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Morphology to Molecular Anthropology: Castes and Tribes of India*

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KEYWORDS Morphopological Variables. Genetic Markers. Population Genetics. Natural and Climatic Regions. Ethnic Groups. Linguistic Groups.

ABSTRACT Within the various fields of research of the present Biological Anthropology the study of human evolution as well as the study of genetic variation in modern man, hold an eminent place. An important branch of Biological Anthropology is therefore Population Genetics, which deals on the one hand with exact genetic descriptions of human population, but which on the other hand tries to find out the reasons for genetic differences among them. To study these genetic differentiation processes in man, which are obviously still ongoing, reliable population data are necessary. Biological Anthropologists are, however, not only interested in the ethnic and geographic variation of the numerous genetic markers of the **human blood**, but are also concerned with the variation of **anthropometric, morphological and dermatoglyphic traits**. Human population studies using traits began with early population descriptions and currently utilise multivariate procedures for detecting evolutionary processes. The development of new techniques in **molecular biology** rendered possible to elucidate human variability and human prehistory. It may be concluded that there are differences in the occurrence of the frequencies of various biogenetical traits (genetic markers of blood, other genetic markers like colour blindness and tasting ability, different dermatoglyphic and somatometric traits) among the population groups inhabiting different geographical zones of India *viz.* North, West, East, Central, South and Islands. From the Himalayan region, some differences in the frequencies and mean values of distribution of various genetic markers and morphological traits have been observed among population groups of Western and Eastern Himalayan regions. Since sufficient studies are not available on the population groups of Central Himalayan region, it has not been possible to observe a differential trend regarding the occurrence of various traits, but it has been observed that the population groups in this area show more similarities with those of Western than Eastern Himalayan region. About the four groups *i.e.*, caste, scheduled caste, scheduled tribe, and community from India, various zones of India and Himalayan regions, conspicuous differences are observed among the scheduled tribes as compared to castes, scheduled castes, and communities. The correlations of frequencies of genetic markers and mean values of morphological traits with various climatic factors and altitude by different ethnic groups although showing significant differences, in general are not high. Nevertheless, it can be concluded that the variations in the frequencies of genetic markers and mean values of morphological traits distribution in the Himalayan region may be due to contacts between the various population groups of Western and Central Himalayas with population groups of Central Asia, and that of Eastern Himalayas with the Northern Mongoloid populations. In Central India admixture with the population groups of West India can be assumed. In South India, a different pattern of allele/haplotype frequencies and mean values is generally observed among the tribal population groups, for which one of the main causes might be seen in small population sizes. Inbreeding is prevalence among certain communities like Muslims, Parsis etc. and in most of the different population groups particularly from South India, which might have also resulted in the marked variation in distribution of frequencies and mean values of different genetic markers and morphological traits. The variations observed for the various morphogenetic traits in the distribution of allele/haplotype frequencies and mean values among the Indian population are due to racial elements present among them in varying degrees, migrations and admixture from time to time and other factors of evolutionary changes like mating patterns, genetic drift, mutation and selection under different environments. However, such a holistic approach should not only consider the anthropometric, dermatoglyphic traits and so far less investigated serum protein and red cell enzyme polymorphisms, but should analyse especially the regional and ethnic distribution of the numerous nuclear and mitochondrial DNA polymorphisms, which turned out to be of highest importance to population genetics.

"About ninety percent population of India is native and for examining the nature of evolution in India, one must look for evolutionary growth on its population from now and earlier also. India has been a crucible of evolution and continues to be so in contemporary times."

-Genetics of Castes and Tribes of India

....Aborigines, who intially arrived in Australia via South Asia may have orignated from India.

Rao et al. 2009 (Times of India, July 23, 2009, P. 17)

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*In loving memory of my colleague and friend Professor Dr. Dr. h. c. H. Walter (Department of Human Biology, Institute of Biology/Chemistry, University Bremen, D-28334, Bremen, Germany)

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There is no truth to the Aryan-Dravidian theory as they came hundreds or thousands of years after the ancestoral north and South Indians had settled in India. The genetics proves that castes grew directly out of trible-like organisations during the formation of the Indian society.
Thangarajan (timesofIndiatimes.com/news/India)

1. INTRODUCTION

Anthropology is the study of man in time and space. The focus of anthropological research is on human population(s) living in an ecological niche. Anthropology can be categorized under the following main heads:

1. Palaeoanthropology
2. Social/Cultural Anthropology
3. Biological Anthropology

1.1. Palaeoanthropology

The research and training in palaeoanthropology is divided in two distinct areas. One emphasizes the methodological training in a Prehistoric Archaeology and the other in Palaeontology

a. Prehistoric Archaeology

The prehistoric archaeology includes a total introduction to the study of geo-chronology through the analysis of such variables as alluvial deposits as also faunal and floral characteristics associated with such deposits on a worldwide basis. Antiquity analysis in terms of the techniques of manufacture as well as their morphology is included as standard components of prehistoric culture. Finally, on the ground of these basics, a thorough study of the various stages of Palaeolithic, Mesolithic, Neolithic and Chalcolithic cultures for the entire Old World is undertaken.

b. Palaeontology

Palaeontology includes the detailed study of the character and distribution of fossil primates. Primate behaviour with specific attention to adaptation attributes is also included within this scheme. Adaptation radiation in both hominoid and hominid evolution forms another important aspect of this course.

1. 2. Social/Cultural Anthropology

Social/cultural anthropology is the study of social institutions and human behaviour in a cross-cultural perspective. It attempts to unravel the underlying designs of human existence with a view to arrive at generalizations having validity, not only at the level of the concerned culture but also at the global level.

1. 3. Biological (Physical) Anthropology

Biological anthropology can be defined as the scientific study of inter-and intra-population variations.

It was in 1951 that S.L. Washburn laid down a distinction between the pre-1951 and post-1951 physical anthropology referred as *Old Physical Anthropology* and *New Physical Anthropology,* respectively. Before 1951, physical anthropology was considered a descriptive study of biological parameters to an understanding of their causes. From 1951 onwards, mathematical models formulated for population biology have become popular for understanding the causes of variation and co-existence of genetic traits. Thus, the orientation of physical anthropology has changed from description to causes to models.

In the descriptive type of physical anthropology, G.W. Lasker has identified five major areas of interest according to which relevant techniques for investigation were devised.

1. The form of bones and teeth
2. Determination of age and sex and ethnic group from bones and teeth
3. Human growth and development
4. Composition of the body and its variation
5. Body build and its application to human engineering.

Although in Lasker's formulation, dermatoglyphics did not figure, it occupied an important place in physical anthropology preceding 1951. Therefore, for completing the list of the old interests, the inclusion of dermatoglyphics is imperative. Since 1951, the various dermatoglyphic traits occupied an important place in biological anthropology. Determined by genetic factors, a few weeks after the conception, they are not affected by environmental factors. This property explains the importance of dermato-

glyphics in population studies. Though up to now it is not possible to calculate gene frequencies for the various dermatoglyphic traits, they are nevertheless good tools in order to record genetic variation within and among the human populations.

However, it should not be forgotten that these interests listed by Lasker were instrumental in generating a wealth of data and are still valuable for accomplishing newer interests. These fields have not been discarded by biological (physical) anthropologists when the New Physical Anthropology, the result of the consanguinity between evolutionary and adaptation theory on the one hand and genetics on the other, had gained ground. With the "New Physical Anthropology", the interests who have come to stay are as follows.

1. Serological studies
2. Biochemical genetics studies especially of various polymorphic systems.
3. Studies of evolutionary factors such as mutation, natural selection, and gene flow.
4. Primatological studies, of their biology and behaviour.
5. Demographic studies, especially of factors that affect inbreeding and genetic drift and the biological consequences of formal kinship and alliance systems.
6. Anthropometric and anthroposcopic studies, with reference to nutritional factors and ensuing demographic characters.
7. Ecological studies dealing with biological and cultural adaptations.

Physical anthropology has achieved new strides after Washburn's 1951 statement. For grasping the laws and processes of human evolution, molecular evidences have been marshalled, leading to the advent of microscopic work in the area. Human cytogenetics has made an outstanding contribution towards the knowledge of adaptation and evolution. Evolution at the genic (elemental) level is that which is being sought through DNA analysis using recombinant techniques. Thus, we haven come a long way from morphological studies (morphological, behavioural, anthropometric, and dermatoglyphic traits - the mode of inheritance of all these characters is still rather unclear) to those of genetic or classical markers (blood groups and protein markers), and to the newly discovered molecular techniques which have provided a new direction and a whole battery of powerful polymorphic systems to study genetic diversity (Cavalli-Sforza and Feldman 2003; Jorde and Wooding 2004). The question, what happens to genes with degradation in biotic environment, acquires a primary place. With these newer and still newer interests, different kinds of techniques have been enunciated to understand nature-nurture relationship in a better fashion. Moreover, there has been a concomitant advancement in statistical methods and we are now in a position to make use of many parameters (Collins et al. 2003; Bamshad et al. 2004; Tishkoff and Kidd 2004; Cavalli-Sforza 2005).

2. INDIAN POPULATION MILIEU

South Asia, constituting mainly the Indian sub-continent, is a panorama of social diversities, racial differences, and rich cultural heritage. However many facets of history, race and culture of this area are still relatively unexplored. Debates and doubts centering on the autochthonous status of the early settlers continue—it is very difficult to ascertain how human groups and settlements were formed in the pre-historic times, whether they were the original inhabitants or migrated from some other place and if they migrated, which route did they take. However, the infiltration and admixture of new racial and cultural elements, from time to time, have made the Indian population more diverse and heterogeneous.

2.1. Skeletal Remains (Hominoid/Human)

Earlier it was pointed out that the first real "ancestor" of man is *Ramapithecus* (named after the Indian god Rama) who lived about 14 million years ago (Fig. 1). Now *Ramapithecus* is no longer considered a hominid ancestor by palaeontologists. From Central India, Narmada Man skull was found in 1982 embedded in a conglomerate containing animal bones and a scattering of Acheulean artifacts by Arun Sonakia (Sonakia 1985a, b). Dates for this material are poorly constrained, but it is probably of Middle Pleistocene age (Sonakia and Biswas 1998). With regard to both its antiquity and phylogenic position, a good deal of controversy is still going on. It is believed by several to be an ante-Neanderthal or *Homo erectus* (Lumley H and Sonakia 1985; Lumley MA and Sonakia 1985). Kennedy et al. (1991) further identified and concluded based on metric and comparative

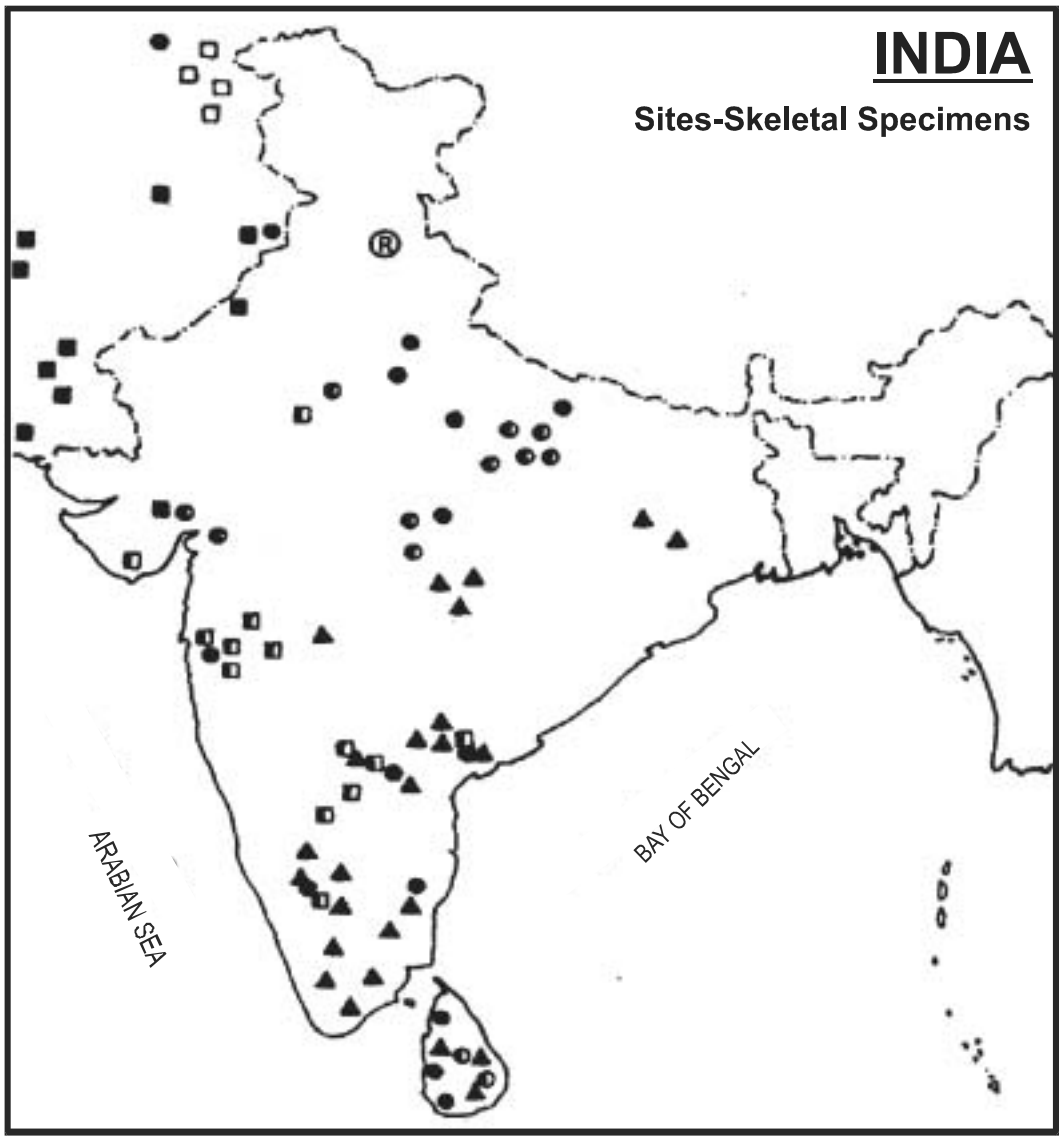


Fig. 1. Prehistoric sites from where skeletal specimens were found from India

investigations that "Narmada Man" is appropriately a *Homo sapiens*. They added, however, that given its broad suite of *Homo sapiens* morphometric characters it is not appropriate to assign Narmada man to a new taxon beyond the trinomial designation of *Homo sapiens narmadensis*. In a more recent publication, Kennedy writes: "In the context of current debates about *Homo erectus* as a valid taxon (is it a species, an evolutionary grade, a paleospecies, or just a collection of specimens certain investigators decide belong together?) In addition, the relationship of middle Pleistocene hominids to anatomically modern *sapiens* (regional continuity [or multiregional] hypothesis versus the mitochondrial Eve-displacement hypothesis), Narmada has a critical role to play. At present, it appears that Narmada is a late middle-Pleistocene representative of early *Homo sapiens* with an impressive suite of anatomical characteristics shared with other early *sapiens* populations from Eurasia and Africa but possessing certain unique features of cranial morphology that may have evolved in India. It does not seem appropriate to assign Narmada to a new taxon" (Kennedy 2000: p. 180). In its overall morphology, the cranial vault is not very different from the African and European hominins (Rightmire 2007). A number of fossil specimens have been recorded from India, but most of the write-ups totally overlook the aspects of ethnic or racial affinities of the specimens.

Kennedy and Caldwell (1984) have attempted in cataloguing the various skeletal (hominoid/ human) remains of India. The research work is mainly confined to the number of specimens, primary dating, and archaeological reference and descriptions of burial circumstances and practices apart from giving an account on ageing and sexing. The write-ups totally overlook the aspects of ethnic or racial affinities of the recorded specimens.

Earlier, in 1972, Sarkar, who was actively working on the study of the ancient races of India, came out with some ethnic description of the various human skeletal remains. In his earlier work, *Ancient Races of Baluchistan, Punjab, and Sind* (1964), he tried to throw some light on the Indo-Aryan problem and suggested the builders of Harappa culture as Indo-Caspians. In his later exhaustive work on the *Ancient Races of the Deccan*, on the basis of examination of human skeletal remains from Langhnaj, Lothal, Nevasa, Chandoli, Hyderabad, Megaliths, Yelleswaram, Piklihal and other sites of the Deccan he postulated that the Dravidian speaking people evolved from the Veddids or Australoids. Even as early as in 1936, Keith also pointed out the evolution of Dravidians from Veddids or Australoids. It is believed that the complexities and variations as one observes in today's population were the results of environmental changes and hybridization. Sarkar also published (1972) the original reports on skeletal remains from Brahamgiri, where he mentioned of, yet another stock: Scytho-Iranian. Other than this, Sastri (1966) is also supposed to have come across a fossil pygmy skeleton (although its hominoid status and antiquity is not clear, as there were no further references to it). He attributed this to the earliest representative of Negrito in India.

Nevertheless, it remains a fact that there is always the problem of disputes arising while identifying the specimens correctly and hybridization or environmental effects, which are often used, as alternative causes for marked changes are no longer taken for granted. Moreover, the repeated allegations that most of archaeologists and other investigators seem to be more preoccupied with the artefacts and other material evidences and do not show much interest in the skeletal remains is also mostly true. Therefore, quite a number of studies (may be of the same specimens excavated earlier) are needed today which may come out with a meaningful fossil study of the Indian sub-continent. In addition, it is hoped that when the number of collections of fossils presumed to be belonging to our ancestral stock would be sufficiently large, it would permit some population studies and the specimens can be used as acceptable population samples.

2.2. Prehistory

2.2.1. Ancient Age

Both prehistory and history of a country together form the background material towards unfolding the pages of emergence of cultures. The problem of terminology in Indian prehistory is well known. This arises naturally due to the difficulty in coinciding the Indian prehistoric ages or cultures (which is based on the material evidence or tool types and assemblages) with the European culture items. Many anthropologists/ archaeologists (Cammiade and Burkitt

1930; Misra 1962) have attempted to solve this problem but still different terms are in vogue. During the long stone age estimated to cover over 5, 00,000 years and forming part of the last geological period namely Pleistocene, and was believed to have been a savage-having no fixed habitation hunting and gathering. It is noted that the great climatic changes of the last glaciations undoubtedly exerted new environmental pressure altering man's number and habitat through changes in the biota stimulating enforced migrations into new environmental niches and changing the life-styles. Changing in the environment and circumstances gradually brought about changes in tools and artefacts, which are the main, and sometimes the only source to reconstruct the physical environment, customs, practices, and social life of a period. However, with further excavations of other associated materials like mammal bones, ornaments etc. terms like Stone Age became more or less irrelevant.

Human occupation in the Indian subcontinent began with a series of stone-tool industries (Fig. 2). The stages in man's progress that are then put forward by Sankalia (1973) are as follows.

1. Primitive Food Collecting Stage or Early and Middle Stone Age
2. Advanced Food Collecting Stage or Late Stone Age/Mesolithic
3. Transition to Incipient Food Production Stage or Early Neolithic
4. Settled Village Communities Stage or Advanced Neolithic/Chalcolithic
5. Urbanization Stage or Bronze Age

2.2.2. The Earliest Human Settlements

The evidence of stone tools in Indian Palaeolithic and certain caves and rock shelters helps only in a very small way to visualize the life of their makers (for the sites *see* Fig. 2). It is more or less clear that they were ignorant of agriculture and house building and had no domesticated animals. The caves and rock shelters might have served as seasonal camps for human being (?). In the Palaeolithic Age, the communities must have been very small and perhaps semi-nomadic.

Piggot (1952) also mentioned that dating is uncertain but earlier man was living in scattered hunting and gathering communities on the alluvial plains and in the marshlands and open parklands of the major river valleys (as suggested by the location and type of tool assemblages).

The epiglacial phase from 10,000 to 50,000 B.C. following the end of Pleistocene more or less coincided with the transitional Mesolithic cultural dispersals. Hunting and gathering remained the main sources of making a living but as vegetation shrank and the bigger game gradually disappeared (presumably due to marked climatic changes) man turned to other sources like water sources, birds or exploitation of plant products as suggested by tool assemblages. Overall, man was mostly dependent upon natural resources during this preparatory stage. In other words, in this period the concentration of population began along river valleys marking the start of a transition to settled living in which food gathering turned into food producing. It was argued that the people who camped in rock shelters, the mouths of caves and in open settlement sites could not have numbered more than a couple of hundred individuals.

Kivisild et al. (2000) have studied Indian mitochondrial DNA variants in the global network of maternal lineages and the peopling of the Old World. They summarized their results as follows: "Both western and eastern Eurasian-specific mtDNA haplotypes can be found in India together with strictly Indian-specific ones. However, in India the structure of the haplogroups shared either with western or eastern Eurasian populations is profoundly different. This indicates a local independent development over a very long time. Minor overlaps with lineages in other Eurasian populations clearly demonstrate that recent immigrations have had very little impact on the innate structure of the maternal gene pool of Indians. Despite the variations found within India, these populations stem from a limited number of founder lineages. These lineages were most likely introduced to the Indian subcontinent during the Middle Palaeolithic, before the peopling of Europe and perhaps the Old World in general. Our demographic analysis reveals at least two major expansion phases that have influenced the wide assortment of the Indian mtDNA lineages. The more recent phase, which according to our estimation started around 20,000-30,000 years ago, seems to correspond to the transition from the Middle to the Upper Palaeolithic. The first expansion phase may reflect a demographic burst immediately after the initial peopling of India around 50-60 thousand years ago. This wave of expansion brought forward also those maternal lineages that can rightfully claim the name of Eurasian Eves" (p. 150).

Roychoudhury et al. (2000) reported mito-

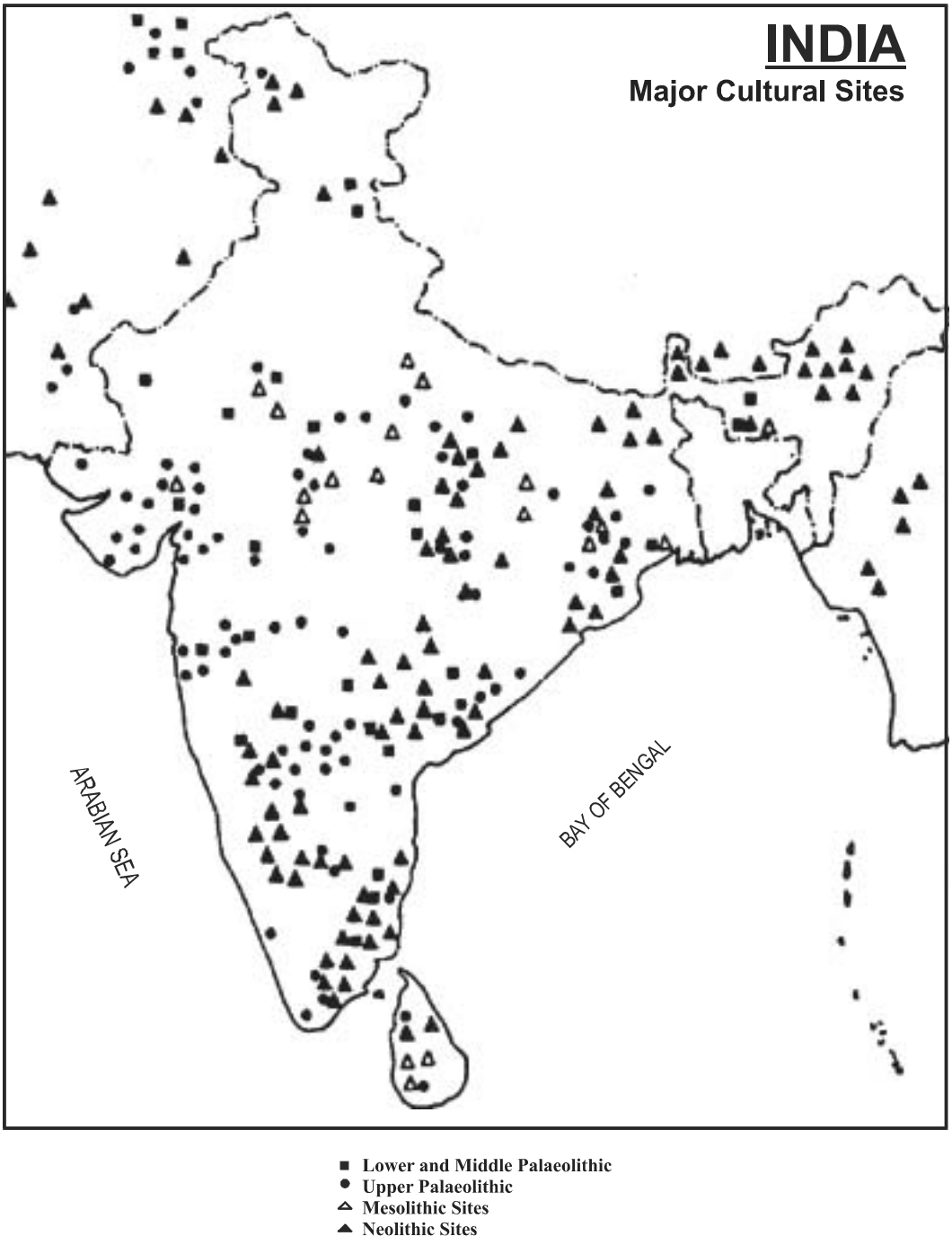


Fig. 2. Major cultural sites found from India

chondrial DNA (mtDNA) profile of 23 ethnic groups of India, which have been drawn from different cultural, linguistic, and geographical backgrounds. They observed that Indian populations were founded by a small number of females, possibly arriving on one of the early waves of out-of-Africa migration of modern humans; ethnic differentiation occurred subsequently through demographic expansion and geographic dispersal. Further, they have found that South-east Asia was peopled by two waves of migration, one originating in India and the other originating in Southern China. Are just 23 ethnic groups from India sufficient for making such an over-generalisation? In doing so, have they considered the previous research work based on the so called traditional genetic markers of blood.

The *Neolithic Age* of the Ancient Orient is approximately dated from 6000 to 4000 B.C. The chief characteristics of this period are the exclusive use of non-metal implements, domestication of animals, and a knowledge of agriculture (for the sites *see* Fig. 2). Corollary to agriculture is the development of village life. Towns also started appearing during the Neolithic phase. Towards the end of Neolithic pottery began to appear and metals came into use around 4000 to 3000 B.C.

The full Neolithic which began in different communities between the seventh and sixth millennium B.C. was not characterized by a uniform step-by-step technological sequence from one type of artefact to another or in the presence of types of ceramic ware or even in house types and settlement patterns, rather it was an adjustment of separate small communities to the ecological resources and advantages of local environments. In other words, the Neolithic does not always imply the universal presence of specified domesticated plants and animals, pottery, polished stone tools and stereotyped settlement patterns. The biological consequences to operate were also not the same throughout India.

Bowles (1977) put forth the interpretation that the ability to control production and storage of life's essentials encouraged the growth of larger permanent settlements and these in turn led to technical innovations, division of labour, the formation of social classes, and ultimately the superimposition of a system of administrative controls. Biologically such developments meant an increase in the demographic dimensions of a limited number of populations (gene pools)-those possessing the knowledge of food production-at the expense of others who retained the earlier type of natural economy and who could not expand numerically beyond the limits set by nature.

As urban centres developed, they attracted a large number of traders, artisans, and labourers from ever-increasing distances, a process accentuated during the metal age with the emergence and expansion of Empires and commencement of the historic period about 3000 B.C. After the first population explosion Asia remained, for a millennium or more, the most favoured quarters and thus by the end of this period, Indus valley developed a comparable Neolithic nexus.

Permanent settlements of substantial size with populations ranging from a few hundreds to two or three thousands began to emerge at such sites as Brahmagiri, Nevasa, Chandoli, Pandu-Rajar Dhibi (in East Indian Neolithic) etc. With complexity in society, trade flourished. The development of trade became an important factor in knitting together the social fabric of local communities into village units and regional societies. However, it may prove impossible to determine how many clusters there were.

Although a negligible number of hominid remains have been found, it is actually thousands of artefacts from a large number of sites, which point to probable contact, and migration either west ward or eastward or both during all major periods. Microliths for example, were found concentrated in the western half, which seems to imply introduction from that direction.

It has been commented that so much is known about the Mesolithic, Neolithic and Chalcolithic periods of Western Asia than of the southern Peninsula that it is easy to overlook the importance of these areas.

India apparently derived much of its Neolithic as well as its Metal age civilization from two sources—one along the Makran Coast and Baluchistan in the west, the other from south-east Asia by way of the Arakan coast and Assam (Fairservis 1971). The knowledge of the first source is documented from numerous sites in the arid regions along the foothill rim of the Indus valley, the second is still largely covered with dense vegetation and is only beginning to be understood (Bowles 1977).

Until recently, it had been thought that the

Indus Valley or Harappan Civilization sites were actually scattered Mesolithic hunting and gathering communities transformed into more concentrated permanent Neolithic and Copper-Bronze Age Settlements. However, the discovery of a number of wall-enclosed complex urbanized mound-based Neolithic settlements in the now dried-up Saraswati riverbed in Rajasthan in Kathiawar and parts of southern Gujarat have changed this view.

