suggest that australopithecine bipedalism was different from, and

costlier than, human bipedalism.

Such differences in the locomotor behaviour can be explained due to the habitat supposed to have existed in eastern Africa- woodland, bushland and dry Savannah with patches of forest along rivers and lakes. Thus, they had to live somewhat less on the tree and more on the ground.

2: Hand-Anatomy And Tool Use

The earliest evidences of hand-manipulations different from apes and sufficiently similar to Homo can be found in *A.afarensis*, though its hand anatomy differs from both . Hands are approximately to human proportions but differ from those of humans in having fingers more curved suggesting great power grip. A precision grip greater than chimpanzee but lesser than the Homo is suggested. *A.afarensis* was spending more time on the land than in the trees hence hand-anatomy had started foreshadowing the characteristic of hands of Homo and different from those of apes. Hominids with their manipulative hands, precision grip, and contemplative brains, have been able to expand their ecological niche so far beyond the physical capabilities inherent in their makeup, one that no other animal has ever had the potential to achieve.

The classical view of anthropologists has been that the use of tools led to the distinction between human and ape-that the split between the Pongidae and the Hominidae resulted from the acquisition of tool-use by one of the ancestral hominoid populations. Others now feel that environmental influences and adaptation to nonarboreal ecological niches were more important for early hominid evolution. However these divergent views are ultimately resolved, it is interesting to learn how far back human technology and culture can be traced.

Recent paleoanthropological findings is that the use of tools antedates the origin of the big-brained *Homo sapiens* by at least a million and a half years. There is now indisputable evidence of the occurrence of modified stone tools 2 million years old found in association with the bones of *Homo habilis*. In other words, tool-use and tool-making developed before hominid brain capacity had undergone remarkable increase. The old idea that a large brain and associated high intelligence were prerequisites for tool use is no longer tenable. The use of tools by primitive hominids may, in fact, have been a major factor in the evolution of the

cerebral cortex and higher intelligence, for once the use and making of tools began to favour survival, there would be high selection pressure for neural mechanisms promoting improved crafting and use of tools. The elaborate brain of *Homo sapiens* may be a consequence of culture as much as its cause. Hominization process, with respect to cultural attainments, had set in much before the modern man appeared on the earth. Oldowan industry of earliest *Homo habilis* clearly proves the point.

Homo erectus had not only perfected stone tools considerably but had also learned how to control and use fire, as revealed by radioisotope dated hearths in caves. With fire, humans could cook their food; they could keep themselves warm in cold weather; they could ward off predators; and they could light up the dark to see. The hearth, no doubt, promoted the development of social organization and allowed an opportunity for the beginning of communication through spoken language.

Neandertal people practiced ritual burial in Europe and the Near East at least 60,000 years ago, suggesting that religious beliefs had developed by that time. By 40,000 years ago or a little later, Cro-Magnon people began constructing their own dwellings and living in communities. The domestication of animals and plants, development of agriculture, and the dawn of civilization followed in relatively quicker that characterize modern humans. The cultural attainments in terms of tool-making and tool use that characterizes modern humans had thus set in at least 2 mya, for which there exist sufficient proof in archaeology since the time of *homo habilis*.

3. Modification Of Jaw And Teeth

Apes are characterized by larger, thick enamelled teeth, large jaw and jaw muscles, large canines, high cuspid molars and a higher ratio of cheek teeth area to body weight. Australopithecines, Paranthropines and habilines differed from apes in some features. *A.ramidus* had teeth which resembled those of Homo in some features- they were smaller with thin enamel and canine were smaller. The dentition, in general, resembled those of Chimpanzee in some aspects. Similarly, *A.afarensis* dentition had some ape-like and some Homo features. The incisors were chimp-like but canines were low crowned and incisor-like. *A.africanus* had dentition similar to those of afarensis except that the cheek teeth were slightly bigger. In *Paranthropus*, front teeth were smaller than those of afarensis and africanus but cheek teeth,

Jaw and Jaw muscles were more massive in them. In *Homo habilis*, teeth were more or less similar to those of *A-afarensis*.

Dental variation among these hominids are peculiar. There is gradual reduction in the sizes of the front teeth, where as there is gradual increase in the sizes of cheek teeth in case of *Paranthropus*.

Such variations in hominid dentition is explained by the climatic changes that occurred around 2.5 mya, opening up more and more Savannah. It is hypothesized that species composition of both plants and animals changed and *Paranthropus* had to survive on low quality food which required prolonged mastication, Larger teeth, Jaw and Jaw-muscles in *Paranthropus* developed due to such responses.

Around 2 to 2.5 mya originated *H.habilis* which is clearly associated with tools. These forms, however, donot show enlarged cheek teeth, Jaw or Jaw muscles. It is supposed that habilines "prepared" their food outside mouth, hence larger cheek teeth, heavy Jaw is absent in them. The enamel is also not as thick as in the Paranthropines.

To conclude, Paranthropines, while displaying a hominid pattern in general, have larger cheek teeth because of ecological reasons. With the advent of tools, the teeth were put to different selection pressure and hence *H.habilis* has smaller cheek teeth in comparison to Paranthropines. Gradually there is reduction in the cusp height of the teeth, a prominent feature of the apes. The ratio between cheek teeth area to body weight was high in Paranthropine where as it is constant for later hominids. Hominization process in dental morphology, thus, consisted of reduction in sizes of teeth, Jaw and Jaw muscles, reduction in cusp-height of teeth, and constant cheek teeth Area. These features are seen to begin with australopithecines and *H.habilis*.

4. Enlargement Of Brain

Earlier Palaeoanthropologists believed that evolution of human brain occurred after bipedalism and changes in the dentition were complete. Recent endocranial cast or endocast studies indicate that encephalisation process progressed along with other changes that characterize Hominids. In the later stages of hominid evolution, the brain evolution consisted more of relative growth of brain and body-sizes i.e. allometric growth rather than simple reorganisation

in hominids).

Endocast studies of *Homo habilis* clearly indicate that its brain volume was significantly greater than those of australopithecines. Body weight of these hominids have been estimated from fossils and the encephalisation quotient determined by computing brain-sizes relative to their body-sizes. These data show that absolute and relative brain-sizes increased during hominid evolution. Furthermore, the increase is not gradual. The period between 4 to 2 mya show insignificant change in brain volume as *afarensis* and *africanus* shows a brain volume below 450cc whereas those of *H.habilis* between 2 to 1.5 mya in the range of 650-700cc. The hominization process that involved evolution of hominid brain can be said to have resulted during this period, between 2 to 1.5 mya.

5. Speech And Language

a. Speech : The speech apparatus of humans consists of three physiological components : the subglottal system that includes lungs and associated muscles which provide the power for speech production; the larynx which communicates the subglottal system to upper supralaryngeal vocal tracts; and the supralaryngeal tracts itself which modulates acoustic energy generated by first two system.

The human supralaryngeal airway differs from that of other primates. In human being the palate has moved backward and larynx downward to achieve unique constructions of supralaryngeal airway different from other primates. Moreover, the round human tongue moving in space defined by the palate and spinal column can generate frequency patterns that define vowels and consonants.

The area of the brain specialised for language and speech are in the region surrounding the sylvian fissure of left hemisphere. This area contains the cortical centres for auditory perception and motor control of face, mouth and larynx for speech production. These motor area for speech and areas for sound perception are closely located to the language areas- the Broca's area (immediately in front of motor area) and Wernicke's area (immediately behind and to the side of the auditory area).

The structures and neural control mechanism necessary for the complex pattern of human speech seem to have evolved during the last 1.8 mya. The comparative anatomy of the living

primates and hominid fossils suggest that evolution of supralaryngeal vocal tract probably started in early African populations of *H.erectus* (Liebeman, 1992). However the hominization process took sometime to complete. There are definite proof that hominids from the Israeli sites of Skhul and Quafzeh had definite human supralaryngeal airways. Neandertals, however, were the only hominids that seemed to have had retained the non-hominid supralaryngeal airways. Endocast studies of such forms indicate that their neural mechanisms had not appropriately developed, whereas those of from Skhul and Quafzeh were capable of producing human speech.

b. Language : Language is an adaptation unique to humans but its biological basis is very difficult to define. The American linguist Noam Chomsky has proposed that a unique "language organ" or language acquisition device (LDC) evolved within the human brain. Although there is no anatomical evidence for a new "organ" it is clear that there exist certain areas such as Broca's area and werricke's area for language (see human brain).

Since languages leave no fossil record, the evidences for its origin are circumstancial, Comparative linguistics were used to estimate a date for a single common language. The recent approaches, however, have used anatomical and archaeological informations to suggest a date of origin for language.

Anthropologists differ in the exact time of origin of languages. One group argues for a relatively recent origin and correlate it with the appearance of modern *Homo sapiens* with modern-sized brains and a fully descended vocal tracts. The tools and artistic culture that flourished in late palaeolithic coincided with development of language and communication. Another group traces origin of language to *Homo habilis* when first appearance of tools and beginning of enlargement of brain took place.

The two conditions have different consequences for the nature of mind. If origin of language is considered late,linguistic changes in brain becomes secondary to the non-linguistic changes, allowing only little to the languages to influence the structure of brain. If its origin is considered early, it is logical to think that it passed through multitude of forms and had major influences on evolution of brain and vocal tract. The diverse language adaptation and its deep integration in human nature point to its ancient origin. It has been suggested that earliest languages were singing, accompanied with gestures.

OUTLINE EVOLUTION OF HOMINIDS

Hominid fossils include following types

1. Australopithecus : These fossils have been discovered from South and East Africa and include *A.Africanus*, *A.afarensis*, *A.ramidus* and *A.anamensis*. The *A.ramidus* and *A.anamensis* are comparatively new finds; the former from Aramis, Ethiopia (1994) and the latter from Kanapoi, Kenya (1995). They had short, upright face and downwardly directed foramen magnum. The post cranial skeleton bear similarities to Homo and it is believed that they used bipedal gait. *A.afarensis* is believed to have existed 3.7 mya; *A.ramidus* 4.4 mya and *A.anamensis* about 4.2 mya. There is a controversy regarding exact nature of relationship of these early hominids.

2. Paranthropus : These fossils have been discovered from south and East Africa and include *P.robustus*, *P.boisei* and *P.aethiopicus*. These were more robust than australopithecines. They had strong brow-ridges, larger lower Jaw and teeth which was quite suitable for herbivorous diet of hard roots and nuts. The cranial capacity is about 1475 cubic centimeters (average) in modern man. As compared to this, the cranial capacities of Gorilla, Chimpanzee and Orangutan are respectively 510, 410, and 450 c.c. In *Australopithecus*. it was about 500 c.c., indicating that there was hardly any brain growth when bipedalism first appeared upon the evolutionary scene. However, there is a theory that the freedom of hands from locomotion and their use in handling "tools" for hunting and defence by *australopithecus* required intelligence to regulate and augment the work of hands, and that this requirement led to a rapid growth or brain, culminating into the modern man, *Homo sapiens*.

3. **Homo Habilis (The Tool-maker)** : Leakey (1960) excavated 16 to 18 lakh years old hominid fossils from Pleistocence rocks of Olduvai Gorge in East Africa. Later (1964), he and his associates assigned these fossils to the genus Homo under the specific name of *Homo habilis* (handy man) because heaps of tools found with these fossils included deliberately sharpened stones, indicating that this prehistoric man was capable of 'making tools'. Its age has been estimated to be 1.5 to 2 mya.

It lived in open grassy lands, moved erect and was omnivorous, but had a larger brain than that of Australopithecus, with a 700 c.c. cranial capacity. The lower jaw was lightly built. The dentition was more like that of modern man,

4. Homo Heidelbergensis : A European discovery of prehistoric man came from Heidelberg in Germany in 1907 in the form of a fossil of toothed lower jaw. It was assigned to this new species. It also belonged to about 10 lakh years old middle Pleistocene. This jaw is heavy, but with man-like dentition. Presumably, it evolved along an offshoot of main human evolutionary line.

5. (a) Homo Erectus erectus (African And Java Man) : Fossils of this form were excavated in Java and China (near Peking) and later in Africa.

It had receding forehead with heavy brow-ridge; Skull cap thick and heavy, flattened in front. Cranial capacity 800 to 1000 c.c. (average 900 c.c.); Lower jaw large and heavy; Teeth large, but quite like those of modern man, except larger canines of the lower jaw.

Java ape man moved erect, made more sophisticated tools of stones and bones, including axes, and lived in small groups in caves. It was ommivorous with meat as the main diet. Possibly, this was the first prehistoric man to make use of fire for hunting, defence and cooking.

5. (b) Homo Erectus Pekinenesis (Peking Man) : Placing Java ape man and Peking man as subspecies of *Homo erectus* has a sound basis because of close similarities between these. The body structure was quite similar in both. Being about 1.55 to 1.65 metres tall. Peking man was somewhat shorter, lighter and weaker. Its lower jaw was also lighter. The only noticeable difference of Peking man from Java ape man was its large cranial capacity which ranged from 850 to 1300 cc (average 1075 c.c.-about 165 to 325 c.c. more).

Like Java ape man, the Peking man was omnivorous and cannibal. There is a clear evidence of use of fire by it. since group-life demands some communication, especially during activities like hunting, fighting, etc., some sort of non-syllabic language was used by these prehistoric men. The tools of Peking *man were relatively more sophisticated, including sharp, chisel-like* tools not only of bones and stones, but also of Quartz.

6. Homo Sapien Neandertalensis (Neandertal Man) : Neanderthal were first obtained from Neander Valley in Germany (1856). Later, many other fossils were excavated in various countries by different palaeontologists. Although all these fossils have been assigned to a common subspecies of *Homo sapiens*,

these clearly fall into two categories - an 'early' or progressive or preneandertal and a later type, recognized as 'extreme' or 'classic Neandertal

The progressives lived about 1.5 lakh years ago. It had arched cranium and forehead, flattened and erect face, moderate brow ridges, all equal-sized molars, and a heavy lower jaw with a small, protruding chin. Its cranial capacity was between 1400 to 1450 c.c.

The "classic Neandertal" appeared about 70-80 thousand years ago and became extinct about 35,000 years ago. It was stronger with a better body-built, but somewhat shorter (about 1.55 to 1:65 metres tall) in size. It had more prominent brow ridges a low and sloping forehead, a broader nose, inconspicuous chin, somewhat shorter legs, slightly arched thigh bones and more powerful molars. Its cranial capacity was generally larger, often somewhat larger even than that of existing man, ranging between 1350 and 700 c.c.

Progressives had, on one hand, several characteristics resembling those of the existing man, suggesting that it was our direct ancestor. On the other hand, some of its characteristics point out its continuity with "classic Neandertal". Considering the "classic Neandertal", some of its characteristics were remarkably different from those of *Homo erectus* and some from those of the man of to-day. These facts indicate that the 'preneanderthal' was an ancestor of the direct evolutionary line of man, but the "classic form" diverged from 'preneanderthal along a dead offshoot of the main line, becoming adapted for a rough and cold climate.

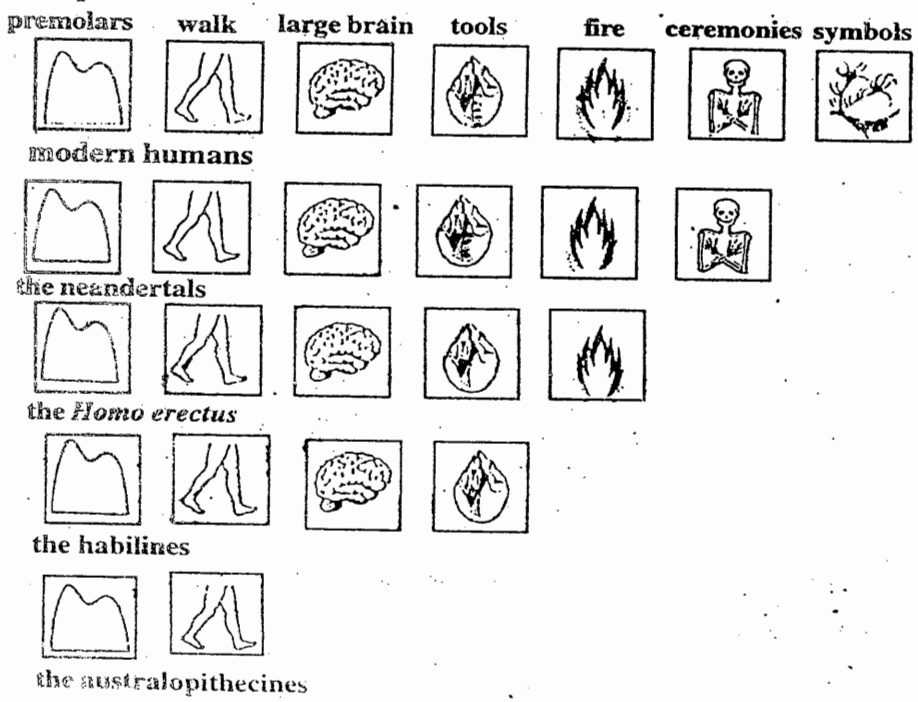
Neandertal men were capable of communicating with each other by some sort of syllabic language. This led to the development of primitive sort of social life associated with some Division of Labour , religion and culture. Evidences of "ceremonial burial" of dead bodies have been often found with their fossils. They used to make tools of bones, stones, quartz and also of flint.

7. Homo Sapiens (Cro-Magnon Man) : Fossils, particularly those excavated in Israel, reveal that about 35,000 to 50,000 years ago a man, anatomically indistinguishable from ourselves, appeared on the evolutionary scene. It has been named Cro-Magnon man because its fossils were first found in 1868 from Cro magnon rocks of France by MacGregor Later, its other fossils were excavated in Germany, Czechoslovakia, Africa and other parts of France. It was an early type of the present man. This is

regarded as the most recent ancestor of to-day's man. It is assigned the subspecies name of Homo sapiens fossilis also by some workers.

Its face was perfectly orthognathous with a narrow, elevated nose, broad and arched forehead, moderate brow ridges, strong jaws with man-like dentition, and a well developed chin. Its cranial capacity was, however, more than ours, being about 1600 c.c. It made excellent tools and ornaments not only of stones and bones, but also of elephant tusks. Its tools included spears, bows and arrows. Use of skin-clothes is also confirmed. Cave paintings done by Cro-Magnon man have been discovered

Homo sapien sapiens (The Man Of To-day) : From Cro-Magnon to the man of to-day cultural evolution has been the dominant feature of human development. Morphologically the transition is marked merely by a slight raising of skull cap, thinning of skull bones, a slight reduction in cranial capacity, and formation of four flexors in the vertebral column.



PROCONSUL-DRYOPITHECUS SIVAPITHECUS (RAMAPITHECUS)

In the miocene from 22 to 7 mya, there lived in the forests of Europe, Africa and Asia certain ape like forms which combined pongid and hominid features. These are fossil hominoids that originated after separation of hominoids and old world monkeys. They are ancestral to apes and some of them might have acted as ancestors of man. They were quadrupedal, lived for most of the times on the trees performing branchiation and occasionally coming on the ground where it could perform limited bipedal locomotion. The growing aridity of miocene and gradual disappearance of forests compelled them to live on the ground where newer agents of natural selection acted to bring about evolution. Those that stayed back in the forests were confronted with different selection agents and evolved into apes. Ancestors of humans ventured out of the forest into grassy savanna were confronted with different set of selection agents and evolved into hominids. *Proconsul-Dryopithecus-Sivapithecus* are fossil apes. For the sake of simplicity, they are referred to as dryoptihecines or dryopiths.

Distribution : A comprehensive list of important fossils find belonging to miocene apes have been given by Pilbeam and others (1992) and is presented here with some modifications :

A. AFRICAN SPECIMEN

1. *Proconsul* : Lake Rusinga, Kenya (E.Africa)
2. *Afropithecus* : Lake Rusinga, Kenya (E.Africa)
3. *Rangwapithecus* : Maboko Island, Fort Ternan, Kenya (E.Africa)
4. *Kenyapithecus* : Fort Ternan, Kenya (E.Africa)
5. *Dendropithecus* : Kenya (E.Africa)
6. *Limnopithecus* : Kenya (E.Africa)
7. *Micropithecus* : (E.Africa)
8. *Turkanopithecus* : Buluk, West Turkana (Kenya)
9. *New Genus* : Monto (Uganda)
10. *New Genus* : Samburu Hills (Kenya)
11. *Otavipithecus* : South Africa

B. EUROPEAN SPECIMEN

1. *Dryopithecus* : France, Germany, Spain etc.
2. *Rudapithecus* : Hungary
3. *Ouranopithecus* : Greece

C. ASIAN SPECIMEN

1. *Sivapithecus Indicus* : Siwalik (India), Potwar hills (Pakistan), Turkey, Nepal.
2. *Lufengpithecus* : Lufeng (China)
3. *Heliopithecus* : Saudi Arabia
4. *Ramapithecus* : India etc.

The different forms, for the sake of description, have been categorized into early, middle and late miocene as mentioned below :

Proconsul And Early Miocene Apes

1. Among the fossil finds of dryopiths, the most nearly complete fossil remains belong to *proconsul*, discovered by L.S.B.Leakey and his wife Mary Leakey from Lake Rusinga, Kenya in 1948. The fossil finds included skull with mandibles including teeth and limb bones. The fossil, when discovered, was thought to be ancestral to the modern chimpanzee and was named after consul, the popular chimpanzee at the London Zoo by Arthur Hopwood of the Natural History museum, London.

2. Proconsul from the early and middle Miocence (23 to 15 million years ago) of eastern Africa diversified into many species. It is the most completely known extinct simian primate. Fossils have come from Kenya and Uganda and show a range in size equal to that extending from large monkeys to female gorillas.

3. The skeleton of *Proconsul* shows a blend of primitive, unique and advanced features. The animal was a monkey-like quadruped without tail but resembled apes in some features of its hands, feet and sacrum. The Pelvis had a blend of monkey-like, ape-like and unique features.

4. Anatomy of humerus, wrist bones and post-cranial anatomy suggest that *Proconsul* was not a brachiator but they do suggest quadrupedal walking and running, perhaps in the manner of some new world monkeys. They were, however, capable of brachiation and bipedalism.

5. *Proconsul* is either the ancestor itself of the hominids or it is very close to it. Many specimen of Proconsul have been discovered from Kenya and Uganda. The genus has been divided into following species (After Pilbeam, 1992)- *P. africanus*, *P. nyanzae* and *P. major*.

Main fossils of *Proconsul* comes from Rusinga island in Lake Victoria (Kenya). *P. africanus* is smaller weighing about 10-15 Kg whereas *P. nyanzae* is bigger weighing about 30-40 Kg.

6. Pilbeam and others (1992) suggest a new relationship between P. nyanzae and P. africanus found at Rusinga - that actually they represent male and female of the same species, P. nyanzae. The conclusion is based upon assumption that only two types of canines are found at Rusinga - long, blade-like "Male" types and short, stubby "Female" type. If there are two species represented at Rusinga, We ought to have four kinds of canines, they argue. The male canine fits with the nyanzae dentition and female canine with the africanus dentition. If it is accepted, then sexual dimorphism displayed in this case would probably be at its zenith in the group. However other explanations are not ruled out.

7. Not much is known about other early miocene apes such as Rangwapithecus and Afropithecus. Other genera such as : *Dendropithecus*, *Limnopithecus*, *Micropithecus* are small forms weighing less than 5 to 10 kg. They were similar to *Proconsul* in many features.

Dryopithecus And Middle Miocene Apes

1. Middle miocene apes are distributed in Europe and Africa. They differ from early miocene apes and approach modern apes.

2. The representative of the group is *Dryopithecus* whose structural detail will follow later on

3. Another example of this group, *Kenyapithecus*, had robust jaw and thick enamel on teeth which suggest powerful biting and prolonged chewing on hard and tough food. Post cranial elements are similar to *Proconsul*. There was sexual dimorphism in canine and body size.

4) The recently discovered *otavipithecus* from late middle miocene of Namibia represents the first South Africa fossil. It is known from a single jaw which lacks thick enamel.

Sivapithecus And Later Miocene Apes

Sivapithecus was discovered from Siwalik hills of India and Potwar hills of Pakistan, Turkey, Nepal etc. Detailed Studies of *Sivapithecus* in 1980 and 1990 indicate that :

1. It is more or less similar to *Proconsul* and *Dryopithecus* except it was more arboreal with feet adapted to vertical clinging. Molars were relatively large with low cusps. It is believed to have given rise to orangutan.

2. *Sivapithecus* shares with the orang-utan several features of the skull and face. These include the absence of a bony sinus in the brow area of the skull, a very narrow bony partition between the eyes, vertically elongated orbits and, most importantly the way the palate joins with premaxilla below nose (naso alveolar clivus). *Sivapithecus* uniquely shares clivus pattern with the orang-utan, which together with other facial features, implies that there is a phylogenetic relationship between the two.

3. In most of the other respects, however, the cranial anatomy of *Sivapithecus* is unlike that of the orang-utan, as is the post-cranial anatomy.

4. Behaviourally, *Sivapithecus* was probably not much like an orang-utan, with no evidence of skeletal adaptions allowing a high degree of limb mobility. Like *Proconsul* and its relatives, these earliest putative members of the orang-utan lineage were not much like their living descendant.

5. All were moderately large, ranging in size from large monkeys to chimpanzees with a few very large species perhaps as large as orang-utan or female gorillas and all appear to have been moderately or even highly sexually dimorphic.

6. Their elbows suggest that climbing and suspension were important in their behaviour. However, some other features of the forelimbs of *Sivapithecus* are monkey-like, implying quadrupedal walking and climbing but not suspension. Other parts of postcranial skeleton also suggest this type of quadrupedalism, with little of the forelimb-dominated suspensory behaviour. Thus hand anatomy suggest suspensory behaviour and feet anatomy quadrupedalism. Pilbeam and others suggest that its foot was adapted to vertical clinging.

A virtually complete skeleton of *Oreopithecus* has been unearthed. This is similar to modern apes in many features of the trunk and limbs. *Oreopithecus* thus seems to have been more

adapted for suspension than was either *sivapithecus* or *Rudapithecus*.

These three Eurasian lineages hence suggest that there was considerable locomotor diversity among late Miocene apes, and that some were still primitive in features of their postcranial anatomy. Not all of them were as adapted for suspension as are all living apes, including the largely terrestrial gorilla which can also show suspensory locomotion.

7. All these late Miocene apes were adapted for life in trees, although they probably came down to ground occasionally. The disappearance of dense forest woodlands may have led to their extinction.

8. The diets of late Miocene Eurasian hominoids were probably quite diverse. *Sivapithecus, Ouranopithecus* and *Gigantopithecus* had thick-enamelled cheek teeth, and may have had diets similar to that of *Kenyapithecus*, with hard and tough food items. However, they differed in body size and in other features of teeth and jaws, especially in the size and shape of the incisors. *Lufengpithecus* had thinner enamelled teeth. *Oreopithecus* had very unusual teeth.

9. By the end of the Miocene, these forms vanished from everywhere except China. The gradual cooler and drier climate of Miocene resulted in replacement of evergreen forests by wooded grassland. This is supported by geochemical evidence from fossil soils in the siwaliks of India and Pakistan. The area vacated by the extinction of apes was soon occupied by the monkeys who were better adapted to live in such habitat. Only the lineage leading to gibbons and orang-utan persisted but became confined to forests of South East Asia. The *Gigantopithecus* was probably a ground dweller which became extinct later on in pleistocene

10. *Sivapithecus* groups shows affinity to the pongo-line and donot bear similarities with *australopithecus* group, the first hominid ancestor discovered so far It suggests that Africa was the site of ape/human split. Because there is no African fossil belonging to the age 18 mya to 5 mya hence nothing can be said definitely about ape/human split.

11. Other later Miocence apes differ from *Sivapithecus* in features of skull. The cranium of *Ouranopithecus* shows a few intriguing similarities to that of African apes, or even to hominids, but whether or not these are phylogenetically relevant is not clear. Although *Lufengpithecus* and *Rudapithecus* have none of the key

features of the ornag-utan clade possessed by *sivapithecus*, each has other features that may place them as more primitive members of this clade. In most respects, however, all except *Sivapithecus* are Variants of a primitive great ape skull.

Characters Of Dryopiths

Dryopiths combine the characters of monkeys, apes and Man. In features of skull it is like monkeys; in features of fore-limb and foot it is ape-like showing incipient ability for brachiation and in features of jaw and dentition it approaches humans.

A. Monkey-Like Features : Resemblances between Dryopithecus and monkeys is a generalized one and donot show any specific similarities to indicate phylogenetic relationship. Dryopithecus seemed to have smaller brain and narrow face like monkeys, indicated by small skull. In the manner of construction of hand bones also the two groups resemble these similarities more due probably to the fact that dryopiths, after their separation from monkey's ancestors had not evolved much with respect to these feature.

B. Hominoid Features : Arrangements of cusps on the 1st lower molar tooth (called y-5 pattern) present in dryopithecus is also present in gibbon, apes and humans and also in fossil Aegyptopithecus in some modified form. In its simplest form, three cusps, 1, 3, 5 are arranged on the check sided and two cusps (2, 4) on the tongue side. Cusp 3 is separated by two grooves from 1 and 5 that form barked part of Y (1 3 5). The Y is completed by a groove between 2 and 4. In humans the pattern is modified Y-5 pattern and in monkeys as + pattern: a condition in which four cusps of molars are arranged as two transverse crests.

Of the two groups of hominoids, namely pongids (apes) and hominids (Homo and its immediate ancestors), Drypithecus resembles with both the groups. In certain features, it is more ape like while in certain other features, it is more human-like, thus regarded as common ancestor of both apes & man.

C. Ape-Like Features :

1. Presence of large incisors which are indicative of frugivorous adaptation.

2. Canines are also large as in modern apes.

3. Its mode of locomotion is controversial. However, the features of the fore-arm and shoulder-girdle indicate that the creatures were brachiators. Such features include :

i. The position of the shoulder spine proves that it was easier for the hands to attain overhead position.

ii. Bending in the humeral head and shoulder joint indicate that there was some medial rotation of the hands

iii. Development of crests in the humerus to provide attachment surface for developed delto-triceps and delto-pectoral muscles, that might have assisted in brachiation.

iv. At elbow joint, the lower-arm radio - ulna, produced into two expanded and extra extended extensions, the olecranon and the coronoid beak, which trap around lower end of fore-arm bone, humerus.

v. Humeral trochlea also expanded to accommodate expanded olecranon and coronoid beaks of radio-ulna. Lewid (1972) has concluded that even if complete brachiation had not developed, they were definitely capable of hanging by the arms and had evolved in this aspect beyond living old world monkeys.

D. Hominid Features :

1. Absence of simian shelf brings dryopiths lower-jaw close to hominid conditions.

2. There is no space between canine and first premolar in lower jaw and hence there is no interlocking of canines like in apes.

3. Incisors and canines are more vertically implanted than the pongids hence dental archade has assumed V-shape (U-shape in pongids and parabolic in hominids).

Origin Of Dryopiths

Since dryopiths were abundant during miocene. it is supposed that it originated from some forms during oligocene. Four fossils of this period compete for the consideration as probable ancestor of *Dryopithecus*. These are :

1. *Propliopithecus*
2. *Pliopithecus*
3. *Dendropithecus*
4. *Aegyptopithecus*

Of the four fossils, *Propliopithecus* combines characters of old world monkeys and hominoids and hence considered ancestral to both. *Pliopithecus* and *Dendropithecus* are miocene forms that are supposed to have given rise to gibbons and siamang. It leaves *Aegyptopithecus* for consideration because it combines character of lower and higher primates and possesses great age, 28 mya. The primitive features include long snout with a relatively small brain case and advanced features include hominoid jaw structure and dentition, eye-sokets and above all, sexual dimorphism. It is supposed that they lived in large, complex social groups.

Aegyptopithecus is the best known oligocene anthropoid. It lived in the evergreen forest where fruits abounded. It was a frugivorous quadruped with adaptations for climbing and leaping. It is considered ancestral to *Proconsul*, a form which itself is considered ancestral to Hominoids (apes and man)

Evolutionary Discussion

Dryopiths are supposed to have originated in Africa. This statement is based on the fact that the *Proconsul*. the earliest of dryopiths, belonged to Africa. It was probably large bodied. arboreal, frugivorous ape with varied positioned repertoire including arm-swinging active climbing especially of vertical supports and occasional bipedalism.

A. Radiations In Asia : One or more species of *proconsul* migrated out of Africa and in the European and Asian Forests and Woodlands underwent modest adaptive radiations. One of the products of radiation is *Sivapithecus* from Asia, which can be linked to *Pongo* (Orang-utan), the sole living Asian great-ape. The oldest well preserved *Sivapithecus* is 12 mya and this would then mark the possible age for an Asian (Pongo) Vrs. African (Pan, Gorilla and Homo) Split. *Pongo* is a highly derived descendent of

Sivapithecus.

B. Radiation In Africa : Our knowledge of what was going on during this time in Africa and adjacent areas is poor. It is not known whether middle and late miocene dryopiths of Africa and Europe are descendants of Proconsul. Thus on the basis of fossil finds the only thing that can be said with certainty at present that African continent was the focal point of dryopiths origin for they are represented in early miocene of Africa only and only later disseminated to Eurasia, including India where only middle and lower miocene forms are found.

However, their branching time can be predicted. Assuming that DNA-DNA hybridization distances are reasonable reflector of time and assuming that *Sivapithecus-Pongo* similarities tell us about evolutionary relationship; given a Pongo lineage diverging at least 12 mya, Gorilla would diverge 9 mya and chimpanzee and man 7 mya. The calibration is based on *sivapithecus-orang-utan* lineage because 12 mya is the minimum age for origin of orang-utan (since no older beds have revealed fossils of *sivapithecus*).

A new fact has emerged in the evolution of drypiths. Upto 1970s there has been a trend to recognise dryopiths as a separate lineage with distinct and different evolutionary potentiality from *Ramapithecus*. It was believed that dryopiths evolved in apes and *Ramapithecus* in man. But in the 1980s there has emerged a trend to recognise the *Ramapithecus* not as distinct line leading to hominids but a part of miocene radiation complex of dryophits leading to greater apes. (pilbeam and others 1990)

Sivapithecus and *Ramapithecus* are remarkably similar in the features of thickness of the enamel of the teeth as well as palato-facial features. The only significant difference between the two is that *Sivapithecus* seems to represent a large canine radiation whereas *Ramaphithecus* represents a small canine radiation. some of the modern paleontologists such as pilbeam & other (1992) believe that miocene radiation complex of dryopiths includes ramapithecus also and that ramapithecus is not a hominid leading to man but a hominoid leading to evolution of apes. Palaeoanthropologists of today believe that *Ramapithecus* was smaller in size than *Sivapithecus* and probably its female. Thus *Ramapithecus* is now included in the *Sivapithecus*.

OREOPITHECUS

Miocene was a period of great climatic change. The growing aridity had dwindled many forests, replacing it with woodland and grassland Savannah. Many related genera of miocene anthropoids were forced to descend on the land where they practised limited bipedalism. *Oreopithecus* was one of such genera belonging to the late miocene of Europe inhabiting woodland Savannah and a contemporary to *Sivapithecus* of Asia. While *Sivapithecus* is now more closely aligned to Pongo line, there is now a days growing realisation that *oreopithecus* more closely represent a hominid line of descent and partially fills the void created by the inclusion of *Ramapithecus* in the *Sivapithecus*.

Oreopithecus, however, is not a new find. The genera has existed for long in anthropological history and has been one of the most controversial fossils. It was first discovered in 1870 in Tuscany, North Italy and subsequently described in 1872 by Grevais. The materials include jaw fragment, teeth and fore-limb bones. In the beginning, its similarities to the old world monkeys were described.

First attempt to see *oreopithecus* fossils not as old world monkey but as a hominid was made by Hurzeler. Such a description of *oreopithecus* was possible because of discovery of new fossils in 1958. In 1958, a complete fossil of *Oreopithecus* was discovered from Italy. It was the first complete fossil of any anthropoid to be have been discovered. The discovery of such a complete fossil thus gave impetus to the studies about its true affinities and phylogenetic relationship.

Taxonomic Relationship Of Oreopithecus : *Oreopithecus* has been differently classified by different workers :

i. Straus (1963) assigned it to its own family Oreopithecidae within the Hominoidea

ii. Szalay and Delson (1979) classified it as cercopithecoid.

iii. Harrison (1986) has placed it in Proconsulidae, suggesting its origin from *proconsul nyanzae*.

Old Monkey-like Features Of Oreopithecus : Judging *Oreopithecus* from its post cranial skeleton, there is no doubt that the group belongs to hominoids and, as a matter of fact, closely resemble hominid. But the main controversial feature of *Oreopithecus* has been its dentition which is unique from several point of view. Teeth, in general, is like hominid but molars are like

old world monkeys in the sense that they are with crests and in some respects shows biolophodont characteristics. However, in several features of anatomy, *Oreopithecus* closely resemble hominids.

Hominid Features Of Oreopithecus :

1. Teeth, in general, are of small size and reflect hominid conditions.

2. Canines are pointed but short and clearly different from monkeys and apes.

3. There is no premolar diastema that accommodates enlarged canines of upper jaw.

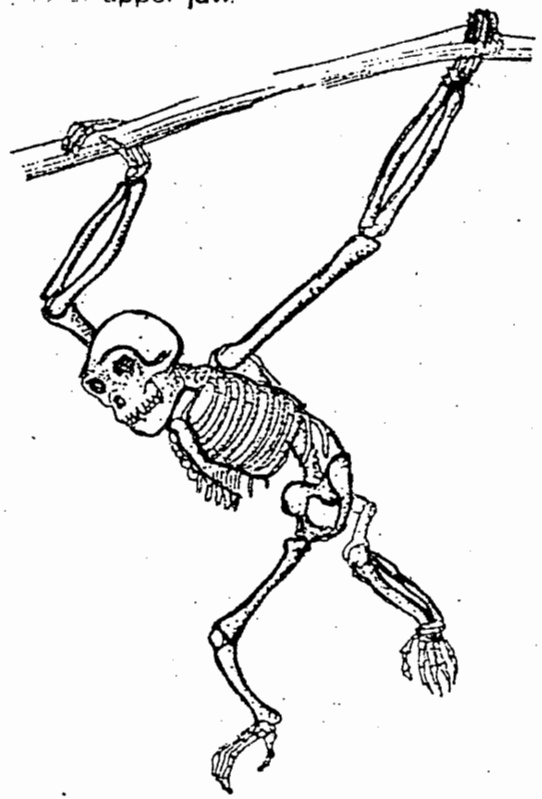


Fig. : Reconstruction of Orepotiphecus, a gibbon-like ape of the Miocene

4. Premolars are similar to humans. First premolar is low crowned. Upper premolar cusps are not heteromorphic.

5. The hand bones also bear marked similarities with hominids. In humerus, trochlear keels are strongly developed. In radio-ulna the olecranon is short and sigmoid notch broad. The ulnar shaft is bowed.

6. Bones of pelvis, leg bones also bear mark similarities to humans. In general, they support the notion that *oreopithecus* was capable of bipedal locomotion. The iliac blade is broadened, the talus neck is short and broad.

Comparing characters of *Oreopithecus* with the list of Andrew (1985) who set forth Criteria for hominoids and hominids, Groves (1992) has concluded that many of the features of *Oreopithecus* is definitely hominoid but different from the Proconsulidae. It means it definitely shared an ancestor with hominids and Hylobatidae after splitting off from the Proconsulidae.

Ape-like Features Of Oreopithecus : *Oreopithecus* approached apes in certain features of its hand anatomy, particularly in the possession of very long arm in comparison to the legs (intermembral index 120) clearly indicates that the creature was a true brachiator. On the basis of anatomy of hands, it has been proposed that *Oreopithecus* was a better brachiator than any of the late miocene apes viz. *Sivapithecus* and *Rudapithecus*. *Oreopithecus*, thus, had more diverse locomotor repertoire.

Evolutionary Discussion : An overwhelming number of features of *Oreopithecus* suggest that it is not a cercopithecoid and it must be considered as a hominoid. Because of its dental specialisations similar to the cercopithecoids, it has not been included in the hominidae and has been allotted a different family of its own, oreopithecidae in the super family Hominoidae. Oreopithecidae is, thus, considered a part of the miocene radiation that produced Hominidae and Hylobatidae. Groves (1992) has stated that *Oreopithecus* must be considered different from apes and *Homo* because they do not show presence of shortened lower molars and symmetrical femoral condyles. There are not many features to base conclusions upon but the two features stated above has necessitated creation of a different family. Oreopithecidae However, there is growing demand that the genus should be placed with hominids. Overwhelming similarities of the *Oreopithecus* with the hominids justify such demands.

AUSTRALOPITHECUS-PARANTHROPUS

They are often divided into two forms - short, slender species of the size of chimpanzee called gracile forms and somewhat largers species with bigger brain size and bigger molars called robust forms. it is now clear that robust forms, which originated later and had larger brains, donot represent main line of hominid evolution but are an aberrant side-line. Hominid evolution was continued with the slender forms and *Homo habilis*. To reflect this growing reallsation, australopithecines are divided into two genera - *Australopithecus* that include slender forms (*A. ramidus*, *A.anamensis*, *A.afarensis* and *A. africanus*), and *Paranthropus* which include robust forms (*P. robustus*, *P. boisei* and *P. aethiopicus*) *A.ramidus* has been discovered in 1994 and *A.anamensis* in 1995.

First discovered by Dart (1925) from Taung in South Africa. hominid status of *Autralopithecus* was confirmed in 1936 when Robert Brown discovered a similar but adult cranium from Sterkfontein. In 1930s and 1940s, Raymond Dart, Robert Brown, Robinson and others discovered many similar fossils at Kromdraai, Sterkfontein, Swartkrans, Makapansgat etc. which finally established that South African ape-man were more human-like than ape-like. In the 1960s and 1970s, many similar fossils have been discovered from Olduvai Gorge in Northern Tanzania by L.S.B. Leakey, and his wife mary Leakey, Afar in the Hadar region of Ethiopia by Johanson & Timothy white. In Omo and Koobi fora by Richard Leakey. In 1994 from Aramis, Ethiopia by white et.al. and in 1995 from Kanapoi, Kenya by Leakey et.al.

Distribution : Distribution of australopithecine outside Africa is doubtful. A fossil from Java has been described by Robinson as *meganthropus* while Clark considers it early *Homo*. In Africa, they are scattered in South & East Africa.

1. South Africa :

Taung, Cape province (1924) *A. africanus*

Sterkfontein, Transvaal (1936-77) *A. africanus*

Kromdraai, Transvaal (1938-54) *P. robustus*

Makapan sgat, Transvaal (1947-61) *A. africanus*

Swart Krans, Transvaal (1948-76) *P. robustus*

2. East Africa :

Tanzania : Garusi(1939), Olduvai(1955-72), Peninj(1964)

Kenya : Around Lake Turkana(Rudolf) : Kanapoi(1965, 1995) Lothagam(1967), Koobi Fora(1968-76) Around Lake Baringo - Chemeron (1965), Chesowanja (1970)

Ethiopia : Omo(1967-73), Afar(1973-76)

Chad : Yayo(1961)

The South African Australopithecines : In South Africa, The australopithecine fossils are found in caves which are formed when water channels run through the limestone underground. Once cave forms underneath the earth, they develop openings into which are washed soil and debris, including bones.

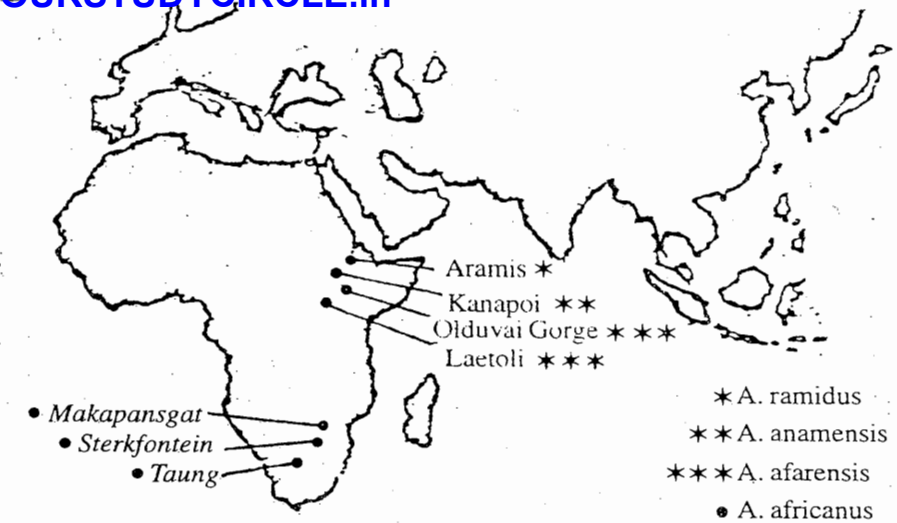
Australopithecine, in most probability, did not occupy these caves. Australopithecine bones were probably introduced into the limestone caves by leopard and other large cats. There is a evidence for this from Swartkrans. The holes in the skull of an australopithecine (SK 54) match the lower canine of a leopard from the same deposit.

The fossils from Taung, Sterkfontein and Makapansgat belong to *A.africanus* or gracile forms whereas fossils from Kromdraai and Swartkrans belong to *P.robustus* (or *Paranthropus robustus*). (Recently, some workers have suggested that robust forms from two sites of South Africa should be included in different species *P. robustus* from Kromdraai *P. crassidens* from Swartkrans).

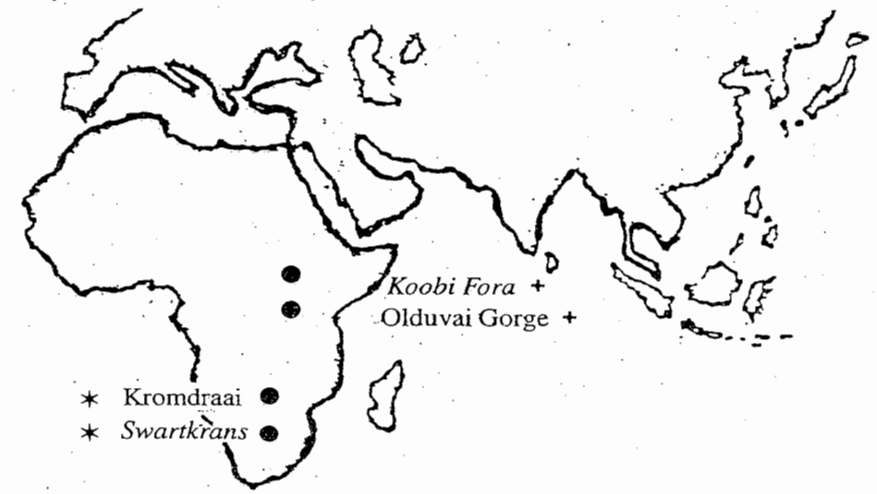
It is now generally agreed that Makapansgat, Sterkfontein and probably Taung, which have *A. africanus* are older (about 3-2 mya) while Kromdraai and Swartkrans with *Paranthropus* are younger (2-1.5 mya).

Initially, it was believed that gracile forms were aggressive predators. This was based on the recovery of broken animal bones associated with the gracile fossils of South Africa. It was thought that breakage pattern and other features implied their use as knives, clubs, spears, and scrapers. The idea is now disputed because patterns of bone-breakage indicate that activities are instead of non-primate predators. Thus, in most probability, autralopithecines did not hunt, rather they were hunted. (Pilbeam, 1992)

The East African Australopithecines : Eastern African australopithecines are found in completely different settings. They are found on the shores of lakes, flood plains, river-valley etc Australopithecines are believed to be inhabitants of these places.



Distribution of australopithecus



Distribution of Paranthropus

✶ P. robustus
✚ P. boisei

Australopithecine sites in East Africa can be dated more accurately. The rift valley had considerable volcanic activity with eruptions of lava containing isotopes of potassium, argon, and uranium. These were deposited in between the sedimentary rocks hence fossil finds of the region can easily be assigned definite age on the basis of such methods as potassium-argon method.

Work in East Africa picked up with the discovery by Mary Leakey in 1959 of an australopithecine Cranium from Olduvai in Tanzania. Initially, it was named *Zinjanthropus boisei*; later on its name was changed to *Paranthropus boisei* and then to *Australopithecus boisei*. These are East African robust forms, different from robusts of South Africa and there is now efforts from several quarters to reallocate its prior name - *Paranthropus* - for graphic expression of its differences with the gracile australopithecines. The hominid was associated with simple stone tools and thus was originally believed to be "tool makers". Largest collection of *P. boisei* comes from Koobi Fora. *P. aethiopicus* is a primitive looking A.boisei discovered from Lake Turkana (Kenya) in 1985

. gracile forms have been discovered from East African sites. *A.afarensis* materials comes mainly from Hadar region in Ethiopia and Laetoli in Tanzania. It was from Hadar region of Ethiopia from where Coppens and Taieb discovered "Lucy". (1973 - 1976)

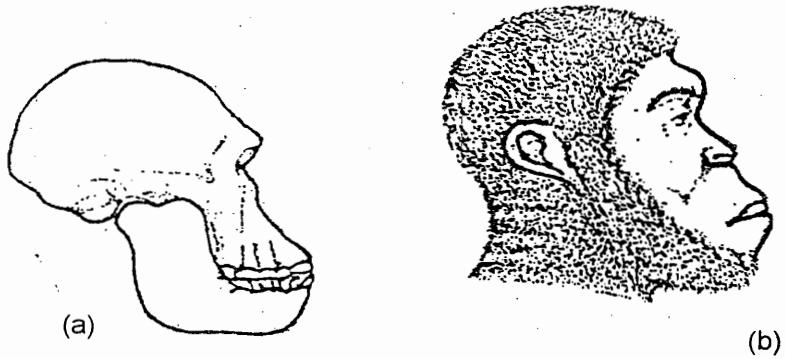
The latest fossils of *Australopithecus* is that of *A.ramidus* coming from Aramis, Ethiopia and *A.anamensis* from Kanapoi (Kenya) the former discovered in 1994 by Tim white et.al. and the latter in 1995 by Leakey et.al.

Gracile Australopithecine

There are two views regarding nomenclature and taxonomy of australopithecines. One divides them in two types *Australopithecus* and *Paranthropus*. the former including gracile forms and latter robusts forms. Other include all forms in one genus *Australopithecus*.

In 1995-96, there are four main species of australopithecus.

.1. Australopithecus africanus : These were lighter or gracile forms measuring 4 ft. and weighing 30-60 Kg. and characterized by smaller, rounded cranium, without sagittal crest, weak supra orbital ridges and modern zygomatic arch. These are supposed to have existed from 3-2 mya.



The Gracile australopithecine (a) skull (b) restoration of individual

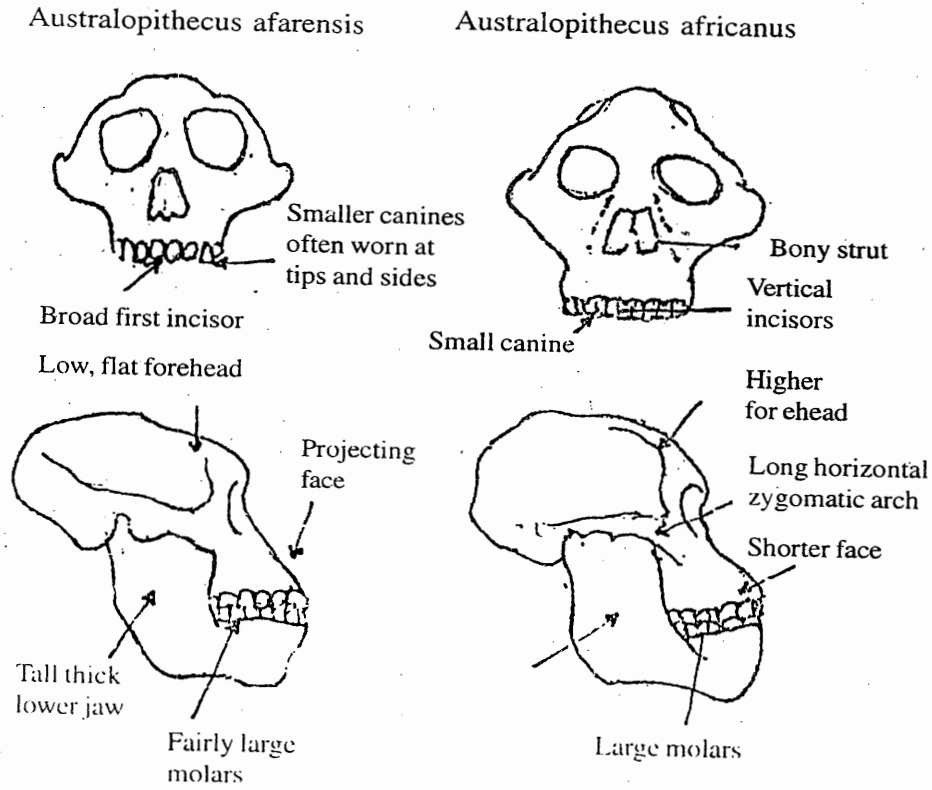


Fig. : Skull of australopithecus

2. Australopithecus afarensis : Its fossils were discovered from Hadar & Laetoli region of E.Africa. These were small measuring about 3.5' weighing 30 to 70 kg and brain volume of 400 cc. Its lower premolar was semi sectoral and canines projected slightly above the level of other teeth. Also, the skull had primitive features such as strong muscle marking on the sagittal crest and temporal and nuchal crest, the hind part of the skull. However, fossil of its foot prints and foot bones show that it might have attained at least a limited bipedal gait. Its age has been estimated to be around 3.77 mya for laetoli specimens though fossils from other places may be older

The taxonomy of A *afarensis* has been a matter of debate since its description in 1978 by Johanson, white and coppens. Some authorities regard all specimens assigned to *A.afarensis* as belonging to one taxon (primarily its discoverers) whereas, others regard the Tanzanian and Ethiopia species as each representing a different species (Leakey, 1981, Tuttle, 1988). Further controversy surrounds the issue of sexual dimorphism and locomotion among these hominids. Fossils discovered in the Afar of Ethiopia in 1990 constitute the first major addition to the *A.Afarensis* since the 1970s. Tim White et al (1993) reported discovery of more fossils from maka, Ethiopia dated 3.4 mya which provide powerful support for the interpretation that *A.afarensis* was a single, ecologically diverse, sexually dimorphic, bipedal pliocene

3. Australopithecus ramidus

Tim white, Gen suwa and Asfaw (1994) discovered 20 fragments of about half a dozen individuals from Aramis, Ethiopia. The evolutionary status of the fossil remains has been discussed by Bernard wood (Nature, volume 371, 1994) and Craig B. Stanford (1995). It is recognised as oldest hominid representing a new species of *Australopithecus, A. ramidus.* It shows following features :

1. It lived around 4.4 mya.
2. It was biped, its lower body was clearly adapted for walking on the grounds.
3. Its limb anatomy predicts that they were able to climb trees to catch ancestors of small colobus monkey.
4. It upper and lower canines were larger than that of *A. afarensis* but more incisiform than ape ancestors.
5. Its lower first molar was narrow and obliquely elongate. Protoconid was large & meta conid small. It is more primitive than that of *A. afarenis*.
6. Teeth enamel was thinner than *A. afarensis.*

7. Upper central incisors were small than that of extant apes,Chimpanzee and Gorilla.
8. Molar crownes were less projecting than that of extinct apes.
9. Foramen magnum was anteriorly placed.
10. Upper limb smaller than apes.

A. ramidus appears to be more primitive than *A. afarensis.* Before 1978, before discovery of *A. afarensis, A.africanus* was considered most primitive hominid leading to man lineage. In 1978, the place was usurped by *A.afarensis* Now it seems the distinction of being oldest and most primitive hominid shall be held by *A.ramidus*

4. Australopithecus anamensis

Leakey et.al (1995) have discovered nine fragments from Kanapoi, Kenya. Leakey claims that the species is about 3.9 to 4.2 mya and ancestral to *A.afarensis* and sister species of *A.ramidus.* It shows following features :

1. The size was in the range of 40-55 Kg, larger than afarensis and ramidus
2. A partial tibia (without shaft) and humerus resemble that of homo.
3. Tooth enemal thicker than *A. ramidus.*
4. First and second molar not different in sizes.
5. Upper molars slope more towards lingual side and lower molars to buccal side in comparison to *A. afarensis.*
6. Molar cusps show different pattern from other australopithecines.
7. Canine with long, robust roots.
8. Sex differences visible in teeth and mandible .
9. Tooth rows parallel.
10. A small acoustic meatus which is narrow ellipse in outline.

The various species of *Australopithecus* show following features :

1. *A.ramidus, A.anamensis, A.afarensis* and *A.africanus* are clubbed together as gracile forms. *A.afarensis* has been discovered from Hadar and Omo (Ethiopia), Laetoli (Tanzania), Lothagam, Tabarin (kenya) etc. *A.africanus* materials comes mainly from Taung, Sterkfontein, Makapansagat (South Africa), and some parts of East Africa. *A.ramidus* was discovered from Aramis, Ethiopia and *A.anamensis* comes from Kanapoi (Kenya).

2. A.ramidus is oldest (4.4 mya), followed by A.anamensis (4.2 mya), A.afarensis (3.77 mya) and A.africanus (3 - 2 mya).

3. The gracile forms had lesser brain size averaging more or less-400 cc. whereas slightly higher for *africanus*-450 cc. For *A.ramidus* it is below 400 cc.

4. The gracile forms had lesser height and body weight than robusts.

5. The teeth of gracile forms were in general smaller than robusts, the total tooth area for the graciles being around 500 mm^2

whereas it being 600 and above for the robusts. The teeth of *A.afarensis* was smaller than *A.africanus*, the tooth area being 460 mm^2 for *A afarensis* and 515 mm^2 for *A.africanus*. For *A.ramidus* it is still lower.

6. Cranium of *A. afarensis* was long whereas it was more rounded in *A.africanus* and other.

7. The skulls of four varieties of graciles differ in detail but ratio to the brain volume/body weight was similar.

8. All graciles had good-sized incisors and pattern of wearing on the teeth is also similar indicating, at least partly, some fruit eating.

