UNIT 3 APPLICATIONS OF GENETIC POLYMORPHISM

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Learning Objectives

After going through this unit, you will be able to:

- comprehend about the enormous genetic variation in humans;
- critically evaluate how these genetic variations are maintained by balanced polymorphisms; and
- explore the possible applications of genetic polymorphisms for the betterment of mankind.
3.1 INTRODUCTION

Physical anthropology primarily studies biological variation in human beings. All the biological and morphological traits exhibit variation and thus are important in understanding not only the variation but even the inheritance pattern shown by most of them. Expansion in the applicability of human genetics to human welfare has created numerous possibilities in reducing the diseases and improving the health status as well as looking into the potential problems like, ethical, moral and practical. It is apparent that numerous polymorphic traits are genetic in nature and are inherited in a simple Mendelian fashion. For example blood group systems, serum proteins haemoglobin variants. With the advent of new and advanced techniques more and more polymorphic traits have been identified and are being used for the welfare of the humankind. Besides considering different types of polymorphisms, the use of DNA technology is quite pertinent for establishing the ancestry as well as solving the problems related to disputed parentage and genetic counselling. The forensic aspect is the latest addition as it not only helps in determining the age and sex of the skeletal material recovered in criminal cases, but also determining the living stature of the individual to whom the bones belong. The reconstruction of the face from the skull using computer graphics and tomography are the latest methods that have been included in the gamut of applied physical anthropology.

3.2 CONCEPT OF GENETIC POLYMORPHISM, TYPES OF POLYMORPHISM

The word ‘polymorphism’ has been derived from the Greek words poly (polloi) meaning many and morphs meaning forms. Ford (1940) has defined polymorphism as “the occurrence together in the same habitat of two or more discontinuous forms of a species in such proportions that the rarest of them cannot be maintained merely by recurrent mutation”. Most of the polymorphic traits are genetic in nature and are inherited as a simple Mendelian fashion. Genetic polymorphic traits are different blood group systems, various red cell proteins, serum proteins and haemoglobin variants, etc. Genes that occupying the same locus on a particular chromosome and control the heredity of a particular characteristic, such as blood type are known as alleles. When more than one version of the same trait is common such as blue and brown eyes or type- A, type- B and type- O blood groups the population is said to be polymorphic for that trait. Humans have long been recognised to be polymorphic for blood groups, skin colour, hair texture, stature and other traits. Genetic polymorphism promotes diversity within a population. It often persists over many generations because no single form has an overall advantage or disadvantage over the others regarding natural selection. The types of polymorphic systems so far discovered have, naturally, reflected the techniques used for detecting them. A polymorphism may be transient; this happens if a favourable gene is spreading through the population. But the majority of polymorphisms, particularly all those discovered in human are not transient; they are balanced polymorphisms and have existed for a very long time. These polymorphic traits are often used in the study of population diversity, movement and relationship between and within various populations.

In recent times, enormous advances in the analysis of such genetic variation have been made. New biochemical and immunological polymorphisms have
been discovered due to advancement of various techniques like iso-electric focusing and more recently a vast array of DNA polymorphisms have been added.

Genetic polymorphism is actively and steadily maintained in populations by natural selection, in contrast to transient polymorphisms where a form is progressively replaced by another. By definition, genetic polymorphism relates to a balance or equilibrium between morphs. The mechanisms that conserve it are types of balancing selection. In many cases, an allele that is harmful in the homozygous condition may produce a heterozygote whose reproductive fitness exceeds that of the normal homozygote. This is called a balance polymorphism. Examples of balanced polymorphisms in humans include persons who are carriers for sickle-cell anemia or beta thalassaemia. Blood group differences, once considered harmless and rather subtle variations, little affected by selection, may in fact be associated with considerable differences in susceptibility to certain diseases. Thus, persons having blood group O are about 40% more likely to develop duodenal ulcer than those belonging to A, B and AB blood groups.

3.3 CLINICAL GENETIC TRAITS: ABO, RH (D), SERUM PROTEINS

Genetic polymorphisms can be found in body fluids and almost every cell of the human body. These polymorphisms are detected by various means viz., plasma proteins like Haptoglobin (HP), Transferrin (TF), and Group specific component (GC); red cell enzymes like Adenylate Kinase (AK), Phosphoglucomutase (PGM), Esterase-D (ESD), Lactate Dehydrogenase (LDH), etc and Human leukocyte antigen [HLA]).