The distinctive features of Harappan Civilization with uniform assemblages of tools, unique methods of water supply, drainage, hypocaust system for heating grand central bath, remarkable individual feature including the ceramic techniques, the systems of weights and measures and the differentiation between the citadel and slave quarters all point to the existence of a complex society with considerable social stratification and complex administrative machinery.

The Indus Valley Civilization extended throughout the entire river basin from the Himalayan foothills and the Doab or Ganges watershed to coastal Gujarat with an estuarine dock at Lothal and an outpost at Thane near Bombay (Fig. 3). About the origin of the Harappan Civilization, practically nothing definite is known. Different versions are put forward—right from Sumerian or a Semitic origin, to the Dravidian and Mundari are often mentioned. Even origins from Baluchistan and Iranian uplands were suggested [Excavations at Harappa were resumed in 1986 under the direction of Dr. George F. Dales of the University of California, Berkeley, and are continuing each year at that site. Drs. Nancy C. Lovell, John R. Lukacs, Brain E. Hemphill, and Kenneth A.R. Kennedy have removed some 100 skeletons from site (Mature Harappan cemetery of R - 37)]

Sastri and Srinivasachari (1980) proposed that at about 3000 B.C., small groups of people from the Iranian uplands inhabited Baluchistan, which was less arid than now. These migrants brought with them the knowledge of agriculture and the organisation of small self-sufficient village communities. In the course of about 500 years, after they had settled in Baluchistan, they migrated in big or small group into the Indus valley.

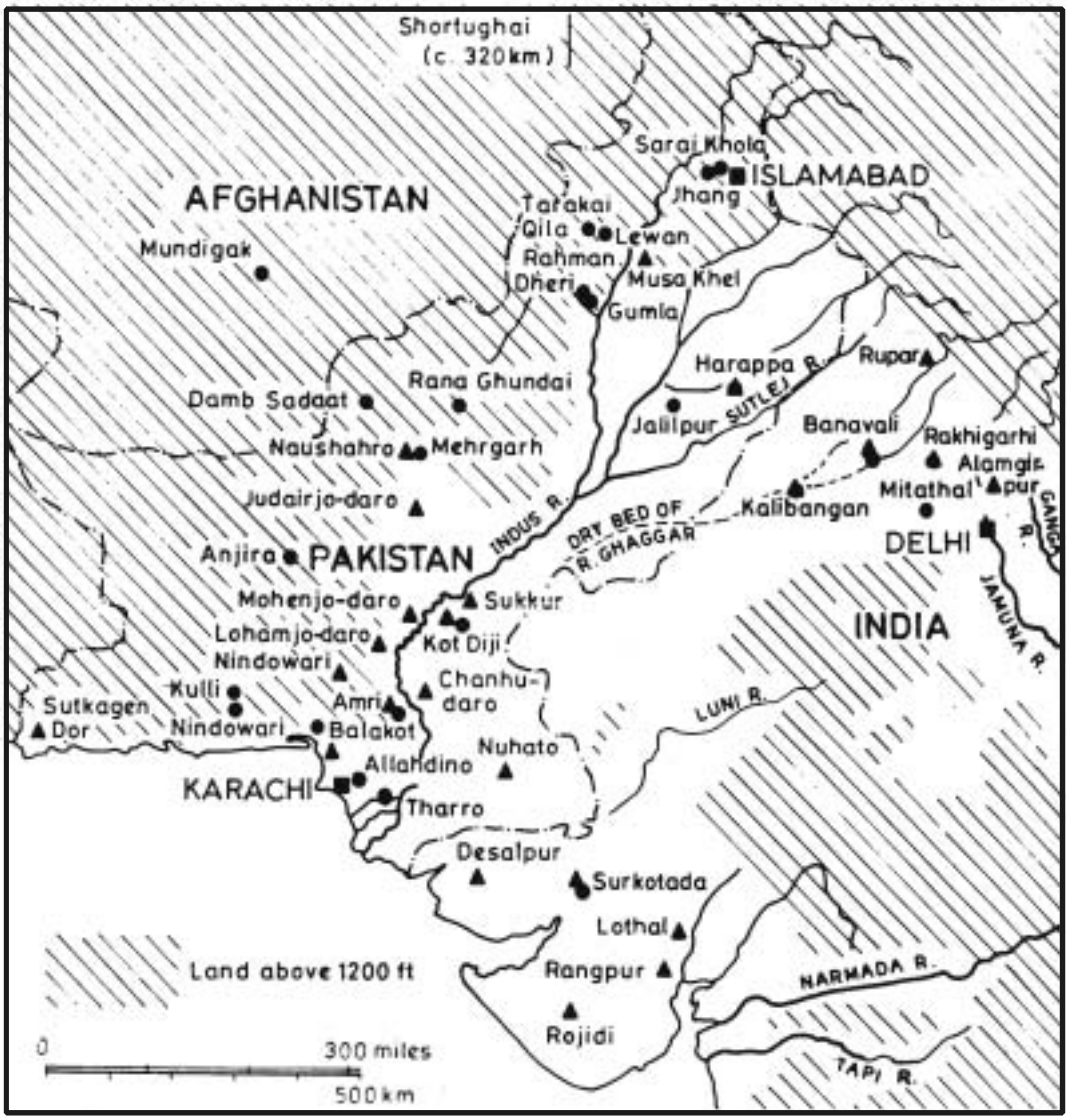
However, the sudden emergence of the urban civilization still baffles the interpreters of Harappan cultures. Some believe that urban civilization was superimposed on the people suddenly by strangers coming from outside at some time in the middle of the third millennium B.C. It is quite impossible to say when Harappan civilization grew up'. The civilization is unique in a sense that it was almost a fully classified state as early as 3000 B.C. It is said that it may well have been evolved by the natives of the soil and foreign settlers induced new ideas which Harappans absorbed and evolved into a distinct mature culture. The Indus Valley Civilization has spread from it southern bases to the Himalayan foothills, up the valley of Kashmir, around 1800 B.C.

The next culture in the chronology, which is known as the Chalcolithic, is dated roughly from 4000 to 3000 B.C. This is called so because the main tool types representing this culture were made of copper along with stone (for the sites *see* Fig. 4), although there was no proper Bronze Age in India as in Europe. However, bronze was not unknown and many bronze materials were found. Here, it should be mentioned that there are hundreds of diverse findings, which suggest that there are still many problems to be solved. It is also noted that early Neolithic and Bronze Age migrations into India have not been clearly defined and skeletal evidence from Baluchistan is far from satisfactory.

Sen (1967) argued that leaving aside the questions of ordered sequence of migrations and demographic fluctuations, there was no skeletal evidence to show that a biologically new element could be held accountable for the development of Indus Valley Civilization. Estimations of total population have varied widely and the rationales for the differences climate, food supply, diseases and technology—and their analyses vary significantly. According to Sarkar (1972), the population of Mohenjodaro and Harappa had been estimated variously between 35,000 and 40,000 with a very high density of population per acre.

It is proved that the settled people knew the valley of Kashmir earlier and Mesolithic artefacts have been found. Excavations in Kashmir also give evidence of earlier proto-urban settlements. Apart from the above, Kashmir also yielded earlier Palaeolithic artefacts which are more allied to those of North India, so it might be conjectured that the builders of Burzahom (Kashmir) crossed the Hindukush by 2000 B.C. or thereabouts.

For the rest of Greater India - the scenario is as follows during the ancient age. About the



■ **Sites of Early Indus Period**
▲ **Sites of Mature Indus Period**

Fig. 3. Sites of Early Indu Period and Mature Indus Period

Ganges Basin, the Deccan and the Peninsular and coastal south is far less known but it is assumed that nothing like the civilization developments had taken place at comparable levels of antiquity. It was not until after the entry of the Aryans that the urban civilization extended into the middle Ganges and parts of the Deccan synchronised with the entry of Aryans. The so-called Chalcolithic, Pre-Harappan and Harappan periods in the Indus valley, Gujarat and western Maharashtra are generally contemporary with the so-called Neolithic of the Deccan and Eastern India.

Towards the end of the stone tool phase, the first evidence of agricultural settlement appeared in Baluchistan in the northwest. This culture spread across the northwest corner of the country

during the next 2000 years, giving rise eventually to the highly developed Indus Valley Civilization, which came to an abrupt end around 1750 B.C. Whether directly related or not, the decline of this civilization coincided with the movement into India from the Iranian plateau and the Caucasus of Aryan peoples speaking an Indo-European language.

2.2.3. Culture Phase and Tools Types

The contemporary culture phase with the tool types and areas of reign may be listed as follows.

1. *Neolithic* - Polished Celts, Pottery limited to hand-made jars, in the east (Assam, Bihar, Bengal and parts of the adjacent Deccan).
2. *Neolithic* - *Chalcolithic* with polished Celts and blade tools, hand-made pottery and wattle and daub houses in Central India, Karnataka, Gujarat and Baluchistan.
3. *Chalcolithic*- *Bronze* with Stone blade and copper-bronze tools wheel-made pottery in the north-west (Sind, Saurashtra, and Punjab).
4. *Chalcolithic-Bronze*- with copper or bronze but no stone tools, wheel-made pottery in north west Sind, Saurashtra and Punjab.

To sum up, during the second millennium B.C., settlements associated with copper and bronze tools spread rapidly down the Ganges valley. Within a matter of centuries, the entire basin had been largely cleared of forests and was supporting a relatively dense population, which at least in its biological aspects, is probably reflected in the majority of the present day inhabitants. Meanwhile, it is believed that there was a spread of Southeast Asian culture complex and a possible minimal immigration *via* Assam and Burma into Bengal and Central India.

2.2.4. Main Tools Types

The terms attributed to different cultures are based on the tool assemblages and types. For example, the Chalcolithic age has come to be known as an age where the tool assemblages were mainly composed of copper artefacts. However, there are scores of tool assemblages reported and analysed and some are still being excavated—it is impossible to give a description of all these tool types here. Therefore, the following is a simplified and short version of the dominant/main tool types found from the Indian sub-continent (for the sites *see* Figs. 2 and 4).

A detailed and extensive account on the prehistory and protohistory of Indian subcontinent can be studied from Sankalia (1962, 1979) and Allchin and Allchin (1983).

Geological age (European)	*Tool types*	*Culture terms*
	Copper	Chalcolithic
Holocene	Polished Celts	Neolithic
	Microliths	Mesolithic
		Palaeolithic
Pleistocene	Bone Points, Harpoons Blades, Burins, Art objects	Upper
	Flakes with Levalosians Techniques	Middle
	Core Bifaces	Lower

2.2.5. Aryans

The Aryans were initially localized to the west of Indus River, but gradually their influence, observed by the presence of Painted Grey Ware pottery extended further east into the western Ganges valley. Aryan influence also appears to have moved south to the Deccan plateau, indicated by the introduction of iron and later of the Northern Black Polished pottery type (Fig. 5), also associated with Aryan cultural levels in the Ganges valley. These Aryan penetrations into the Deccan put into contact, by the end of the first millennium B.C., with other types as revealed by the presence of megalithic burial sites, which were widespread in southern Indian by about 300 B.C. Whether the megalithic builders came from outside India or represented a local development is still not clear.

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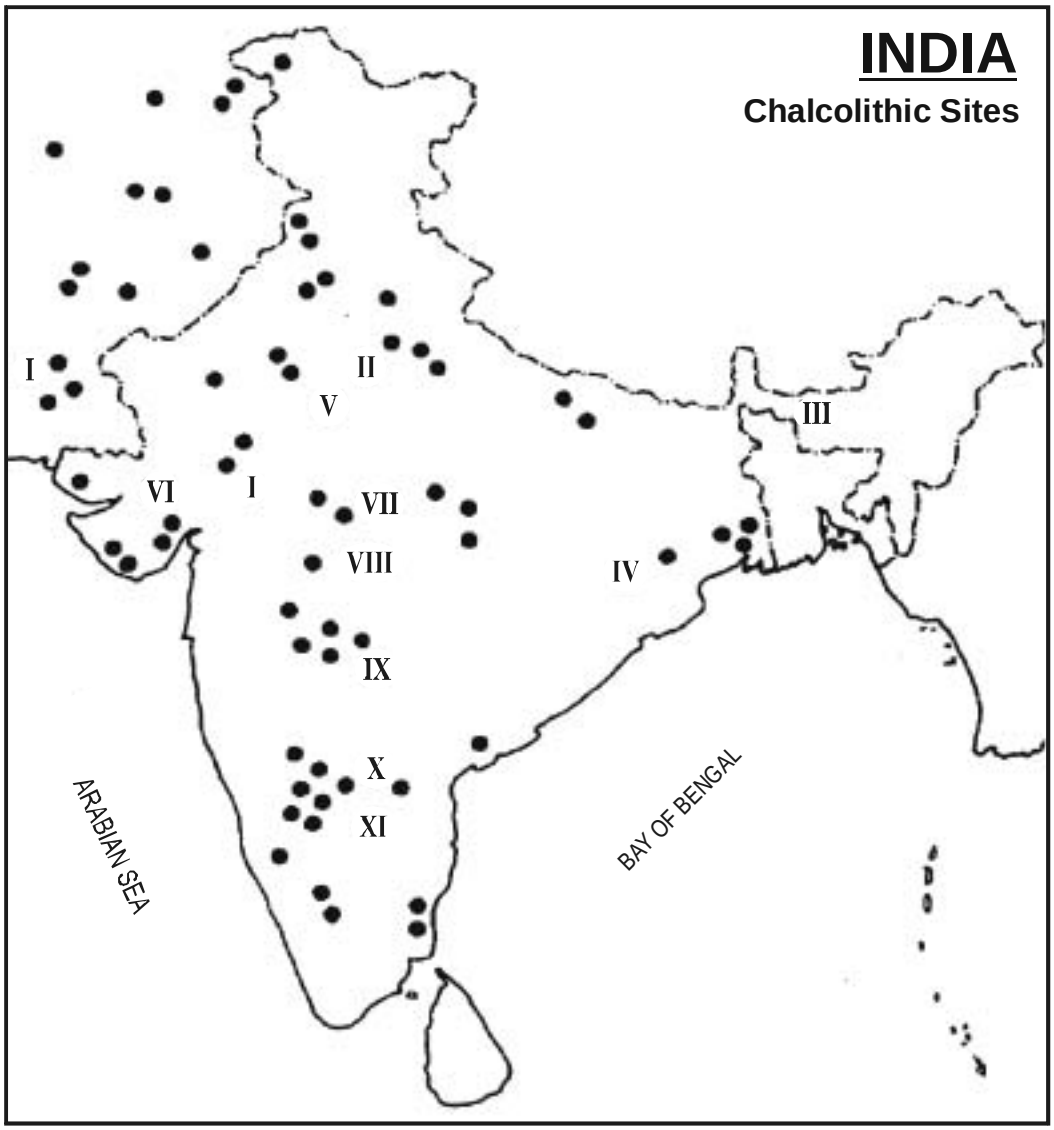
2.3. History

From the fourth century B.C. onwards for 2000 years, India, particularly in the north, was



● Chalcolithic Sites

I	Indus System	VI	Rajputana-Saurashtra
II	Ganges System	VII	Narmada System
III	Brahmaputra System	VIII	Tapi System
IV	Mahanadi System	IX	Godavari Pravara System
V	Chambal System	X	Bhima System
XI	Karnataka System		

Fig. 4. Major Chalcolithic Cultural sites found from India

subjected to repeated waves of penetration by alien people. History testifies that Greeks, Parthians, Sakas (Scythians) and Pahlavas including the Kushans were the first to come in after the Indo-Aryan civilization entered its settled course. The Huns came in somewhat larger numbers at the close of the Gupta epoch. These successions of peoples from outside India were assimilated into Hindu society. On the west coast, Jews and Parsis came after fleeing from their own homelands. Arabian Muslims, Persian Muslims, Turks, and Afghans, whose total number was very large, came to India from time to time. The Muslim immigration into India began even before the Arab invasions of the Sind quite early in the eighth century A.D. and ended with the establishment of the Mughal Empire in the sixteenth century. This was the last major movement, which produced some perceptible changes in the composition and culture of the indigenous population. The Muslims did not accept the Hindu religion but they made converts to their religion. The Europeans—Portuguese, Dutch, French and British started their intrusions from 15th century A.D. onwards and the Indo-European community grew from these infusions. In the east Shan peoples from Southeast Asia entered eastern part of India (Assam) (Thapar 1992, 1995).

2.4. Racial Classification

Anthropologists distinguish groups of people based on common origin, living, or having lived, in certain defined regions and possessing differing characteristic features in their appearance. However, one should remember that there are no strict lines of demarcation between races. All these groups blend imperceptibly into one another with intermediate types possessing various combinations of physical characteristics. Modern man is biologically uniform in basic features (for example upright posture, well-developed hand and feet, prominent chin, absence of bony eye brow, an intricately structured brain encased in a big skull with a straight high forehead and 46 number of chromosomes) and polymorphous as regards many secondary features. Scientists consider all human beings as belonging to a single species, *Homo sapiens*. The variations found in groups living in different geographical areas reflect only a differentiation within the single species due to host of biological, social and other factors. In anthropology there are two schools of thought on the origins of man and the major races—the polycentric and the monocentric schools. The polycentric theory (Franz Weidenreich, U.S.A.) claims that modern man evolved in several regions relatively independent of one another and that peoples developed at different rates. This theory claims that modern man evolved from the "oldest" and "old" people in each region and that this gave rise to the formation of the major races—Caucasoids, Negroids, Mongoloids, Australoids, etc. On the other hand monocentrists (for example Henri-Victor Vallois and G. Olivier in France, Francis Howell in the U.S.A., Kenneth Oakley in Britain, Vsevolod P. Yakimov, U.S.S.R.) consider modern man to have evolved in a single region. The ancient *Homo sapiens* who evolved there did not possess clearly distinguished traits of any of the modern races. It was only when human groups spread geographically and settled in definite territories that racial types evolved. That is why the races of modern mankind resemble one another so closely. This resemblance is a sign of their common origin, of their emergence in a single region. Darwin more than 100 years ago, ventured to predict- that one day it would be found that man had originated in Africa.

Mourant (1983) in his book *"Blood Relations"* stated that it is almost certain that man evolved from his pre-human ancestors and emerged as a unique tool-making animal somewhere in tropical Africa and that we are therefore, in a sense, all of African origin. Using five polymorphic restriction sites on b gene cluster, Long et al. (1990) worked out, the evolutionary histories and relationships among Africans, Eskimos and Pacific Island populations and reported an African origin for modern *Homo sapiens* and a phyletic structuring in the major geographical regions. It is probably rather over a million years ago that man entered Asia from Africa; bones of the early human species, *Homo erectus* have been found in China as well as in Java, which could have reached only through Asia. Moreover, to reach Europe, which he probably very soon did, he must have passed through south-west Asia. India has served as a major corridor for the dispersal of modern humans out of Africa (Cann, 2001, 2003; Kivisild et al. 2003; Palanichamy et al. 2004; Cavalli- Sforza 2005).). It probably was in Asia that Eurasian man, by now of the modern *Homo sapiens* species, diverged from African man, and then became

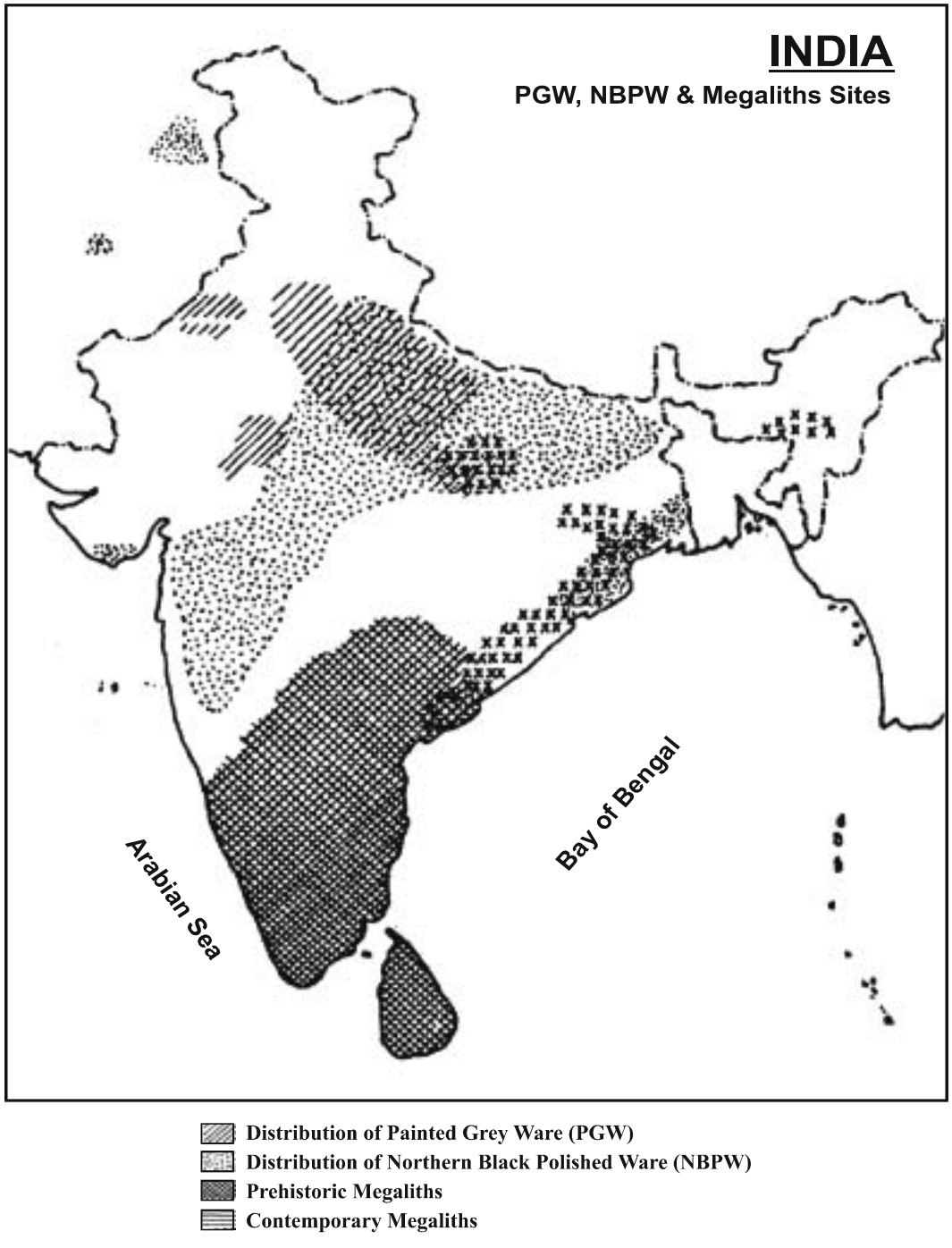


Fig. 5. Distribution of Painted Grey Ware (PGW), Northern Black Polished Ware (NBPW), Prehistoric and Contemporary Megaliths sites from India

differentiated into Caucasoid and Mongoloid types. Another differentiation, which probably took place in Asia, is that of the Australoids, perhaps from a common type before the separation of the Mongoloids. The Caucasoids and the Mongoloids almost certainly became differentiated from one another somewhere in Asia and Caucasoids subsequently spread to the whole western part of the continent and thence to Europe and North Africa (Mourant 1983). The divergence lines among the three major races—Negroid, Caucasoid and Mongoloid—estimated by Nei and Roychoudhury (1982) by using a number of genetic markers, reported the divergence between the Negroid and the Caucasoid-Mongoloid groups seemingly to have occurred about 110,000 ± 34,000 years ago. On the other hand, the divergence between the Caucasoid group and the Mongoloid group seems to have occurred about 41,000 ± 5,000 years ago. This corresponds to the time when classic Neanderthals were living. These estimates of divergence lines are much earlier than the estimates of Cavalli-Sforza and Bodmer (1971) (20,000-50,000 years ago), but they are not unreasonable in view of the fossil records available (Birdsell 1972).

The Mongoloids are the most numerous of the three major races of mankind and China in the centre of the Mongoloid area has the largest population of these than any country in the world, so the Chinese must be taken as the typical Mongoloids. The ancestors of Japanese passed through Korea to reach Japanese Islands, where they found ancestors of the present Ainu. Through an area to the south of China, extending from the Vietnamese border to the tip of Malaya peninsula, through this there must have passed Homo erectus very long ago on his way to Java; ["Sundashelf, a dry land as the route from Asian mainland to Java is now so well accepted that Shutler and Braches (1987) in their review of the paleoanthropology of Pleistocene island Southeast Asia see it as the route to Java from the Asian mainland for all migrating land mammals" (p. 186) *cited from* Tumer II (1990]. than perhaps (some- forty thousand years ago) the ancestors of the Australian aborigines. Then came the Indonesians, and finally the Mongoloids in narrower sense, represented by the Mons and the Khmers, the Tibeto-Burmans and the Thais, all of whom probably entered the region before 1000 B.C. (Mourant 1983).

The populations of Siberia are important in supplying evidence regarding the original peopling of the American continent. This took place perhaps about thirty thousand years ago; it was through the Bering Strait, which was then dry land owing to the recession of sea level accompanied by last glaciation. Perhaps about thirty thousand years ago, populations of Mongoloid physical type moved into northeastern Siberia and thence into America (Mourant 1983).

The differences between Mongoloids and Caucasoids appear rather sharp as one crosses the mountains in the northern boundary of the Indian sub-continent. The passage from India to Burma is somewhat more gradual, probably because contact here has been present for a long time and some mixing has taken places, whereas the Mongoloids north of the mountains were probably fully differentiated in the Far East before the retreat of the ice allowed them to enter Tibet (Mourant 1983).

In Asia, Australoid people now live in South of India, the deep ocean between India and Australia means that the direct ancestors of the Australians could not have set out from there. We must picture both India and south-east Asia as being at one time inhabited largely by Australoids who were driven by technologically more advanced people from the north, in the one instance into southern India and Sri Lanka and in other, across Burma and Malaysia and so ultimately through Indonesia and New Guinea to Australia (Mourant 1983).

A number of racial classifications of human populations have been reported in the literature, but there seems to be no agreement about these classifications among anthropologists. However, the human populations are broadly divided into three major races: Caucasoid, Negroid, and Mongoloid. Many anthropologists have considered two more major groups *i.e.*, Amerind and Australoid or Oceanian (Boyd 1963). These schemes of classification of human populations were largely based on morphological and anthropometric characters. In the last few decades, however, new methods with elaborate statistics and biometry along with the latest concepts on human genetics have added fresh dimension to the study of human population groups.

To the Indian subcontinent came several waves of immigrants at different periods of history and entered into the ethnic composition of the population at different levels from a very early

phase of human civilization. The intrusions of these people with several racial elements have left the strains of various developed races together with their ethnic and cultural substrata in the land, thus representing the elements of all the main divisions of mankind.

In India, the range of somatic variations in different physical traits of its people is remarkably wide. To account for the heterogeneity and to highlight the underlying pattern of the observed variations, earlier European anthropologists, like Charles de Ujfalvy (1884) and Captain Drake-Brockman, Sir TH Holland (1902) and Waddell (1900) measured groups from various parts of India and attempted various taxonomic classification of the Indian peoples. During the early part of the last century, the schemes of classification of Indian people were largely based on morphological and anthropometric characters. The list of various classifications that have been given on the people of India by different authors is as follows.

1. Risley's Classification (1915)
2. Giuffrida-Ruggari's Classification (1921)
3. Haddon's Classification (1925)
4. v. Eickstedt's Classification (1934, 1952)
5. Guha's Classification (1935, 1937)
6. Roy's Classification (1934-38)
7. Sarkar's Classification (1958)
8. Biasutti's Classification (1959)
9. Roginskij and Levin's Classification (1963)
10. Büchi's Classification (1968)
11. Bowles's Classification (1977)

So many classifications on the people of India have been reported and almost all seem to make some sense. An attempt has been made to evaluate the distribution of various racial strains/ elements present in the peoples of India and this is represented in Figure 6 (This figure has been drawn while taking into consideration the classifications reported by Guha and others).

2.4.1. Negrito Element

It is generally admitted that the Negrito represents the oldest surviving type of man and it is possible even that they preceded Neanderthal man by whom, according to Grifth-Taylor, they were displaced and disposed. In any case, Negrito seems to have been first inhabitants of South East Asia. The traces of the stock are still to be seen in some of the forest tribes of the higher hills of the extreme south of India and similar traces appear in the inaccessible areas of Assam and Bengal, and Burma, where dwarf stature is combined with frizzly hair which appears to have resulted from recent admixture of pure Negrito stock of the Andamans with blood from the main land of India or Burma.

If Negrito was the earliest inhabitants of Southern Asia, they must have been displaced or supplanted by the Proto-Australoid. This dolichocephalic type appears to have its own origin in the west. The view that the Australian is connected with the Neanderthal man, though repeatedly rejected by authorities, seems to die hard since Hrdlicka (1927) apparently regards the Neanderthal as having contributed to existing human types, while Sewell (cited from Iyer 1936) appears to revert to the theory of Australian origin and in his account of Mohenjodaro skulls he definitely associates Indian Proto-Australoid type with Australian aborigines on the one hand and with Rhodesian skull on the other.