9. Anatomy of hand and feet differ only partially. Some see groups as habitual bipedal whereas majority holds all the groups as neither predominantly arboreal nor fully bipedal. However, latter condition is indicated more. The skeleton of *A.africanus* was more adapted for bipedal locomotion but details of its muscular construction was different from modern apes or human. It is concluded that they might have moved like modern baboons, placing emphasis on bipedalism. It is thought that this group might have moved out to forage on the ground in the day using bipedalism and then congregate in caves or trees in the night.

10. Social system of living apes and monkeys is predicted, to some extent, on the range of body size and habitat. On this basis, it has been guessed that gracile may have lived as multimember group or a single male with a harem.

11. The archaeological discovery of stone artefacts barely overlaps the most recent gracile australopithecine. Hence it is uncertain as to what extent these creatures made and used these weapons.

Robust Australopithecines or Paranthropus

There are two or three species of *paranthropus* :

A. Paranthropus robustus : These were massive or robust forms of South Africa measuring 3 ft, 11 inch and weighing around 40-80 Kg. and characterized by larger, flat cranium and cranial capacity, pronounced supra orbital ridges, distinct saggital crest and massive zygomatic arch. Large strong rooted premolars and molars indicate a harsh vegetarian diet. These are supposed to have existed from 2.3 to 1.8 mya.

B. Paranthropus boisei : It is robust of East Africa,

measuring 4'4" and 40 to 80 Kg in weight. Previously referred to as *Zinzanthropus boisei* by its discoverers L.S.B. Leakey and Mary Leakey (1959) the fossils were discovered from olduvai Gorge (Tanzania), Turkana (Kenya), Omo (Ethiopia) of East Africa. The robust features were more pronounced. It is supposed to have existed from 1.8 to 1 mya. *A.aethiopicus*, a find of 1985 looked like primitive *A.boisei*.

Paranthropus shows following features :

1. *Paranthropus* has been discovered from both South Africa and East Africa. The South African form *P.robustus*, measured 3.11" in height and 40-80 Kg. in weight. The East African form *P.boisei* was slightly taller, 4.4 Ft., but apparently no heavier. Their brain-size was larger (500 cc). In general, they are believed to have existed from 2.5 to 1 mya, following graciles in evolution.

2. There has been found size differences in the mandibles of *P.boisei* indicating differences between the body-size of males and females being twice as is found in modern gorillas.

3. Robusts had broad face, tall mandibles and larger molars indicating a diet that involved the processing of large amount of food and generation of much force between the teeth. The diet suggested range from seed to bones but most probably it included a pulpy food with hard covering.

4. Robusts moved in a similar way to graciles.

5. Studies of the pattern of formation of the hard enamel of teeth suggests that growth and development of the dentition was faster in robusts than in modern humans and apes.

6. The social structure of robusts may also have involved multiple groups or a harem.

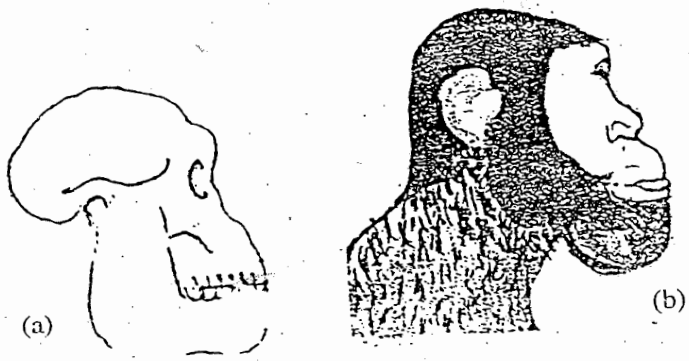
7. Archaeological findings of bony artefacts belonging to the age of robusts have been recorded.

8. The advent of robust form may have been part of a more widespread evolutionary event around 2.5 mya when there became a cooler climate with opening up of more grassland and woodland. Many vertebrates became extinct at this time and many appeared for the first time.

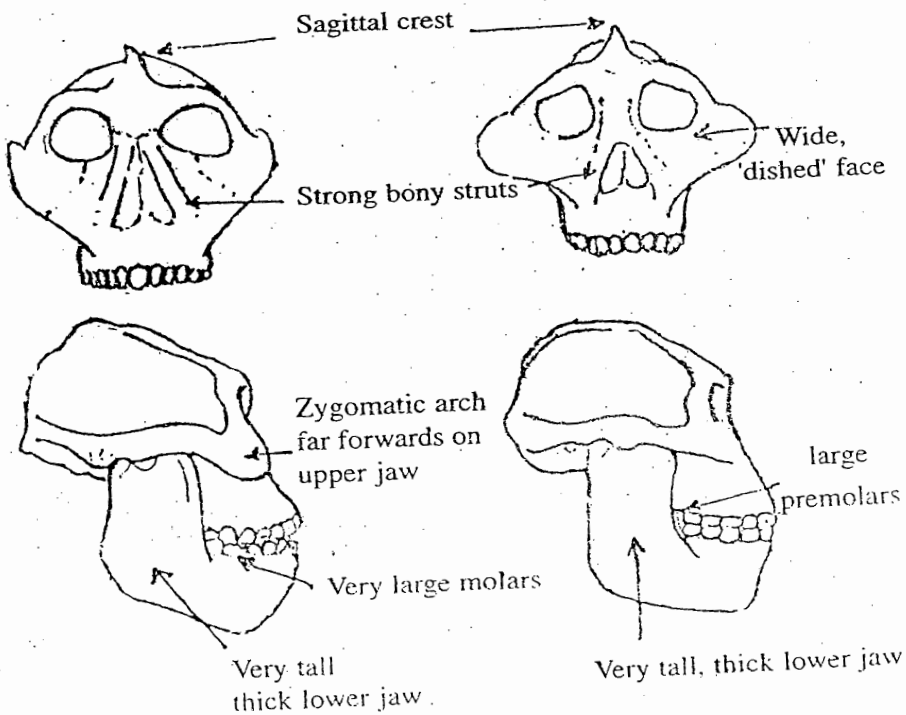
Features	Australopithecus		Paranthropus	
	Australopithecus afarensis	Australopithecus africanus	Paranthropus boisei	Paranthropus robustus
Height (ft)	3.5'	4.0'	4.4'	3.1-1'
Weight (kg)	30 - 70	30 - 60	40 - 80	40 - 80
Bodily features	Light build; some ape- like features (eg.shape of thorax; long arm relative to legs; curved fingers and toes: marked to moderate sexual dimorphism)	Light build: probably relatively long arms; more human features: probably less sexual dimorphism	Very heavy build; relatively long arms; marked sexual dimorphism	Heavy, build relatively long arms moderate sexual dimorphism
Brain size	400 ±	450 ±	500 ±	500 ±
Skull form	Low, flat forehead: projecting face: prominent brow ridges	Higher forehead, shorter face; brow ridges less prominent	Prominent crests on top and back of skull: very long. broad, flattish face: strong facial buttressing	Crest on top of skull; long broad. flattish face; moderate facial buttressing
Jaws/teeth	Relatively large insicors and canines; gap between upper incisors and canines moderate sized molars	Small incisor-like canines: no gap between upper incisors and canines: larger molars	Very thick jaws; small incisors and canines; large molar-like premolars very large molars	very thick jaws; small incisors and canines large molar-like premolars; very large molars
Distribution	Eastern Africa	Eastern Africa	Eastern Africa	Southern Africa
Known date (millions of years ago)	3.77	3 - 2	1.8 - 1	2.3 - 1.8

General features of Australopithecus and Paranthropus

A. Skull and Brain : 1. Brain-size, ape-sized and ranged between 400 to 530. But if compared with relative body size it is more than chimpanzee and gorilla. It is smaller than human average but more than that of miocene apes hence signifies an increase in brain size.



The paranthropus (a) skull (b) restoration of individual
Paranthropus robustus Paranthropus boisei



2. Increase in brain involved expansion of cerebral cortex, especially parietal and association areas. In humans, these areas are related to language production suggesting that austrolopithecines had developed some form of symbolic communication system based on sound (the precursor of language). The increase in cerebellum relative to rest of brain as compared to apes allowed fine control of movements during locomotion and manipulation by hands.

3. Receding fore-head.

4. Sagittal crest-reduced in graciles but pronounced in robusts.

5. Supraorbital ridge reduced or absent in graciles but pronounced in robusts. Development of such crest and ridges indicate developed masticatory muscles.

6. Face concave resulting from flat nasal bones and prognathism.

7. Foramen magnum located downward as in man indicating erect posture of australopiths.

B. Dental Arcade : Graciles were omnivores and robusts were vegetarian. Many vegetations have silica hence molars of robusts show greater wearing pattern than gracile (Dietary hypothesis of Robinson).

The dental arcade is largely man-like with some pongid features suggesting adaptation to mainly vegetarian diet. It showed following characters-

1. Mandibles (lower jaw) are massive and chinless like pongids but parabolic and without simian shelf like humans.

2. Incisors are small and canines are only slightly projecting, showing they were largely vegetarian.

3. Premolars are large but bicuspid like modern man. Early gracile forms, however, had semisectoral first lower premolar like *Ramapithecus*.

4. Molars are also large but develop in series. In modern man, it also develops in a series $M_1 > 2 > 3$. Wearing pattern of the molar crowns is similar to modern man and is downward. Molars, however, show some pongid feature in the sense that it possesses Y-5 pattern of Dryopithecus.

5. Muscles for mastication such as masseter and temporalis well-developed.

C. Limb Bones And Locomotion : Australopithecus were, in all probability, bipedal which is supported by following evidences:

1. Later australopithecine fossils are mostly associated with dry-climate, like savanna. This habitat necessitates moving on ground because trees are sparse.

2. Presence of lumbar curve in the backbone.

3. Short and broad Ilium (of pelvis)

4. Torsion-angle of femur and presence of linea-aspera on it for attachment of muscle.

5. Straightening of Knees.

6. Weight bearing structure of ankle bones.

7. Well-developed arches in foot.

8. Fore-limbs without any signs of weight-bearing activity.

9. Discovery in 1978, of foot-prints providing further evidence.

However, the australopithecine bipedalism differ from human bipedalism because they had long ischium-bone (as opposed to short in humans) and no gluteus medius and gluteus minimus (which stabilizes pelvis during walking). Napier opines that this would have resulted in Jog-trot like bipedal locomotion in quick, short steps with bent knees and hip. The gait seems to be physiologically inefficient calling for disproportionately high out-put of energy, prompting individuals to take to high-energy food-stuff.

Evolutionary Discussions

Australopithecus possesses a small brain case, & massive projecting jaw and a few other minor simian features but it is characterized by overwhelming hominid features such as details of skull construction, dental-arcade, limb-bones for erect posture and bipedal locomotion and manipulation of tools. Simian features can be accounted for by way of common inheritance from a hominoid ancestor that also gave rise by divergent evolution to the modern anthropoid apes. On the other hand, hominid characters are characters of its independent acquisition demonstrating that australopithecines were representative of the hominid and not the pongid line of evolution.

There are two theories that explain evolution of australopiths:

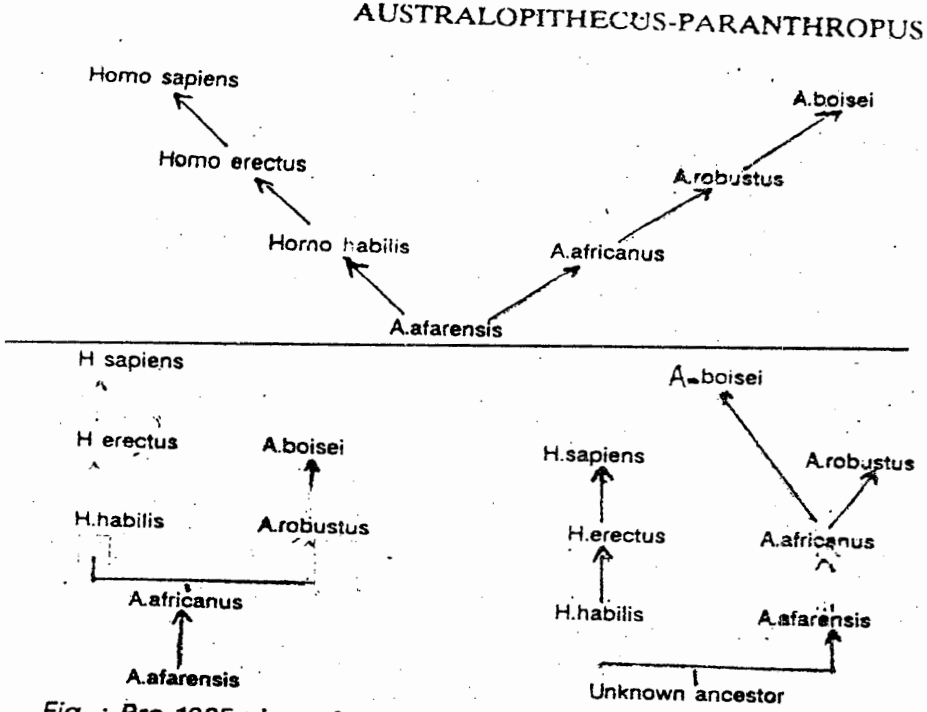


Fig. : Pre-1985 view of australopith evolution

i. Two Branch Theory : Two branch theory was proposed in 1979 by the discoverers of *A.afarensis*, Donald C.Johanson and his colleague Timothy White and the theory remained generally accepted till 1985. The theory stated that *A.afarensis* split into two branches- an australopith line represented by *A.africanus* to *A.robustus* to *A.boisei*; and a Homo-line represented by *Homo habilis* to *Homo erectus* to *H.Sapiens*. The branching was supposed to have occurred 3 mya into these two bipedal hominid lines. The australopith line showed a progressive increase in robustness : larger bodies, a shortening of the face but with increasingly massive jaws & facial structures, increasingly larger and flatter molars & premolars with a corresponding decrease in size of canines and incisors and some increase in brain size (from the 350-450cm^3 of *A.afarensis* to over 500 cm^3)

Thus according to this theory, *A.afarensis* 3 mya gave rise to *A.africanus* of the same height living upto 2 mya. It was thin (gracile). Next came *A.robustus* which showed marked increase in robustness in body, face, jaws & teeth and lived from 2.3 to 1.6

mya. Finally the last and the most robust form, *A.boisei*, lived in E.Africa from roughly 1.8 to 1 mya.

The second branch of the Johanson-White model, the *Homo* line, also shows a shortening of the face but there is marked decrease in the size of both the cheek teeth and the front teeth. There is massive increase of the size of brain also. This line begins with a transition from A.afarensis to *H.habilis*, the first hominid who made and used tools, and lived in Africa from roughly 2-1.5 mya. They had human like teeth and larger brain than australopiths (600-800cm^3). Earlier its height was supposed to be between *A.afarensis* and *H.erectus* but in 1986 its complete fossils were discovered and it became known that it was of the height of *A.afarensis* (3-3^1/$_2$ ft tall) and had ape-like long arms that dangled below the knees.

Variants of two branch theory, differing in details, have been described by various workers :

All the variants of the two-branch theories consider *A.afarensis* basal to all other forms of australopithecines. The position of *A.africanus* varies in the different schemes. Some consider it as ancestral to both australopithecine and Homo-line; There is one scheme which considers *afarensis-africanus-robustus-boisei* line evolving parallel to the *Homo* line.

However, there are many workers who suggest that hominid evolution may not have been so simple, isolated and clear-cut in its operation. Instead, there is possibility that three or more hominid lineages may have been evolving, interacting with each other.

ii. Three branch theory : The two branch theory of Johanson and White was generally accepted until the discovery in Northern Kenya in 1985 by Alan Walker of a complete new type of hominid skull called *A.aethiopicus* (earlier known by its museum number KNM-WT 17000). The skull is dated about 2.5 mya and is the most robust form ever found. It has massive teeth and Jaws of *A.boisei*, combined with a primitive ape-like brain. Thus *A.boisei* did not evolve in the last lag of australopith evolution, but as its age indicates, it originated directly from *A.afarensis*. Thus, majority of anthropologists believe that early hominids had three branches instead of two one to homoline, second to *boisei*-line and the third to *africanus-robustus* line.

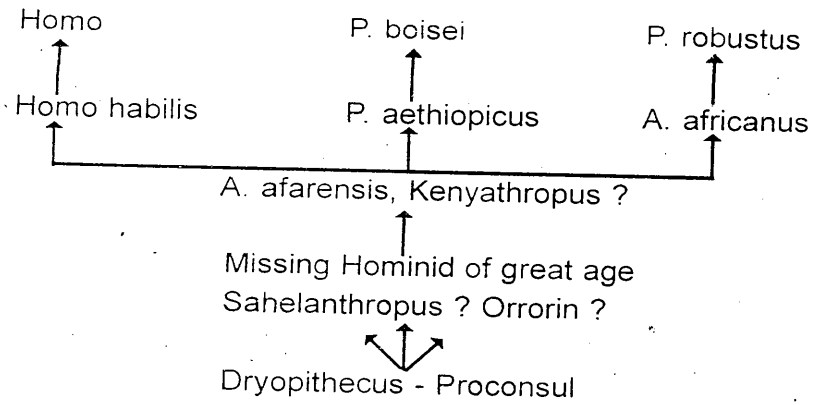


Fig. : Prevailing view of australopith evolution

Prevailing view in 2011-12

Prevailing view is not much different from one in the 1990s. Most workers agree that *A.afarensis* is ancestral to both robustus - *P.boisei* and *P.robustus* and that *P.aethiopicus* served as intermediate to *p.boisei* and *A.africanus* served as intermediate to *p.robustus*. Efforts however are on to search an acestral hominidae of great age that fills the gap between Dryopithecus - Proconsul of 12-15 mya of age and *Australopithecus* of 4 mya. Initially, *Australopithecus ramidus* and *A anamensis* were considered but later on it was found out that they represent pongid line of evolution and were thus renamed *Ardipithecus ramidus*. In the recent time, three hominids of great age are considered — ***(i) Sahelanthropus tchdensis :*** Which is 7 mya old. ***(ii) Orrorin tugensis :*** Which is 6 mya old. There is some evidence of bipedalism and smaller teeth. ***(iii) Kenyathropus platyops :*** Which is 3.5 mya old. It is believed that genus *Homo* split either from *A.afarensis* or *K.platyops*. This genus, therefore, represent a branch point for *Homo*. This species showed bipedalism and had smaller teeth. The species was discovered in Lake Turkana, Kenya in 1999 by Justus Erus.

HOMO HABILIS

Bernardwood (1994) has emphasized the difference between australopithecines and *H.habilis*. Foramen magnum in *H.habilis* is further forward than australopithecines. Teeth is narrower than those of australopithecines but not as small as in *H.erectus*.

Bernaardwood (1994) divides *Homo habilis* in two species :

a. H.rudolfensis : The specimens with broader faces, heavier jaws and larger grinding teeth.

b. H.habilis : with narrower faces, jaws and smaller grinding teeth.

First fossil of *H.habilis* was discovered in Olduvai Gorge (Tanzania) by Louis Leakey in 1960-61. The find consisted of only a few cranial materials and others. It was regarded as intermediate between autstrlopithecine and *H.sapiens* because fragments of skull bones measured a cranial capacity of 700 cc, well above the value of australopithecines. The cheek teeth, though longer, were narrow than australopithecines. Since there were only fragmentary materials, it became controversial whether the fossils represented any significant advance over other australopithecine materials which seemed to overlap the time of its existence i.e. between 2-1 mya. However, many similar fossils have been discovered since then from olduvai, omo, Koobifora and East Turkana. Age of such fossils have been estimated to be around 2-1.5 mya. Perhaps most famous of all these fossils is KNM-ER 1470 from Koobi fora, found in 1972. This skull has a large brain (volume about 750 ml) and was originally dated to more than 2.6 million years ago. However, this was subsequently revised to about 1.9 million years ago, a date that tallied with the Olduvai record of *H.habilis*. The braincase has a more human shape than that of the australopithecines, but the face is very long, broad and flat, with prominent australopithecine-like cheekbones. Although no teeth were preserved, the sockets and spaces for them were large than that of modern human. The fossils are characterized by following features:

1. There are several crania belonging to it and there are disagreement as to how many species are being sampled because they show variation of cranial capacity ranging from 650cc to 800cc. The cranial capacity, however, was greater than in australopithecines and approached *H.erectus*.(Pilbeam et.al.1992).

represent any camp sites but mere places where they often collected and performed various activities. Others believe that these were camp-sites where habilines lived for longer periods of time.

7. The remains however, do not indicate that how meat was obtained - by scavenging or by hunting. It also do not provide information about regularity of the meet needed. Pilbeam (1992) is of the opinion that some of the animals were hunted while others represent carcasses. Such aggregates appear to be result of activities of so short duration that scattered bones and stone fragments can be conjoined. Other aggregates are fairly heterogenous and perhaps involve activities spanning more than one, single life-time.

8. *Homo habilis* originated from some gracile australopithecines and represent, in a short span of time massive increase in the brain-size. The earliest australopithecines date about 4 mya and earliest *habilis* around 2 mya. While the former has an average brain size of 400 cm^3 where as latter has 700 cm^3 slightly less than double in just two million years.

Pilbeam (1992) opines that such a rapid increase in brain size resulted due to strong selection forces. Hunting must have involved some sort of group activity and vocalization, meaning enlargement of Broaca's area. Making of tools and its use must have had involved refinement of many sensory and motor areas of brain. If such activities are being controlled by cortical areas of brain, there would definitely be a strong selection for such features leading to rapid enlargement of brain.

9. The distribution and period of *H.habilis* and *Paranthropus boisei* overlap. Both are found in East Africa during 2 to 1 mya. But fossils of *P.boisei* far outnumber those of *habilis*. According to Pilbeam (1992). It may result due to better preservation of large sized boisei. However, there is still another possibility. Because *P.boisei* were herbivorous they may have represented larger biomass. *H.habilis*, because it was omnivore and more dependent on meat, may had lower biomass, with fewer individuals in the community.

10. Pilbeam(1992) on the basis of brain-size, has predicted the changed life-patterns of *habilis*. According to him, a larger brain would involve longer gestation, bigger new borns, greater longevity. This would have placed greater metabolic demands on the mothers both pregnant and lactating, because brain tissues are

brain size / body size

There has been quite some controversy with respect to body size versus cranial capacity. It was supposed earlier that it was larger than australopithecines in body-size hence slight increase in cranial capacity doesnot indicate in a meaningful way evolutionary advancement of the group. Later fossils, however, have shown that it was of the size of *A.afarensis* hence any increase in cranial capacity truly reflects evolutionary advancements.

2. The endocast studies show development of frontal lobe, the seat of higher mental abilities, not found in australopithecines but present in us. The brain case is rounded. The top of the skull was more rounded with lesser crests than that of australopithecines.

3. The teeth, in general, show human affinity, particularly premolars which have two ridges like humans. However, the size of teeth vary - they are bigger in bigger brained habilis.

4. Their mandible in less massive than that of australopithecine. Dental arcade was more parabolic.

5. Hind limb morphology clearly approached human's foot.

6. There is evidence that *H.habilis* was a tool maker and around 2 mya we find first archaeological traces of tools. Such tools are best sampled at olduvai Gorge and East Turkana, and also from South Africa.

The habiline "tool Kit" found at olduvai Gorge is usually referred to as the Oldowan industry. It includes three types of tools:

a. Cutting tools : A stone flake hold between the thumb and fingers makes good cutting tools.

b. Scraping tools : Such tools may have been used for scraping meat from bone or for scraping fat from skin.

c. Tools to make tools : It includes hammer stones which can be used in striking a flake off another stone to make a tool with a sharp edge. It is also called core.

Analysis of edge wear on the flakes show that these were used to cut a range of objects - meat, wood and plants. The hammer stones or cores were used for cracking bones, or hard nuts and seeds also. Many aggregates of such stone tools and bones have been found. There has been some lively debate over significance of such aggregations of tools and bones.

Pilbeam (1992) maintains that such aggregates do not

represent any camp sites but mere places where they often collected and performed various activities. Others believe that these were camp-sites where habilines lived for longer periods of time.

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energetically costlier.

11. The brain enlargement was perhaps cause and effect of dietary shifts in *habilis*. Enlarged neural tissues place greater nutritional demands on the individuals and assumption of meat probably satisfied such demands. To acquire meat eating involved learning of newer and newer skills which resulted in growth of neural tissue. The dietary shifts and enlarged nervous tissues were perhaps mutually stimulatory.

The dietary shifts in *habilis* is represented by nature of tools discovered in the consecutive beds of olduvai Gorge and Koobifora. The earlier flakes are naturally sharp edged flakes. Such tools would have been used to cut plant materials. Later on, there appears 'artificially sharp edged flakes". Such tools we4re perhaps used in cutting meat. Such shifts in diet may have been necessitated by some environmental change.

12. It has been stated earlier that *H.habilis* shows great variation of cranial capacity. Some fossils from Koobi fora (KNM ER 1813 and KNM ER 1805) are small brained, (500 cc) while some (KNM-ER 1470) large brained, but former with more rounded skull whereas the latter with a crest at mid-line of skull like australopithecines.

The meaning of this great variation in morphology is still unclear but it may be that *H.habilis* was not the only human-like inhabitant of eastern Africa between 1.6 and 2.4 million years ago (Stringer,1993).

Confirmation of this complexity has come from a recent discovery at Olduvai which the finders have nick named the Dik-dik Hill hominid (OH 62). Features of the fragmentary skull are said to be Homo-like, yet the skeletal bones of this small-bodied hominid closely resemble those of the australopithecine 'Lucy' (*Australopithecus afarensis*) from Hadar in Ethiopia. It is unclear whether this fossil shows that *Homo habilis* was very variable in morphology and body size or that there were two kinds of early Homo, one large and the other small. Bernardwood (1994) maintains there were two.

13. The traditional view is that oldowan culture represents the earliest stages of human culture that differentiates *Homo* from the apes. In recent times, there has been much debate over this traditional view. Tom Wynn and McGrew reported in Man, vol 24 (1990) that they could find nothing in the tools themselves, in the way they were made, or in the way they were used, that implied

that Oldowans were smarter than modern apes. Their contention was that the earliest tool makers were no more sophisticated culturally than chimpanzee.

McGrew has studied tool-using habits of chimpanzee which include making termite "fishing" sticks, stone and wooden hammers for cracking nuts, anvils and ant probes. The fact that apes can use tools was first shown by Richard Wright at Bristol Zoo. He taught an Orangutan to knock a flake off a cobble using a second cobble, and then use the flake to cut a string to gain access to food.

Like oldowan tool-maker, chimpanzee have been found to be selective in type of stone used for making tool and carry it to far off places. Toth, Savage-Rumbaugh and others have performed experiments with a pygmy chimpanzee (*bonobo*) called Kanzi at Language Research Centre in Atlanta, Georgia. They have reported in their book "The ape at the brink of the Human mind" that chimpanzees are capable of producing oldowan-like tools. In 1993, Kanzi was awarded with the CRAFT annual award for outstanding Research pertaining to Human technological origins.

A recent book entitled "Chimpanzee culture" edited by Wrangham McGrew, de waal and Heltne brings out different facets of chimpanzee culture.

14. Several workers propose that these are not true *Homo*. Their teeth are large relative to their body size and their skeleton suggest that they had limb proportions closer to the australopithecines than to true Homo. They even suggest placement of these fossils in a separate genus.

Two million year old "pebble tools" from Olduvai Gorge.

HOMO ERECTUS
AFRICAN JAVA AND PEKING MAN

Homo erectus, originally described as *pithecanthropus erectus*, the Java ape-man, ranged across Africa, into Eurasia, from over 1.6 to 0.12 mya. A complete discovery of *H-erectus* fossil from west of lake Turkana in Kenya in 1984 has completely revolutionised our understanding about this group of human ancestors. This hominid was characterized by a primitive face with considerably large brain than any of the australopithecines, approaching the lower limit of brain capacity in modern humans. This hominid made stone tools and knew use of fire and was probably the direct ancestor of *Homo sapiens* who replaced it. It is supposed to have evolved side by side *Paranthropus* up to 1 mya and became extinct by 0.12 mya in the wake of competition from more efficient *Homo* forms.

Dubois in 1891, collected a skull cap with a few associated teeth and bones, notably femur from solo region of Java. The owner of the bones was named *Pithecanthropus erectus* meaning erect ape-man. W.C.Pei and others (1921-29) discovered several fossil skull & teeth from Zhoukoudian near Beijing province of China. The fossils were studied in detail by D.Black who assigned the name *Sinanthropus pekinensis* to it.

These two earlier finds from Java and China were supplemented by two more finds from these two regions. Von Koenigswald discovered several fossils from Eastern Java during world war II. Similarly, Weidenreich (1943-46) also discovered several fossils from a cave near Peiping (China). Because of similarity of the Javan and the Chinese fossils, the different generic name were done away with and initially a new name was assigned to them - *Pithecanthropus pekinensis* - to accommodate one part of the name from both fossils. Since it had stood erect, and to remove any doubt about its limited regional existence, the name was changed to *Pithecanthropus erectus*.

Detailed studies of the fossils in 1960s revealed that these fossils bear remarkable similarities with human differing only in cranial capacities and a few other cranial elements. Mayr (1960) advocated that similarities of the fossils with humans is enough to bring it in the same genus : *Homo*. To bring home the point that fossils are sufficiently different from humans at the same time, a new name was created from it by Beuttner Janusch : *Homo erectus*. However, the term "Pithecanthropine" is sometimes used

to denote such forms.

Since 1984, Several *Homo erectus* fossils have been discovered from Africa (see distribution) and thus it has been possible to compare and contrast the different fossils in Africa, Java and China. Discovery of further materials from China and Java have pointed out obvious differences in the *erectus* populations developing in such isolated places and hence there has been growing movement to reflect such features of their evolutionary consequences. Since all the forms are basically same but sufficiently different from each other, the fossils of each region has been assigned a different sub-specific level.

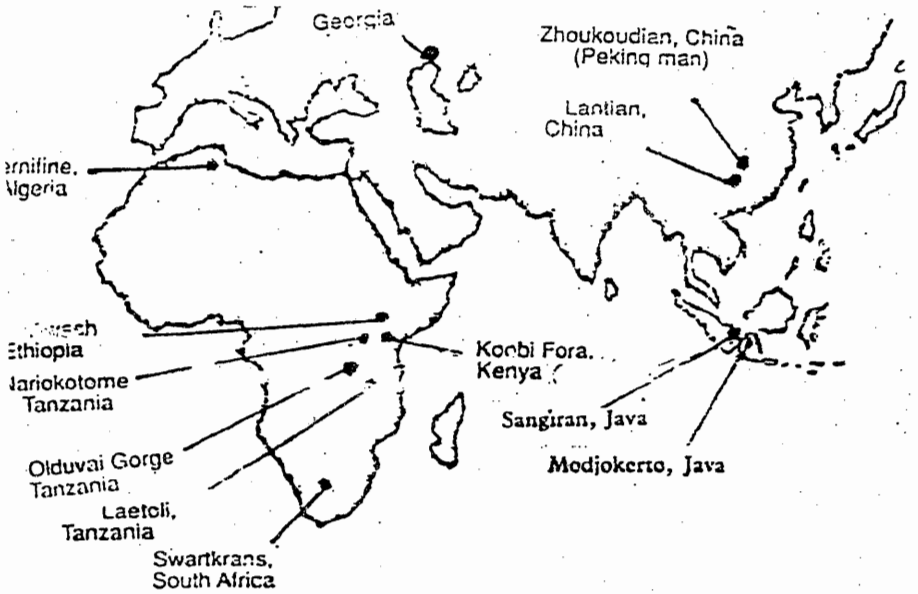
Most African fossils and some Javan fossils have lowest cranial capacity (775-940 cc). Most Chinese fossils have moderate cranial capacities (940-1225) whereas fossils from India, *Homo erectus narmadensis* has highest cranial capacity (1155-1421). Some believe narmada man to belong to later period

H.erectus : Glaciations And Evolution : Origin of *H.erectus* is often described with respect to different glaciations experienced in Northern Continents during pleistocene. Pleistocene started around 1.6 mya and the period from 1.6 mya to present is often divided into five glacial and four interglacial period. Pleistocene is divided into Upper pleistocene (1.6mya - 0.7mya), Middle pleistocene (0.7 mya - 0.125 mya), and Late pleistocene (0.125 mya - present). *H.erectus* fossils are found from Upper pleistocene to Lower Middle pleistocene.

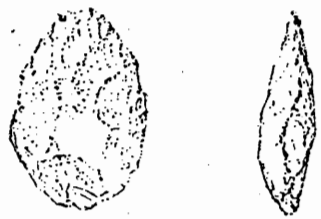
Human origin and evolution in pleistocene is intimately associated with glaciation and intervening interglacial periods. During glaciation there occurred large scale inundation of forest and other terrestrial ecosystems by ice and increased Sea-level and consequent contractions of human population in few pockets. During intervening post-glacial periods, there were re-spread of forest and other terrestrial eco-systems allowing for the mingling of human races. This periodic isolation and mixing of population facilitated rapid speciation of human being as well as other animals.

Africa : The earliest example of *H.erectus* are from northern Kenya on the east side (Koobi Fora) and west (Nariokotome) of Lake Turkana At the former site, two skulls (KNM-ER 3733 and 3883) and various fragments have been found while at the latter nearly complete skeleton of a boy (KNM-WT 15000) was discovered in 1984. These specimens are characterised by brain

sizes of about 800 to 900 ml and a long and low skull. the brow ridges were prominent, but the face is somewhat less projecting than in some *H.habilis* fossil and has a more pronounced nose. The Nariokotome boy's skeleton shows that, although not fully grown, he was already nearly 5ft 6in. tall and heavily built. He had the long-legged build expected of tropical humans, but had some unusual features in his spinal column.



Homo erectus Major sites of discovery



stone tools manufactured by Homo erectus

Other example of early *H.erectus* are known from Olduvai.

Tanjania where a skull dated about 1.2 million years ago was discovered in 1960. This robust skull (OH9) had a brain capacity of about 1050 ml, and an enormous brow ridge. Later finds from Olduvai (less than 1 million years old) is OH12 which either represent an extreme variant of the *erectus* type of an entirely separate species. Elsewhere in Africa, fossils attributed to *H.erectus* have been found in adjacent to Kenya Baringo) and in Algeria (Ternifine, now called Tighennif), Morocco (Sale and the Thomas quarries). Ethiopia (Melka Kunture and Bodo [illegible]) and South Africa (Swartkrans).

China : Chinese fossils have been discovered from Zhoukoudien near Beijing. It includes skull, mandibles and a few post cranial elements dated 0.5 to 0.25 mya. Younger and older Chinese specimens come from Hexian (0.26 mya), Gong Wangling (0.8 mya) and Yingkon (0.2 mya).

Java : Javan fossils are mostly from Sangiran dated 0.7 to 1.0 mya and somewhat younger fossils from Solo (0.12 mya) and Trinil.

In India, it has been discovered from Hathnora, near Hoshangabad in Narmada valley and it has been given the name *H.erectus narmadensis* by its discover, Sonakia (1985).

Presence of *H.erectus* in Europe is doubtful. However, a lower jaw from Dmanisi in the Republic of Georgia has been a probable contender. Excavations at Dmanisi (Georgia) led to the discovery in late 1991 of a well preserved early human mandible. The fossils dates between 1.8 to 1.6 mya. Gabunia and Vekua (Nature vol 373 No.6514, Feb. 1995) have identified the mandible as belonging to the species *H.erectus*. It is the earliest known representative of *H.erectus* in Western Eurasia. It shows a number of similarities to the African and Chinese representatives of this species, African affinities being more visible.

Bernardwood (1994) and some other palaeoanthropologists divide *erectus* fossils into 2 groups-

1. H.ergaster : the earlier kind which arose in Africa and then migrated out of Africa.

2. H.erectus : those descendants of *H.ergaster* who migrated into Asia.

He concludes that *H.ergaster* is our true ancestor. As to the evidence for this division, he mentions about the presence of sharp shelf at the back of the skull where neck muscles attach. This is

less pronounced in *H.ergaster* and earliest *H.sapiens* but well developed in *H.erectus*.

Java man	Peking man
1. 6.5 to 1.75 meters tall with a weight of about 70 kg.	1. Peking man was somewhat shorter and lighter.
2. Legs long and erect, but body slightly bent while moving.	2. Peking man stood more upright than Java man.
3. Slightly prognathous.	3. Prognathism was less marked.
4. Small skull with average length and breadth 18.5 and 13.0 cm, cranial index 70.0.	4. Larger skull with average length and breadth 19.4 and 14.0 cm cranial index 72.2.
5. Lower vault of skull (10.5 cm).	5. Higher vault 11.5 cm.
6. Cranial sutures close earlier.	6. Cranial sutures close comparatively later.
7. Occipital region is broad and rounded.	7. Occipital region is narrow and elongated.
8. Frontal sinus is large.	8. Frontal sinus is small.
9. Chin inconspicuous.	9. Chin was comparatively more developed.
10. Nose broader and flattened.	10. Nose was not as broad and flattened as in Java man.
11. Low and receding forehead.	11. Forehead receding as in Java man but with bump-like region.
12. Brow-ridges high like those of apes.	12. Brow-ridges were high as found in Java man but separated from forehead.
13. Skull bones less thick.	13. Skull bones comparatively more thick.
14. Cranial capacity 800-1000cc (average 900 cc) less than peking man.	14. The main difference between the two. Peking's man cranial capacity ranged from 850-1300cc (average 1075cc)

15. Lower jaw large and heavy.	15. Lower jaw was lighter than Java man.
16. Teeth large, with larger molars, diastemsa between upper canine and lateral incisors.	16. Teeth were shorter in comparison. No diastema between upper canine and lateral incisors.
17. The tools of Java men were less advanced.	17. Tools of peking man were more advanced.

Impelling Causes Of H.erectus Evolution : Majority put the time of origin of *H.erectus* at the beginning of pleistocene, some 2 mya. For about 1 million year *Homo* existed side by side with *Paranthropus*. Australopithecines radiated to give rise to *Homo erectus* on the grounds of feeding habit - australopithecines remained specialised small object feeder, while *Homo* gradually adapted for an omnivorous diet with emphasis on hunting and meat eating. Naturally the two groups are differentiated mainly on the basis of dentition, jaw and skull. *Australopithecines* premolars & molars are large with massive jaw, *flaring* of zygomatic arch, development of sagittal crest. In *Homo*, premolars & molars are small with small jaw, reduced Zygomatic arches, and no sagittal crest.

It is hypothesized that first glaciation resulted in large scale destruction of forests, leaving only a few pockets with nuts and seeds. *Australopithecines* remained confined to these vestiges of forests. But *Homo*, with slightly larger brains and enhanced mental capacities, could not remain satisfied and extended his area of interaction and reached out to far and wide and adopted omnivorous habits. His mental faculties helped him not only in devising ways and means to kill his prey but also to fight with the freezing temperatures by use of fire.

Characters Of H.erectus

Characters of *H.erectus* can easily be grouped under two categories - advanced and primitive. It was because of its advanced characters vis-a-vis *Australopithecus* that it was placed in genus *Homo*, and it was because of its primitive features that it was denied a rank equal to modern man and kept in a separate species- *H.erectus*.

A. Advanced Features Of H.erectus

1. Cranial capacity of *H.erectus* ranges from 775 to 1421, highest in Narmada man from India. This is very close to average cranial capacity of modern man i.e. 1450CC.

2. Height of cranium is more than width like us.

3. More anterior placement of foramen magnum*[1] indicating an erect posture.

4. Dental arcade more parabolic than *Australopithecus*, nearing that of *H.sapiens*.

5. Dental morphology similar to modern man, all being of same size and shape.

6. Taurodontism (extension of pulp-cavity) present.

7. Linea aspera*[2] well developed in femur

8. Zygomatic arch*[3] thin like *H.sapiens*.

9. Sagittal crest*[4] reduced or absent as in *H.sapiens*.

10. Parietal lobe of brain well developed signifying development of language as means of communication and thinking-process.

11. Sexual dimorphism was not much pronounced because selection favoured larger females for carrying and brith to infants with larger brains and bodies. There is no pelvic evidence but, as suggested by Pilbeam and others (1992) females delivered immative young ones like us.

Such advanced features of *H.erectus* were combined with a number of primitive facial features on which ground they were placed in a species different from *H.sapiens*.

B. Primitive Features Of H.erectus

1. Sloping forehead. It is vertical in us.

2. Prominent brow-ridge extending as a bar of bone across nasal root & both orbits. It is slight or nearly absent in us.

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*[1] *Opening of skull through which spinal cord passes out*

*[2] Attachment site for muscles in femur.

*[3] *Bones below eyes & above cheeks.*

*[4] *Top of skull.*

3. Angular occipital region*[1]. It is rounded in us.

4. Widest part of cranium at the level of ears. It is at higher level in us.

5. Flatter nasal area. It is somewhat elevated in us.

6. Bones of cranium thick, the thickness being in the range of 7-10mm. It is 5.2mm thick in us.

7. Mandible larger that make the face prognathous*[2]. It is smaller in us.

8. No chin, though there is thickening of mandible in side called mandibular torus.

9 Teeth larger, molars with divergent roots - not so in us.

10. First molar is largest in *H.erectus*. In *H.sapiens* third molar is largest.

11. Molars of *H.erectus* show fine wrinkles and a thickened ring of enamel (cingulum) around the base.

12. There are several mental foramina (passage for nerves & blood vessels) in the jaw of *H.erectus*. In modern humans, there is one mental foramina on each side of the jaw.

13. The greatest width of the lower jaw is at the level of 3rd molars. In modern humans, the greatest width is at the level of 2nd molar because tooth rows slightly turn inside in us.

14. X-ray studies show that outer wall of the femur is twice as thicker as that of *H.sapiens*.

15. Average Height 5 - $5\frac{1}{2}$, Average weight - 53 Kg.

Socio-cultural Behaviour

a. Tool-Culture : *H.erectus* was tool-maker and its stone-tool culture correspond to the lower palaeolithic chellean and Acheulean traditions. The sites bearing tool-fossils are spread from N.W.Europe to S.E.Asia. Tool-industry of *H.erectus* shows two distinct phases - in the initial phase only large choppers and hammers were used whereas in the later phase hand axes and flakes (blades, knives) predominated.

*[1] *Back of skull.*

*[2] *Protruding, projecting.*

The new tools, different from oldowan of *habilis* consist, of *bifaces*, which were symmetrical and large in size. Even quality and consistency of the tool differ. The earliest Acheulean of Africa, Europe and Asia contain fewer bifaces and little differ from earlier oldowan.

The second phase is marked by the presence of flakes which was prepared differently from those of oldowan flakes. The technique, known as "Levailois" flaking consisted of preparing the final shape of the flake before removing it from core than after. Judging by the abundance of tools and smaller teeth and faces of *erectus* people Pilbeam (1992) opines that these people prepared food more than the *habilis* people. The increasing use of fire is also indicative of this fact.

b. Use Of Fire : Evidences from China prove that *H.erectus* were the first user of fire. They may have used fire for warmth, protection from wild animals, and hunting. It also provided for centres of increased working capacity in terms of working hours. It may have also helped in splitting stones from bigger rocks. Presence of charred bones near the oldest known (0.75 mya) hearth from Escale (France) indicate that fire may have been used for cooking. Pilbeam & others (1992), on the basis of smaller teeth and faces conclude that they used to cook food and prepared it more than *habilis* did.

c. Hunting : Tools indicate their use in hunting, though there is no unequivocal support for planned and coordinated hunting of large and herd animals. There is also no evidence for transporting of large amounts of meat or its storage. The simple technology would have allowed such transportation over distances of only a few or tens of kilometres(Pilbeam, 1992).

d. Cannibalism : Some fractured hominid bones and skulls with enlarged foramen magnum from china indicate technical removal of human brains from skull. E. Adamson Hoebel has suggested that cannibalism was practised among *H.erectus* for ritualistic, gustatory and survival (in time of stress) purposes.

e. Language And Communication : Studies have proved that development of language is not a function of enlarged brain, or higher brain-body ratio hence can not be predicted on the basis of fossils. However, it is supposed that tool-making and its use, hunting and group-living acted as selective forces and those with developed memory-sites in occipital lobe, thinking-sites in frontal lobe and different motor-areas in cerebral cortex were favoured by

...e natural selection. This resulted in gradual development of brain. Pilbeam (1992) believes that capabilities for symbolic behaviour was developed.

f. Sexual Behaviour : Although females approach males in body-size, there is marked differences in the facial features of males and females. Males had bigger faces with more massive brow ridges like apes. Thus "Intra male competition" was more biologically regulated, in contrast to *H.sapiens*. The slow pace of technological advancement also indicate a non-human type of behaviour (Pilbeam 1992).

Theories Of Origin Of H.erectus

Homo Habilis Theory Of Origin : This theory is supported by Leakeys, Napier, Johanson, White, Pilbeam and others besides a host of other workers. They maintain that *Homo habilis* existed around 2 mya, just before advent of *H.erects*. Its cranial capacity was 750cc, matching with the cranial capacity of East African & Javan *Homo erectus* which are supposed to be most primitive *H.erectus*. Its certain cranial features was more advanced than *Australopithecus*, approaching *H.erectus*. These characters included more rounded skull with lesser crests, less massive mandible with dental arcade, more parabolic and smaller teeth than *Australopithecus*.

Conclusion

Judging by their duration of existence, 1.7 mya to 0.12 mya it can be safely concluded that *erectus* was a successfully adapted group. Prolonged anatomical and archaeological stability also point to the same fact. There is no doubt that in many of the physical features and behaviour the *erectus* group was advanced over those of apes. A brain capable of generating some kind of speech, use of symbols, controlled use of fire, omnivory with meat eating a significant component obtained by hunting and scavenging are features of advancement over previous hominids. However, in order to judge its proximity with Homo sapiens, one must recognize the percentage of biological and cultural component in the behaviour. Pilbeam (1992) finds the biological component of the behaviour being greater. It is a real problem to reconstruct such a system. Unless that is done, it is very difficult to have a true picture of *erectus* population structure and behaviour.

EARLY OR ARCHAIC SAPIENS

(Including Some Progressive Neandertals)

This group is very flexible and various finds included in this category show neandertal and erectus affinities in varying degrees so that some of the workers place them in different groups. Fossils such as Ehringsdorf skull, Fontechevade skull, Steinheim skull, Swanscombe skull etc have been frequently included in the progressive neandertals. Such fossils are included with the archaic sapiens here for clarity. The term archaic sapiens itself now has much broader meaning and include neandertals too. Thus there is no sharp dividing line between archaic sapiens and progressive neandertals whose time of existence sufficiently overlap. There should not be any effort to commit any fossil to any of the two groups. Classic neandertals are easily recognised from these two groups because of possession of neandertal complex of characters by them. Progressive neandertal and archaic sapiens lacked such complex of characters.

The period between 1.0 to 0.125 mya is marked by a group of hominid fossils which resembled *H.erectus* on one hand and *H.Sapiens* on the another. The group resembled to modern sapiens more than resembled the later neandertals with the modern sapiens. Placed between the two poles, *erectus* and *sapiens*, the group was more closer to *erectus* than to sapiens (Pilbeam and others, 1992). Thus the group foreshadowed much in advance the characters possessed by the modern sapiens and is collectively known as "early sapiens". They originated several thousand years before the last *erectus* became extinct. The proximity between *H.erectus* and early sapiens is so close that many consider early *sapiens* as geographical variant of erectus.

These fossils are marked by the characters that are intermediate between the *H.erectus* and *H.sapiens*. Cranial capacities average 1000cc. Skull is long and low, rounded or moderately angulated occipital, thin skull bones: large browridges; robust skeleton. Contrary to the later neandertals, the face is not projecting forward.

A few important representatives of this group is discussed here.

The Mauer Jaw : The famous fossil was discovered in a gravel pit at mauer, near Heidelberg, West Germany in 1908. Stringer(1981) assigns a date of 0.35 to 0.45 mya. The fossil has

1. It had all its teeth in place

2. The site of discovery abound in animal fossils such as those of elephant, horse, wild boar, bison, wild cat, red deer etc.

3. The jaw is very large and massive. The ascending rami is broad and square in shape (height 6.6 c.m., breadth 5.0 cm). In modern man, the breadth of lower jaw is 3.7 c.m.

4. The condyloid process is at a higher level than the coronoid which is blunt and rounded. In this character the jaw resembles that of gibbon.

5. The horizontal ramus is very high and massive. Its lower border is concave, a feature of baboons.

6. The angle of the jaw is truncated and the meeting place of two sides of mandible (mandibular symphysis) is very thick. These characters resemble with those of ape's Jaw.

7. The Jaw is parabolic like human's. In apes, it is U-shaped.

8. Dental series is continuous without diastema (=gap) as in modern man. In apes there is diastema in the jaw in which fits projected canine.

9. The teeth are of ordinary size like those of modern sapiens. Incisors are normal and canines do not project from the level of other teeth. Premolars and molars are typically like those of modern sapiens

10. The jaw displays more simian features whereas teeth display more human features.

Rhodesian Man (Broken Hill Man)

A few bones of skull and limb were discovered in 1921 at Broken Hill mine, Rhodesia by Twigelaar. Though its geological age is uncertain, it is believe that the form existed during last lag of *erectus* i.e. about 0.2 mya. The fossil bones show following features -

1. The skull reconstructed from available bones indicate to be narrow and long in the shape.

2. The cranial capacity has been variously measured to be from 1280-1400 cc.

3. Supraorbital ridges are prominent and fore-head is receding.

4. Maxillae and palate are massive.

5. Orbits are high and enlarged.

6. Teeth, in general, are like those of modern sapiens.

7. Face is muzzle like in appearance.

Rhodesian man exhibits *erectus*, *neandertal* and *sapiens* features at the same time hence its taxonomic status has been a matter of controversy. Though in some features it resembles neandertals, typical neandertal complex of characters is lacking hence its inclusion in neandertals is disputed. It shows definite advancement over *erectus* and possession of some *sapiens* feature. Hence, majority of workers consider the sample having closer affinities with modern man.

Saldanha Man (South Africa)

In 1953, Keith, Jolly and singer of the University of Capetown (South Africa) discovered fossils of skull cap and fragments of lower jaw in a village near Saldanha Bay, near Capetown. The fossil was designated Saldanha man. It shows following features

1. The skull is typically like Rhodesian man in being long and narrow with prominent supra orbital ridge.

2. The jaw is typically like the Mauer jaw in shape and dimension. It is, however, slightly less massive than the Mauer jaw. Because the fossil finds indicate some sapiens feature at the time of *erectus* it is included in the early sapiens.

Steinheim Skull

In 1933, a skull without lower jaw was discovered from Steinheinam - Murr in Germany. The fossil find is estimated to have existed 0.7 mya (middle pleistocene) and thus a contemporary of *H.erectus*. The skull shows following features :

1. The skull was long and narrow.
2. Cranial capacity is estimated to be over 1000 c.c.
3. Supraorbital torus pronounced
4. Occipital part a bit rounded.
5. Facial prognathism not marked.

Steinheim skull was more complete than swanscombe skull and is more similar to *erectus* skull in having lesser cranial capacities. However place of highest width of skull is higher than *H.erectus*. In some features they also approximate neandertals hence several workers place it along with progressive neandertals.

But as Pilbeam and others (1992) opine any such division of neandertal should be avoided and neandertals must be characterized by a complex of neandertal characters. Similar is the view of Erik Trinkaus (1984), the authority on neandertal study. Hence Steinheim skull is described here along with early *sapiens*.

Swanscombe Skull

Fragments of skull bones were discovered in 1935 and again in 1955 from Swanscombe, kent (England). On the basis of these bones (parietal and occipital) the entire skull has been reconstituted. The skull shows overall similarities with the Steinheim skull, differing only in minute details :

1. The cranial capacity is greater than that of steinheim, being in the range of 1300 cc whereas it is slightly more than 1000 cc for Steinheim skull.

2. The bones are unusually thick. Thus greater cranial capacity brings it closer to modern *sapiens* whereas greater thickness of bones brings it closer to erectus.

3. Its period is estimated to be middle pleistocene (0.7 mya)

The Fontechevade Skulls, Arago Skulls, Mauntmarin Jaw

From a stalagamite deposit in a cave at Fontechevade (France) two skulls were discovered in 1947 by Henri-Martin. One of the skull was fragmentary whereas another was nearly complete. The skulls show following features.

1. The cranial capacities of the brain is estimated to be around 1400 CC.

2. The skull resemble Swanscombe in the sense that they are unusually thick.

3. These skull differ from Steinheim and swanscombe in the sense that it lacked heavy eye-brow ridges.

4. other features of skull is similar to modern *sapiens*.

5. Its age is estimated to be lower pleistocene (around 0.12 mya).

6. The fossil foreshadows modern sapiens. Fossils similar to Fontechevade skulls have been found from France (Arago skulls and Mauntmarin Jaw). These have characters similar to Fontechevade skulls.

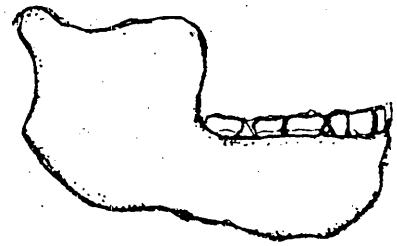
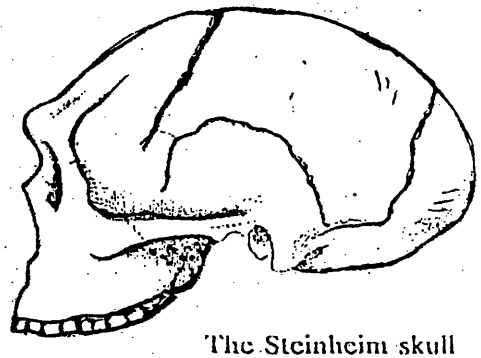


Fig. : Mauer jaw



The Steinheim skull

Vertesszollos Skull

Two sets of fossils have been discovered from vertesszollos (Hungary). Specimen I included a few broken and eroded teeth whereas specimen II included an occipital bone. The fossil has been designated *Homo erectus palaeohungaricus*. It shows features of erectus, neandertals and modern sapiens.

Evolutionary Significance Of Early Sapiens : These intermediate forms, which have been discovered from Asia, Africa and Europe, occur during 1:0 to 0.12 mya. During this time they must have co-existed side by side *H. erectus*. Such forms that belong to lower pleistocene are more similar to *H-erectus*; those belonging to middle and upper pleistocene are more similar to *H.sapiens*. The transition of characters from those like that of *H.erectus* to that of *H.sapiens* is not sudden and discrete; rather it represents small, quantitative shifts from *H.erectus* to *H.sapiens*. Intermediate forms of pleistocene thus represent gradual shift from *H.erectus* to *H.sapiens*.

The evolution of *H.sapiens* from *H.erectus* must have depended upon nature and frequency of genetic exchange among the different groups during the early pleistocene and concomitant isolation and separate selection pressure during the middle and late pleistocene. Evolution of *H.erectus* was accelerated by glaciation and interglaciation which forced periodic mixing & isolation. During interglaciations, there must have occurred frequent genetic exchanges. Glaciations would have definitely been marked as periods of isolation and selection.

NEANDERTAL MAN

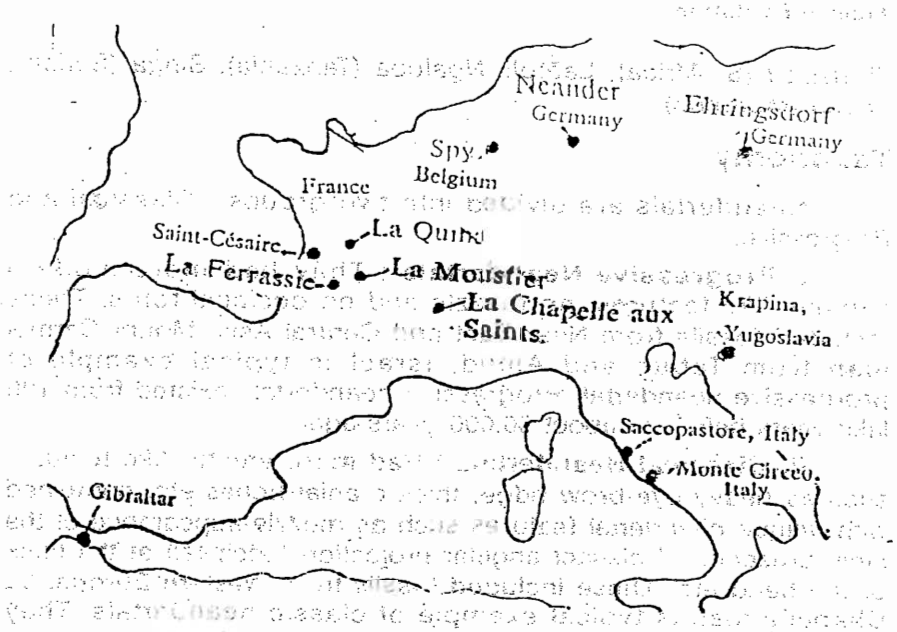
From 1,20,000 years ago to 30,000 years ago distinctive group of people, collectively called Neanderthals/Neandertals*[1] lived in Europe. More than 250 remains, in varying completeness, of such people have been found in Europe, Near East and Central Asia. They had cranial capacities approaching those of modern man, with certain features resembling *H.erectus* such as heavy eye-brow ridge and low-cranium. A few characters such as forward projection of the jaws etc. were complete new acquisition. On the basis of anatomical similarities with modern man, they are included in the same species, though in a separate sub-species i.e. *Homo sapiens neandertalensis*. There is now opinions to keep the group in a separate species, *H.neandertalensis* (stringer,1992). Their culture correspond to old stone age known as "Mousterian" which is characterized in the initial stages by hand axes, and flakes in the later stages. Socio-cultural development had reached a stage when people attached values to individual and society and showed belief in supernatural.