3.3.1 Human Blood Group Systems

a) ABO Blood Group

The first human polymorphism discovered was the ABO blood groups (Landsteiner 1901). This initial discovery opened an unseen world of biological diversity for anthropologists and geneticists. The ABO blood group system is the most studied and well known of the simple genetic traits in humans. This genetic system is located on chromosome 9. There are three major alleles (A, B and O) in the system: A and B behaves as codominant alleles, and O is recessive.

All the common blood types, such as the ABO blood group system, are genetic polymorphisms. Here we see a system where there are more than two morphs: the phenotypes are A, B, AB and O are present in all human populations, but vary in proportion in different parts of the world. The phenotypes are controlled by multiple alleles at one locus. These polymorphisms are seemingly never eliminated by natural selection; the reason came from a study of disease statistics.

The worldwide variation and clines for the A, B, and 0 alleles suggest that mechanisms of evolution (gene flow, genetic drift, and natural selection) have played a role in their distribution and frequency. Worldwide, the 0 allele is the most common (about 63%), while A is next at about 21%, and B at 16%. There is, however, much variation, with the frequency of 0 ranging from about 40% to 100% in populations across the world. The ABO blood
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The B allele frequencies among the population of Indian sub-continent are the highest in the world. Currently more than 160 red blood cell antigens are identifiable. Most have been implicated in blood transfusion reacting and presumably are involved in mother-foetus exchanges. The frequencies of most genetic variations in a population have a spatial gradient slope. Geographical distribution of blood groups (the differences in gene frequency between populations) is broadly consistent with the classification of “races” developed by early anthropologists on the basis of visible features.

b) The Rh System

The discovery of the Rh blood group system was an important scientific breakthrough because it finally explained some unexpected transfusion reactions and haemolytic disease of the newborn (HDN). The clinically important antibody discovered by Levine and Stetson (1939) is now recognised as the Rh system located on chromosome 1. For simplicity’s sake, red cells are often subdivided into “Rh+” and “Rh-.” The Rh+ designation comes from the presence of the major D antigen and Rh-, from the absence of D antigen. Several antigens of the Rh system are defined as the products of three loci: C, D and E, and antigens C, c, D, d, E, e have been extensively analysed. However, there are few populations in India studied with five antisera are reported. Forty-five antigens have been identified in the Rh system, making it one of the more complexes of the polymorphic systems in humans. For the Rh system the populations of the Indian subcontinent show high frequencies of the D allele with most common haplotype (the combination of the sites along one chromosome) observed in Indian population is CDe. For other blood group systems (K, Fy, JK and P) the number of studies in different regional and ethnic groups is limited.

c) The blood group system and selection

Apart from the studies on the distribution of O, A, and B genes in ABO blood groups as well as the distribution Rh(D) blood group system several studies have been conducted to find the relationship between blood groups and environmental interaction especially diseases. Statistical research has shown that the various phenotypes are more, or less, likely to suffer a variety of diseases. For example, an individual’s susceptibility to cholera and other diarrheal infections is correlated with their blood type: those with type O blood are the most susceptible, while those with type AB are the most resistant. Between these two extremes are the A and B blood types, with type A being more resistant than type B. An analysis of the data showed that persons with blood groups A and AB have a disadvantage when exposed to smallpox. This suggests that the pleiotropic effects of the genes set up opposing selective forces, thus maintaining a balance.

Rh-induced incompatibility between mother and foetus, known as erythroblastosis fetalis, is caused by antibody D, Which crosses the placenta and reacts with red cells of the foetus. This is the most common cause of severe haemolytic disease of the newborn (HDN). The possibility of producing a child with HHD occurs when the mother is Rh- and the father is Rh+, i.e., an incompatible mating because the mother lacks an antigen
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Because fetal red cells enter the mother’s circulatory system primarily during labour, HDN is not common in the first pregnancy. Apart from the ABO blood group, the other erythrocyte polymorphisms, serum protein and red-cell enzyme polymorphisms, the HLA system, etc., are available.