So many views on the Negrito problem in Indian ethnology have been reported in the literature. Guha (1928, 1929) observed the presence of Negrito racial strain from the solitary character of hair form (frizzly type) which he found among the Kadars who live in the interior of the chain of hills running from the Anamalais to Travancore. Guha (1961) wrote to Sharma (personal communication) that frizzly type of hair occurs not only among Kadars but among Irulas and the Pulayans also. Guha (1961) disagree with the hypothesis that there had been admixture of African slaves with the Malabar people; giving the reason that if it has occurred in that case, it should have been in the coastal areas, where Zamorins of Calicut imported African slaves but not in the interior of the hills 100 miles away. He further added that there is no sign of any African culture among the Kadars. However v. Eickstedt (1939) stated that genuine Negro frizzly hair never has been found in South India. The problem probably arose because the distinguishing words, spiral, woolly or frizzly, have been applied in a vague manner. Sarkar stated that the sporadic cases of frizzly hair might not be Negritoid at all. They may be independent mutations. Whether they are genetically related to Negro or Melanesian frizzly hair group, only further genetic researches can disclose.

Banerjee (1959) reported the presence of intermediate or mixed types of hair among the

Kadar and accounted its origin as due to admixture with Negroid elements.

Rakshit (1965) suggested that the alleged Negrito Dravidian tribes of south India *viz.*, the Kadar, Irula, and Pulayan etc. are in all probability, the foetalized derivatives of Australian basic type.

From the genetic structure of Kadar of Kerala, Saha et al. (1974) evaluated their findings with the other (Sarkar et al. 1959) and observed that there is a little to support that a proportion of Kadar show Negritoid traits. However, they added that there is slender evidence, which supports the possibility of past African Negro admixture on a small scale. The postulated genetic reconstruction of ancestral Kadar population by them suggested that they may have been similar to Melanesian and Australian aboriginal populations, but their original genetic structure has been modified through incorporating genetic elements not only from Black Africans but also from surrounding Dravidian populations.

To study the molecular genetic evidence Mountain et al. (1995) used a small sample of (n=7) of Kadars, without any definite conclusion.

Sarkar (1954) has discussed the Negritos of the Andaman in the light of the process of pygmy formation. Steatopygia, infantilism, and dwarfism are probably the effect of endocrine derangements and the reproductive physiology of the Andamanese appears to have been affected as well. The Andamanese appear to have been facing extinction long before they were exposed to civilization. The Andamanese were probably peopled in the quaternary times during a glacial period when the fall of sea level brought lower Burma in direct contact with the Islands.

Negrito populations occupy parts of the Philippines, Northern Malay Peninsula, Andaman Islands and New Guinea has a number of morphological characters similar to those of Pygmies and Bushmen of Africa. Because of this similarity, some anthropologists have hypothesized a common origin of the Negrito populations. However, Nei and Roychoudhury (1982) analysed the genetic relationship and reported that despite some morphological similarity between the Negritos of Southeast Asia and the Pygmies and Bushman of Africa the genetic distance analysis shows them to be genetically different. This result supports Coon's (1965) thesis that the Pygmies and Asian Negritos developed their phenotypic similarity by adapting to similar environmental conditions independently rather than by common descent.

Further Nei and Roychoudhury (1993) suggested a southern route of migration from Africa to Australia in the Pleistocene period to explain the similarities among some populations in Africa, Southeast Asia and Australia and similar observations have also been made by Cavalli-Sforza et al. (1994) and Schurr and Wallace (2002).

Murhekar et al. (2001) studied the red cell genetic abnormalities among Great Andamanese and observed that they are the surviving representatives of Negrito populations that were distributed over the entire Southeast Asia in ancient times, which were genetically different from other African populations. Using mtDNA material, Endicott et al. (2003) and Thangaraj et al. (2003) observed that the Andamanese are more closely related to other Asians than to modern day Africans. Kashyap et al. (2003) studied the aboriginal groups (Great Andamanese and Jarawas) of Andaman and Nicobar Islands and observed that the distinct genetic identity of the aboriginal populations of the Andaman Islands and other Asian and African populations deciphered by nuclear and mitochondrial DNA diversity suggest that (i) either the aboriginals of Andaman are one of the surviving descendents of settlers from an early migration out of Africa who remained in isolation in their habitat in Andaman Islands, or (ii) they are the descendents of one of the founder populations of modern humans.

2.4.2. Proto-Australoid Element

The earliest stratum of Indian populations was a long-headed, dark skinned, broad-nosed people. Their physical features are closely akin to modern aborigines of Chota Nagpur, Central India and the primitive tribes of South India. They are original inhabitants, the so-called *'Adi-basis'* of India. In the hymns of *Rig-Veda* the oldest sacred texts of the Hindus, they are mainly addressed as *'Dasa'* (Barbarians) or *'Dasyu'* (ugly, sub-human) described as *'Anas'* ('a-nas' = noseless or 'an-as' = without a mouth), *Krishnagarba* (Dark skinned), *'Mridhravak'* (Hostile speech) not worshiping *Vedic* gods with whom Aryan speaking tribes fought during their advent into India from Transcapia.

Various authors have classified them and so far, there has been no agreement on this. Lapicque (1920) was probably responsible for the term Pre-

Dravidian. Ruggeri (Chakladar 1921) named it 'Australoid-Veddaic', while Chanda (1916) favoured the term *'Nishada'*. v. Eickstedt (1934) used the term Weddid for those having closer affinity with the Veddas of Ceylon. Sewell and Guha (1929) in trying to find out the physical affinities of the Nal race have described Tamils and the Veddas as descendants of the original Proto-Australoid and Proto-Negroid blend. They have also found the Proto-Australoid type occurring among the Mohenjodaro skeletal remains. Hutton (1933) used the term Proto-Australoid exclusively in his census reports. He even put Veddas under Proto-Australoid. The term Proto-Australoid owes its origin to Dixon (1923). Hooton (1930) introduced changes in Dixon's terminology and replaced term Proto-Australoid as Pseudo-Australoid while he similarly renamed Proto-Negroid as Pseudo-Negroid.

The Papuas of New Guinea and the Australian aborigines of Oceania are often called Australoids. Guha (1937) used the term 'Proto-Australoid' to designate the indigenous people of India presumed to have racial affinities with Australian Aboriginals. It was observed in the morphological traits that there seems to be a regular gradation, the shortest and smallest being the Indian tribes, then come Veddas of Ceylon (Sri Lanka) and lastly the Australians. The Indian tribes retaining the more basic characters and the two extra Indian groups having developed some of the features in a more marked manner. The most appropriate term to apply to them therefore is Proto-Australoid, which shows best the genetic relationships between the three. Sarkar (1954) pointed that so long, the Australoid is regarded as one of the basic stems of mankind and its prototype is unknown, the use of the term Proto-Australoid seems to be unjustified.

Sanghvi (1976) compared allelic variability observed among tribal populations in India and Australia to study the postulated ancestral relations between Indian and Australian Aboriginal people. He concluded that the search for appropriate weights for individual alleles to be considered in genetic distance analysis of problems for racial origins has not so far been rewarding.

Simmons (1976) reported on the basis of the blood group genetic data, presently available, that the Veddoids, and other aboriginal peoples of South India relate most closely to the Indian populations, and neither they nor the Veddhas relate in any obvious blood groups genetic make-up to the distant Ainu, or to the even more distant Australian Aboriginals.

Kirk (1976) searching for specific markers, which might link Australian Aboriginals with the Veddahs of Ceylon and the "Veddoid" populations of South India and stated that so far no specific markers common to any of these sets of populations have been found. By contrast, the Veddahs of Ceylon do have some genetic markers in common with groups of Southeast Asia, particularly TF CHI and the abnormal haemoglobin *HB*E*. The 'Veddoids' of South India, however, have neither of these markers that possess the abnormal haemoglobin *HB*S* and having no transferrin variants in the populations which he studied. It is only in the north east of India that transferrin allele *TF*CHIi* is found while allele *HB*E* is not uncommon among tribal populations such as Oraons, Konda Reddis and Koya Dora. Roychoudhury (1984) studied genetic relations between Indian Tribes (Toda, Irula, Kurumba of South India); Veddah of Sri Lanka with the Aboriginals of Malay, New Guinea and Australia by genetic distance analysis and found the tribes of South India and Sri Lanka are genetically closer to each other than to the Aboriginals of Southeast Asia and Oceania. He concluded that despite their morphological similarity there is no genetic evidence to suggest that the Indian tribes and Australian Aboriginals are biologically related.

Pietrusewsky (1990) reported from the craniofacial variation that Australians represent a biologically distinct population, sharing ancestral ties with Melanesians but not with the recent populations of Asia and the rest of the Pacific. The latter represent a second major population complex.

Rao and his colleagues (2009) have sequenced 966 complete mitochondrial DNA genomes from Indian 'relic populations' and found certain mutations in the DNA sequences of the Indian tribes which are specific to Australian Aborigines, which shows that aborigines, who initially arrived in Australia via south Asia, may have originated from India (Times of India, July 23, 2009, P. 17)

2.4.3. Mongoloid Element

The Mongoloids are mainly presented in the northern and northeastern zones of the

Himalayan ranges, valleys, and eastern frontiers. Regarding the Mongoloid element, Hutton is of the view that it may be said to fringe upon the area to Indo-European languages. There is very considerable overlap in the places. In all the overlapping areas, the Indo-European languages are definitely intrusive and the Mongoloid element in the population is strong enough to retain its own languages. It is possible that the extension of Mongoloid physical elements has gone a good deal further than the present range of their language would suggest. One of the Mohenjodaro skulls has been identified as definitely Mongoloid and from the lowest stratum of the excavation have been recovered terracotta figurines with unmistakable Mongoloid features having the typical sloping narrow eyes of caricatures of that type.

On the other hand, Eastern Bengal is strongly suggestive of mixed Mongoloid and Proto-Australoid strain. Buxton suggests that the Pareoean (race inhabiting South China, Burma, or Southern Mongoloid) element extends to southern India. Burma, of course, is almost completely Mongoloid and though the existence of other strains is not doubted, they are no longer easy to isolate. There are Proto-Australoid elements too. In some of the hill tribes and on the Assam side, a Melanesian strain is to be expected.

Mongolian features have been observed among the tribes of Central and Eastern India, the tribes occupying such States as Bihar, Orissa, Madhya Pradesh, and Andhra Pradesh, in the latter state in areas adjoining Orissa and Madhya Pradesh. The list includes almost important Mundari speaking (Munda Group of Austro-Asiatic Family) tribes like the Munda, Santal, Ho, Juang, Saora, Gadaba etc., and number of Central Indian Dravidian speaking tribes like the Maria, Muria, Kondh, and Oraon etc. The occasional presence of Mongolian features among the central and eastern Indian tribal groups foetalized derivative is of Australian types as suggested by Rakshit (1965).

2.4.4. Other Racial Elements

Amongst the earliest arrivals into Indian subcontinent were long-headed people of Palaeo-Mediterranean stock, who came in successive waves. They were closely related with the Proto-Mediterranean or Proto-Egyptian Brown Race and were long, narrow-headed people, having medium to tall stature, possessed relatively long, narrow faces, low orbit, and vertical forehead with protruding occiput and mesorrhine nose. Later waves of this race belonged to the more basic stock of the Mediterranean race. Their skeletal remains have been recovered from the Chalcolithic sites of the Indus Valley (Harappa 1963; Mohenjodaro 1931) etc. and further west from the Aeneolithic sites of Iran and Mesopotamia. They now form a dominant element among the populations of North India and the upper classes.

The next wave was allied to the so-called Oriental Race of Eugen Fischer (1923). They were relatively broad-headed, medium in stature, and broad faced, thus closely related to the brachycephalic Alpine and Armenoid racial types of Europe. Their major concentration was in Asia Minor, Pamirs or the Iranian plateau, from where they are supposed to have infiltrated into India during the third to second millennium B.C.

The early evidence of these elements was found among a few of Chalcolithic crania from Indus Valley sites and later among Iron Age crania from Adittanallur in the Tinnevally District of South India (1963). The origin of the broad-headed strain allied to Alpine and Armenoid lies primarily among the brachycephalic hordes of prehistoric *Homo alpinus* stock of Central Asia. However, the original source of brachycephaly in Western India appears to have come from Scytho-Iranians who had infiltrated from the ethnic intrusion of the Sakas, Huns, Kushans, and Abhiras. Today the stronghold of this type is in Bengal, Rajasthan, and Gujarat.

The Dinaric type (medium to light pigmented, hook-nosed, acrocephalic, round head) finds expression among the population of Bengal and Orissa and were mixed with varying degrees of the Mediterranean element. It is also to be seen in Kathiwar, Kannanda and Tamil areas. The latest great racial movement into India was associated with a long-headed, tall, delicate-nosed, fair-skinned people having a long face with well-marked chin, possessing blue eyes more akin to the so-called Nordic Race (pure blond or near blond, long heads) of Europe. During the close of the third or at the beginning of the second millennium B.C., they were supposed to have entered India across the northwestern frontier from the Eurasiatic steppes between south-western Russia and Siberia. Based on linguistic and cultural evidence, they have been described as Indo-European, Indo-Iranian, or Aryan people,

who were Proto-Nordics. The area of their civilization was said to be in the Aralo-Caspian Basin.

Abe and Tamura (1983) and Abe (1985) used multivariate analysis to classify the people of India (South) and Sri Lanka. Based on morphological types, Malhotra (1978) stated that Negrito, Australoids, Mongoloids and Caucasoids have contributed to the biological composition of the people of India.

Mourant (1983) classified the peoples of the Indian region broadly into three zones - tribal peoples of Australoid type, living in pockets chiefly in the south, the Caucasoids of slender type and with rather dark skin mostly speaking Dravidian languages occupying the main southern part of the region and more robust Caucasoids, with paler-skins and speaking Indo-European languages, in the north. The people of the Himalayan regions are partly or wholly Mongoloid.

If the millions of population of India are members of some great branch of humanity, it is strange to note, all or nearly all, who have sought to explain the differentiation of population of India into racial types, have sought the solution of this problem, from outside the peninsula. They have never attempted to ascertain how far India has bred her own races. They have proceeded on the assumption that evolution has taken place long ago, far too away but not in India, the great anthropological paradise (Keith 1936). No doubt, India has been invaded repeatedly but it is a fact that 85 per cent of the blood in India is native in the soil. It is necessary that our eyes should be more directly focused on the possibility of India being an evolutionary field both now and in former times.

In India, the range of somatic variations in different physical traits of its people is remarkably wide. Based on these variations a number of European and Indian anthropologists attempted various taxonomic classifications of the Indian peoples. Among Indians all the major racial elements, namely Caucasoid, Mongoloid, Australoid, and Negritos have been reported. In general, all the classifications given by different authors agree that Himalayan mountain complex region populations have Caucasoid (Aryan and/or Dravidian) and Mongoloid racial elements in Western and Central Himalayan region and Australoid (Pre-Dravidian), Caucasoid (Aryan and/or Dravidian) and Mongoloid racial elements in Eastern Himalayan region. Whereas in Indus-Ganga-Brahmaputra plains region, the people from north are having predominantly Caucasoid-Aryan and Caucasoid-Dravidian racial elements and towards western side Caucasoid (Aryans, Dravidians) and Australoid (Pre-Dravidian) racial elements, towards East India, from West Bengal, the racial elements present are similar to that observed among peoples from Eastern Himalayan region, albeit Mongoloid racial element is present in lesser degree. Among populations from Orissa and Bihar the Caucasoid (Aryan and Dravidian) and Australoid (Pre-Dravidian) racial elements are present. Among Central Indian populations, the picture is similar to that observed from Bihar and Orissa. Towards South India the major racial elements are Caucasoid (Dravidian) and Australoid (Pre-Dravidian), whereas among Andamanese, Negrito-like traits are present and in Nicobarese, Mongoloid affinities are observed.

In general, the Australoid (Pre-Dravidian) racial element is predominant among scheduled tribes, whereas among scheduled castes also Australoid racial element is present, but it varies in degree among regions/zones and as scheduled caste populations are having admixture with Caucasoids (Aryan and/or Dravidian) in varying degrees. Mongoloid racial element, which is predominant among populations inhabiting Eastern Himalayan region is also observed among peoples living in inner areas of Western and Central Himalayan regions.

Apart from this, some more populations with different racial elements entered India and were assimilated into the local people. The Australoid (Pre-Dravidian) are supposed to be the original inhabitants of India, while the rest are considered to have come in successive waves of immigration of known and sometimes unknown antiquity.

Barnabas et al. (1996) used mitochondrial DNA to study the ancestry and interrelationship of and their relationship with other World populations and concluded that the Indian population is closer to Caucasians and has an admixture with Asians. The North Indian population appears to have a recent admixture of Caucasian mtDNA types which is absent in people of South India. This study conforms to already known observation from a long time.

A study by Centre for Cellular and Molecular Biology (CCMB) and Harvard Medical School, Harvard School of Public Health and the Broad Institute of Harvard and MIT researchers on

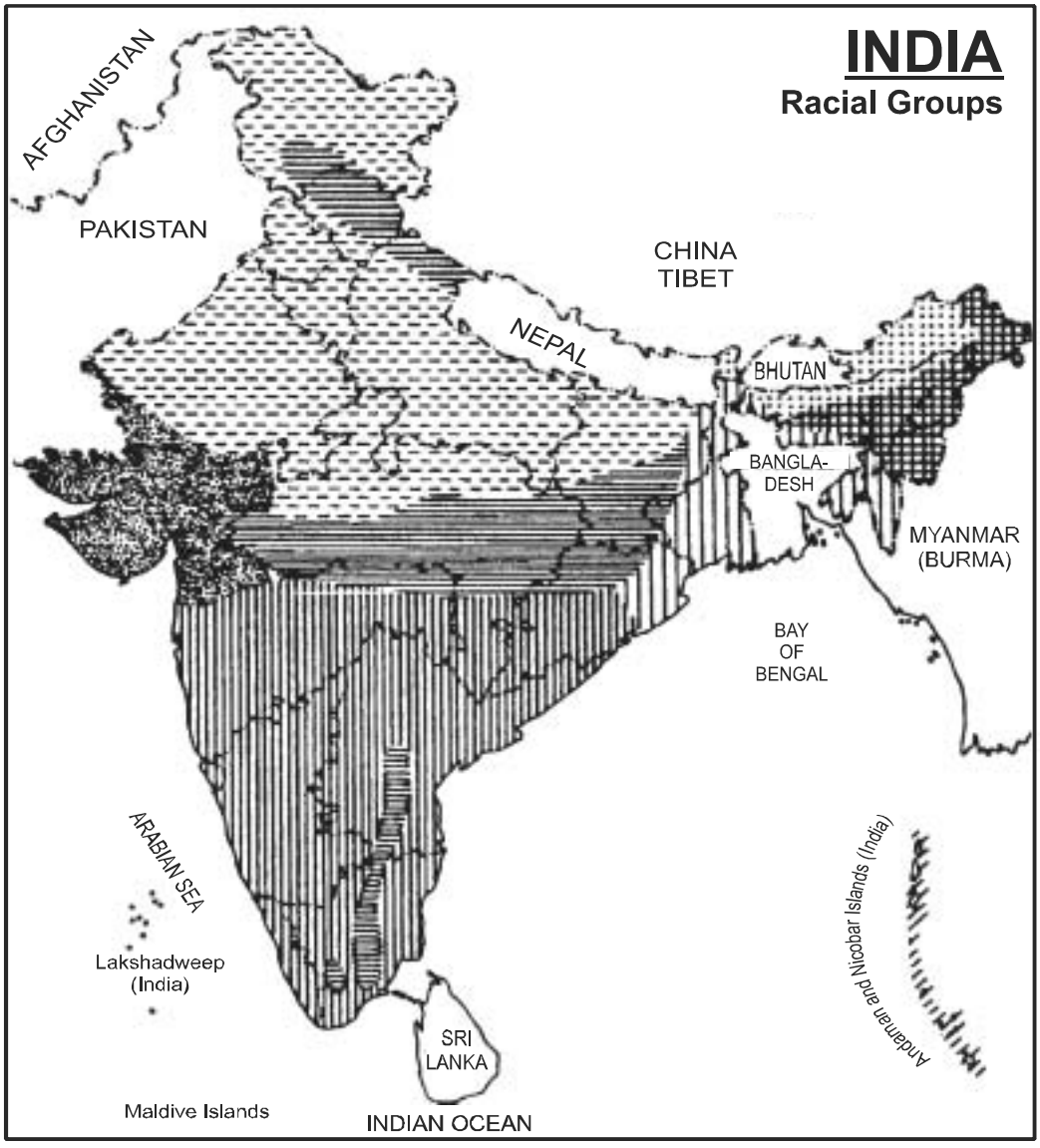
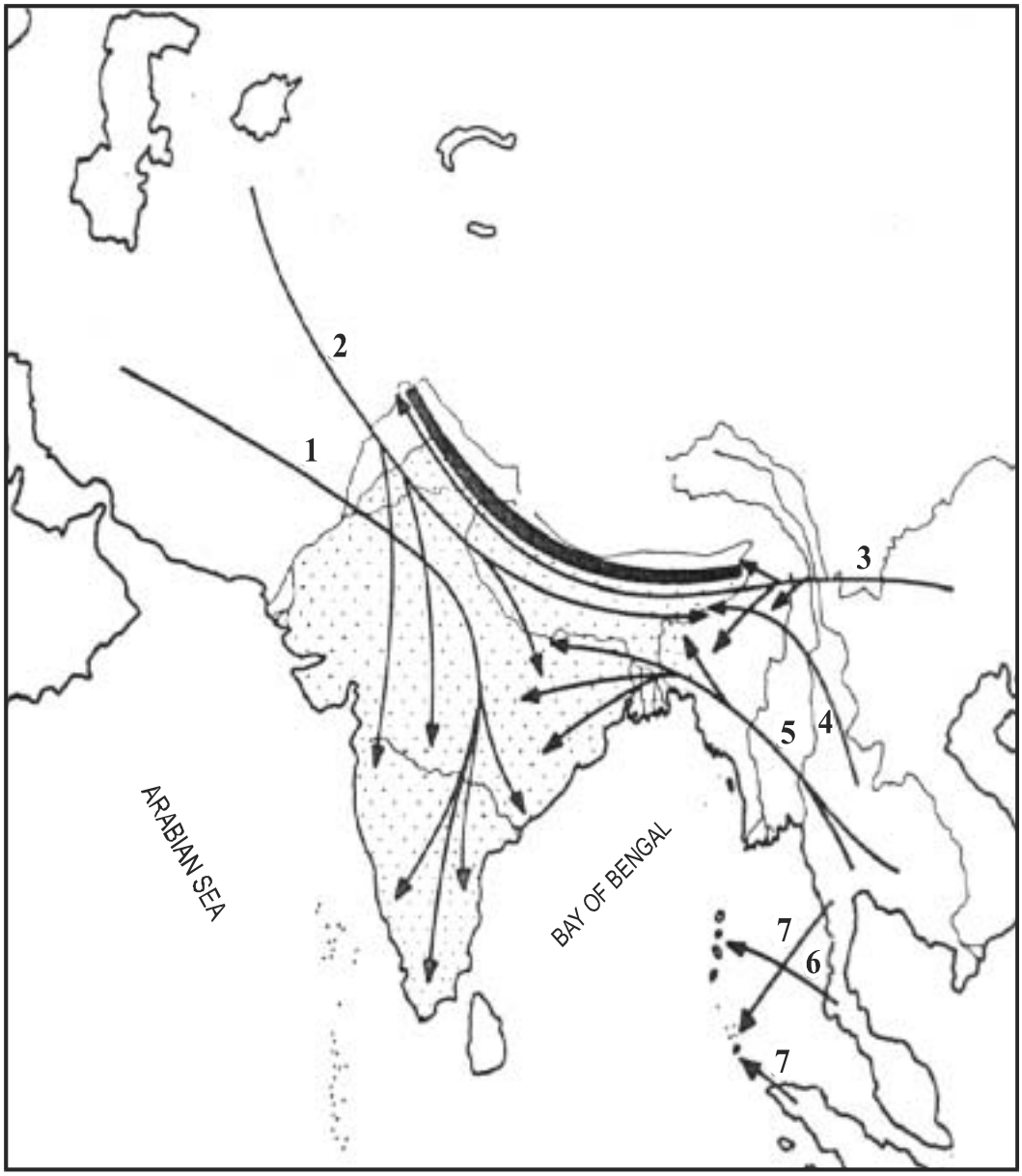


Fig. 6. Distribution of various racial strains present in the people of India



1 Early Caucasoids (Dravidians)
2 Later Caucasoids (Indo-Aryans)
3 Early Mongoloids (Various groups)
4 Later Mongoloids (Ahom)
5 Austro-Asiatics (Various groups)
6 Andamanese
7 Nicobarese
Dots = Original distribution of the autochthonous Indian tribal populations

Fig. 7. Racial migration

ancestral Indian populations says there is a genetic relationship between all Indians and more importantly, the hitherto believed "fact" that Aryans and Dravidians signify the ancestry of north and south Indians might after all, be a myth. The study analysed 500,000 genetic markers across the genomes of 132 individuals from 25 diverse groups from 13 states. All the individuals were from six-language families and traditionally "upper" and "lower" castes and tribal groups.

Thangarajan of CCMB said there was no truth to the Aryan-Dravidian theory as they came hundreds or thousands of years after the ancestral north and south Indians had settled in India.

The genetics proves that castes grew directly out of tribe-like organizations during the formation of the Indian society. Thangarajan noted that it was impossible to distinguish between castes and tribes since their genetics proved they were not systematically different. It reveals that the present-day Indian population is a mix of ancient north and south bearing the genomic contributions from two distinct ancestral populations - the Ancestral North Indian (ANI) and the Ancestral South Indian (ASI). Thangarajan said that the initial settlement took place 65,000 years ago in the Andamans and in ancient south India around the same time, which led to population growth in this part. He further added that at a later stage, 40,000 years ago, the ancient north Indians emerged which in turn led to rise in numbers here. However, at some point of time, the ancient north and the ancient south mixed, giving birth to a different set of population. And that is the population that exists now and there is a genetic relationship between the populations within India.'

The researchers, who are now keen on exploring whether Eurasians descended from ANI, find in their study that ANIs are related to western Eurasians, while the ASIs do not share any similarity with any other population across the world. However, researchers said there was no scientific proof of whether Indians went to Europe first or the other way round.

Migratory Route of Africans

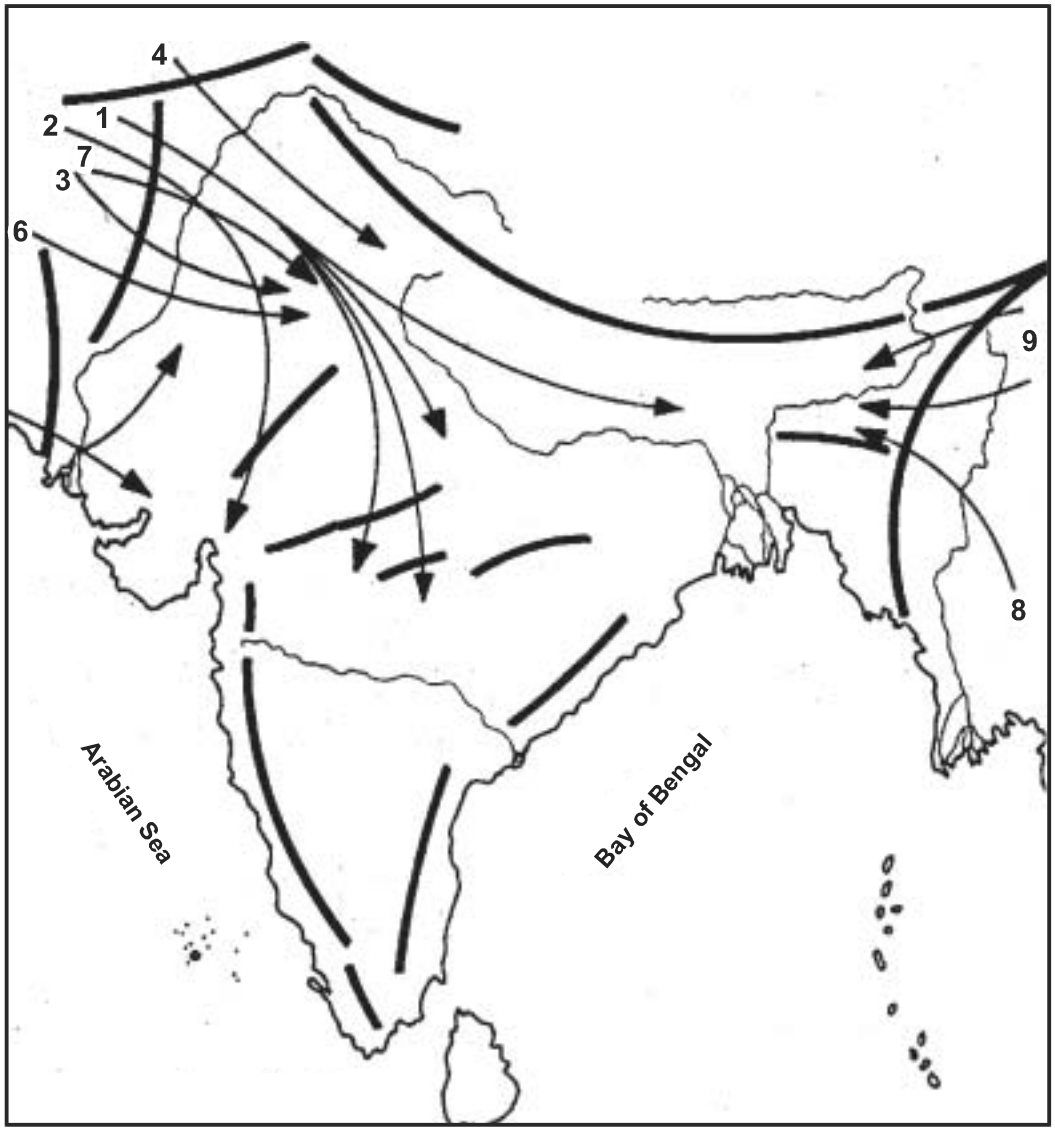
Between 135,000 and 75,000 years ago, the East-African droughts shrunk the water volume of the lake Malawi by at least 95%, causing migration out of Africa. Which route did they take? Researchers say their study of the tribes of Andaman and Nicobar islands using complete mitochondrial DNA sequences and its comparison those of world populations has led to the theory of a "southern coastal route" of migration from East Africa through India. This finding is against the prevailing view of a northern route of migration via Middle East, Europe, south-east Asia, Australia and then to India.[timeso findia.indiatimes.com/news/india/Aryan-Dravidian-divide-a-myth-Study/articleshow/5053274.cms (Retrieved on 29. 09. 2009)]

The various classifications given above were initially based on geographical regions, linguistic families, caste groups, and/or religious groups and were followed by scientifically oriented somatometry and somatoscopy. Finally, few genetic markers, like blood groups, were also taken into account. The picture thus emerged was complicated and uncomprehensive as India from the fourth century B.C. for 2000 years, particularly in north received wave after wave of immigrants [Indo-Aryans, Greeks, Parthians and Sakas (Scythians), Kushans, Huns, Arabs, Turko-Afghans, Mongols (from north and north west directions), Shan (from eastern side)] from different directions and thus took on the character of a miniature museum of races commingling in all sorts of permutation and combinations.