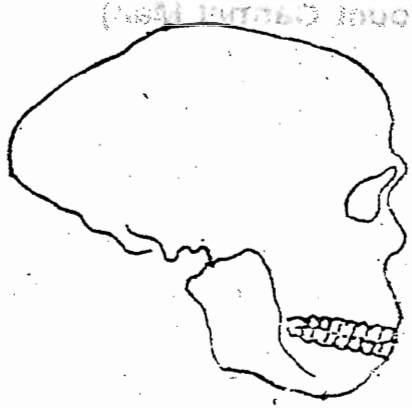
Distribution : Neandertal man was discovered in 1848 from Rock of Gibraltar but it went unnoticed. In 1856 Neandertal skeleton was again discovered from Neandertal valley in Dusseldorf, Germany. Since then more than 275 fossils have been found from Portugal in West to Russia in East. In its true sense, the term neandertal is restricted for the people of fourth glaciation living in Europe, Near East and Central Asia. There is no knowledge about the neandertals from East and South-east Asia and Africa.

i. In Europe : Fossil finds include from Gibraltar (1848 and 1926) Spy I and II from Belgium (1886) Krapina from Yugoslavia (1899-1905), Le Moustier from France (1908-09), La Chapelle aux Saint from France (1908), La Ferrassie from France (1909-1921) La Quina from France (1908-1921); Regourdou and Saint-cesaire from (France) etc.

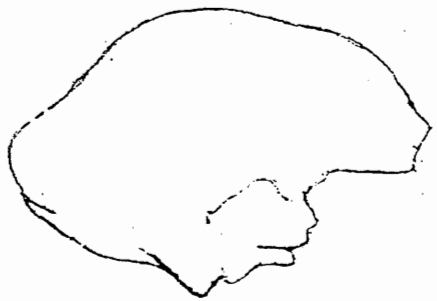
ii. In Near-East And Central Asia : Fossil finds include Galilee from Palestine (1925), Tabun and Amud and Kebara (Mount Carmel), From Palestine, now Israel (1931-32), Teschik-Tasch from Uzbekistan; Kiik-Koba from crimea, Russia; Shanidar from Iraq. Other groups of humans belonging to the same period were living in Africa and Central Asia. Their fossils have been found from

*[1] *Both are correct word Neandertal is according to new terminology.*





classic neandertal
La Chapelleaux Saints from france



Progressive Neandertal

Florisbad (S. Africa), Laetoli, Ngaloba (Tanzania), Singa (Sudan), Irhoud (Morocco).

Taxonomy

Neandertals are divided into two groups : Classical and Progressive.

i. Progressive Neandertals : They had more modern sapiens like features, no muzzle and no occipital torus. These included fossils from Near East and Central Asia. Mount Carmel man from Tabun and Amud, Israel is typical example of progressive neandertal. Progressive neandertals existed from 120 lakh years before to about 50,000 years ago.

ii. Classical Neandertals : Had more erectus-like features such as heavy eye-brow ridge, thick cranial bones etc. combined with unique neandertal features such as muzzle-appearance of the face, presence of distinct angular projection (occipital) at the back of the head etc. These included fossils from Western Europe. La Chapelle man is typical example of classic neandertals. They existed later than progressive neandertals. Their age is roughly 75,000 years to 30,000 years ago.

Progressive Neandertals (Mount Carmel Man)

In 1931-32 Skeletons belonging to progressive neandertals were recovered from two places in Mount carmel, Palestine. The first cave yielded skeleton of an adult female, consisting of a mandible with teeth and other bones while the second site yielded fragmentary remains of about ten individuals. The Mount carmel man is characterized by following features :

1. The cranial capacity, though large, was less than the classic neandertals. It was in the range of 1400 cc, closer to the average of modern man.

2. The skull was longer than the La chapelle and was less broad giving a higher caphalic index.

3. Skull was comparatively high vaulted.

4. Forehead was less receding and occipital region was slightly projecting.

5. The supraorbital torus, though slightly present, did not make a continuous, rounded ridge as in La chapelle man.

6. Orbits were comparatively more rounded.

7. Maxilla did not project in muzzle like fashion.

8. The nose was less broad with nostrils less widely separated.

9. Lower jaw, though slightly larger than modern man, had distinct chin.

10. Skull was less rough, suggesting lessr development of attachment surfaces in comparison to that of La chapelle.

Classical Neandertals (La Chapelle Aux Saints)

It was discovered in 1908 in a cave in Correnze, France. The finds included cranial and postcranial materials along with such tools as flints, scrapers, points and fossil remains of rhinoceros, reindeer, bison, hyena etc. The age of the fossil has been estimated to be upper pleistocene and the culture is mousterian. Best descriptions of La Chapelle man comes from Boule and H.V.Vallois (Fossil Man : 1957). Later studies have proved that La Chapelle man was not a true representative of neandertals because the Skeleton had belonged to a diseased person, suffering from arthritis. La chapelle man can be considered, thus, as a prototype of classic neandertals.

The main difference between classic neandertals and those of progressive types consisted of differences in skull. Both were similar, in post cranial features.

Characteristic Of Skull : The skull-characteristics of La chapelle man consisted of following.

1. The cranial capacity was in the range of 1600 cc.

2. The skull measured 208mm in length and 155mm. in breadth, giving a cephatic index of 74.5.

3. The skull was large, especially from lower end and behind. It is upper and anterior part of brain which is associated with higher mental abilities. Neandertal brain was thus enlarged at wrong places. It was low vaulted hance looked flattened (platycephalic).

4. Forehead was receding and occipital region protruding.

5. The supraorbital ridge was heavy, rounded and continuous torus as present in apes and erectus.

6. Orbits had greater transverse diameter than the vertical diameter.

7. Maxilla or upper jaw projected in a muzzle-like fashion.

Incisors worn out quickly and completely by the age of 40 years. This signifies that they were used in holding objects and cutting them. We still find many human populations who use frontal teeth in similar fashion. This was accompanied with reduction and recession of jaw-muscles which receded back. Use of canine and incisors as third hand and receding of the jaw-muscle produced the peculiar muzzle-like appearance of neandertal's face.

The muzzle-like face benefited in another way. It kept the nasal cavities far away from the brain so that inhaled air is warmed more. The nasal apertures were large and pyriform that provided more surface area for the warming up of the inhaled air.

8. The nose was broad with large, wide and pyriform nasal aperture.

9. Lower jaw was large and strong with very much reduced chin. Its ascending rami were large and broad.

10. The whole surface of skull was rough, indicating presence of muscular impressions.

Characteristics Of Postcranial Elements : The classical neandertals were slightly shorter than the progressive type but were heavier with well developed musculature and short, wide phalanges. The different elements of postcranium showed following features :

1. The vertebral column was short and stout in comparison to progressive neandertals.

2. Ribs were strong indicating large thorax.

3. Humerus was short, strong, with a large head like those in modern man. Structure of shoulder blade (scapula) and upper arm bone (humerus) indicate great development of a muscle, teros muscles, that pull the hands down. The teros muscle helped in throwing activities.

Same was the case with the muscles of the hand;. The fingers were large, robust, terminating in thick pads and large nails that increased the grasping strength. The two phalanges of the thumb were of the same length whereas our first phalanx is one-third of that length. This features endowed the hand with extraordinary force so as to grasp the object with the Centre of the thumb and not at the extremity as is in our case.

4. Radius had strong curvature.

5. Fingers were comparatively shorter.

6. Femur was strong with large head. Short and stout bones of skeleton with larger areas for powerful muscular attachment was characteristic of neandertal. Length of leg bones and vertebral column indicate that neandertals were shorter averaging 5.1" to 5.5", women being shorter than men. This small stature was due in part to the short legs, in which the shortness of the lower leg (shin) was particularly marked.

According to Trinkaus (1983), the shortness of the limbs were adaptation for protection against cold and conservation of body heat because shorter limbs limit the quantity of heat lost. This adaptation is astonishing since predecessors of neandertals were living in a more cold climates and did not show such curious adaptations. Pertes (1984) explains that neandertals lived in a dwelling that failed to protect them. It were nothing but shallow depressions in the earth surrounded by blocks of stones which must have cooled rapidly once the fire went out. Modern man took shelter in caves that protected them sufficiently from the cold.

Limbs were shorter but stouter. We have seen that hands and shoulders were specifically built to help "throwing activity". The bones and muscles of legs were built for rapid movement for brief periods. This exceptionally powerful hand and feet is clearly manifest in the tools in their possession. The main tools were chipped stone tools which did not require multiplication of force by lever mechanism. Their strong arm and hand compensated for this technical deficiency. With advent of modern man and development of lever mechanism the hand became suited for precision work.

7. As is mentioned before, the skeleton had belonged to a man suffering from arthritis of legs. The femur thus appears bowed forward and the knee-joint wrongly suggested that neandertals walked with knees bent.

They had upright erect posture. Early restorations seemed to indicate that these people did not have a fu ipright posture but later investigations have shown this interpretation to have been incorrect, having arisen from the fact that the first specimen restored was pathological, the skeleton of an individual suffering from severe arthritis.

8. According to Trinkaus (1984) the pubic bone of neandertal is wider than the first and present modern man. Pubic bone is present in the pelvic girdle (Hip bone) to which attaches bones of leg. The pelvic girdle of two sides unite in the middle forming a pelvic cavity. Babies, at the time of birth, has to pass through this

pelvic cavity. A small pelvic cavity would not allow large sized baby to pass through it.

If pubic bones are wider, pelvic cavity would become larger and hence would allow larger babies. Since neandertals had wider pubic bones it is believed that they had longer gestation-period of 11 or 12 months that resulted in the birth of comparatively mature babies. Evolution of modern man is characterized by diminution of pubic bone hence shortening of pelvic cavity and gestation period to nine months. The situation was advantageous to neandertals because they had no necessary social structure to keep immature new borns alive hence female neandertals delivered comparatively mature babies. It is only after development of complex culture of modern human beings that it has become possible for the females to deliver immature babies and save them. A shorter gestation period is definitely more advantageous than long gestation period on many counts. Stringer (1992), however, contradicts the explanation and holds that it was because of difference in the way Neandertals walked. He maintains that difference in pubes would not result in difference in birth canal.

9. The histological examinations of the bones of neandertals indicate a low life expectancy. The oldest of the neandertals are around 50 years of age, a majority being around 40.

Having gone through the different aspects of neandertal's physical and cultural traits, one is convinced that their traditional image of a brute creature with bent knees and shoulders is not justified. Having approximately the same height as modern man, he is built with heavier bones and powerful muscles. He presents a mixture of archaic and modern traits which makes him a very complex human group, similar and different from us at the same time.

Socio-Cultural Behaviour

The culture of Neandertals is designated as Mousterian culture of middle paleolithic which is continuous on one hand with the Acheulian of lower paleolithic of *H.erectus* and the upper paleolithic of early *H.species* on the other. Mousterian is named after a cave, Le Moustier in France. The culture is marked with butchering activities. Acheulian is named after St.Acheul, France. The culture is characterized by bifacial and flake tools.

The culture is characterized by following features :

i. Tool-making : Existence of diverse tools, predominated in

the earlier part by hand axes and flake tools such as "Point" in the later part. A "point" is made by hafting into a spear. Scrapers and blades were also found. Bone tools predominate at "Pin-Hole Cave", England which was used for ripping, hammerings, cutting, digging etc. Concave - bones were used as containers. Diversity of tools indicate existence of multiple culture and movement of population.

ii. Rock Shelters : Neandertals were hunting and gathering nomadics who wandered in the search of food, water and shelter but dwelled at the mouth of caves in times of bad weather. Molodara I (Russia) show mammoth bones nearby such a cave that had hearths. It is supposed that they may have constructed huts and wind breaks out of grass, leaves and sticks.

iii. Language : Language development in neandertal is doubtful. Poor development of pharynx show their inability to pronounce vowels.

iv. Clothing : Presence of bone-needles at certain sites indicate tailoring activity and it is belived that they may have used fur clothes.

v. Ritualistic Burials : At certain places ritualistic burials with animals are indicated such as Mt.Carmel (palestine), Teschik-Tass (Russia), Shanidar (Iraq) etc. where dead body is associated with goat or bear skull. Presence of family cemeteries are also indicated.

vi. Society And Religion : Group activities such as hunting, migration may have led to the formation of nomadic society with interpersonal relationship. This may have paved the way for leadership and political system. To keep society in harmony some sort of religion must have appeared. Ritualistic burials are testimony to this fact.

vii. Bear-cult : Large scale hunting of large bears, measuring 9' and use of its skull in ritualistic act probably comprised a test of manhood.

viii. Neandertal's Philosophy : Neandertals perhaps had awareness of dignity of individuals and interdependence of individual and society. La chapelle-aux-saints man had severe Arthritis and Shanider I had undergone surgical operation of right hand, But both survived to maturity. Shanidar IV was laid to rest with eight varieties of flowers. These instances indicate conversion of man as an animal species into man as human being.

Theories Of Origin Of Neandertals

A. Neandertal Phase Of Human Hypothesis : The theory favours a single line human evolution and maintains that early sapiens evolved in neandertals most of which became adapted to cold conditions. Other neandertals developed in isolated pockets into next higher form of man, cro-magnon. Due to some reasons those adapted to cold conditions became extinct later on and human evolution was led by cro-magnon. The theory thus considers neandertal as specialized stage in human evolutionary progressions.

B. Dual Phase Of Human Hypothesis : Put forward by G.Kennedy (1980) the theory holds that ever since the post erectus days there had existed dual lineage - one through Laetoli hominid, Fontechevade man embarked upon the path of human evolutioin, and the second through Steinheim, Swanscombe, Ehringsdorf, Krapina, La chapelle auxsaints etc ended with neandertals.

C. Varied Phase Of Human Hypothesis : According to this theory it is wrong to think of neandertal origin as a mono-line origin in which all the forms had received its genes from *H.erectus* and crossed through the neandertal stage, or as bi-split origin in which neandertal-origin and modern sapiens origin were separated in watertight compartments. It was rather like several smaller streams coming together and joining to form course of a river while others separating at certain places receiving water from whole channel and going away from it.

As Moody has stated, origin of neandertals, and therefore human evolution, cannot be depicted by one or two line of descendance from H-erectus; It is an interwoven and interlaced phenomenon with immense possiblity of hybridisation in which many ancestral line crossed and recrossed as new forms arose, differentiated, and passed on their genes to descendants in varying proportions. The theory supposes that no one hominid living at a certain time was the ancestor of all hominids living at later time, rather each later hominid received his collection of genes from varying predecessors some of whom contributed more than others. According to this theory *H.erectus* may have received some of its genes from australopithecines but not all its genes from it; Neandertals may have received some of its genes from *H.erectus* but not all its genes from it. Some of its ancestors may still be hidden in the bowel of the earth and thus still unknown to us.

How influencing this process of hybridisation can be on the

course of human evolution is amply clear by the Dorothy Garrod's data of fossils discovered by her from Mount carmel, Israel. In lower beds at Tabun, she discovered fossils resembling steinheim, an early sapiens. In still higher beds were fossils resembling modern sapiens more and a the same time with some neandertal features. At skhull, in still higher beds, are fossil that are very modern in some respects with slight neandertal features, not much enough to be called neandertal The specimens, in all probability, seem to be hybrids. Neandertal complex of traits is never at full bloom but presence of neandertal genes are indicated.

Mount carmel people, thus, during their course of evolution, seem to have exchanged - es with classic neandertals.

Causes Of Extinc.

The nenadertal complex of trait started developing since the beginning of fourth glaciation, 1,20,000 years ago, and completely disappeared 30,000 years ago. What purpose had the traits originated for and why did it vanish? The answers to these and similar questions are not clear-cut. Various theories have been proposed that explain neandertal's extinction.

1. Physical Extermination : The theory proposes that more evolved people from elsewhere hunted lesser evolved neandertals. However, there is no evidence of hunting of neandertals by more evolved people.

2. Competitive Exclusion : The theory proposes that change in ecological conditions made neandertals unfit to exist while another group thrived. However, no change of ecosystem is indicated around 40,000 to 30,000 years ago and similar food and game hunting continued as before.

3. Over Specialisation : Presence of robust features indicate that neandertals were specialized for cold climate and became extinct when conditions normalised. it has been, however, estimated that the coldest period of Pleistocene existed around 25,000 years ago. Had the theory been correct, neandertals would have existed at least for that period.

4. Total Assimilation : The theory considers that when more evolved people invaded neandertal's territory, they intebred with it and neandertal's genes were completely assimilated by this more evolved group.

MODERN HOMO SAPIENS

(CROMAGNON, GRIMALDI AND CHANCELADE MAN)

Palaeoanthropological findings indicate that humans similar to us were distributed in the Africa, Europe, South west Asia, south Asia, South east Asia, Australia and Americas. The earliest of these fossils to be discovered was from Cro-magnon (France) in 1868 hence men of this period are often designated by this name. The age of cromagnon is believed to be around 30-40 thousand years, though earliest of such fossils belong to Africa.

African finds, which mainly come from Border cave, Klasies river mouth, Omo-Kibish (Ethiopia), Singa (Sudan), Jebel Irhoud (Morocco) are the oldest and date around 0.1 mya. Those from South west Asia e.g. Qafzeh (Israel) and Skhul (Israel) are also similar in age to African fossils. Other fossils are comparatively of later origin. European fossils are from Grimaldi (Mediterranean coast) cro-magnon (France), chancelade (France) Gonbecapelle (France) Brux and Brno, predmosti (Czechoslovakia), Velika Pecina (Yugoslavia), Bacho Kiro (Bulgaria), Hahnofersand (W.Germany) etc. Asian fossils are from zhoukoudian (upper cave, China), Willandro lakes of Australia and Niah of Borneo. All the fossils, except those from Africa and Qafzeh and skhul are 30-40 thousand years old.

All fossils, though grouped together, are different to some extent. Those from cro-magnon are typical, belonging to Aurignacian culture of upper palaeolithic. Grimaldi man also belongs to same period but bear some Negroid characteristics, particularly in the projecting characteristics of the Jaw. It is believed that they represent incursion of a Negroid race from Africa into south Europe. Some fossils, e.g. chancelade man, belongs to Magdalenian culture which succeeded aurignacian and solutrean cultures in some parts of Europe. This period is characterized by extreme arctic severity and hence chancelade man bears close resemblances with modern Eskimos.

A. Cro-Magnon Man

1. Lartet in 1868 discovered five skeletons from a cave Cro-magnon in les Eyzies, France belonging to two adult men, one woman, an infant and an old man.

2. Its age has been estimated to be 30-40 thousand years (late pleistocene). Associated finds belong to aurignacian culture of

upper palaeolithic consisting of bone and stone tools, cave-paintings, sculptures, stone statues of female figures etc.

3. The animal bones belong to mammoths, cave bear, Woolly rhinoceros etc.

4. Individuals were tall around 180 cm with large and massive skulls with cranial capacity ranging form 1550 cc to 1650 cc. The skull was very long but short in breadth (dolicocephalic). Browridges were small and divided contrary to the large, undivided of earlier forms. The skull was characterized by presence of prominent parietal tuberosities laterally so that skull appeared pentagonal in outline.

5. There were disharmonious combinations of face and skull-skull was narrow and long but face broad, short and flat. Orbits were rectangular and nose long and narrow (leptorrhine). The skull had marked prognathism.

6. The lower Jaw possessed well marked chin. Both front and cheek teeth were smaller.

7. The postcranial elements included bones of fore limbs and hind-limbs. With regard to limb proportions, the leg is long compared to thigh and the fore-arm is long compared to arm. Longer legs, longer distal limb segments indicate efficient bipedal walking.

8. femur is developed with linea aspera which suggest a strong musculature. Individuals were thus tall with well developed musculature. Pelvis of females indicated birth of less mature babies and thus longer socialization.

9. According to some anthropologists cromagnon man didnot become extinct at the end of upper palaeolithic but continue to the present. People with such characteristics can be found in Dordogne, France (after Collignon) and canary islands (after Verneau).

10. Evolutionary possibilities of cromagnon is unclear. Fossils similar to it have been discovered form Border cave, River clasies, omo from Africa and Qafzeh and skhul from S.W. Asia dating 0.1 mya Whereas non of the European fossils are older than 40 thousand years. It is not known when and where transformations to modern sapiens occurred. We donot know even interaction between archaic and modern sapiens. According to Pilbeam (1992) it cannot be that archaic sapiens were transformed into modern sapiens everywhere or this transformation occurred in a small,

isolated pocket. Modern sapiens are homogenous species. DNA and mitochondrial DNA studies indicate that early modern sapiens developed in Africa and replaced archaic populations in the different continents. Cro-magnon man may have had some inter relationship with these African ancestors with which it shared genes in the formation of modern humans.

11. Culturally, these people were much advanced than the earlier forms. Their tool kit included more new devices: the bow and arrow, spear thrower, complex bone-tools, methods of food storage, improved hearths, clothing. Larger dwellings. Faunal remains indicate a planned hunting.

Burial was much elaborate with cromagnon people. Graves are often associated with goods that indicate changes in the belief system and existence of social class. There are found evidences of camp-sites with dense populations of hunter-gatherers.

Cave-paintings are elaborate and, though their meaning can never be fully deciphered, they encode information about hunting, critical life transition such as puberty and other belief-systems. They probably represent symbolically coded information which must be transmitted between generations to ensure adaptive behaviour (Pilbeam, 1992).

B. Grimaldi man

1. Skeletons of a woman aged 30 and a boy aged 15 were discovered form a cave called Grotte des Enfants in the village Grimaldi on the Mediterranean coastal region. The manner of placements of the skeleton indicate burial.

2. Along with the skeletons have been found remains of aurignacian culture, similar to those of cromagnon and included such tools as flints, Knives, scrapers, saws etc.

3. The skull was more long and narrow compared to cromagnon skull and hence these skulls were classified as hyper dolicocephalic. But the cranial capacity was lower than that of cromagnon man (1250-1450 cc).

The skull contrary to the pentagonal symmetry of cormagnon, had elliptical contours because parietal tuberosities found in cromagnon was absent in Grimaldi man.

4. Face, like cromagnon, was short but below cheek bones it was more narrow hence face presented a triangular outline. The face resembled Negroid in features of feebly developed supra

orbital ridges and bulged forehead. The orbits, like cromagnon man, was rectangular i.e., low in height incomparison to its breadth. The lower border of the nasal aperture, similar to the Negroids, were not sharp. The alveolar border was U-shaped and had marked prognathism. Face, thus, had many similarities with Negroids.

5. Lower jaw, too, had many similarities with those of Negroids. It was strong, broad with thick body but low ramii. The chin was poorly developed and alveolar margin projected forward.

6. The teeth were, in general, larger and molars were like those of australoids in having 4 cusps in upper and 5 cusps in lower series. It was thus sufficiently different from Europeans in which 3 cusps in upper and 4 cusps in lower molars are found.

7. In postcranial skeleton, the hind limbs were very long compared with fore-limbs indicating less-energetic bipedalism. The fore-arm was longer than arm, and leg was longer than thigh. Such proportions resemble Negroids and they are often compared with Bushmen and Hottentots of South Africa.

8. Both cromagnon and Grimaldi belong to the late pleistocene and represent early populations of Europe. Judging from the similar post-cranial elements, both seem to equally capable of efficient non-energetic bipedalism and efficient hand-manipulations. But from the point of view of cranial elements, the two appear to be different racial groups though both show admixture of Negroid characters. Such Negroid characteristics are particularly well-developed in the Grimaldi man, hence it is supposed to represent a late incursion of African race into European territory. Cromagnon man, on the other hand had, diluted Negroid characteristics hence supposed to have made incursion into European territory much in advance and to have undergone sufficient hybridization with the local population.

C. Chancelade Man

1. Skeleton of a man with its hand folded on the chest and its knees touching its jaw was discovered from a cave near chancelade, France in 1888

2. As stated earlier, the fossils belong to magdalenian culture, which succeeded aurignacian and solutrean cultures in some parts of Europe. As stated earlier, chancelade man resembled in many features to modern day Eskimos.

3. The skull was long and narrow (dolicocephalic) with high cranial capacity (1500-1700 cc). The parietal tuberosites were also developed. In such features the skull of chancelade man resembled cromagnon man. However, sagittal crest in chancelade man was more developed than it was in the cromagnon man. Dolicocephalic head with sagittal crest is feature of Eskimos.

4. Facial skeleton of chancelade man differ from those of cromagnon. Face was long and broad and thus was inharmony with skull. The orbits were quadrilateral and cheek-bones were prominent. Such features resemble those of modern Eskimos.

5. Lower Jaw had unique proportions - the ramii were very broad but the body was very narrow. Prominent chin was also indicated. The masticatory apparatus was thus powerful and similar to those of Eskimos.

6. Most of the differences between chancelade man on the one hand and Grimaldi and Cromagnon on the other consisted in the postcranial elements. The limb bones of chancelade man was shorter with upper limb being longer than the lower limbs. In such features it resembled modern Eskimos.

7. It is hypothesized that chancelade man were ancestors of modern day Eskimos which are distributed in North America. It is believed that with the retreat of glaciation the ancestors of Eskimos moved from Europe to North America where they evolved in Eskimos. Some anthropologists, however, differ and consider different origin of Eskimos.

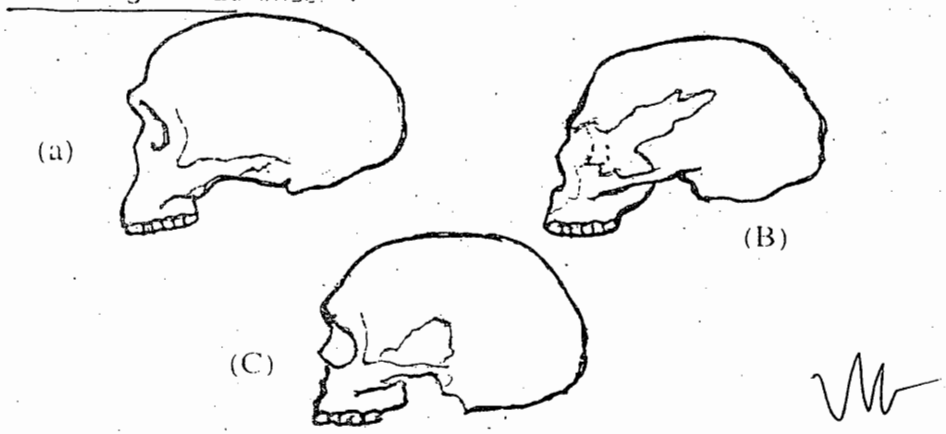


Fig. : Early modern Homo sapiens crania (a) Jabel Irhound, Morocco, (b) Skhul, Israel (c) Qafzeh, Isra...

RECENT ADVANCES IN HOMINID EVOLUTION AND DISTRIBUTION

In the last 10 to 15 years the most controversial issue regarding human evolution has been as to which of the fossils should get honour of being the oldest hominid. Traditionally this hor our was conferred upon *Ramapithecus* However, discovery of more complete fossil of this taxon has led to its recognition not as a hominid ancestor but as a hominoid, thus leaving the place of oldest hominid ancestor open and wide.

Downfall Of Ramapithecus : Most of the interpretations about *Ramapithecus* was based on dental findings by Lewis (1930) in Shivaliks (India). and Lewis (1955) in Kenya. On such meagre fossils, the dental arch and skull and post cranial structure was reconstructed. It showed presence of a rounded jaw, a man-like dentition, arched palate and a more upright face. Such findings led to the belief that *Ramapithecus* was the earliest representative of hominidae - and a direct ancestor of australopithecines. Its age was great - 12-15 mya. It was supposed that usual course of human evolution is *Dryopithecus* - *Ramapithecus* - *Australopithecus* - *Homo erectus* - man.

Jolts to this kind of belief came during 1970s due to some biochemical studies and fossil finds. From China, many skull belonging to *Ramapithecus* had been found during 1970 and it was possible to study the characters, as it were present, in greater details. The earlier conclusions about parabolic nature of the jaw became doubtful.

Doubts about *Ramapithecus* had stated gathering from another angle too. The downfall of *Ramapithecus* from the status of hominid ancestor to a hominoid ape ancestor may be said to have accelerated with biochemical analyses by Wilson and Sarich in 1970 of different proteins of primates By such studies, they have proved that orang-utan is distantly related to chimpanzee - gorilla and human trio. They had constructed a molecular clock by calculating percentage difference in the proteins of these primates, evaluated against the back drop of time-scale of primates evolution. They had calculated ape - human separation to be around 4-5 million years ago. *Ramapithecus* was of great age, 12-15 mya and it did not fit as ancestor of hominids. Next blow to the status of *Ramapithecus* as hominid fossils came around this time from the discovery of *Sivapithecus* from Pakistan India and Turkey. *Sivapithecus* was unmistakably similar to *Dryopithecus* on

one hand and *Ramapithecus* on the other. Moreover, among the living apes, *Sivapithecus* had clear affinities with the orangutans. It seemed that *Ramapithecus* is similar to, and no different from, *sivapithecus*. Assuming *Ramapithecus* to be equivalent to *Sivapithecus*, its great age (12-15 mya) was easily explained.

it was, however, not an easy task to dethrone the *Ramapithecus* from the status it had gained from earlier studies. In addition, Simons was the ardent saviour of *Ramapithecus* and he was not prepared to buzz even slightly from his earlier observations that declared *Ramapithecus* a hominid fossil. Initially, David Pilbeam was also hesitant, but growing evidence on biochemical and palaeontological fronts led him to withdraw himself from his earlier observation. Simons commented that David Pilbeam might think that he hard "burnt his fingers" but he did not find a reason to withdraw his conclusions.

In case of *Ramapithecus*, there were two potential problems - firstly, the structures were so close that it was easy to be confused, and secondly, there was a problem of preconception or set in thinking. As Pilbeam (1982) himself confessed "I know, *Ramapithecus* being a hominid, would have a short face and a rounded jaw - so that was what I saw". Pilbeam and others were not uniquely guilty of this error. It often occurs when it comes to analyse fragmentary fossils. Pilbeam (1982) accepted later on that *Ramapithecus* had no parabolic dental arch.

Another misinterpretation for the evolutionary potentiality of the *Ramapithecus* sprang from presence of thick enamel on its cheek teeth, a feature it shares with *Australopithecus*. At one point in the *Ramapithecus* affair, this shared thick enamel was regarded as the main anatomical argument for making a direct ancestral link between *Ramapithecus* as the accepted hominid ancestor of *Australopithecus*. This supposedly unique link meant - or was interpreted to mean - that *Ramapithecus* must, therefore, be a hominid too. In fact, thick cheek-tooth enamel turned out to be something that many of the Miocene apes had and not a specialization uniquely shared by hominids.

By 1982, most of the palaeoanthropologists had changed their opinions and accepted *Ramapithecus - Sivapithecus* link.

Australopithecus adiba - a "game changer"

Scientists have long held that genus Homo evolved from *A-afarensis* which is more than 3 million years old. Another fossil of *Australopithecus* has been discovered from Malapa, Johannesburg, South Africa in 2008 which has been named *Australopithecus Adiba* Lee R Berger of the University of Witwatersrand (S.A.) and Richard Potts of Smithsonian Institute in recent articles (2011) have declared the fossil to be unique- it combines the features of *Australopithecus* and *Homo*; its age is around 2 million years ago, a time when *Homo* arose. It has been claimed that this fossil contains a stop action snap-shot of human evolution, representing a vital moment of transition from *Australopithecus* to *Homo*. *A.adiba*, thus, is poised to be immediate ancestor of *Homo*, representing a transitional connecting – link between *Australopithecus* and *Homo*.

Researchers have revealed new details about the brain, pelvis, hands and feet, Jaw and teeth of *A.adiba*.

1. Brain, though smaller in size like that of *Australopithecus*, is enlarged just behind the eyes, an area where frontal lobe of brain is situated. Frontal lobe is predominantly an association area which is involved in cognitive behaviour, a higher mental ability
2. Pelvis of *A.adiba* is more similar to humans than other *Australopithecus*. It is supposed to have resulted in more efficient and energy-saving walk in comparison to other *Australopithecus*.
3. Hand contains longer thumb and shorter fingers which could have helped precision – grip, an ability which is required for tool – making.
4. Facial features suggests that it had a longer nose than other *Australopithecus* for better respiration
5. All teeth except incisors have been found. On the basis of facial features the incisors were reconstructed. All teeth are surprisingly small- a feature of *Homo*.

It is supposed that *A. adiba* may become an immediate ancestor to *Homo*, an ancestral from between *A. afarensis* and *Homo* displacing *A.afarensis* from the place of immediate australopithecine ancestor of *Homo*. If this happens, it will prove to be a "game-changer" in our understanding of human evolution

Last decade is characterized by generation of diverse genetic data from both extinct and extant individuals based on mt MRCA and y-MRCA the details of which could be found elswhere. Together with fossil data it has resolved some mysteries of human evolution.

New Fossil Finds

(A) Hominids of great age : So far fossil data is concerned we have read about *Ramapithecus* and ultimate fate meted out to this taxon. Initially it was considered hominid of great age. Last decade is also characterized by discovery of fossils which have been classified as hominids of great age. This includes- ***(i) Sahelanthropus tchadensis :*** It is a fossil hominid that lived approximately 7 million years ago. ***(ii) Orrorin tugensis :*** It is considered second oldest known hominid ancestor. The fossils were discovered in Tugen hills of Kenya and dated around 6 mya. Fossil find indicate bipedalism around the time of the split between humans and Chimpanzee. ***(iii) Kenyathropus platyops :*** This species is supposed to be ancestral to Homo. It is a 3.5 to 3.2 mya old extinct hominin species discovered in Lake Turkana, Kenya in 1999 by Justus Erus. The fossil find includes a broad, flat face with a toe bone that suggests it probably walked upright Teeth are smaller. It is believed that genus *Homo* split either from A afarensis or Kenyanthropus *platyops*. Thus this genus contains the branch point of genus *Homo* from earlier hominin species. ***(iv) Homo antecessor :*** It is an extinct hominin and a potential distinct species dating from 1.2-0.8 mya discovered by Carbonell, Arsuaga and de Castro. *H antecessor* is one of the earliest known hominins in Europe. It is supposed that controlled used of fire was not characteristic of *Homo erectus* but only of a later species of *Homo* such as *Homo antecessor*.

(B) New finds of Australopithecines : (1) *Australopithecus garhi* : It is a gracile australopithecine species whose fossils were discovered in 1996 by Berhane Asfaw and Tim White, an American paleontologist. It was dated 2.6 mya, older than *H. habilis*. It is associated with stone tool implem... which is 1.0 million years older than stone tool implements of *H*... Previous assumption that oldowan culture of *H. habilis* wa... culture of human ancestors is now doubtful. **(2) *A...bahrelghazali :*** The fossil was discovered by Michel... thropologist and professor at the college de Fra... Africa. The finds included skull and jaw re... Ghazal valley, Korotaro, in Chad. The fi... 2001 and the specimen was given th... of his close friend Abel Brillanceau w... The fossil has been dated 3.6 mya ...

...rs ...w up ...Man : ...he fossil ...The fossil ...erthals. ***(ii)*** ...derthals and ...Portugal). It is ...odern humans

Qu... ago. Africa modern Lake Mun... Lake Mung...

Complete Neanderthal genome unraveled

Of all the human ancestor's fossil DNA, Neanderthal genome, both mitochondrial and nuclear, abound probably because of comparatively younger age of the fossils and presence of better fossilizing conditions.

A project to reconstruct the whole Neanderthal genome was started in 2005 at Max Planck Institute for evolutionary Anthropology, Leipzig, Germany. As the project was a huge one Max Planck collaborated with 454 Life-Sciences (a Roche company) in 2006. In 2008, Richard E Green et.al. at Max Planck institute published the full sequence of Neanderthal mitochondrial DNA. Writing in Nature afterwards, James Morgan asserted that mitochondrial DNA of Neanderthal indicates that it lived in small and isolated group and probably did not interbreed with human populations. Based on mt DNA studies the divergence time between Neanderthal and modern humans was calculated to be 5,00,000 years ago. Awante Paabo, Director, Max Planck Institute has tested more than 70 Neanderthal specimens and found enough DNA to sample from a 38,000 years old bone-fragment of a femur found at Vindija Cave, Croatia. He asserts that 99.5% of their nuclear DNA is common to humans. In 2009, the Max Planck Institute announced that the 'first draft' of a complete Neanderthal genome is completed. Comparing and contrasting Neanderthal genome with that of modern humans have started and we are shortly to receive some startling revealation about Neanderthal- modern humans connections.

In addition to Max Planck, Neanderthal genomes are being studied by various other groups, details of which can be found elsewhere (see chapter multiregional continuity model). Edward Rubin ,director, Lawrence Berkely National Laboratory, California has also sequenced a fraction (0-00002) of Neanderthal nuclear DNA derived from Vindija femur bone . He asserts that it is 99.5 to 99.9% identical to modern humans. On the basis of nuclear DNA sequencing, he calculates the time of divergence to be 3,53,000 years ago and a complete separation about 88,000 years ago. Both Paabo and Rubin assert that despite sharing a common genome the two species. *H. Neanderthal* and *H.sapiens* did not interbreed.

That there is no admixture of Neanderthal genome and human genome is also supported by work of Noonan. The variant of microcephalin gene , causing primary microcephaly (small headedness), which is suggested to be of Neanderthal origin, was not found in Neanderthal genome. Nor was the MAPT variant present in Neanderthal genome. This is very old variant found primarily in Europeans.

However , evidences opposite to it also exists and some genes are shown to be commonly shared by Nendertthal and humans. A recent extraction of the Neanderthal DNA shows that it has the same version of the FOXP2 gene. FOXP2 encodes a protein, a transcriptional factor, which plays a role in human language . FOX P2 proteins of human and chimpanzee has also been compared and it was found that it differs only by two amino acids (Nature 2009)

find consists of a mandibular fragment, a lower second incisor, both lower canines, all four lower premolars, affixed in dental alveoli. It is symbolized KT-12/H1. In features it is similar to A.*afarensis* which is believed to be common ancestor of both *Australopithecus* and *Homo*. The claim is difficult to substantiate as the KT-12/H1 specimen was locked away from anthropological community till 2001, contrary to the international code of Zoological nomenclature, 1999. Also, it is the only Australopithecine find from central Africa. If found true, it will represent third window of early hominid evolution, apart from East and South Africa. **(3) *Ardipithecus ramidus*** : (Previously named *Australopithecus ramidus)* In 1992 and 1993 a team led by Tim White found in total 17 specimens of hominid fossils at Aramis, Ethiopia. More fragments were discovered in 1994, amounting to 45% of total skeleton. The fossils were originally described as an Australopithecine, but White and his colleague later published paper, renaming the *Australopithecus ramidus* as *Ardipithecus ramidus*. Between 1999 and 2003, a multidisciplinary team led by Sieshi Semaw discovered bones and teeth of nine *ramidus* individuals. Two species of *Ardipithecus* is presently recognized. *Ardipithecus* ramidus which lived about 4.4 mya during early Pliocence and *A. Kadabba* dated to approximately 5.6 mya. *Ardipithecus* represents pongid line of evolution.

(C) "Peking Man" more ancient : Though there has not been any new finds of *Homo erectus* in the last decade, there has been some studies on the dating of the fossils found earlier. Guanjun Shen et.al. have reported in nature (march 12, 2009) that Peking man, *Homo erectus*, which was thought to be 5,50,000 years old is now estimated to be 7,50,000 year old, about 2,00,000 years older than previously thought. Shen and his colleagues employed a new dating method based on the radioactive decay of ^{26}Al and ^{10}Be (aluminium and beryllium). Zhoukoudian caves, near Beijing, have yielded richest fossil remains of *Homo erectus*- remains of nearly 40 individuals, including six fairly complete hominin cranium and bones.

(D) Earliest modern humans : *(i) Homo sapiens idaltu :* It is an extinct subspecies of *Homo sapiens* that lived about 1,60,000 years ago in Ethiopia. "Idaltu" in Saho- A far means elder or first born and represents the oldest known anatomically modern humans and classified as extinct. ***(ii) Quafzeh-Skhul man :*** From Israel have been dated around 100000 years ago. These humans seem to have either gone extinct or retreated back to Africa 70,000 to 80,000 years ago. ***(iii) Mungo Man :*** The oldest fossil of modern humans found distal from Africa that are well dated is one from Lake Mungo, Australia. It consists of two fossils : Lake Mungo 1 (LM-1) and Lake Mungo 3 (LM-3). It was discovered in 1996 and has been dated 42,000

years ago. ***(iv) Tianyuan Man :*** The fossil has been found from Tianyuan Cave near Beijing, China. The find includes 34 bone fragments of a single individual and has been dated around 42,000 to 39,000 years ago.

(E) New finds of cromagnon man : Several fossils of early European Modern Humans (EEMH) have been discovered in last decade. These include — (i) Several fossils from Mladec (Czech republic) dated 31,000 yrs. ago. (ii) Some fossil bones, tibia & fibula, from kootenai (Russia) dated 32,000 yrs. ago. (iii) cranial and post cranial elements from Pestera Muierilor dated 30,000 yrs. ago. (iv) Kant's cavern (England) fossil is dated 30,000 yrs. ago. (v) Pelosi 1 and Pelosi 2 are 23,000 & 24, 000 yrs. old fossils of Cro-magnon whose mt DNA was sequenced. It was found that haplogroup type N_1 is predominant which is a feature of Europe and central Asia. (vi) Hofmeyr skull which was discovered by Grine (1952) from South Africa has recently been analysed by Katerina using latest mapping and measurement technique. It belongs to Cro-magnon dating 36,000 ± 3,000. It is oldest modern human from sub Sahara and supports **"Recent Out of Africa"** model.

(F) Recent hominids : *(i) Homo floresiensis* (The Hobbit Man) : Extending east of Java island of Indonesia is the Sunda island of Flores. Fossils of human ancestor has been found which has been named *Homo floresiensis*. The fossil is remarkable for its small body and brain and survived until relatively recent times, 14,000 years ago. It is supposed that *Homo erectus* invented raft to reach the island of Flores which is always surrounded by deep body of water. *Homo floresiensis* was described first in Nature (2004). Jungers et. al (2009) have reported discovery of post cranial elements from which partial assembly of foot is possible. Thus it is now possible to reconstruct hobbit man from head to toe. ***(ii) Minatogawa Man :*** Japan 16000-14000 years — The fossils have been discovered from Okinawa, Japan and belongs to four individuals. It has been dated 16000 to 14000 years ago.

(G) Hybrid hominids : Some fossils have been discovered which show up admixture of characteristic of two hominins. These include -***(i) Oase Man :*** In 2002 a fossil was discovered from Pestera cu Oase, Romania. The fossil was dated 35000 years B.P. belonging to early modern humans. The fossil characteristically showed features of archaic *Homo* and Neanderthals. ***(ii) Lagar Velho Man :*** In 1999, a possible hybrid between Neanderthals and Cro-Magnon fossil child was discovered from Lagar Velho (Portugal). It is dated 24,500 years ago. The fossil primarily belongs to modern humans with Neantherthal traits.

Toba Catastrophe Theory : Stanley H. Ambrose of Illinois University proposed in 1998 that a super volcanic eruption occurred 70,000 to 75,000 years ago in the lake Toba, Sumatra (Indonesia) that plunged the earth, which was already in ice age, into deep colder spell. This resulted in world's human population being reduced to 10,000 or even a mere 1,000 breeding pairs, creating a population bottleneck in human evolution. The eruption was the mightiest in the last 25 mya history of the earth and deposited 15 centimeteres thick ash layer over the entire Indian subcontinent, the Toba ash layers being 6 meteres thick at one site in Central India. In his book, "The winds of change : climate, weather and the destruction of civilization", Eugene Linden (2006) writes "Toba eruption lowered global temperature between 3° to 5° C. The snow line became lowered by about 9000 ft. This left only two species of human ancestors on the earth - *Homo neanderthalensis* and modern humans, *Homo sapiens*. Genetic evidences suggest that all humans alive today are descended from a very small population, 1,000-10,000 breeding pairs 70,000 years ago. Among these, as a recent work by the archeologist Michael Petraglia suggest, the largest survivors were from India. Genetic studies suggest that the modern humans spread from East Africa 60,000 to 70,000 years ago and Toba eruption occured 75,500 to 65,500 years ago. What happened to Indian survivors during the times of Toba? There is no clear-cut answer to the question.

Sahara Pump Theory : The Sahara Pump theory is a hypothesis that explains human migrations between Eurasia and Africa via Levantine land bridge. Levantine is the land area in western Asia bordering eastern shores of Mediterranean. Sahara region in Africa experiences periodic wet and dry ages due to various formations in the atmosphere. During wet times, there is plenty of rainfall and area abound in plant and animal species. When they turn dry the entire area is arid and there is no water in the region. It is converted into desert with no vegetation. Inhabitants of Sahara migrate to occupy the area surrounding the Sahara - in north the Atlas mountain, in the south western Africa, in the south east Ethiopian highland and Kenya, and in north east Asia via Sinai. The flux of fauna to the surrounding region caused by periodic alteration of Saharan environment is known as Sahara Pump. The Sahara Pump has caused migration of not only a number of animal species such as antelopes, horses etc but also *Homo*. The Sahara Pump has been used to date at least three waves of human migrations from Africa- (i) *Homo erectus ergaster* into south east and East Asia. (ii) *Homo heidelbergensis* which is direct ancestor of both *Homo neanderthalensis* and *Homo sapiens*. (iii) *Homo sapiens* 60,000 years ago, the modern sapiens.

Monogenism vs. Polygenism and archaeogenetics : The debate whether human beings have originated only once and evolved into various races (Monogenism) or separate race of human beings have originated separately and have no evolutionary connections (Polygenism) is an older one. Supporters of Polygenism held that human races had been created as separate species from transmulation of species from apes, with no common ancestor. Charles Darwin as early as in 1871 had indicated about a common descent (Monogenism) where as Carleton S. Coon (1962) favoured Polygenism and stated that *Homo sapiens* arose five times from *Homo erectus* in five separate places. "The Recent African Origin" of modern human supports Monogenism. With the advent of archaeogenetics i.e. the analysis of fossil DNA recovered from archaeological remains in the 1990s it became possible to date the "Out of Africa" migration with some confidence. With the study of mitochondrial and y-chromosome variations and its distribution pattern, the monogenism has now firm roots.

THEORY OF DISTRIBUTION OF MODERN HUMANS

There are two main theories of human origin & distribution.

The Single African Origin Model (Out Of Africa Model)

The theory holds that anatomically modern *H. Sapiens* evolved in Africa 0.1 to 0.2 mya. Members of this population migrated out of Africa replacing archaic human groups through Asia and Europe. The racial differences occurred in them within the past 0.1 mya. (Stringer,1988).

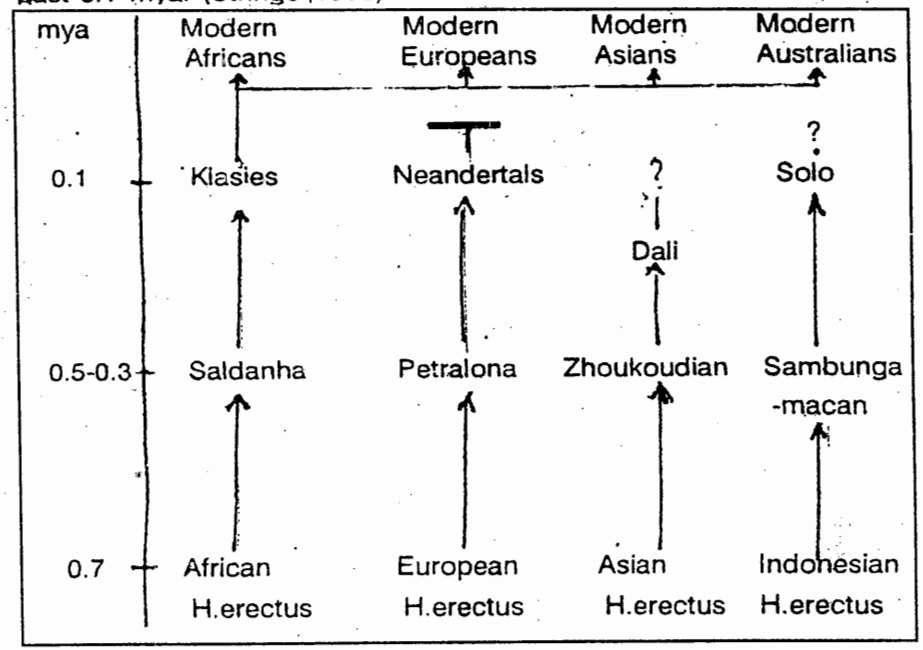


Fig. : *out of Africa model (Replacement model) of human origin. H. erectus developed in each region but all except those of Africa became extinct at some point of time which is known for neandertals and not known for Dali and Solo. Similarity among modern humans is explained by expansion of the form living in Africa which replaced other forms (After Howells 1992).*

Multiregional Continuity Model

Proposes continuous evolution over the past million years, with racial variations developing early and similar modern human traits developing in all the erectus through early sapiens (Wolpoff, 1989 Thorne and Wolpoff, 1992). The persistence of specific morphological features within regions over the past million years support regional continuity whereas identification of anatomically modern fossil specimens from Africa 60,000 years before they are found elsewhere provides support for a single African origin.

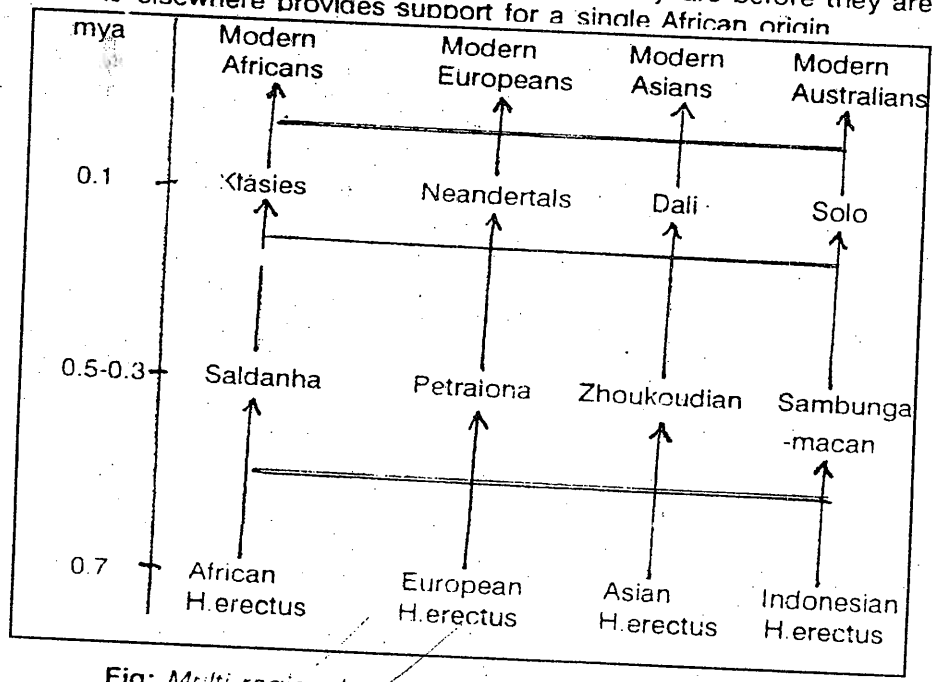


Fig: *Multi regional continuity Model: Starting from H. erectus, each region had its own representative which are identified at different levels. Similarities among them was due to gene-exchange among them at all levels. (After Howells, 1992)*

There has been many efforts to prove efficacy of the either of the models and majority are in favour of out of Africa model suggesting that modern humans evolved in Africa.

A) Evidences for "OUT OF AFRICA" Model : See page 657 for a detailed discussion on this and other related topics.

B) Evidences for Multiregional hypothesis :

Support — Wolpoff theorized that human species arose in Africa two million years ago as *H-erectus* and then spread out allover the world, developing adaptations to regional conditions.

(A) Fossil evidences for multiregional hypothesis : Wolpoff and other multiregionalists maintain that fossil evidences are more reliable than genetic evidences which are liable to drifts, bottlenecks etc.

1. Neanderthals — In 1999, a possible hybrid between neanderthal and *Homo sapiens* fossil child was discovered from Lagar velho, Portugal, aged 24,500 years ago. There has been some dispute over the hybrid status of the fossil child. In an article appearing in the "Proceeding of the National Academy of Science" in 2007, Eric Trinkaus has discussed the current issue. He maintains that early modern European fossil reflect features of both predominantly an early African modern human ancestor and a substantial degree of admixture of modern humans and neanderthals.

2. Early Modern Human : Further evidences for multiregional hypothesis comes from fossils of early modern humans discovered in early 2000.

(a) Tianyuan Man : In 2003 fossil of early modern human was discovered from Tianyuan cave near Beijing, China. It is dated 42,000 - 39,000 year B.P. a most ancient early modern human in eastern Eurasia. It has typical modern and some archaic traits such as large hamulus (Hook type portion of a bone such as pterygoid, lacrimal, hamate etc) length, anterior to posterior dental proportions, rounded distal phalangeal tuberosity etc.

(b) Oase Man : A human fossil was discovered in 2002 from Pestera Cu Oase, Romania which belonged to an early modern human. It is dated 35,000 years B.P., and considered oldest early modern hu-

man in Europe. The fossil shows characters which are admixture of archaic Homo, early modern human and neanderthal character.

B. Genetic evidences :— Proponents of multiregional hypothesis see genetic sequences of several loci in the human genome with million year old genes. These data of deep genetic lineages are explained in the multiregional theory framework as a result of heredity from structured ancestral population. The data are not interpreted in light of the Recent African Origin (RAO) hypothesis, postulating recent replacement.

The hypothesis was put forth by wolpoff in 1988. The theory holds that human evolution from the beginning of pleistocene 2.5 million years ago to 1,20, 000 years B P has been within a single continuous human species evolving worldwide to modern *Homo sapiens*. Proponents of multiregional origin point to fossil and genomic data as support for their hypothesis. The theory supposes gene flow and sexual reproduction between modern and ancestral human populations. Though there is no evidence for contribution of neanderthal mitochondrial DNA (37genes) or Y-DNA (78 genes) to the modern human, there are evidences for the autosomal DNA (20-25 K genes) which make up vast majority of human genome. Multiregionalists list a number of genes which show very ancient history. Such genes include :—

(i) ALMSI — ALMSI protein is encoded by ALMSI gene located on the short arm of chromosome 2 on the plus strand. It is 24161 bases in length organised into 23 exons. The encoded protein has 4, 167 aminoacids. It has been found that the protein has ancient and complex history.

(ii) CMAH — Cytidine Monophosphate - N - acetyl neuraminic acid hydroxylase like protein is an enzyme that in human is encoded by the CMAH gene. The pseudogene shows 2.9 million years ago history.

(iii) ASAHI — N- acylsphingosine Amidohydrolase gene, producing

Acid ceramidase related to mental activity, has TMRCA (Time for most Recent Common Ancestor) 2.4 ± 0.4 million years ago.

iv) PDHAI — Pyruvate dehydrogenase, a locus on X-chromosome, has TMRCA of 1.86 million years ago.

v) RRM2P4 — Ribonuleotide reductase M2 subunit pseudogene has TMRCA of 2.3 million years ago.

vi) Microcephalin — Microcephalin is one of the six genes causing microcephaly (small headed) when in homozygous state. Evidences indicate Neanderthals as the possible source of this gene.

Criticism :— A competing theory of multiregional hypothesis, namely the Recent African origin (RAO), also known as Recent out of Africa (RoA), has emerged as near consenus view since 1990s. It proposes that modern humans arose in Africa around 100-200,000 years ago, moved out of Africa 50-60,000 years ago and replaced *Homo* such as *Homo erectus* and Neanderthals.

Ancient mitochondrial sequence, extracted from 37,000 years old Neanderthal specimen and that of from modern humans are completely different. Same is true for nuclear DNA. However, the largest example of sequenced Neanderthal nuclear DNA comprised 1 million base pairs compared to human nuclear genome size of roughly 3 billion base pairs. This amounts to comparison of only 0.033% of the genomes, hence this logic is not much supportive to "Recent out of Africa" model.

DIFFERENT RATES OF SOMATIC EVOLUTION

Allometric Growth : All animals are characterized by differential rates of growth of their body parts compared to the overall growth of their body. In horses, for example, there has occurred increase in overall size of its body but its face has increased more relative to the body-size. This becomes possible because rate of growth of its face is greater than the rate of growth of its body.

Primates, including humans, are also characterized by such allometric growth. In human, for example, when baby is born it has large head and small legs. Head and legs, thereafter, donot grow at the same rate - head grows slowly in comparison to legs so that legs become enormous in size relative to head. During foetal life, however, the trend is opposite - head grows faster relative to the legs so that head is large relative to legs when baby is born. Different body parts, indeed, reflect different rates of growth.

Allometric growth can be positive, isometric or negative. When a body part grows faster than the overall body-size, the allometric growth is positive. When both body-part and overall body-size grow at the same rate, the growth is termed isometric. Negative allometric growth results when a body-part grows at slower rate relative to overall body-size.

Rate-genes : Those genes that control rate of metabolic processes and the times in the life-history of which such processes occur are termed rate-genes. Those rate-genes that are active during embryonic period is of greater significance than those which are active after birth because environment becomes additional factor too in latter case. During embryonic times itself, those rate-genes that affect rate of growth of the parts and organs of the developing individual is of greater significance. These rate-genes by controlling relative rates of growth of different parts determine the nature of the resulting adult. Mutations in such rate-genes, hence, have far-reaching consequences, more than the mutations in ordinary genes. Natural selection favours those mutations in the rate-genes which result in optimum sizes of the different parts of the body. Such allometric growth, therefore, are favoured over other allometric growth patterns. When the rate of growth of a part of the body results in a size which is hot beneficial for the organism concerned, natural selection interferes and weeds out such mutation from the population. Natural selection, thus doesnot

favour a mutation is a rate-gene which results in growth rate of an organ or part which ultimately becomes liability for its possessor. Natural selection interferes only in later stages when such organs or parts have become overgrown or over reduced in a manner as to harm survival of the species. If biotic and abiotic components of environment are adverse, the organism may become extinct too. Natural selection, thus, favours those rate-genes which bring about rate of development of different parts of body in a manner to provide maximum survival of the species. In the long course of evolution, organisms are thus characterized by different rates of somatic changes that result in optimum sizes for the different parts of the body, apart from the overall size of the body.