3.3.2 Haemoglobin Variants

Besides ABO blood groups, more than 200 structural variants of human haemoglobin are reported but only three of them, HbS (sickle cell trait), HbE, HbC are found in fairly large areas of the world with heterozygote frequencies of about 10 percent or higher. The Khmer populations of northern Cambodia and adjacent areas of north-eastern Thailand in Southeast Asia show the highest concentration of HbE (55.2%). This haemoglobin variant (HbE) has been found in high frequencies in eastern India among the Ahom, Khasi, Assamese and Totos, among whom it ranges from 20% to 58%. In comparison to HbE, the study on HbS or sickle cell haemoglobin has been carried out much more extensively in India. It is well established that the HbS gene is widely distributed in India except in the eastern region particularly Bengal and Assam. It could also be noted that sickle cell gene is mostly found among the tribal populations. A few other variants HbD in the north-west of the Indian sub-continent, HbO (in the) Indonesia in Celebes attain heterozygote frequency 5 percent. However, a great majority of Hb variants are rare and do not reach a gene frequency of one percent.

3.3.3 Balance Polymorphisms

Evidence is now strong that many polymorphisms are maintained in human populations by balancing selection. Such a balance is seen in sickle-cell anaemia, which is found mostly in tropical populations in Africa and India. An individual homozygous for the recessive sickle haemoglobin, HbS, has a short expectancy of life, whereas the life expectancy of the standard haemoglobin (HbA) homozygote and also the heterozygote is normal (though heterozygote individuals will suffer periodic problems). The sickle-cell variant survives in the population because the heterozygote is resistant to malaria and the malarial parasite kills a huge number of people each year. This is balancing selection or genetic polymorphism, balanced between fierce selection against homozygous sickle-cell sufferers, and selection against the standard HgbA homozygote’s by malaria. The heterozygote has a permanent advantage (a higher fitness) so long as malaria exists; and it has existed as a human parasite for a long time. Because the heterozygote survives, so does the HgbS allele survive at a rate much higher than the mutation rate.

3.3.4 Lactose Tolerance/Intolerance

There is considerable interest today in investigating genetic base of difference in human metabolism energy and material transformation within cells as these differences interact with culture and health. Lactose intolerance and alcoholism are to be mentioned in this regard. The ability to metabolise lactose, a sugar found in milk and other dairy products, is a prominent dimorphism that has been linked to recent human evolution.
3.3.5 G6PD (Glucose-6-Phosphate Dehydrogenase)

Glucose-6-phosphate dehydrogenase human polymorphism is also implicated in malarial resistance. G6PD alleles with reduced activity are maintained at a high level in endemic malarial regions, despite reduced general viability. Variant A with 85 percent activity reaches 40 percent in sub-Saharan Africa, but is generally less than 1 percent outside Africa and the Middle East.

3.3.6 Genetic Variability of Major Histocompatibility Complex (MHC) in Human Populations

Human major Histocompatibility complex (MHC) molecules are called human leukocyte antigens (HLA), in short, the genetic control of the body’s immune system, which were discovered in 1958 (Dausset 1958) and is located on chromosome 6. It is well known that several HLA genes exhibit an extremely high degree of polymorphism. In particular, the HLA-A, HLA-B and HLA-C genes in class-I and the HLA-DR and HLA-DQ genes in class-II are highly polymorphic in various ethnic groups. Thus, these genes are very useful for tracing an evolutionary history of human populations.

The genes of the major histocompatibility complex (MHC) are highly polymorphic, and this diversity plays a very important role in resistance to pathogens. This is the type of genetic variability involved in acceptance or rejection of organ transplant, defence against cancer and resistance to diseases such as malaria or measles.

3.4 DNA POLYMORPHISM: STR AND SNP

The study of protein polymorphism has indicated that the extent of genetic variation in natural populations is enormous. However, the total amount of genetic variation cannot be known unless it is studied at the DNA level. The results so far obtained indicate that the extent of DNA polymorphism is far greater than that of protein polymorphism.

3.4.1 What is DNA Polymorphism?

Non coding nucleotide sequences that contain base pair variations that do not appear to have a phenotypic effect on the individual are referred to as human DNA polymorphisms. A DNA polymorphism is any DNA variant recognisable by a change in DNA sequence that occurs with a frequency of greater than 1 per cent. Mutation change nucleotides over the course of evolution. Other evolutionary forces, such as natural selection and random genetic drift, determine the fate of new mutations. Most mutations are eliminated from population. Some mutations at a particular DNA site reach polymorphic frequencies (that is over 5 per cent of individuals in the population carry the mutation) and are called polymorphic DNA site. Recognisable DNA polymorphisms, or marker DNAs are now being used to locate genes that cause genetic diseases.