From the section of Indian population milieu of this chapter it may be evaluated that migration from different places formed the Caucasoid (Dravidian, Aryan) and Mongoloid components of India's populations, whereas the original inhabitants who have been classified as Negrito and/or Proto-Australoids may be referred as Nishada (Pre-Dravidians). It is worthwhile to mention here that the racial classifications are currently only of academic interest and are seldom used for categorizing populations, as the population composition at any time is influenced by mating patterns, migrations, genetic drift, mutation and selection under different environments. It should not be forgotten that racial categories are artificial constructs, which have not been able to withstand the test of time. Populations have always intermixed, with the consequence that the pure type ('race') was nothing but a figment of imagination. We dissociate ourselves from the old race concepts.

3. HUMAN POPULATION GENETICS

Biological Anthropology deals with the comparative biogenetics of man. Within the



Mountain ranges

1	Indo-Aryans	2000 - 1400 BC
2	Yüechihs and Sakas	2nd Century BC
3.	Kushanas	First Century AD
4	Huns	5th-6th Century
5	Huns	8th Century
5	Arabs	10th-11th Century
6	Turko-Afghans	12th-13th Century
7	Mongols (Timur)	before 13th Century
8	Ahoms	before 13th Century
9	Tibeto-Burmans	

Fig. 8. Waves of penetration by alien peoples

various fields of research of the present Biological Anthropology, the studies of human evolution as well as the study of genetic variation in modern man hold an eminent place. An important branch of Biological Anthropology is therefore Population Genetics, which deals on the one hand with exact genetic descriptions of human population, but which on the other hand tries to find out the reasons for genetic differences among them. To study these genetic differentiation processes in man, which are obviously still ongoing, reliable population data are necessary. The comprehensive reviews on the human population genetics have been given e.g. by Mourant et al. (1976), Steinberg and Cook (1981), Tills et al. (1983), Roychoudhury and Nei (1988), Bhasin et al. (1992), Cavalli-Sforza et al. (1994), Cavalli-Sforza and Cavalli-Sforza (1998), Walter (1998), Cavalli-Sforza (2000), Bandelt et al. (2006), Stone et al. (2007), Reddy (2008). The existence of genetic variation in man is caused by many factors, among which selection, migration and gene flow, genetic drift and founder effects are the most important ones. By means of many examples, Vogel and Motulsky (1997) and Jobling et al. (2004) have shown the importance of these factors for the understanding of genetic variation in man. Morant et al. (1978) have reviewed the associations between genetic markers of the blood and diseases, which are of considerable interest in this connection. A critical appraisal of the available human population genetic studies has shown a high incidence of genetic and genetic-environmental disorders like abnormal haemoglobins S and E, glucose-6-phosphate red cell enzyme deficiency, etc. (WHO 1966, 1967; Livingstone 1983; Yoshida and Beutler 1986; Honing and Adams 1986; Luzzatto and Mehta 1989; Beutler 1990; Bhasin et al.1994; Mao 2007).

Biological Anthropologists are, however, not only interested in the ethnic and geographic variation of the numerous genetic markers of the *human blood*, but are also concerned with the variation *of anthropometric and morphological traits*. They also help to understand extent and mode of genetic variation in man and contribute, too, considerably to our knowledge on evolution processes within the human species (Comas 1964). Biological relationships and distances between human individuals and groups can be assessed by the use of anthropometric data at least as successfully as this can be done by the use of serological traits with known modes of inheritance (Spielman and Smouse 1976). The obvious reason is that anthropometric dimensions are also genetically determined even if the polygenic nature of the genetic control and the environmental effect on the development of their phenotypic manifestation cannot be spelled out in detail (Brace and Hunt 1990; Brace et al. 1991). However one has to take into account, however, that some of these anthropometric traits, *e.g.* body height, are not only inherited by an unknown number of different genes but they are also determined by non-genetic factors of different kind, which makes it somewhat difficult to interpret ethnic and/or geographic differences in the distribution of these traits in a satisfying way.

Since 1951, also the various *dermatoglyphic traits* occupy an important place in Biological Anthropology. Determined by genetic factors a few weeks after conception they are not affected by environmental factors and it is a property that explains the importance of dermatoglyphics in population studies. However, up to now, it is not yet possible to calculate gene frequencies for the various dermatoglyphic traits they are nevertheless good tools in order to record genetic variation within and among human populations (Cummins and Midlo 1943; Holt 1968).

Human population studies using dermatoglyphic traits began with early population descriptions and currently utilise multivariate procedures for detecting evolutionary processes. Birdsell (1952) stated that complex genetic traits (polygenic) would be more useful than simple genetic traits in tracing widely separated or distantly related populations. Rife (1954) observed that the polygenic nature of dermatoglyphic variables would make them less subject to random genetic drift, and in addition they would be free of assortative mating effect. Newman (1960) made a similar review and reported that anthropometric variables were highly susceptible to extensive post-natal alteration by the environment, while blood group alleles might reflect too much recent evolutionary activity from gene flow and suggested that dermatoglyphic traits would possess advantages in being less subject to environmental influences, but would also be less affected by gene flow. Therefore, dermatoglyphic traits would be most suitable for classifying older and more basic relationships between populations. Rothhammer et al. (1977) applied this idea and observed that polygenic (e.g. dermatoglyphic) traits evolve at a slow rate as compared with monogenic systems,

and are thus less susceptible to evolutionary forces, particularly genetic drift.

The various *morphological and behavioural characters* can be utilised profitably, too, to investigate genetic variation within and among human populations (Boyd 1950), though the mode of inheritance of all these characters is still rather unclear.

Human cytogenetics has made an outstanding contribution to the understanding of human evolution (Vogel and Motulsky 1997; Kalz and Schwanitz 2004; Bhasin 2005; Décsey et al. 2006; Ibraimov and Karagulova 2006a, b). Its contribution to the concern of human population genetics, however, is rather insignificant, at least yet, and the expectations, which arose from Court Brown's book "Human Population Cytogenetics" (1967), were not fulfilled. Nevertheless cytogenetic population studies should not be given up.

The development of new techniques in *molecular biology* rendered possible to elucidate human variability and human prehistory. Application of DNA techniques within anthropology permits analyses of molecular variability in both human and non-human organisms, to test hypothesis about human origins and behaviour.

Types of Molecular Markers: Human genome is composed of three billion base pairs - these are "Chemical Letters" of which DNA is composed - out of which only a small fraction (4 percent) – actually belong to structural genes. Human genome consists of 3300 Mb of Nuclear DNA and 16.6 Kb of Extra Nuclear Mitochondrial DNA. Following is the list of various molecular markers that can be studied using nuclear and mitochondrial DNA.

1. Restriction Fragment Length Polymorphisms (RFLPs) studied using restriction endonucleases - which cut at specific DNA sequences (3000 polymorphic sequences - mostly bi-allelic)
2. Single Nucleotide Polymorphisms (BAs/SNPs) (Bi-allelic – or single nucleotide polymorphisms (BA/SNPs) are available in human genome)
3. Minisatellites or Variable Number of Tandem Repeats (VNTRs) Jeffreys et al. (1985) working with myoglobin gene came across a 33bp sequence, which when hybridised with some restriction enzyme digested total genomic DNA and produced a complex pattern of multiple DNA bands. This ladder of DNA fragments was individual-specific and was called a DNA fingerprint. Each band of DNA fingerprint represents a sequence repeated in tandem fashion and can be considered as one allele at a number of independent loci in human genome. These VNTR alleles also known as minisatellite alleles, show a co-dominant Mendelian inheritance and each locus – specific VNTR has numerous alleles showing a very high level of heterozygosity.
4. Microsatellites or Short Tandem Repeats (STRs) (Smaller core sizes (di-, tri- or tetra nucleotides) popularly known as Short Tandem Repeats (STRs) or microsatellite polymorphisms)
5. Alu Insertion/deletion Polymorphisms
6. Mitochondrial DNA (mtDNA) markers inherited only through the maternal line. mtDNA is found outside a cell's nucleus, in the mitochondrial organelles that manufacture the chemicals and provide our cells with their energy. A man does not pass his mito-chondrial DNA on to his offspring. Mitochondrial DNA therefore follows an unwavering path through the maternal lineage and is useful material for studying female migration routes.
7. Y-chromosome DNA Markers: chromosome Y is inherited in its entirety from an individual's father; he in turn inherited it from his father. The chromosome therefore gives researchers a tool to probe an individual's male lineage since its DNA provides material for studying male migration routes.

The correct and appropriate evaluations of all kinds of anthropological population data require good and reliable *statistical methods*, and fortunately, there has been a concomitant advancement in these methods including those for multivariate analyses of data. Jacquard (1974) and Nei (1987) have published recommendable statistical textbooks.

The unit of studying genetic variation in man is a "breeding population", also referred to as a "Mendelian population". Following Harrison (1988) one can point out that "the collective unit of evolution is the population and it is in populations that all the forces we have considered operate" (p. 326). Thus, selection, gene flow, genetic drift, founder effects etc. are acting on and in populations and shape their specific genetic profiles in the course of time. The "breeding population" is the minimal integrated unit of evolutionary changes. As far as delineating evolutionary factors are concerned, the

"breeding population" as a unit of study meets almost every logical requirement and any change in its genetic profile from one generation to the next will constitute an evolutionary change.

The impact of the population approach on the study of genetic variation in man has been to focus attention on "breeding populations" as biological or evolutionary units in man and to describe them in terms of gene frequencies or if this is not possible (anthropometric, morphological, dermatoglyphic, etc. traits) in terms of phenotype frequencies and mean values, respectively. Such exact and comprehensive descriptions are the basic requirements for the understanding of genetic variation in man and thus for the analysis of the various evolutionary factors, which caused this variation in the course of time.

The populations of India and other South Asian countries offer great opportunities to study genetic variability. Perhaps, nowhere in the world people in a small geographic area are distributed in such a large number of ethnic, caste, religious and linguistic groups as in India and other South Asian countries. Not all these groups are entirely independent; people belong concurrently to two or more of these groups. People of different groups living side by side for hundreds or even thou-sands of year try to retain their separate entities by practicing endogamy.

The aim of the paper is to study of micro-evolutionary processes as they are reflected in genetic and morphological traits in human populations of Indian region. This variability has been studied in terms of natural regions, climatic factors, climatic regions, political division of India, ethnic groups, traditional occupational and linguistic groups.

4. THE PRESENT STUDY

The data on the various biological traits have been collected, arranged, and categorised in the book entitled *"The Distribution of Genetical, Morphological, and Behavioural Traits among the Peoples of Indian Region"* by Bhasin et al. (1992). Bhasin also published a *"Classified and Comprehensive Bibliography on the Biology of the Peoples of Indian Region"* in 1988. In the present work, the data have been analysed from the studies reported till 1987, and from Ph.D., M.Phil. and M.Sc. dissertations and the unpublished work of the various authors. In this study, different biological traits have been analysed in relation to various factors like Regional Groups, Ethnic Groups, Traditional Occupational Groups and Linguistic Groups and the results have been arranged and categorised as follows.

4.1. Arrangement and Categorisation of Biological Traits

The mean weighted values of various serological and morphological traits have been calculated, arranged, and categorised under the following heads:

1. Genetic Markers in Human Blood
2. Other Genetic Traits
3. Dermatoglyphics
4. Anthropometry

The following is the list of various aspects studied under the above-mentioned categories:

4.1.1. Genetic Markers in Human Blood

The genetic loci are classified into the following groups:

(1) Blood Group Systems
(2) Serum Protein Systems
(3) Red Cell Enzyme Systems
(4) Haemoglobin Variants

The gene symbols used in this book are after Race and Sanger (1975) and Human Gene Mapping (1985). The list of the genetic markers in human blood reported is listed with gene symbols and chromosome location as follows:

4. 1.1.1. Blood Group Systems

S. No.	*System*	*Gene Locus*	*Year of Investi-gation*	*Investigator*
1.	ABO	9q34.1-q34.2	1900	Landsteiner
2.	P	22q11.2-qter	1927	Landsteiner & Levine
3.	MNSs	4q28-q31	1927	Landsteiner & Levine;
			1947	Walsh & Montgomery
4.	ABH	19cen-qter	1930	Lehrs; Putkonen
5.	Rhesus	1p36.2-p34	1940	Landsteiner & Wiener
6.	Lutheran	19q12-q13	1946	Callender & Race
7.	Kell	7q32-qter	1946	Coombs et al.
8.	Duffy	1q21-q25	1950	Cutbush et al.
9.	Kidd	18q11-q12	1951	Allen et al.
10.	Diego	17q12-q21	1954	Levine et al.;
			1955	Layrisse et al.

4.1.1.2. Serum Protein Systems

S. No.	*System*	*Gene Locus*	*Year of Investigation*	*Investigator*
1.	HP	16q22.1	1955	Smithies
2.	GM	14q32.33	1956	Grubb
3.	TF	3q21	1958	Smithies
4.	GC	4q12-q13	1959	Hirschfeld
5.	KM	2p12	1961	Ropartz et al.
6.	CP	3q23-25	1967	Shreffler et al.
7.	C3	19p13.3-p13.2	1967	Wieme & Demeulenaere
8.	ORM	9p32	1969	Johnson et al.
9.	BF	6p21.3	1972	Alper et al.
10.	AHSG	3q27-q29	1977	Anderson & Anderson
11.	PLG	6q26-q27	1979	Hobart; Raum et al.
12.	F13A	6p25-p24	1979	Board et al.
13.	F13B	1q31-q31.1	1980	Board et al.

HP=H aptoglobin, GM = Gammachain-Marker, TF = Transferrin, GC = Group specific component, KM = Kappachain-Marker, CP = Coeruloplasmin, C3 = Complement System 3, ORM = Orosomucoid, BF = Properdin Factor B, AHSG = a2-HS-Glycoprotein (H = Heremans, S = Schmid), PLG = Plasminogen, F13A=Factor 13A, F13B = Factor 13B.

4.1.1.3. Red Cell Enzyme Systems

S. No.	*System*	*Gene Locus*	*Year of Investigation*	*Investigator*
1.	ACP1	2p25	1963	Hopkinson et al.
2.	PGD	1p36.3-p36.13	1963	Fildes & Parr
3.	LDH B	12p12.2-p12.1	1963	Boyer et al.; Nance et al.
4.	LDH A	11p15.1-p14	1964	Latner
5.	PGM1	1p22.1	1964	Spencer et al.
6.	PGM2	4p14-q12	1965	Hopkinson & Harris
7.	AK1	9q34.1	1966	Fildes & Harris
8.	SOD A	21q22.1	1967	Brewer
9.	PGM 3	6q12	1968	Hopkinson & Harris
10.	ADA	20q12-q13.11	1968	Spencer et al.
11.	PGI	19q13.1	1968	Detter et al.
12.	PGK	Xq13	1971	Chen et al.
13.	CA II	8q13-q22	1971	Moore et al.
14.	ESD	13q14.1-q14.2	1973	Hopkinson et al.
15.	UMPK	1p32	1974	Giblett et al.
16.	PGP	16p13.3	1978	Barker & Hopkinson
17.	ALADH	9q32-q34	1981	Battistuzzi et al.
18.	G6PD	Xq28	1956	Carson et al.

ACP1=acid phosphatase 1, PGD = 6-Phosphogluconate-Dehydrogenase, CA I = Carbon anhydrase I, LDH B = Lactat dehydrogenase B, LDH A = Lactate dehydrogenase A, PGM 1 = Phosphoglucomutase 1, PGM 2 = Phosphoglucomutase 2, AK 1 = Adenylate kinase 1, SOD A = Superoxide dismutase, PGM 3 = Phosphoglucomutase 3, ADA = Adenosine deaminase, PGI = Phosphoglucomutase - Isomerase, GPT = Glutamat-Pyruvat-Transaminase, PGK = Phosphoglycerate kinase, CA II = Carbon anhydrase II, ESD = Esterase D, UMPK = Uridin-5-Monophosphat kinase, GLO 1 = Glyoxalase 1, PGP = Phosphoglycolat Phosphatase, ALADH = d-Aminolaevulinat Dehydratase, G6PD = Glucose-6-Phosphate dehydrogenase.

4.1.1.4. Haemoglobin Variants

S. No.	*Haemoglobin*	*Gene symbol*	*Gene Locus*
1.	Haemoglobin Alpha	*HBA*	16p13.3
2.	Haemoglobin Beta	*HBB*	11p15.5

4.1.2. Other Genetic Traits

The gene symbol and chromosome location of these characters are as follows:

S. No.	*Genetic traits*	*Gene symbol*	*Chromosome location*
1.	Colour Blindness	*CB*	X
2.	Phenylthiocarbamide taste	*PTC*	3(?)

4.1.3. Dermatoglyphics

The following traits were analysed under this head:

4. 1.3.1. Finger Dermatoglyphics

(a) Patterns (b) Ridge-Count

4, 1.3.2. Palmar Dermatoglyphics

(a) Palmar Main Line Formulae (b) Patterns on Palmar Areas

4.1.4. Anthropometry

The studies are reported here on the adults for the following measurement and indices:

1. Stature 2. Cephalic Index 3. Nasal Index 4. Total Facial Index.

4.2. Identify and Distinguish the People

The populations of India and other South-Asian countries offer great opportunities to study socio-cultural and genetic variability. Perhaps, nowhere in the world people in a small geographic

area are distributed as such a large number of ethnic, castes, religious and linguistic groups as in India and other South Asian countries. Not all these groups are entirely independent; people belong concurrently to two or more of these groups. People of different groups living side by side for hundreds or even thousands of year try to retain their separate entities by practicing endogamy.

India is a multi-cultural country. Anthropologists are committed to grasping the dynamics of communities and populations. As anthropology combines the premises of a biological as well as well as socio-cultural study, it looks at the diverse sections of human beings with dual perspective, one derived from its branch called biological anthropology, and the other from social/ cultural anthropology. How communities and populations continue to retain their identity, in social and cultural terms on one hand and biological on the other, and how they acquire the characteristics of the others because of cultural borrowing or interbreeding are the questions anthropologists systematically investigate. India with more than 1000 million people has the second largest population in the world and it is one of the world's top twelve megadiversity countries and has vast diversity of human beings, fauna, flora, and environmental regimes. Its present population includes stone-age food gatherers, hunters, fisher-folk, shifting agriculturists, nomadic herders, entertainers, as well as those engaged in mechanized and chemicalised agriculture, mechanized fishing, tapping offshore oil and natural gas, running atomic power plants and producing computer software. Human groups carrying a diversity of genes and cultural traits have peopled India. We have almost all the primary ethnic strains Proto-Australoid, Mediterranean, Mongoloid, Negrito and a number of composite strains. It is homeland of over 4000 Mendelian populations, of which 3700 endogamous groups are structured in the Hindu caste system as '*jatis*'. Outside the preview of caste system, there are a thousand odd Mendelian populations, which are tribal autochthones and religious communities. Like any other plural society, India offers a cauldron where the processes of unification as well as of fragmentalisation are unceasingly taking place. This presents a situation of cultural, biological, and environmental richness and diversity, and one where the constant interactions between communities are aiding the formation of bridges, thus creating a sense of unity. It is in these terms that India offers an ideal case for examining unity in diversity both biological and socio-cultural perspectives. (Bhasin et al. 1994; Lahr and Foley 1998; Bhasin and Walter 2001; Cann 2001; Bamshad et al. 2004). In the present paper, an attempt has been made to give an outline of Indian population milieu

For the biogenetical study of the people of India, researchers have generally used the following criteria to identify and distinguish the people: 1. Regional Groups, 2. Ethnic Groups, 3. Linguistic Groups, and 4. Religious Groups.

It should, however, be kept in mind that these are the convenient units of study, although there are significant levels of overlapping between them. For example, an occupational group pursuing traditional job inhabits a region, shares religion with other categories, belongs to one or the other language group, and has an aggregation of ethnic properties. However, in the human population genetic studies, out of these criteria one is chosen (Bhasin 1988).

In the present study, an attempt has been made to analyse the above-mentioned biogenetical traits into 1. Regional Groups, 2. Ethnic Groups, 3. Traditional Occupational Groups and 4. Linguistic Groups.

4.2.1. Regional Groups

These can be divided into the following groups:

1. Natural Regions of India
2. Climatological Factors and Climatic Regions of India
3. Political Division of India

Each region has its own characteristics and a brief description of each one will give an idea of what it constitutes of.

4.2.1.1. Natural Regions of India

The natural regions have broad uniformity in their characteristics, such as relief, geomorphological history, drainage, climate, soil, natural vegetation, and wild life. Broadly speaking the Indian sub-continent may be divided in the following natural regions (Fig. 9).

1. The Himalayan Mountain Complex
2. The Indus-Ganga-Brahmaputra Plain
3. The Peninsular Plateau and
4. The Islands

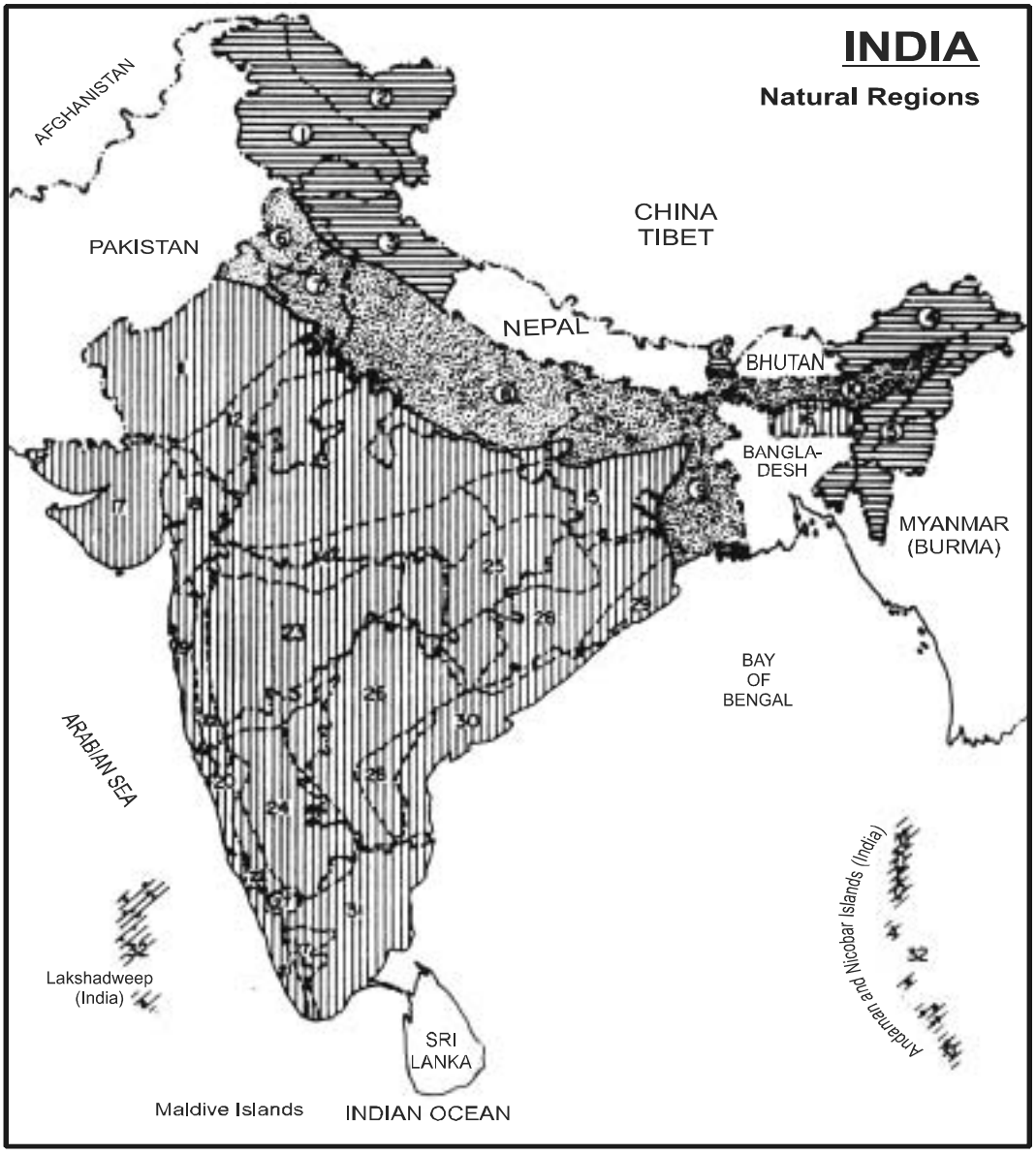


Fig. 9. India-Natural Regions

NATURAL REGIONS

THE HIMALAYAN MOUNTAIN COMPLEX 1.Kashmir 2.Karakoram, Ladakh & Baltistan 3. Himachal Himalayas & Kumaon 4. Eastern Himalayas 5. Purvanchal Hills THE INDUS-GANGA-BRAHMAPUTRA PLAIN 6. Punjab Plain 7. Indo-Gangetic Divide 8. Ganga Plain 9. Ganga Delta 10. Assam Valley THE PENINSULAR PLATEAU 11. The Desert 12. Aravalli Hills 13. Central Vindhyan Uplands 14. Khandesh & Satpura-Maikal Ranges 15. Chota Nagpur Plateau 16. Meghalaya Plateau 17. Kachchh & Kathiawar 18 Gujarat Plains 19. Konkan Coast 20 Goa & Kanara Coast 21. Kerala Coastal Plain 22 Westem Ghats 23 Deccan Lava Plateau 24. Karnataka Plateau 25. Wainganga & Mahanadi Basins 26. Telangana 27. Southern Hills Complex 28. Eastern Ghats 29. Orissa Delta 30. Andhra Coastal Plain & Delta 31. Tamil Nadu THE ISLANDS 32. Andaman and Nicobar Isls & Lakshadweep.

4.2.1.2. Climatological Factors and Climatic Regions of India

Various climatological factors (Rainfall, Humidity, and Temperature) and Altitude have been considered to study correlations with different biological traits. The values for the climatological factors are after "Climatological Tables of Observations in 1931-1960" Meteorological Department, Government of India, New Delhi.

A climatic region generally possesses a broad uniformity in climatic conditions produced by combined effects of climatic factors. India can be divided into the following climatic regions after Köppen's method, based on the monthly values of temperature and precipitation (Fig. 10):

(1) Tropical Savannah Type, (2) Monsoon Type with Short Dry Season, (3) Monsoon Type with Dry Season in High Sun Period, (4) Semiarid and Steppe Climate, (5) Hot Desert Type, (6) Monsoon Type with Dry Winters, (7) Cold Humid Winters Type with Shorter Summer, and (8) Polar Type.

4.2.1.3. Political Division of India

India is a Union of States. Comprising 25 States and 7 Union Territories, according to the Census 1991, there are 4689 towns and 587,226 inhabited and 47,095 uninhabited villages in the country. The country had 466 districts in 1991.