Rate Of Different Somatic Systems

1. Body-size : Primates evolved from insectivore ancestors and Tupaia or tree-shrew is a living model of such earliest primates. Its body-size is that of a small rat. Animals, in due course of evolution, tend to increase in size. It is partly because of reason that smaller animals fall easy prey to predators. Larger body-size is of adaptive value hence genes that increase the overall size of the body is favoured by natural selection, other factors remaining constant. Alteration in such a trend is witnessed when dietary, locomotor or some other preferences are involved. During the course of human evolution, earliest hominids such as *A.ramidus*, *A.anamensis*, *A.afarensis*, *A.africanus* etc. were of smaller sizes than the later hominids. Body-sizes have decreased only in response to demands such as increased arboreality, extreme fluctuations of temperature or other physical factors etc in which natural selection has favoured a small body-size such as Eskimos. However, there is witnessed no great changes in overall body-size in hominid line after emergence of *Homo erectus* and body-size has remained more or less constant thereafter. Brain, on the other hand, has continued to expand thus resulting in greater brain to body-size ratio.

2. Rate Of Brain-evolution : Primates have a larger brain for its body size than most non-primate mammals. It is because growth-rate of brain is greater than the growth-rate of the body. This applies not only to adults but to every stage in development. All primates, including humans, follow a growth trajectory similar to mammals, but at every corresponding stage primates have about twice the proportion of brain to body.

It is assumed that relatively larger brain for body-size of

primates correlates with an increase in intelligence. The superior visual and manual skills of monkeys and apes, which makes them so well adapted to life in trees, could be attributed to their proportionately enlarged brains. One thing must be made clear at this stage. when we speak of increase in brain size is faster than rate of body growth we speak in terms of comparison to other reference animal group e.g. mammals. In mouse-lemur brain represents 3% of body-weight; in humans brain represent 2% of body weight. Brain always grows at slower rate than body-growth so that larger animals have smaller percentage of brain weight. A ratio of brain to body size decline with increasing body-size. Among mammals, brain-size scales to body-size with a power function of 0.75 i.e, with a unit increase in the body-size, the corresponding increase in brain weight is only 0.75. When we say larger brain for body-size we mean that other mammalian genera of the same body-size has relatively smaller brain-sizes. Relative brain and body-size is thus always spoken of in comparison to other mammals.

Different primates differ in brain-sizes relative to body-sizes. It is often stated that apes have larger brain than monkeys. It is true only for absolute brain size. When the scaling-effect is taken into account, apes are not different from monkeys in relative brain-size. Indeed, the gorilla has a small brain, relative to body-size, compared with monkey. The highest value for relative brain size to body size in non-human primates is not found in apes but in new world capuchin monkey. Thus, in matter relating to brain versus body size, capuchin monkey is closest to humans.

Compared with anthropoids (as I have already stated that brain versus body size is always compared with some reference group), the human brain is three times bigger than expected. This represents a dramatic increase in a few million years. The rate of increase in brain size in humans when compared to apes is thus fascinating. In general, all anthropoids have bigger brains in comparison to body-sizes than the prosimians (aye-aye is an exception).

Endocast studies and limb-skeleton of fossils give indications of brain to body-size in hominid ancestors. The brains of australopithecine hominids fall within the range of modern great apes, with a mean weigh of approximately 450 grams (assuming that 1 cubic centimetre of brain weight 1 gram). Encephalisation probably first exceeded the ape range at least 2 million years ago, with the appearance of *Homo habilis*. The fossil KNM-ER 1470

from Koobi Fora in Kenya is a highly encephalised specimen of this group, with a brain weight of approximately 750 grams.

The brains of *Homo erectus* weighed almost 1000 grams. Brain size continued to increase without a corresponding increase in body size until the appearance of the first *Homo sapiens*. Early *Homo sapiens* brains were as large as ours. The Neandertals of Europe and the Middle East also had a modern brain size, and many have argued that Neandertals should hence be included in *Homo sapiens*.

Neandertal brain was, however, large at wrong places. The size of brain is a crude estimate of intelligence. It is believed that much of the evolution in brain in *Homo sapiens* involved not increase in size but changes in internal circuits of the brain. All primate foetuses, including those of humans, follow a common brain and body growth curve in which the brain is about 12 per cent of body size and both grow at about the same rate. In most primates, this pattern changes around the time of birth as brain growth slows but body growth continues. In human infants, this slowing of brain growth does not occur until more than a year after birth while body growth follows patterns similar to those of the great apes. As a result, the shape of the curve described by human brain and body growth differs from that of other primates. considering the size of brain of human foetus at the time of delivery its body-size is negligible because it is the size that can be supported during pregnancy by the mothers. Immaturity of body-size needs longer parental care which is important for socialization process, A larger brain to body ratio at the time of birth thus has direct bearing on the cultural evolution of man.

Different rate of brain growth in different primates or mammalian groups seem to be puzzling at first instance. If larger brains means greater efficiency, why do some groups show slower rate of brain-growth ? Martin (1992) explains the riddle on the grounds of metabolic costs involved in maintaining a larger brain. Large brain can be carried only when high energy diet is available. Large brains are expensive - In humans it represents 2% of body weight and consumers 20% of body's energy. A higher rate of brain growth cannot be supported in a species if it is not capable of enhanced use of rich diet.

3. Rate Of Teeth And Jaw Evolution : It is evident that rate of brain evolution is dependent upon efficient nutritional capabilities. Jaw, dentition and alimentary canal are central to such capabilities. Relative increase in brain size from australopithecines

to modern humans depended on a shift in feeding habits that led to increased energy turnover.

Compared to mammals, primates are characterized by gradual reduction in both number of teeth and tooth-area relative to the body-size. The reduction in incisors is not as marked as in the premolars and molars (cheek-teeth).

The tooth area in relation to body-size was high in hominid ancestors such as australopithecines and as evolution occurred through *erectus* to modern humans there has been a decrease in the tooth area. The rate of growth of teeth relative to the body-size has thus relatively decreased.

Ancestral hominoid were largely frugivorous as they were forest dwelling. During miocene when increasing aridity destroyed forests and opened up savannah and woodland savannah, ancestors of humans were forced to adapt to seed-eating for which rotary motion of jaw is needed. For this, larger and heavier jaw, high cuspid molars and premolars were not required. There was thus selection for smaller jaws. As jaws shortened, the teeth were cramped and reduced in size Molar cusps gradually became more rounded to allow rotary motion.

Development of tools also facilitated selection for smaller cheek teeth and canines in hominid ancestors. As tools were progressively used more and more as weapons, canines lost its selection value for agoni display. Canines were reduced in size as its interlocking in diastema obstructed rotary motion of the Jaw also. Development of tools and use of fire did much of the preparation of the food outside mouth. It was thus obvious that a larger lower jaw and tooth area must have had proved a liability and hence natural selection favoured small jaw with reduced tooth area. Contrary to the brain, teeth in primates and humans thus show decreasing rate of growth with respect to body-size.

4. Relative Length Of Limbs All limbs are shorter with respect to body-size in primates practising tree-quadrupedalism whereas all limbs are longer with respect to body size in primates practising land-quadrupedalism. Short limbs in the tree-quadrupedalism serve to keep centre of gravity more stabilised hence danger of falling from tree is minimized. Most new world monkeys, which are highly adapted to tree-quadrupedalism have shorter limbs with respect to body-size. Longer limbs increases the speed of the animals on land where there is no fear of falling. Longer limbs have adaptive value on the land hence rate of limb development on land is greater than rate of overall size.

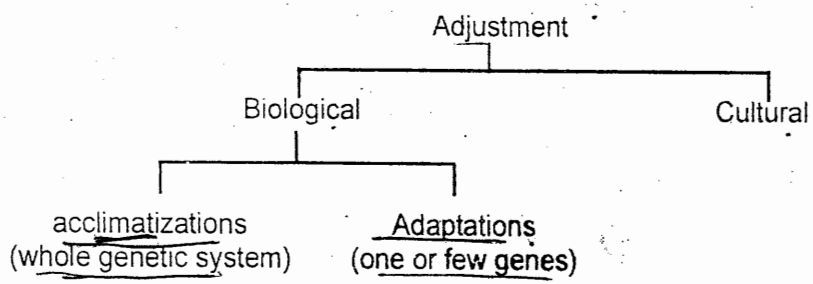
HUMAN ECOLOGY : AN INTRODUCTION

Biological evolution of humans into sapiens is marked with rapid geographical distribution, extending its range into diverse types of ecological habitats. This ecological diversification of human species was significantly aided by cultural evolution in the form of tools, use of fire etc. In the form of *Homo sapiens*, modern humans thus adapted to almost total range of terrestrial environment. This capability of adaptation springs from human ability to mould and modify the ecological habit to suit its purpose. Where the features of environment is difficult to be changed or modified, humans have sufficiently moulded and modified its own behaviour, thus displaying to a great extent adaptive behaviour.

The ability to mould and modify the elements of environment suitable for existence is found in other animal groups too eg. birds in the form of nesting, courtship behaviour, brooding etc. In lower vertebrates, the process of aestivation and hibernation are the modes of survival in adverse environments. But human ability differ significantly from these lower forms in that the human ability is largely non-genetic and a learnt behaviour whereas it is genetic and innate behaviour in case of lower animals. Not only these survival mechanisms are largely non-genetic and behavioural in origin, but they are also transmitted to the next generation in the form of accumulated information. This process of transmission of accumulated information is major construct of culture and hence it is cultural behaviour that has significantly aided in the adaptation of population to diverse environments.

Genetic mechanisms also seem to have contributed to some extent in this human adaptability. The "reaction-range" of several genetic traits are sufficiently broad so that the favourable traits are elicited in a given environment that ensures maximum survival. This genetic variation is superimposed upon overall genetic similarity of the human species. Such genetic variation is expressed in biochemical, physiological, immunogenetical and other aspects of functions. Changes in these features along with behavioural changes ensured by cultural components are crucial for human survival. Human adaptability, therefore, includes both a biological component and a cultural component.

Human adjustments occur in the following way:

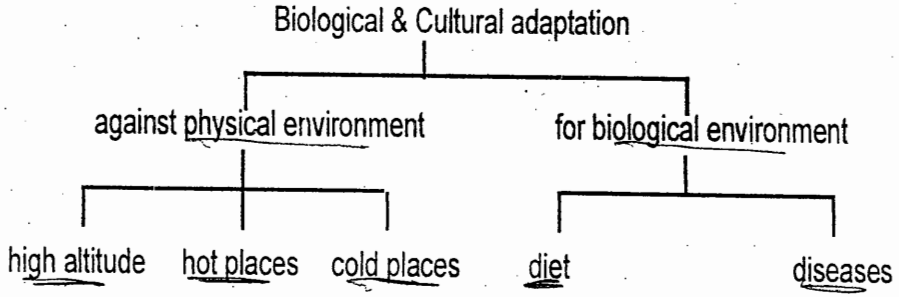


In **biological adjustments**, there are changes in the structural and plysiological system of organism whereas in cultural adjustments human populations use methods and practices learnt from its ancestors over long period of time for its survival. Changes in height, pigmentation, facial feature etc in response to a particular physical environment is biological adjustment whereas use of certain diet, dress, activity-pattern, rituals etc are cultural adjustments.

Biological adjustments can be acclimatizations and adaptations. **Acclimatizations** are changes in physiological processes in response to changed environment. It is always temporary changes and species-wide ie. if individual reverts to original environment, the changes vanish. This characteristic adjustment is shown by all the individuals of a species. Acclimatizations involve whole genetic system and not a single or few genes. Since acclimatizations are long historical process almost whole genetic system is responsible for it. Acclimatization for high altitude and heat stress is typical example of this category. Entire human species react similarly in such conditions.

Adaptations, on the other hand, is a permanent change structure and physiology of an organism. Different populations

of a species may be adapted differently to live in its environment. An eskimo has small limbs to prevent loss of heat whereas has normal trunk length so that maximum metabolic energy is generated. Also, they have cold genes which keep their limbs warm and save them from frost-bite. An african, on the opposite, lives in hot environment. He does not have 'cold genes' for limbs their hand and foot is cold hence suffer most from frost-bite if they are sent to snow-laden areas. Adaptation occur in cold climates and at high altitude (for physical environment) and also for food and against diseases. A variety of cultural adaptation has also occured in response to diet and diseases.



Sometimes it is difficult to classify an adjustment as acclimatization or genetic adaptation for example, level of melanin in skin. Dark skin colour is adaptive in regions of high radiation because it protects skin from UV damage, whereas light skin colour is adaptive in regions of low radiation because it allows penetration of more UV-radiation. There is thus genetic adaptation in the melanin content of the skin. It shows acclimatization effect too. It is known that exposure to high radiation increases melanin content of the skin and such capability is the species-wide. Moreover, intake of sufficient Vitamin D doesnot affect growth in individuals with high pigmentation in low radiation areas. Human adaptation, with reference to melanin content, thus seems to involve genetic differences, genetic plasticity (acclimatization) and behavioural responses.

ADAPTATION TO HIGH ALTITUDE

Since atmospheric pressure drops at high altitude there is shortage of Oxygen to tissues and biological adjustments tend to correct this shortage. It involves both acclimatization and adaptation

A. Acclimatization :

1. Increased Breathing Rate : Hypoxic condition stimulate appropriate nervous centres to cause instant increase in breathing rate to 65%. If person remains at high altitude, this rate increase to five fold. Initially this much increase is prevented because of blowing off of large amounts of CO_2 and consequently change in the blood alkalinity that suppresses the neural centres. In a few days, this inhibitory effect resulting from low CO_2 is removed and breathing rate increased five-fold.

2. Increased RBC And Haemoglobin : Hypoxic conditions stimulate Kidneys to secrete erythropoietin that increases RBC count and haemoglobin level from 15 gm/dl to 22 gm/dl in latter case. The total blood volume also increases by 20-30% hence net increase in haemoglobin comes around to 50% to 90%. This increase in blood volume and haemoglobin is a slow process and evidenced after few weeks of acclimatization.

3. Increased Lung Surface : Increase in lung surface means that more oxygen can diffuse to the blood. This increase in lung surface is brought about by increased volume of lung due to increased breathing and expanded blood capillaries of lungs.

4. Increased Tissue Blood Supply : Increase in cardiac output and growth of additional capillaries in the tissues ensures increased tissue blood supply thus removing hypoxic condition.

5. Cellular Acclimatization : It has been claimed that hypoxic condition causes increase in mitochondria and some other

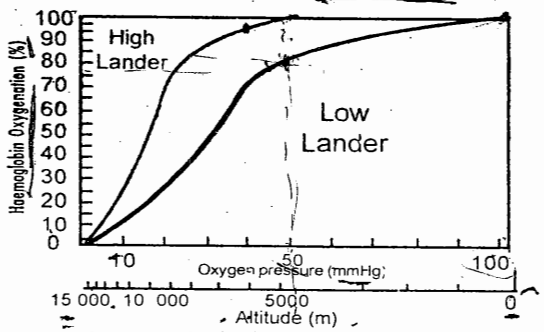


Fig. : The oxygen dissociation curve.

cellular enzyme systems. Oxygen inhaled is ultimately utilised by mitochondria for energy - transduction.

6. Shift of Oxygen-dissociation curve to right : At high altitude there forms diphosphoglyceric Acid (DPG) which displaces oxygen from $Hb0_2$ hence dissociation of Hbo_2 becomes rapid and 0_2 is readily available to tissues.

B. Adaptation

The permanent inhabitants of high altitudes show following adaptations.

1. Their chest size is greatly increased giving a high ratio of ventilatory capacity to body mass. Sherpas of Nepal are exception to this. In them, compensatory adaptations are found in blood. Ventilation capacity of high-landers do not rise they descend to low lands.

2. Their body size is decreased to reduce the body mass. Lower body mass can be supported by decreased gas exchanges (O_2-uptake).

3. Size and weight of babies born tend to be smaller. High level of nutrition and care do not come in the way.

4. Their heart particularly the right side of heart, is greatly increased to ensure supply of larger amounts of blood to lungs for oxygenation.

5. Some physical attributes, such as shape of nose, skin colour etc. are adaptive. Nose is shortened to reduce nasal passage-way, and nostrils directed upward.

6. The most important adaptations in high altitude inhabitants is capacity of their haemoglobin to extract oxygen i.e. combine with oxygen at lower partial pressure of oxygen (PO_2). The pressure of oxygen at which haemoglobin is saturated (arterial value) is very low (40 mm of Hg) in high landers whereas it is high (100 mm og Hg) in low landers. The venous values, the pressure at which O_2 is delivered to the tissue, do not vary much in high landers and low landers. It is precisely 25 mm of Hg for the latter and 40 mm of hg for formers. The oxygen dissociation curve for the high landers is thus situated left to those of curve of low landers.

ADAPTATIONS TO HEAT

Human species developed in tropical Savannah type climate hence we are quite capable of tolerating moderate heat and a temperature of 30^0c (±) 5^0c is well tolerated. Problem arises when temperature gets above 35^0. Heat load is first lessened by radiation and then, if core-temperature does not come down, hypothalamus of brain is activated for sweating. Sweating takes away a lot of heat as heat of evaporation, cooling skin which ultimately lowers core temperature.

If the heat load continues for some days, there is developed heat acclimatization with less sweating and a lower core temperature. The heat acclimatization disappears if heat load is removed. There can be individual differences in the heat acclimatization but all populations tested are more or less similar with respect to heat acclimatization.

1. Heat Is Tolerated First By Thermal Gradient : This occurs due to raditation of heat from body to surrounding air.
This is possible because of vaso-dilation i.e. dilation of blood vessels.

2. Heat Adaptation By Sweating In Low Vapour Pressure Area : When heat is not tolerated by thermal gradient, our sweat glands become active and sweating occurs. The sweat evaporates from surface and provides evaporative

Human skin is covered by more than 1.5 million sweat glands. The number of active glands does not vary significantly among human populations : any differences appear to be the result of acclimatization rather than genetics.

. Lack of hair also ensure that evaporation takes place rapidly providing cooling effect. In principle, a small body will improve heat tolerance because the surface area for heat loss will be greater in relation to the heat producing mass of the body. Long extremities will also be advantageous, as these increase conductive and radiative cooling.

3. Heat Adaptation By Thermal gradient Only In High Vapour Pressure Area

Evolution in such hot humid climate has taken a different turn than dry hot climates of the desert. The latter favour a small individual because in smaller individuals the ratio of surface area to body weight is higher (for example for infants it is as high as 0.6 Cm/gm whereas in large individuals it is 0.027). The smaller body weight generates less metabolic heat and larger surface area dissipates it. In moist, humid hot climate there is no heat loss by sweating, the only means being the thermal gradient and heat loss through the skin. The surface area hence increases in such cases along with increase in length of extremities such as limbs and ear. Such increase in extremities has occurred in Nilotics of Africa.

4. Heat Acclimatization Is The Final Stage Of Heat Tolerance: When young men from hot and cold climates are first exposed to a heat load, there are substantial differences in their heat tolerance. However, if these individuals then work in the heat for 10 days the difference between them disappears, because heat acclimatization is a universal human capability.

During acclimatization sweating rate rises under a given heat and work load. Body temperature falls down and strain on the cardiovascular system decrease. It has also been observed that salt excretion in the sweat declines over the period of acclimatization so that the danger of serious symptoms from electrolyte imbalance in the body also decreases. Heat acclimatization appears to be specific to the heat load since further heat acclimatization will occur if heat load is increased and acclimatization is completely lost if the heat load is not maintained on a fairly continuous basis.

All population tested so far show ability to heat acclimatize. However minor differences can be produced by the climate in which an individual develops. If individual is exposed to high heat load since infancy a greater numbers of sweat gland are activated, distributed all over the body. Such individuals can be slightly more efficient in heat acclimatization than the persons who have not developed in a climate with high heat load.

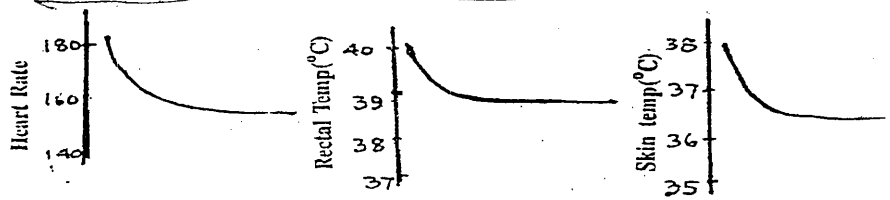


Fig. : Acclimatisation to heat as shown in men undergoing treadmill test for 60-90 min, daily have gradully lowered pulse rate, body and skin temperature.

5. Culture and heat : Human populationshave developed elaborate mechanisms to reduce heat exposure. In the recent past, houses in the hot deserts were built so as to keep inside temperatures cool during maximum day time heat, clothing usually covered almost all of the body so as to reduce radiative heating. In hot wet environments housing was open and clothing minimal to promote sweat evaporation. While these responses date from the development of agriculture, even hunters and gatherers tend to restrict physical activity during mid day in hot climates. These cultural adaptations to heat may simply be responses to the discomfort people feel, but the performance of many physical and mental tasks tend to decline at air temperatures above 28^0c, and heat stress imposes a measurable, if slight, metabolic cost on all human activity.

ADAPTATIONS TO COLD

Man, because of its savannah origin, is a poor tolerant of cold and rely more on cultural adaptations than bilogical adaptaions. Thogh presence of hair which traps a layer of air, and, subcutaneous fat is imporant for biological adaptation Our adaptation against cold chiefly consists of narrowing down the blood vessels of the extremities of the body, including skin whenever we are faced with a cold spell. When blood-vessels are narrowed down there is less flow of blood to the extremities and consequently, less heat loss. This narrowing down of blood-vessel and discontinuity of blood-supply to the extremity of blood supply to the extremity should not continue for long because cold will adversely effect the cells and several tissues can be frostbitten. Thus, narrowing down of the arteries is succeeded by its expansion.

The pattern of vessel constriction (vaso constriction) and vessel expansion (vaso dilation) can be seen by immersing a finger in freezing water. In most people, there occurs vaso-constriction immediately. Subsequent response varies. For some, finger temperature drops to water temperature and stay there. For others, it falls to water temperature but then rise and fall in short cycles (Lewis cycles). Others have consistent higher temperature than freezing water.

The basis for such an effect is known as 'Habituation'.

The biological basis of habituation is very simple. The part of the body which is experiencing cold immediately sends impulses to the brain. The impulses are recorded in the special sensory cells of our skin which are specialised for thermal sensation. Brain interprets the sensation and accordingly responses are sent by return signals to the affected part for vasoconstriction. If this circuit is pressed for too long, the return signals from brain weakens. Once the cold stimulus to sensory cell is removed, the return signals from brain also stops. Adaptation to extremity cooling is, thus, simple biological phenomenon.

Population Adaptation Is Marked In Both Whole Body And Extremity Cooling : Population differences in adaptation to cold has been studied for many populations both in extremity cooling and whole body cooling.

i. Population Differences In Whole Body Cooling : A study comparing Australian aborigines with white people has been recorded. Later on experiments on Bushman of South Africa was also conducted. Such experiments show that Africans are best adapted against whole body cooling. They maintain higher temperature during freezing condition. Europeans are the second. Aborigines and inuits are the worst and their body temperature falls much lower, thus threatend by frostbite. Their limbs become numb during night and the fire that they use during night often burn their

ii. Population Differences In Extremity Cooling : Population differences in extremity cooling was reverse to whole body cooling. In a comparison between native African, European, American, Indians, Arctic American Indians and Inuits the relative levels of extremity cooling was highest in native African followed by Europeans, Americans, Indians, Arctic American Indians and Inuits. A native African maintains the lowest cooling characterized by lowest rewarming tendency. Such a response for extremities is unadaptive in cold climate because of danger of frost bite. This is also supported by the fact that during Korean wars the soldiers who suffered most the frostbite were Africans. Inuits maintain the highest extremity temperature. Adaptation against cold in case of extremities is thus maintenance of a high skin temperature to combat frostbite.

Such studies show that adaptations against cold is genetic. But it could not be taken as conclusive and final statement because no genes involved with cold adaptation has been

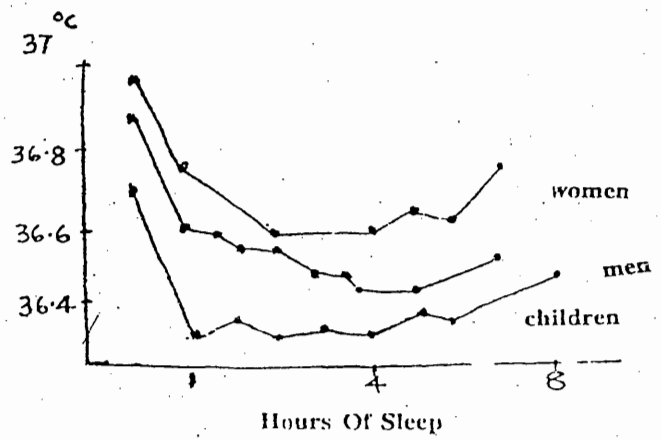


Fig. : The rectal temperature of Quechua Amerindians sleeping in unheated houses (temperaturs below freezing)

described.

Existence of such a gene is indicated only in certain Arctic fishes which produce anti-freeze proteins. No such substance has been isolated in people inhabiting colder regions. Till such a substance is isolated and the gene is indicated, both genetic origin of adaptation and acclimatisation process shall be held equally important in adaptation against cold.

Acclimatization has some role to play : Man, because of its tropical origin, shows poor acclimatisation against cold stress. A few studies indicating acclimatization in cold adaptation is also on the record. It has been found in North Atlantic fisherman that cold exposure for many years may enhance their response to cold adaptation. The debate genetic Vrs. Acclimatisation in cold adaptation shall continue till a final verdict is delivered in favour of one of them.

Culture Material And Behavioural Adjustment Are More Important : The genetic component and acclimatization in cold adaptation is uncertain and definitely played lesser roles than cultural practices and behavioural adjustments of human ancestors and modern humans. The nature of clothing, the way of constriction of shelters and use of fire are definitely most important of all cultural practices.

Such culture materials and behavioural adjustments sometimes lead to tragic conditions if they are not used judiciously in adaptation against cold. For example, Melanesia group of people use smoky fire during night to drive off mosquito. This has resulted in high incidence of respiratory ailments in this group. People in N.E.Siberia use insulated boxes to sleep. Hypoxic symptoms frequently develop in these individuals. Australian Aborigines frequently sleep naked between fire. Since they are known to drop their extremity temperature, it becomes insensitive and often burnt.

5. Cultural Adaptation has influenced Genetic Adaptation : This is evident from clothing pattern of Inuits. They have unique clothing which warms the body-core but leaves the extremity cold. The heated body core supplies heat to the extremities and they are kept warm. This saves them from frostbite. This is an unique case of reversal of mechanism of cold adaptation found in Savannah climate. In Savannah, vasoconstriction of extremity is utilised in cold adaptation; in Inuits vasodilation is utilised for the purpose

ADAPTATION TO DIET

The teeth and bones of fossil men reflect to great extent the nature of their diet. It has been found that in due course of time the teeth and mandible of human ancestors became progressively smaller in size, reflecting a change from vegetarian diet to carnivorous diet. Recent researches, however, indicate that meat was never a predominant diet of human ancestors and gradual shortening of teeth and jaw might reflect evolution of tools and technology, and the mastery of cooking.

There are several limes of evidences which show that meat was not a predominant diet of human ancestors. Firstly, plan of our digestive system does not suit a carnivorous diet and its tools, technology and fire that has adapted our alimentary canal to meaty diet. Secondly, energetic studies of hunting shows that even with techniques of recent past, hunting is not energetically favourable. Thirdly, studies of primitive hunting and gathering societies reveal that they never depend on predominant meaty diet.

A predominantly meaty diet would mean deficiency of several vitamins and minerals as well as carbohydrates thus predisposing the subjects to various nutritional stresses. The fact that our ancestors were chiefly herbivores with frequent additions of meat in their diet lead us to conclusion that they might not have suffered any major nutritional stressful conditions. All essential minerals and vitamins could have been available through plant materials whereas meat could have supplied essential amino acids.

Hunters And Gatherers : It is difficult to reconstruct the diet of hunters and gatherers because their diet get modified once they come in contact with the outsiders. However, several San tribes of South Africa are without much external influences and their diet might reflect a genuine diet for hunters and gatherers. Thus Lee (1979) working with Kung San of South Africa found that their diet was predominantly of plant origin, including 20 species of nuts, roots, dried fruits, etc. The food was well diversified with somewhat rich supply of mongongo. It also included meat, forming 1/3 of daily intake of food. The diet of hunter-gatherer Kung San of South Africa is so diverse that they rarely suffer from any nutritional stresses. It is believed that most of the hunter and gatherers similarly include variety of substances in their diet and thus generally not inflicted by nutritional stresses.

AGRICULTURISTS AND PASTORALISTS

They depended on cultivated plants and domesticated animals for food Below is given a table which shows complexes of food in agriculturist society.

Table : Some food complexes in the world as of A.D.1500.

Regions	Plant Diet	Animal Diet
North China	Millet, oates, soybeans, apricot, peach, radish	Pigs, chickens, cattle
South China and South-East Asia	Rice, soyabeans, bananas, coconut	Chickens, cattle
South-west Asia	Wheat, barley, peas, carrots, dates, olives	Goats, sheep, cattle, camels
Mesoamerica	Maize, kidney beans, squash, tomatoes	Turkeys, dogs
Andean Area : Highlands Lowlands	Potatoes(white), chenipodia, maize, sweet potatoes, tomatoes, lima beans	Llama, alpaca
Africa - South of the Sahara	Millet, oil palm	Chickens
Melanesia and Polynesia	Taro, sweet potatoes, breadfruit, coconut	Chickens, pigs

Source : Baker (Human biology, 1992)

Eurasian Communities : It is evident from the table that diet of Eurasian populations was more diverse and balanced. Wheat and millets, while providing substantial carbohydrate, was also rich source of protein. Plenty of foods and vegetables offered a rich supply of essential minerals and vitamins. It is thus evident that Eurasian people may not have suffered nutritional stress to any significant extent. There may have been exception with south East Asian populations ranging from Indonesia to Japan and a small strech of Indian Peninsula where rice cultivation is still predominant for food purposes. These areas, in absence of major domesticated animals for food, must have experienced deficiency of Vitamin B complex - chiefly Vitamin B_1. In times of short supply of different food items, thus, Vit B_1 - deficiency must have been a common problem.

South American Communities : In the South and central America, on the other hand, the situation may not have been as satisfactory as witnessed in Eurasia. In majority of South American

population a potato based diet was prevalent whereas in central American population a maize-based diet was more common. Diets of both the regions of America was inferior to those of Eurasian diets, particularly lacking source of minerals and vitamins. These regions, therefore, must have witnessed nutritional stresses arising due to shortage or lack of minerals and vitamins.

Between the two Americas, the situation was more satisfactory in the South. Here potato-based diet lacked protein but it was reinforced with chenopodium which possessed good quantity of protein. Besides, they had domesticated nerbivores which supplemented their diet with essential amino acids and fats. Last, but not the least, the Andean mountain range caused different climatic conditions resulting in fast exchange of food, bringing in diversity in their diet. Even in present day times, when the socio-economic condition of this area is quite low and undernutrition quite prevalent, no fragment of population suffer from any serious nutritional stress.

Central American Communities : Maize-based population of central America probably were worst sufferers. Maize contains inferior proteins in comparison to those of chenopodium and wheat, available to the South American populations. Central Americans lacked domesticated animals thus they were also short of meat. Dogs and Turkeys were common domesticated animals but food of such animals overlapped those of humans. Thus any effort to raise such domesticated animals in large numbers would definitely have meant sacrifice of high energetic plant food to obtain much lower energy yield these animals provided in the form of meat.

Maya was another civilization which was also primarily maize-based. It is supposed to have undergone the similar trauma of nutritional stress as suffered by other populations of central America. The civilization had, by 1000 AD, a population of about 3-5 million and quite a few big cities. By early sixteenth century when Spanish arrived here, the cities were replaced by a few towns and population reduced to 800 thousand in 1528. There was no warfare or serious climatic change over this period.

The real cause of decline of population of Maya is unknown. It may have been due to poor soil quality, some maize disease, or some human disease. The skeletal remains belonging to this period show that people in this period had some nutritional stresses causing slow statured growth and multiple skeletal defects.

~~ADAPTATION TO DIET~~

There are some concrete evidences to the fact that maize-based diet lack certain essential ingradient and is a source of potential nutritional stresser. Niacin is one such thing. Its deficiency results in pellagra. As late as early 1900s, maize-based diet has been prevalent in South US in lower socio-economic strata. There are historical evidences that people of lower socio-economic strata of South US suffered from pellagra to a great extent in the earlier decades of 20th century.

Herding Societies :

studies of herding societies reveal that the energetic cost of herding animals would be so high that the populations could not be supported by the meat provided by their herds.

This finding conforms to the fact that most herding societies either practise limited form of agriculture or trade their herds for food which is higher in energetic yield. Thus usable nitrogen is traded for a greater quantity of usable carbon. Studies of Turkana (Kenya) herding population and those of population of gangetic plains (India) suggest that use of herds primarily as source of milk may provide a more efficient use of energy input than the eating of meat.

The trade between Pygmoid hunters of Central Africa and Bantu agriculturists provides an unique example of protein-carbohydrate trade. Pygmoid hunters provide meat to some agriculturist group who, in return, provide carbohydrate necessary for adequate energy intake. In modern times, the relationship is weakening because of a sedentary life led by Pygmoid.

Lactose Intolerance : A Stressful Situation : Studies of lactose intolerance shows that a populations best adapted to its traditional nutrient environment, and changes in that environment are likely to be stressful.

It all started with the US sending dehydrated milk to several countries, short of food. At several places it induced diarrhoea and it was later found out that many population and/or individuals are characterized by absence of lactase, the enzyme that breaks down lactose, the milk sugar. Studies suggest that the production of lactase is genetically controlled.

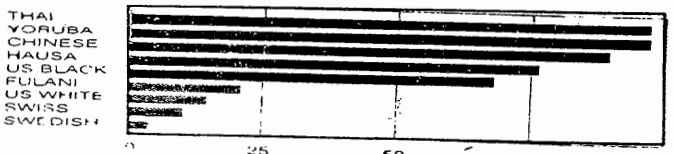


Fig. The percentage of la. tose intolerant individuals in selec human population: Kretchmer (1973); modified Baker (1992)

ADAPTATION TO DIET

Lactose intolerance is associated with the traditional uses of milk by human populations. The fermentation-process breaks down lactose into digestible form - as it is found in yoghurt and most cheeses. Therefore, problem arises if milk is used in its fresh form such as milk, cream etc. The data available indicates that very high frequency of intolerance appears in those populations which are non users whereas lowest levels of intolerance occurs in those populations, such as Eurasian populations, that have been using unfermented milk products.

Modern Society

Disruption of traditional diets and introduction of new food stuffs caused nutritional stress in many societies. The estimate of such a stress in earlier times is not known completely but by the beginning of 20th century epidemics of goitre, pellagra and beri-beri became common one. In urban areas, movement of

Though nutritional stresses are declining in the contemporary society, a very apparent change in body-form is taking place. children in modern society are growing faster, maturing sexually at an earlier age and developing into taller adults. It is generally attributed to better nutrition, but absence of many infectious diseases as well as increased genetic heterosis are also indicated. However, such a feature is not an indicator of fittest physique. Pariskova has reported that Tunisian children are shorter and grow slower than Czech children but the former are physiologically more fit. It may be that rapid growth and larger size is selectively beneficial. Similarly, body weights also show increasing trend but causes are largely unexplained. One hypothesis blames our appetite for tasty food, another indicates reduction in the required physical work such as that of Samoans, the heaviest population of the world (Baker et al 1986).

Baker (1992) on the basis of accumulating evidences donot favour either diet/physical work theory. Several populations had the genetic endowment to store fats fast in times of plenty to tide over periods of acute scarcity. While such a genetic endowment had definite selective advantage in environments characterized by periods of plenty interrupted by those of shortages, in the present conditions of continuous and adequate food supply would result in development of obesity as is found in Polynesian and certain other populations.

In present day world if there exists malnutrition and inequitable food distribution there are technologies and educational approaches to deal with the situation. Solutions depend on use of mechanical energy for food production and human energy input in its equitable distribution. Given the political will on the part of affluent nations this is not a distant dream.

ADAPTATION AGAINST DISEASES

Taxonomy Of Infectious Diseases : Human beings are affected by following category of organisms,

1. Virus : These are DNA/RNA particles with protein that survive within the cell. Among the many viral diseases which affect people are herpes simplex, cold, measles, mumps, chicken-pox etc.

2. Bacteria And Fungi : This taxonomic group includes the staphylococcus, streptococcus, and other lethal forms of infection. Some are symbionts in our alimentary canal.

3. Protozoans And Helminthes : This includes Entamoeba, Giardia, roundworm, hook worm, pinworm etc.

Infectious diseases are diseases caused by viruses, bacteria and multicellular animals such as helminthes. Infectious diseases were established due to chance contact with the hosts, ourselves, and it evolved along with us. As we adapted according to the needs of our environment and underwent definite changes in the long course of our evolution, so have these organisms adapted to the changed microenvironment present inside us. Only by going through these changes have they ensured their survival. Adaptation of causative organisms of these infectious diseases to their changed habitat thus initiated co-evolution in them along with the human host. In this coevolution, the infectious disease organisms have been at advantage because every generation cycle of host involves their several generations. The extent of damage inflicted

Culture and diseases The type of diseases menifested in human group is largely reflected in manner of food production, population density, natural environment, contact with other populations and method of sanitation. For example : It will be clear in coming pages that societies which did not observe proper sanitation were inflicted with more infections. Similarlay, large scale migration in Hawaii and other Islands Caused measles to a great extent.

Co-Evolution of People And Disease :

Genetic adaptations of humans : Human hosts showed two types of adaptations-behavioural and genetic. Behavioural adaptations stemmed largely from cultural practices that commanded observance of certain rules and practices. It is doubtful, however, that this form of adaptation was in any way superior to the genetic adaptation.

Genetic adaptation, on the other hand, seems to have played a greater role in human adaptations against infectious

diseases. Though there is no data regarding number of mutations introduced for this purpose, there are indirect evidences about their superior role in human adaptations. During 16th to 19th century there occurred large-scale migration from Europe to North and South America and islands of pacific ocean. There occurred large scale death and infertility in the aboriginal population of North America during this time. Though they lacked certain cultural sanctions and practices as high as 14% death in Fijians from measles cannot be explained only by lack of adaptive behaviour. On the other hand, low death rate among Europeans from such diseases cannot be explained through adaptive behaviour either. There must have been involved a genetic element in Europeans that lacked in Americans. In the 20th century, mortality and infertility among Americans is very much reduced, indicating development of a genetic adaptation. One such example of genetic adaptation against infection is sickle-cell trait (SCT). Persons suffering from SCT have defective haemoglobin. Once malarial parasites enter into such RBC, it gets deformed and such RBCs are detected by spleen and destroyed. Thus mutation in the haemoglobin gene that causes SCT proves to be a sort of genetic adaptation against infectious disease, malaria.

The best form of genetic adaptation against diseases seems to be elaboration of antibodies, a type of proteins that are formed by special type of WBC called Lymphocytes. Once antibodies evolved, man seemed to have in its possession a weapon par excellence to fight infections.

Genetic adaptations of Diseases : On the other hand, in the recent years it has become known that parasites are capable of antigenic variation in one generation of its life cycle. Humans elaborate some types of antibodies against parasites and parasites escape from its clutches by forming another variety of antigens. This is a sort of hide and seek between pathogens and hosts. Parasites are capable of forming a variety of antigens not only during its long course of co-evolution but during its life-cycle spanning only one generation. It is thus able to deceive human defense system and perpetuate itself. Who is a dominant partner leading this game of hide and seek? There is no clear-cut answer. The situation apparently seems to be a circular one. Are humans capable of forming a great many varieties of antibodies because invading parasites are characterized by plenty of types of antigens, or are invading parasites forced to evolve a great many varieties of antigens because humans are capable of forming plenty of types

Hunters And Gatherers : In hunters and gatherers average life expectancy was low and very few people lived beyond 50 years. The causes for this low life expectancy are not clear but do not appear to be primarily the result of infectious diseases. Accidental and traumatic death appears to be the main cause as did such predators as reptiles and carnivores. Social mortality in the form of infanticide, geronticide, cannibalism and warfare may have also contributed.

The relatively low incidence of childhood deaths compared to early adult deaths in recent foraging groups is reason for believing that infectious disease was not a major cause of death. This mortality pattern contrasts with recent agriculturalists where the many bacterial and viral infections produce high mortality rates in infants and young children, but result in the immunity of most young adults to high-fatality infections.

Agriculturists : Growth and development of agriculture and consequently permanent settlement formed large aggregates of humans where many infectious disease could develop. Most of the bacterial diseases and some viral disease that invoke short term immunity could have been present. Contrary to viral disease, bacterial diseases do not need large aggregates of population and large-scale migration for its perpetuation. Among parasitic diseases, those that require a domestic animal as its intermediate host, must have spread. Among viral diseases, it is believed that a few, slow viruses such as chicken pox and Kuru could have been present.

Kuru : In new Guinea it has been found that agricultural population often suffer from a delayed lethal viral disease of nervous system which progressed over a period of up to a year before death. The virus appears to be a human limited one, only the chimpanzee proved susceptible. The virus remains resident in significant quantities only in the brain and neural tissue. It also appears to be a delicate virus which can be transmitted only by brain and neural tissue to blood contact or possibly by the ingestion of relatively uncooked brain tissue. It was closely associated in the new Guinea with frequent cannibalism. The disease could have established only when population have had become a denser one.

Tapeworms : A very common form of tapeworm which affects human population is *Taenia solium*, which is normally acquired by eating poorly cooked pork. The eggs of the tapeworm are produced by the mature worm in the human digestive system. it is consumed by pigs. Once in the pig's digestive tract, the eggs hatch, producing embryos, that penetrate the intestine, circulate in the blood, and finally develop somewhere in the pig into a

bladder-like form called cysticercus. Finally, when the cysticercus is eaten up by people in the undercooked pork, it infects man. Human can become infected by cysticercus larva if eggs are directly engulfed. Thus pigs from Bali (which were infected with the tapeworm) were given to the agriculturists of New Guinea. In Bali, where the population often ate poorly cooked pork but were careful in personal cleanliness, it was limited to tapeworm infections. New Guinea populations didnot dispose of their excreta safely hence the eggs were often directly engulfed by people. As a consequence, the people were infested by not only the tapeworms, but also the embryos. These embryos formed cysticercus in all parts of the body, including the brain. Within the brain, many dysfunctions occurred, Including epileptic-type seizures. Many societies prescribe rigid hygienic proscriptions to ward off such infectious diseases.

Towns And Cities : Most of viral infections, especially those which stimulate long-term or lifetime immunity, are more recent. It include measles, mumps, whopping cough and polio-myelitis that must have resulted due to dense population and large scale mobility as is shown by the table following :

*Endemicity of measles in islands with population of 500 000 or less, all of which had at least four exposures to measles during 1949-64**

Islands	Population	Annual Population input	% months with measles (1949-64)
Hawaii	550 000	16 700	100
Guam	63 000	2200	80
Tonga	57 000	2040	12
Bermuda	41 000	1130	51

After Fenner (1970). modified BAKER (1992.)

It is evident from table that measles was constantly present only in Hawaii where the population exceeded 500 000. It is believed that within a self-contained human population measles would disappear in a population below 500 000 persons. Measles

prevalence was affected by high reintroduction rates in Guam that, at the time, had a high turnover of US military personnel, and Bermuda, which had many tourists. On the other hand, even relatively large populations, like in Tonga, had few visitors during those times and were measles free much of the time. These data suggest that the human forms of the childhood diseases probably did not exist until some agricultural centres developed dense population clusters with high levels of personal interaction. This may have happened 6 or 7 thousand year ago.

Epidemics :

Trade between Europe and Asia had started around 2500 BC. The plague was introduced from Asia to Europe because of such trades. By the late Middle Ages epidemic diseases [introduced from South Asia] were rapidly spreading through Europe; most notably the bubonic plagues which were usually spread from rat hosts via fleas to people. These highly lethal diseases were initially slow to spread since the carrier rat species first had to arrive and disperse prior to the disease. Later, the epidemics were restricted to people living in urban areas which were infested by the host rat species. Finally, with the development of new plague foci in central Asia and a from which could be spread by human contact, the massive Black Death of the mid-fourteenth century hit Europe.It is believed that about one-third of Europe's population died in this epidemic.

Most massive mortality of humans occurred in western hemisphere and Pacific island when it come in contact of Europeans. The arrival of the Europeans created the possibility for a major exchange of diseases. The only disease which may have been transferred from the western hemisphere to Europe is syphilis. Certainly, an epidemic of this venereal disease began in the Mediterranean region shortly after contact with the Western Hemisphere began.

Americans, however, were great sufferers due to diseases introduced by Europeans. It was Cortez's army that introduced small pox in Mexico. Pizarro's "conquest" of the Inca Empire followed the small-pox epidemic which had killed the Inca, his successor, and a large percentage of the population by several years.

The extent of population decline in the Western Hemisphere related to the arrival of the Europeans is unknown, but it is estimated that the total population of native Americans was reduced by between 50 and 60 percent. This may have resulted due to absence of genetic adaptation in Americans.

IMPACT OF AIR POLLUTION ON CARDIOVASCULAR FUNCTIONS

Air-pollution is a by-product of human civilization though it has been increased to several fold more by our reckless conduct without concern to maintenance of air quality. Large scale and rapid industrialisation is necessary to meet the demands of burgeoning population. Such industries generates and release in the air in dangerous proportions several pollutants and populations have to pay the price in terms of health hazards. It was originally thought that India, being a less industrialized country, faces no immediate threat to human health. Such an euphoria has died down because ill maintained industrial units and vehicles pour more pollutants and many of our cities have crossed the limit of 150 SPM (mg/m^3) laid down by the WHO.

Table : *Annual Summary of Air Quality*

City	SPM
Ahmedabad	217
Bombay	184
Calcutta	522
Delhi	433
Hyderabad	143
Jaipur	308
Kanpur	432
Madras	155
Nagpur	199

Dangerous consequences of air-pollution on human health is revealed in the episodes of air-pollution which occasionally strike. Some of the episodes of air-pollution throughout the world with associated deaths can be cited to show seriousness of its effects on human health. Most of the episodes were caused by leakage of dangerous pollutants from some industrial units which are main source of air pollution.

Mechanism of action Most pollutants enter human body through lungs because it is richly supplied with blood -vessels Many pollutants have known action on the haemoglobin and sufficiently lower concentration of oxyhaemoglobin. Carbon monoxide, for example, has greater affinity for haemoglobin than oxygen has. There is thus formation of more carboxyhaemoglobin at the cost of oxyhaemoglobin. This reduces supply of oxygen to the various tissues of the body, including heart and brain, seriously hampering their function.

Effects Of Pollutants On Human Health

1. Sulphur dioxide (So_2) : It is an irritant to mucous membrane. Some of sulphur dioxide is oxidised to sulphur trioxide in presence of water vapour, forming Sulphurous and sulphuric acid respectively. Sulphur trioxide is much stronger than sulphur dioxide, causing severe bronchospasms at relatively low levels of concentration.

2. Carbon monoxide (CO) : Carbon monoxide has a strong affinity for haemoglobin and form carboxyhaemoglobin, COHb. This reduces the ability of the haemoglobin to carry oxygen to the tissues. CO has about two hundred times the affinity than oxygen for attaching itself to the haemoglobin, so that low levels of CO can still result in high levels of COHb. Both brain and heart severely suffer due to lack of oxygen and a paralytic and heart attack can be precipitated in case of high Co-level.

3. Oxides of Nitrogen (NO & NO_2) : Only two out of seven oxides of nitrogen are thought to affect human health. These are nitric oxide (NO) and nitrogen dioxide (NO_2). Haemoglobin possibly react with oxides of nitrogen though there is no positive evidence that nitric oxide exposure is a health hazard associated with community air pollution. NO_2 is irritant to the eye and nasal mucosa.

4. Hydrogen Sulphide (H_2S) : It is well known for its rotten egg like odour. Exposures to hydrogen sulphide for short periods can result in fatigue of the sense of smell, though it has no ill-effects on human health. In fact, mercaptans are often added to natural or manufactured gas supplies so that leakage of gas will be noticed.

5. Ozone (O_3) : Ozone is a gas that has an irritant action on the respiratory tract, reaching much deeper into the lungs than the oxides of sulphur.

6. Fluorides : Fluorides, present in air, range from those which are extremely irritant and corrosive like Hydrogen fluoride to relatively non-reactive compounds. Fluorine is a cumulative poison even in low concentrations.

7. Lead : Automobile exhaust create concentration in the atmosphere inorganic lead of about 1-3 $\mu g/m^3$, with high values in areas of heavy traffic Inorganic lead affects gastro-intestinal tract, liver and kidney, fertility, pregnancy, and mental development of children.

8. Hydrocarbon Vapours : These form photochemical smog is presence of water and sunlight. It is a major contributor to eye and respiratory irritation.

9. Carcinogenic Agents : Carcinogenic agents are responsible for cancer. The incomplete combustion of hydrocarbons and other carbonaceous materials give rise to polycyclic organic compounds such as 3, 4 benzpyrene which is carcinogenic.

10. Insecticides : DDT has been found in mother's milk in western countries and even in India. Insecticides have effect on brain. It can initiate labour and abortion.

11. Radioactive Isotopes : Iodine 131, Phosphorous 32, Cobalt 60, Strontium 90, Radium 226, Carbon 14, Sulphur 35, Calcium 45, and Uranium are the chief radioactive isotopes that can be released in the air by nuclear reactors, radioactive isotopes for scientific, medical, Agricultural and industrial use and testing of nuclear bombs in the atmosphere etc. The serious health effects are anaemia and cancer. Radioactive isotopes also cause genetic defects and sterility as well as embryo defects and congenital malformations.

12. Allergic Agents : Organic allergens have their origins in living things like plants (pollen grains), yeasts or moulds, or in animal hair, fur, or feathers. These cause hypersensitive reactions in skin or respiratory tract. The incidence of bronchial asthma is particularly high in garden city of Bangalore. People who have never exhibited tendencies earlier have, on coming to Bangalore, had attacks of asthma. A study identified 75 types of air-borne pollen and 120 types of spore present all the year around in the city atmosphere. According to the study, the pollen of *parthenium* was the highest in quantity (41%), followed by grass pollen (28.8%), the Cassia species (11.8%) etc. The study revealed housewives & office workers to be greater sufferer.

OCCUPATIONAL DISEASES

Many occupations, particularly industrial operations, are characterized by handling and/or release of harmful substances. Industrial workers, hence, may be exposed to various types of occupational hazards.

Chemical agents act in two ways : inhalation (dusts and gases), and ingestion (chemical substances such as lead, mercury, arsenic, zinc, chromium, cadmium, etc).

The main chemical hazard is because of inhalation of dust particles. The size of dust particles varies between 0.1 and 150 μ. Particles smaller than 3μ are directly inhaled into the lungs and are mainly responsible for pneumoconiosis. Pneumoconiosis is a lung disease which is characterized by lung fibrosis and other complications leading to CardioVascular malfunction.

Following are the occupational diseases associated with the inhalation of dust particles.

DUST	DISEASE
1. Silica	Silicosis
2. Asbestos	Asbestosis
3. Cotton dust	Byssinosis
4. Coal dust	Anthracosis
5. Sugar cane dust	Bagassosis
6. Tobacco	Tobaccosis
7. Iron	Siderosis
8. Hay or grain dust	Farmer's lung

Nitrogen dioxide is known to cause occupational disease. Manufacture of nitric acid, high nitrate fertilizers, electric arc welding, mining utilising nitrogen compounds as explosives are instances that involve occupational diseases.

1. Silicosis : Silicosis is caused by inhalation of dust containing free silica or silicon dioxide (SiO_2). The mining industry (coal, mica, gold, silver, lead, zinc, manganese, and other metals), pottery and ceramic industry, sand blasting, building and construction work, rock mining etc. cause release of silica and

threaten health of workers.

The main symptoms of silicosis are cough and pain in the chest. In some cases silicosis may lead to 'Silico-tuberculosis'. Reduced oxygenation of blood causes various cardiovascular complications in few months to six years of age.

2. Asbestosis : The inhalation of asbestos dust causes a disease known as 'Asbestosis' which harms the lungs. Asbestos has also been reported to cause ailments like chest pain, cough, asthma, lung cancer etc, the risk of lung cancer being high in cigarette smokers among workers exposed to asbestos.

The dust particles of asbestos act slowly on the lung taking as long as 25-30 years and in some cases even 40 years to manifest their presence by causing illness that may, by then, be incurable. For this purpose, many countries have prescribed occupational exposure limits.

3. Byssinosis : It is due to inhalation of cotton fibre dust. The symptom is chronic cough ending in chronic bronchitis (respiratory disorder).

India has a large number of textile industries employing nearly 35% of factory workers. About 20% of textile mill workers are victims of byssinosis.

4. Anthracosis : This is a disease resulting due to deposition of fine coal dust in the lungs of coal-miners. Over the years, the coal dust destroys mucous membrane of lungs and predisposes coalminers to subsequent pulmonary infections.

5. Tobaccosis : This is a disease resulting due to inhalation of raw tobacco dust by the workers engaged in processing of tobacco products. The raw tobacco also damages mucous membrane of the lungs and opens the floodgates of recurrent secondary pulmonary infections.

6. Siderosis : This is an occupational disease in the workers of steel and iron manufacturing. Very fine dust of iron is inhaled and deposited in the lungs. The blood- vessels of the lungs are damaged and fine particles of iron enters into blood circulation and are deposited in the joints. This occupational disease, besides causing lung-damage, also results in severe joint pain.

7. Farmer's Lung : Farmers are exposed to fine dust of hay or grain which accumulates in the lungs. The damage is mainly to mucous membrane of lungs and nasal mucosa.

IMPACT OF SMOKING ON CARDIOVASCULAR FUNCTION

Smoking is prevalent in most of the industrialized as well as developing countries, though it is more prevalent in the former. There has been many surveys of industrialized countries and ratio of smokers to non-smokers is very high. In third world, in terms of prevalence, people of Latin America have more smokers among them than the population of the continents of Asia and Africa, lowest being in Africa. Surveys have been conducted for most Latin American, Asian and African countries. Smoking is more common in urban than in rural areas. Among women, it is found to be prevalent in urban high status group, though rural women also smoke. Cigarette smoking is popular in third would among university students, particularly medicos. African & Asian surveys indicate that smoking is gradually increasing in the countries of third world.

The US surveys indicate opposite trends. Between 1975 and 1990 there has been marked decline in proportion of male smoking. This has been accompanied by a change in smoking habit, so that filter cigarettes now account for 90% of US consumption. In addition, there has been reduction in tar and nicotine content of the cigarette. This is probably due to dissemination of the knowledge about ill effects of smoking on health.

Smoking And Cardiovasculr Functions : Survey : There has been quite a few surveys by WHO in UK involving British doctors and general population. Like USA, in UK also there has been a late realisation of health hazard associated with smoking and hence there is marked decrease in smoking among doctors of UK. Consequently, percentage of mortality in doctors of UK as compared to general population by coronary heart disease has significantly decreased: In a report of the Royal college of Physicians, it has been estimated that in countries where smoking is established it is responsible for 90% of lung cancer death, 75% of death from bronchitis and 20% from ischaemic heart disease. Giving a break-up for a recent survey, the report said that there occurred 70,000 deaths form lung-cancer and other lung-ailments and 1,80,000 from coronary heart disease; smoking thus caused 63,000 (90%) in the first and 36,000 (20%) in the second category totaling 99,000 deaths.

Smoking as a contributory factor to cardiovascular diseases

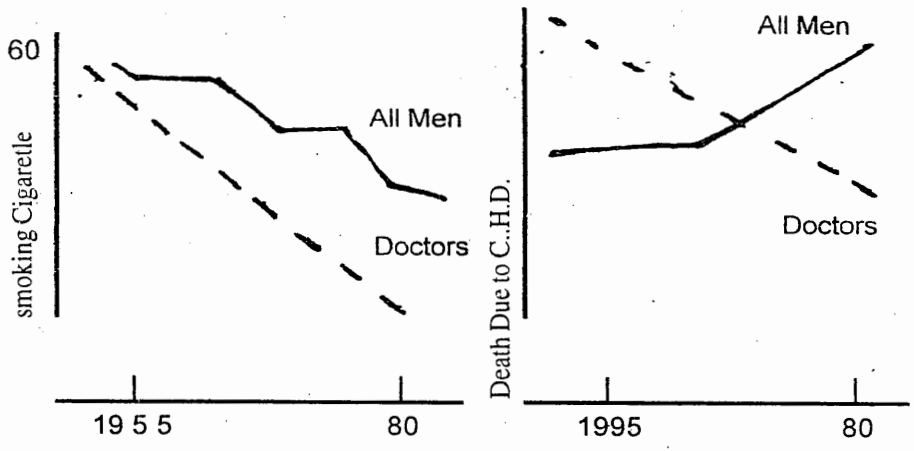


Fig. : Changes in death rare from Coronary heaart disease in eleation to changes in smoking habits (WHO survery) (per 1000 per yr.)