The DNA sequence in the human genome comprises a string of approximately 3 billion nucleotides, which is packaged as sub-strings in the haploid set of 23 chromosomes. DNA is not only present in the nuclear region of the cells but are also present in the mitochondria of the human cells known as mitochondrial DNA (mtDNA) comprises 16,569 nucleotides. Mitochondrial DNA are
transmitted only through the females, hence both the males and females receive their mt DNA from their mothers only. The hyper variable region of the mtDNA has five to ten times greater mutation rate than nuclear DNA. mt DNA is present in a high copy number and can be recovered from skeletal remains, hair-shaft, etc., which are poor sources of nuclear DNA.

### 3.4.2 DNA Polymorphism versus Biochemical Polymorphism: What are the Advantages in Population Genetics?

Traditionally population genetic studies have used blood group, red-cell enzyme and serum protein polymorphisms. Such polymorphisms are generally in the functional regions of the genome, and therefore under effects of natural selection. This leads to restricted level of variation. Further, not all polymorphisms can be detected using the traditional starch-gel electrophoresis technique. DNA polymorphisms, especially those that are in the non-functional regions of the genome, are ‘neutral’ polymorphisms, and therefore exhibit much greater levels of variation. This property makes DNA polymorphisms extremely useful for population genetic studies. Further, because at the DNA level one can detect a much greater number of polymorphisms, it has become easy to pick and choose polymorphisms in any region of the genome. This has facilitated the reconstruction of heliotypes and the study of haplotype variation, which is far more informative for population genetic studies.

### 3.4.3 How is DNA Polymorphism Detected?

The simplest method of detect known single-nucleotide DNA polymorphisms by use of restriction end nucleases. Such polymorphisms are called restriction fragment length polymorphisms (RFLPs). Fragments of different length produced by the restriction enzyme can be distinguished by the altered mobility of the restriction fragments on gel-electrophoresis. These variations in the nucleotide sequence are not expressed phenotypically because these variations are due to sequence differences in the non-coding region of the genome. The gold standard is, of course, DNA sequencing. DNA polymorphism detection has been greatly facilitated by the invention of the polymerase chain reaction (PCR) technique, which requires nanogram quantities of DNA. In early 1980s, several groups of molecular biologists began to map the human genome using restriction fragment length polymorphisms (RFLPs).

### 3.4.4 Short Tandem Repeats (STR) or Microsatellite

Short tandem repeats are composed shorter and simpler repeat sequences (two to six nucleotides) in contrast to the RFLPs. These STRs are highly variable and each of the STRs is determined by a separate locus. These repeats can be amplified faithfully with the Polymerase chain reaction (PCR), enabling precise allele designations in population surveys on the basis of their DNA sequence. STRs were first used in forensic case work for the identification of human remains in Persian Gulf War in 1991.

### 3.4.5 Single Nucleotide Polymorphisms (SNPs)

Single nucleotide polymorphisms (SNPs) are sites in the individual genome that have at least two different nucleotide bases at the same location. This point mutations or substitution of a single nucleotide, do not change the overall length of the DNA sequence in that region. Presently. The SNPs are used as tools for
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studying variation within human populations or between different populations. Over the past years, a large number of different SNP technologies have been developed based on various methods of allelic discrimination and detection platforms.

3.4.6 What are the Applications of DNA Polymorphisms in Anthropology?

It is impossible to exhaustively list all possible applications. The more important ones are:

a) Inferring population histories and affinities,

b) Reconstructing mutational patterns and dating occurrences of mutations in populations,

c) Relating inferences in demographic histories of populations,

e) Mapping disease genes, and

f) Tracing trials of disease and other genes.

The best way to study population an affinity is by comparing DNA sequence of individuals from different populations, since not only is DNA analysis more informative than analysis of proteins but it is also direct and unambiguous. Genetic distance analysis based on DNA polymorphisms indicated a major division of human populations into an African and a Eurasian group. This is consistent with the postulate that earliest forms of modern human originated in Africa and subsequently gave rise to all non-African populations.

3.5 FORENSIC AND LEGAL TRAITS: INDIVIDUAL IDENTIFICATION AND CRIME DETECTION

Forensic anthropology is the application of the science of physical anthropology to the legal process. Forensic anthropology is an “applied” science. It borrows methods and techniques developed from skeletal biology and Osteology and apply them to cases of forensic importance. In this lesson, we discuss forensic anthropology as an applied science in brief as it has been taken up in detail in the first unit of this block.