India-Political and Ethnic Zones: The weighted mean values of various biological traits have been classified into 25 States and 7 Union Territories (U.T.) which have been categorised as follows (after Bhasin, 1988):

I. North India, II. West India, III. East India, IV. Central India, V. South India, and VI. Islands. Himalayan Region may be divided into three divisions, *i.e.*, A) Western Himalaya, B) Central Himalaya, and C) Eastern Himalaya as follows (Fig. 11):

I. North India:

(A) Western Himalaya (S. No. 1, 2):

(1) Jammu and Kashmir, (2) Himachal Pradesh, (3) Punjab, (4) Chandigarh (U.T.), (5) Haryana, (6) Delhi (U.T.), (7) Uttar Pradesh (*Uttaranchal* (Previously referred as Uttarakhand or Gaganalaya): A separate state of Uttaranchal came into existence in November, 2000, comprising of following eleven hill districts: Almora, Bageshwar, Chamoli, Champawat, Dehradun, Nanital, Pauri Garhwal, Pithoragarh, Rudra Prayag, Tehri Garhwal, Uttarkashi and two plains districts - Hardwar and Udham Singh Nagar - of Uttar Pradesh. Dehradun is the capital of new State).

(B) Central Himalaya (S.No.7, Eight Districts of Uttar Pradesh)

[(i) Almora, (ii) Chamoli, (iii) Dehra Dun, (iv) Garhwal (Pauri), (v) Naini Tal, (vi) Pithoragarh, (vii) Tehri Garhwal, and (viii) Uttarkashi.] and 8. Rajasthan

II. West India:

(1) Gujarat, (2) Maharashtra, (3) Goa*, (4) Daman and Diu* (U.T.) (*The frequency distributions for the State of Goa and Union Territory of Daman and Diu have been listed under Goa, Daman and Diu.) and (5) Dadra and Nagar Haveli (U.T.)

III. East India:

C) Eastern Himalaya: (S. No.1 to 8 and Darjeeling District of West Bengal)

(1) Arunachal Pradesh, (2) Assam, (3) Nagaland, (4) Manipur, (5) Mizoram, (6) Tripura, (7) Meghalaya, (8) Sikkim, (9) West Bengal, (10) Bihar (*Jharkhand:* A separate state comprising the following 18 districts of Bihar came into existence in November, 2000: Bokaro, Chatra, Deoghar, Dhanbad, Dumka, East Singhbum, Garhwa, Giridih, Godda, Gumla, Hazaribagh, Kodarma, Lohardaga, Palamau, Pakur and Palamau, Ranchi, Sahebganj, West Singhbhun. Ranchi is proposed as the capital of new State), and (11) Orissa

IV. Central India:

(1) Madhya Pradesh (*Chhattisgarh:* A new state comprising sixteen districts of Madhya

Pradesh came into existence in November, 2000: Bastar, Bilaspur, Dantewada, Dhamtari, Durg, Janjgir-Champa, Jashpur, Kanker, Kawardha, Korba, Koria (Baikunthpur), Mahasamund, Raigarh, Raipur, Rajnandgaon and Sarguja. Raipur is the capital of the new State.

V. South India:

(1) Karnataka, (2) Andhra Pradesh, (3) Tamil Nadu, (4) Kerala and (5) Pondicherry (U.T.).

VI. Islands:

(1) Lakshadweep (U.T.) and (2) Andaman and Nicobar Islands (U.T.).

4.2.2. Ethnic Groups

An aggregation of biological and socio-cultural characteristics constitutes an ethnic group. Within the category of Ethnic Group, we include Castes, Scheduled Castes, Scheduled

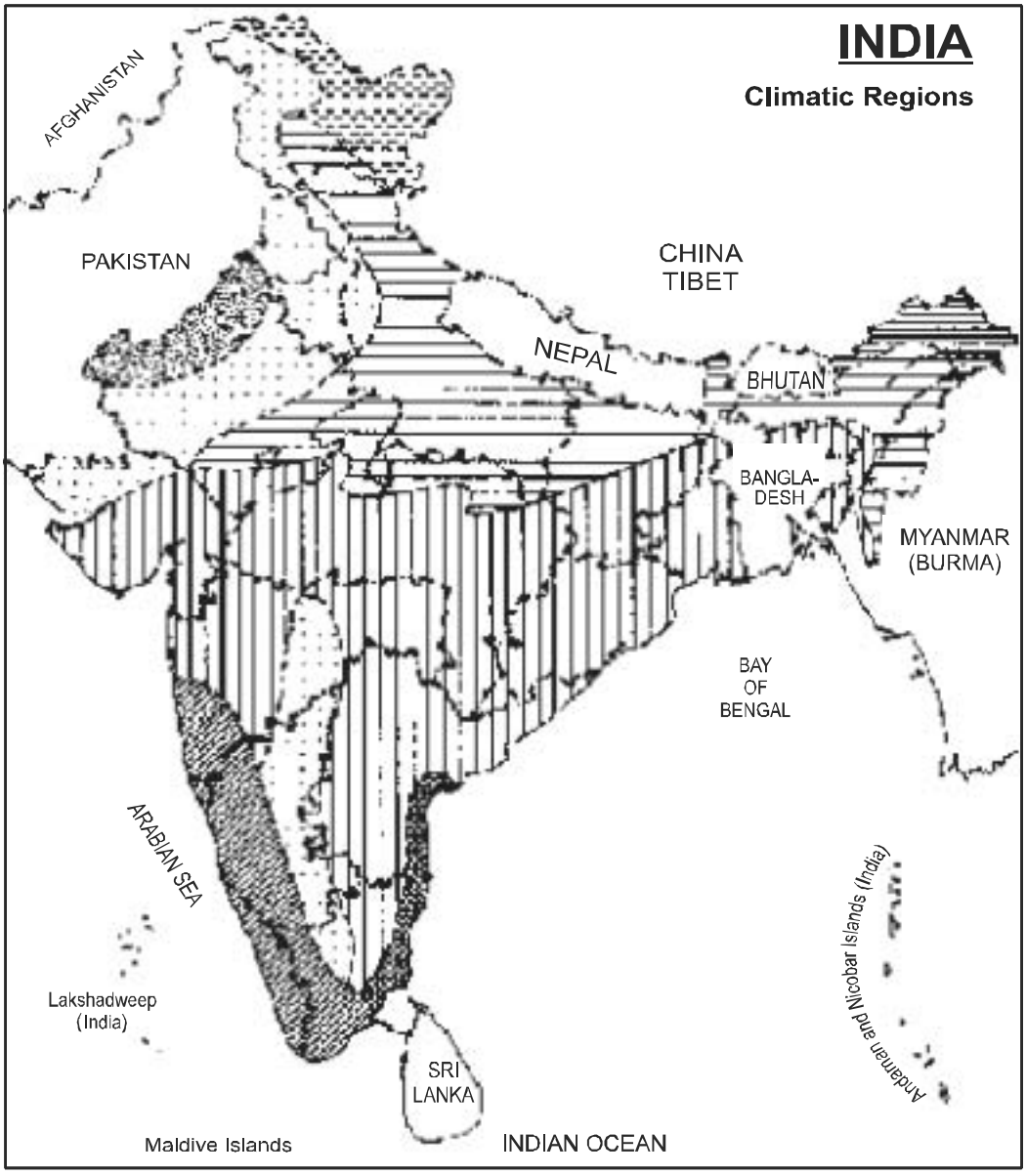


Fig. 10. India - Climatic Regions

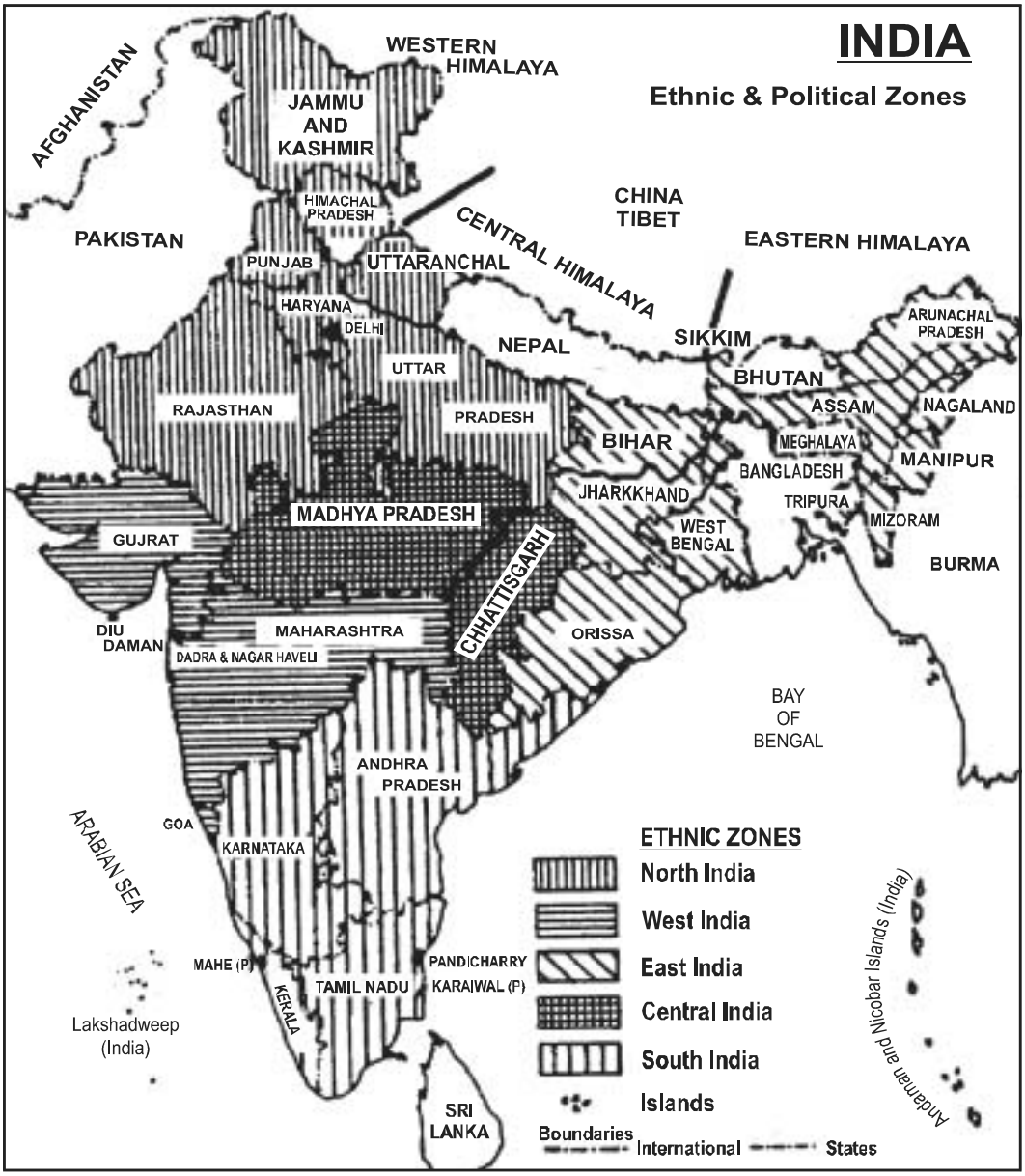


Fig. 11. India-Ethnic and Political Zones

Tribes, and Communities (the names of Scheduled Castes and Scheduled Tribes after Manual of Election Law 1982, Government of India, New Delhi, *see* appendix (II) for the list of Scheduled Castes and Scheduled Tribes). Biological anthropological studies of such ethnic groups as well as "Communities" have been reported in India. By Community, we generally refer to a group of people who may have occupational, linguistic, religious, or regional characteristics (Bhasin 1988).

4.2.2.1. Castes

The Indian society is highly stratified and is divided into castes, scheduled castes, scheduled tribes etc. It should be understood at the outset that our intention is not to give the detailed account of individual castes, their ceremonies, and their machinery for regulating their relation with other castes, nor of their own internal conduct, but to examine caste in terms of Mendelian population groups.

Ethnographic and genetic evidence both support that Hindu Castes have been highly endogamous for a considerable length of time (Karve 1968; Bhasin et al. 1994; Bamshed et al. 2001; Bhasin and Walter 2001; Misra 2001; Wooding et al. 2003). Although level of genetic differentiation between castes is relatively small, genetic distances observed suggest that gene flow is limited (Bhasin et al. 1994; Bamshed et al. 1998; 2001; Bhattacharya et al. 1999; Bhasin and Walter 2001; Dutta et al. 2002; Lakshmi et al. 2002).

It has been reported that paternally inherited DNA was overall more similar to Europeans than to Asians but, unlike in the case of maternal inheritance with no significant variation in affinity across the castes and this may be due to the migrating Eurasians populations are likely to be mostly males who integrated into the upper castes and took native women. Inter-caste marriages practices, while generally taboo, are occasionally allowed, in which women can marry into an upper caste and move up in the social hierarchy, whereas, such upward mobility, is not permissible for men because caste labels of men are permanent, but women, by means of their limited mobility, cause a gene flow across caste barriers (Bamshed et al. 2001; Basu et al. 2003; Kivisild et al. 2003)

It cannot be said when and in what circumstances the caste system originated. However, many theories have been put forward, which are as follows:

(1) Based on Colour

It is generally believed that in the early Vedic period there were no castes in Punjab. Only the fair-skinned invaders called themselves Aryans and they called the dark skinned aborigines as *Dasyus, Dasas,* or *Asuras*.

The term *Varna* (colour) is often confused with caste (*Jati, Jat*), though it is far from having the same meaning. The Rigvedic society was divided into four classes based on *Varna,* three categories of twice-born (*Dvija*)—Brahman, Kshatriya and Vaishya, and fourthly the Sudra below whom were the outcastes.

(2) Based on Purushukta

In the *Purushukta* of the *Rig-Veda,* there is a *mantra* interpreted by scholars as such: "The Brahmans were born from the mouth of God, the Kshatriyas from his arms, and the Vaishyas from the thighs and Sudras from his feet". Some people regard this *Mantra* as the basis of the caste system.

(3) Based on Division of Occupation

After the Aryan invasion into Ganges valley, the stratification in the Indian society began. Social mechanisms were built up in order to carry on the organization of production and supply of services. One such well-known mechanism was caste. Caste was not wholly an economic structure. Yet undeniably, it was built up based on monopolistic guilds that were endogamous, each of these guilds grew up into separate caste. Exchange of goods and services was a highly stratified affair and each caste specialized in certain type of industry or delivery of goods. Therefore, each unit in the economic structure was virtually a monopoly of one caste and every tribe if possible was brought into more than one caste according to their specialization. Each caste or tribe was allowed to preserve its diverse socio-cultural pattern as long as it did not give rise to conflicts with Brahmanical priesthood. Brahmans were trying for the uniformity of the rites and practices at a community level, local communities were allowed to carry on their modified version at family level.

Traditionally, each caste was associated with hereditary occupation and had a limited monopoly over it *e.g. Brahmans* (priestly and learning); *Kshatriyas* (warrior and aristocracy); *Vaishyas* (landowners and traders); and *Sudras* (crafts and service). For details about castes see Ghurye (1969), Hutton (1981).

4.2.2.2. Scheduled Castes, Scheduled Tribes

The Scheduled Castes and Scheduled Tribes were enumerated from 1951 census onwards. The President by a special order scheduled traditional

occupational particular castes among Hindus and Sikhs in particular areas for special treatment that also applies to tribes irrespective of their religious persuasion. Fifteenth Presidential Orders issued under the provisions of Articles 341 and 342 of the Constitution have specified the Scheduled Castes and Scheduled Tribes. They listed in Scheduled Castes and Scheduled Tribes Orders (Amendment) Act 1976.

The constitution prescribes protection and safeguards for the Scheduled Castes and Scheduled Tribes, and other weaker sections either specially or by way of insisting on their general rights as citizens to promoting their educational and economic interests and of removing the social disabilities. However, in spite of all Governmental efforts, even when following the same profession as their neighbours, the Scheduled Castes and scheduled Tribes often have an inferior social status and are ruthlessly exploited by their employers and by money lenders. In the Census of India (1991), 16.5 per cent of the population enumerated as belonging to Scheduled Castes or another 8.1 per cent as belonging to Scheduled Tribes (Table 1).

Table 1: Percentages of Scheduled Castes and Scheduled Tribes to total population of India (1961-91)

Year	*Scheduled Castes*	*Schedueld Tribes*
1961	14.67	6.36
1971	14.60	6.94
1981	15.75	7.76
1991	16.48	8.08

In addition, some state governments have also specified other categories of people known as 'Other Backward Classes' and Denotified Nomadic and Semi-Nomadic communities.

4.2.2.3. Communities

The population groups which have not been identifiable on the basis of caste system or are not denoted as tribes, have been referred by some authors on regional basis like Punjabis, Bengalese etc., by others on religion basis like Hindus, Muslims, Sikhs etc., by others on language basis like Telugus, Tamils etc. These authors have not specified or defined explicitly their caste and/or specific groups. All these groups classified under the category of community.

Confusion may be created if we assume that the surname attached to a name is the 'caste' name. Quite often, these may be misspelt or substituted with occupation, locality, or religion. Quite often, as in the case of low castes that originally did not have the custom of writing a surname, caste, or '*Gotra'* name, use a high caste surname to identify them. Such identification is thus fallacious. A caste group is best identified by tracing its social relationship, especially that of marriage. Endogamy most often defines the operational limits of a caste group. However, wider identification is possible with a region, language, or occupation. Even then it is found that an endogamous group, even where it is cross-cutting geographical boundaries is likely to be identifiable as a social group in terms of caste ranking, social interaction, language, culture and sometimes even as a political grouping.

4.2.3. Traditional Occupational Groups

In the traditional society, there were occupational guilds. The *Chaturvarna* system with its division into *Brahman* (priestly caste), *Kshatriya* (warrior caste), *Vaishya* (landowners and traders) and *Sudra* (labouring caste) based on occupational differentiation. The occupations are grade manual labour is looked down upon, and those dealing with swine-herding, scavenging, butchery, removal of night soil are regarded as polluting (Bhasin 1988). The caste-based division of occupation is 1. Priesthood, 2. Warfare, 3. Trade and Commerce, 4. Agriculture, 5. Animal Husbandry, 6. Artisan, and 7. Menial Workers (Table 2).

4.2.4. Linguistic Groups

According to Grierson (1903-1928), India has 179 languages and 544 dialects. Of these languages (the separate enumeration of dialects is irrelevant, since they also come under "languages"), 116 are small tribal speeches of the Tibeto-Chinese family; these are found only in the northern and north-eastern fringes of India and are present among less than 1per cent of the entire population of the country. Nearly two dozen more are likewise insignificant speeches of other language groups; or they are languages not truly belonging to India (Census Centenary Monograph No.10, 1972; Gazetteer of India 1973).

Although the Schedule VIII recognizes fifteen

Table 2: Caste based on division of occupation

Social status	*Social group*	*Economic activities*	
		Traditional occupation	*Primary occupation*
I. High Castes	Brahamans	Priesthood	Priesthod, Agriculture, Trade and Commerce, Armed Forces
	Kshatriyas or Rajputs	Warfare	Agriculture, Trade and Commerce Armed Forces
	Vaishyas (Banias)	Commerce	Trade and Commerce, Agriculture
II. Backward (Middle)	(a) Jats, Reddies, Kammas, Vokalligas etc.	Agriculture	Agriculture, Trade and Commerce, Armed Forces
	(b) Ahir, Gollas, Gujars	Animal Husbandry	Animal Husbandry, Agriculture, Trade and Commerce
	(c) Porter, Barber, Teli, Lohar etc.	Artisan	Artisan, Agriculture, Agricultural Labourers
III. Low Castes	Chamar, Dom, Bhangi, Khatik	Menial Workers	Menial Workers, Agricultural Labourers

languages in India, there are innumerable dialects, which change after few scores of kilometers. Linguistic diversity is an important factor in the formation of regional groups, and it reflects the regional differentiation. The four- fold regional division can be seen for the major languages, *i.e.*, (i) the Dravidian region of the south; (ii) the Indo-Aryan regions of the north and north-west; (iii) the Mon Khmer and the Tibeto-Burman region of the northeast and the Himalayan region; and (iv) the Austric region of the Aravalli-Vindhya-Chota Nagpur complex (Fig. 12).

Chronological sequence in the matter of the advent into India of the three groups other than Aryan has not been established. It is not clear as to who came first - the Austro-Asiatic, Tibeto-Chinese or Dravidians. But the fact remains that all these three groups were in India when the Aryans came.

Renfrew (1987, 1989) and Cavalli-Sforza et al. (1994) reported that Indian sub-continent had experienced massive gene flow from at least two Neolithic episodes of migrations. Firstly about 10-15 thousands years ago, when agriculture developed in the fertile cresent region, a part of an eastward wave of human migration entered India and brought Dravidian languages (Renfrew 1989) mainly, Elamo-Dravidian languages (Ruhlen 1991), which may have originated in the Elam province (Zagros Mountains, Southwestern Iran) and are confined to southeastern India and to some isolated groups in Pakistan and northern India. The next was the arrival of pastoral nomads from the central Asian steppes to the Iranian plateau about 4000 years before present, brought with it the Indo-European language family, which eventually replaced Dravidian languages from most of Pakistan and northern India, perhaps by an elite-dominance process (Renfrew 1987, 1989, 1996, Cavalli-Sforza et al. 1988; Quintana-Murci et al. 2001).

These languages are again divided into sub-families and groups as follows:

4.2.4.1. Language Classification-—Indian Languages

The family, branch, group, and language of India are as follows:

I. Austro-Asiatic Family

Mon-Khmer Group (Mon-Khmer Branch)
Munda Group (Munda Branch)

II. Tibeto-Chinese Family

Siamese-Chinese Sub-Family
Tai Group
Tibeto-Burman Sub-Family
Tibeto-Himalayan Branch
Bhotia Group (Tibetan Group)
Himalayan Group (Pronominalized/Non-Pronominalized Himalayan Group)
North-East Frontier Group (North Assam Branch)
Assam-Burmese Branch
Bodo Group (Bara or Bodo Group)
Naga Group
Kachin Group
Kuki-Chin Group
Burma Group

III. Dravidian Family

South Dravidian Group
Central Dravidian Group
North Dravidian Group

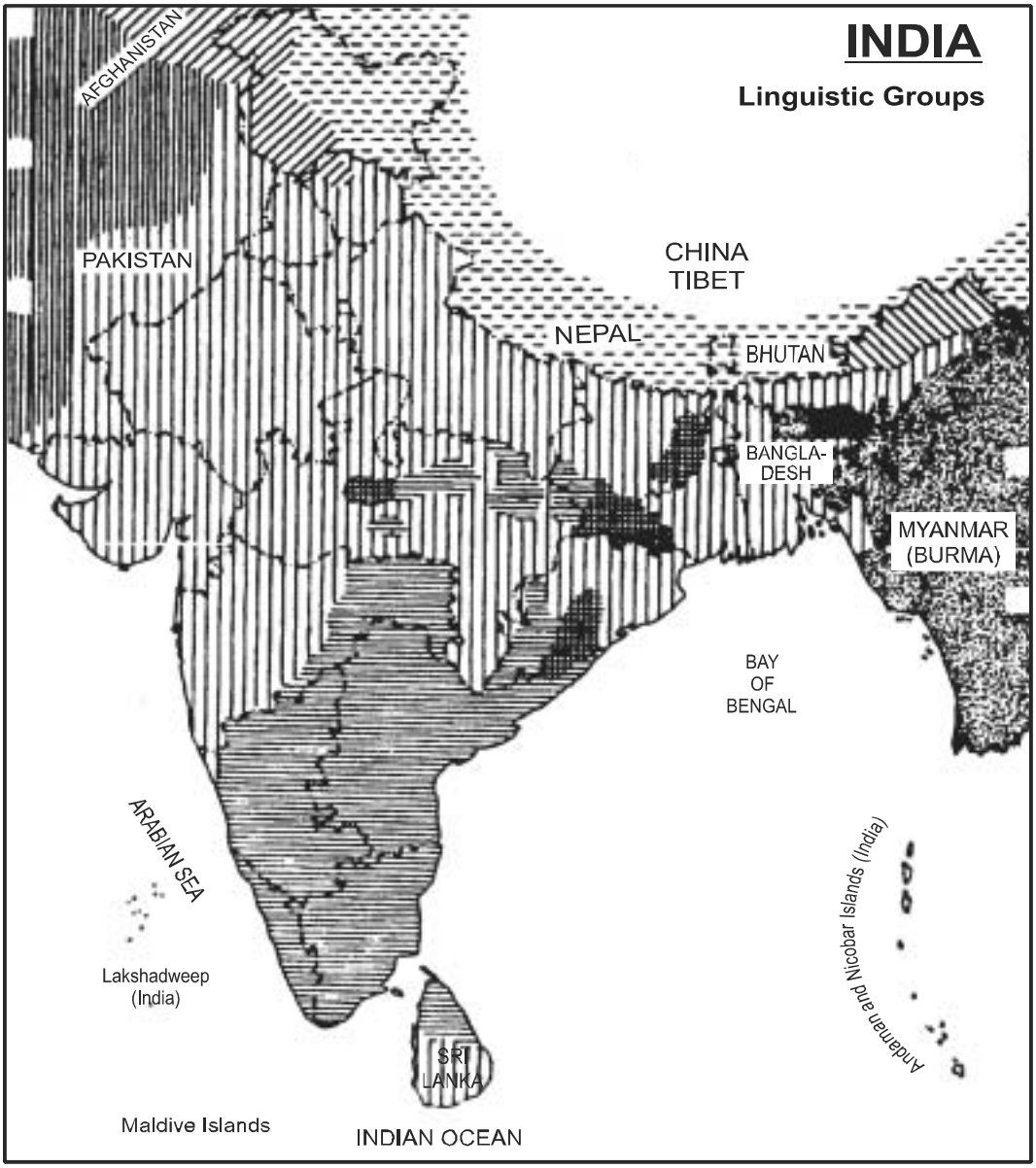


Fig. 12. India - Linguistic Groups

IV. Indo-European Family Aryan Sub-family

Dardic (or Pisacha) Branch
Kafir Group
Khowar Group
Dard Group
Indo-Aryan Branch:
Outer Sub-Branch
North-Western Group
Southern Group
Eastern Group
Bihari Group (Bhojpuri, Maithili and Magahi Sub-Group)
Mediate Sub-Branch/Inner Sub-Branch:
Mediate Group/Central Group/Pahari Group
Mediate Group/Central Group
Pahari Group
Eastern Pahari
Central Pahari
Western Pahari

4.3. Some Problems in Distinguish People and Sampling

A few studies are available in which researchers have identified and attempted to distinguish the people of Indian region to study the biological diversity and that are almost similar to that reported by Bhasin (1988); Bhasin et al. (1992, 1994), Bhasin and Walter (2001), Bhasin (2006d).

However, in some of the studies pertaining to the people of Indian region, one finds number of problems in the categorisation of the population groups into ethnic groups, in not specifying the place of the data collection and other sampling details, besides in many other details pertaining to the principles of population genetics.

There are number of articles with such problems. However, I take a recently published one such article (Sahoo et al. 2006; PNAS, 103: 843-848) as a case in point. This work included eighty different ethnic groups categorised as caste (Upper, Middle and Lower) and tribal groups. While going through the list one finds that Nepali (people of Nepal are referred as Nepali and a heterogeneous group) have been categorized as Upper Caste Group. There is a substructure within the Nepali population and it would have been appropriate to specify precisely to which caste and/ tribe these samples pertain to.

We should take necessary precautions while classifying ethnic groups into castes and tribes and if it is difficult to categorise any group than it may classified as community.

Another example is of categorization of an ethnic group into Scheduled Caste or Scheduled Tribe; Chaubey et al. (2008) classified Mushar (This ethnic group is spelt as Musahar in the List of Scheduled Castes and Scheduled Tribes Census of India-1991) from Uttar Pradesh, Bihar, Jharkhand as Scheduled Tribe whereas in the Census 1991, Musahar group is listed as Scheduled Caste. While classifying any group into Scheduled Caste or Scheduled Tribe, one must check the name from Census Report.

Quite a good number of studies undertaken by the researchers of the different Universities/ Institutes from abroad in collaboration with their counterparts in India have reported findings on various population groups of India. One cannot but be skeptical about the reliability of the samples collected for them by their collaborators in India who themselves (or those recruited by them for the purpose of sample collection) may not often be familiar with the population structure of India. Consequently, the population samples, more often than not, were not representative as they are usually drawn from City Hospitals etc. without due regard to their backgrounds (Name, Caste/subcaste, complete address of the residence, city etc. in urban areas whereas in rural areas it may be helpful to record besides other details the District, Tehsil, Panchayat Circle or Patwar Circle, Village and House No. etc.). Tragically, in most of the above studies involving foreign investigators, the sampling details are often not found and in most cases, these investigators are not in a position to furnish such data when queried. It is indeed not fair to the scientific community. These information are required in general (in the population genetics perspective) but also because if any one has observed some rare variants then the family of that subject may be contacted and their sample can be procured and analysed. The reproducibility in such situations is very important. One may hope the future investigators would take recourse to insisting on sample/sampling details while procuring samples from abroad and publishing articles based on such materials.

4.4. Statistical Analysis

4.4.1. Mean Weighted Values

To discern the pattern of regional groups, ethnic groups, traditional occupational groups and linguistic groups using the frequency data,

the mean weighted values of the biological traits calculated and estimates for the various groups are presented.