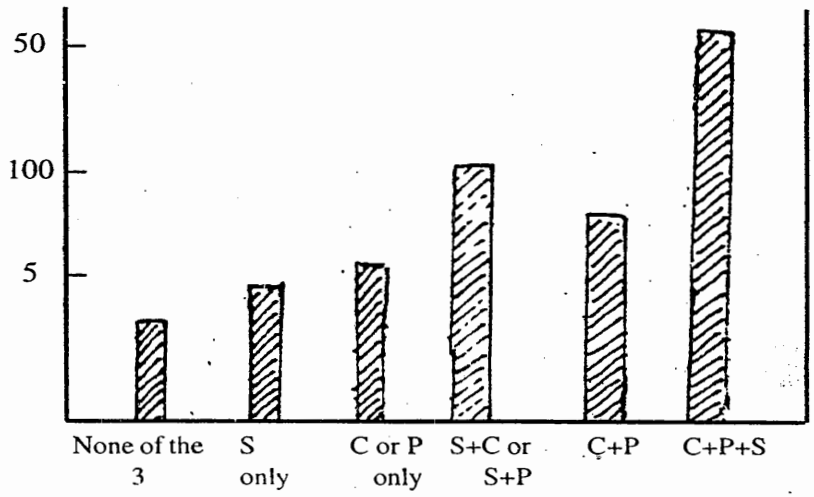


Fig. Ten Year incidence of first major coronary event in relation to cigaretee smoking, serum cholesterol, and BP in white adult meals in USA (W.H.O., 1980). S = Smoking C= Cholestrol in serum>2.5 g/I.P. = Blood pressure, diastolic > 120.

is even more significant because it is synergistic with other risk factors such as hypertension and high blood cholesterol. The fact has been established in a systematic study of over 1 million people in USA (man) and UK (females).

A systematic study of nine metropolitan cities has been carried out by WHO and contributory factors to the cardiovascular diseases estimated. It was established that smoking together with hypertension make up significant factor though it varied in different cities. .

Table : *Smoking as risk factor in cardiovascular disease*

Towns	smoking and hypertension as risk factor in Acute myocardial infarct
Auckland	50%
Bombay	12%
Capetown	49%
Edinburgh	52%
Heidelberg	40%
Los Angeles	27%
Melbourne	45%
Singapore	14%
Tel. Aviv.	50%

Mechanism : Cardiovascular functioning is adversely affected because of decreased oxygen uptake in the lungs by the blood due to various reasons. Carbon monoxide (CO) of smoke has higher affinities for haemoglobin, forming carboxyhaemoglobin and this hampers oxygenation of haemoglobin. Besides it also causes chronic bronchitis and emphysema of lungs and diminished pulmonary functions. After prolonged exposure to smoke irritants, the bronchial tubes narrow down which causes difficulty in breathing. With emphysema, the situation complicates. In emphysema, the air-sacs in the lung breakdown into larger spaces. The lung area where exchange of gases occur thus get reduced, forcing the patient to take much large breaths. This causes onset of heart failure. In UK and USA, the chronic obstructive lung disease, chronic bronchitis and emphysema rank second only to artery disease.

Smoking And Pollution : In study, the prevalence rate of various lung ailment was compared in west Indies, African and England whites. It was found that there was less cough and phlegm in the smokers of West Indies than the UK. It was probably due to healthier climate of Jamaica. This and several other studies indicated that harmful effects of smoking is enhanced in the industrialized countries due to presence of high level of pollutants in the atmosphere whereas relatively non-polluted atmosphere of developing country doesnot allow harmful action of smoking to multiply.

Ethnic variations have been found in the susceptibility of various populations of Africa to Airways obstruction due to smoking. Also, In a study of Pakistani adult males it has been found that forced vital capacity and forced expiratory volume donot differ in smokers and non-smokers. However, they differed in certain other statistics. There is also sex-differences in smoking effects. In a study of Delhi (India) adults, it was found that chronic Cor pulmonale, a pulmonary hypertension, is equally prevalent in female and male smokers, whereas in other parts of world there is male preponderance. The fact that males and females of various populations differ in susceptibility to Cor pulmonale indicates sex-differences and ethnic variations in cardiovascular functioning due to smoking.

Effect Of Bidi & Cigarette : In third world, particularly in India, Bidi is smoked. Bidi smoke, compared to American cigarette, contains higher level of co, hydrogen cyanide and acrolein, tumour promoting volatile phenols, and other carcinogenic agents. In a survey of Bombay (India) by Jussawala and Deshpande (1971), it was found that bidi-smoking involves greater risk of lung cancers and cardiovascular diseases.

Pollutants	Bidi : 2 puffs/min	Cigarettes : 2 puffs/min
Carbon monoxide	7.7 vol %	3.5 vol %
Ammonia	284 μg	180 μg
Hydrogen cyanide	903 μg	445 μg
Phenol	250 μg	150 μg
Other volatile phenol Carcinogenic Hydrocarbons	264 μg	173 μg
Benzopyrene	78 μg	47 μg

PHYSICAL ANTHROPOLOGY AND DEFENCE DESIGNS

Anthropometry is the branch of Physical anthropology concerned with the measurement of the human body. Anthropometric surveys provide information on the range and variation of body shape. Size and fit are important issues because they can significantly affect the utility of equipment, clothing, or work space. For example, a computer key board may be designed for the Indian market, with the right spacing for the average Indian to rest his or her hands on the "home keys". Before such computers are marketed in other countries say Nepal, it is important to know whether it is equally comfortable for a typical Nepalese hands. The same may be said for automobile seating or airoplane cockpits where reach or field of vision may be critical factors.

There was a time when equipments were designed with little concern for the physical characteristic of the users. Physical anthropologists as experts of human anatomy were first involved in the designing of defence equipments during world war II. Since then anthropometric research has played significant role in engineering designing of many technologies, from Jet-fighter ejection seats to analyzing human posture in zero gravity based on skylab experiences.

The term Anthropometry was first coined by Queflet (1871). It was, however, Martin, a German Scientist, who published in 1928 the famous title "Lehrbuch der Anthropologie". The revised edition of this book in three volumes, co authored by Salter is still a significant work (1957). Knussmann (1990,1992) has recently edited two volumes based on Martin's work.

Designing of any product or equipment considering human variability is a complex one, and it needs participation of three groups of people, viz. the users, the anthropologists and the manufacturers Role of anthropologists is crucial, particularly if the efficiency of equipment is dependent on human variability. Anthropologists are supposed to provide basic data on human variability in such a simple manner that it is easy to understand and ready to apply.

Three factors that collectively determine the quality of man-machine relationship are efficiency, safety and comfort (Malik et.al.1995). Design that do not consider human variations lead to

poor job. performance, low job-satisfaction, waste of time and increased morbidity.

Gun Turrets : Anthropometric data has had been very reliably taken and intelligently applied by anthropologists for Airforce. It improved flying efficiency of the pilots thus saving much money on procurement of large number of pilots. After 1942, its spread to other fields of human activities has improved work efficiency in other fields by reducing discomfort of people. It is not that anthropometric data has not been used in military services, but it was primarily used for physical or medical description.

A gun-turret is a movable enclosure containing the gunner, wearing protective clothing and equipment, a pair of machine guns and a sighting mechanism. The gun turret is so designed that the gunner has all the free movement of his body needed. It has to be scientifically designed because any extrusion from an aircraft adds air-resistance. Hence, such areas as offering resistance must be reduced to minimum without compromising efficiency of the gunner.

Such improvements in US gun-turrets greatly increased efficiency of crewmen, reduced their discomfort of long occupancy in a cramped enclosure and insured effective means of escape from an aircraft in emergency, or in removal of a casualty. With the increased efficiency of crewmen, the losses to the airforce were effectively curtailed.

Cockpit Size And Seat Configuration : Scientists have made study of cockpit space and established parameters for cockpit size in different types of air-craft. They were also instrumental in designing various seat configurations for both fighters and bombers. Such improvisation largely aided in reducing cockpit fatigue and discomfort by proper body support.

Use Of Mock Up : Engineering design of defence equipments is necessarily a three-dimensional problem which cannot be solved by two dimensional studies alone. Hence, full-scale mock up is manufactured with everything that a crewmen will bear : clothing, inner-line gloves, helmets, masks and goggles, boots and parachute. This has vastly improved gun-turret and cockpit size designing: This increases initial costs but is more than compensated by improved operator acceptance and saves from a possible error that might lead to rejection of the design.

Flight Clothing : Application of anthropometric data in the flight clothing has been vital. Individual designers have their own

schedule of sizes so that clothings sometimes fit no one. Flying Helmets is one such problem. To provide correct size-control, anthropologists have sculptor-carved wooden head forms in four statistically derived sizes-extra-large, large, medium and small. Sets of these head forms are supplied to helmet manufacturers as standards. It has been found that the helmets follow the ratio of 10:40:40:10. This is a great and immediate help to purchase departments.

Physical anthropologists are also concerned with designing of oxygen masks and make its correct fit with the help of a set of seven statistical sizes and shapes of sculptured face-forms. Similar is the case with the garments. Body-sizes of females are also taken to procure flight clothing and other garments for service women.

Such anthropological efforts bring about two sided advantage- operational efficiency and economic benefits-the latter to agencies such as government, manufacturer. Such studies indicate the least number of sizes in which a garment would have to be fabricated, the values of dimensions necessary for each size, and the number of garments required in each size.

Jet Engines : Anthropometric engineering is applied in the Jet engines and it is perhaps the most important engineering programme. The Jets fly over altitudes above 50,000 ft. At such altitudes, human body can swell up due to reduced atmospheric pressure. Dr. J.P.Henry, a medical physiologist, invented a concept called the "partial-pressure suit" - a one piece perfectly fitting, non-stretch garment with air tubes connected to it so that when air-pressure dropped, air could be introduced in the spaces within the clothing that could prevent muscles from expanding. The unit served the purpose but there were severe sizing dilemmas. Each suit has to fit like skin from neck to wrists and ankles, but there were no anthropological data.

Once the garments are available there is conducted "fit test", they are checked for conformity to the specified dimensions by trying them on a sample of 50 or more subjects, selected to show the full range of body-size in the target population. The subject, after he dons it, goes through all the motions required to show whether that size actually is comfortable fit.

It was found that stature and weight generally yield the highest correlations with other bodily dimensions and could become the diagnostic dimensions for complex, fitting garments.

Numerous "height-weights" sizing programmes have been tested in the forces of all the countries the world over.

The Ejection Seat And Car Passenger Safety : Originally this used to be a simple metal bucket seat mounted in the aircraft in type of gun, so that in an emergency, the pilot could fire the seat and himself out of the aircraft, and after freeing himself from the seat, take to his parachute. This seat was invented by the Germans during world war II.

Any such device must take into account centre of gravity to avoid excessive rotation of the seat as it enters the airstream at high speed. The centre of gravity is determined by the man-equipment-seat combination. Since limbs are flayed in the air, it is important to know centre of gravity of the limbs. For such purposes, hence, centre of gravity of limbs are known from a large sample of population. Later on, many studies were conducted for knowing moments of inertia of living subjects in a variety of fixed positions on a compound pendulum, nude and with full-pressure suit. Such datas has helped refine crew accommodation in the space capsules as well as cockpits and seats of advance fighter aircraft and automobiles. This has reduced the severity of damage during accidents.

Anthropomorphic Dummy : Physical anthropologists started studying the G-forces generated when living subjects, strapped to a seat on moving sled, stopped suddenly against a barrier. The experiments were hazardous and dummies displayed little mobility of the body and centre of gravity. A sophisticated dummy was drawn up after considerable research of anthropological, engineering and orthopaedic literature. Such dummies are now regularly manufactured for variety of tests situation. Such dummies enable engineers to approximate the trajectories of human bodies in crashes, and to obtain some idea of the forces involved.

Design Requirements : Design requirements may be classified into three groups ;

a. Work space design

b. clothing and personal equipment design

c. Component and devices.

Workspace design includes designing of any space for human occupancy during work, recreation, rest, education, travel, treatment etc. The designing aims to ensure that operator has adequate work space and proper location of controls, displays and

devices (Malik et.al. 1991). Designing of automobile interior, aircraft cockpits, seating apparatus, doors, tunnels etc are some of the examples where workspace designing is needed. The measurements required in designing workspace include reach limits, body clearance, eye location etc.

Clothing and personal equipment design include designing of garments, press suits, helmets and gloves etc. The designing of such things assure proper fit, minimise restriction of movements. The body measurements that are generally required for designing clothing and personal equipment includes circumferences, body contours, limb movements etc.

Designing of components and devices include designing of small appliances such as knobs, levers, switches, handholds etc.

There Is No Average Man In Designing : Clearance and reach are the important aspects of anthropological designing.

A door whose size is designed on the basis of average height would obstruct the one half of population above the average value. Similarly a control set up at an average height will hardly be approachable by shorter half of the population. These are the examples of clearance and reaches separately. If an equipment is designed taking averages of the two, the equipment would be practically suitable to none.

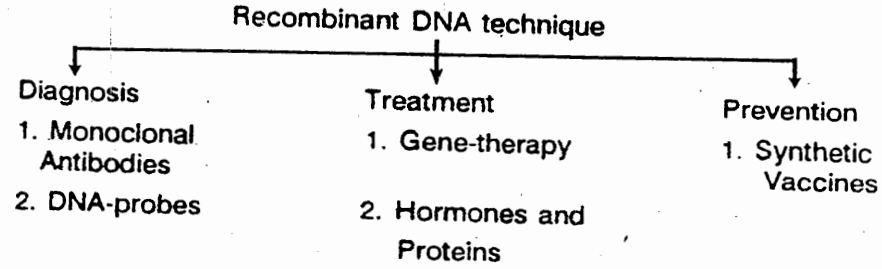
Hence, in the design anthropometry, there is no average man. It is percentiles of the normal distribution curve. While designing for clearances, it is to be based on 95 or 99 percentiles, and for reaches it is to based on 1st or 5th percentiles.

The front of a car with its steering wheel, windglass, clutch, breaks, door, several accessories cannot be designed keeping in view an average man. As already stated, where reach is crucial, it is always the lowest percentiles, and where clearance is required, it is always the highest percentiles. The thinking that large female can be represented by average male and the children are miniature adults has equally proved wrong so far anthropometric designing is concerned.

95-99%.
1-5%.

RECOMBINANT DNA TECHNIQUE IN HEALTH AND MEDICINE

Recombinant DNA technique has contributed significantly in the spheres of diagnosis, treatment and prevention of the diseases. Efforts in these three areas of health and medicine can be summarised in the following way.



1. Monoclonal Antibodies : These are specific antibodies produced by lymphocytes through hybridoma technique. The technique was developed by Kohler and Milstein in 1975 who were awarded Nobel prize in 1984. Hybridomas are fused cells resulting from fusion of antibody-producing lymphocyte cell and myeloma (Cancer) cell. The resulting hybridoma can synthesize antibodies continuously, and is immortal-a feature of cancerous cell. The cell can be tested for different antibodies and selected for elaboration of a specific antibody. Such monoclonal antibodies can be used for diagnosis, therapy and prevention.

In diagnosis, monoclonal antibodies are used in blood typing, pregnancy test, presence of pathogens such an viruses and bacteria. For therapeutic use, monoclonal antibodies are so designed that they will neutralize the effect by one defined antigen. Sometimes, they are also designed by genetic manipulations to carry cytotoxic substances to target cells such an Cancer cell . Monoclonal antibodies that inhibit male gametes of malarial parasite and merozoite infested RBC has been developed, and a malarial vaccine is in the process of development.

2. DNA Probes : DNA probes are short segments of DNA that recognise complementary sequences in DNA and thus allows identification of specific DNA-sequences. Such DNA-probes are generally labelled with radioactive 32p though other labels may be used. In recent times, DNA probes have been devised that donot

use labelled radioactive substances but depend on specific chemical reactions. DNA probe against specific parasite can hybridise with the similar DNA sequences and allow its identification. Identification of the causative organisms by conventional methods require cultivation of stool samples on a variety of different media in a variety of different ways. Using DNA probes, such identification can be easily accomplished using stool or blood samples.

Such DNA probes have been elaborated for *Leishmania* causing Kalaazar. *Trypanosoma* causing sleeping sickness, *plasmodium* causing malaria, *Schistosoma* causing schistosomiasis, *Wuchereria* causing elephantiasis, *Taenia* causing taeniasis etc. By application of DNA-probes and other techniques a major disorder of haemoglobin, thalassaemia. in the cypriot community of Britain has been sufficiently brought down. There are some advantages of DNA-probes. No culture of pathogen is required if it exist in sufficient quantity. However, if its number is less, polymerase chain reaction (PCR) can be employed to enhance DNA level. DNA-probes can be used to test Pathogens which are difficult to culture such as viruses.

3. Gene-therapy : The process has been separately described elsewhere. Though the procedure promises cure of many genetic diseases in future, currently it is used in introduction of functional genes in individuals who are characterized by non-functioning of some of their genes resulting in deficiency of gene-products eg. ADA-deficiency.

4. Hormones And Proteins : In recent times, recombinant DNA-technique has been used for elaboration of many hormones and proteins which were earlier obtained by sacrificing great number of animals such as cattles and pigs. Among hormones, important are human growth hormones and Insulin.

Insulin or Growth hormone producing genes of humans can be introduced in bacteria using plasmid vectors. Genetically altered bacteria produce copious of such substances. Similarly, interferon, which is used in treatment against some tumour viruses, were previously sold at the rate of 16 million U.S dollars per 50 mg, costing a patient 150 dollars per day. With the genetically engineered interferon, this cost will come down to one dollar per day. The genetically engineered insulin is being marketed by trade name Humulin and GH as trade names prototropin (USA) and somatonorm (UK) under license from Genentech (USA).

In addition, several other proteins for therapy are also being produced. Factor VIII is important for blood-clotting. Persons suffering from haemophilia lack this substance hence such patients used to receive transfusion of VIII. Factor VIII is now being commercially produced by genetically altered bacteria.

Urokinase is a thrombolytic substance which dissolves blot clots formed in the vessels, causing heart attacks and paralytic attacks. Commercial production of the enzyme through genetic engineering has substantially cut down the price of this drug.

Somatostatin or growth hormone inhibiting substance (GIH) is used to treat excess growth. Conventionally it is obtained by brain of sheep or goats. Somatostatin is now being produced by genetically altered bacteria.

Below is presented a table enlisting important proteins and hormones being produced by recombinant DNA technique-

Table: Proteins and hormones produced by recombinant DNA technique

Protein and hormone	Disease
Insulin	Diabetes mellitus
Growth Hormone	Dwarfism due to GH-deficiency
Factor VIII	Haemophilia A
Factor IX	Haemophilia B
Interferon	Infections, Cancer
Somatostatin	Excess growth
Urokinase	Dissolution of blood clot

5. Synthetic Vaccines : conventional vaccines are inactivated germs or their antigens. Use of such germs or separation of their antigens sometimes has the risk of contamination. Synthetic vaccines have been produced in three different ways using biotechnology-

a. **Separation** of a pure antigen using monoclonal antibody and then using it as vaccine.

b. **Synthesis** of a vaccine using a cloned gene.

c. **Synthesis** of peptides to be used as vaccine.

The first method has been used in separation of antigens that elicit interferon synthesis. When such antigens are injected, there occurs synthesis of interferon.

In the second method, genes for certain antigens are separated from their causative organisms and transferred to bacteria. Bacteria produces such antigens in large quantities which are used as vaccines. Hepatitis B virus antigens has been commercially produced and used in many countries. Gene of malarial parasite encoding for circumsporozoite (CS) protein has been obtained. It is used for synthesis of CS protein, which is used as vaccine. The third method of vaccine production consists of synthesis of peptides that include antigenic regions. SPF-66, malaria vaccine elaborated by Patarroya (1987) is a synthetic peptide.

Similarly, foot and mouth disease virus antigens and feline leukaemia virus antigens have been synthesized.

Using the three approaches against many diseases such as Rabies virus, foot and mouth disease virus, *Salmonella typhimurium* causing typhoid, *Vibrio Cholerae* causing cholera, hepatitis B-virus causing hepatitis Plasmodium causing malaria, Feline leukaemia virus causing cancer, Taenia causing Cysticercosin either have been synthesized or are in various stages of production.

In recent times, vaccines are being elaborated for fertility control. Three types of fertility vaccines are being developed in India simultaneously. National Institute of Immunology has developed vaccines that elicits antibodies against HCG (Human Chorionic Gonadotrophin)- a pregnancy hormone secreted by placenta. A group of scientist at Indian Institute of science (IISc), Bangalore are developing vaccine that elicits antibodies against FSH and another group of scientist at the IISc are developing vaccines that elicits antibodies against vitamin carrier proteins.

6. Transgenic Animals : Recombinant DNA technique, no doubt, is being increasingly used in the diverse areas of diagnosis, therapy and prevention of genetic and non-genetic diseases. In addition, such techniques have also resulted in production of many transgenic animals such as fishes, pigs, cattles etc. which are known for their improved quality of proteins, thus ensuring enhanced supply of such substances which are important from human health point of view.

FORENSIC ANTHROPOLOGY

Forensic anthropology, as an applied discipline to physical anthropology, was recognised way back in 1972 and role of physical anthropologist in forensic science was defined by CC show (1973) as "a person with specialised knowledge of human sexual, racial, age and individual variations to the problem of medical jurisprudence". Forensic anthropology, thus, employs every means to identify a person through the anthropologically significant marks or remains of his or her body, however a trivial one.

Aim And Scope : The aim and scope for such identifications can arise in various situations. For example, it would be required to establish identify of a person at some crime situation; or identify a person in disputed parentage; or identity of persons at the site of accidents ; or identify persons as a follow up measure in immigration laws.

Areas Of Operation : There are three or four areas in which a forensic anthropologist can operate -

(i) He can either study the finger prints

(ii) or he can study the skeletal remains left at the site,

(iii) or he can study the DNA left at the site even in a trivial proportion such as in saliva, semen, blood or scratches of skin tissues.

1. Study of Fingerprints : According to Nath (1989) forensic anthropologists are capable of playing a crucial role in such identification. Anterior surface of our fingers bear unique ridges so that they leave a unique pattern of such friction surfaces when they come in contact of some surface. Sometimes, such finger prints are visible and can be directly photographed for further studies. Sometimes, plastic prints, such as those on plastic or waxy substance, can also be photographed by differential exposure to light. Most difficult to be photographed are the latent prints which are not visible to the naked eye. Such prints are formed because of differential distribution of sweat over our palm which leave an impression over the surface. Such prints can be formed on smooth surfaces such as door-handle, or rough surfaces such as textiles and fruit pealings (Nath 1984) such latent fingerprints can be made visible by sprinkling fine black or gray powder. The moisture in the finger print shall adhere the powder and make it visible. Alternatively, any of the following chemicals can be used to develop the latent prints: bromine, iodine fumes,

silver nitrate, osmic acid, Tannic acid etc. Since sweat contain, besides water, a few chemical substances such as Na, K, Ca, lactic acid, fatty acid, amino acid, glucose etc. chemical used in developing latent finger prints react with such chemicals to make finger print apparent. Once a finger print is obtained, next comes the identification of the ridge-pattern. There may be 75-150 ridge characteristics on which ground one is required to look for the variations. A few of such characteristics are ridge ending, fork, lake formation, break, return angle formation, trifurcation, bifurcation etc. All India forensic science congress (1973) has ruled that a minimum of eight characteristic patterns of ridges is essential to establish an identity.

Finger print studies can be helpful, besides locating suspect at the crime situation, in identification of deceased person, person suffering from amnesia, for licensing procedures in automobiles, fire arms, in impersonation cases etc.

2. Identification Through Skeleton And Tooth : First of all, it is necessary to establish whether bones are related to human being, which can be easily done on the basis of comparative anatomy. By matching the bones with each other, and in certain cases if bones are fresh and uncontaminated, blood group typing may establish the number of persons represented at the site of accident. Next important step is the identification of sex of the persons. If all teeth have not erupted and basisphenoid suture at the base of skull has not fused, the skull belongs to a sub-adult and sex identification in such cases cannot can be performed. Skull of females tend to be smaller, smooth, gracile, small to medium, with lesser developed supra orbital ridges, mastoid process, occipital torus, cheeck bones, mandibles, palate, teeth, foramen magnum and occipital condyles. Frontal and parietal eminences are, however, prominent and projecting, with larger orbits that have sharp margins. In the post cranial skeleton, pelvis is the most important and sub-public angle and greater sciatic notch can differentiate between sexes.

Determination of age of the bones is also important which is achieved by either teeth or bone. In bones, important criteria are unification of ossification centres, cranial suture closure and age-related pathological changes in the bones and joints. Age wise, there are definite identification points -

a. Infants show an ossification centre at the lower end of humerus.

b. Children show unification of two bones of hip region (pelvis) - pubis and ischium

c. Adolescents show fusion of coracoid process with scapula, olecranon with utra, triradiate cartilage with acetabulum

d. Adults show fusion of inner ends of clavicle bones, articular facets of ribs, all epiphyses of wrist and knee, elbow and shoulders, the sacral vertebrae with each other. The fusion of such epiphyses with their respective shafts is good indication that bones belong to an adult person.

e. Mature persons, around 40, show fusion of xiphoid process with sternum

f. Senescent persons, around 60, show fusion of manubrium with sternum. The laryngeal and costal cartilages ossify around this age.

In addition, two skeletal elements reveal age-changes from birth to death. These are Pubic symphysis that connects two sides of pubes, and bones of hand. Public symphysis, however, shows some alterations in females during pregnancy which can be identified only by experts. Among hand bones, the entire wrist bones are cartilaginous at the time of birth. Gradually, through the years, different epiphyses are ossified, with the ossifications progressing in females in advance to those of males.

Determination of age by tooth is based on five features - attrition (wearing down of occlusal surfaces due to mastication) Periodontosis (loosening of the gums), secondary dentine (formed in the pulp cavity), Cementum apposition (apposition of cementum at and around the tooth) and Root transparency (transparency of the tooth as revealed in section). Age of the tooth is calculated by assigning numerical values (0,1,2,3,4 etc.) to the degree of changes to each of the five features ($A_n + P_n + S_n + C_n + RT_n$) and added to obtain point value for the age. As age increases, so the point value.

3. DNA Fingerprinting : There are instances when one has to settle relationship between individuals, and also when there is no skeletal remain or finger print at the site of crime to locate the probable culprit but only traces of blood, hair root, skin fragment in the nail of deceased, semen etc. In such conditions DNA fingerprinting has been found to be very useful.

As human beings, we all share the similar genes. But such genes constitute only 5% of our total DNA. Genetics has

established that we all may be similar in 5% of DNA that functions as genes ; in rest of 95% of DNA we all vary much. This 95% DNA, which is apparently functionless, shows unique arrangement of DNA bases in the sense that some bases are repeated most often : there may be short repeats of 9-40 base pairs; intermediate repeats of 200-300 base pairs, or even long repeats of above 1000 base pairs. In such repetitive DNA, the sequence of bases vary, but often it tend to be G-C rich.

One such short repetitive sequence of DNA was discovered in DNA during study of B-globin gene, located in its flanking region : several such locations are now known. These short segment of DNA, called minisatellites, have repetition of such short sequence thousands of times. Such minisatellites have been found to be hypervariable i.e they differ greatly between unrelated individuals. This polymorphism is due to the variation in the number of repeats (n) arising from the loss or gain of the repeat sequences through mutations. Consequently, the alternative name for such loci is variable number Tandem Repeat (VNTR). Many repeated sequences have evolved from one or more common core ancestral sequence. Thus each hypervariable locus has some sequence similarity with many other loci. This can be demonstrated by using any such locus as a probe for detecting any sequence with sufficient sequence similarity to permit hybridization (Jeffreys et.al 1985a). The multi - locus probes described by Jeffreys and colleagues were derived from an intron of the myoglobin gene and shown subsequently to hybridize to other autosomal genes. Other suitable probes include the insulin, α-globin (Fowler et.al 1988). Since unrelated persons contain different number of such repeats, DNA fragments generated in DNA of two persons will be of unequal length. This can be separated by gel electrophoresis. The two DNA will give completely different patterns because of differences in the number of such repeats. On the contrary, if individuals are related, DNA profiles of such persons will resemble closely, the degree of resemblance of DNA patterns depending upon their closeness in relations. Such similarities and differences in the DNA patterns is determined by southern blotting technique. In Southern blotting technique, the pattern obtained on gel after electrophoresis is blotted on a filter paper and this filter paper is used in hybridization experiments with DNA probes. Records of DNA fingerprints of identified criminals may be preserved for identification. DNA-Profiling has been used in following areas :

1. Except identical twins, DNA profiles of two persons are

never the same. This fact is taken advantage of in forensic science when it is often necessary to try to match a blood or semen stain with a sample from a particular suspect.

The value of such a technique has been greatly enhanced by polymerase chain reaction (PCR) in which small quantity of DNA can be produced in thousands of copies under suitable enzymatic conditions.

The first criminal court case to use DNA fingerprinting evidence was in Bristol, UK, in 1987. In this case DNA provided the link between a burglary and a rape. The following year, DNA fingerprinting evidence was used in the USA. DNA evidence is now widely used in Western countries especially in UK and USA. It is worth noting that DNA evidence has also been used to prove innocence as well as guilt. Indeed, it is easier to prove innocence that guilt as shown by the recent bitter debate in the USA over interpretation of data (Chakraborty & Kidd 1991, Lewontin & Hartl 1991, Roberts 1991,1992). Proponents of DNA fingerprinting claim that the probability of two DNA samples matching by chance is very low about one in a million ($\frac{1}{1000000}$ or 10^{-6}). Since the issue is very much debated, an example will be cited in the case of Andrew Deen who was convicted of rape in 1990 in Oxford. David Pringle (New Scientist Jan 1994) has criticized the manner in which a DNA fingerprint is considered as an evidence against a crime. It was pointed out that Forensic experts answer the question what is the probability that the defendant's DNA profile matches that of the crime sample, assuming that the defendant is innocent ? For the jury, it must try to answer a different question : What is the probability that the defendant is innocent, assuming that the DNA profile of the defendant and the crime sample match ? Both the question outwardly look similar but lead to completely different answers. He stressed upon odds of innocence which may lead to different conclusions. The odds of innocence are the ratio of the probability of innocence to the probability of guilt.

Citing an example, he explained that if a crime is committed by an unidentified youth in Oxford, all the 30,000 youth could be possible perpetrators. Hence this implies prior odds of 30,000 to 1 in favour of the defendant's innocence. If the probability of a random DNA match with a suspect were 1 in a million, then the Posterior adds of his innocence would be $30{,}000 \times \frac{1}{1000000}$ 3391 it is this figure 33:1 which should be considered by the Jury

and not the figure of 1 in a million.

2. Another use of DNA profiling is to resolve cases of disputed parenthood. If a child's DNA fingerprint does not resemble with its presumed father, some other person may be involved. This has been useful in immigration cases. DNA fingerprinting to resolve immigration case was applied in Britain in 1984 when a Ghanian boy was refused entry in Britain by immigration officials who were not satisfied that the woman claiming him as her son was his mother. Analysis of serum proteins and erythrocyte antigens and enzymes showed that the alleged mother and son were related but could not determine whether the woman was the boy's mother or aunt. The father was not available for analysis nor was the mother certain of the boy's paternity. DNA fingerprints from blood samples taken from the mother and three children who were undisputedly hers as well as the alleged son were prepared by Southern blot hybridization to two of the mini-satellite probes. The pattern in the child's and the women's DNA finger prints were sufficiently similar for the boy to be allowed residence in Britain.

3. Sometimes it becomes necessary to identify a dead person on the basis of DNA left in his or her mortal remains. In such cases, the DNA fingerprints of deceased is obtained and matched with supposed relatives - mother, father, sister and other close relatives. A greater similarity in the DNA indicates relatedness. In such identification, even mitochondrial DNA can be used. DNA was used to confirm that skeletons found in Ekaterinburg, Russia, were the remains of the last Tsar and his family (Gill et al. 1994).

The DNA fingerprinting for such an analysis has been taken recourse to in our country also. In the ill-famed Naina Sahni Tandoor case, (1995) the body of a woman, supposed to be Naina Sahni of Delhi, was almost completely burnt to ashes. To establish her identity, DNA fragments from her remaining bones were extracted and matched with those of her parents. Sufficient similarities were found in DNA profiles of the sample recovered and their supposed parents. Thus her identity was established.

Mini satellite alleles vary not only in the number of copies of the repeat but also in the sequence of the repeat. That is, along any one individual mini-satellite the individual repeats may have different sequences. With one particular hypervariable locus, DIS8, two classes of repeat unit have been identified that differ by a single base substitution which creates or destroys a HaeIII

restriction site. Jeffreys et.al. (1991) have developed a method for displaying the sequence pattern of these two repeat units along mini satellite alleles. This produces DNA profiles which can be digitized and stored in computer databases for forensic applications. UK police has been using such databases crime prevention and detection since 1994 and a bill for the same has been cleared in USA for its application from 1995.

In the recent years, use of single locus probe has also been practised. In such cases, DNA fragments are separated by size and four bands are identified and probed for a allele at that locus. This allows for a simple and quick method.

Future Prospect : Science of Forensic anthropology has not been given its due place either in the university curriculum or in the fields of its practical applications. The latter may be an outcome of the former situation. There are hardly a dozen of universities that impart teaching of forensic anthropology. Moreover, even students passing out from such centres do not have facilities of adequate training programmes. A few forensic laboratories that exist in our country do not have any programme to train such passouts. Thus there exists a gap between physical anthropologists passing out from universities and their actual involvement in the forensic acts.

In addition, there exists a wide gap between theoretical education given to the students of forensic anthropology and existent conditions of most of our forensic laboratories. Strengthening of teaching at the graduate and postgraduate levels of the forensic anthropology will be of no advantage if conditions of our laboratories do not improve. To achieve an all round progress of forensic anthropology, things must improve on both the fronts- theoretical education at Universities as well as its practical utility in the forensic laboratories. Improving the education without improvement in the laboratories will be exercise in futile, and improvements in the laboratories cannot even conceived of without improving the education. Let us hope and pray that our this child, barely over 20 years old, may gain some vitality and stimulus for development in coming years.

PARENTAGE DETERMINATION

In the recent times there has been increased instances of theft/exchanges of newborns in maternity hospitals. This leads to claims and counterclaims by real and alleged parents, the cases ultimately coming in the purview of courts of justice. There occur instance of rape in which the victim becomes pregnant. In such cases, justice hinges on the identification of the father of the child. There are also cases of alleged illicit and extra-marital relationship of wives on the basis of which husbands seek divorce. In such case, parenity of the child born of the wives is doubted, calling for parentage determination. In short, parentage determination occur for maternity and parenity determination and delivery of judgment by a court of law hinges largely on the outcome of parentage determination tests.

Methods of determination-exclusion and inclusion

It should be cleared at the outset that most of the methods applied for parentage determination exclude parentage— meaning that it says that Mr. & Mrs. so and so cannot be the parents of the child in question. It doesnot says that Mr. & Mrs so and so are the parents of the child in question. However, it should be mentioned that some european court of law such as Norway, Germany etc consider positive inclusion parentage determination. There are two bases of such considerations— Presence of rare alleles in alleged father, and, similarity of many morphological, morphometric and dermatoglyphic characters. A Norwegian court of law considered presence of brachydactyly, a rare allele, as evidence of similarity in alleged father and son. Similarly, a German court considered presence of a rare rh-allele as evidence of similarity. If such alleles are absent in mother the relationship between alleged father and the child becomes all the more strong. But such conventions are fraught with dangers— a rare allele may be present in the near relatives of accused who may be penalized for no fault of his Similarly, morphological, morphometric and dermatoglyphic characters are determined by polygenes and

polygenic inheritance is much variable.

Another point that should be kept in mind is that every child inherits only 50% characteristics of its parents hence it can differ from its parent in many of the characters. Hence, it is necessary to evaluate the child on as many criteria as possible and final co-efficient of probability should be calculated on the basis of sum of probability of each characteristic.

Methods of Parental Determination

(A) Morphological analysis.

(B) Dermatoghyphic analysis

(C) Genetical analysis—

(1) Serological analysis- ABO, MNS, Rh - system

(2) Biochemical analysis

(3) Immunological analysis

(4) Non-Serological analysis

(5) Mendelian structures

(6) Chromosomal analysis

(7) DNA- Fingerprinting

While evaluating a child on genetical analysis, probability of inheritance of each characteristic is noted and added to give value of X. The probability of inheritance of such characteristics in general population (Y) is also noted and likelihood of paternity (LOP) is calculated by the formula— $\text{Lop} = \frac{X}{X+Y}$

(A) Morphological analysis : This includes morphoscopic and morphometric characteristics- mosphoscopic characters are those which can be viewed only whereas morphometric characters can be measured. Morphoscopic characters include hair, eye, nose, lips, chin, ear etc which has variability in its shape, size and organisation. Morphometric characters include Head-index, face-index, nasal-index etc which also vary. (Readers are advised to go through "morphological criteria of Races") since such characters are determined by alleles, their similarity indicate common origin.

(B) Dermatolglyphic analysis: Dermatglyphic prints can be obtained from palm, fingers, soles and big toe. It is hereditary, doesnot change with time and not influenced by environment. it shows racial variations hence also used in determination of races (see "racial criteria") The characteristics of dermatoglyphics which are significant for parental determination are Palmar ridge Counts- a-b count, b-c count, e-d count and a-d count, Main-line formula and Main-lime index, Finger ridge count and Finger-Pattern.

(C) Genetical Analysis : Under this category is included serological and other analyses.

1. Serological analysis : Under this caterogy are included various blood group-systems which are multiple allelic system in many cases. The different blood group systems which are used in paternity determination is as follows—

a) ABO System : There are three alleles in this system - I^A I^B and I^O out of which a person can possess two alleles. Below is given types of blood group in ABO System and its allelic determinants—

Blood Group	Allelic determinants
A	$I^A I^A$, $I^A I^O$
B	$I^B I^B$, $I^B I^O$
AB	$I^A I^B$
O	$I^O I^O$

It is clear that group A can be homozygous-A or heterozygous-A. Similarly, grooup B can be homozygous-B or heterozygous-B. during fertilization, each parent contributes one allele to the progeny.Below is given parental blood group, its genotype and possible blood groups in the progency—

Parental blood group	Possible parental genotype	Possible children
A x A	$I^A I^A$ x $I^A I^A$	A
	$I^A I^A$ x $I^A I^O$	A
	$I^A I^O$ x $I^A I^O$	A & O
B x B	$I^B I^B$ x $I^B I^B$	B

	$I^B I^B$ x $I^B I^O$	B
	$I^B I^O$ x $I^B I^O$	B & O
A X B	$I^A I^A$ x $I^B I^B$	AB
	$I^A I^A$ x $I^B I^O$	AB & A
	$I^A I^O$ x $I^B I^O$	A, B, AB & O
	$I^A I^O$ x $I^B I^B$	AB & B
A x AB	$I^A I^A$ x $I^A I^B$	A & AB
	$I^A I^O$ x $I^A I^B$	A, B, & AB
B x AB	$I^B I^B$ x $I^A I^B$	B & AB
	$I^B I^O$ x $I^A I^B$	A, B, & AB
A x O	$I^A I^A$ x $I^O I^O$	A
	$I^A I^O$ x $I^O I^O$	A & O
B x O	$I^B I^B$ x $I^O I^O$	B
	$I^B I^O$ x $I^O I^O$	B & O
AB x O	$I^A I^B$ x $I^O I^O$	A, B
O x O	$I^O I^O$ x $I^O I^O$	O
AB x AB	$I^A I^B$ x $I^A I^B$	A, B, AB

It is clear from above chart that progeny blood group depend on parental genotype and not on parental group (Phenotype). For example, as shown in case of third parental mating, A x B, if parents are heterozygous A and B, all the four blood group A, B, AB & O is possible. Thus, we mainly depend on exclusion— There cannot be B and AB children from A x A matings; there cannot be A and AB children from B x B matings; there cannot be B and AB children from A x O matings; there cannot be 'A and AB children from B x O matings; there cannot be O children from AB x A, AB x B and AB x AB matings; there cannot be AB children from A x A B x B, A xO, B x O, AB x O matings, and lastly, there cannot be A, B and AB children from O x O matings.

Parental Groups	Impossible Progeny Groups
A x A	B, AB
B x B	A, AB
A x O	B, AB
B x O	A, AB
AB x A, AB x B, AB x AB	O
A x A, B x B, A x O, B x O, AB x O	AB
O x O	A, B, AB

Thus, presence of B or AB child from A x A mating type is excluded and confirm that the child does not belong to the couple. Similarly presence of O child from AB x AB mating type is excluded and confirm that the child does not belong to the couple.

There are, however, situations where a child's blood group is possible with both the alleged father's blood group. If disputed child belongs to group A and mother is O and the two alleged fathers are A and AB, no alleged father can be excluded and hence we have to take recourse to inheritance of other blood groups.

(b) Rh-System : This antigen was considered to be determined by one pair of allele D/d, and the genotype D/D and D/d resulting into Rh^+ and d/d into Rh^- type. Later on, Fisher and Wiener suggested involvement of many alleles, making it also a multiple-allelic system. According to Fisher, there are 6 alleles in the system— C, D, E, c, d and e, with three alleles remaining together forming eight allelic complexes— **CDE**, **CDe**, **cDE**, **cDe**, **Cde**, **CdE**, **cdE**, and **cde**. In the Weiner system. these are also referred to as R_z, R_1, R_2, R_0, R′, Ry, R″ and r— respectively. There can be 36 possible genotypes such as CDE/CDE, CDE/CDe, CDE/cDE etc. A cdE/Cde parent cannot have a cDe/CDe progeny.

(c) MNSs-System : There are two alleles, M and N and three genotype MM, MN, NN in MN-System. Similarly another system Ss- is closely linked to MN-system. There are two alleles in Ss-system and three genotype- SS, Ss and ss and together the two systems form 9 possible genotype— MSMS, MSNS, NSNS,

MSMs, MSNs, NSNs, MsMs, MsNs, NsNs. A NSNs child cannot be obtained from MSMS x MsMs parents. Large number of such exclusion progeny types can be deduced and knowledge thus obtained can be utilized in parental determination.

In addition to these common blood antigens, there are several other types of blood antigens which can be used for parenal determination. These blood antigens are rare. These blood antigens include Diego (Dia, Dib), Kidd (JK^a, JK^b) Lewis (Le, le), Duffy (Fy^a, Fy^b), Lutheran (Lu^a, Lu^b) etc. If, for example, parental genotype is JK^a/KJ^a x JK^a/JK^a, JK^b child can be born not out of this mating.

(2) Biochemical Analysis : This includes analysis of wide variety or protein and enzymatic systems present in our body. Since enzymes are proteins, they are primary derivative of genes and inherited mostly in Mendelian fashion from parents. The various protein and enzymes that are used in parental determination is as follows—

Enzymes or Proteins	Phenotype	Genotype
Haemoglobin	Hb-A, Hb-S,	Hb-A/H-b-A, Hb-A/Hb-S
	Hb-C, Hb-D	Hb-S/Hb-S, Hb-C/Hb-C
	Hb-E etc.	Hb-D/Hb-D etc.
Haptoglobin	1-1, 2-2, 2-1	Hp^1/Hp^1, Hp^2/Hp^2, Hp^2/Hp^1
GC (Group Specific) component	Ge^1, Ge^2, Ge^{2-1}	Ge^{1-1}, Ge^{2-2}, Ge^{2-1}
Adenylate Kinase	AK^1, AK^2	AK^{1-1}, AK^{2-2}, AK^{1-2}
Caeruloplasmin	CP^A CP^B	AA, BB, AB
Adenosine Deaminase (ADA)	ADA-1, ADA-2	ADA^{1-1}, ADA^{2-2}, ADA^{1-2}

Such analyses can be effectively used in parental determination e.g. in case eg. Adenylate kinase, 1-1 and 1-1 parental types can not give birth to 2-1 child.

(3) Immunological analysis : This includes variability in the constant region of immunoglobulins (Haplotype), mostly IgG one system described in IgG is Gm-System which has several variants such as GM(1)+, GM(1)-. GM(1)+ parental types cannot give birth to GM(1)- type progeny.

Another area of immunological analysis used for parental determination is the Histocompatibility (HL-A) system. As discussed elswhere, it is responsible for tssue antigen and responsible for graft rejection. There are 5 closely linked loci- A, B, C, D and Dr on short arm of chromosome 6. There are 19, 27, 7, 11 and 7 alleles on each A, B, C, D, and Dr. loci, generating enormons number of haplotypes. Every individual, though unique in possession of HL-A haplotype, does inherit the type from its parent in mendelian fashion. Alleles present in child but absent in alleged parents indicate parental exclusion.

(4) Non-Serological Criteria: This includes roling ability and tasting ability. Non-roller and Non-taster (r/r and t/t) parents can never give birth to roller and taster children. Similarly, non-secretor (se/se) parents cannot give birth to secretor children. (secretors secrete blood group antigen, A, B, H in saliva)

(5) Mendelian Character Inheritance : There are some characteristics which are determined by a pair of alleles such as anonychia, chin fissure, Mid-digital hair, Darwin's tubercle, achondroplasia etc. If none of the parents have Darwin's tubercle, its possession by the child exclude such parentage because this and other characteristics listed above are controlled by atosomal dominant gnee.

Genetical methods, alone or along with morphological and dermatoghyphics, have been variously utilized by Indian Courts of justice to solve problem of parental determination. The leading institute in India specialised in the process is Forensic science Laboratory, Madhuban, Haryana. Its assistant Director, K.P.S. Kushwaha (1992)has solved many cases of parental determination and thus helped courts of law to arrive at their judgments. He has used serological and non-serological genetic analyses to solve problems. While investigating a case of alleged illicit child born to his wife, as claimed by her husband, Kushwaha (1992) performed

a variety of genetical analyses to arrive at conclusion. A brief account of his results is as follows:

Genetical analyses	Mother	Father	Son	Parentage
ABO system	A	B	B	Possible
Rh-system	CcDe	CcDe	CcDe	Possible
MN-system	MNSr	MMSr	MNss	Possible
ADA	1-1	2-1	1-1	Possible
Adenylate Kinase	1-1	2-1	1-1	Possible
Haptoglobin	2-2	2-2	2-2	Possible
GC component	2-1	1-1	2-1	Possible
Secretor Status	Se/Se	Se/Se	Se/Se	Possible

Based on such informations, the likelihood of paternity was calculated to be over 93%, indicating strong probability that his social father is also biological father of the alleged illicit child.

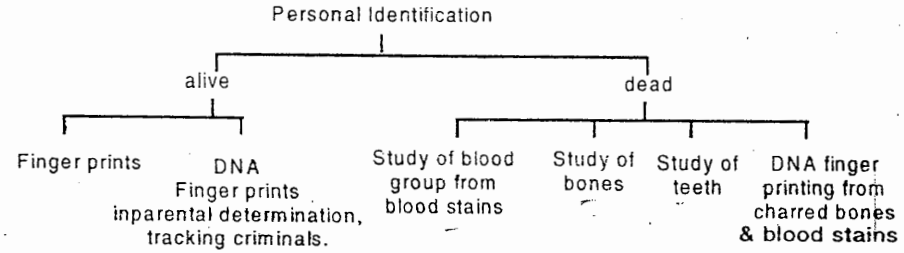
(6) Chromosomal Analysis : Chromosomes often undergo various structural and numerical variations and presence/absence of such chromosomal variations are good indicator of paternity. of special interest in such cases are satellite chromosomes and Y which frequently undergo structural variations.

(7) DNA Fingerprinting : It has been discussed in detail under Forensic anthropology. The minisatellite and its distribution-pattern (VNTR) in on individual's DNA-profile is made known by the process of (i) DNA-Cleavage (ii) gel-electrophoresis (iii) Southern blotting (iv) DNA-Probing and (v) Radio autography. The pattern is matched with the patterns obtained from alleged parents. Since minisatellites show mendelian inheritance, a child posseses one copy of maternal and one copy of paternal minisatellite and the child's DNA-pattern matches with both parent's pattern.

The process of DNA-fingerprinting has been utilised in the paternity determination in case of Deepa Murmu in the State of Jharkhand (2001). Deepa Murmu charged a government official of her rape and held the person as father of her child. DNA-prints of all concerned were examined at centre of cell and Molecular Biology (CCMB), Hyderabad and found to be true.

PERSONAL IDENTIFICATION

There are instances when it is required to identify a person-either alive or dead. If alive, he/she may have left his/her finger prints. Dermatoghyphics in such cases become the basis of identification. If dead, he/she might have left some bodily remains and blood stains. Basis of identification in such cases become study of blood group from blood stains, study of bones and teeth and DNA finger printing from cells present in root-hair cells or bone marrow cells.



Personal identification from finger-prints & DNA-Finger Prints : This process is mostly followed to identify a criminal whose finger-print record is often registered with police. Criminal, if not wearing gloves, leave finger-prints at the site of crime. Visible print is directly photographed, plastic prints (on glass etc) photographed in differential light exposure, and, latent print is photographed after treating the objects with carbon powder. All India Forensic science congress has ruled that inorder to identify a person eight characteristics of fingerprint should match. Similarities many be in matter of palm or finger prints, loops, arches, breaks, bifurcations, trifurcations, fusions, lakes etc.

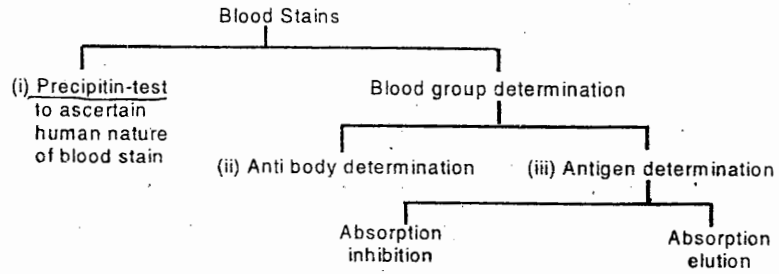
DNA fingerprints can be used to solve cases of parental determination related to parental disputes, immigration disputes and child born to a rape victim. In such cases identification of the child is crucial. During rape, semen stains may be left on the clothes of victim. Sperms from such stains are extracted and DNA fingerprinting performed to identify the perpetrator of the crime.

Criminals often leave traces of hair and skin in the nails of victims. Root hair cells from hair can be extracted and DNA-fingerprinting can be performed to identify the criminal if there is

record of DNA finger prints of criminal is registered with the police. The process of DNA fingerprinting is discussed in the chapter forensic anthropology.

II. Identification of dead persons: Materials belonging to a person that can be obtained from site of accident are blood stains, bones, teeth and cells in bone-marrow. Person can be identified on the basis of such materials.

(A) Identification from blood-stains: Blood-stained clothes are often recovered from site of accident. Firstly, it is made sure that blood belongs to human beings and, secondly, its group is ascertained so that it can be matched with the blood-group profile of missing person under investigation.



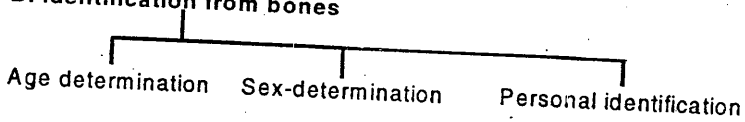
(i) Precipitin-test to ascertain human nature of blood is simple. Blood Stain is scratched, dissolved in normal saline and treated with human anti-sera. A ring develops between serum of blood stains and anti-sera added. This is **ring-test.** Alternatively, another technique, called **immunodiffusion**, is performed. Small pockets are created in agar gel and serum and anti-sera is put in the pockets. Substances diffuse in the gel and form antigen antibody complex where they meet. This is indicated by precipitate forming in between pockets of gel. Once human nature of blood is ascertained, next step comprises identification of blood group. It can be antibody determination or antigen determination. It follows the principle that blood group A has antigen-A and antibody anti-B; Blood group B has antigen-B and antibody anti-A; AB has both antigens and no antibody where as group O has no antigen and both antibodies— anti-A and anti-B.

(ii) Antibody determination: In antibody-determination, blood stains are taken on two slides and mixed with blood cellsof group and group B. It first slide belongs to group A, it will have

antibody anti-B and hence blood of group B will form precipitate. Opposite will happen to second slide. If precipitate forms on both slides, blood belongs to group O and if no precipitate forms blood belong to group AB. Thus, in antibody determination we use antigens present in blood cells.

(iii) Antigen-determination: Two samples of blood stains is reacted with antisera-A and antisera-B. Anti-sera is then recovered and its strength analysed. Strength of anti-sera, which has reacted, will fall down. If strength of antisera A has fallen, the group is A. This is process of **absorption-inhibition**. In alternative method of **absorption-elution**, anti-sera is used to form antigen-antibody complex and washed to remove unreacted antibodies from antigen-antibody complex and amount of attached antibody determined by fresh RBC. For example, if blood group on a slide belonged to group A, it will react with antibody anti-A and anti-A will remain on slide. It will complex with RBC with group A.

B. Identification from bones



Bones recovered from site of accident can be used for age and sex determination as well as personal identification. For the first two, readers are referred to chapter Forensic anthropology.

For personal identification, bones are used to find out height of a person so that it can be matched with recorded height of the individual. There are several processes but one which is used most often is the process of Duepertius and Handem. The index for the male and female is different hence this method is performed after ascertaining sex of the individual.

For males, index is as follows—

Length of the bone			Constants	
			Cm.	Inches
Femur	x	2.238	+ 69.089	27.200
tibia	x	2.392	+ 81.688	32.161
Humerus	x	2.970	+ 73.570	28.965
Radius	x	3.650	+ 80.405	31.655

For females, index is as follows—

Femur	x	2.317	+ 61.412	24.178
Tibia	x	2.533	+ 72.572	28.572
Humerus	x	3.144	+ 64.977	25.581
Radius	x	4.876	+ 73.502	28.938

C. Identification from Teeth: Teeth is the hardest substance in body and resist degradation to the maximum extent. Accidents, however severe, is sure to leave teeth intact. Hence forensic odontology serves to identify persons where other measures fail.

Forensic odontology can be used to calculate age of the person. There are two methods- first is the examining extent of wear happened to teeth. The points to be noted is accretion, secondary dentine, periodontosis, cementum opposition and root-transparency (discussed in Forensic anthropology). Second is observing milk and permanent teeth that errupt at constant time. The time for dental erruption is as follows—

For milk-teeth—	Lower incisors	—	5-12	months
	Upper incisors	—	6-14	months
	First premolar	—	13-20	months
	Canine	—	13-30	months
	Second pre molar	—	18-38	months
For Permanent teeth—				
	Lower incisors	—	6	yrs.
	Upper incisors	—	8	yrs.
	First premolar	—	9	yrs.
Second premolar		—	10	yrs.
	Canine	—	11-12	yrs.
	First & 2nd molar	—	12-13	yrs.
	Third molar	—	17-25	yrs.

If all permanent teeth except IIIrd molar has errupted, a person is never less than about 13 years of age.

Dental profile of a person is also important for personal. Identification Partially broken teeth, overlapped teeth, cavities

filled with gold etc form important landmarks for identification. In our country, Dr. Arun Ganguli, the leading Forensic odontologist, Kolkata has solved many cases related to forensic odontology. A few classical cases of this area can be mentioned. **Hitler and Iva** were supposed to have committed self-immolation and only their charred bones and teeth were recovered from site of accident. It was finally confirmed in 1975, after forensic examination of the teeth, when details of teeth matched with dental profile of Hitler. The famous **Frankfurt Murder case** was solved on the basis of forensic odontology. A retired military personnel was charged with a case of rape and murder. His conviction in the case was almost final when the defence counsel struck a vital clue for the innocence of his client. The personnel had no canine since long. It was broken early in his life. It was mentioned in his identification certificate. There was cut mark on the cheek of the woman raped and murdered. The cut mark included impression of both canines. The judge agreed with the point.

(D) DNA- finger printing: Dead persons can be identified from bone-marrow cells present in charred bones. Identification of Naina Sahni on the basis of charred bones recovereed from Tandoor furnace is classical example.

The method can also be used to identify a person from blood stains found on the clothes or in the surrounding. In such cases, blood cells are separated and DNA is extracted from lymphocytes and DNA Finger printing is performed. Details of the process is mentioned in the chapter 'Forensic anthropology'.

KINANTHROPOMETRY (ANTHROPOMETRY OF SPORTS)

Definition and history : Kinanthropometry or anthropometry of sports evalutes physical structure of individuals in relation to gross motor functions. The field of kinanthropometry goes beyond the measurement of structure characteristics of the human being such as size, shape etc. and includes such aspects as maturation, nutrition and body composition too.

Though anthropometry has long association with sports, the term Kinanthropometry is relatively newer, having been used first in 1972 by Bill Ross. It was first included in Olympic scientific congress (OSC) at Quebec in 1976 prior to Montreal Olympic games in 1978. International council of sports science and physical Education (ICSSPE, UNESCO) founded an international working group on Kinanthropometry (IWGK) at Brasilia. This group has been driving force behind most initiatives for the development of Kinanthropometry.

Kinanthropometry And Nature - Nurture : Shukla et.al. (1992) have emphasized relative roles of heredity and environment in the final outcome of phenotype and has suggested a greater role for genetic endowment. Phenotypic variations is size, physique & body composition, metabolic powers and capacities, strength, speed and skill, Cardiovascular adaptations are related to outstanding performance of an athlet. Environment can shape positive genotype into a fit type by way of training though even this varies with age and individual. Kinanthropometry thus aims at selecting fit genotypes that are not hampered by extraneous factors of nutritional stress and infectitious diseases so that individuals attain their fullest potentialities.

Physique And Sports : A sport needs not only muscle strength but coordinated body movements. For different sports, co-ordinated body movements are required in different ways. Thus, individuals with a certain anthropometric characteristics are supposed to perform better than others. Anthropometric studies of individuals in such cases can help select players who can have better potentialities in a particular sports than others. This not only enhances quality of performance in a sport but also curtails or minimizes expenditure on individuals who because of their unfavourable anthropometric standards, are less fit for a particular sport.

For classification of physique, the system followed most often is that of MoreHouse and Rasch who classified physique on the basis of height-weight index.

Height Category	Weight Category	Suitable for Evetns
Tall	Heavy	Wrestling
	Medium	Boxing
	Light	Sprinting-jumping
Medium	Heavy	Throwing
	Medium	Long distance swiming
	Light	Games-Hockey, football
Short	Heavy	Weight-Lifting
	Medium	Gymnastic
	Light	Skating

Each category of the table can be justified

Skaters : Since they perform great balancing act hence they must be short to keep centre of gravity low. They have to be light because they have to show high activity level.

Gymnast : They have to be short because of balancing act. In addition, development of muscle is also required. Their fat-level is significantly lowered (Parizkova, 1962)

Sprinters, jumpers : They are tall persons with greater

lengths of their limbs in comparison to their trunk length. Greater the length of trunk more will be frictional force of the wind encountered during running. Also, a larger weight of trunk on the legs is sure to exhaust muscles of the leg sooner. Such aspects of body, hence, is not suitable for a runner. According to Shukla (1992) jumpers also have long lower extremities than upper one because a greater trunk volume proves a dragging force in jumping.