Anthropometry deals with the quantitative assessment of human physiques. When we take these methods and apply them to unknown modern human remains, with the aim of establishing identity or manner of death, then we are practicing the forensic application of Osteology. Forensic anthropology involves the application of these same methods to modern cases of unidentified human remains. Through the established methods, a forensic anthropologist can aid law enforcement in establishing a profile on the unidentified remains. The profile includes sex, age, ethnicity, height, length of time since death, and sometimes the evaluation of trauma seen on bones.

3.5.1 Individual Identification and Crime Detection

The anthropologist(s) can assess metric and non-metric characteristics of the bones to determine the minimum number of individuals, sex, stature, age at death, time since death, ancestry and race, health, and unique identifying characteristics such as healed breaks or surgical scars. Sometimes the forensic
anthropologist must determine whether the remains found are actually human. Occasionally, positive identification can be established from such remains, but often only an exclusionary identity can be drawn. However, the primary responsibility of a forensic anthropologist is to provide law enforcement with a biological profile of the deceased (age, sex, ancestry, stature, and individualising characteristics) to help narrow down the possible identity of the decedent.

Forensic anthropologists apply standard scientific techniques developed in physical anthropology to identify human remains, and to assist in the detection of crime. In addition to assisting in locating and recovering suspicious remains, forensic anthropologists work to suggest the age, sex, ancestry, stature, and unique features of a decedent from the skeleton.

### 3.5.2 Identification of Sex

In general the human skeleton provides ample evidence of its sex and age: the bones of the female, for example, are less robust than those of the male and the ridges which provide attachments for muscles and tendons are less prominent in the female. The pelvis, thigh-bones and skull are particularly noted for their sexual characteristics. The female pelvis, constructed to meet the needs of childbearing, has several features – notably wider hips – which distinguish it from the male. Apart from general appearance, a number of measurements can be conducted on pelvic bones which can help in establishing sex. The difference in ratio between the lengths of the pubis and ischium (known as the ischium-pubis index) is commonly used for this purpose. The skulls also have a number of important features which help to determine the age and sex of a skeleton.

### 3.5.3 Identification of Age

Age is determined by studying a number of skeletal features in humans, principally the skull, teeth and centres of ossification. As the young human body develops from soon after conception until early adulthood, the growth of the bones is regulated by centres of ossification which gradually fill out and fuse together to give the bones shape and size. This process is established in a regular pattern which enables the skilled anatomist to give a reliable estimate of age to within one or two years. Examination of the growing ends of the bones epiphyses is especially relevant. The teeth also become important later in the identification of a specific individual, particularly the age.

### 3.5.4 Reconstruction of Height

Using the Regression Formula for Estimating Living Stature with standard errors obtained from the average of the Long Bone Length of both right and left humeri, ulnae and radii, femurs, tibiae and fibulae, an estimate of the decedent height could be assessed.

### 3.5.5 Identification of Decedents

*Racial Affiliation:* In the present day it is very difficult to comment on the racial affiliations on examining the skeletal remains. One could comment on the basis of the cranial index or nasal index as Caucasoids generally have mesocephalic heads, the Negroids possess Dolichocephalic heads while the Mongoloids have brachycephalic heads. Similarly the Negroids have very broad nose, while the Caucasoids have long nose and the mongoloids have small nose.
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Forensic anthropologists frequently work in conjunction with forensic pathologists, odontologists, and homicide investigators to identify a decedent, discover evidence of trauma, and determine the post-mortem interval. Though they typically lack the legal authority to declare the official cause of death, their opinions may be taken into consideration by the medical examiner. In fact, a forensic anthropologist is now an integral member of most mass disaster teams.

### 3.5.6 DNA Profiling

DNA profiling is a way of identifying a specific individual, rather than simply identifying a species or some particular trait. It is also known as genetic fingerprinting profiling. As a technology, it has been around since 1985, when it was announced by its inventor, Sir Alec Jeffreys. DNA profiling is currently used both for identifying paternity or maternity and for identifying criminals or victims.

DNA uses a specific type of DNA sequence, known as a microsatellite to make identification much easier. Microsatellites are short pieces of DNA which repeat many times in a given person’s DNA. In a given area, microsatellites tend to be highly variable, making them ideal for DNA profiling. By comparing a number of microsatellites in a given area, one can identify a person relatively easily.