4.4.2. Distance Measures

All distance measures have something in common that they manipulate variations in allele frequencies and come up with a product that performs the same function. Reviews of the theory underlying genetic distance measurement have been provided by Balakrishnan (1975), Cavalli-Sforza (1973), Cannings and Cavalli-Sforza (1974), Chakraborty (1976), Edwards (1971), Goodman (1972), Morton (1973, 1975). Many of these authors have pointed out the close mathematical relationship between the various distance indices.

A measure of distance, which provides the possibility of combining both sets of data (quantitative as well as qualitative traits including allele/haplotype frequencies), is given by Hiernaux (1965). Thus in a final step of distance analysis Hiernaux distances have been computed on the basis genetical markers, dermatoglyphic traits and anthropometric traits.

The present work is based on the frequency data obtained by a large number of authors. The number of publications examined exceeded 3000. For references and distribution of the various biological traits *see* Bhasin (1988) and Bhasin et al. (1992), respectively.

In the present study, we have constructed dendrograms under the heads—for (a) Genetic markers; (b) Dermatoglyphic traits; (c) Anthropometric traits; and (d) All the traits combined—in (i) Regions, (ii) Ethnic groups, (iii) Language family, (iv) Regions and Ethnic groups combined and (v) Language families and Ethnic groups combined.

5. RESULTS AND DISCUSSION

5.1. Genetic Markers in Human Blood

5.1.1. Blood Group Polymorphisms

5.1.1.1. ABO System

The frequency of allele *ABO*B* is higher (0.233) among Indian populations as compared to allele *ABO*A* (0.186). From the Himalayan mountain complex towards the peninsular region the frequencies of alleles *ABO*A* and *ABO*B* decrease and that of allele *ABO*O* increase. Among the different ethnic groups the allele *ABO*B* is higher (0.230-0.248) as compared to allele *ABO*A* (0.173 - 0.181) except among scheduled tribes where alleles *ABO*A* and *ABO*B* are almost similar (0.213 and 0.218, respectively). This shows that the differences are well marked between scheduled tribes and other populations. Among castes, scheduled castes and communities the differences are observed invariably in relation to their proximate category *e.g.*, between castes and scheduled castes, communities etc.

Generally, areas either with a sparse distribution or completely devoid of scheduled tribes is preeminently scheduled caste areas. The main concentration of scheduled castes is in Indus-Ganges-Brahmaputra plains. Numerically major scheduled castes such as Pasi, Dusadh, Dhobi, Bhangi/Mehtar, Koli, Mushahar, Rajbanshi, Bagdi, and Namasudra predominate this area. Agglomeration of scheduled castes—Madiga, Adi Dravida, Mala, Paraiyan, and Adi Karnataka is in the south. Numerically minor scheduled caste populations are in dense concentration in an elongated belt stretching over northwestern Himalayas and immediate adjacent Punjab plains, whereas the entire southern peninsula exhibits a sparse distribution of minor scheduled castes, except for Telangana plateau and a few clusters in the coastal areas. The differences for the frequencies of alleles *ABO*A* and *ABO*B* among scheduled castes from North and East India are not significant as compared to scheduled castes from South India. Further, the differences observed among various occupational groups from South India are high as compared to other zones.

The scheduled tribes which show marked differences from other populations bear a strong correlation for their distribution with the areas heavily forested and highly inaccessible. The numerically major scheduled tribes (Gond, Bhil, Santal, Oraon, Mina, Munda, Khond, Kachari group, Ho, Naga, Kol, Soara/Savara, Koli, Khasi and Kawar) are concentrated mainly in the central-western and northeastern parts of the country. A very thick cluster of scheduled tribes occurs in Santal Parganas, Ranchi and Singhbhum districts of Bihar and Bastar Plateau and Chhattisgarh Basin of Madhya Pradesh. From the Bastar Hills in the south-west up to Darjeeling district in northeast, there is a continuous strip of tribal

concentration, which is thickest in South Bihar. The next large concentration is at the convergence of three states—Gujarat, Maharashtra and Madhya Pradesh—lying in between south Arvali Hills and eastern Rajasthan plateau in north and lower Narmada valley in the south. The third concentration exists in the eastern hill areas and Assam valley. The numerically minor scheduled tribes in India live in the hills and plateau of southern and eastern parts of the country. The principal abodes of minor tribal groups are Chhota Nagpur plateau, Orissa plateau, Malabar Coast and its immediate adjacent uplands of Tamil Nadu, eastern hills and western part of peninsula.

The distribution of *ABO*A* and *ABO*B* allele frequencies in the distinct areas of tribal concentration is as follows.

In the eastern hill areas—Assam valley and Meghalaya plateau which constitute the Eastern Himalayan region is mainly inhabited by peoples with Australoid (Pre-Dravidian), Caucasoid (Dravidian and/or Aryan) and Mongoloid admixture in varying degree and they are mostly tribals. From Eastern Himalayas, in Purchaval hills and Meghalaya plateau the frequency of allele *ABO*A* is quite higher as compared to *ABO*B*, whereas in Assam valley as observed from Western and Central Himalayas, the frequency of allele *ABO*B* is higher as compared to *ABO*A*.

Western peninsular plateau is shared by southern districts in the Aravali hill region of Rajasthan, Gujarat plains and Malwa plateau and northwestern Maharashtra inhabited mainly by Mina and Bhil tribal groups. Among scheduled tribes the frequency of allele *ABO*B* is little higher as compared to allele *ABO*A*.

The north-eastern peninsular plateau region is embracing tribal populations in the forested hills and plateaus of Bihar (Santal, Oraon, Munda, Ho), Orissa (Khond, Gond, Santal) and Madhya Pradesh (Gond, Bhil, Kol) states which are mainly Australoid (Pre-Dravidian) having admixture with neighbouring populations in less degree, and in them allele *ABO*B* is higher as compared to allele *ABO*A*.

The southern peninsula shows a relatively thinner concentration of major scheduled tribes - Naikda, Kurumba (Karnataka) Koya, Yandi (Andhra Pradesh), Malayali, Irula (Tamil Nadu), Kadar, Kurumba (Kerala). The tribals are Australoids having little Caucasoid (Dravidian) admixture, among whom allele *ABO*A* is higher as compared to allele *ABO*B*, and allele *ABO*O* is low as compared to other ethnic groups of the zone.

Among the populations with Mongoloid affinities which speak the Mon Khmer group of Austro-Asiatic languages, Himalayan group, North East Frontier group, Naga group, Kuki Chin group of Tibeto-Chinese languages, the frequency of allele *ABO*A* is higher as compared to allele *ABO*B*. Among the speakers of southern group of Indo-European and Central Dravidian group of Dravidian languages the frequency of allele *ABO*B* is little higher as compared to *ABO*A*, whereas in rest of the groups allele *ABO*B* is higher than *ABO*A*.

The frequency of allele *ABO*A*2 is 0.025 among Indian populations. Among the population groups with Mongoloid affinities and scheduled tribes, the frequency of this allele is negligible as compared to other groups.

The pattern of distribution of the ABO alleles in Indian population is argued to be influenced by selection *via* smallpox, cholera, and plague. It has been suggested that the advantage of group B could be due to long-standing selection against group A by smallpox, as well as, against group O, especially by cholera and plague (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.1.1.2. MNSs System

It can be pointed out that the allele *MN*M* is predominant (0.648) over *MN*N* (0.352) among Indian populations. The frequency of allele *MN*M* is high in the Himalayan mountain complex moreover, as one move towards Indus-Ganga-Brahmaputra plains region, this frequency gradually starts decreasing but towards southern peninsula, it reaches a maximum. The frequency of allele *MN*M* is quite low in scheduled castes in Indus-Ganga-Brahmaputra plains and similar between caste and scheduled caste from South India. The frequency is quite high among the populations with Mongoloid affinities from Eastern Himalayan region (0.771) and highest is observed among scheduled tribes (0.747). The frequency of allele *MN*M* is also observed quite high among scheduled tribes from southern peninsula (0.725), whereas from western peninsular plateau the frequency is quite low among scheduled tribes (0.597). The scheduled tribes from northeastern peninsular plateau show differences as observed from Orissa and West Bengal with high frequencies as compared to

Bihar and Madhya Pradesh. Among the speakers of Indo-European languages the frequency of allele *MN*M* is quite low as compared to other language families.

Where MN system has been studied with anti-S or/and anti-s sera, it has been found that the *S* allele is more associated with M as compared to N. Among the Indian populations, the frequencies of *MNS*MS, MNS*/Ms, MNS*/NS* and *MNS*Ns* haplotypes are 0.195, 0.430, 0.091 and 0.262, respectively. The lowest frequencies of haplotypes *MNS*MS* and *MNS*NS* are observed among populations with Mongoloid affinities from Eastern Himalayan region. The frequency of haplotype *MNS*Ms* is high and that of *MNS*Ns* low among scheduled tribes as compared to other ethnic groups of India as well as among the scheduled tribes from eastern peninsular plateau and southern peninsula whereas among the scheduled tribes of western peninsular plateau, the frequency of *MNS*Ms* is low and *MNS*Ns* high. The frequency of *MNS*Ms* is highest and that of *MNS*MS* and *MNS*NS* are lowest among speakers of Tibeto-Chinese languages as compared to other language families (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.1.1.3. P System

The allele *P*P1* frequency is 0.416 among Indian populations; it is low in the Himalayan mountain complex but gradually starts increasing and reaches maximum towards Southern peninsula. The frequency is quite low among populations with Mongoloid affinities from Himalayan region and among scheduled tribes of western and northeastern peninsular plateaus and southern peninsula. The highest frequency of *P*P1* is observed among speakers of Dravidian languages (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.1.1.4. Rhesus System

Among the various Indian population groups the highest frequencies are observed for *RH*CDe* (range 0.340 to 0.960, frequency 0.632) and *RH*cde* (range 0.000 to 0.444, frequency 0.177). Against that, all the other Rh haplotypes are showing much lower frequencies as is seen from the following figures.

*RH*cDE*	0.097	(0.000-0.366)
*RH*cDe*	0.056	(0.000-0.413)
*RH*CDE*	0.012	(0.000-0.133)
*RH*Cde*	0.021	(0.000-0.173)
*RH*CdE*	0.001	(0.000-0.036)
*RH*cdE*	0.004	(0.000-0.091)

The frequency of allele *RH*D* is 0.803 among Indian populations (varies from 0.532 to 1.000). Among the populations with Mongoloid affinities from Eastern Himalayan region, the frequency is quite high (0.938). In different ethnic groups allele *RH*D* is in high frequency among scheduled tribes from western, northeastern and southern peninsular regions as compared to other ethnic groups. Lowest frequency of allele *RH*D* is observed among the speakers of Indo-European languages. The frequency of allele *RH*D* is high in East India and from there it starts decreasing in all directions.

In India in the Rhesus system when different antisera have been used, the frequency of haplotype *RH*CDe* is highest (0.632) followed by *RH*cde* (0.177). From East India and South India zones the scheduled castes are showing differences with other ethnic groups for the frequencies of *RH*CDe* and *RH*cde* whereas in North India castes and scheduled castes are showing almost similar frequencies. The frequency of haplotype *RH*CDe* is quite high and that of *RH*cde* low among the population groups with Mongoloid affinities from Eastern Himalayan region and scheduled tribes of India (0.723, 0.707 and 0.048, 0.093, respectively). The frequency of *RH*CDe* is high and that of *RH*cde* low among scheduled tribes of western and northeastern peninsular plateau as compared to southern peninsula. Quite interesting results have been observed among populations with Mongoloid affinities in which so-called African haplotype *RH*cDe* is present in high frequency along with quite high frequency of haplotype *RH*cDE* which is not observed, in general, from other parts of the world. Among the speakers of Indo-European languages, the frequency of haplotype *RH*CDe* is lowest (0.606) and *RH*cde* highest (0.206). A high frequency of *RH*cDe* is observed among speakers of Mon Khmer group of Austro-Asiatic and that of *RH*cDE* in speakers in Tibeto-Chinese languages (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.1.1.5. Lutheran System

The allele *LU*A* is absent among most of the Indian populations and in general the frequency is 0.016. Among the scheduled tribes the frequency is quite high (0.033) and allele *LU*A* is almost absent among the speakers of Dravidian languages (0.001) as compared to Tibeto-Chinese (0.028) and Indo-European (0.022) languages (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.1.1.6. Kell System

The frequency of allele *KEL*K* is low among Indian populations (0.038); however, quite high frequencies are reported among different ethnic groups from West Bengal. The allele is either absent (among scheduled tribes) or present in low frequency (0.014 in caste populations) among populations with Mongoloid affinities from Eastern Himalayan region. The frequency of allele *KEL*K* is low among scheduled tribes as compared to other ethnic groups of India, but among the scheduled tribes from western and southern peninsular regions the frequencies are high as compared to rest of the ethnic groups. The frequency is high among Indo-European language speakers (0.041) as compared to speakers of Tibeto-Chinese (0.017) and Dravidian (0.010) languages (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.1.1.7. Duffy System

The frequency of allele *FY*A* is 0.530 among Indian population with a quite wide range (0.136 to 1.000). The frequency is high in the Himalayan mountain complex region, starts decreasing towards Indus-Ganges-Brahmaputra plain, and again gradually starts increasing towards southern peninsula. Among the populations with Mongoloid affinities from Eastern Himalayan region the frequency is quite high (0.737) and it is highest among scheduled tribes (0.811) as compared to other ethnic groups from this region. The differences are well marked among different ethnic groups from zones and India and among them; the frequency is high among scheduled tribes. However, differences are observed from western and northeastern peninsular plateaus and southern peninsular scheduled tribes, wherein among the latter, the frequency is high. The frequencies of *FY*A* are quite low among the speakers of Mon Khmer and Munda groups of Austro-Asiatic and Southern, Eastern and Central groups of Indo-European languages as compared to other groups. Selective advantage of *FY* allele against malaria has been observed from Africa. From India, most of the studies reported are using only anti-FY (A) and therefore it is rather difficult to evaluate selection factor in this area (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.1.1.8. Kidd System

The allele *JK*A* frequency is 0.529 among Indian populations (varies from 0.309 to 0.817) and the frequency is high among caste populations (0.628) whereas among scheduled castes and scheduled tribes the frequency is almost similar (0.532 and 0.535, respectively). The frequency is low among the populations with Mongoloid affinities from Eastern Himalayan region (0.481). Among the speakers of Indo-European languages the frequency is high (0.547) as compared to speakers of Tibeto-Chinese (0.475) and Dravidian (0.432) language families (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.1.1.9. Diego System

*DI*A* allele which is usually referred to as a Mongoloid allele is present in quite low frequency 0.014 (varies from nil to 0.034) among populations with Mongoloid affinities from Eastern Himalayan region. However, sporadic cases of this allele have been reported among other ethnic groups of India. The allele *DI*A* is present among the speakers of Tibeto-Chinese and Indo-European (0.018 and 0.015, respectively) languages (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.1.1.10. ABH Secretor System

The allele *ABH*Se* frequency is 0.524 among Indian populations (varies from 0.216 to 0.863). The frequency is high in Himalayan mountain complex and starts decreasing towards western and northeastern peninsular plateau and then towards southern peninsular region, it starts increasing gradually. The differences among the various ethnic groups from South Indian region are well marked with other zones, as observed among scheduled castes population among whom

the frequency of *ABH*Se* is quite high (0.730) as compared to Indus-Ganges-Brahmaputra plains (about 0.450). In general, the frequency is low among scheduled tribes of India than in other ethnic groups. However, the differences are observed among scheduled tribes from western and northeastern peninsular plateaus among whom the frequencies are high as compared to southern peninsular region. The frequency is low among the speakers of Indo-European languages (0.514) as compared to those of Dravidian and Tibeto-Chinese (0.556 and 0.585, respectively) languages.

Overall, in the Indian region, there are marked clines at the extremes of which frequencies are widely different. This emerges from the data on blood group polymorphisms, wherein the population groups differ significantly in their ABO frequencies. Significant variations in the frequencies of the MN and Rhesus blood groups can also be seen but they are much less than the ABO system. The other blood group systems show less frequency variations, which reasonably may be attributed to lack of data (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.1.2. Serum Protein Polymorphisms

5.1.2.1. KM System

The frequency of allele *KM*1* is 0.114 among Indian populations (varies from 0.021 to 0.328). The frequency is quite high in the Himalayan mountain complex and then starts decreasing towards the peninsular region. The frequency is quite high also among populations with Mongoloid affinities from Eastern Himalayan region (0.189) and it is highest among scheduled tribes (0.247). Among the different ethnic groups, the frequency is high among scheduled tribes (0.131) as compared to others, and similar pattern is observed among western and northeastern peninsular plateaus, whereas from southern peninsular region the frequency is quite low among scheduled tribes (0.059) as compared to other ethnic groups. The frequency of *KM*1* is less than 0.10 among the speakers of different languages except Tibeto-Chinese, among whom the frequency is quite high (0.224) (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.1.2.2. GM System

The most common GM haplotypes around the world and the groups with which they are primarily associated with are as follows:

The frequency of haplotype *GM*5* is high (0.355) as compared to that of *GM*1* (0.276), *GM*1,5* (0.269) and *GM*1,2* (0.100). Similar pattern is observed in various zones of India except in East India where *GM*1,5* is quite high (0.405) and this haplotype is observed in high frequency in scheduled tribes and among the populations with Mongoloid affinities from Eastern Himalayan region. In general, the frequencies of *GM*1*, *GM*1,2* and *GM*1,5* are high in the Himalayan mountain complex region and then these start declining gradually towards peninsular region. The differences are well marked between the scheduled caste and caste populations from Indus-Ganga-Brahmaputra plains than from southern peninsular region. Among the speakers of Tibeto-Chinese, Munda group of Austro-Asiatic and North and Central Dravidian group of Dravidian languages the frequency of *GM*1,5* is quite high, whereas among Indo-European and Dravidian speakers the frequency of *GM*5* is quite high (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.2.2.3. Haptoglobin (HP) System

The frequency of allele *HP*1* is 0.160 among populations of India (varies from nil to 0.406). In the Himalayan mountain complex the frequency of allele *HP*1* is high and it starts declining towards peninsular region. The scheduled castes of Indus-Ganges-Brahmaputra plains region have

Group	*Common*	*Haplotype*
Europeans	*GM*3,5*	*GM*3;5,10,11,13,14,26,27*
North East Asiatics, Europeans	*GM*1,17;21*	*GM*1,17;21,26,27*
South East Asiatics, American Indians	*GM*1,2,17;21*	*GM*1,2,17;21,26,27*
North East Asiatics	*GM*1,17;15,16*	*GM*1,17;10,11,13,15,16,27*
South East Asiatics	*GM*1,3;5*	*GM*1,3;5,10,11,13,14,26,27*
Black Africans	*GM*1,17;5*	*GM*1,17;5,10,11,13,14,26,27*
Black Africans	*GM*1;5,6*	*GM*1,17;5,6,11,24,26*

1. Gamma-1 and Gamma-3 allotypes [G3M (28) expected] which are separated by a semicolon.

low frequency as compared to castes and communities, whereas from South India, the frequencies of *HP*1* allele are low and similar among scheduled castes and scheduled tribes.

From the western and northeastern peninsular plateau, the frequency of allele *HP*1* is low among scheduled tribes as compared to other ethnic groups. However, among the populations with Mongoloid affinities from the Eastern Himalayan region (0.192) and among the scheduled tribes of this region (0.189) the frequency of *HP*1* allele is high. In general, the frequency of *HP*1* allele is low among scheduled tribes (0.135) and it is falling closer to scheduled castes (0.147) as compared to other ethnic groups. The frequency is high among speakers of Mon Khmer group of Austro-Asiatic (0.209) and Tibeto-Chinese (0.189) languages from Himalayan region followed by Indo-European languages (0.180) as compared to speakers of Munda group of Austro-Asiatic (0.109) and Dravidian (0.130) languages. In India, hypohaptoglobinaemia (HP O) phenotype has been reported in almost all the population groups studied. It is reported that it has a selective advantage in malaria since this phenotype is present in high frequency (0.30 to 0.40) among some population groups from West and Central Africa. However, from India, it is difficult to evaluate this association because the frequency of this phenotype is quite low among Indian populations and it is present among majority of the studied groups (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.2.2.4. Transferrin (TF) System

Among Indian populations common transferrin allele found in most individuals is *TF*C* (0.991), while *TF*D* and *TF*B* alleles are present in quite low frequencies (0.008 and 0.001, respectively). The frequency of *TF*C1* subtypes is high among scheduled tribes as compared to populations with Mongoloid affinities among whom a low frequency is observed particularly from the states of Assam and Manipur. The frequency is high in West India and from here, it starts decreasing in all directions particularly in East India. The *TF*C3* allele referred as specific marker of European populations, is present in high frequency among populations of North India as compared to others. The frequency of *TF*D* is high in scheduled tribe and scheduled caste populations and it gives high correlations with mean annual temperature. Walter and Bajatzadeh (1971) observed that the frequency of *TF*D* in tropical regions is more frequent than in non-tropical regions and in India it is observed high in tropical savannah type climatic region. The frequency of *TF*D* is high in Munda group of Austro-Asiatic (0.025) and Dravidian (0.014) language families. The rare allele *TF*Chi* reported from Bihar among Oraons and variants of D are also observed among tribals of Andhra Pradesh, but it is not certain whether they are *TF*Chi* or not (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.2.2.5. Group Specific Component (GC) System

The frequency of *GC*1* is 0.747 among the Indian populations (varies from 0.591 - 0.911). In the Himalayan mountain complex the frequency of the allele is low and it starts increasing towards peninsular India. In the Himalayan region the frequency of the allele is almost similar in Eastern and the Western Himalayan regions (0.752 and 0.756, respectively) than in Central Himalayan region (0.688). The frequency of the allele is almost similar among scheduled tribes from western, north eastern and southern peninsular regions, as well as from Eastern Himalayan region among scheduled tribes with Mongoloid affinities (0.740, 0.752, 748, and 0.746, respectively). The frequency of *GC*1* allele is low among scheduled caste populations from Indus-Ganga-Brahmaputra plain region as compared to southern peninsular region. The frequency of *GC*1* is low among speakers of Indo-European languages and high among that of Austro-Asiatic languages (Munda group).

Population	*Allele Frequency*		
	*GC*1S*	*GC*1F*	*GC*2*
Europeans	0.55-0.60	0.10-0.20	0.20-0.30
Africans	0.07-0.17	0.64-0.84	0.06-0.07
Mongoloids	0.15-0.38	0.39-0.80	0.11-0.32
Iraqis	0.59	0.22	0.17
Indians	0.50	0.25	0.25
American Indians	0.29-0.64	0.13-0.47	0.09-0.38
Australian Aborigines	0.59	0.31	0.03
Melanesians	0.25	0.24	0.34
Polynesians	0.30	0.44	0.26
Micronesians	0.21	0.59	0.28

The distribution of GC suballeles shows an interesting fluctuation in frequencies. The *GC*1S*

frequency starts rising from Southeast Asia and East Asia reaching its peak in India, Europe and Middle East, declining again through East Africa and down to South Africa where it has minimum value (below 0.20). In contrast, Africans are characterised as having the highest frequency of the *GC*1F* allele (above 0.60). Values of the allele fall to below 0.20 in Europeans but rise again in East and Southeast Asia (0.50). Among Chinese and Japanese the frequencies of *GC*1F* are 0.480 (varies from 0.390 to 0.588) and 0.484 (ranges from 0.421 to 0.579), respectively, whereas among Mongoloids of Southeast Asia the frequency is high (0.535, varies from 0.354 to 0.795). However in the Pacific area there are relatively stable values of the *GC*1S* and *GC*1F*, each allele having frequencies in the range of 0.27 to 0.40.

The frequency of *GC*1S* allele is high from most of the states and union territories of India (0.492) as compared to *GC*1F* (0.250). The differences are observed among the populations with Mongoloid affinities from Western Himalayan region where *GC*1S* is high as compared to Eastern Himalayan region and among some populations from this region the frequency of *GC*1F* is higher than *GC*1S*. Among Siddi population of African descent the frequency of *GC*1F* is higher than *GC*1S* as also observed among Africans whereas in Onges (Negrito) from Andaman the frequency of *GC*1S* is quite high (0.614). For the distribution of *GC*1F* and *GC*2* a cline associated with increasing *GC*1F* and decreasing *GC*2* allele frequencies is present between northern and southern regions as observed by Constans et al. (1985). However, they added, that due to limited knowledge, it is not possible to establish selective pressure, if any (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.1.3. Red Cell Enzyme Polymorphisms

5.1.3.1. Adenosine Deaminase (ADA) System

Among the Indian populations the frequency of allele *ADA*1* is 0.882 (varies from 0.500 to 0.985).The frequency is low in Indus-Ganga-Brahmaputra plains region and starts increasing towards Himalayan mountain complex and peninsular region. Among the populations with Mongoloid affinities from Eastern Himalayan region and in scheduled tribes from this region (0.834) the frequency of *ADA*1* is low (0.829) as compared to western (about 0.880), northeastern (0.921) and southern (0.863) peninsular regions. The frequency of *ADA*1* is low among Tibeto-Chinese speakers as compared to others (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.1.3.2. Adenylate Kinase (AK1) System

The frequency of allele *AK1*1* is 0.924 among Indian populations (ranges between 0.795 and 1.000). The frequency is high among the populations from Himalayan mountain complex and it gradually starts decreasing towards peninsular region. Usually the frequency of *AK1*1* is high among scheduled tribes as compared to other ethnic groups. In the scheduled tribes with Mongoloid affinities from Eastern Himalayan region the frequency is higher (0.974) as compared to western, north eastern and southern peninsular regions from where the frequency is low (about 0.940) among scheduled tribes. Among the speakers of Munda groups of Austro-Asiatic, Dravidian and Indo-European languages the frequency of allele *AK1*1* is low (about 0.919) as compared to Tibeto-Chinese language speakers (0.976) (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.1.3.3. Red Cell Acid Phosphatase (ACP1) System

The frequency of allele *ACP1*B* is higher (0.756) than *ACP1*A* (0.242), whereas *ACP1*C* occurs in very low frequency (0.002) among Indian populations. The frequency of allele *ACP1*A* is high among scheduled castes from Indus-Ganga-Brahmaputra plains region (about 0.260) as compared to southern peninsular region (0.189); the frequency is high among scheduled tribes from western (about 0.240) and southern peninsular plateaus(0.235) as compared to north-eastern peninsular plateau (about 0.200), and among scheduled tribes with Mongoloid affinities from Eastern Himalayan region (0.214). The allele *ACP1*C* is present in quite low frequency in the Himalayan region. This frequency of allele *ACP1*A* is quite high among speakers of Indo-European languages (0.255) as compared to other languages. The effects of selectively acting ecological factors such as mean annual temperature on acid phosphatase alleles is reported by Walter (1976). In view of the marked

quantitative differences in the enzyme activity of the different phenotypes of this system, the role of differential selection in bringing about the existing variability of this red cell enzyme in various populations from different ecosystems could have been substantial (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.1.3.4. Phosphoglucomutase (PGM1) System

The frequency of allele *PGM1*1* is 0.700 among Indian populations (varies from 0.442 to 0.950). In the southern peninsula the frequency is low and from there it starts increasing towards North India. Among the scheduled castes from Indus-Ganga-Brahmaputra plains region the frequency of *PGM1*1* is low as compared to other ethnic groups whereas from southern peninsular region the frequency is higher among scheduled caste populations than among other groups. The scheduled tribes inhabiting western and north-eastern peninsular plateau, have high frequency of *PGM1*1* as compared to other ethnic groups and similar pattern is observed from Indian region also, whereas from southern peninsular region and eastern Himalayan region the frequency of this allele is low among scheduled tribes as compared to caste and scheduled caste populations. However, the frequency of *PGM1*1* is almost similar among scheduled tribes from all these regions except from western region where it is high. Among the speakers of Munda group of Austro-Asiatic languages the frequency is low (0.668) whereas among Dravidian and Tibeto-Chinese and Indo-European speakers the frequency shows less differences (0.695, 0.700 and 0.703, respectively). The frequency of subtype *PGM1*1S* is low among scheduled tribes as compared to other ethnic groups. From the states of East India (West Bengal) and South India (Karnataka and Andhra Pradesh), the frequency of *PGM1*1*S is high (0.726, 0.733 and 0.745, respectively) as compared to North India (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.1.3.5. 6-Phosphogluconate Dehydrogenase (6-PGD) System

Among the Indian populations, the frequency of allele *PGD*A* is 0.959 (varies from 0.754 - 1.000). The frequency is low in Himalayan mountain complex and gradually starts increasing towards peninsular region. The frequency of *PGD*A* is higher among scheduled caste populations and low among caste populations of India. From north-east peninsular plateau and southern peninsular region, the frequency of *PGD*A* is high (about 0.970) among scheduled tribes as compared to western peninsular plateau (0.925) and from Eastern Himalayan region among scheduled tribes with Mongoloid affinities (0.850). Among the speakers of Bhotia group and Himalayan group of Tibeto-Chinese languages low frequencies are observed (0.790 and 0.868, respectively) followed by Pahari group of Indo-European languages (0.885) from the Himalayan region as compared to other speakers of rest of the languages. Saha and Tay (1990) reported that hypoxia prevailing at a high altitude might have acted as selective pressure on 6-PGD locus giving rise to higher *PGD*B* frequency. Tills et al. (1971) have assumed this already. Among Indian populations (n=120) Walter et al. (1991) observed a statistically significant positive correlation between *PGD*B* frequencies and altitude: $r = + 0.320$, $p < 0.001$. In the different population groups of India, the corresponding correlation coefficients are as follows: Castes (n=24), $r = + 0.684$, $p < 0.001$, Scheduled Castes ($n = 13$) $r = + 0.545$, $p = 0.054$, Scheduled Tribes ($n = 45$) $r = + 0.205$, $p = 0.177$, Communities ($n = 38$) $r = + 0.206$, $p = 0.215$ ((For details see Bhasin et al. 1994; Bhasin and Walter 2001). These data confirm the assumptions of Tills et al. (1971) and Saha and Tay (1990). Further detailed studies are required, however, in order to prove this presumed selective pressure on the 6-PGD locus - A rare variant Kadar is reported among Kadar tribals of Kerala in quite high frequency (about 17 per cent), which might have some adaptive significance (Saha et al. 1974).