Weight-lifters : Tanner (1964) has studied anthropometric characteristics of weight-lifters. It has been found that in champion weight lifters the limb height is less than the trunk height. It is natural because taller individuals are at disadvantage because they have to lift the weight to a greater height and this would require greater strength to overcome the gravitational pull. Hence the stature is found to be small in champion weight lifters. Shukla et.al. (1990) have made anthropometric studies of weightlifters of India and have arrived to similar conclusions.

Throwers : On the basis of Indian Studies, Sharma and Shukla (1982 to 1989) and others have shown that throwers have indicated significantly higher values in all anthropometric measurements. They are taller and heavier, have longer upper and lower extremities, the amount of body fat is more and cover larger body surface areas in comparison to other sports persons.

Cricket, Hockey, Football, Tennis, Badminton Etc. : Some sports such as football, cricket , hockey, badminton etc. require more use of either fore-limb or hind limb or both. In case of foot ball, anthropometric characteristics of hind-limb such as femur versus tibial length, patellar height, metatarsal lengths, size of arches of the foot etc. have been found to be crucial. Similarly, plays such as cricket, hockey, tennis, badminton etc. involve more use of hands than feet and hence such anthropometric characteristics as humeral/radioulnar length, size of the metacarpals and phalanges etc. are crucial.

Swimmer : In swimming, persons are supposed to stay for quite some time daily in water and hence they are at great risk of catching cold. Most of the successful swimmers, particularly those of cold-waters, are found to have a uniform layer of subcutaneous fat which protects them from cold water. The fat layer however, has not been found excessive for it may act as dragging force.

Aerobic and Anaerobic Power : For persons who have to apply great force in sudden jerk such as weight-lifter must have high aerobic power whereas those persons who have to play games and sports for long duration such as long-distance runner must have high anaerobic power. In former, high lung-capacity is requred: in latter high level of blood-alkali is required.

Maturity-level : Sports persons should have even-maturity-neither fast maturer nor slow-maturer. It can be found out by ossification of their bone-joints which reveals their biological age which must match with their chronological age.

Genes and Anthropometry :

sports anthropometry has travelled a long way in short span of its history of less than fifty years. Initially, sports anthropometrists relied upon physique only. Later on, after discovery of latest diagnostic tools such as ultrasound, soft-xray, CT scanning etc it became possible to analyse deep seated muscle. And now, a new category of genes have been discovered which make athlets.

American journal of Human Genetics (2003) has reported a study conducted by Australian Institute of sports, Canberra. According to the study, there are definite genes for short distance running and long distance running. For short distance running, the gene responsible is Alpha Actinin- 3 (ACTN-3) and for long distance running, the gene responsible is Alpha Actinin-2 (ACTN-2), ACTN-3 gene synthesizes a protein which can combine with glucose and is released in between muscles which are contracting very fast in short distance runner. Glucose provides energy for fast contracting muscles. Also, there are two copies of ACTN-3 gene in short distance runners. Gene ACTN-2 in long distance runner synthesizes a protein which keeps level of lactic acid low in muscles.

Redesigning Of Sport Article

Anthropometric studies of sports involve another aspect too. Though there exist international sizes of the various sports articles, sometimes there is need to redesign such articles to suit anthropometric standards of certain indigenous ethnic groups. For example, the hockey-sticks of national standards donot suit juniors. Dr. Sachindra Narayan (1988) redesigned such sticks for the juniors of certain groups of chotanagpur (Bihar). With the redesigned hockey-sticks the chotanagpur boys became Indian National champion in 1995.

Another example of the sort comes from Sauria Pahariya of chotanagpur (Bihar). They are shifting cultivators, short-statured people expert in Archery. As they are short-statured, the National standards does not suit them hence they were unable to accept it as a sports. Dr. Narayan (1988) redesigned the archery for Sauria Pahariya and now they excel at this sport.

NUTRITION, MALNUTRITION AND ASSESSMENT OF MALNUTRITION

There are four classes of nutrients-protein, Carbohydrate, Fat & minerals and vitamins

1. Protein : It is made-up of aminoacids which are of 22 types. Some of it can be synthesized in our body where as others must be supplied in the diet. The former are called non-essential amino acids and the latter essential amino acids. *Essential amino acids include leucine, isoleucine, lysine,methionine, phenylalanine, threonine, tryptophan and valine.* Histidine is essential during infancy for sustaining the growth. Protiens help the child to grow as the constituent amino acids are necessary for the synthesis of tissues in the body; is essential for the formation of digestive juices, hormones, plasma proteins,enzymes, vitamins and haemoglobin etc., and act as powerful buffer substance to maintain acid base equilibrium in the body. It is also a source of energy for the body. Animal Proteins contain most amino-acid whereas plant-protein is deficient in some essential amino-acid. But animal flesh is high in fat content hence some flesh is added in vegetarian diet.

2. Carbohydrates : Carbohydrates furnish more than 50%of energy requirement in all the societies. These are cheap and readily obtained food and hence included in higher percentage in the diet of people belonging to the low economic strata. Both carbohydrates and fats serve as energy yielding substances hence are largely replaceable by one another. However a minimum amount of both must be included in the diet. Dietary deficiencies of carbohydrate leads to ketosis, a metabolic disorder in which certain toxic metabolites accumulate in our blood due-to excessive breakdown of fat. Excessive breakdown of proteins also occur and hence its repairing and building activity is impaired.

In adults, the daily in take of carbohydrate is commonly in the range of 300-500 gm (1200-2000 Kcal).

3. Fats (Lipids) : Fat is concentrated source of energy. A healthy European or American obtains 35 to 40 percent of his calories from fat. Diet of persons in the less affluent societies such as ours may provide less than 10 percent of Calories from fat. Triglyceride is the most important lipid. This is ester of three molecules of fatty acid and one molecule of glycerol. Compound lipids are esters of fatty acids. glycerol (or related compounds) and nitrogenous bases. Those containing phosphate groups are called phospholipids.

Some fatty acids such as Linoleic acid, Linolenic acid, arachidonic acid are essential fatty acids, not synthesized in our body hence we must take them in our diet. Its shortage causes skin-disorders.

Classes of malnutrition : There are two classes

A. Protein - Energy Malnutrition B. Micronutrient malnutrition

A. Protein - Energy malnutrition (PEM) - It is of three types :

1. Mild to moderate undernutrition : If the food deficit continues for a long period the child becomes slow and less energetic. Growth-lag in weight is pronounced. The child looses interest in environment and very much irritated. As the nurtient deficit exaggerate with onset of infection the child shows kwashiorkor or merasmus.

2. Marasmus : A marasmic child has deficiency of all nutrients . The body weight is less than 60 percent of the expected weight for the age. The fat in the adipose tissues is severely depleted because it is used up for providing energy. The contour of muscles is evident under the thin and wrinkled skin. Loose folds of skin are prominent over the inner side of thigh. The skin appears dry and inelastic and is prone to be infected. The hair is hypopigmented. The abdomen is distended due to wasting and hypotonia of abdominal wall muscles. Gaseous distension occurs due to bacterial fermentation of unsplit sugars in the colon. The mid arm circumference is reduced. Reduction of mid arm circumference is best indicator of protein energy malnutrition.

3. Kwashiorkor : Markedly retarded growth and edema are two essential features of Kwashiorkor. The edema starts in the lower extremities and later involves upper limbs and the face. Muscles of the upper limb are wasted but the lower extremities appear swollen. Kwashiorkor generally develops in the older child when, after the birth of next child, it is weaned. The child suffers mainly due to undernutrition of protein and a high proportion of carbohydrate in diet. With the onset of kwashiorkor the undernourished child becomes lethargic, listless and apathetic. He takes little interest in the environment and does not play with his toy. Appetite is impaired and it is difficult to feed him orally. The hair is thin, dry, brittle and devoid of their normal sheen. It becomes straight and hypopigmented. The length of the hair that grow during the period of nutritional deprivation appears reddish brown. During the phases of better nutrition, the growing part of the hair gets appropriately pigmented. This gives appearence of alternate bands of hypopigmented and normaliy pigmented hair. These children often suffer from recurrent episodes of diarrhea, respiratory and skin infections.

B. Micronutrient Deficiency

1. Sodium And Chloride : 2gm of NaCl is needed daily for osmotic balance and transport of substances across the

membrane. It is available in plenty.

2. Phosphate : 0.88gm of phosphate is needed per 70kg body weight .It is required in DNA and RNA, high energy substances, tooth and bones . It is available in plenty.

3. Iron : The daily intake of iron should not be less then 12mg which should be increased during pregnancy.

4. Calcium : Most natural food contain small amount of calcium. Milk, milk products and millet like 'Ragi' are rich sources of calcium. Infants require only 500 to 600 mg of calcium per day. An intake of 400 to 500 mg per day is adequate for the body needs from the age of 1to 10 years.Thereafter, during the pubertal spurt of growth, calcium requirement is higher, in the range of 600 to 700 mg per day. Adults require about 400to 500 mg of calcium per day.

5. Iodine : Iodine is present in the secretions of thyroid gland. Lack of iodine in the diet leads to increased secretion of protein from thyroid glands leading to endemic goiter. Sea foods and vegetables grown on iodine rich soil are good sources of iodine. Salt is being iodated. Adult persons require about 150 micrograms of iodine per day. Growing children, pregnant and lactating women need larger allowances of iodine.

6. Fluorine : Fluorine prevents dental caries. It acts probably by reducing the solubility of the enamel in acids produced by bacteria. Sea food and tea are good sources. Average range of safe and adequate fluorine in the diet is 1.5 to 4.0 mg of fluoride per day. Younger persons need a maximum of 0.25 mg per day to avoid mottling of teeth.

Excess of fluoride in the diet results in dental fluorosis which *presents as mottling of the teeth in regions where the drinking* water supply contains more than2 parts per million of fluoride.

7. Zinc : Zinc is a part of several enzyme system of the body e.g. carbonic anhydrase. A syndrome of growth failure, hypogonadism, anaemia and hepatomegaly due to zinc deficiency was described in West Asia. Animal foods such as meat and fish are rich sources of zinc. Intensive cultivation of soil in North India over hundreds of years has led to deficiency of zinc in its soil. The deficiency is reflected in the low levels of zinc in the food crops grown in this area. Adults and children need 22 and 10 mg of zinc daily respectively.

enlargement of liver

8. Magnesium : Magnesium is an essential element,

necessary for the oxidative phosphorylation enzymes.Deficiency of magnesium may be associated with malabsorption syndrome,protein-energy malnutrition, chronic renal failure and diarrhoea. Clinical manifestation include irritability, tetany and increased or decreased reflexes. Magnesium is present widely in plant foods and meat. In the first six months of life, the infant requires 40 mg of magnesium, in the second six months the allowance is 60 mg/day.Older persons require 3.0 to 4.5 mg /kg of magnesium per day.

9. Copper : Copper is present in enzymes tyrosinase, uricase and oxidation-reduction enzymes. Copper helps in the absorption of iron. Liver, kidney, shellfish, nuts, rasins and dried legumes are good dietary sources. Infants require 80microgram/kg of copper per day. Older children need 40 microgram/kg/day while 30 microgram/kg/day is sufficient for adults.

10. Cobalt : Cyancobalamin (Vitamin B_{12}) contains four percent of cobalt. Human requirements of cobalt relate only to the needs of vitamin B_{12} synthesis.

11. Vitamins : Vitamins are organic compounds that are needed in small quantities in several functions of our body systems. Most of them are not stored in the body hence its daily supply is essential. Broadly, there are two groups of vitamins-water soluble (vit B complex and vit C) and Fat soluble (vit A, D, E and K). As already stated , Vitamins are essential for life and maintenance of normal health. These act as cofactor in many enzyme systems and are therefore essential for various body functions such as energy production, hydrogen transfer and synthesis of fats, amino acids,nucleic acids and nucleoprotein. Any aberrations in these critical mechanisms cause profound changes in the nervous system and integrity of skin and mucous membrane. These are required in very minute quantities in the diet.

The Indian situation on micronutrient deficiencies projects a grim picture even today. Of all the micronutrient deficiency, vit A deficiency is the most tragic. Studies have shown that morbidity and mortality due to gastrointestinal and respiratory infection is greater in vit A deficient children. In some pockets of country the incidence of corneal xeropthalma is between 0.5 and 1/thousand preschool children. The National Nutrition Monitoring Bureau (NNMB) data indicates a decline in the prevalence of Bitot spots from about 2% in 1975-79 to about 0.7% in 1988-90 in the ten states of India surveyed. This is still higher than WHO criteria (< 0.5%). A recent survey indicates a 0.04% of total blindness (due to vit A deficiency) as compared to nearly 2% about two decades ago.

Anaemia, due to iron deficiency, is another micronutrient disorder of reproductive age group and young children. Haemoglobin surveys of populations in different areas reveal that 88% among pregnant women suffer from anaemia, and about 26% have severe anaemia (with Hb level < 8 g/dl.).

Goitre, a condition resulting from iodine deficiency, which was earlier confined to Himalayan and Sub-Himalayan region has now spread to areas south of Vindhyas (M.Mohan Ram, 1994, National Institute of Nutrition, Hyderabad, India). In India, no state is free from the ill effects of iodine deficiency disorder (IDD) of which goitre is the simpler form and cretinism the severe manifestation. A survey conducted by the Indian council of Medical Research (ICMR) in 14 districts of different states indicates that the prevalence of endemic cretinism is India is very alarming.

Assessment of malnutrition : or Nutritional Anthropometry

Various methods, particularly biochemical ones, exist for the evaluation of nutritional status of a population. Such measures are, however, highly technical and require participation of skilled technicians along with a number of instruments and biochemical substances hence unsuitable for a developing country like India. In recent years, international consensus has been achieved to a large extent for defining the nutritional status of persons with the aid of anthropometry. Various recommendations for such assessment has been made by WHO working group (1986) and UNO (1990) in the recent years. Though contribution of heredity in the growth and development is not denied, it is still maintained that the same genotype is capable of different growth potentialities in different environments. This is the underlying assumption for use of anthropometry in nutritional assessment of populations.

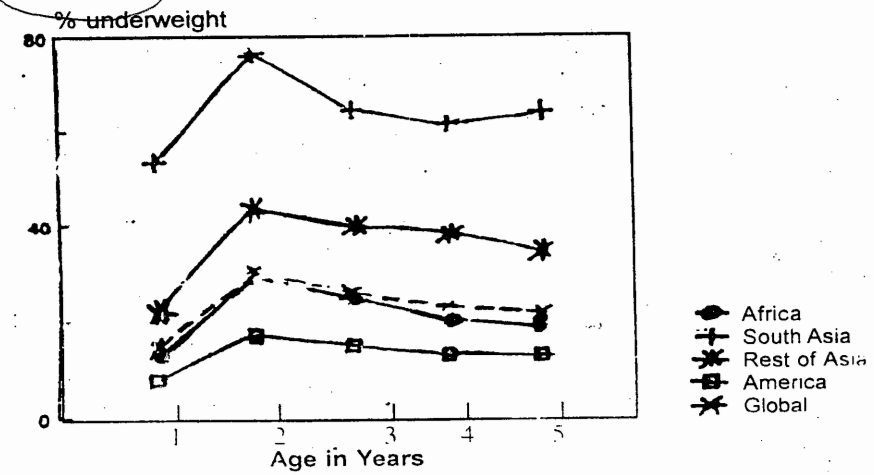
Concept Of Reference Population : The reference population for assessment can be international such as one by National Centre for Health Statistics (NCHS), US which is widely used as international reference population, or it can be national. There are points in favour and against both the Criteria. National reference population does represent acceptable growth in a given environment and thus may represent a true picture of nutritional status, whereas international reference population may "over estimate" the true extent of existing malnutrition because of high standards set by it. However, such arguments in favour of a national reference population can be effectively met with. There are diverse ethnic groups in India with sufficiently different anthropometric measurements. Moreover, well-fed children of different ethnic groups (including Indians) have the same growth potential as Americans, and genetic differences have little effect on their growth potentialities compared to environment effects. If a standard is to represent a target, it has to be derived from well to do groups, hence NCHS data is much in use for nutritional assessment of children.

Indices And Nomenclature For Deficit In Indices : There are mainly four indices the first three commonly used for children, and last for adults. For children, three indices widely used are -

1. *Weight For Height (cited earlier) :* **deficit in this index is known as wasting.**

2. *Height for age :* **deficiency in this index is known as stunting.**

3. *Weight for age :* **deficiency in this index is known as underweight.**



There exists geographical variations in the three indices

4. *Body Mass Index (BMI) :* This is an index of weight/height (Wt/ht^2) in which weight is taken in grams and height in centimetres squared.

Concept Of Indicator And Cut-Off Point : An index is simply a number. Indicator represents use of index, with cut-off point, for making an assessment. Thus, weight for height with a cut off at 80% of the reference is an indicator of wasting.

To illustrate, 3 feet tall boys in a population weigh between 20 to 33 kg. The reference population for the same height may indicate a median of 30 kg. 80% of this reference comes to $\frac{30 \times 80}{100} = 24$. Thus 24 is the cut off point and all boys below 24 kg should be considered wasted.

The cut off point vary with index. While it is 80% for weight for height and weight for age, it is 90% for height for age because any serious reason for stunting might interfere with life. Thus cut off point for this index is raised.

In addition to use of percent of median of reference population as cut off points, there are other indicators of malnutrition too, namely percentiles and SD or Z scores. Usually the 3rd and 97th percentiles are utilized as cut off points to define undernutrition and obesity respectively. SD or Z sore is below (-2) for under nutrition and above (+2) for obesity. A table depicting the various indices and cut off point is presented.

Table : Cut-Off Points In Relation To Three Basic Indices

Indices	Nomenclature for deficit of Index	Cut-off points for defining malnutrition		
		Percentile of reference median	Percentage of reference median	Z or SD score from reference median
Weight-for-height	Wasting	< 3rd	< 80%	< -2
Height-for-age	Stunting	< 3rd	< 90%	< -2
Weight-for-age	Underweight	< 3rd	< 80%	< -2

Mid-Arm circumferencce method

Mid-arm circumference (AC) has some practical utility. In normal children between one and five years of age, mid-arm circumference is virtually age independent, increasing during that period by only 1 cm. The mid-arm circumference (is widely used as a measure of thinness and the conventional cut-off points to define malnutrition are : (i) AC 14.0 cm-normal nutritional status; (ii) AC 14 to 12.5 cm-mild / moderate undernutrition; and (iii) AC < 12.5cm severe undernutrition. Based on such cut-off points, multicoloured bands in a tape have been suggested (Shakir's tape) where the colours green, orange and red correspond to the ranges described above, respectively. Similarly, people have attempted to make bangles with an internal diameter 12.5 cm for easy detection of malnutrition. The advantages of AC are its simplicity, particularly for screening children in emergency situation. The two measures of thinness, weight-for-height and AC usually show significant correlations of the order of 0.6-0.7.

Assessment of Adults

Assessment of Adults is on the basis of BMI and weight for height

Table : useful critical limits - weight for height and weight / height^2 for adults

S.No.	Form of malnutrition	Limits of indices	Weight for height (%)	Wt/ht^2 (BMI)
1.	Severe undernutrition	Lower than (Mean - 4SD)	< 60	< 1.40
2.	Mild form of undernutrition	(Mean - 4SD) to (Mean - 2SD)	60-80	1.4 - 2.0
3.	Normal	(Mean - 2SD) to (Mean + 2SD)	80-120	2.0 - 2.5
4.	Mild form of overweight	(Mean + 1SD) to (Mean + 2SD)	110-120	2.5 -2.8
5.	Overweight	(Mean + 2SD) to (Mean + 3SD)	120-130	2.8-3.0
6.	Obesity	(Mean + 3SD) to (Mean + 4SD)	130--140	3.0-3.3
7.	Severe Obesity	(Mean + 4SD) and above	140 +	3.3 +

Studies indicate that Body Mass Index (BMI) of 3.0 or above is associated with extra risk to life because of heart disorders, diabetes etc. Those with extremely low values of BMI have higher incidence of infection disorders and ill-health. The BMI for men and women differ - it has been proposed to be 2.5 for males and 2.4 for females (Royal college of Physicians); and 2.78 for males and 2.73 for females (NCHS data). It may be rounded to closer figure of 2.80. Anthropologists and nutritionists indicate a critical limit of BMI of 3.0 to be of use for classification of adults.

Weight for height (%) and BMI donot distinguish between overweight due to excess fat and that due to excessive muscular development. Measurements of fat folds at triceps or biceps has also been indicated for use together with BMI values. Critical limits of BMI together with ratio of waist/hip circumference have been found useful for differentiation of overweights from obese (Gopalan, 1994). Waist-hip ratio (WHR) provides an indication of the predominance of fat storage in the abdominal region relative to that in the gluteal region. A high WHR indicates central fat distribution. The WHR useful for males is 0.95 and for femals 0.85

PROBABILITY AND STATISTICS IN GENETICS

One of the reasons for success of Mendel in discovery of laws of inheritance lay in the fact that Mendel's work was a laborious one. He obtained seeds from a plant, counted it, again sowed it and counted the types of plants obtained from the seeds. At first, he concentrated on one character and later included in the study more than one character. By such laborious methods he was able to discover the probability of different types of offspring from a given type of parental cross.

ADDITIVE FUNCTION OF PROBABILITY

While performing monohybrid cross, Mendel observed that if a pure tall plant is crossed with a dwarf plant, all the plants were tall in F_1. When F_1 was selfed, 1/4 were pure tall, 2/4 were hybrid tall and 1/4 were dwarf. Since the three classes are mutually exclusive, one has to add up to find out total number of a type of plant. For example, we will have to add 1/4 tall + 2/4 tall to obtain total number of tall plants because the two classes are mutually exclusive - one is pure tall and another hybrid tall. It can never be both at once. We can understand the phenomenon by a simple analogy. What is probability of getting an ace in a pack of cards ? Probability of getting an ace of a colour is 1/52. Since there are four colours hence probability of getting an ace of any colour is 1/52 + 1/52 + 1/52 + 1/52 = 4/52 = 1/13. We are adding up because events are mutually exclusive - We can have one ace at a time.

MULTIPLICATIVE FUNCTION OF PROBABILITY

If two events are not mutually exclusive, probability of their occurence together is found out by multiplying their individual probabilities.

In a dihybrid cross, probabilities of RR (Pure round), Rr (heterozygous round) and rr (wrinkled) is 1/4, 2/4 and 1/4 respectively. Also, probabilities of YY (pure yellow) heterozygous yellow (Yy) and green (yy) is also 1/4, 2/4 and 1/4 respectively. Hence probabilities of different classes obtained by Mendel in dihybrid cross can be found out by multiplicative function of probability because two events are not mutually exclusive.

RR 1/4	YY	1/4	(1)	RRYY	1/4 x 1/4 = 1/16
	Yy	2/4	(2)	RRYy	1/4 x 2/4 = 2/16
	yy	1/4	(3)	RRyy	1/4 x 1/4 = 1/16
Rr 2/4	YY	1/4	(4)	RrYY	2/4 x 1/4 = 2/16
	Yy	2/4	(5)	RrYy	2/4 x 2/4 = 4/16
	yy	1/4	(6)	Rryy	2/4 x 1/4 = 2/16
rr 1/4	YY	1/4	(7)	rrYY	1/4 x 1/4 = 1/16
	Yy	2/4	(8)	rrYy	1/4 x 2/4 = 2/16
	yy	1/4	(9)	rryy	1/4 x 1/4 = 1/16

Thus, there are nine genotypic classes— 1,2,4 and 5th classes making round and yellow (9/16) ; 3rd and 6th making round and green (3/16) 7th and 8th making wrinkled and yellow (3/16) and 9th class making wrinkled and green (1/16).

We can find out ratio of offspring by the same method in a trihybrid cross.

YYRRTT x yyrrtt

1/4 RR
- 1/4 YY
- 2/4 Yy
- 1/4 yy

2/4 Rr
1/4 rr

- TT 1/4 — RRYYTT = 1/4 x 1/4 x 1/4 = 1/64
- Tt 2/4 — RRYYTt = 1/4 x 1/4 x 2/4 = 2/64
- tt 1/4 — RRYYtt = 1/4 x 1/4 x 1/4 = 1/64

We can understand the phenomenon by a simple analogy. In a pack of Cards, there are 13 diamonds and one king of diamond. What is probability of finding a king of diamond? Since the two events are not mutually exclusive we can find out the probability of getting king of diamond by multiplying probabilities of getting a king and probability of getting a diamond. In a pack of cards (52), the probability of getting a diamond is 13/52=1/4. Since there are 4 kings in a pack of cards, probability of getting a king is 4/52 = 1/13. Hence, probability of getting a king of diamond = 1/4 x 1/13 = 1/52.

Statistical Operations

(i) **Finding mean-** This is basic to most statistical operations.

Polygenic traits such as I0, height, sugar-level, blood pressure etc show great range of variations and it becomes necessary to find mean value of observations. This is calculated by formula $\frac{\Sigma x}{N}$ where Σ x is sum of observation and N is the number of observations.

Example : Calculate mean difference of height in DZ twins —

No. of obs	Pair-diff.	Obs (X)	Mean ($\overline{X}$)
1	150-160 cm	10	$\frac{\Sigma x}{N} = \frac{30}{5}$
2	155-160 cm	5	
3	153-157cm	4	
4	152-156 cm	4	=6
5	156-163 cm	7	

(ii) Finding mean in grouped data

This is calculated by formula $\frac{\Sigma fx}{\Sigma f}$

Example: Calculate mean age of a population of 10 individuals having ages with frequency listed in brackets —

10 (2), 15 (1), 20 (2), 25 (3), 30 (2)

Variables (x)	Frequency (f)	f.x.
10	2	20
15	1	15
20	2	40
25	3	75
30	2	60
	Σ f=10	Σfx=210

$$\overline{X} = \frac{\Sigma fx}{\Sigma f} = \frac{210}{10} = 21.0 \text{ Years}$$

(iii) Calculating Variance —

It is calculated by the formula —

$$\frac{\Sigma(x-\overline{X})^2}{N}$$

Example : Find out variance in height of DZ twins cited in Example 1.

No. of obs	obs (X)	Mean ($\overline{X}$)	$x-\overline{X}$	$(x-\overline{X})^2$
1	10		+4	16
2	5	30	-1	1
3	4	5	-2	4
4	4	=6	-2	4
5	7		+1	1
	Σ x=30	6		$\Sigma(x-\overline{X})^2$= 26

$$\text{Variance} = \frac{\Sigma(x-\overline{X})^2}{N} = \frac{26}{5} = 5.2$$

(iv) Calculating 't'- value

t-test is performed to test whether two samples belong to the same population or not and the formula is—

$$\frac{\text{Difference in means}}{\text{Diff in standard error of means}}$$

$$= \frac{\overline{X} - \overline{Y}}{\sqrt{(S.E.m_1)^2 + (S.E.m_2)^2}}$$

Where $\overline{X}$ = mean of one sample

$\overline{Y}$ = mean of another sample

S.E.m1= Standard error of mean 1

S.E.m2= Standard error of mean 2

(Difference is calculated by the operation given above)

Example : ABO Blood group was studied in two tribes and results were as follows-

	O	A	B	AB	Total
Tribe I	40	90	50	20	200
Tribe II	45	50	40	20	155

Find out whether the two tribes belong so same population not.

Tribe I

N	X	$\bar{X}$	$(X-\bar{X})$	$(X-\bar{X})^2$
O	40		-10	100
A	90	50	+40	1600
B	50		+0	0000
AB	20		-30	900
4	200			$\Sigma(x-\bar{X})^2 = 2600$

Mean = 50

variance = $\frac{2600}{4} = 650$

S.D. = $\sqrt{\text{variance}}$

= $\sqrt{650} = 25$

S.Em = $\frac{S.D}{\sqrt{N}} = \frac{25}{\sqrt{4}}$

= $\frac{25}{2} = 12.5$

Tribe II

N	X	$\bar{X}$	$(X-\bar{X})$	$(X-\bar{X})^2$
0	45		6	036
A	50	$\frac{155}{4}$	11	121
B	40	=39	1	001
AB	20		-19	361
4	155			$\Sigma(x-\bar{X})^2 = 519$

mean = 39

variance = $\frac{519}{4} = 129$

S.D. = $\sqrt{\text{variance}}$

= $\sqrt{129}$

= 11.3

S.Em = $\frac{S.D}{\sqrt{N}} = \frac{11.3}{\sqrt{4}}$

= $\frac{11.3}{2} = 5.6$

$$t \text{ value} = \frac{\text{Diff of means}}{\text{S.Em diff}}$$

$$= \frac{50 - 39}{\sqrt{(12.5)^2 + (5.6)^2}}$$

$$= \frac{11}{\sqrt{187.61}} = \frac{11}{13.70} = 0.800$$

Degree of freedom = 4 + 4 - 2 = 6

Level of Significance = 5%

Table value of t= 2.45

Since calculated value of t = 0.80 which is much smaller than table value of t (2.45) at 6 df and 5% level significance. It is, therefore, inferred that there is no significant difference between the tribes and they belong to same population.

(v) Chi-square test (f^2-test)

It becomes necessary sometimes to find out whether numbers obtained in different categories in a test conform to a definite ratio or not. For example, if out of 1000 plants, 750 are tall and 250 dwarf, it conforms to 3:1 ratio. But, if out of 1000 plants, 800 are tall and 200 dwarf, there is no direct 3:1 ratio and one has to perform chi-square test to find out whether number conform to 3:1 ratio or not. The formula is —

$$f^2 = \frac{\Sigma(obs - Exp)^2}{Exp}$$

Where obs= observed ratio

Exp= Expected ratio

Example :

In a monohybrid cross, out of 1775 plants, 1270 were tall and 502 dwarf. find out whether results conform to 3:1 ratio.

	Tall	Dwarf	Total
obs =	1270	502	1772
Exp =	1772 x 3/4	1772 x 1/4	
=	1329	= 443	1772

$$f^2 = \frac{(obs-exp)^2}{Exp}$$

For tall = $\frac{(1270 - 1329)^2}{1329}$

= $\frac{(-59)^2}{1329}$

= $\frac{3481}{1329}$

= 2.6 approx

For dwarf = $\frac{(502 - 443)^2}{443}$

$\frac{(59)2}{443}$

$\frac{3481}{443}$

7.8 approx

$f^2 = 2.6 + 7.8 + 10.4$

Degree of freedom = 2-1 = 1

Level of Significance (P) = 0.5

table value of $f^2 = 3.841$

Since our calculated value of chi-square = 10-4 which is much higher than table value of chi square (3.841). hence ratio 3:1 is not suitable to it.

Concept of degree of freedom : It is given by formula n-1 and for t-test $n_1 + n_2 - 2$ where n is the number of variable classes. For example, there are two variable classes in length of plants— tall & dwarf. The degree of freedom is 2-1 = 1. In dihybrid cross, since there are four classes (9:3:3:1), the degree of freedom will be 4-1 = 3. For analogy, if 100 is made of two numbers, we are free to say only one number ; for another number we are not free. If we say 20, the another number must be 80.

5% or 0.05 level of significance: It means that an event, which doesnot have chances to occur at least 5 times in a trial of 100; has no chance to occur at all.

In addition, correlational studies are performed in family studies where we are supposed to find out co-efficient of Correlation. The formula and method to obtain it is mentioned with family studies in the topic "genetic analysis of man". Probability and statistics find widespread uses in the field of genetics.

GENE MAPPING

All the genes of a species are contained on different chromosomes that the species possess. Gene-mapping provides an opportunity to know which gene is located on what place of which chromosome. Methodology used have-taken different recourses hence we have different approaches.

Gene-mapping

(1) Linkage maps or Cross-over maps or Genetic maps	(2) Cytogenetic maps or Cytological maps	(3) Molecular or Physical maps

First two methods map the chromosome hence called chromosome-mapping.

(1) Linkage maps : Such maps discover relative distances of genes on chromosome. In preparing linkage maps, 2-point, 3-point or 4-point test-cross is made in which a dihybrid or, tri-hybrid or, tetrahybrid is mated to double-recessive, triple recessive, or quadruple recessive individuals respectively.

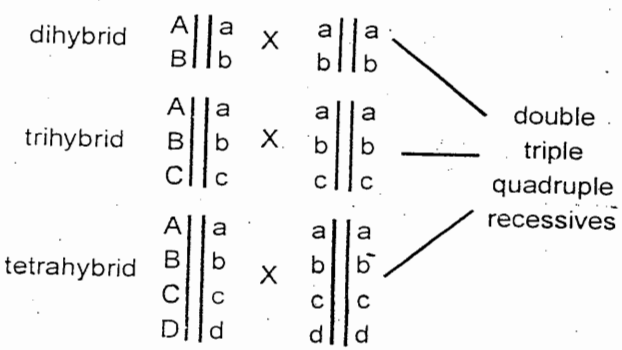
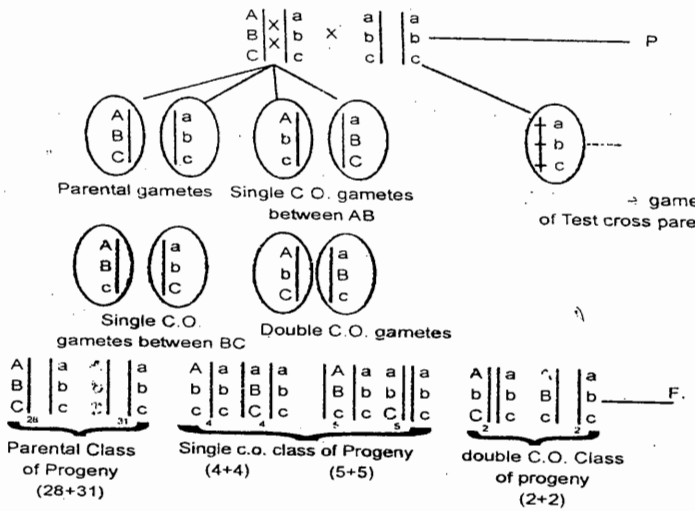


Fig: A dihybrid, a trihybrid & a tetrahybrid matings with double, triple and quadruple recessives, respectively.

The hybrids form different types of gametes and different types of progency is obtained. The frequency of cross-over progeny can be known and distances of the genes in the chromosome is calculated.

Example : In a trihybrid tests-cross —



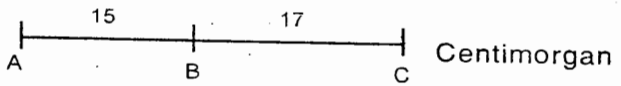
Suppose total Progeny = 81

Recombination Frequency between A andB=

$$\frac{4+4+2+2}{81} = \frac{12}{81} = 0.15 \text{ or } 15\%$$

Recombination Frequency between B and C

$$\frac{5+5+2+2}{81} = \frac{14}{81} = 0.17 \text{ or } 17\%$$



(2) Cytological maps

(a) Linkage Studies: Cytological maps are constructed on the basis of data from studies that iink phenotypic changes or single gene disorder to chromosomal rearrangements. Banding pattern of a chromosome is definite and microscopically visible. Even when portions of the chromosome are shifted by structural changes the specific bonds can be identified. Loci of particular genes can be determined by a detailed comparison of mutant phenotype relative to mutant banding pattern. Gene for polyposis coli (bowel cancer)

and changes in the long arm of chr-5; Gene for Duchenene musculer Dystrophy (DMD) and deletion in short arm of X-chromosome is typical example of this category.

(b) Somatic cell hybridization: This is a process by which a gene is aligned to a specific chromosome. Human cell and mouse-cell is fused in presence of sendai Virus or polyethylene glycol to obtain a hybrid cell which is cultured in a specific medium. It is found that human chromosomes are gradually eliminated from hybrid cell, leaving ultimately one human chromosome. Thus panel of human cell-lines with different chromosomes can be obtained and human proteins different from mouse protein can be eluted from culture medium and examined. The gene for the protein will be located on the chromosome of a specific cell-line. It is difficult to identify hybrid cells. For this, human cells (TK^-) and mouse cells ($HGPRT^-$) are specific. **TK** is Thymidine Kinase which is essential for pyrimidine synthesis. **HGPRT** is Hypoxanthine Guanine phosphoribosyl Transferase which is essential for purine synthesis. Aminopterin blocks major pathway for DNA syntheisis. The cells are cultured in **HAT medium** (containing hypoxanthine, Aminopterin & thymidine). Both mouse and human cells are unable to grow because they lack one of the enzymes whereas hybrid has both the enzymes and grow in the medium.

(c) In-Situ hybridization: Copy-DNA is obtained from mRNA of a known protein.

mRNA
↓ reverse transcriptase
Complementary DNA
↓ 32p + other substances
Copy DNA
↓
used as probe

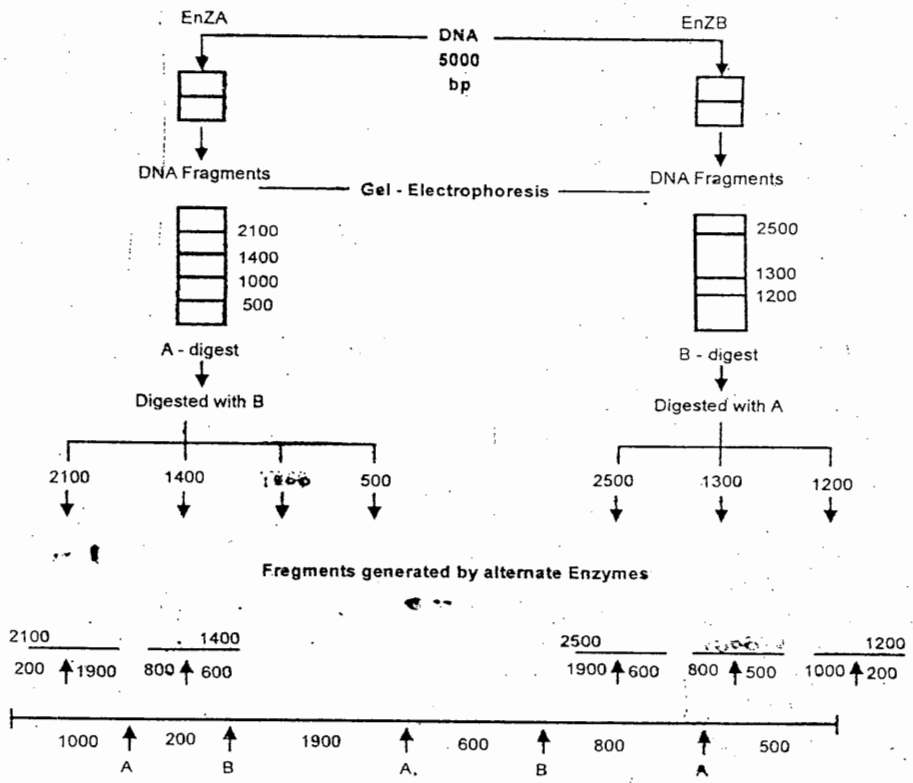
The copy DNA is applied to well spread metaphase chromosome. It hybridizes with the corresponding portion on a specific chromosome.

(3) Physical or Molecular Maps: In this method genes are mapped in terms of base-pair distances. The process is also referred to as gene-mapping. There are two approaches in gene-mapping—

(a) upside down method (Restriction mapping)

(b) Bottom-up method (contiguous method)

1. Restriction mapping: This is the method used by Cerela Genomics. In the first step, two samples of same DNA is cut by two different restriction enzymes. DNA fragments are separated by gel-electrophoresis. In the next step, fragments from one enzyme is digested with another anzyme and vice-versa. Since restriction enzymes always cut at specific points, the sequence of bases at a specific cut point by a specific enzyme can be known and this information can be used to map bases on the segment of DNA selected for the study (several copies of the segment of DNA under study is obtained by gene-cloning or PCR).



At respective points, the bases are those which are specifically identified by a restriction enzyme.

(2) Contig mapping- This is the, process adopted by Human Genome Project.

In this process, DNA of a chromosome is broken into very small pieces, cloned and base-sequance is analysed. The process,

In the contig mapping, or bottom-up approach, we start with individual clones. Later on, by detecting overlapping of DNA segments in clones, the latter are arranged in a large number of contiguous sets of overlapping clones (Contigs). This coalesce into a map of the whole genome. The method gives high resolution information but has gaps. Restriction mapping, howerver, gives information about distantly spaced genomic regions but donot give high resolution information. Both types of maps are useful and can be combined.

Human Genome Project (HGP)

The project started in 1990 with the co-operation of many countries, especially National Human Genome Research Institute (NHGRI) in USA. Initially, it was estimated that in a genome of 3.2×10^9 bases, there are approximately 50,000 genes. Now it seems that there are only less than 25,000 genes. It means 1% of human genome synthesizes proteins.

Though the project was to submit its report by 2005, there was a tough challenge by the Craig venter's **celera genomics** which announced to publish the sequencing by 2001 itself. However, Collins of **HGP** and Craig Venter of celera genomics joined hands to publish the draft in 2001. By 2006, complete sequences with the accuracy of 99.9% were published for all 24 chromosomes, including sex chromosomes, x and y.

Human Epigenome Project (HEP)

There are now convincing evidences that characters are controlled and inherited not only by base seqences of DNA but also by other factors not associated with DNA sequences. This includes a variety of DNA changes involving histones (a protein required for packing of DNA in chromosome) such as modifications of histones (acetylation, phosphorylation, methylation, ubiquitinylation etc), occurrence of histone variants, non-histone proeins etc. Initially, these changes were studied at the individual gene level but now efforts are on to study it at the whole genome level, thus opening up a new horizon in the field of genetics — **epigenomics**. Human epigenome project, started in 2000, is an initiative to study epigenetic changes at the whole genome level so that diseased states produced by such epigenetic changes can be understood and drugs can be directed against such epigenetic changes.

The project was initially started by Stephan Beck (UK) and Alexander Olek (Germany) in 1998 but a consortium was formed in 2000 with the wellcome Trust Sanger Institute (UK), epigenomics AG (Germany) and the Centre National de genotypage in Every (France). As a Pilot study, DNA methylation profiling was carried out on the human Major Histocompatibility Complex (MHC) locus, which is located on chromosome 6, and by 2005 it was extended to chromosomes 13, 20 and 22.

Advantages of Gene-mapping

Genes, being the genetic material, are responsible for all anatomical and physiological characteristic of a species. Their precise number and location on the chromosome must be known in order to get complete genetic picture of the species. In case of humans, this is all the more important because if concerns betterment of human species. Expertsagree that main advantage from gene-mapping shall accrue to the field of medicine in all its hence spheres namely diagnosis, therapy and prevention.

a) It will become easier to diagnose a genetic disease. If all normal genes are known, any deviation from the normal can be detected from infancy so that corrective measures can be taken at appropriate time.

b) Precise knowledge of position of genes can boost the frontiers of gene-therapy. Once gene is located, its primary product, protein, can be known and its nature ascertained. Treatment of various ailments can become easier if full genetic picture of an individual is known. Persons may be issued 'genetic card' which can help physicians in treating an individuals.

c) It can also help in prevention of diseases because even infectious diseases afflict persons of a particular genotype. Hence, susceptibility of a person to various infectious diseases can be known and suitable vaccination recommended.

d) There is distant possibility of a designed baby. In recent times, techniques were developed to separate X and Y bearing sperms so that a couple can have child of a preferred sex. Now comes the possibility of changing the genotype of a baby by selectively silencing some genes and implanting others.

The complete sequencing of humen gene will take some time. After that, only sky will be limit in the area of genetic diseases. But the question arises— How much are we as country going to get advantage from such exercises? We are plagued with starvation deaths, deaths due to infectious diseases, dowry-deaths and deaths due to superstitions. 75% of our population is devied safe drinking water which is source of major illnesses. Western nations, having fulfilled their objectives on such frontiers, can aspire such achievements 15% of all infant-deaths and 50% of all childhood deaths in US is because of genetic reasons. It is their requirement also. But we, as a poor nation, must concentrate first on primary health and education, safe drinking water, proper disposal of excreta, control of mosquito and housefly and a host of other problems which make our life miserable.

MEDICAL ANTHROPOLOGY

Primitive people had knowledge of medicinal plants which were used as trial and error. The knowledge about such plants is restricted to the medicine man of the rural/ethnic people. As civilisation progressed, the early physician were guided by these observations. Vedic literature (1000-2000 BC) cites **248 botanical** drugs (Sharmah, 1968-69)

However, due to modernization, use of ethnomedicines by common people decreased. This negative growth is proportional to the extent of civilization. But tribesmen are still in possession of some rare drugs, mainly derived from plants, which are used to cure a variety of ailments. According to WHO, 60% Population of non-industrialized and 40% of industrialized countries still utilize traditional system of medicine. Ayurveda, siddha and Unani together use 1100 medicinal plants whereas tribesmen use over 5000 medicinal plants for treating a variety of ailments (Raghunathan, 1995). In India, there are altogether 427 tribal communities comprising 8% of total india's population (Anonymous, 1985). They are estimated to occupy 1.5% total geographical area (Gupta 1995). Such medicines generally abound in the vicinity of settlement of the tribe. In addition to herbs, several tribes use animal parts/organs to treat different ailments:

A. Animal parts or body used for treatment : Dimasa Tribe of Assam valley uses meat of terrestrial snails for treatment of jaundice. The same tribe uses meat of aquatic snails for the treatment of Leuchorea. Kuki tribe of Assam uses horn of Sambhar for treating ectoparasites.

B. Plants used as ethno medicines : Tribes are settled in valleys and forests which abound in plants of herb, shrub and tree nature. The various parts of plants are used as ethno-medicines— it can be root, leaves, fruits, bark, seeds etc. These are either taken raw (tender leaves) or grinded and used with water/milk/honey in prescribed doses for a definite period. It also may be in form of decoction.

Some of the common ailments that are cured using ethno-medicines are fever, cough, dysentery, toothache, indigestion, bleeding from wounds, helminthic parasites.

Some plant medicine used by us it also used by many tribes such as use of neem plant (*Azadirachta indica*) in various infections, use of *solanum nigrum* by kuki in toothache, use of onion (*Allium cepa*) in fracture by kuki tribe, use of Tulsi (*ocimum sanctum*) by Dimasa and other tribe to treat a variety of elements are few examples. There are scores of such examples.

There are two main disturbing aspects in the overall scenario: one

concerns the lack of interest in survey and documentation of these biodiversities which are scattered throughout our country. In recent times, however, has been some attempts to fill this void and National Institute of Science communication and information Resources (CSIR) organised a seminar in 2001 at Guwahati (Assam) to assess these ethnic biodiversities, particularly of North-East India. Similar efforts are needed in other parts of country. The second aspect is gradual destruction of these herbal medicines which are being destroyed by different agents knowingly or unknowingly. There is need to conserve such biodiversities lest they are lost forever.

1. Lepcha, Bhutia, Sherpa tribe— (After A. S. Chauhan 2001) These are tribes of Sikkim. They use ethnomedicines for the following ailments—

i) Cuts, wounds & Sexual diseases- N=Panch Anguli (*orchis*)

2) Sexual impotency— Root of N= Ginseng (*Panax*)

3) Family Planning— Tuberous root of N=Githey abortion (*Dioscorea*)

4) Measles— Fruits of N= Ban baigum (*Cestrum*)

5) Blood dysentery-Petals of N-Guras (*Rhododendron*)

2. Tai Tribe (After Gogoi, 2001) — This includes many sub-tribes such as Aho, Phake, Aiton, Turung, Khamti etc in indian territory adjoining Thailand. The herbs are used against following ailments—

1) Malaria— *Clerodendrum, Alstonia, Gnetum, Cuscuta, Punica, Scoparia* etc.

2) Bone-fracture— *Bryophyllum, Artemisia crimum, Plantago* etc.

3) General Tonic— *Desmodium*

4) Scabies— *Verbena*

5) Anti-inflammatory—*Curcuma, Ricinus*

3. Khasi Tribe— (After Ayesha Ashraf Ahmed, 2001) These are inhabitants of Khasi hills of Meghalaya. The herbs are used for following ailments—

1) Cuts and wounds— Goat weed (*Ageratum*)
2) Toothache— Bat thri (*Solanum*)
3) Multidesease— Pa Theng (*Potentilla*)
4) Cough and Asthama— Pine needles (*Pinus*) kept below pillows.
5) Dysentery— Bat soh khnai (*oxalis*)

6) Cataract & other eye diseases— Unopened Pitcher from pitcher plant. The fluid of pitcher is also prescribed for diabetes, urine problems, gynecological problems etc. (*Nepenthes*)

7) Sun burn, skin-cracks- Fruits of *Meyna*

8) Umbilical infection- By Hneria stem

9) Joint pain - *Cuscuta*

10) Headache- Leaves of *Gaultheria*

11) Leucoderma- bark of *Gynocardia* (*Soh-ling*)

4. Mizo Tribe : (After Dutta & Dutta 2001) : Mizo tribe uses many ethno-medicines in different ailments —

i) Inflammatory glands— They use roots of certain plants such as Tubal (*Raphidophora*), huahkhar (*Colysis*) etc.

ii) Snake-bite— They apply crushed juice of roots of Hruidum (*Butea*), Vawmdawng (*cissus*) gangmula (*sonchus*), Dudebra (*vitis*). Dudebra is also used by Bru-tribe and gangmula by Chakma.

iii) jaundice— The extract of Knahkiah (*callicarpa*) Theipui (*Ficus*) etc.

iv) Fever— Decoction of stem bark of Lungkhup (*Haldia*), Thingkhawilu (*vitex*).

5. Chakma Tribe : (After Dutta & Dutta 2001)

i) Prevent child-birth bleeding— Scrapped root bark of Zoeng (*Amaranthus*), Sialtuai (*Ardisia*)

ii) Heart-trouble— The root of plemts Sialtuai (*Ardisia*), Arpatil (*Murrya*) and vawmdawng is grinded, mixed with water and a hot iron dipped into it.

iii) Jaundice— The roots of plants Kaihapui (*Smilex*), Phaktel (*Bridelia*) is used.

6. Bru Tribe : (After Dutta & Dutta, 2001)

i) Cough and cold— Roots of Vaingai (*Plumeria*) Purunvar (*Allium*) etc are used.,

ii) Infertility— Bulb, nut and roots of Sanghar- vaibel (*Aginara*), Kuva (*Areca*), Vawm dawng (*cissus*), Panbnah (*Piper*) is used.

iii) Abdominal Turmour— The paste of roots of Chapau (*Thevesia*) humtiang kohha (Phloga Centhus), khuy mmurmu (*Musaenda*), Tratuba (*Clerodendrum*) Nagabang (*claoxylon*) and

Muiktituin (Ardisia) is applied on the abdomen from below. A Bru young girl (6) Tiabung was cured by this therapy.

iv) Difficult urination— Roots of Phunchawng (*Bombax*) is used.

v) Fracture, bone setting— The paste of stem and leaves of Dulairu and Makhat (*Rhaphidophora*) Lehpong (*Pothos*), Hnahkiah (*callicarpa*) is used.

7. Bawm tribe : (After Dutta & Dutta, 2001)

i) Contraceptive— Whole plant of herb Mitthi- sunhlu (*Phyllanthus*) and fruits of tree Reraw (*Terminalia*) are used. Two teaspoonful of powder is taken twice daily for 2 months.

8. Kuki Tribe : (After Dutta & Dutta, 2001) Kuki is a dominant tribe of Barak valley, Assam and uses several ethno-medicines for several ailments such as—

i) Dysentery— Bark of Haitai (*Mongifera indica*), Leaves of Kolding (*Psychotria*)

ii) Fever— Bark of Moban liche (*Alstonia*)

iii) Parasitic infection— Leaf of kamitri (*Alocacia*)

iv) Body pain— Leaves of Refugelat (*Mikania*)

v) Bleeding— Leaves of Refugelat (*Mikania*)

vi) Pyrrhoea— Leaf juice of Ruirimst (*spilanthes*)

vii) Teeth problem— Root of Launonga (*mimosa*)

viii) Elephantiasis— Cardiosparmum

9. Jayantia, Meitei, H'mar, Deb Burma, Halam, Rongmei Kuki and Dimasa Tribe of Assam: (After Saha & Dutta 2001)

These tribes of Assam valley use same herbs to treat similar ailments

i) Fever— Bark of *Alstomia* (*Rongmei & Kuki*)

ii) Malaria— Leaves of *Azadirachta* (*Mettei & Dimassa*)

iii) Stomach problems— Leaves of *Centella* - Kuki, Dimasa and Halam.

iv) Bleeding — Leaves of *Mikania*- Meitei, H'mar, Deb Burma, Kuki & Halam.

v) Abdominal problems— Tender leaves of Psidiwn guajara- Rongmei, jayantia, Kuki, Meitei and H'mar.

10. Monpas and Sherdukpens: (After A.K. Das 2001)

These are dominant tribes among 25 of Arunachal Pradesh. They are relatively isolated from civilized world and are in possession of Knowledge about ethnomedicines. Some of them include—

i) Tuberculosis— Rhizome of Sueta Ralia (*Aconus*)

ii) Leprosy— Whole plant of clematis.

iii) Gonorrhoea— Seeds of Sissoo (*Dalbergia*)

iv) Bone-fracture— Shang Shun Sheng (*Gaultheria*)

v) Goitre— Leaf of Nakhrang sheng (*Pogostemom*)

vi) Asthma— Swertia (*Whole plant*)

vii) Cancer— Seeds of Blagar Sheng (*Viburnum*)

viii) Ulcer & appendicitis— Seeds & leaves of Merep Sheng (*Ficus*).

ix) Hysteria, Epilepsy— Leaves of *Taxus*

x) Blood pressure— Root of Menang Zougi Sheng (*Girardinia*)

It is in the interest of civilized societies that such biodiversities existing at the Tribal and village level should be conserved so that ailing humanity is not denied some posible chances of therapeutic intervention.

11. Oraon, Munda, Santals and other tribes: (After Binod Kumar & A.K. Sinha, 2003) These tribes are distributed in Jharkhand and adjoining areas in Madhya Pradesh. Tribes of North-West (Palamau, Gumla, Lohardaga) include oraon Asur, Virhor, Nagesia, Brizia, Ghasi, Mahli, Kishan etc among which Oraon is the dominant. Asur is regarded to be one of the oldest tribes, engaged in Iron-ore excavations. South East (Ranchi) has the Munda dominant tribe. In the recent years there has been a serious effort to document ethnomedicines of this region.

Following herbs are used by these people—

i) Migraine— Bariari

ii) Constipation— Bengsag (Brahmi)- *Baccopa monieri*

iii) Milk & Sperm formation— Satavar- *Asparagus racemosus*

iv) To enhance labour pain— Murgichundi

v) Tuberculosis— Munzini- commercial production by Dabur

vi) Family Planning— Roots of Galfulli- one dose after m.c./ month

DEMOGRAPHY : NATURE, SCOPE AND RELATIONSHIP WITH PHYSICAL ANTHROPOLOGY

Demography deals with the analysis and measurement of fertility, mortality, migration and net change in population. Because of its area of operation it is similar as well as different from many basic and social sciences. It is closely related to sociology, geography, economics, human ecology, Physical anthropology and culture.

Sociology studies the demographic events in the perspective of social norms. Since populations are societies, the different demographic events are conditioned by social factors. The study of social factors influencing demographic events is the core-issue of sociology. **Geography** studies population in a narrow way. It performs geo-climatic studies, cropping-pattern and level of food-supply and process of urbanisation. **Human ecology** studies demography in terms of population population explosion and extent of environmental damage caused due to it. **Culture** and demography is also closely related because demographic differences can partly be ascribed to the cultural differences.

Physical anthropology is concerned with physical attributes of man, both past and present. These physical attributes are influenced by evolutionary attributes such as inbreeding, endogamous breeding, assortative mating, out breeding (gene-flow) etc that brings about changes in gene-frequency. Those evolutionary attributes, in turn, are influenced by demographic attributes such as marriages, fertility, fertility-differentials mortality, migration etc. Demography, thus, is defined in two ways— in narrow sense and broad sense. In **narrow sense**, demography is numerical portrayal of human population which takes into account births, deaths, diseases and migration (Hauser and Duncan) Whipple and Barckley, on the other hand, have taken **broader view**. They maintain that biologists, sociologists, economists, statisticians, medicalmen, geographists etc have all contributed to the subject. For example, natality is dependent upon menarche, menopause, endocrinological control of reproduction ie. the whole reproductive biology of man which is a subject area of biology. The various devices that are utilised for populational control is an exclusive area of medicalmen. Marriages are governed by social norms hence there are also heve to be taken into consideration while describing natality. Many, such as spengler, Vance, Boughe, Ryder, Losimer etc, prefer a common path— they favour both demographic analysis and 'Populational Studies' to be part of demography. They favour both the quantitative

and qualitative aspects of populations to be included in study of demography.

DEMOGRAPHIC VARIABLES

Population-size, rate of grouth of population, population-structure and distribution are influenced by different factors which are referred to as demographic variables. The different variables are —

1) Fecundity 2) Fertility
2) Morbidity 4) Mortality 5) Migration

(1) Fecundity— Fecundity refers to the potential of a women to bear child. She is sterile if she is unable to bear child. A fertile woman can bear a child / 9 to 11 months. However, this potentiality is seldom realised. Fecundity is influenced by suckling because it blocks pituitary-ovary axis and consequent ovulation. In addition, her physical health, diseases, psychological level etc also influence fecundity. Thus menstruation may be stretched upto 1-2 years after child birth.

If reproductive age of women is considered to be ranging from 15-49 years, she can bear about 20 children. But we seldom find this many number of children born to a female. The fertility of a women is much less. There are several biological, economic and social theories explaining fertility differential which will be discussed elswhere.

(2) Fertility— It is capacity of a woman to bear a live child. It differs from fecundity. A woman who can conceive is fecund but if repeatedly suffers from miscarriages, she is infertile. A woman who is exposd to intercourse but does not conceive is infecund. Unmarried women, widow, married women using fertility control measures are not infecund. One to three percent of women in different societies are infecund.