DNA profiling has a high success rate and a very low false-positive rate, making it an extremely popular form of paternity and maternity verification.

In forensics, DNA profiling is very attractive because it doesn’t require actual fingerprints, which may or may not be left behind, and may or may not be obscured. Because all of the DNA sections are contained in every cell, any piece of a person’s body, from a strand of hair to a skin follicle to a drop of blood, may be used to identify them using DNA profiling. This is useful in the case of identifying a criminal, because even a drop of blood or skin left at the crime scene may be enough to establish innocence or guilt, and it is virtually impossible to remove all physical trace of one’s presence. DNA profiling is useful in the case of identifying victims because even in cases where the body may be disfigured past identification, and teeth or other identifying features may be destroyed, all it takes is a single cell for positive identification.

### 3.6 SUMMARY

The polymorphism occurring while gene replacement is in process is transient, since as soon as the favoured allele is fixed the population becomes monomorphic. However, many characters in human populations are more or less permanently polymorphic. One of the most obvious examples of such ‘balanced polymorphism’ is sex. Others that occur in many human populations affect the blood-group systems, secretor status, haemoglobins, red cell enzymes and serum proteins. Non-coding regions of DNA from homologous chromosome pairs also demonstrate an average of one nucleotide difference for every 250-nucleotide sequence. The nucleotide differences are called polymorphisms. Humans have such extensive polymorphism that each person’s DNA is as individual as his or her fingerprints. These polymorphisms then become genetic markers that can be raced within members of the family just as genes are traced.

The role of genetics is emerging as an increasingly important aspect of health care. A number of RFLPs associated with human diseases are now being used in
prenatal diagnosis and to determine delayed-onset diseases and dominant and recessive carriers. A number of RFLPs have now been cloned: those for cystic fibrosis, Duchenne’s muscular dystrophy, sickle-cell anaemia, thalassaemia, haemophilia A and Huntington’s disease etc. Information from a genetic test can be used to diagnose disease, identify risk as for future disease and predict treatment response.

Genetic polymorphisms provide us with the ability to predict inter-individual differences in susceptibility to clinical disease. Biomarkers of susceptibility include: polymorphisms in drug/carcinogen metabolism, in DNA repair capacity, and in genes that control cell growth. Wide variations in drug/carcinogen metabolism have been widely investigated and clearly shown to be an important determinant of individual cancer susceptibility and adverse drug reactions. Such polymorphisms in drug/carcinogen-metabolising enzymes may be due to heritable and/or to environmental factors; and the modern application of metabolic phenotyping and genotyping methods to epidemiological studies has provided new insights into such gene-environmental interactions.

Polymorphisms in DNA repair or processing of DNA damage have long been evident from rare hereditary disorders involving defective DNA repair or chromosomal stability. Today, about 130 different genes have been shown to be involved in DNA excision or base repair and polymorphisms in gene-specific DNA adduct repair have been correlated with biological outcomes (mutations, drug sensitivity). Moreover, lower DNA repair proficiency has recently been associated with increased susceptibility to cancers of the skin, brain, lung, stomach, breast, bladder, head/neck, and colon. While over 100 genes have been identified that serve as positive (proto-oncogenes) or negative (tumor suppressor genes) regulators of cell growth, as well as the cell cycle and apoptosis (e.g., cyclins, cytokines, chemokines, caspases, etc.), these have been largely associated with rare hereditary disorders involving greatly increased human cancer susceptibility.

Besides, the advent of DNA technology has gained wide acceptance in criminal offences involving biological evidences such as murder, sexual assault, in case of mass disaster, paternity disputes, in identification of mutilated bodies and exhumed skeletons.

Anthropology is on the verge of becoming a purely applied science. Advance scientific and technical know-how on the human genome project are enabling us to understand the rich genetic resources India possesses. India with diverse population has incredible scope to move forward in the field of genetic epidemiology and to develop effective strategies to prevent both infectious and complex lifestyle diseases like Type2 diabetes, obesity, hypertension, cardiac diseases, cancer and others.

References


Applications of Genetic Polymorphism

Suggested Reading


Sample Questions

1) What is genetic polymorphism?
2) What do you mean by balanced polymorphism?
3) What is DNA fingerprinting? State its significance in forensic anthropology.
4) What is HLA?
5) How would you determine age and sex of the skeletal material?