5.1.3.6. Esterase D (ESD) System

The frequency of *ESD*1* allele is 0.729 in populations of India (varies from 0.418 to 0.978). In the Himalayan mountain complex region the frequency of this allele is high and starts decreasing towards peninsular region. Among the scheduled castes of Indus-Ganga-Brahmaputra plains region the frequency of *ESD*1* is high (about 0.740) as compared to southern peninsular region (0.678). The frequency is low among scheduled tribes (0.690) as compared to other

ethnic groups. From western peninsular plateau region, the frequency of *ESD*1* is high among scheduled tribes (about 0.780) as compared to northeastern (about 0.650) and southern (0.683) peninsular plateaus and also among scheduled tribes with Mongoloid affinities from Eastern Himalayan region (0.687). Among the speakers of Munda group of Austro-Asiatic family the frequency is low (0.604) followed by Bodo group (0.640), Kuki Chin group (0.635) of Tibeto-Chinese family, Central and North Dravidian groups (0.646 and 0.639, respectively) of Dravidian family as compared to different groups of Indo-European family (0.758) (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.1.3.7. Glucose-6-Phosphate Dehydrogenase (G-6-PD) System

The frequency of *G6PD*Def* is 0.045 among Indian populations (varies from complete absence to 0.271). From the Himalayan region, the frequency is quite high (0.087) as compared to non-Himalayan region (0.043). Among the scheduled tribes, the frequency of *G6PD*Def* is high (0.055) as compared to other ethnic groups. The frequency of the allele is low among scheduled tribes of southern peninsular region (0.026) as compared to other regions. From Eastern Himalayan region, among the scheduled tribes with Mongoloid affinities, the frequency of *G6PD*Def* is quite high (0.111). In general, the frequency of *G6PD*Def* is comparatively higher in North and West India zones, which indicates considerable stability of the allele in these areas, whereas in South India it is uniformly low except in Andhra Pradesh and Tamil Nadu and from East India, the studies are too few to evaluate. Among the speakers of different languages, the frequencies are high in Mon Khmer group, North East Frontier group, Bodo group and Pahari group of Himalayan region and low among the speakers of Dravidian languages (Bhasin et al. 1994; Bhasin and Walter 2001; Bhasin 2006a). Kotea et al. (2001) reported that G6PD Orissa (44Ala→Gly) is the major polymorphic variant which has been observed among tribal groups of India and it is not found among urban populations among whom most of the G6PD deficiency is due to G6PD Mediterranean (188 Ser→Phe) variant. The studies available from different ecological settings are not sufficient to evaluate this genetic marker precisely and its connection with prevalence of malaria (For details see Bhasin et al. 1994; Bhasin and Walter 2001; Bhasin 2006a).

5.1.4. Haemoglobin Variants

Among Indian populations, the incidence of haemoglobin variants is 0.005. *HB*S* allele with a frequency ranging from nil to 0.410 is present among various populations of India with a general frequency of 0.031. It is more prevalent among the scheduled tribes, followed by scheduled castes populations and is almost absent in the caste groups. Its frequency is high in semi arid steppe type (0.071) followed by tropical savannah type (0.039) climatic region. It is present in high frequency in Central India followed by South, West, and North India. The frequency is quite low in East India and the trait is absent in Islands zone. With regard to origin of sickle cell gene, Kan and Dozy (1980) is of the view that Indian and West African sickle cell gene mutations arose by separate events. Kulozik et al. (1986, 1987) were the first to report that the *HB*S* allele is strongly associated with the Saudi Arab haplotype. Subsequently Labie et al. (1989) also confirmed this finding in a larger set of Indian populations. They also found several atypical haplotypic backgrounds on which the *HB*S* allele occurred in various population groups from India. The *HB*E* allele is observed in high frequency among the population groups of East India, particularly among the populations with Mongoloid affinities from Eastern Himalayan region in which the frequency is 0.237. The frequency of *HB*E* is high in speakers of Mon Khmer group of Austro-Asiatic family, as well as among the speakers of Tibeto-Chinese family from Eastern Himalayan region. Heterogeneity of the *HB*E* allele has been recently observed both in South-East Asia and North-East India. Selective advantages of *HB*S* and *HB*E* against malaria could not be corroborated in the Indian populations. The low frequency of *HB*E* allele at high altitude is suggested due to relaxation of selection. It has been observed that most of the studies reported in the literature involve case studies and reports from hospitals, which cannot be regarded to represent population surveys, since such studied samples are usually heterogeneous. Further, most of the studies in India have not given any details about the ethnic groups, social and environmental factors etc. Therefore, it is rather difficult to study the

relationship of abnormal haemoglobins with different factors in India (For details see Bhasin et al. 1994; Bhasin and Walter 2001; Bhasin 2006a).

5.2. Other Genetic Markers

5.2.1. Colour Blindness

The frequency of colour vision defects is 0.036 in population groups of India (males only) which varies from complete absence to 0.231. It is present in low frequency in scheduled tribes as compared to other ethnic groups. In different zones, it is high in North (0.038) and South India (0.040) than in other zones. In the Himalayan region a low frequency is observed from Eastern (0.029) as compared to Western (0.032) and Central (0.036) regions. In occupational groups, it is low among agriculture groups and high in priesthood, warfare and trade and commerce groups. A similar pattern is observed from different language families *i.e.* low frequency in Austro-Asiatic and Tibeto-Chinese families as compared to Dravidian and Indo-European families. The validity of the theory of relaxation of selection among different ethnic groups explains to some extent the status of colour blindness in tribal population groups *i.e.* low frequency among them as compared to other ethnic groups, particularly caste groups, but it remains to be further evaluated and more quantitative data are required ((For details see Bhasin et al. 1994; Bhasin and Walter 2001; Bhasin 2006b).

5.2.2. Taste Sensitivity

Among population groups of India, the frequency of the taster allele (*T*) is 0.457 (varies from 0.108 to 0.912). It is present in high frequency among scheduled castes and in low frequency among community. Among the different zones, it is present in high frequency in population groups of Islands, followed by North and South India and in low frequency in West and Central India, where it is low in scheduled tribe groups in general. In Himalayan region, its frequency is high (0.533) as compared to non-Himalayan region (0.426). From Eastern Himalayan region, the frequency of allele *T* is low among populations with Mongoloid affinities (0.538) as compared to the Mongoloid populations of East Asia and Southeast Asia (0.70) which may be due to high frequency of goiter in this region. High frequency is observed in Austro-Asiatic and Tibeto-Chinese families than in Dravidian and Indo-European families For details see Bhasin et al. 1994; Bhasin and Walter 2001; Bhasin 2006c).

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5.3. Dermatoglyphics

5.3.1. Finger Dermatoglyphics

5.3.1.1. Finger Patterns

The distribution of the frequencies of different finger patterns (in percentage) may be generalised among major population groups as follows.

Whorls: Mongoloids (47) > American Indians (43) > Europeans (36) > Africans (27)
Loops: Africans (64) > Europeans (60) > American Indians (52) > Mongoloids (51)
Arches: Africans (9) > American Indians (5) > Europeans (4) > Mongoloids (2)

The frequency of loops is higher (53 per cent) than whorls (44 per cent) whereas the frequency of arches is 3 per cent among Indian population groups. The frequency of whorls is high in the Himalayan region and it gradually starts decreasing towards south of India, and the frequency of arches is low in East India and it starts increasing in all directions. In different zones, high frequency of whorls is observed from Islands (50 per cent) followed by Central (47 per cent), East (45 per cent), North (43 per cent), South (42 per cent) and West (39 per cent) India and the frequency of arches varies in between 2 and 4 per cent in these zones. From Himalayan region, the frequency observed for whorls is 46 per cent from Eastern and little less (45 per cent) from Western Himalaya. The highest frequency of whorls is observed among scheduled tribes from India, Islands, Central, East and South India and regions of Himalaya in general. In the language groups, the highest frequency of whorls is found in Tibeto-Chinese language family (49 per cent) and lowest in Indo-European language family (42 per cent) (For details see Bhasin et al. 1994; Bhasin and Walter 2001)

The whorl: loop (W: L) ratio appears to be approximately as follow.

Austro-Asiatic Family: Mon Khmer group	40:60
Tibeto-Chinese Family	50:50
Austro-Asiatic Family: Munda group	48:52
Dravidian Family	44:56
Indo-European Family	43:57

5.3.1.2. Total Finger Ridge Count (TFRC)

The mean value of TFRC is 141.26 from India and a low value has been observed among scheduled tribes as compared to other ethnic groups. The value is high in Indus-Ganga-Brahmaputra plains region and it starts decreasing towards northern as well as southern directions. From the various zones of India, the highest mean values are reported from Islands (167.97) and Central India (151.91) from where only scheduled tribes have been reported, followed by East (146.57), West (141.53), North (140.88), and South (131.48) India. The value is low among populations of Himalayan region (136.08) as compared to non-Himalayan region (142.24). In the different zones of India and regions of Himalaya, in general, high mean values are observed for caste or scheduled caste groups. From the language families, high mean value of TFRC is observed for speakers of Indo-European (142.79) and low for that of Dravidian (137.10) (For details see Bhasin et al. 1994; Bhasin and Walter 2001)

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5.3.2. Palmar Dermatoglyphics

5.3.2.1. Three Main Line Formulae of Wilder

Wilder (1922) observed that the three most common main line formulae in various populations with different racial elements were 11.9.7.-., 9.7.5.-. and 7.5.5.-. and concluded that the 11.9.7.-. type is essentially the European formula and the 7.5.5.-. type the African formula. The frequencies of three main line formulae as observed among different populations are as follows (after Steggerda et al. 1936).

Europeans: 11.9.7.-. (28 to 31 per cent) > 9.7.5.-. (17 to 26 per cent) > 7.5.5-. (9 to 10 per cent)
Africans: 7.5.5.-. (35 to 45 per cent) > 9.7.5.-. (16 to 22 per cent) > 11.9.7.-. (10 to 13 per cent)
Mongoloids: 7.5.5.-. (24 to 35 per cent) > 9.7.5.-. (19 to 32 per cent) > 11.9.7.-. (9 to 23 per cent)
American Indians: 9.7.5.-. (36 per cent) >11.9.7.-. (21 per cent) > 7.5.5.-. (18 per cent)

The order of preponderance observed for three main line formulae among different zones, regions, ethnic groups, and speakers of various languages is well marked as may be observed from the summarized distribution as follows (For details see Bhasin et al. 1994; Bhasin and Walter 2001)

Zone: North and West India
Region: Western and Central Himalaya
Ethnic Group: Castes, scheduled castes and communities
Language: Indo-European Family
11.9.7.-. > 9.7.5.-. > 7.5.5.-. or 9.7.5.-. ≥ 7.5.5.-.
Zone: Central and South India
Ethnic Group: Scheduled tribes (also of Bihar state)
Language: Dravidian Family
11.9.7.-.>7.5.5.-.>9.7.5.-.
Zone: East India
Region: Eastern Himalaya
Ethnic Group: Scheduled tribes
Language: Austro-Asiatic and Tibeto-Chinese Families
7.5.5.-.>9.7.5.-.>11.9.7.-.
Zone: Islands
Ethnic Group: Scheduled tribes (Also of Orissa state)
9.7.5.-.>11.9.7.-. or 7.5.5.-.

In India, the order of preponderance is 11.9.7.-.>7.5.5.-.>9.7.5.-. in Central and South India, whereas in North and West India, it is 11.9.7.-.>9.7.5.-. >7.5.5.-. and similar pattern is observed from Western and Central Himalayan regions; from East India the order is 7.5.5.-.>9.7.5.-.>11.9.7.-. and similar distribution is recorded in Eastern Himalayan region. From Islands, the tribal groups show the order 9.7.5.-.>11.9.7.-.>7.5.5.-. Among the caste groups the order is 11.9.7.-.>9.7.5.-.>7.5.5.-. and in scheduled tribe groups it is 11.9.7.-.>7.5.5.-.>9.7.5.-. whereas among the population groups from Eastern Himalayan region the order is 7.5.5.-.>9.7.5.-.>11.9.7.-. and similar pattern is observed in different language families *i.e.* among speakers of Indo-European languages the order is 11.9.7.-.> 9.7.5.-. >7.5.5.-., among Dravidian speakers it is 11.9.7.-.>7.5.5.-.>9.7.5.-. and in Tibeto-Chinese and Austro-Asiatic speakers the preponderance is of main line 7.5.5.-. , followed by 9.7.5.-. and 11.9.7.-. (For details see Bhasin et al. 1994; Bhasin and Walter 2001)

5.3.2.2. Palm Configurational Areas

1. Hypothenar Area

In India, the frequency of patterns on hypothenar area is 33 per cent and it is high from East India (36.5 per cent) and low in South India (29.9 per cent). From the Western and Central Himalayan regions, the frequency is over 25 per cent as compared to Eastern Himalayas where it is 20 per cent. Among the ethnic groups, the frequency for the presence of patterns is high among scheduled tribes (35.4 per cent) as compared to rest of the ethnic groups, where it is

almost similar (castes - 30.1 per cent, scheduled caste - 29.0 per cent and community - 29.9 per cent). Among the various linguistic groups, a little high frequency is observed among Indo-European language family (31.8 per cent) followed by Dravidian language family (30.0 per cent) and low frequency is found in Tibeto-Chinese language family (24.7 per cent) (For details see Bhasin et al. 1994; Bhasin and Walter 2001)

2. Thenar/First Interdigital Area

The presence of patterns from India in on thenar/first interdigital area is 15 per cent. From Central India, a high frequency is observed (17.7 per cent), followed by North (16.5 per cent), and South (15.1 per cent) India. From the Western and Central Himalayan regions, the frequency is over 15 per cent as compared to Eastern Himalayan region (less than 10 per cent). Among the different ethnic groups, high frequency is observed in caste and community 15.9 per cent followed by scheduled caste (15.2 per cent) and scheduled tribe (14.4 per cent). High and almost similar frequencies (16.2 and 15.8 per cent, respectively) as compared to speakers of Austro-Asiatic (10.4 per cent) and Tibeto-Chinese (9.6 per cent) language families represent the Indo-European and Dravidian language families (For details see Bhasin et al. 1994; Bhasin and Walter 2001)

3. Second Interdigital Area

Among the various Indian groups, the frequency of patterns in second interdigital area is 8.2 per cent for the presence of patterns. From the different zones, a low frequency is observed from East (3.4 per cent) and South (5.7 per cent) India. In the Himalayan region, the frequency is low in Eastern region (about 2 per cent) as compared to Western and Central regions (8.5 per cent). Among the various ethnic groups, the frequency is low in community (6.6 per cent) and high among caste (9.1 per cent) groups. In the language families, a high frequency is observed among speakers of Dravidian (9.2 per cent) and Indo-European (8.3 per cent) languages as compared to that of Tibeto-Chinese (3.4 per cent) and Austro-Asiatic (3.7 per cent) languages (For details see Bhasin et al. 1994; Bhasin and Walter 2001)

4. Third Interdigital Area

From India, the frequency of the patterns in

Table 3: Distribution of Palmar Patterns among Different Population Groups

Population	*Presence of patterns*		
	High	*Intermediate*	*Low*
Europeans	Hypothenar, Third Interdigital	Thenar/First Interdigital and Second Interdigital	Fourth Interdigital
Africans	Thenar/First Interdigital, Second and Fourth Interdigitals	Hypothenar and Third Interdigital	
Mongoloids		Fourth Interdigital	Hypothenar, Thenar/First, Interdigital, Second and Third Inter digitals
American Indians	Thenar/First Interdigital	Third and Fourth Interdigitals	Hypothenar, Second Interdigital

Table 4: Distribution of Palmar Patterns among Different Linguistic Groups

Population	*Presence of patterns*		
	High	*Intermediate*	*Low*
Tibeto-Chinese	Fourth Interdigital	-	Hypothenar, Thenar/First Interdigital, Second and Third Interdigitals
Munda group (Austro-Asiatic)	-	Hypothenar, Thenar/ First Interdigital, Second and Third Interdigitals	Fourth Interdigital
Dravidian	Hypothenar, Third Interdigital	Thenar/First Interdigital	Fourth Interdigital
Indo-European	Hypothenar, Third Interdigital	Thenar/ First Interdigital	Fourth Interdigital

the third interdigital area is 43.1 per cent. The frequency is low in East (31.1 per cent) and South (36.1 per cent) India as compared to Central (57.3 per cent), West (53.8 per cent), and North (47.7 per cent) India. From the Himalayan region, the frequency is about 40 per cent in Western and Central regions, whereas in the Eastern region it is quite low (about 25 per cent). Among the ethnic groups, the frequency for the presence of patterns is high in caste (49.1 per cent) and community (46.3 per cent) groups as compared to scheduled tribes (40.4 per cent) and scheduled castes (39.2 per cent). The frequency of patterns is high in Indo-European language family (49.5 per cent) and low in Tibeto-Chinese language family (24.7 per cent) (For details see Bhasin et al. 1994; Bhasin and Walter 2001)

2.2.5. Fourth Interdigital Area

The frequency for the presence of patterns fourth interdigital area among Indians is 60.7 per cent. Among various zones, the frequency is observed high from Central (73.2 per cent) followed by East (64.8 per cent), North (63.5 per cent), West (59.0 per cent) and South (56.0 per cent) India. From the Himalayan region, the high frequency is present in Eastern region (75 per cent) as compared to Western and Central regions (65 per cent). Among the various ethnic groups, the frequencies are almost similar (caste - 61.7; scheduled caste - 60.9; and scheduled tribe - 61.4 per cent) except among community (54.9 per cent). In the linguistic groups, the highest frequency is observed from Tibeto-Chinese family (76.4 per cent) and lowest in Dravidian language family (36.0 per cent) and Austro-Asiatic (Munda group - 56.5 per cent) languages speakers who are mostly tribals (For details see Bhasin et al. 1994; Bhasin and Walter 2001)

5.4. SOMATOMETRY

5.4.1. Measurement

5.4.1.1. The Stature

Among Indian populations stature is on an average medium (163.06 cm) among whom caste people are taller as compared to scheduled castes whereas tribal groups are short in stature, suggesting that the basic substratum of ethnic elements have been in favour of short stature individuals. In view of the advantages of the smaller body size in both 'undernourished' and 'hot climate' the smaller stature among the tribal groups might have developed in the process of adaptation to these conditions. The inhabitants of Punjab, Delhi, and Rajasthan are in general taller than the populations of other regions, which show a gradient of stature distribution from northwest to east and south positions of Indian subcontinent. Among occupational groups, the taller stature is found among pastoralists, which indicates that this occupation may involve selection for efficiency of a long distance walking. The speakers of Austro-Asiatic, Tibeto-Chinese, and Dravidian languages are shorter in stature as compared to Indo-European language speakers (For details see Bhasin et al. 1994; Bhasin and Walter 2001; Bhasin 2006e).

5.4.2. Indices

5.4.2.1. The Cephalic Index

The value of cephalic index varies from dolichocephaly to mesocephaly in India except a few population groups from West, East, and South India, and Islands among whom brachycephaly has been observed. The mean value of cephalic index in India is 76.06, which is mesocephalic. In various zones, the distribution of cephalic index is mostly dolichocephaly in North and Central India and brachycephaly is absent. On the other hand, among West, East, and South Indian populations, mesocephalic cephalic index is predominant and brachycephaly is observed in low frequency, while the Islanders are mostly brachycephalic. In the Himalayan region, a low mean value of cephalic index is observed from Western Himalayan populations, which are more dolichocephalic than Central and Eastern Himalayan populations, which are mesocephalic. The mean value of the index is low in scheduled tribes as compared to other ethnic groups. Among the scheduled tribes from northeastern peninsular plateau and southern peninsular region, the value of cephalic index falls in dolichocephalic as compared to western peninsular plateau region with mesocephalic index. Among the scheduled tribes with Mongoloid affinities from Eastern Himalayan region, also the value of index is in the range of mesocephalic class (77.57). Among the speakers of Tibeto-Chinese languages the value of cephalic

Table 5: Classification of Stature and Indices

Particulars	*Stature*	*Cephalic Index*	*Nasal Index*	*Facial Index*
INDIA	L. Med. (163.06)	Meso (76.06)	Meso(78.53)	Meso (88.34)
Natural Region				
Himalayan Mountain Complex	L. Med. (162.13)	Meso (76.38)	Meso (70.68)	Lepto (88.33)
Indus-Ganga-. Brahmaputra Plains	Med. (164.15)	Dolicho (75.87)	Meso (72.13)	Meso (87.00)
Peninsular Plateau	L. Med. (162.77)	Meso (76.07)	Meso (78.01)	Meso (85.64)
Islands	Short (155.50)	Meso (78.64)	Meso (79.98)	Meso (86.10)
Zones of India				
North India	Med. (164.70)	Dolicho (73.65)	Meso (70.13)	Lepto (88.33)
West India	L. Med. (163.09)	Meso (78.24)	Meso (75.86)	Meso (84.52)
East India	L. Med. (163.05)	Meso (76.82)	Meso (77.06)	Meso (86.27)
Central India	L. Med. (160.32)	Dolicho (74.96)	Meso (82.09)	Meso (87.45)
South India	L. Med. (161.23)	Meso (76.07	Meso (77.99)	Meso (86.61)
Islands	Short (155.50)	Meso (78.64)	Meso (79.98)	Meso (86.60)
Regions of Himalaya				
Western Himalaya	L. Med. (163.38)	Dolicho (74.00)	Lepto (65.51)	Meso (89.92)
Central Himalaya	L. Med. (163.13)	Meso (76.71)	Meso (72.85)	Meso (87.71)
Eastern Himalaya	L. Med. (161.20)	Meso (78.09)	Meso (75.56)	Meso (85.47)
Ethnic Groups				
Caste	Med. (16.25)	Meso (76.20)	Meso (74.78)	Meso (86.45)
Scheduled Caste	L. Med. (162.11)	Dolicho (75.96)	Meso (75.61)	Meso (85.79)
Scheduled Tribe	Short (157.75)	Dolicho (75.81)	Meso (74.49)	Meso (86.26)
Community	Med. (164.18)	Meso (76.17)	Meso (71.57)	Meso (86.58)
Language Family				
Austro-Asiatic Family	Short (158.89)	Dolicho (75.63)	Meso (81.72)	Meso (85.68)
Tibeto-Chinese Family	L. Med. (161.37)	Meso (77.67)	Meso (73.87)	Meso (86.47)
Dravidian Family	L. Med. (161.34)	Dolicho (75.52)	Meso (77.55)	Meso (86.54)
Indo-European Family	Med. (164.52)	Dolicho (75.99)	Meso (74.23)	Meso (86.42)

L. = Lower, Med. = Medium

index is high (77.67 - mesocephalic), while low values are observed among speakers of Munda group of Austro-Asiatic (75.18) and North and Central Dravidian groups of Dravidian languages (73.67 and 75.41, respectively - dolichocephalic), who are mostly tribals (For details see Bhasin et al. 1994; Bhasin and Walter 2001; Bhasin 2006e).

5.4.2.2. The Nasal Index

It is of mesorhinae type (75.53) among Indian populations (varies from 51.40 - leptorhinae to 96.75 chamaerhinae). The value of index is low in Himalayan mountain complex region and it starts increasing towards peninsular region. The value is high among scheduled castes from southern peninsular region as compared to Indus-Ganga-Brahmaputra plain region. Among scheduled tribes, the value of the index is high (79.49) as compared to other ethnic groups and higher values are observed from western, north eastern and southern peninsular scheduled tribals, whereas from Eastern Himalayan region among the scheduled tribes with Mongoloid affinities the value of the index is low (76.69). The value is high among the speakers of Austro-Asiatic and Dravidian languages as compared to Indo-European and Tibeto-Chinese language speakers. Global variation in the human nasal index is viewed as the result of an adaptive response to climatic variability, but it is not universally accepted as a reflection of climatic adaptation (For details see Bhasin et al. 1994; Bhasin and Walter 2001; Bhasin 2006e).

5.4.2.3. The Facial Index

It is mesoprosopic among various populations of India and from all the zones of India except North India (leptoprosopic). In the Himalayan region mesoprosopic type is predominant except in Western Himalayan region where leptoprosopic type is found. The value of index is high in the Himalayan region and gradually starts declining

towards south. Leptoprosopic facial index is observed among caste groups from West Bengal and Tamil Nadu, Kerala, and Pondicherry of South India. Europrosopic type of facial index is observed among caste groups of Gujarat and scheduled caste groups of West and South India zones. However, generally a high frequency is observed among community or caste > caste or community > scheduled tribe > scheduled caste except from West and South India where high values are observed among scheduled tribes. The differences observed among speakers of various languages are quite low (Dravidian ≥ Tibeto-Chinese ≥ Indo-European ≥ Austro-Asiatic) (For details see Bhasin et al. 1994; Bhasin and Walter 2001; Bhasin 2006e).

5.5. Among the Various Traditional Occupational Groups

Among priesthood and warfare (higher caste groups), trade and commerce (middle caste or Vaishyas) and agriculture, animal husbandry, artisans and menial workers (backward and scheduled castes) the distribution of frequencies and mean values of various biogenetical traits studied show similarities among the higher and/or middle with backward and/or scheduled castes populations, which indicates gene flow among these occupational groups (For details see Bhasin et al. 1994; Bhasin and Walter 2001). An explanation of this can be found in the fact that scheduled castes may have in them a sub-stantial trace of gene flow from the higher castes from generations past (Majumdar 1965).

5.6. Among Islanders

From Andaman and Nicobar Islands, a few biological traits are studied among Andamanese and Onges considered to be of Negrito affinities and Nicobarese who have Mongoloid affinities. Due to their small number, it is rather difficult to evaluate the studies based on a few subjects and a limited number of traits studied. However, the frequencies and mean values observed among them are different from the other Indian populations, which may be attributed to genetic drift instead of ethnic characteristics (Bhasin et al. 1994; Bhasin and Walter 2001).

5.7. Correlations

The correlations between climatic factors and altitude and different ethnic groups viz. caste, scheduled caste, scheduled tribe and community with various biogenetical traits (genetic markers in human blood, other genetic markers, dermatoglyphic traits and somatometry measurement and indices) have been calculated. Although many genetic markers and somatometry traits show significant correlations, generally the values are not high (For details see Bhasin et al. 1994; Bhasin and Walter 2001). Further, no correlation between climatic factors and dermatoglyphics among different ethnic groups has been found and Hiernaux and Froment (1976) also reported similar results.

5.8. Genetic Differentiation

The present study, we believe, is based on data from the largest number of Mendelian genetic markers so far used in India, as well as, from polygenic traits like dermatoglyphics and somatometry. Before evaluating the dendrograms based on the frequency data from genetical, dermatoglyphic and somatometric traits and all the traits together for various zones, different ethnic groups and four language families, an attempt has been made to review the studies available on genetic distances in India under the following heads.

1. Subgroups of an Ethnic Group into the Same or/and Different Regions
2. Various Ethnic Groups into the Same or/and Different Regions

5.8.1. Subgroups of an Ethnic Group into the Same or/and Different Regions

Genetic distance estimates have been used to study the genetic relationship of subgroups of an ethnic groups into the same or/and different regions. It has been observed that if the genetic distance among them is small, then genetic differentiation among them is also at an early stage.

The process of differentiation by fission with very little inter-caste migration has taken place in the recent past as reported from West India among four groups of Lohanas (Sindhi, Cutch, Halai and Punjabi) by Bhatia et al. (1976a), Saraswat groups (three Saraswat Brahmans and one Goan Catholics ethnologically related to Saraswats) by Bhatia et al. (1976b), a nomadic group Dhangar (22 castes of Dhangars) by Malhotra et al. (1978), from South India different subcastes of Brahmans of Andhra Pradesh by

Srikumari et al. (1986), and among three subpopulations of Naikpod of Andhra Pradesh by Muralidhar et al. (1989).