Measurement of fertility is essential to assess increase in population. Fertility is measured in the following ways—

i) Crude Birth Rate- The expression for Crude Birth Rate is—

$$CBR = \frac{B}{P} \times 1000$$ [B = Total births, P = Mid year population]

ii) Corrected Birth Rate- The expression for corrected Birth Rate is —

$$\text{Corrected BR} = \frac{B + 100}{P} \times 1000$$ [100 is the cases of birth which may be unreported as in developing societies]

iii) The General Fertility Rate- The expression is —

$$GFR = \frac{B}{Pf\ 15\text{-}49} \times 1000$$ [male is excluded and female of 15-49 age group (mid year)]

iv) Age-specific Fertility Rate or Age-specific Birth Rate- The expression is —

$$ASFR \text{ or, } ASBR = \frac{bi}{Pi} \times 1000$$ [bi= birth in the female of age i; mid year population of women of age i]

v) Total Fertility Rate- This is sumtotal of all age-specific birth rates. There are seven age-groups in reproductive age (15-20, 20-25, 25-30, 30-35, 35-40, 40-45, 45-50). The ASBR is calculated for all seven categories and added. It is multiplied by age-interval (5) and divided by 1000 to find out number of children born/Women.

Calculation of TFR

Age of mothers	No. of children born	No of women in age-grup	ASBR
15-20	200	2000	100
20-25	150	1000	150
25-30	350	3000	116
30-35	750	7000	107
35-40	250	3000	83
40-45	100	2000	50
45-50	75	1000	75

Σ ASBR = 680

$$TFR = \frac{\Sigma ASBR \times \text{Age-interval}}{1000}$$

$$= \frac{680 \times 5}{1000} = \frac{3405}{1000} =$$ 3.4 child/woman or 340/100 or 3400/1000

vi) Gross-reproduction Rate- It gives the rate of birth of female child who are potential mothers. If in 3400 children cited above, the ratio of male : female is 52 : 48 the number of female child = $3400 \times \frac{48}{100} = 1632$

$$GRR = \frac{1632}{1000} = 1.6$$

Expression is GRR= $\frac{\Sigma bif}{1000}$ where Σbif is all female child born

vii) Net Reproduction Rate (Robert Kuczynski)- It takes into account mortality of mothers and daughters (potential mothers). This is accomplished by using a life-table for females which shows how an original cohort of 1 lakh girt-babies at birth diminishes by five year periods becouse of death. The exmenssion is—

$$NRR = \sum \frac{Bx}{Px} \cdot \frac{Lx}{lo}$$

Where Bx/Px is the age-specific fertility rate and lx/lo is the proportion of new born girls surviving to the midpoint of age-interval x. The summation of all interval in the child bearing represents the aggregate fertility within the age groups of the survivors Lx from birth when they numbered Lo.

Example—

Age-group	Fertility rate (2)	Survival factor (3)	(2) x (3)
15-20	0.0216	0.964	0.0208
20-25	0.0856	0.960	0.0823
25-30	0.0866	0.955	0.0827
30-35	0.0493	0.950	0.0468
35-40	0.0236	0.942	0.0222
40-45	0.0060	0.932	0.0057
45-50	0.0004	0.916	0.0004
			0.2609

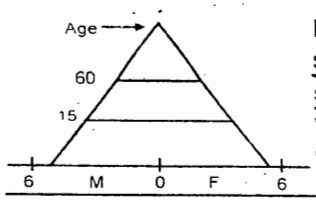
Female net reproduction = 0.261 x 5 = 1.3 thus female population is more than replacing itself.

COHORT FERTILITY

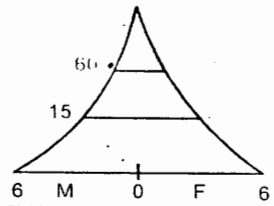
All the female babies born in a year are called whort and whort fertility studies reproductive experiences of these same women through their child bearing years.

AGE-PYRAMIDS OF SEX COMPOSITION

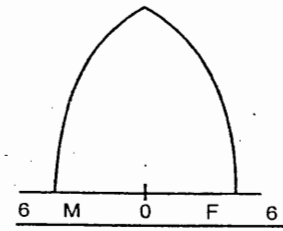
When the age and sex composition of a population are plotted graphically we find pyramids. There are five types of pyramids—



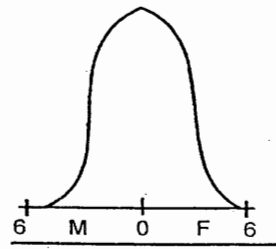
First type : This is broad based, gently sloping pyramid characteristic of primitive society with high birth and death rate eg. world before 1650; median age is low and dependency ratio high.



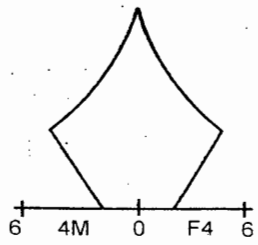
Second type : This is characteristic of developing societies like India, Mexico, Srilanka which have reduced infant mortality but has not been able to reduce fertility. Base is broader than I and sides bow sharply median ages are falling and total dependency ratio is highest.



Third type : This is characteristic of societies with low birth rate and low death rate e.g. USA and western Europe upto world war II. Its median age is the highest.



Fourth type : It is a bell-shaped curve is produced recently in US, Canada. Such curve is produced when BR and DR is kept low for hundred of year and reversal of trend occurs in fertility rate but death rate kept low. It has a declining median age.



Fifth type : Such a pyramid results when death rate is low and birth rate is decreased drastically eg. Japan, France.

(3) Morbidity- It is necessary to know the number of morbid people in society, the nature & type of their morbidity, the rate of morbidity and secondary causes of death with reference to age, sex, seasons and territorial distribution. This is expressed in terms of per thousand per year. Though there is no regular survey the

data entered into clinics and hospitals come handy. To know the secondary cause of death, it has been made compulsory to mention in the death-certificate the secondary cause of the death, certified by a competent health official. These activities lead to deciphering of level of morbidity in the society and possible relationship between morbidity and death. This will enable authorities therapy and diagnosis of the morbidity.

(4) Mortality- Any fact regarding mortality shows the general health of society. Death rate is defined as crude death

$$\text{rate} = \frac{D}{P} \times 1000 \quad \frac{\text{Total deaths}}{\text{Total population in the middle of year}} \times 1000$$

The following are the different categories—

(a) Age-Category— The death-rate is calculated for different age groups.

(b) Sex-Category— The death-rate is calculated on the basis of sex, for different age-groups.

(c) Embryonic, neonatal & postnatal category— It is advantageous to register embryonic death (death during gestation), neonatal death within four weeks after delivery of child and post-atal death (child death between 4 to 52 weeks)

(d) Morbid Category— WHO has divided causes of deaths into five classes—

1. Infectious, parasitic and respiratory deaths
2. Deaths due to circulatory system
3. Cancer
4. violence-deaths
5. Genetic deaths such as diabetes mellitus, hypertension

The information in different categories enable us to recognise the reasons of death in different categories. Measures needed to combat infant and childhood deaths would be entirely different from measures needed to combat maternity or cancer deaths. Health facilities can be improved to a great extent if such informations are at the hands of our policy makers. There are other advantages of mortality studies also. Such studies can provide informations about number of widows, orphans etc in the society so that proper planing can be initiated for them. Also, projected population of a country in future cannot be known unless birth-rate and death-rate is unknown. All the future planning of a country depend upon its projected future population which cannot be worked out unless death rate is known.

It is essential for making life-table also.

$$\text{Infant mortality rate} = \frac{DC}{B} \times 1000$$

(DC= Death of children of different age group
B = Births recorded)

$$\text{Age-Specific death rate} = nMx = \frac{nDx}{nPx}, 1000$$

Where nMx = mortality rate
nDx = Deaths between two ages (30-31)
nPx = No of persons in that age group (Mid year Population)

Death rate and Life Table : Information obtained by death-rates is utilized to construct life-table. Though an ancient Roman practice, the method came in vogue from 18th. Century when life-insurance companies started their operations in a big way. It is difficult to predict the age upto which a person can survive. However, a probability can be expressced. The life-table is a life-history of a cohort of people as it is diminished gradually by death. The record begins at the birth of these individuals and continues until all died. Life table is thus a multiple decrement table. Life-table has following characteristics—

1- It is constructed for a cohort consisting of many people, say 10 thousands or 1 lakh.

2. Since it is not completed till all members of this colrort die, it is constructed not by one but several persons who themselves die during the process.

3. Cohort persons need not reside at one place but it is import to keep their record.

4. The cohort is sex-selective ie. boys and girls are not included in the same cohort, particularly in a country like india where ASDR is very different for the two sexes.

5. Life-table can be constructed by demographers for a hypothetical cohort also.

7. The fundamental information in construction of life - table is actual deaths (dx) in column 4 which determines number of survivors to the next group (fx) in column 5.

8. A life-table is a mathematical model portraying mortality and survival chances at a particular time among a population cohort

and provide a basis for measuring longevity.

9. A life-table is constructed from behind forward and not from forward behind.

1	2	3	4	5	6	7	8
Age x	**qx**	**px**	**dx**	**fx**	**Lx**	**Tx**	**ex**
0	.12356	.87644	12356	1,00,000	93822	4997173	50.0
1	.01488	.98512	1304	87644	86992	4805822	54.8
↑							
96	.960493	.09507	28	32	18	—	—

Fig : Life table (abbrv) for age 0,1 and 96

qx = Death per person
px = survival per person
fx = no. of person s[illegible]
dx = actual death
Lx = No. of person living in a year
Tx = No of person-years lived in a year

10. The different columns used in the table convey the following— (Jumbled here)

Column 1 - Various ages

Column 4 - Actual deaths

Column 3 - This shows survival per person. It can be obtained by 1-qx (1-.12356)

Column 2 - If deaths in column 4 for the age 0 are 12356 out of 1,00,000 then death per person will be .12356. In the age 1-2 there were 1304 deaths in 87644 hence death/person $=\frac{1304}{87644}=.01488$

Column 5 - Shows number of persons surviving to the next group. If out of 1,00,000 babies, 12356 die in the year 0-1 then 87644 will attain age 1.

Column 6 - Shows the number of persons lived in a particular year and is calculated by adding the population at the beginning and end of year and dividing it by 2.

Column 7 - This is number of person-years lived in a year. This is cumulative frequency of persons lived calculated for the last year to 0. 'Person-year' lived is calculated by adding days of survival of all persons in that year. Suppose, out of four persons starting on jan 1, they die one by one on 6th April, 19th Sept, 10th October and 31 Dec, the four persons lived for— 95+262+283+365+=1005=2.75 year.

Column 8 - This is life-expectancy and can be calculated by dividing Tx by fx (column 5). This can be calculated only after column 7 is fully calculated ie. when the last person is dead. (After srivastava 1994)

5. Migration and Population change : Fertility, mortality and migration are three important tools of population change. Migration is not a business or pleasure trip, rather it involves permanent (or at least for considerable period of time) departure for a place which is not nearby. Migration can be internal or international. **International migration** may involve covering less distance (eg. from Bihar to Nepal) than **internal migration** (eg from Kanyakumari to kashmir).

Migration is an important component of change in the size and distribution of population. **Net internal migration** (balance of in-migration and out-migration) changes the distribution of population and regional settlements. **Net international migration** (balance of emigration & immigration) changes the size of population of a country. Both types of migration redistribute people in terms of resources, labour force participation, job opportunities, housing-facilities etc. Inter regional migration is both a cause and consequence of differences in the rates of development of different regions.

Models of Migration- Models of migration are actually explanations of causes and consequences of migration put forth by various workers.

(1) Ravenstein's model (1885) : Ravenstein model describes both pull and push factors as causes of migration. Unemployment, oppression, discrimination etc at the original place of habitation are the push factors whereas development of commerce and industry in urban areas are the pull factors. Migration is inversely related to distances between points of migration, first occurring to nearby places and then to far off places. The stream is generally from rural to urban areas.

(2) Neo-Classical models: These models were givben by neo-economists who argued that if wage-differentials exist and if there is no hindrance and if people are economic men then people will migrate from places of low wages to places of high wages till wages of different places are more or less equal and so is the marginal productivity of labour at all the places.

3. Lewis Model : Lewis opines that in the rural areas there is massive disguised under employment/unemployment. Too many people work on the small farm "spoiling the broth". If they are shifted in orderly manner from place of negative productivity to a place of

marginal product-

positive productivity it will be good for both the places. Lewis advocates orderly transfer of surplus manpower from the rural/ agriculture sector to the urban/manufacturing sector.

4. Todaro Model: Todero in his writing "Thought process thesis about the migration" defines migration in terms of "income expected at the new place". Migrants bear temporary difficulties in the hope of permanent incomes in the long run. This creates regional imbalance. He therefore, advocates that jobs should be taken to man "so that" man have not to move to jobs".

5. Lee's Model : In lee's model, migrants are people who are either over ambitious or are those who cannot get any job at the place of their original residence to suit their skills, knowledge, or aspirations or who donot find total environment (rural setup, sociocultural conditions, climate etc) agreeable.

6. Gravity Models: In such models, two places are compared to two masses and according to theory of gravitation, gravitational force between two masses is a function of product of the masses themselves and inversely proportional to distance.

If a region has low employment intensity, low income generation, less number of function and facilities if is said to have low mass and region of high mass will attract factors unless distance constraints come in the way; Distance constraints may occur due to costly transport, cultural distance, political distance (national boundaries) etc.

Measurements of migration

(1) Direct method- This is performed by registration authorities. The balancing component of growth is given by—

$$P_T = P_0 + B - D + M_1 - M_0$$

Where P_0 is initial population, B is all births, and D all deaths plus net balance of in migration and out-migration.

(2) Indirect method— This is referred to as residual method. Population changes between two census not attributable to the difference between births and deaths is assumed to be migration. The formula is—

$$M = P_1 - P_0 - B + D$$

Where P_1 is population at the time of second census and P_0 at first census. B and D are birth and deaths.

In-migration, out-migration and migration-differential: In-migration is equal to the population of the area minus those born

in the area itself (immigration). Out-migration is equal to total population born in the area minus those still residents in the area.

if 10,000 people immigrate and 10,000 people out migrate from a city, net-migration is zero but gross-migration is 20,000.

Differential migration is calculated per 100 ro 1000 of population and the expressions is—

$$DM = \frac{Mt}{M} - \frac{Nt}{N} .100$$

Where Mt is the number of migrants of a particular character; M is the total of all migrants; N is the number of all non-migrant and the Nt is the non-migrant of the same character as Mt.

Example : In a population of 5,00,00,000 in Delhi, in-migrants from Bihar are 15,000 and Bihari out-migrants 2,000. Suppose total population of Biharis in Delhi is 20,00,000 and gross migration in Delhi is 1,00,000. The Differential migration for Biharis in Delhi will be—

$$\text{DM for Biharis} = \frac{17,000}{1,00,000} - \frac{19,83,000}{4,99,00,000} \times 100$$

$$= 0.17 - 104 \times 100 = 13$$

(After srivastava, 1994)

Effects of Migration : Migration can occur in various ways eg. rural to rural, rural to urban, urban to rural. It also depends on extent of migration and streams of migration. Rural to rural migrations generally occur from regions of high population density/ or low productive area to regions of low population density/high productive areas. This will have positive effect as unemployment at the original place will be reduced and its per capital income increased. Migration to barren lands shall improve the productivity at the place of migration. Other effects, in short, are—

Positive effects

1) Favourable change in demographic characteristics- it is because of, separation of the spouse.
2) Shift in woman's responsibility.
3) Money sent for various farm related activities.
4) Higher wages and better living.
5) Education and skills.
6) Importance of hygiene etc etc.

Negative effects

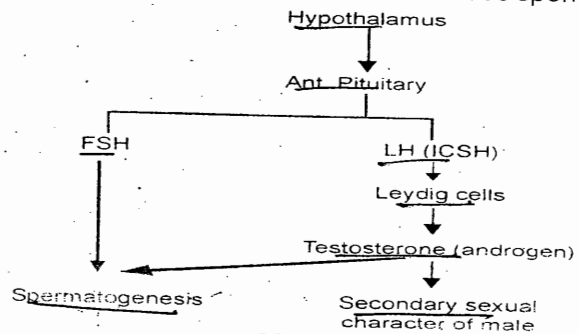
1) Over populatioin of urban areas.
2) Growth of prostitutions.
3) Neglect of villages etc etc.

MALE REPRODUCTIVE PHYSIOLOGY AND MALE-FERTILITY CONTROL

Unit-Seminiferous tubule: Human male reproductive gland consist of a pair of testes which is present in a fold of skin, the scrotum, and hangs outside the abdominal cavity. The unit of testes is seminiferous tubules which fills up the testes. The testes is surrounded by fibrous tissue, called capsule, which extends interiorly and divides the cavity of the testes (septa). Thus there are compartments inside testes, occupied by seminiferous tubules.

Structure of seminiferous tubule- If a cross-section is cut various generations of cells are found in the tubule. Starting from outside, the first generation is **spermatogonia** which can be arranged in several layers. It divides mitotically and thus its number increases. Spermatogonia increase in size and forms **primary spermatocytes**. Primary spermatocyte undergoes first meiotic division forming **secondary spermatocytes**. These cells attach to specific diploid cells found there, called sertoli cells. **Sertoli cells** brings about maturation of sex-cells. Spermatids later develop tail and are released in the cavity of seminiferous tubule and become fully mature spermatozoa. **Cells of Leydig or Interstitial cells** are present in the testes but lie outside the seminiferous tubules. It secretes a hormone, called testosterone (androgen). This is male sex-hormone. This not only brings about formation of spermatozoa (spermatogenesis) but is also responsible for secondary sexual character of male such as growth of bodily, facial, axial and pubic hair, deepening of voice, growth of muscle etc.

Hormonal control : Hypothalamus in our brain secretes gonadotrophin- Releasing Hormone (GnRH) which acts upon anterior pituitary. Anterior pituitary secretes two hormones - FSH (Follicle) Stimulating Hormone and LH (Luteinizing Hormone). The second hormone, LH, is also Known by the name of ICSH (Interstitial cell Stimulating Hormone). The latter acts upon cells of leydig to cause release of testosterone. FSH combines with Testosterone to cause spermatogenesis.



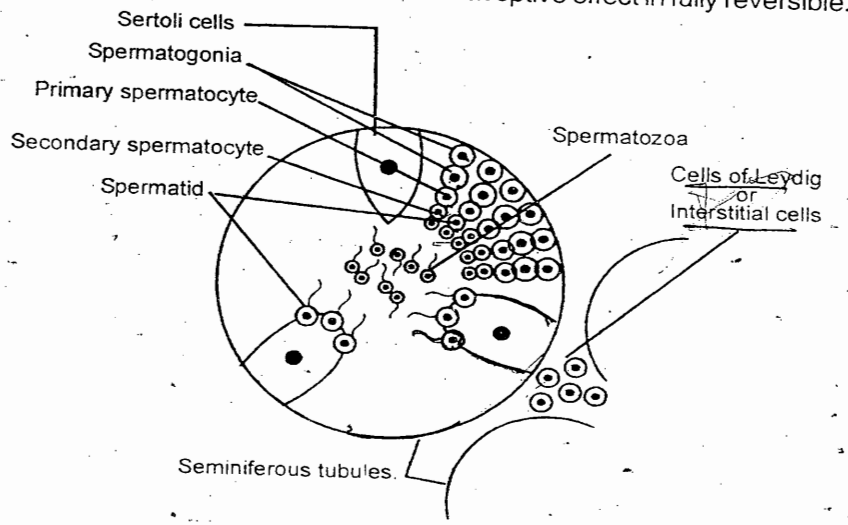
Male-Fertility Control

Receptor analog;

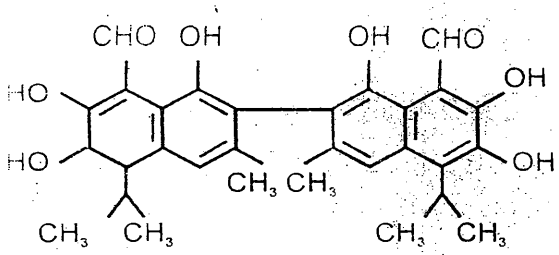
Circuit I— All three points in the circuit GnRH- LH - Testosterone can be depressed by use of their receptor analogs which blocks the receptor sites of these hormone. One of the androgen receptor analog is cyproterone acetate which blocks functioning of androgen. Synthesis of androgen is also inhibited by use of inhibiting enzymes. Alternatively, antibodies can be produced against androgen. In all these methods, it is ultimately androgen whose function is blocked. Androgen, besides spermatogenesis, is also responsible for a number of physiological activities. Thus, absence of testosterone causes loss of libido, loss of muscle, negative nitrogen balance, osteoporosis etc.

Circuit II : Depression of the circuit GnRH - FSH- spermatogenesis- sperm is better approach because it leaves testosterone level unaltered. Sertoli cells, which help in sperm maturation, secrete a hormone, called Inhibin which selectively depress FSH. If **inhibin** is isolated, it can be effectively used to depress FSH centres and thus spermatogenesis.

Alternatively, the enzymes responsible for maturation of sperm can be either inhibited or inactivated. One such enzyme is LDH (lactic dehydrogenase). It has been found that **Gossypol**, a phenolic compound from seed, stem and roots of cotton plant, *Gossypium*, inhibits the enzyme LDH and prevents spermatogenesis. Gossypol does not interfere either with the androgen-level or libido and its contraceptive effect in fully reversible.



T. S. of Testis



Gossypol

In addition to such contraceptive steps, male fertility is also controlled by use of synthetic barriers such as condoms (for example. Nirodh), and, Operative measures such as vasectomy in which vas deferens is cut.

FEMALE REPRODUCTIVE PHYSIOLOGY AND FEMALE FERTILITY CONTROL

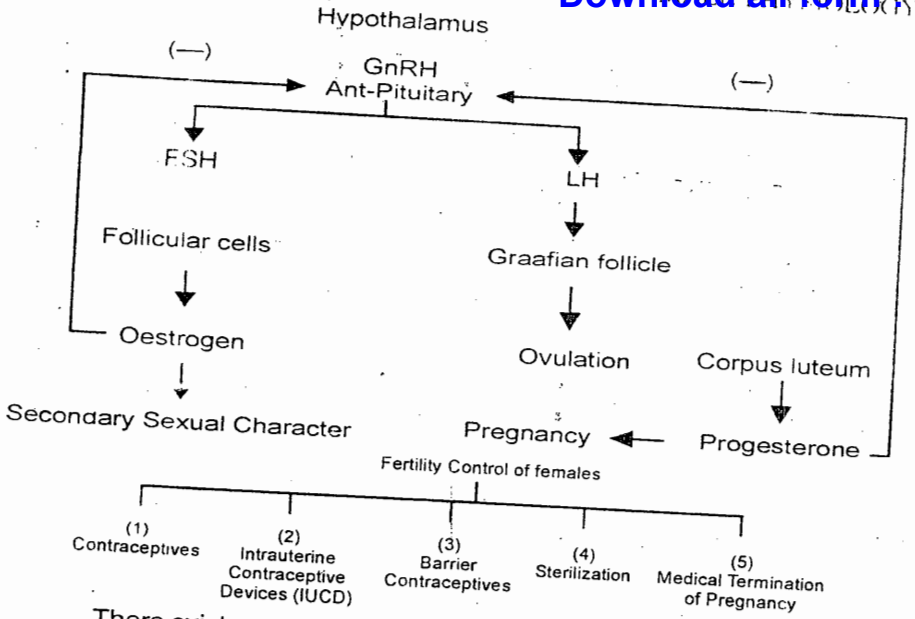
Female reproductive gland is a pair of ovary present in the abdominal cavity. It ovulates eggs, caught in the oviduccal funne from where it is transported through oviduct to uterus where fertilization takes place and embryo implanted. A section of ovary shows that it is made up of connective tissue in which there are several ova. A girl is born with all her ova that she will shed in her life time and no ova is formed after birth of the girl child. Ovulation (discharge of ova) occurs once in a month after puberty in a woman.

The different generations of sex cells in ovary are oogonia, primary oocyte, secondary oocyte, ootid and ovum. No. of oogonia is fixed at birth and donot increase. It increases in size and enter first meiosis as primary oocyte. The division is completed in ovulatory month. After completion of first meiosis it is secondary oocyte. Second meiosis and fully maturation of ovum occurs after penetration of sperm into ovum. During both these divisions eggs give off polar bodies.

The ova are present in the form of follicles— Primary folicle, secondary follicle and graafian follicles in which an ovum, in various stage of development is surrounded by a group of cells called follicular cells which provide nutrition to the growing ovum. An ovum must be made haploid before it is fertilized with sperm so that diploid zygote is formed. Meiosis in ovum is a very discontinuous process. All the ova at the time of birth of girl-child enter into meiosis I and halted at metaphase. This is called metaphase block.

Such ova are surrounded by one layer of follicular cells. When ova is about to be ovulated, it enters second meiosis and secondary oocyte is formed. Follicles now are called secondary follicles. surrounded by many layers of follicular cells. A cavity, called antrum, appears in the secondary follicle. It is filled with fluid called liquor folliculi. This is called graafion follicle. As the quantity of this fluid increases, the follicle becomes heavier sinks at the bottom of ovary, touches and erodes its lower wall. In the mean time, fluid increases internal pressure on the ova which is released with a burst and captured in oviducccal funnel of fallopian tube.

Hormonal control: All the changes are under hormonal control-with the attainment of puberty, hypothalamus is activated to release GnRH which acts upon anterior pituitary to cause release of FSH andLH. FSH causes growth of follicular cells which secrete a hormone called oestrogen. Oestrogen is responsible for secondary sexual character of females such as growth of axial and pubic hair, breasts, vagina and sub-cutaneous fat at crucial places of body. Level of LH increase and its peak is reached on about 14th day of a menstrual nycle when ovulation occurs. Released ova travels down the fallopian tube. It is surrounded by a membrane called zona pellucida. If It is not fertilized, it is absorbed in the system. If fertilized, it immediately undergoes second maturation division and changed into mature ova. The follicular cells remain inside ovary and are transformed into endocrine orgen, called corpus luteum. It secretes a hormone, called progesterone, the pregnancy hormone. Progesterone causes the layers of uterus to develop in anticipation of a pregnancy. The corpus luteum is supported by LH for next 12 days after which a rising level of progesterone inhibits LH secretion. In absence of LH, there is no corpus luteum and hence no progesterone and endomtrial layer of uterus, which had grown too much, is eroded and comes out as menstrual bleeding. In the event of fertilization, however, a embryo is implanted in uterus, placents formed and after 12 days a hormone called hCG (human chorionic gunadotrophin) secreted by the placenta which retrieves corpus luteum and level of progesterone is maintained. Since progesterone has inhibitory action on pituitary, no PSH and LH is secreted till pregnancy continues and hence no another ovulation and pregnancy while one pregnancy is continuing



There exists several procedures for female ferility control. The most common is use of contraceptives which is available in the form of pills and implants. Pills can be steroidal and non-Steroidal. **Steroidal pills** either has progesterone alone or combined with oestrogen. It blocks LH and thus ovulation. But it has some adverse side-effects. It lowers anti-thrombin III activity hence thrombus or blood clots is formed which may precipitate heart-attack. **Non-Steroidal pills** are mainly antibodies against hCG which support corpus lutenm, against vitamin-carrier protein, against FSH, against progesterone to check endometrial growth of uterus and thus implantation of egg (eg. Saheli, CDRI, Lucknow) **Implants** were developed in Finland which has six matchstick sized silastic tubes implanted in upper arm. This causes slow release of progesterone. **Intrauterine contraceptive devices (IUCD)** include copper-T, loop etc which are implanted in uterus and prevent fertilization. **Barrier contraceptives** include vaginal diaphragm with spermicidal cream (eg. TO-DAY) Sterilization include tubectomy in which fallopian tubes are removed either by laproscopic or abdominal method. **Medical Termination of Pregnancy (MTP)** can be achieved surgically, upto 3 months of gestation. Alternatively there are abortion drugs which has Prostaglandin (eg. Preglandin). It causes muscle contraction when inserted into uterns. The method is in common use in Japan which requires 3 day hospitalization. It terminates 3-5 months of pregnancy. The drug is sold with strict regulations.

Use of **inhibin**, which is secreted by follicular cells of graafian follicles is also being tested. It suppresses FSH and hence follicular maturation.

BIOLOGICAL THEORIES OF POPULATION

Theories can be divided into three groups—

(1) Sexual behaviour-related theories— These theories suppose passionate behaviour between two sexes to be reason of fertility.

(2) Food-fertility nexus- related theories— These theories suppose food to be reason of fertility.

(3) Population-density related theories— These theories suppose population-density to be reason of fertility.

(1) Sexual behaviour related theories—

Two theories are important under this category-

a) Malthusian theory of Population

b) Robert Ardrey's theory

a) Malthusian theory of Population: Thomas Robert Malthus (1766-1834): Malthusian essay "Essay on the principle of population as it affects the future happiness of mankind" is an essay which ran only a few pages but exhorted people the world over, some rejecting the theory as a childish writing, others acclaiming it to be a realistic manuscript depicting the real state of affairs in different societies concerning population and food

Theory— There are four cornerstones to tl

(a) Geometric progression of the population: Malthus believed that, because of passionate behaviour of male and female sexes, our population shall double in one generation time- 25 to 30 years. Thus, population shall increase by geometric progression— 2, 4, 8, 16, the transition coming in a generation time.

(b) Arithmatic progression of food production: Because of law of diminishing returns, Malthus believed that increase in food production in a generation time may not double. It may increase by arithmatical ratio.

(c) Positive checks by Nature (Miseries): Malthus believed that under such circumstances there would be a massive shortage of food and people will die of hunger. Before this happens there is a check on population growth by the nature which is experienced by us as "miseries". Malthus listed about eleven such miseries which reduces the population-size before it overgrows. These miseries are bad food, bad health, pollution by industries, diseases, famine, wars, epidemics, infanticide, urbanisation, infant mortality .

(iv) **Preventive checks:** Mankind, according to Malthus, can be spared from these miseries if he voluntarily controls the growth of population. For this, Malthus didnot support use of family planning measures because he believed that such practices bring about social and moral degradation. Women practising such family planning measures were dubbed 'special prostitutes' and 'conjujal frauds'. Instead, for preventive check, he suggested late marriage of women and chastity before marriage.

Malthusian essay has been dubbed as 'Black demon' by Godwin and "School boyish" by Marx. It was accused of seeing a black cat in a black hole which was not there. Hence many workss didnot take it seriously and pronounced it 'scarecrow'.

It is true that all that is supposed by Malthusian theory is not correct, Malthus supposes a geometric rise in population. It is not true for all populations but only for developing societies— the population of underdeveloped and developed societies are more or less constant (refer density related theory). Food-production can double in a generation-time as was possible with measures undertaken under green revolution. Positive checks, which is thought to eliminate large number of people and bringing population to small size may not actually do so. Transport and communication facilities is so much developed in modern world that remotest of the world can be reached in shortest possible time. With several governmental and non-governmental organisations at work, food items can be sent to any part of world struck with famine. Similarly, most of the diseases and epidemics, which used to cause immense loss of life in past, are now tamed. Pollution is now being continuously monitored. Healthcare facilities have also increased immensely. The "miseries" of Malthus is no longer a misery. Suggestion of late marriage of girls as "preventive check" is also fraught with dangers as girls can be enticed in large number by males, creating another social problem. The suggestion of abstinence during married life is niether practical nor scientific because it can lead to serious psychological and physiological problems in both partners.

Judging from idealistic point of view we find several drawbacks in the malthusian essay. It is, however, not so if it is judged from realistic point of view. Geometric progression of population is witnessed in the developing societies. Green revolution increased the quantum of food production but seriously compromised quality of environment and hence was abandoned in many areas.

Also, rise in production does not guarantee food for all if there isno equitable distribution of food and lack of purchasing power. Reliefs are distributed during flood, famine, epidemics etc, but how much of it does land into real hands? There is an organised loot of relief materials and hapless people remain a mute spectators to all such morbid affairs. Condoms and pills, decried by Malthus, is being more misused than used. It has brought moral degradation in adolescents and emboldened unmarried girls to experience sex either for sake of fun or money. Extra-marital sex, prostitution has become safer.

Malthusian message is thus loud and clear : Unless we practise sexual and moral restraint and work hard for the development of agriculture our doomsday is not far. India has added as much populatoin between 1951 and 1991 as was the total population of the world in 1650. The world is adding 100 crore persons every year. About 50 crore in the world face near starvation and 150 crore suffering from malnutrition.

Famines were rampant in Ethiopia, Sudan, Somalia, Chad etc in 1992. Most of the socialist countries were facingshortage of bread in 1990s. All growth models of developing countries should keep malthusian remedies in mind while formulating developmental strategy.

(b) Robert Ardrey's Theory

The theory supposes that animal species and primitive societies practise populatoiin control long before food supply becomes a consideratoin. For example, cholainaickens of manjeri, Kerala (Cave-man)are aware of herbal prescriptions used in family planning. In case of animals also the rate of population growth declines with the decline in food availability. This may happen because of lack of breeding places, lack of parental care, reduction in litter-size etc.

(2) Ford-Fertility nexus related theories

These theories hold that food in some way is related to fertility. Important theories are —

(a) Theory of De castro: This theory supposed that less consumption of protein by females is the cause of high fertility. Less protein consumption leads to fatty degenaration of liver, causing it to become weak. A weak liver isunable to neutralise excess oestrogen which circulates in high level and causes fertility to rise.

Below is given Birth Rate (BR) and average protein consumption of selected countries (1952

Countries	BR	animal protein consumption (gm)
India	33	8.7
USA	17.7	61.4
Taiwan	45.6	4.7

Thus, Castro suggested high intake of protein by females in the reproductive age group. The theory was proposed in the book written by castro in 1952 entitled 'The geography of Hunger'. Experiments on rats by Slonakar were the basis of castro's observatoin.

(b) The theory of Thomas Doubleday (1790-1887): Doubleday maintained that plethoric state is unfavourable to fertility whereas scarcity enhances fertility. He also observed that vegetarian diet increases fertility whereas non-vegetarian diet decreases it. He also asserted that leanness is favourable to fertility. It seems that consumption of animal fat and leading a sedentary life adds to body fat and interferes with the fertilization process. It is supposed that deposition of fat in the female reproductive tract reduces its contractility and prevents fertilization.

(c) The theory of Herbert Spencer (1820-1902): Spencer tried to explain his population theory on the basis of evolution. He maintained that lower forms of life have high genesis because there is low individuation where as higher forms of life have low genesis because there is high individuation. By analogy, people have high genesis because there is low individuation, or we can say that because there is low individuation in poor hence there is high genesis. Rich people have low genesis because there is high individuation.

High genesis	Low genesis
Poor, Lower forms ↓↑	↓↑ Rich, Higher forms
Low individuation	High individuation

(III) Density-Fecundity Nexus theories

(a) Therory of Pearl and Reed: With certain contradictions, the theory proposes that as density grows, there is fall in fertility and population finally finds a plateau. The population experiences different stages of growth in transition from low density to high density, explained by logistic curve (S-Curve) of population.

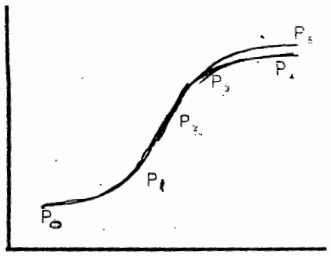


Fig: The stages of growth of population as shown by logistic curve.

The curve shows following

i) P_0-P_1— It is the stage of least density represented by mostbackward society such as hunters and gatherers, where death rate almost equals birth rate and population is nearly static.

ii) P_1-P_2— It is stage of high growth of population, represented by developing society. Here, death-rate falls but birth-rate is still high and population rises with increasing rate.

iii) P_2-P_3— As the society progresses there is gradually concern for the population checks, leading to substantive fall in birth rate. Population is still rising but with decreasing rate. Thestages P_1-P_2 and P_2-P_3 are the stages of demographic transition.

iv) P_3-P_4— By the time society becomes most dense, its birth-rate falls substantially and equals death rate, hence there is no net rise in population. The population finds a plateau and is stabilised. In the meantime, the population will reach the maximum level. Hence, earlier a population finds a plateau, the better.

v) P_3-P_5— This is similar to P_3-P_4 except that the population is slow rising as in US and Western Europe in recent times.

(b) Sadler's theory: The theory, which runs in 1300 pages, has almost nothing to offer. The theory was put forward in 1830 in lifetime of Malthus, and took half of entire book in criticising Malthus. Sadler believed that hard work and privation increases fertility whereas as population becomes denser there is less manual work and less time for privation because there are many other intellectual pursuits. All this leads to lower fertility.

FACTORS OF DIFFERENTIAL FERTILITY

What are the factors that determine fertility? There is not one view hence a number of theories. But most of them agree that it is K.A.P. (Knowledge, Attitude and Practice) about the family planning that determines the fertility. This includesuse of oral pills, intrauterine Devices, use of condoms, vasectomy and termination of pregnancy. Besides, a number of biological, social and economic theories have been proposed to explain differential fertility.

I. Biological Factors
II. Economic Factors
III. Social Factors

I. BIOLOGICAL FACTORS OF FERTILITY RATE

According to Davis and Blake there are 8 important factors—

A. Exposure Factors —

(1) Proportion Married: Marriage age of girl in different society differs eg. in kerala and west Bengal marrriage age of girls is high hence low fertility- In UP, Bihar etc marriage age is early hence high fertility.

B. Deliberate marital fertility control factors —

(1) Contraception: Measures which prevent fetilization such as use of contraceptive pills or surgical intervention preventing fertilization.

(2) Induced Abortion : Measures which causes termination of pregnancy.

C. Natural marital fertility factors—

(1) Lactational infecundability: Suckling deepresses hypothalamus— No LH-RH— No LH & FSH from Pituitary— No ovarian follicle's maturation— No ovulation— No fertilization— No menses- No pregnancy (upto 2yrs).

(2) Frequency of Sexual intercourse:
Normally, higher the frequency of intercourse, greater the chance of pregnancy.

(3) Sterility : Both sexes are afflicted **Males** - azoospermia, low sperm count, non-motility of sperm, **Females-** Amenorrhea, constriction of oviduccal funnel and fallopian tube, physical or psychological trauma etc.

(4) Spontaneous intrauterine mortality: May occur due to reason such as Blood group incompatibilities (Rh^-mother & Rh^+child) chromosomal changes- structural or nmumerical, maternal mistake, maternal medication etc.

(5) Duration of the fertile period
Female fertile period ranges betweent ages. 15-49

Infecundability

Benefit cost

Age at menarche is determined more rigidly by heredity but **age at Menopause** has environmental bearing hence early menopause will lead to less fertility.

II. ECONOMIC THEORIES OF DIFFERENTIAL FERTILITY.

(1) Theory of Leibenstein (Benefit-cost ratio): There is high infant mortality in poor societies hence there is de e to compensate the loss because children are viewed as having h gh benefit-cost ratio. In rich societies, children are viewed as having lo benefit-cost ratio because high expenditure involved in upbringing of the child.

(2) Becker's theory of behavioural economics: Becker put forth his views on fertility in "an economic analysis of fertility" and received Nobel prize in 1992 for his behaviou al economics of fertility. Theory explained why there are more children to some rich prople.

Like most economists, Becker also believed that K.A.P. (Knowledge, Attitude Practice) about the family planning is the most inportant factor that determines fertility. Next is the income. Higher the income, more is the aspiration for "home made durable goods".

(3) Easterlin's theory of Parental aspiration : Easterlin contradicted Becker. He maintained that if aspiration of parents are high than the high income, the person is actually poor and will not be able to afford more children. He will have lesser number of children. Poor persons with high aspiration will also have fewer children. The aspiration relate to having a good level of living for the parents themselves. High income with low aspirations is associated with high fertility.

(4) Distress from Unemployment-Inflation Combine: Population-explosion has resulted into more and more unemployment. Scarcity of Commodities has led to inflation. Most of the amenities, including education, health, housing, clothing, food and drinks have become costlier. Two-child norm is giving way to 'one child norm' or 'no child norm' in some countries.

(5) Rising socio-economic status of women: With the rise in literacy of women and their rising economic status, they assert that they have greater control over their body and it is she who generally decides whether to go in for long gestation periods. In under developed societies, because of poor socio-economic conditions of women, there is crime of repeated pregnancies commited on them.

III. SOCIAL FACTORS OF DIFFERENTIAL FERTILITY

(1) Age at marriage : Fertility period of women ranges from 15 to 49 on average . Hence if a woman marries late eg. the age of 30 years, she has obviously lost the first fifteen years of her potential fertility period. Marriage age of women in different societies differ. In Kerala and West-Bengal, marriage-age is high

hence low fertility. Conversely, in U.P. and Bihar marriage age of girls is lower hence high fertility occurs in them.

(2) Polygamy: Polygamy is prevalent in many societies. In this form of marriage several females tie nuptial knot with single men or vice-versa. In either case, fartiltiy is affected.

(3) Widowhood: Fertility is affected by death of husband of a woman.

(4) Separation and Divorce: Psychlogical conflicts, divorce separate husband and wife, thus affecting fertility.

(5) Post-Partum abstinence: Husband and wife are separated for a long period after birth of a child. This custom also affects the fertility.

(6) Celebacy: Many women either donot marry or perform homosexual acts to satisfy sexual urge, thus affecting fertility.

(7) Frequency of Coitus: In developed societies there are many means of recreation hence frequancy of coitus is reduced. In undeveloped society coitus is the only means of recreation hence high fertility.

(8) Spacing-practices : Children upto 3 years need constant attention hence parents "space" pregnancies. It can be achieved by abstinence during and after ovulation ie- 14th to 18th day of menstruation.

(9) Family-system: In joint families, fertility is high because there is always sufficient number of persons who can look after two or more children at a time.

(10) Rational approach: Parents verify their potentiality and ability to satisfy physical and emotional needs of children and decide about number of children.

(11) Social customs and beliefs: There is strong desire to have male child because it is custom in many societies that funeral pyre of parents is lit by a son. This is believed to be essential for final rest of the soul. Thus, not withstanding, number of female children, children are born till a male child is born.

(12) Superstitions: Children are viewed as 'gift of God' hence many niether use any contraceptive device nor opt for termination of pregnancy. There is also fear of sin against using contraceptive devices.

(13) Higher desire for social capillarity(Dumont's Hypothesis): As women are getting educated they aim for higher, independent social status and avoid wasting time in repeated pregnancies and child-care.

In addition to such biological and socio-economic factors, a new dimension is being added—Political factors. Many governments have refused to rely on only natural factors for decline in fertility. Many of them have come out with reward and punishment for following or not following one or two child-norm.

SEROGENETICS AND CYTOGENETICS OF REPRODUCTIVE PHYSIOLOGY

Male and female in humans possess specialized sex-gland, testes and ovary, respectively, which are concerned with exocrine function of formation of sperm and ova, respectively. The event of formation of sperm and ova is regulated by a number of serum factors some of which are produced locally, at the level of gonads, and some distally at the level of brain. These serum factors include a variety of hormones and enzymes. These cells, producing serum factors of reproduction, are specialized cells.

The axis of reproductive physiological event can be briefly summarised as thus:

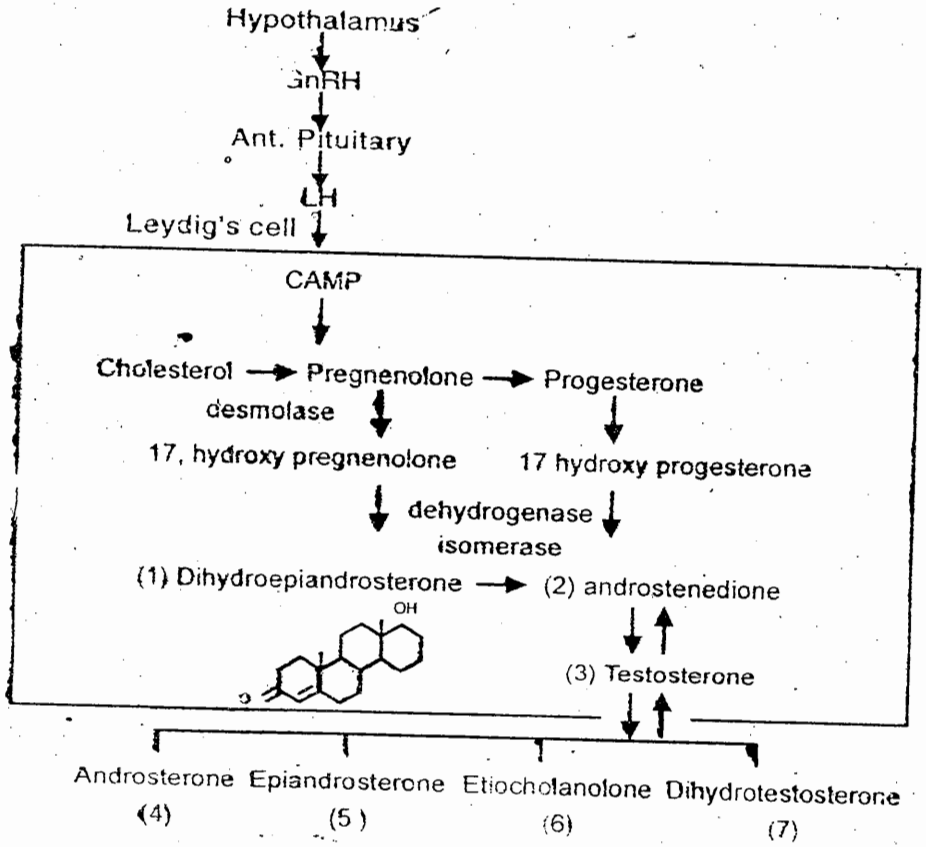
Hypothalamus
↓ Gonadotrophin-Releasing hormone (GnRH)
Anterior Pituitary
↓ Gonadotrophins (LH and FSH)
Gronad
↓
Gonadal steroids (eg. Testosterone, Oestrogen)
↓
Reproductive Functions.

All gonadal steroids are derived from cholesterol and contain pentanoperhydrophenanthrene nucleus. Testosterone is a C-19 steroid and oestrogen a C-18 steroid, derived from testosterone. Cholesterol is a C-27 (27 cerbon atoms) steroid and a system of enzymes called desmolese system cuts six carbon atoms to form C-21 compound pregnenolone. Progesterone (C-21) testosterone (C-19) and Oestrogen (C-18) are derived from pregnenolone.

Serogenetics of Male System

In hypothalamus, there are specialized neurons called ventromedial and Arcuate nucleus which elaborate a serum protein called Gonadotrophin-Releasing Hormone (GnRH). This is also referred to as Luteinizing Hormone-Releasing Hormone (LH-RH). Target cell of this hormone is in the anterior pituitary, producing LH and FSH. Evidences are that LH-RH alone can cause release of both LH & FSH. LH is known to activate adenyl cyclase of cells of Leydig or interstitial cell and thus fermation of cAMP occurs in these cells. cAMP activates enzymatic system of Leydig cell.

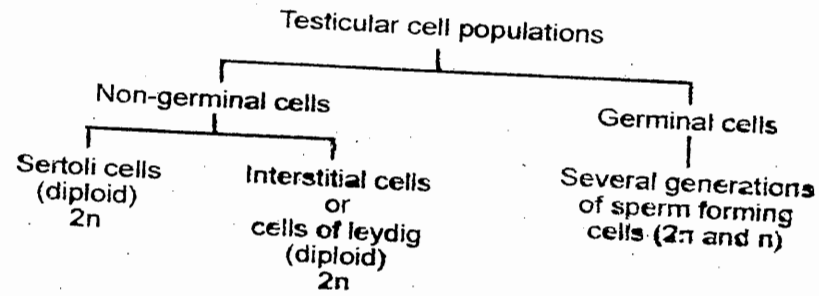
Formation of male sex-hormone, testosterone, occurs in Leydig's cells. Testosterone is a steroid which is derived from cholesterol, the parent steroid. Cholesterol is transported from serum into cells of leydig with the help of a serum lipoprotein called low-density lipoprotein (LDL) This complexes with cholesterol and bind to receptors in the cells of leydig transporting cholesterol inside. Leydig's cell can also synthesize cholesterol because it has rich smooth Endoplasmic reticulum. Cholesterol in presence of cAMP and enzymatic systems, is converted into pregnanolone which is the first derivative in Leydig's cell, giving rise ultimately to testosterone. Testosterone, after its biological functios are over, is metabolized in liver in the form of androsterone, epiandrosterone & Etiocholenolone. Testosterone, in some target cells, is converted into dihydrotestosterone. Thus, there are three androgens (1,2,3). There are four metabolic products of androgens (4,5,6,7) which are not biologically active at all.



Almost 100% of testosterone in the blood serum is bound to protein.. about 40% is bound to a β-globulin called gonadal steroid binding protein or androgen binding protein (ABP); about 40% is bound to albumin, 17% to other proteins (After Hadley, 1984) In activation of testosterone involves oxidation of OH-group and and reduction of Keto group (=o)

Cytogenetics of male System

Tests is characterized by following cell populations—



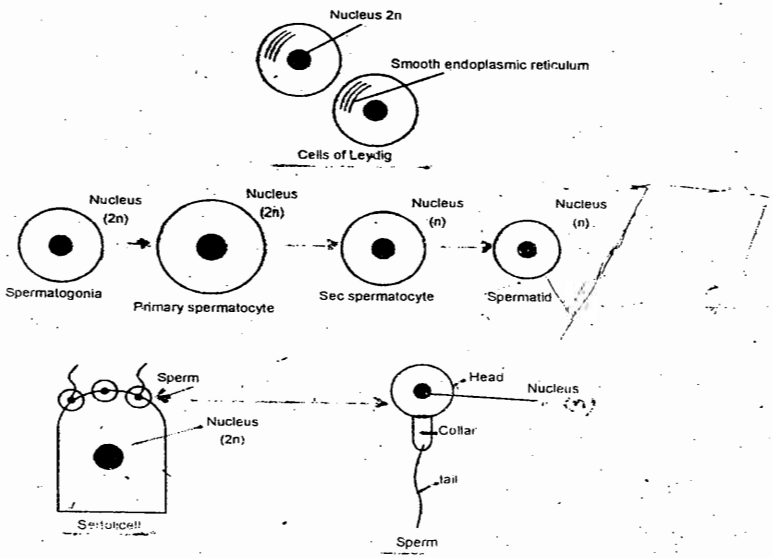
Sertoli cells: are tall columnar diploid testicular cells which help in maturation of sperms. Spermatids, after their formation from secondary spermatocytes, get attached to sertoli cells, differentiate and form tail. sertoli cells are specialized in storing androgens which is secreted outside the seminiferous tubule. Androgens diffuse from outside the tubule into sertoli cells and nourish maturing sperms. Sertoli cells are responsible for synthesis of a hormone, called inhibin, which acts upon pituitary to decrease levels of FSH. FSH of pituitary and testosterone of testes together control sperm formation (See male physiology)

Cells of Leydig or Interstitial cells: are small, rounded diploid testicular cells which lie outside semiferous tubules. These are source of testosterone, a steroid which is synthesized from cholesterol. Cholesterol synthesis occurs in smooth endoplasmic reticulum hence cells are rich in this organelle. After bio-synthesis of cholesterol, the next steps of conversion to testosterone occurs in mitochondria where larger cholesterol molecules are cleaved into smaller testosterone molecules. The cells, therefore, are rich in mitochondria also.

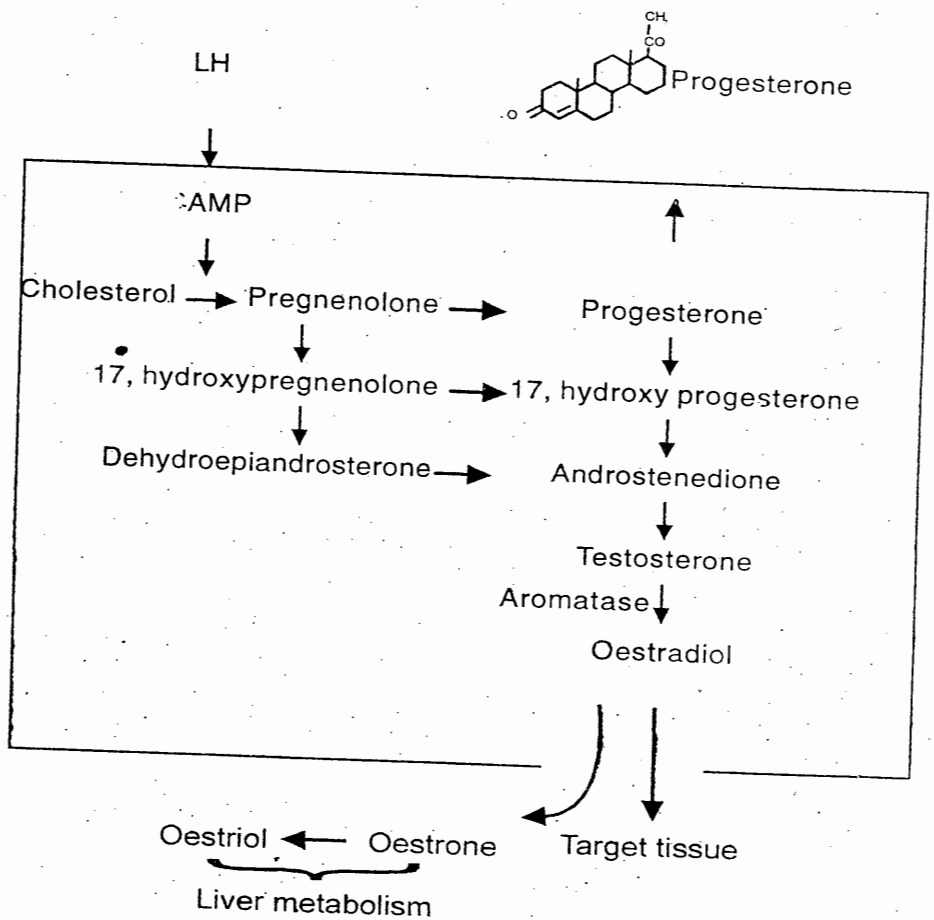
Germinal cells: This include several generations which are characterized by following ploidy—

Spermatogonia
(2n)
↓ mitosis
Primary Spermatocyte
(2n)
↓ Ist meiotic division
Secondary Spermatocyte
(n)
↓ 2nd meiotic division
Spermatid
(n)
↓ maturation on sertoli cells
Spermatozoa
(n)

Spermatogonia (2n) are fast dividing diploid cells which enlarge to form primary spermatocyte. Primary spermatocyte (2n) undergo first meiotic division and converted to secondary spermatocyte (n). Secondary spermatocyte divide by 2nd meiotic division and form spermatid. In spermatids, thus, all chromosomes are made up of single chromatid. Sperms, after maturation, leave testes via epididymis and reach seminal vesicle where it is nourished by seminal fluid. At the time of discharge, seminal fluid gets prostatic fluid which enhances sperms motility.



Serogenetics of Female system: Female sex hormone is oestrogen and pregnancy hormone is progesterone. Oestrogen is secreted by thecal cells of ovary, the cells of ovary that surround follicles. Some oestrogens are also produced by granulosa cells, cells, that sorround ovum, which are required for maturation of ova. Oestrogen is a C-18 steroid formed from testosterone (a C-19 steroid) in presence of an enzyme, aromatase. This conversion occurs mainly in thecal tissues. The level of oestrogen is highest during FSH/LH peak before ovulation (14th. day of menstrual cycle)



Oestrogen is metabolized (oxidised) in oestrone in lever.

It may be further hydrated to oestriol. Hence, three oestrogens are excreted in urine as glucuronides. During pregnancy the placenta is additional source of oestrogen. Adrenal gland and adipose tissue are other places of oestrogen formation (stallion produces highest level of oestrogen!)

Another hormone of ovary is **progesterone** which is secreted by corpus luteum. Granulosa cells, after ovulation, are transformed into corpus luteum. Corpus luteum cells lack smooth endoplasmic reticulum system, essential for steroid formation. Hence corpus luteum absorbs rich quantity of cholesterol for progesterone formation.

Prolactin (PRL) is a hormone from pituitary which is required for breast development and milk secretion. The plasma level of PR rises during pregnancy and continues a few months after birth of child. It initiates maternal behaviour hence also known as "hormone of maternity".

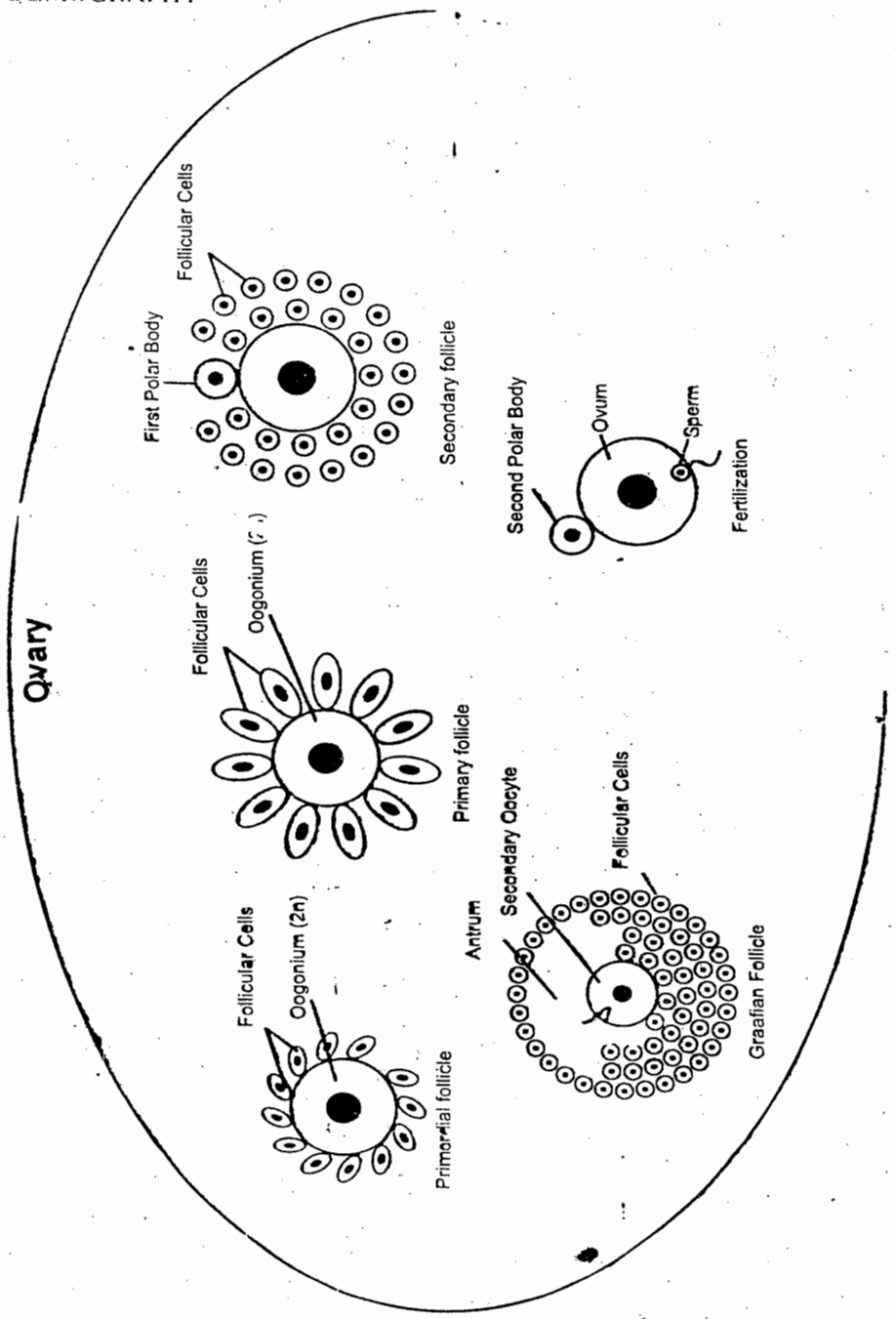
Granulosa cells also secrete a hormone called **inhibin**, which has negative feedback on FSH secretion from pituitary.

Two more hormones are involved in Female reproduction—oxytocin and relaxin. **Oxytocin** is secreted by hypothalamus and released by pituitary. It contracts the muscle of milk-follicles and ejects milk. The hormone also initiates labour-pain. **Relaxin** is secrected by uterus and dilates vagina for child birth.

Cytogenetics of Female System

Except descendants of Primary oocyte, all the cell populations of ovary are diploid. The **primordial follicles**, present at birth, has diploid oogonia surrounded by diploid, flat one layer of granulosa cells. **Primary follicles** has diploid primary oocytes surrounded by one layer of tall granulosa cells. Primary oocyte is larger than oogonia. Primary oocyte forms a polar body (n) and is converted into Secondary oocyte (n)

Secondary oocyte has half the number of chromosome and most cytoplasm whereas polar body has half of the chromosome and little of cytoplasm. The meiosis I, which is completed before ovulation, starts at birth of girl child and held up in metaphase stage till the month it is ovulated. It may be in 14th year or in the 44th. Year of women. Metaphase I thus has longest duration. The secondary follicle has secondary oocyte and is surrounded by multilayer follicular cells and forms graafian follicles. Secondary oocyte passes out from ovary during ovulation. Next maturation division (ie. meiosis II) occurs at the time of fertilization when sperm enters egg. Granulosa cells secrete a membrane, zona pellucida, at the time of ovulation to which sperms attach before fetilization.



ECOLOGICAL RULES OF EVOLUTION

Different factors of environment, both physical and biological, affect organisms and during evolution there has been more or less similar type of adaptations in various groups of animals against such factors. Such unity of mode of adjustments against a given set of ecological demands is referred to as ecological rules of evolution. Such rules include—

1. Allen's Rule : The rule states that in hotter areas the extremities (limbs, ear etc) tend to be increased and in colder areas tend to be decreased in size. This happens to increase surface area of body in former case and to decrease it in the latter case. With the increase in surface area, more blood below the skin comes in contact with the surrounding air and heat is lost. Opposite happens in colder areas. eg. shorter limb & tail in arctic fox.

A glimpse through the different racial stocks adjusted to their place of origin supports the contention. Populations eg. Niolotic Negro, which are inhabitant of hot, humid climate tend to have longer legs and are tall because sweating is ineffective in them and loss of heat is mainly through radiations. Conversely, populations in hot, dry climate tend to have shorter limbs. In both cases, surface area increases. In latter, the net volume and surface area is kept low to avoid heat-contracting (sun-stroke). Eskimo, inhabitant of colder areas, has short limbs.

2. Bergmann's Rule : It states that there is large bodies in colder climates eg. bears in Alaska.

A glimpse through different native racial stocks moots the point. People in temperate region, some places of which remain in the freezing conditions such as siberia, tend to be heavier and bulky, their trunk length being greater than limb-length. A larger body means greater body-mass and a greater body-mass means more metabolic heat needed by these people.

3. Gloger's Rule : The rule states that there is black pigmentation in hotter areas wheras it is absent in colder areas.

Black colour doesnot provide comfort in strong sunshine. A black feels more discomfort in sunshine than a white. But black colour absorbs strong sunshine at the surface and prevents if from reaching deep into skin lest it destroys Vit D. white skin, on the contrary, allows meagre sunshine in temperate regions to penetrate into skin for synthesis of Vit D. Vit-D is linked with calcium absorption and bone-formation. Human races show variation in pigmentation according to amount of sunshine.

4. Jordavi's Rule : The rule states that closely related species and sub-species are not found in the same geographic range and usually separated by some barriers. The rule underlines

importance of geographic isolation in speciation of animals. Unless a parental population is isolated it cannot develop genetic differences and form new species. The new species thus formed will resemble the original species from which it has descended but will occupy a different territory.

The case of *Australopithecus* evolution proves he point. It is found that evolutionary progression of *A. afarensis* occured in eastern Africa whereas those of *A. africanus* in South Africa. Similarly, *Paranthropus boisei* evolved in eastern Africa and *Paranthropus robustus* in South Africa.

5. Gause's Rule : The rule states that two species with identical ecological requirement cannot occupy the same ecological niche for long. Either one is driven away, or becomes extinct. Ecological niche of a species is that place in ecosystem in which a species performs its functions, feeds and reproduces. Two or more than two species occupying the same niche will face serious threat of food-shortage because both will use the same food. Thus, food will be a limiting factor. Another is the space-problem. Animal species requires a sufficient large breeding space and its litter size is reduced if there is overcrowding

6. Cope's Law : The rule states that animals in course of evolution tend to increase in size until nature imposes a restriction on this size-increase.

The rule seems to be true. Even in human evolution, our ancestors namely, *australopithecus, Homo erectus* were less than five feet in height but man of today is more than five feet in average height. Evolution permits increase in height in individuals on land because there is no as much balancing act required on land as in the tree. The increase in height in our ancestors must have facilitated them with a distant sight so that carnivores could be avoided, fruits could be obtained from tall bushes, and, locomotion could be rapid. Dinosaurs among animals are classic example of this increase in size. They increased to fantastic sizes till a drop of temperature due to formation of mountains (and also a possible collision of meteorite with the Earth causing no sun-rise for years and no vegetation) made these masters of mesozoic look pathetic-no place to hide from freezing temperatures and no food to eat.

This increase in size occurs generally in the herbivores. Carnivores, in order to catch its prey, have to spend a good amount of energy and it would be energetically not favourable for them to hunt with larger bodies.

Dollo's Law : The rule states that evolution is largely irreversible. Evolution is defined as phenotypic changes in an organism which adjusts the organism to the environment in better way. Since environment keep on changing and environment of the past cannot have a replica in the future hence exactly similar demands can never be placed on organisms from environment. Evolution, therefore, is irreversible.

DNA-PROFILING

(New Vistas in DNA-Fingerprinting)

Readers are referred to DNA-fingerprinting described in Forensic anthropology. The original methodology developed by Alec Jeffreys involved a probe with a sequence which was complementary to a large number of minisatellites (ie. **Multilocus Probe, MLP**) in human DNA. It produced numerous bands. This method of hybridization had some limitations— It needed large amounts of DNA; the bands produced couldnot be aligned to a chromosome and the results couldnot produce a computer Database.

Wong et al. (1987) developed a **single Locus Probe (SLP)** method which detects only one minisatellite per probe. Thus, if individuals are homozygote for the minisatellite, two bands will be found (its length will differ in two parents from whom it was inherited) and if individual is heterozygote (having inherited minisatellite from only one parent), only one band will be formed.

In the Original method, the probes were ^{32}P labelled and detection was achieved through autoradiography of an x-ray film placed over the nitrocellulose filter (nylon membrane). The time for hybridization differed— if only small amounts of DNA was available, the result on-x-ray film could approach 2 weeks. In a later development a chemiluminiscent method was employed in which an alkaline phosphatase was bound to the probe(Giles et al 1990). After hybridization, the nylon is sprayed with a solution containing a phosphated luminiscent substrate. In the area from where substrate is removed by alkaline phosphatase an unstable intermediate is formed which emits light which can produce image on photographic film. Results are produced in 1-2 days.

In the SLP method once this process is complete and recorded, the probe can be removed with alkaline detergent and another probe, which will detect another locus can be applied. This process can be continued with **sequential probing** until a sufficient discriminating result is produced.

SLP has become the standard method in forensic sciences. It became known as DNA-Profiling as any one SLP test was not sufficient to identify uniquely an individual. By combining four or more DNA profile test produced a near unique genetic definition of an individual.

FOSSIL TYPES AND AGE-DETERMINATION

Fossils are remains or impressions of past life.

Fossils can form in following ways :

Preservation of hard parts : Bones and teeth are the hardest part of the body and can be fossilized as such in sedimentary rocks.

Preservation of Soft parts : Many fossils are preserved in ice or amber (secretion of plants). Mammoths in ice and insects in amber are example. (see fossil DNA in multidisciplinary study of fossil types.)

Petrifaction : The organic part of the organism is degraded and replaced by inorganic material. Many bones are petrified bones.

Moulds and Casts : Fossils of brain is generally obtained in this form. When brain is disintegrated, sedimentary materials deposit in the cranium and take shape of brain. When skull bones disintegrate, the brain-casts one released. Brain-cast can be formed by obtaining one or few skull bones. (See endocast studies in multidisciplinary apprcach of fossil study)

There are various methods of determination of age of fossils such as.

(A) ABSOLUTE METHOD - Absolute age of fossils is calculated.

(B) COMPARATIVE METHOD - Ages are compared.

(A) ABSOLUTE METHOD :

1. Radioactive carbon method : When uv-rays stirke on nitrogen, C^{14} is formed, This C^{14} is present in environment with normal carbon C^{12}. Plants take up C^{14} in photosynthesis and animals when they eat plants. When animals die, the C^{14} losses radioactivity and converted to C^{12} at a fixed rate. The half-life period of C^{14} is about 5568 years. It is in this time that half of the C^{14} is converted into C^{12}, thus decreasing the ratio of C^{14} : C^{12} by half. By obtaining the ratio of C^{14} : C^{12}, the age of fossil can be calculated.

2. Potassium-Argon method : C^{14} method is handicapped In the sense that its half-life period is short and is operative with carbon only. Radioactive potassium is converted into Argon and its half-life period is over million year.

3. Uranium-lead method : Radioactive uranium is converted into lead and its half-life period is above 3 mya.

(B) Comparative methods

4. Aminoacid racemization : L- aminoacid is converted into D-aminoacid and their ratio can give antiquity of forms.

5. Aminoacid replacement : Antiquity of living organisms can be compared by finding out shifts in aminoacid content of a protein.

INDIA AS CRADLE-LAND FOR HUMAN EVOLUTION

Fossils of ancestral humans from India is meagre. The notable finds are the following :

1. *Palaeopithecus krishnaii :* (From Siwalik hills)
2. *Sivapithecus :* (From Siwalik hills)
3. *Ramapithecus :* (From Siwalik hills)
4. *Homo erectus narmadensis :* (From Hathnora, Hoshangabad, Narmada Valley)
5. *Gigantopithecus bilaspurensis :* (From Bilaspur)

Palaeopithecus Krishnaii was discovered from siwaliks. Detailed study of the fossil has indicated that the fossil is ancestral to Gibbons.

Ramapithecus, when discovered first in 1930 by Lewis, evoked great interest because of its old age (12-15 mya). Anthropologists badly needed a hominid ancestor of *H. erectus.* The fossil included a broken jaw and all the derivations were wrongly interpreted and the fossil was declared to be the most ancient hominid.

Sivapithecus was initially considered ancestor of Ramapithecus, but as Pilbeam (1990) has suggested, both are similar except canine. *Sivapithecus* has larger canine, *Ramapithecus* has smaller canine. It is suggested that *Ramapithecus* is female of *Sivapitheucs* and both gave rise to orang-utan.

Sonakia, Who discovered Homo erectus fossils from Narmada Valley, initially gave it an ealier age. Later on, by strict age-determination, it proved to belong to the group of early or archaic sapiens. The line probably indicates one of the incursions of african or chinese *erectus* into Indian territory.

Gigantopithecus bilaspurensis is similarly an offshoot of *erectus* evolution that ended in blind alley.

Thus India, in the matters of hominid evolution, can be rated only after Africa, Java and China. However, there has been no serious attempt to discover the fossils and many may be hidden in the bowel of the earth.

EPOCH			MAJOR EVENTS IN PRIMATES EVOLUTION
Pleistocene			First-known humans *(Homo)*
			3.6
Pliocene	Late		
	Early		First-known hominids *(Australopithecus)*
			5.2
Miocene	Late		
	Middle		Spread of African mammals, including hominoids into Eurasia.
	Early		First-known lorises First-known old World monkeys Early apes *(Procosnul)*
			23.3
Oligocene	Late		New World monkeys (platyrrhines) apper in S. America.
	Early		Primates disapear from Europe First-known tarsiers.
			35.4
Eocene	Late		Early Old simians
	Middle		Adapids and omomyids common in N. America, Europe and Asia.
	Early		First-known modern-looking primates (adapids and omomyids)
			56.5
Palaeocene	Late		
	Early		
			65.0
Cretaceous	Late		First-known archaic primates (plesiadapiforms)

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Evidences for 'OUT OF AFRICA' Model

Besides fossil evidences, other evidences come from nuclear DNA (microsatellite), mitochondrial DNA, Y-chromosomal DNA etc.

A. Support from microsatellite study : It has been found in a study by Bowcock (1994) that microsatellite such as CA repeats have highest variation in Africa. This is, however, not the case with other alleles. The reason for this discrepancy has been stated to be bias in the initial selection of the allele.

B. Support from mitochondrial DNA study : The mitochondrial DNA is present in the mitochondria and consists of about 16,500 base pairs, far less than nuclear DNA. Because offspring receive mitochondria only through egg and not through sperm, there is maternal lineage of the mitochondrial DNA. There is no recombination hence no shuffling of mitochondrial DNA, the only method by which it changes is through mutation. Rate of mutation in mitochondrial DNA is much higher than nuclear DNA. A study with 12 restriction endonucleases demonstrated that it contains about 200 polymorphic sites, different patterns present in different lineages.

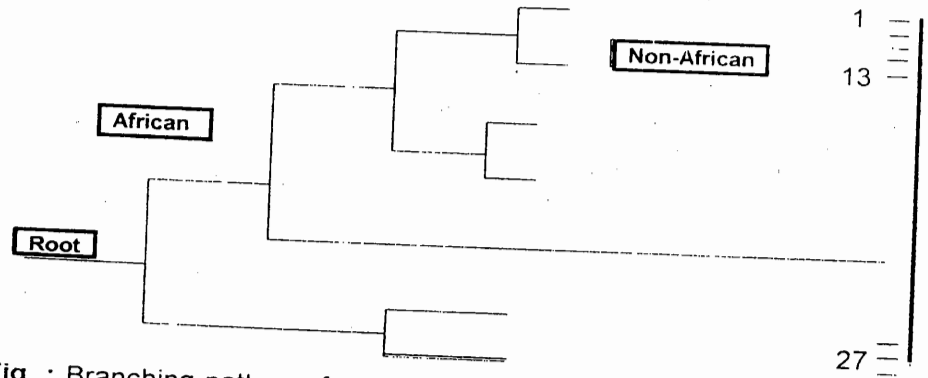

Fig. : Branching pattern of mt DNA variation. All lineages next to root are african. All the nodes (1) (2) (3) are found in Africans whereas non-Africans show only node (1). Africans carry 14 out of 27 sequences belonging to all the three nodes. Non-Africans carry only 13 sequences belonging only to node (1).

A schematic phylogenetic tree illustrating the general pattern of relationships among mt DNA sequences shows that the branches next to the root

(i.e. the last common ancestor of all human mt DNA lineages) consists exclusively of African sequences indicating that the oldest lineages are found among Africans. Further more, African lineages are found throughout the tree. A conclusion is that Africans, with a subset of mitochondrial variation, migrated out of Africa, leaving other variations behind. Thus, all non-Africans carry a sub-set of African mt DNA plus new variations acquired with lapse of time.

(C) Support From y-chromosome variation : As mt DNA is matrilineal, so the y-chromosome is patrilineal — from father to son. Y is paired with x but it has portions that do not pair with x and genes in such unpaired regions are passed to offspring unshuffled, like the mt genes. Rate of mutation is very low in y - chromosome in comparison to autosomes because y is single. The effective population size is also low for y because it is carried only by males whereas autosomes are carried by both males and females. Fewer mutations accumulate in y-chromosome hence extent of DNA sequence variation in y-chromosome is low. Therefore, techniques have been devised to study particular variable nucleotide (SNPs, single nucleotide Polymorphism) that are then studied in populations. In agreement with the mt DNA trees, y-chromosome trees show that Africans carry most ancestral lineages as well as considerably more genetic variation than non-Africans.

There are, however, two discrepancies between mt DNA and y-chromosomal variations. While most recent common ancestor (MRCA) (see chapter MRCA) estimates for mt DNA puts the age around 0.1 to 0.2 mya, MRCA estimates for y-chromosomal DNA puts the age around 60,000 years (Pritchard et. al. 2000). The second discrepancy relates to geographical clustering which is more for y-DNA and less for mt-DNA. Thus, a few y-DNA variation are characteristic of a population whereas mt DNA variations for a population are large. Paabo (2002) is of the opinion that it is because of more migrations for females than for males ("women on the move" hypothesis). It probably reflects the predominance of patrilocal societies, in which wives tend to move into their husband's natal households.

(D) Evidences from Other Nuclear DNA Sequence Variation : Autosomal DNA sequence variation includes microsatellite variation, single copy DNA variation, MHC (Major Histocompatibility Complex) variations and variations of xq 13.3.

Microsatellite variation has been discussed earlier. These are short nucleotide repeats that have a high mutation rate and are highly variable in length. Studies show that majority of length variants and thus greatest diversity is found among African genome. Alu-family is a short 300 bp interspersed repeat which replicate and jump around in the genome and give

rise to Alu-insertion polymorphism. Watkins and others (2001) have shown that ancestral sequences i.e. absence of Alu-insertion sequences is typical of Africans.

So far single-copy DNA variation is concerned, DNA sequences encoding B-globin, lipoprotein lipase, pyruvate dehydrogenase, melanocortin I receptor has already been published and many are in the pipeline. In general, these sequences show that the ancestral sequence is found among Africans and the age of the MRCA range from 0.7 (melanocortin 1 receptor MCIR) to 0.15 (pyruvate dehydrogenase) mya.

MHC and MCIR variability do not give any clue. These DNA sequences are related to immune response and pigmentation, respectively. Pigmentation and immune response are direct target of selection operating upon individual traits rather than influenced by population events such as migrations, bottlenecks or founder principle. For instance, there is local selection for sickle - cell anaemia gene in African population which provides immunity against malaria. Level of pigmentation is decided by the amount of sunshine and type of antibodies elicited is decided by the nature of pathogens present in the environment.

Variation at Xq 13.3

Present on the long arm of x chromosome is the region 13.3 which contains about 10,000bp. The region is non-coding hence not direct target of selection. Its recombination rate is about eight times lower than the average x-chromosomal recombination hence not much reshuffling of ancestral DNA sequences is caused. The situation is more advantageous in males because males carry only one X and there is no probability at all of xq 13.3 recombinations.

Two sorts of variations in xq 13.3 have been studied in populations — root-variation and variable nucleotide sites. Root sequence is carried by both Africans and non-africans, therefore not informative regarding its origin. Nine branches emanate from Root-sequence and Africans are present on all nine, whereas non-Africans on only four. In total, there are 33 variable sites in xq 13.3 region. Africans represent 24 whereas non-Africans only 17.

To conclude, all genetic evidences indicate that Africans carry more genetic diversity including variants not found out of Africa, and non-Africans carry less genetic diversity with variants also found in Africa. Of the 10 genomic regions such as mt DNA, y-chromosome, xq 13.3, Lipoprotein lipase, Pyruvate dehydrogenase, Melanocortin I receptor, B globin, dys 44, GK and Z FX, nine have ancestral sequences found in Africans. The observation that 90% of the ancestral sequences across the genome are African

in origin is not explained by multi-regional theory unless it is presumed that African founding population was much larger than the European and Asian founding population. Even in this grossly asymmetric relative population sizes, the contribution of non-Africans to the human gene pool will be minimal.

(E) Evidences from Linkage disequilibrium : Apart from evidences from DNA sequences, history of a genetic locus can also be estimated by variation along the sequence on a chromosome correlate between sites as a result of mutation and recombination. For example, assume that two SNP (Single nucleotide Polymorphism) occur in a DNA sequence. One SNP carries nucleotide A 30% times and nucleotide G 70% times whereas another SNP carries nucleotide C 70% and T 30% times. If recombination has acted for long priod of time to exchange information between chromosomes, the haplotype fequency will be as follows.

SNP 1.

SNP2		A = 0.3	G = 0.7
	C= 0.7	A - C= 0.21	C - G = 0.49
	T=0.3	A - T = 0.09	G - T = 0.21

Table : Linkage equilibrium. In linkage disequilibrium, haplotype C-G = 0.7 and A-T = 0.3 with absence of A-C and G-T haplotypes.

Thus, if the frequencies of haplotypes is larger or smaller, linkage disequilibrium is said to exist between the SNPs. Linkage disequilibrium indicates that not much time has elapsed since the (a) mutations generated SNPs b) two variants came into contact through migration.

Therefore, greater the extent of linkage disequilibrium between pairs of variable loci in a population , the younger the genetic variation in that population. Tishkoff et.al. (1996 a, 1996b, 1998, 2000) have studied linkage disequilibrium in CD4 locus, PLAT locus, myotonic dystrophy locus, Plasminogen Activator locus, and Reich (2001) on a genome wide scale. All studies indicate that gene-pool in Africa is older than outside Afica because linkage disequilibrium is less in Africa than outside.

Our genetic picture, overall, conforms with replacement hypothesis (out of Africa model) than with the regional continuity model. However this does not preclude that some of the genes of selective advantage from archaic human penetrated into modern human gene pool.

Evidences from Parasites

1. Evidences from louse genes

A louse is an obligate ectoparasite of most mammalian species. There are about 3000 species of lice of which 3 are classified as human disease agents. Analysis of louse genes indicate that the populations of *Homo sapiens* grew after a small band of early humans left Africa sometime between 1,50,000 and 50,000 years ago. All variations in the louse genes are traced back to louse genes present in Africa of this period.

2. Evidences from *Helicobacter pylori* genes : *Helicobacter pylori* is a bacterium that inhabit human stomach and duodenum that causes various degree of ulcers . It has been found that genetic diversity in the bacteriam *H.pylori* decreases with geographic distance from East Africa, the birth place of modern humans. Based on genetic diversity data, researchers have claimed that bacteria seemed to have spread from East Africa around 58,000 years ago. The evidence also suggests that human ancestors were infected with *H.pylori* before they migrated out of Africa.

What is a Haplotype ?

1. There are a group of enzymes called 'Restriction endonucleases'. These enzymes cut or cleave DNA at specific sites which include specific DNA bases. For example, an enzyme may cut at the following specific site –

A G A T A T C T

T C T A T A G A

Such sites are called 'palindrome' or inverted repeats as is evident in the two strands of DNA.

2. If DNA of any individual is cleaved by a restriction endonuclease, its DNA will be cut in pieces wherever such specific sites are present, reducing the long, continuous DNA thread into a number of pieces or fragments. Because these specific sites are distributed randomly on the DNA, the size of fragments will differ.

3. The fragments of DNA can be separated according to the size if we adopt a process called 'gel electrophoresis' in which DNA fragments are put to electrophoresis in a gel medium. In the medium, smaller fragments of DNA move faster hence travel greater distance and larger fragments travel slowly hence cover less distance. On the gel, we get a continuous smear of DNA, starting from larger to smaller fragments.

4. The gel platform is calibrated so that we can know what the size of a DNA is in a particular region of the gel. The calibration is in the form of kilo base (kb) i.e. 1000 base pairs (bp). A 10 kb fragment means that it is made up of 10,000 base-pairs.

5. Suppose, if the DNA contained a gene for sickle-cell anemia, this gene can be searched on the DNA fragments. For this, we adopt a practice called 'Southern blotting'. In this process, DNA fragments on the gel are blotted on a nitrocellulose filter paper.

6. The DNA fragments are now transferred from gel to filter paper. We get a DNA probe for the sickle cell anemia gene. A DNA probe is radioactively labeled complementary DNA of a specific gene we are looking for. We put DNA probe on the filter paper and allow the hybridization to occur with the sickle cell anemia gene.

7. The filter paper is washed so that whatever excess DNA probe present on the filter paper that has not hybridized with the gene for sickle cell anemia is washed out. Now we have only those radioactive DNA probes that have hybridized with the sickle cell anemia gene present on the DNA fragments.

8. This can be found out by exposing the filter paper to autoradiography. Since Calibration is maintained from gel to filter paper to x-ray film, we can find out what the size of the fragment is with which the DNA probe has hybridized. Because the DNA probe is for sickle cell anemia gene, hence the gene must be present on that fragment.

9. Suppose we get the gene on a 10 kb fragment when it is cleaved by restriction endonuclease A. Suppose we get it on a 9 kb fragment if cleaved by enzyme B; on 7 kb fragment if cleaved by enzyme C. The Haplotype in this case is A10 B9 C7 for the gene sickle cell anemia. Thus, in molecular genetics, a haplotype is a set of restriction fragment sites closely linked to one another and to a gene of interest.

10. For individuals of a population genetically closely related the same haplotype i.e. A10 B9 C7 will be found. This can be given a name, say, Haplotype X.

11. Individuals from genetically different populations may show up restriction fragment length, say, A5B7 C10 for the gene sickle cell anaemia . It is different haptotype, say, haplotype Y.

12. For one restriction endonuclease enzyme say A, the gene for sickle cell anaemia goes with a fragment size of 10 kb in a one population and with DNA of 5 kb in another population is referred to as Restriction Fragment Length Poly morphizn or RFLP For classification of RFLP see genetic analysis of Man.

13. The term haplotype is also used in classical genetics.

The MRCA
(Most Recent Common Ancestor)
IAP
(Identical Ancestor Point)
TMRCA
(Time of Most Recent Common Ancestor)

MRCA: MRCA of any set of Organism is the most recent individual from which all organisms in the group are directly descended. The term is often applied to human genealogy. The MRCA of a set of individuals can sometimes be determined by referring to an established pedigree. However, sometimes it becomes difficult to identify the MRCA and only an estimate of the time at which the MRCA lived can be given. Such estimates are based on DNA tests and mutation rates.

The term MRCA is used to denote common ancestor of individuals of a species. However, a common ancestor of two species can also be indicated through a separate term, Last Common Ancestor (LCA) or the equivalent term **concestor** is sometimes used in place of MRCA. The term MRCA may also be used to identify a common ancestor via specific gene pathway in which ancestry of an individual gene is explored via coalescent pathway. In such pathway alleles of a gene shared by all members of the population is traced back to a single ancestral copy, known as Most Recent Common Ancestor (MRCA).

Two pieces of genetic elements namely mitochondrial DNA and a part of y-chromosome is not shuffled and passed from generation to generation unaltered – mitochondrial DNA from mother and y-chromosome from father. Hence, MRCA can also be considered matrilineally and patrilineally, in former case through mitochondrial DNA and, in the latter case, through y-chromosomal DNA. It is because mitochondrial DNA is passed to the offsprings through ovum, sperm contributing practically no mito-chondrial DNA, hence if a mother has only sons and no daughter, the inheritance of her mitochondrial DNA will be disrupted. Similarly, y-chromosome is passed only to males and inherited via males, hence if a man has only daughters and no son, inheritace of his y-chromosome will be disrupted. Matrilineal and patrilineal MRCA must have had a number of contemporaries at her and his times but only they were able to continue their genetic elements through unbroken lines of inheritance whereas their contemporaries failed to do so.

Approximate dates of matrilineal, patrilineal and general MRCA can be calculated on the basis of Single Nucleotide Polymorphism (SNP) and rate of mutations on the basis of above estimates. Approximate dates of matrilineal, patrilineal and general MRCA has been calculated to be approximately 1,60,000 years ago. 60,000 years ago and 2,000 to 5,000 years ago, respectively.

Matrilineal MRCA as stated above, has been derived through study of common variations in mitochondrial DNA, patrilineal MRCA has been derived through study of common variations in y-chromosomal DNA, General MRCA has been derived through study of single gene pathway.

(A) Mitochondrial Eve or mt - MRCA

Mitochondrial Eve is the female counterpart of y-chromosomal Adam, although they lived at different times the former 1,50,000 – 2,50,000 years (average 1,60,000 years) BP (1 January 1950) and the latter about 60,000 years BP, probably in the East Africa in the region of Tanzania and areas South and west of it.

Mt Eve lived during a period of time when *H.sapiens* were developing as a separate species. As an individual she lived in a small population (between 4000-5000 females capable of producing offspring at any given time). Mt eve would have been contemporary to fossils found in Ethiopia near Omo river and at Hertho. namely *H. sapiens idaltu*.The fossil is dated 1,60,000 years ago.

Mt eve is traced from every individual to his/her mother and continue from each of these mothers to their mothers and so on. Going back through time these lines converge on one ancestral mother. This female was nicknamed 'Eve' because she bore the template of mitochondrial genome whose replica can be traced in every human being.

Mitogenomes are passed from mother to offspring. Only rarely father's mitogenomes are passed to the offspring and that too it is in so less in quantity that it rarely reaches to the germ cells of offspring. So recombination between maternal and paternal mitogenomes is almost non-existent.

All complex animals can also trace their ancestory back to a mitochondrial MRCA (Most Recent Common Ancestor). Chimps and humans share a mitochondrial MRCA. Further back in time, the human/ chimp MRCA share an earlier MRCA.

Mitochondrial DNA replicates faithfully and produces a clone to be inherited by offspring. Only rarely, once in 10,000 years, a stable mutation occurs and perpetuate down the progeny line.

Such a mutation occurred in the basal stocks and thus Lo and L1 lineages were differentiated. It is unknown which of the two lineages is

ancestral because each lineage accumulated multiple mutations after this split. Hence both lineages can be considered as having arisen from an ancestral mitogenome. To-day, Lo is restricted to African population whereas L1 is ancestral haplogroup of all non-Africans, as well as most Africans.

(B) Y-Chromosomal Adam (Y-MRCA)

Most Recent Common Ancestor (MRCA) in genetics of a group is the most recent individual from which all organisms in the group are directly descended. Y-MRCA is the individual from which y-chromosome of all living men are descended. Y-chromosomal Adam is thus male counterpart of mitochondrial Eve (mt Eve). By analyzing the y-chromosome DNA males in all region of the world, Spencer Wells and Rhodes has concluded that all humans alive today are patrilinealy descended from a single man who lived in Africa 60,000 years ago. The approximate dates of y-chromosomal Adam and mt-Eve differ- while an age of approximately 60,000 years ago has been estimated for y-chromosomal Adam, it is more than. 1,60,000 years ago for mt-Eve-approximately 1,00,000 years apart.

This difference in the ages of y-MRCA and Mt-MRCA can be explained. It is important to understand that y-Adam was not the only male of his time. He must have co-existed with a large number of human males. None of the y-Adam's male contemporaries, however, have a direct unbroken male line to the present day. Either their lines died out entirely, or at least one generation within each line produced only daughters who could not pass their male parent's and ancestor's y-chromosome to their own children.

If this can happen in the male line, the same can happen in the female line also. Great age of mt - MRCA will be revised if a woman produces only male child, ensuring no inheritance of mitochondrial DNA to her offspring, or she dies out without leaving any offspring. Had the above conditions existed equally in the two sexes, there would not have been much difference in the dates of y-MRCA and mt-MRCA. The solution to the above paradox lies in the statistical dispersion of the probability distribution for a palaeolithic man to have living descendant. In comparison to a palaeolithic woman. While fertile woman had more or less equally distributed chances of giving birth to a certain number of fertile children, chances for fertile men varied widely, with some fathering no offspring and some fathering many. Chances of bottlenecks in male line, thus, is greater than in female line. This difference in variance in the number of descendants of male and female parents was first pointed out by Bateman (1948) in case of fruitfly , *Drosophila*.

We should understand that in the ancient past, our y-MRCA was not the y-MRCA of entire population and in the future one of his descendants may take over. The y-MRCA of all humans alive today is different from one for humans alive at some point in remote part or future. As male lines dies out a more recent individual becomes the new Y-MRCA. Such situation are less likely to occur during the period of rapid population growth but likely to occur during bottlenecks.

IAP: The MRCA had many contemporary companions at his or her time. Some of the contemporaries of MRCA left no descendants and thus they are ancestors of no one in the current population; others may be ancestral to some but not the entire current population.

As we push back further in time, the MRCA had its ancestors in past. Eventually we reach a point in time when all humans can be divided into two groups: those who left no descendants today and those who are common ancestors of all living humans today. This point in time is referred to as Identical Ancestors Point (IAP). From this point back, all the living individuals share the same set of ancestors, all the way to the single-celled organisms. On the contrary, from this point forward, the entire living person receive genes in dramatically different proportions.

The Identical Ancestors Point for *Homo sapiens* has been estimated to be between 15,000 and 5,000 years ago with an estimate of human MRCA living about 2,000 to 5,000 years ago

Thus, IAP estimate is about three times as distant as MRCA. Matrilineal and Patrilineal MRCA estimates are far more remote – 1, 60,000 years and 60,000 years ago, respectively.

It is incorrect to assume that MRCA or its ancestor passed all its genes to its offspring. In sexual reproduction, a parent passes only half of its genes to the next generation. The percentage of genes inherited from MRCA becomes smaller and smaller at every successive generations as genes inherited from contemporaries of MRCA are interchanged through sexual reproduction.

Coalescence time or Time of Most Recent Common Ancestor (TMRCA)

Coalescence time is a measure of average genetic distance of genes in extant populations to predicted sequence of the mt DNA MRCA. TMRCA is significant because it can be used to describe population structure and indicate places and culture of ancient ancestors. The coalescence studies conducted in 2007 estimate TMRCA of the Lo/L1 split in modern humans to 1,94,300 ± 32,500 years BP. According to coalescent theory, this would place the number of females in the effective population at below 5000 females.

DISTRIBUTION OF MODERN HUMANS

Recent Single Origin Hypothesis (RSOH)
or,
Recent out of Africa model (ROAM)
or,
Replacement Hypothesis

The hypothesis that human had originated in Africa was published in Charles Darwin's "Descent of Man" in 1871. The concept was speculative until the 1980s when it was supported by the study of mitochondrial DNA and non-recombining DNA of y-chromosome of male humans combined with evidences based on physical anthropology of archaic specimens. According to both genetic and fossil evidences, archaic *Homo sapiens* evolved to anatomically modern humans solely in Africa between 2, 00,000 to 1, 00,000 years ago, with members of one branch leaving Africa by 60,000 years ago and over time replacing earlier human populations such as Neanderthal and *Homo erectus*. According to this theory, around the above time frame, one of the African sub-populations went through a process of speciation prohibiting gene flow between African and Eurasian Human populations. The recent single origin of modern humans in East Africa is the near consensus position held within the scientific community.

Alternatively, some support the original "Out of Africa" migration, in this case by *H. erectus* and not by *Homo sapiens* – two million years ago. Still another hypothesis is the multiregional hypothesis of origin of modern humans. "Recent out of Africa" model is evidenced by study of mitochondrial DNA and y-chromosome of human populations. Mitochondrial Eve is the name given by researchers to the woman who is defined as the matrilineal most recent common ancestor for all currently living humans. Derivatives of her mitochondrial DNA is found in all living humans. Similarly, y-chromosomal Adam is the name given by researchers to the man who is defined as patriarchal most recent common ancestor for all currently living men. Mitochondrial DNA from mother is inherited by all sons and daughters where as y- chromosome is inherited by sons only. Studies of mitochondrial variations and y-chromosomal variations have indicated that all variants of these structures possessed by all humans today can be traced back to the African population.

In mitochondrial DNA, following are the haplogroups in African populations: (See figure)

L_0, L_1, L_2, L_3, M and N. Haplogroup L_0 is one of the earliest branches from Most Recent Common Ancestor (MRCA) and found in high proportion in South and East Africa. These groups branched off early in human history and remained relatively genetically isolated. L_1 is believed to have evolved in East Africa about 0.17mya to 0.15 mya whereas L_2 around 0.1mya to 90,000 yrs ago and L_3 in a later date 90,000 to 70,000 yrs ago. L_1 and L_2 which have descended from L_0 represent about two-third of mitochondrial DNA which has remained in East Africa. According to recent African origin hypothesis, a small group of L_3 bearers of East Africa left Africa and populated the whole world.

Some workers believe that only a few people left Africa in a **single migration** that went on to populate the rest of the world. It is estimated that from a population of 2,000 to 5,000 in Africa, only a small group of possibly 150 people crossed the Red Sea. This is because, of all the lineages present in Africa, only the daughters of one lineage, L_3 are found outside Africa. Had there been several migrations one would expect more than one African lineage outside Africa. L_3's daughters, the M and N lineages, are found in very low frequencies in Africa. A possible explanation is that these mutations occurred in East Africa shortly before the exodus and by the founder-effect became the dominant haplogroups of rest of the world after the exodus from Africa. Haplogroup N is predominant in Europe and Haplogroup M is absent in Europe. (One theory presumes that the small European founder population initially expressed both haplogoups M and N and could have lost Haplogroups M through random genetic drift resulting from a bottleneck).

Alternatively, some workers have proposed a **Multiple Dispersal Model**, in which there were two migrations out of Africa – one across the Red Sea to South Asia through Coastal route represented by Haplogroup M and another group of migrants with haplogoup N followed the Nile from East Africa heading northward. This group then branched in several directions, some moving into Europe and other heading east into Asia.

Whether single migration through Red sea and subsequent bottleneck, or multiple migrations through Red sea and Nile, the reasons for such migration(s) is not known. Migrations occurred because human ancestors were probably searching for food or escaping climate change. The Red Sea is about 20 KM wide but believed to be much narrower and shallower at that time. There may have been islands in between which could be

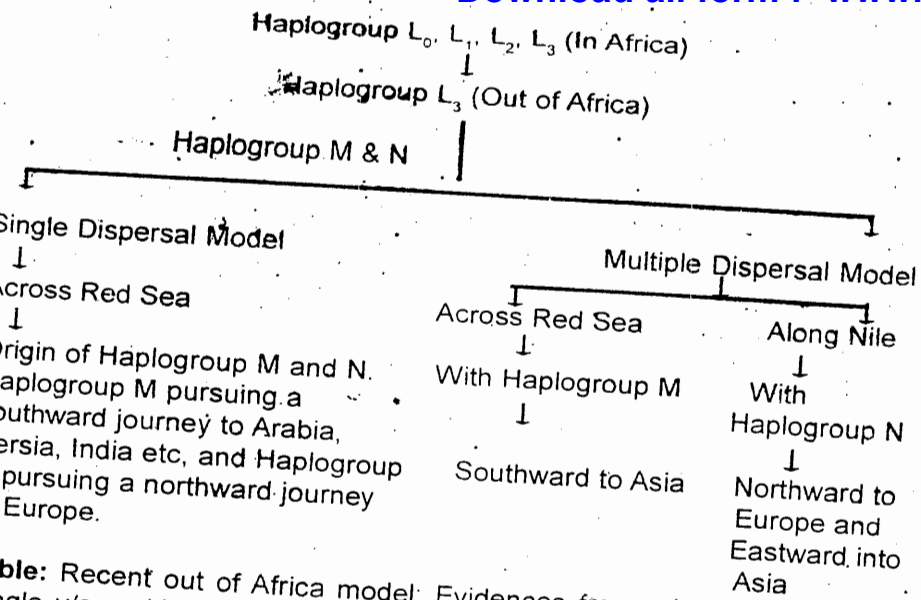

Table: Recent out of Africa model: Evidences from mitochondrial DNA: Single v/s multiple dispersal models. Single dispersal model has more evidences.

reached by simple rafts. Shells of ancient origin indicate that the diet of early humans included sea food obtained by beachcombing, a hunting exercise in the intertidal zone.

In the y-chromosome, there are two groups – haplogroup A and haplogroup B. Haplogroup A is found mainly in the southern Africa's Khoisan ethnic group which has lighter skin and epicanthic fold. It represents the oldest and most diverse of the human y-chromosome haplogroup. Haplogroup B is found mainly in Sub-Saharan region of Central Africa. After haplogroup A, it is the second oldest and one of the most diverse human y-haplogroup present in most human populations. The other y-chromosome haplogroup are Haplogroup C, Haplogroup D,E and F descending from more ancient haplogroups DE and CF. More than 90% of male not native to Africa are descended in direct male line from first bearer of haplogroup C and F, both descendants of haplogroup CF.

South Asia -Australia – East Asia

Most studies support single migration to south followed by rapid northern migration of a subset of the group. The people who took southern route spread to West Asia, Arabia and Persia until they reached India. India appears to be the first major settling point because 60% of Indian population

belongs to haplogroup M and the haplogroup M has the greatest diversity in India indicating that it is here where mutations may have occurred. The indigenous people of the Andaman Islands also belong to M lineage. The Andamanese are thought be an offshoot of earliest inhabitants of Asia because of their long isolation from mainland Asia. They are evidence of the coastal route of early settlers that extends from India along the coast of Thailand and Indonesia all the way to the Papua – New Guinea. Because haplogroup M is found in high frequencies in New-Guinea where people have dark skin and afro-textured hair, it is believed that both are the part of the same wave of migration that occurred around 60,000 years ago across Red Sea in the **Great coastal migration**. Both New Guineans and African contain the same version of MCIR (one of the genes for melanin production) except a single silent mutation. Hence, though Andamanese - New Guineans and Africans differ at a number of loci, selections for some loci has continued similarly. It supports the hypothesis that present day remnants of the ancient phenotype can be seen among Andamanese, New Guineans and contemporary Africans (others suggest that this could be due to convergent evolution).

The group which went north radiated to Europe , eventually displacing the Neanderthals. They also radiated to India. The former group, the Southern branch, reached Australia between 55,000 and 30,000 years ago. Australia was populated upto 10,000 years before Europe because colder region of the north was avoided by humans. Also; in Australia, 46,000 years ago, all large mammals weighing more than 100 kg, suddenly became extinct. The new settlers were likely to be responsible for this extinction. While some settlers crossed into Australia others may have continued eastward, eventually to China and Japan. This coastal migration is confirmed by the dominant presence of haplogroup M (mitochondrial DNA), which is a descendant of haplogroup L3, and haplogroup C (Y-DNA) which is a descendant of haplogroup CF. There is, however, some discontinuous distribution of haplogroup M and N; M being predominant lineage in Eastern India and SE Asia whereas Haplogroup N being predominant lineage in East Asia and Australia. This can be explained by founder effect and bottleneck. Founder effect occurs when a genotype multiplies in barren land; bottleneck occurs when a genotype survives during a natural calamity.

Northward migration to Europe

Europe was colonized by northwest migration from 45,000 years to 15,000 years before where modern humans competed with Neanderthals. Because Neanderthals were well adapted for colder regions, existing there for well over 0.2 million years, modern humans with superior technology

and language, eventually replaced Neanderthals. After 30,000 years ago, there is no record of Neanderthals whose last refuge was Iberian Peninsula which includes modern day Spain, Portugal etc.

Central and Northern Asia:

In Central and Northern Asia, three mitochondrial DNA haplogroups appeared between 30,000 to 50,000 years ago:

- Haplogroup A (descendent of haplogroup N)
- Haplogroup B (descendant of haplogroup R), and
- Haplogroup G (descendant of haplogroup M)

The bearers of these haplogroups subsequently colonized Siberia and Russia.

The Americas:

The Americas were occupied by the people who crossed from Siberia into Alaska. At this time sea-levels were lower and a land bridge of the lost continent of Beringia connected North America to Eurasia. There is much controversy about when Americas were colonised and how many migrations there were. Controversial findings in Chile (Monte Verde) indicate a human presence in America by upto 33,000 yrs ago. The oldest undisputable evidence of human presence in America is findings related to the **Clovis culture**. The culture existed 11,500 yrs ago and is characterized by a particular tool kit adapted to the hunting of large mammals such as mammoths which became extinct around this time.

Personal genetic maps

David Bentley (2008) of Iplumina cambridge Ltd (UK) and Jun wang (2008) of the Beijing Genomics Institute. Shenzen (china) have sequenced two personal genomes the former of an African individual from the Yoruba ethnic group of west Africa and latter of an East Asian individual Both have used powerful next generation genome sequencing technology, designated Illumina (formerly solexa) massive parallel sequencing technique that enables 100 million DNA fragments to be sequenced in a parallel on a chip. The genome has been matched with other individual genome available — that of J. D. watson and Craig venter. Personal genetic maps will become a clinical tool in near future supporting diagnosis, prevention and therapy of human diseases.

Behavioural Modernity (Cultural Evolution of Man)

re-historic age is divided into three Stages —

. Stone age or lithic age 2. Copper - Bronze age 3. Iron - age

tone - age is divided in old-stone age (palaeolithic), mid stone age (Mesolithic) nd New stone age (Neolithic). Lower palaeolithic period, which spans from 2.5 mya to 1,00,000 years ago, contain much of the cultural activities of the early *lomo* such as *Homo habilis* Homo *erectus* etc. whereas middle palaeolithic which spans from 300,000 years ago to 30,000 years ago. and upper palaeolithic, which spans from 40,000 years ago to 10,000 years ago, contain cultural activities of more evolved Homo such as *Homo neanderthalensis* and *Homo sapiens* including ro-magnon. The periods are associated with characterstic stone tool implements which are indicative of existence of a unique tool-making industry in various periods. hese periods of specific cultural activities are given specific names. Following are he different cultures that existed in the old stone age in the different parts of world om an estimated 2.5 million years ago to 10,000 years ago. **(See Chart)**

Social organisations

. The social organisations of the australopiths is comparatively unknown. Even ocial organisation of lower palaeolithic humans such as *Homo habilis* and *Homo erectus* is also unknown though it is believed that from 1.7 million years onward, here evolved in human ancestors such as *Homo habilis*, *Homo ergaster. Homo erectus etc.* the tendency to invent central camp-sites or home-bases and incorporate them into their foraging and hunting strategies. However, definite evidence for he existence of camp-sites and home bases as indicated by presence of hearths nd shelters dates back to 500, 000 years ago.

2. Regarding existence of monogamous vrs polygamous life-styles, workers are of iew that sexual dimorphism (differences between male and female morphology) was more pronounced in australopiths and *Homo erectus* in camparison to modern humans hence earlier forms were polygamous. It has been found that greater he sexual dimorphism, larger is the chances of polygamy.

3. Human societies from palaeolithic to early neolithic farming tribes lived without states and organised government. There are evidences that lower palaeolithic people were not grouped into bands though during the end of lower palaeolithic *Homo rectus* possibly began living in small bands similar to middle and upper palaeolithic ocieties and modern hunter-gatherer without a settled life. A band-society is a mall kingroup consisting of 30-50 individuals. Band societies sometimes organised nto ' macrobands' for activities such as celebrations and acquisition of abundant esources. By the end of palaeolithic around 10,000 BP people began to settle down into permanent locations and began to rely on agriculture for subsistence.

4. Evidences exist about long-distance trade between bands for rare commodities such as ochre (pigment to create light yellow brown and red colour), which was often used for religious purposes such as rituals as early as 1,20,000 years ago. During middle palaeolithic, exchange of other resources may have occurred to ensure survival during lean times.

Pre-Historic Age

1. Stone Age

(A) Palaeolithic (Old Stone Age)

(i) Lower Palaeolithic
(2.5 mya - 100, 000 yrs ago)

*** Oldowan**
It is the first known tool complex in prehistory which includes simplest known flakes; derives its name from olduwai gorge from where *Homo habilis* fossils were discovered. 2.0 mya in Africa.

*** Acheulean**
It extended across Africa and much of west Asia and Europe, tools more sophisticated than oldowan.

*** Clactonian**
Tool industry of *Homo erectus* associated with flint*1 tool of Europe - Also called Hoxinian or the Holstein stages.

*1**Flint** is a hard stone, a form of silica, but less lustrous

(ii) Middle Palaeolithic
(Circa 300,000-30,000 yrs. ago)

*** Mousterian**
predominantly flint tools associated primarily with *Homo neanderthalensis;* mainly scrapers, first discovered from Moustier (France).

*** Aterian**
Stone tools associated with human fossils around Atlas mountain and northern Sahara in Africa.

(iii) Upper Palaeolithic
(40,000 - 10,000 yrs. ago)

*** Chatelperronian**
Industry of chatelperron, France that extends into spain.

*** Aurignacian**
Culture of Europe and South-West Asia; derives its name from Aurignac, France. It began 36,000 years ago and lasted until 26,000 year ago;
It belonged to early modern humans.

*** Gravettian**
European Industry

*** Solutrean**
Advanced flint tool making industry, derives its name from solutre, Eastern France, appeared around 19,000 years ago; belonged to modern humans.

*** Magdalenian**
later culture of Western France, derives its name from La Magdeleine, Tursac, France; belonged to modern humans.

(B) Mesolithic
(Middle Stone Age)
(10,000-9,000 yrs.ago)

(C) Neolithic
(New Stone Age)
(9,000-8,000 yrs.ago)
- Domestication of animals, agriculture, pottery & textile

2. Copper Age

3. Bronze Age

4. Iron Age

5. In general, middle and upper palaeolithic societies were possibly fundamentally egalitarian and may have rarely or never engaged in organised violence (or war) between groups. Howerver, resource-rich environments, such as Sungir, Russia (about 30,000 years ago) may have had more complex and hierarchical societies such as tribes. Tribes differed from other middle and upper palaeolithic societies in the sense that it was often engaged in endemic warfare to protect its rich resources, had a formal division of labour and formal leadership in chiefs or monarchs.
6. Apparent egalitarianism in middle and upper palaeolithic has been recently explained on the basis of primitive communism, a brainchild of Marx and Friedrich Engels referring to the collective right to basic resources in preagrarian societies. Christopher Boehm (1999) has hypothesized that egalitarianism may have evolved in palaeolithic societies because of a need to ensure a stable food supply. According to Raymond C. Kelly it resulted from a low population density, cooperative relationship between groups and collaboration in hunting expeditions.
7. Lower, middle and most of the upper palaeolithic seems to be a period of gender equality with there being no division of labour between males and females. It is only in the later upper palaeolithic that sexual division of labour appears with men engaged in hunting and gathering food and women procuring small game-animals or driving herds with men. This ensured most efficient procurement of food. Archaeological evidences suggest that individual women enjoyed high status in their communities. The earliest known palaeolithic shaman (c 30,000 BP) was female. Jared Diamond suggests that status of women declined with the adoption of agriculture because women in farming societies have more pregnancies and expected to do more demanding work than their counterparts in hunter-gatherer societies. The presumably higher status enjoyed by women in palaeolithic and mesolithic societies is corroborated by the fact that these societies were probably matrilineal.

State of Art and Music

1. There are only two examples of lower palaeolithic and two examples of middle palaeolithic art. The art form of lower palaeolithic are venus of Tan-Tan and elephant bone pattern whereas art forms of middle palaeolithic are two bracelets and use of ochre in rock-art. Venus of Tan-Tan is an alleged artefact found in Morocco. It is 6 cm long quartzite rock which depict faceless human form dated between 300,000 to 500,000 years ago. This is supposed to have been created by Acheulean tool user such as *Homo erectus*. The first art form created by modern humans is in the form of two bracelet from Blombos cave (South Africa), dating 75,000-80,000 years ago. This is a piece of bone decorated with beads of Nassarius shells. It is indicative that human ancestors collected stones and bones for aesthetic qualities. There are also evidence of rock-art and use of ochre such as one from Bilzingsleben.

2. The art form of upper palaeolithic, dating 40,000 to 10,000 years ago, is much varied and rich. It includes cave-paintings, venus figurines, animal carvings and rock paintings. Upper palaeolithic art can be divided into two groups — figurative art such as cave paintings which depicts animals etc and non-figurative which consists of shape and symbols. Cave paintings have been interpreted in a number

of ways. Physical Anthropologist Abbe Breuil considers it as a form of magic designed to ensure a successful hunt. The hypothesis is, however, doubtful because it depicts such animals as lions and saber - toothed cat which were not hunted for food, and existence of half-human, half-animal beings in cave paintings. The anthropologist Lewis-williams has suggested that palaeolithic cave-paintings were indications of shamanistic practices because half-human, half-animal paintings and remoteness of these caves are reminiscent of modern hunter-gatherer shamanistic practices. Symbol- like paintings are more commonly found in paintings than depictions of animals and humans and unique symbols might have been trademark of different ethnic groups.

3. Venus figurines have been variously described as representing goddesses, pornographic imagery, apotropaic amulets used for sympathetic magic and even as self-portrait of women themselves. Guthrie maintains that these figurines, along with painting of powerful beasts, display fantasies of adolescent males during the upper palaeolithic. The abundance of such female imagery has led some workers to believe that upper palaeolithic society had a female-centered religion and a female-dominated society.

Music

Though there is no direct evidence of this form of art from palaeolithic, it is supposed that music may have developed from rhythmic sound of daily activities such as cracking nuts by hitting them with stones. Maintaining a rhythm while working is an energy efficient practice. Humans used flute like bone-pipes and animal skin drums in rituals.

Religion and beliefs

1. James Harrod and Vincent W. Fallio have recently proposed that religion and spirituality arose in oldowan societies or even earlier and rituals were used in their socieities to strengthen social bonding and group cohesion. Use of burials by krapina man, Croatia (30,000BP) and Qafzeh man (1,000,00 BP) have led Philip Lieberman and others to believe that middle palaeolithic men may have had a belief in after-life.

2. Cut marks on the Neanderthals at Cobe-Grenal and Abri Moula in France suggest that Neanderthals, like some contemporary cultures, may have practised ritual defleshing for religious reasons.

3. Neanderthal societies also practised the earliest form of totemism or animal worship in addition to religious burial. A bear-cult was widespread among middle palaeolithic neanderthal as is evident from a number of neaderthal sites. Bear-cult involved a type of sacrificial bear ceremonialism in which a bear was shot with arrows and finished off by a shot in the lungs. The bear was buried near a clay bear statue covered with bear fur, the body and skull buried separately. Additional evidences of animal worship comes from Tsodito Hills (c 70, 000 B.P.) in Kalahari desert in Africa. Here a giant rock resembling a Python is accompanied by large number of coloured spear heads which were offerings to the Python god. Hunter and gatherer tribe, Kung san tribe, which is descendants of people who devised Tsodito hills ritual, worship pythons even today.

4. Existence of general anthropomorphic images and half human-half animal images in the upper palaeolithic indicate that people believed in polytheism (worship of multiple deities). At the same time, these may indicate existence of shamanistic practices similar to those of contemporary tribal societies.

5. According to Vincent W. Fallio, ancestor-cult first emerged in complex upper palaeolithic societies. Elites of these societies, like present day Tlingits of north west America, used special rituals for ancestor worship to solidify their control over their subjects. Religious practices of such societies were thus divided into two spheres-popular religion and elite religion.

Diet & Nutrition

1. There are evidences that palaeolithic people consumed both plant food and animal flesh proportions of which varied according to the regions of their habitat. Hunter - gatherers in tropical regions such as Africa consumed more plant-based diets, while population in colder regions such as Northern Europe consumed more meat. It is probable that palaeolithic-mesolithic people, who were hunter-gatherer, experienced lesser malnutrition and famine in comparison to Neolithic farming tribes because former had access to wide variety of wild plants and animals where as latter were dependent on a small number of cultivated crops. It is also probable that palaeolithic and mesolithic people suffered less from diseases of affluence (type II diabetes, cardio-vascular diseases, obesity etc) in comparison to agriculturist neolithic people who were dependent on less number of crops in their diet, and led a stationary life. It is because of this reason that even in the contemporary society a dietary regimen known as palaeolithic diet or cavemen diet, or stone age diet is prescribed as a preventive measure against the diseases of affluence.

2. Large seeded legumes were part of palaeolithic diet as is evidenced from mousterian layers of Kebara cave (Israel). Recent evidences indicate that wild cereal grains were processed and consumed as early as 23, 000 years ago. Recent archaeological evidences also indicate that wine making originated in palaeolithic when early humans drank the juice of naturally fermented wild grapes from animal skin pouches. Horticultural activities were scant except in tubers and bananas which were cultivated from 25,000 BP in South-East Asia. Pastoralism and animal husbandry for milk and meat was practised in late upper palaeolithic. Europeans domesticated reindeer as early as 14,000 BP for their meat and milk. Use of shellfish and other fishes in diets of human ancestors is an ancient practice. Evidences of cooking of shell fishes from neanderthal sites in Italy dates back to 1,10,000 BP and from *Homo sapiens* sites in Pinnacle point (Africa) dates back to 1,64,000 B.P. There are evidences of hunting of large catfishes from Congo with specialised barbed fishing points as early as 90,000 years ago.

It is, therefore, seen that as hands became free from locomotion, ancestors of humans engaged themselves in various cultural activities that probably became the selection criteria for enlarged brain cortex and the two becoming mutually cause-and-effect of each other as is evidenced from *H.habilis* onward.

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