The differences observed among the subgroups of an ethnic group in the same or different regions may be due to either isolation, that is, due to cultural factors and/or geographical distance or due to admixture with the neighbouring populations of different racial elements/ genetic make up, as observed from Central Himalayan (North India) region among the Bhotias—a scheduled tribe (out of five groups of Bhotias, three namely Tolchha, Jad, Marcha are close to each other and show affinities with Tibetans, and Lepchas and two groups—Rang and Johri Bhotias are falling apart from them and are nearer to Rajputs of Kumaon and Shrestha Newars of Nepal) as reported by Tiwari (1984).

Among the three groups of Vania Soni, the Vania Soni of Surat (West India) are showing marked variation from Vania Soni of Saurashtra and Gujarat, apparently due to their geographical distribution (Undevia et al. 1978).

Among the four migrant groups of fishermen of Orissa (East India), Reddy et al. (1987, 1988, 1989) observed differences for the genetical, dermatoglyphic and anthropometric traits due to geographical distribution of these groups and concluded that the anthropometric measurements demonstrate high inter-group variation than dermatoglyphics.

Among Vaidiki a subsect of Brahmans of Andhra Pradesh (South India) studied from three different locations by Char et al. (1983) the differences due to geographical location, which also relate to ethnic history were observed.

Banerjee et al. (1992) studied genetic differentiation among three Hindu low caste groups (Poliya, Deshi, and Tiyor) from West Bengal, East India who are the descendants of the Koch, Indo-Mongoloid populations and they observed that they are having closer genetic affinity.

Das et al. (2002) studied the three subpopulations (Boro-Deshi-Dinajpur District, Boro-Deshi-Malda District, and Chhoto Deshi-Malda District) of the Koch Scheduled Caste of West Bengal, East India. They observed that Boro Deshi-North Dinajpur and Boro Deshi-Malda are showing closer affinities as compared to Chhoto Deshi –Malda.

Reddy et al. (2001) reported genomic diversity based on 3 STR loci (CSF1P0, TPOX, and TH01) among the 7 subpopulations of the pastoral caste, Golla, of Southern Andhra Pradesh, India. They observed that the UPGMA tree suggests a relatively earlier separation, hence the distinctiveness, of Kurava population whose position among the Gollas is disputed. The relatively earlier separation of Punugu from the rest of Golla subpopulations is also depicted. The clustering of the remaining 5 Golla populations is consistent with the microgeographic affiliations; for example, the Doddi, Puja and Karnam distributed in the western parts of the district tend to cluster together although the Pokanati and Erra, distributed in the eastern region do not form a compact cluster. Further, they studied by comparative analysis the phylogenetic position of the Gollas vis-à-vis the other Indian populations, which was based on the 3 STRs with 16 other Indian populations. The cluster of populations in the UPGMA dendograms portrays the underlying social, ethno-historical, and geographical backgrounds of the Indian populations well, both at the local, regional, and national levels. They observed that the Mongoloid populations clearly separated from the non-Mongoloid populations, lower castes from the upper and middle castes, and the local Golla populations from the extreme south are distinctly separated from the eastern as well as northern populations. They found that even the microgeographic variations within the Gollas seem to have been faithfully depicted.

Further, according to Karve (1961) the subcastes are not always segments split off from the same caste and, in most cases, are probably the result of the lack of fusion of different racial elements. Segments of both the autochthones and the immigrants become separated from the present groups due to migrations, and different segments going to different regions assumed or were given different ranks. The groups maintained strict endogamy and usually made certain clusters based on similarity of economic pursuits. Karve and Malhotra (1968) made an attempt to test the validity of Karve's hypothesis that many so-called subcastes are independent social realities, sharing with other subcastes a social status and function but lacking the biological affinity which would be expected if they were a result of splitting, by studying the distances among eight endogamous groups of Maharashtrian Brahmans (Maharashtra-West India). They concluded that the scanty historical records also suggest independent origins. Similar findings were also

reported by Dutta and Gulati (1976) among nine endogamous groups of Kumbhars (potters) from Maharashtra (West India) *i.e.* Kumbhar as a group is not a genetical category but a social category (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.8.2. Various Ethnic Groups into the Same or/ and Different Regions

A number of studies are available in which genetic distances are used to establish the genetic relationship between the various ethnic groups (caste, scheduled caste, scheduled tribe and community) from the same or/and different regions. These studies are helpful in understanding the intra-or/and interethnic group differences which may be due to either different racial elements present among various Indian populations in varying degrees or/and various population variation factors like mutation, natural selection, migration, genetic drift etc. From such investigations, the authors have attempted to study the differentiation of biological rank of various ethnic groups that exist in various parts of India.

About the racial composition, Majumdar (1965) has suggested that caste is a composite racial structure with an upper segment represented by the immigrant Mediterranean, Alpine elements, and lower segment represented by the Proto-Australoid autochthonous racial stock. Hypergamy brought into existence a large number of mixed castes of artisans, which formed the intermediate segment. On this was superimposed the four-fold division of society which was known to have existed in Iran.

Bhasin and Khanna (1992) reported genetic structure of nine population groups of North India -Jammu and Kashmir (Bodhs and Tibetans of Leh District; Baltis of Kargil District; Pandits and Muslims of Kashmir; Gujjars and Dogras caste groups - Brahmans, Rajput and Ramdasias of Jammu District) for eleven polymorphic traits and they observed two clusters – the first for the three population group from Ladakh region namely Bodhs, Baltis and Tibetans with Mongoloid affinities and rest of the population groups of Jammu and Kashmir districts with Caucasoid affinities.

Walter et al. (1993) studied genetic variation for three polymorphic traits (HP, GC and PI) among eleven populations groups of North India - Jammu and Kashmir (Baltis, Bodhs and Tibetans from Ladakh; Brahmins, Rajputs, Scheduled Castes, Khatris, Mahajans and Gujjars from Jammu and Pandits and Muslims from Srinagar). They observed that Baltis, Bodhs and Tibetans who are from same racial origin (Mongoloid) and affiliation to the same language family (Tibeto-Chinese) form one cluster. A second cluster is formed by majority of Jammu and Kashmir populations, which, however is composed of two clear-cut subclusters. One of them comprises the Khatris and the Pandits, the other one the Rajputs, Gujjars, Brahmins, Muslims, and Scheduled Castes, with the exception of Mahajans all the groups with Caucasoids affinities and Indo-European language speaking populations are found in one cluster.

Trivedi et al. (2002) reported only the frequencies of nine microsatellite loci among four population groups from Ladakh (North India) namely Argon, Balti, Drokpa, and Buddhist.

Tandon et al. (2002) have reported only results of genetic diversity at 15 fluorescent-labeled short tandem repeat (STR) loci in four populations – Thakur, Khatri, Kurmi, and Jat of Uttar Pradesh (North India).

Bhasin et al. (1985) have observed no intergroup differences in the same ethnic group i.e. scheduled tribes (Vasava, Kotwalia, Chaudhuri, and Gamit) from the same region (West India - Surat District, Gujarat).

Gaikwad and Kashyap (2002) reported only results of polymorphism at fifteen hypervariable microsatellite loci in four populations namely Marathas, Desasth Brahmins, Chitpavan Brahmins, and Dhangars of Maharashtra State (West India)

From the state of Karnataka (South India) Rajkumar and Kashyap (2002) have reported results on four population groups (Iyengar Brahmin, Gowda, Lingayat, and Muslim) for the distribution of 15 STR loci of the Powerplex TM 16 multiplex system.

The geographical proximity of eleven major tribal populations from South India - Andhra Pradesh (Chenchus - two groups, Kolam, Savara, Jatapu, Koya, Rajgond, Pardhan, Konda Reddi, Lambadi and Yerukula) was studied by Blake et al. (1981) from dendrogram. They observed that the pattern of clustering among tribal populations of Andhra Pradesh is consistent with their geographical positioning in general (these patterns are also consistent with their migration histories) except for certain aberrations.

Also from the analysis of anthropometric and genetic distances between five Gondi speaking populations (Raj Gonds, Kolams, Manne, Koyas and Plains Maria Gonds) of Central India (Andhra Pradesh and Maharashtra states) Pingle (1984) reported that closer the geographical distance between populations, the closer the genetic as well as morphological similarity between them. This is more so in populations, which due to their having adopted a settled agricultural occupation are less mobile. The low mobility in turn results a small marriage distance thus restricting the spatial distribution of genes to a smaller area.

Saha et al. (1988) have studied the genetic relationship of Oraons (Veddoid) of Eastern India (Bihar and Jalpaiguri) with eight Australoid tribes of Central and Southern India (Bhils, Malayaran, Kadar, Kota, Toda, Irula, Kurumba, and Chenchu) and two caste Hindu Groups (Tamils and Nayar) of Southern India. Oraons are believed to have migrated from Southern India, settled in Bihar several centuries ago and eventually moved to Chota Nagpur (Icke-Schwalbe 1983). Some of the Oraons migrated to Jalpaiguri district of North Bengal. By genetic distance analysis, the authors observed that Oraons are nearest to Bhils of Madhya Pradesh. The Oraons and Bhils are nearest to Kurumba and Irula tribes of Nilgiri Hills, where-as the Kota of Nilgiri and Chenchus of South India are the most distant tribes.

Trivedi et al. (2002) reported results of eight Indo-Caucasian populations represented by Baniya (East India - Bihar), Dehshast Brahmin (West India - Maharashtra), Bengalee Kayastha (East India - West Bengal), mixed Punjabi (North India - Punjab), Indo Mongoloids represented by Kuki and Hmar (East India - Manipur), Indo Proto-Australoid – Ekere and a mixture of Proto-Australoid and Indo Caucasian – Reddy (South India - Andhra Pradesh) for D1S80 alleles 14 and 15 which have been reported absent among most of the population groups but observed among Dehshast Brahmin.

Ghosh et al. (1977) studied the Kota of Nilgiri Hills (South India) and found a closer relationship between Kota and Toda than Kota and any other tribal population in the Nilgiri Hills (South India); whereas Saha et al. (1976) reported that Toda, a tribal group, which is considered to be distinctive by virtue of culture and appearance is closely related to the Brahman than to any other tribal group. Similar observations have been made by Ghosh et al. (1977) *i.e.*, Kota relationships with Hindu populations are somewhat closer in neighbouring Kerala (South India) than in geographically remote populations in North India, from where they are supposed to have originally migrated.

Studies are also available which indicate common origin of certain ethnic groups, as for example from Orissa (East India) five tribes namely Bodo Gabada (speaking Indo-Aryan Oriya language), Ollaro Gabada, Konda Paroja (speaking different dialects of Dravidian language) and Bareng Paroja and Pareng Gabada (speaking variants of Austro-Asiatic Munda speech) are speculated to be of common Veddoid origin (Das et al. 1968). Chakraborty and Yee (1973a) studied these tribes and observed that Bareng Paroja and Oallaro Gabada groups are quite close to one another. This cluster is far away from another cluster generated by Bodo Gabada and Pareng Gabada tribes, whereas Konda Paroja is placed between these two clusters. Chakraborty and Yee (1973b) also reported on anthropometry basis that the relative positions of the five populations seem to be the same as observed with genetic markers.

From South India in order to study the earlier hypothesis that Chenchu, Irula and Yanadi originated from the same stock, Reddy et al. (1983) studied their genetic relationship but their results failed to support the contention.

Biological rank differentiation exists in various parts of India as reported by Risley (1915) and Guha (1931) by anthropometric and somatoscopic observations, but they observed that this does not occur in Northern India.

Bhasin et al. (1983a, b) from their studies from Himachal Pradesh (North India) in the first instance among Brahmans, Rajputs and Scheduled Castes of Kulu district and Swangalas (a Hindu scheduled tribe group) and Bodhs (a Buddhist scheduled tribe group) of Lahaul tehsil and in the second among different Gaddi groups and Pangwalas of Chamba and Kangra districts observed no genetic differences. They reported that this is in agreement with the historical evidence and traditions, which connect their origin to those people who sought refuge in these mountain ranges from the plains from time to time, and also inter-group marriage was in vogue and the genetic differentiation among them was at an early stage.

From Punjab (North India), four endogamous groups (Jat Sikh, Ramdasia Sikh, Khatri, Brahmin) are close to each other out of five (including

Bania) reported by Sehgal et al. (1986). There is no definite clustering of the groups with their biological rank as has been observed by Das et al. (1978) among five endogamous groups of Delhi – North India (Rajput, Chamar, Gujjar, Ahir and Jat).

Kamboh (1984) studied the genetic relationship between various ethnic group—Brahmin, Kshatriya, Vaish, Shudra, Miscellaneous Hindus (Ahir, Gujar, Jat) and Miscellaneous Non-Hindus (Muslim, Christian, Sikh) from North India and observed closeness of three Kshatriya groups (Rajput, Arora, Khatri) with Brahmin as compared to Vaish and Scheduled castes. He also studied tribal and non-tribal groups of South India and observed differences between these groups. Further, he found closeness of South Indian non-tribal groups with the caste groups of North India.

From North West India among 14 population groups from three states—Rajasthan – North India (Udaipur district: Paliwal Brahmin, Rajput, Oswal Mahajan, Bhil Tribe, Meghwal, Meena Tribe), North India - Punjab (Patiala district: Jat Sikh, Ramdasia Sikh, Mahajan Agarwal), and Himachal Pradesh – North India, (Kangra district: Brahmin, Chowdhury, Gaddi Rajput, Chamar and Nepalis), Papiha et al. (1982) studied genetic relationships. They showed with the genetic distance calculations that tribals and low caste groups are closer, but well separated from the high and middle caste groups. They concluded that there is a slight possibility of disruptive selection, but the analyses suggest that the differences in genetic structure in North-West India are more likely to be due to their breeding structure, differential migration, and ethnic affiliation. Furthermore, within a given geographical area, the internal structure regulates genetic differentiation of the various sub-populations. At the less local level, both geographical distance and major ethnic affiliation exert a primary influence.

Racial admixture and genetic isolation among Kanets (scheduled tribe) and Kolis (scheduled caste) of Kinnaur of Himachal Pradesh – North India are reported responsible for genetic differentiation by Papiha et al. (1984) since they observed that Kanets of Puh and Koli are falling apart from rest of the three Kanet groups from Kalpa, Sangla and Nachar.

Biological rank differentiation has been observed from West India among nine endogamous groups of Maharashtra (caste groups—Desasth Rigvedi and Chitapavan Brahmans, Maratha, Chandrasenya Kayastha Prabhu; Scheduled caste—Nava Budha; Tribals—Bhil, Pawara, and Katkari and a migrant group—Parsis) studied by Mukherjee et al. (1979) who observed two clusters, one of tribal groups and another consisting of rest of the six groups.

Mastana and Papiha (1994) have studied the four endogamous groups (Brahmin, Maratha, Gujarati Hindu Patel, and Parsee) from Maharahtra, West India and found that the Brahmans and the Marathas are closely joined by the Patels while the Parsees are clearly isolated.

Al-Maghtheh et al. (1993) studied of Parsi from Western India using four DNA probes from the short arm of the human X chromosome and reported affinity between the Parsis and the population from Southern Europe (Spanish). It is difficult to agree with their observation.

From East India - Assam, Danker-Hopfe et al. (1988) observed that two Hindu high castes are closely related and they form one subcluster. They also reported that Sheikhs (Muslims) are more closely related to the Brahmans and Kalita to Kaibartas (scheduled caste) when genetic traits are considered, and to Kalitas when anthropometric traits are considered, these observations can reasonably be explained based on their Caucasoid origin. Further, they observed from anthropometric measurements a distinct position of Ahom- a Mongoloid group belonging to Siamese-Chinese group from other Mongoloid groups namely Chutias, Deuris, Mishings, and the Morans who belong to Tibeto-Burman language family. Similar results have been reported by Mukherjee et al. (1989) who reported that Brahmins, Kalitas, Kaibartas and Muslims who belong to Caucasoid groups and Indo-European language family make one cluster and Ahoms, Sonowals, Rajbanshis, Chutias, Karbis (Mikir) who have strong Mongoloid affinities make another cluster.

Chattopadhyay et al. (2001a) studied nine fluorescent-based STR loci among four tribal groups with Mongoloid affinities (Garo, Naga, Kuki, and Hmar) from North Eastern part and Eastern part of India.

Dutta et al. (2001) reported STR data for the AMP STR profiler plus loci among four populations from West Bengal – East India (Brahmin and Kayastha) and Manipur – East India (Meitei and Manipuri Muslims).

Dutta and Kashyap (2001a) studied genetic

variation at four minisatellite loci (D1S7, D4S139, D5S110, and D17S79) among three population groups of West Bengal (East India) – Brahmin, Kayastha and Garo and observed similarities among Brahmin and Kayastha groups, whereas Garo group is falling apart from them.

Dutta and Kashyap (2001b) used three tetrameric STR loci (HumTHO1, TPOX and CSF1PO) and also observed that two Hindu high castes – Brahmins and Kaysthas are closely related and form one cluster whereas population with Mongoloid affinities namely Meitei, Kuki, Naga, Hmar are making another cluster with Chinese, however they observed that Manipuri Muslims are falling apart from these groups in East India.

Again Chattopadhyay et al. (2001b) investigated the nature and extent of genetic variation at 3 tetrameric STR loci (HUM HPRTB, F13B, and LPL) among 8 population groups of West Bengal and Manipur regions (East India) of India. Of which, two groups from West Bengal belong to Caucasoid and six (one in WB and five in Manipur) belong to Mongoloid stock. Mongoloid groups show similarities in some alleles and differences in some other alleles in STR loci. For example, Manipur Muslims show differences in STR allele frequency when compared to other four regional populations. Similarly, Garo, one of the Mongoloid populations of West Bengal differ in allele frequency from their counterparts in Manipur region. Heterozygosity values are higher for Caucasoid than Mongoloid groups. The overall gene differentiation for STR loci is 5.3%. The clustering pattern for the eight populations shows distinct clusters for Caucasoid and Mongoloid groups, whereas Manipur Muslims stand apart from others. They observed similar results as obtained from classical genetic markers.

Further Dutta et al. (2003) reported results of five population groups from North-East Region (Meitei, Kuki, Naga, Hmar and Manipur Muslims) studied for VNTR markers(four minisatellite loci D1S7, D4S139, D5S110 and D17S79) and observed that populations with Mongoloid affinities (Meitei, Kuki, Naga and Hmar) are falling closer to each other whereas Manipuri Muslims are falling apart from them.

Chattopadhyay and Kashyap (2001) studied genetic variation at six DNA loci: HLADQA1, LDLR, GYPA, HBGG, D7S8, and GC among three castes, four tribal and one religious group from West Bengal and Manipur (East India). They observed very low genetic distance between the Brahmin and Kayastha communities in relation to the Garo. Genetic affinities among the populations of Manipur reveal very close association between the Meitei, Naga, Hmar, and Kuki.

From Sikkim (East India), Bhasin et al. (1986b) studied 13 populations and they observed three clusters—the first one of the population groups with Caucasoid affinities with some Mongoloid admixture [Brahmins, Chhetris and Pradhans (Newars)], the second of population groups with Mongoloid affinities and certain degree of Caucasoid admixture (Bhutias of North Sikkim, Sherpas, Scheduled castes, Tamangs and Gurungs) and the third one of population groups with Mongoloid affinities [Lepchas of North and Rest of Sikkim, Bhutias of Rest of Sikkim, Rais and Limboos (Subbas)]. They concluded that the genetic relationship of 13 Sikkim populations under study reflects fairly well their ethnic and linguistic affiliations.

Kashyap et al. (2002) reported results only of 15 STR loci in three population groups of Sikkim (East India) namely Nepali, Bhutia, and Lepcha.

From East India - West Bengal, ten endoga-mous groups [Rarhi Brahmin, Vaidya (caste groups); Rajbanshi, Bagdi and Jalia Kaibarta (scheduled caste groups); Rabha, Garo, Mech, Munda and Lodha (tribal groups)] which encompass all social ranks in the caste hierarchy and cover almost the entire geographic area of the state were studied by Chakraborty et al. (1986). They observed that overall genetic differentiation is not in accord with the classification based on caste as two low ranking scheduled castes are in close proximity with the high castes, which suggests gene flow in past generations. They further observed that three different clusters of groups emerge from the present data providing support for the anthropologic assertion that in Bengal, Proto-Australoid, Caucasoid and Mongoloid racial elements generally co-exist. However, these three components are not uniformly present in all groups. Geographic separation of these groups is a strong determinant of the gene differentiation that exists among them. However, they added that these findings are in qualitative agreement with the postulates given in the ethno-history of these populations but none of these results is conclusive.

Ashma and Kashyap (2002) have reported the results of 15 STR loci among four population groups namely Brahmin, Bhumihar Brahmin, Rajput, and Kayasth from Bihar (East India).

Differences have been reported among low caste Hindus of West Bengal and Tribals (Bihar and Orissa), Eastern India by genetic distance analysis by Roychoudhury (1981). He observed two clusters, one made by the low caste Hindus, and the other by tribal groups. Further, he found that the genetic relationship of the Bengalis is closer to the North Indians than to the Bhutanese, Nepalese, Tibetans and Chinese, and Bhutanese, Tibetans and Chinese are closer to each other than the Nepalese.

Sahoo and Kashyap (2002) reported four caste groups from Orissa (East India) namely Oriya Brahmins, Khandayat, Karan, and Gope using 16 STR loci, but the results have not been discussed.

Mukherjee et al. (2000) studied five tribal groups from Madhya Pradesh , Central India (Muria and Halba of Bastar District; Kamar, Chinda Bhunjia and Chaukutia Bhunjia from Raipur District (These districts are now in new State of Chhattisgarh)They analysed 16 polymorphic loci, of which nine were insertion/ deletion polymorphisms (Indels) and the remaining seven were RFLPs. They observed that Muria and Kamar are close to each other. From ethno-historical accounts, it is known that both these groups are descendants of Dravidian speaking Gonds. The two subscribes of the Bhunjias Chinda and Chaukhutia are genetically close to each other. The Halbas are genetically distinct from these two clusters of populations as they are Indo-European speakers and do not share any common ancestry with the Gonds. The genomic affinities of these tribal groups correspond closely with their ethnohistorical and linguistic affinities.

The results of two pentanucleotide STR and thirteen tetranucleotide STR markers have been reported among four population groups – Agharia, Satmani, Dheria Gond and Teli of Central India (Chhattisgarh) by Sarkar and Kashyap (2002).

Kashyap et al. (2002) reported the results of 16 STR loci in five endogamous populations of India namely Bhumihar from Bihar (East India), Reddy and Sakunapakshollu of Andhra Pradesh (South India), Naga of Manipur and Nagaland (East India) and Khandait of Orissa (East India).

From South India genetic analysis of nine endogamous groups (caste groups—Brahmin, Nayar, Izhava, Scheduled Castes; Religious Groups—Muslim and Christian, and tribal groups—Malayaran, Irula, Kurumba and Toda) was reported by Saha et al. (1976). They observed that tribal groups stand apart from Hindu population groups as well as from each other.

Similarly, from Andhra Pradesh (South India), some endogamous groups belonging to Brahman, Vysya and Sudra (except Kshatriya) have been investigated to study the genetic differentiation by Char et al. (1989) and they observed that the separation of the caste populations in the dendrograms fits well with social rank in the hierarchy of the Hindu caste system.

From Andaman and Nicobar Islands (Islands), Kashyap et al. (2003) studied the polymorphism at fifteen autosomal short tandem repeat (STR) loci, mitochondrial control region sequences and eight Y chromosomal STR loci in 194 blood samples, of which 94 samples were from the Andaman Negritos (24 Great Andamanese and 70 Jarawas) and 100 Nicobarese, a Mongoloid group of Nicobar Island and evaluated their relatedness with similar ethnic groups of India, South-east Asia and Africa. They observed that the aboriginal populations of the Andaman Islands – the Great Andamanese and the Jarawas constitute an independent cluster, separating out from all other populations (Hmar, Lusai, Mara, Lai, Hong Kong Chinese, Nicobarese, Saora, Juang, Paroja, US Caucasian, US Hispanic, US African American, West African) selected in the study . They found that the Nicobarese show a close affinity with the Mongoloid population of South-east Asia whereas the distinct genetic identity of the aboriginal populations of the Andaman Islands and other Asian and African populations deciphered by nuclear and mitochondrial DNA diversities suggest that (i) either the aboriginals of Andaman are one of the surviving descendents of settlers from an early migration out of Africa who remained in isolation in their habitat in Andaman Islands, or (ii) they are the descendents of one of the founder populations of modern humans.

Balakrishnan (1978) has studied genetic relationship between tribal and non-tribal populations of India. He observed that the two groups are distinct from one another and obtained four clusters (two each in tribal and non-tribal groups). He suggested that these might be termed Caucasoid-Aryan, Caucasoid-Dravidian, Australoid, and Mongoloid based on location and nature of the populations in each cluster. He also reported considerable homogeneity among populations of North-West India (Balakrishnan 1978). That homogeneity is increased in certain

regions by excluding the tribal populations was pointed out by Balakrishnan (1981).

Roychoudhury (1977) investigated gene diversity in Indian population. He observed that a small fraction of total gene diversity is attributed to the genetic differences between Indian populations. Further, he found that the genetic distances between Indians and three major races of mankind, Caucasoids, Mongoloids, and Negroids indicate that Indians are closer to Mongoloids than to Caucasoids or Negroids. Balakrishnan (1981) observed that the opinion of Roychoudhury (1977) that there is no justification in classifying Indian populations genetically appears to be a cry of despair. According to him, the choosing of populations by Roychoudhury does not appear to be a correct procedure. Further to Roychoudhury's observation that Indians are closer to Mongoloids than to Caucasoids, Balakrishnan reacted by saying that it was a finding, which does not tally with whatever is known about immigrations into India.

Mukherjee et al. (1999) reported 4 STR loci (CSF1P0, TPOX, TH01, VWA) among eight caste and tribal population groups of Eastern India (Agharia, Gaud, Tanti (Caste groups) of Orissa; Bagdi, Brahmin (Caste groups) and Santal (Tribe) from West Bengal; Brahmin and Chamar (Caste groups) from North India (Uttar Pradesh) and they observed genetic similarity with geographic proximity of habitat but not with socio-cultural proximity.

Majumder et al. (1999) studied 8 human-specific insertion/deletion loci among 14 ethnic populations of India (Caste Groups - Agharia, Gaud, Tanti and Tribe – Munda from Orissa – East India; Caste Groups – Bagdi, Brahmin, Mahishya and Tribes – Lodha and Santhal of West Bengal - East India; Caste Groups – Brahmin, Rajput, Chamar and Religious group – Muslim from North India - Uttar Pradesh; and Tribe – Tipperah or Tripuri from Tripura – East India). They observed that the affinities among caste populations do not correlate well with their socio-cultural affiliation. Instead, populations that occupy closer geographical habitat show, largely, closer genomic affinity, as the Upper Caste Brahmin groups sampled from distant geographical regions of Uttar Pradesh and West Bengal do not show close genomic similarity, but the Brahmins of West Bengal are genetically close to low caste populations (Mahishya and Bagdi) who reside in close geographical proximity. Similarly, the Brahmins (Caste Group) of Uttar Pradesh show close genomic affinities with two other populations – Rajputs (Caste Group) and Muslims (Religious Group) – inhabiting contiguous geographical regions, whereas Chamar (Scheduled Caste) is genetically quite distant from Brahmins, Rajputs and Muslims of Uttar Pradesh. Out of the four tribal groups three tribal groups (Santal, Lodha and Munda) are linguistically Austro-Asiatic and the fourth (Tipperah) is Tibeto-Burman and this group falls apart genetically, whereas Lodhas and Munda show close genomic affinities and form a distinct cluster which also includes another middle caste group (Gaud) who occupy overlapping geographical habitat with them. They further observed that Indian populations are genetically between Caucasoids and Mongoloids.

About higher than predicted heterozygosities coupled with a high level of genetic differentiation, they provided two explanations

1. inflow of genes into the populations under study have been high (resulting in higher than predicted heterozygosities), but different study populations have had different sources of genes (resulting in high levels of genetic differentiation), and
2. an early inflow of genes into a population followed by a rapid expansion of this population (resulting in high heterozygosities) and subsequent splits of this population into largely isolated (endogamous) populations (resulting in high levels of genetic differentiation).

Mourant (1983) observed that Caucasoids and Mongoloids show some fairly definite blood group differences, but the two 'races' resemble one another more closely than either of them does the Negroids. The differences are largely quantitative ones of gene frequencies rather than qualitative presence or absence of particular genes. However he further added that the difference between the two 'races' (Mongoloids and Caucasoids) appears rather sharp as one crosses the mountains on the northern boundary of the Indian sub-continent. The passage from Indian to Burmese is somewhat a more gradual one probably because contact here has been present for a very long time and some mixing has taken place. On the other hand, the Mongoloids north of the mountains were probably fully differentiated in the Far East before the retreat of the ice allowed them to enter Tibet.

Attempts have been made to study the genetic relationships between Indian populations and the people of neighbouring countries and it has been demonstrated that the Sinhalese in Sri Lanka are closer to the Tamils and Keralites of South India and upper castes of Bengal than they are to the populations like the Parsis and Iranis in Western India who have been shown to be genetically affiliated to the Persian and Turkoman speaking peoples in Iran, respectively (Kirk et al. 1977).

Papiha and Mastana (1999) analysed four VNTR loci in five Indian population groups (Punjabi, Northwest India; Brahmin and Gujarati, Western India; Muslim, South India; Bengali, Northeast India) and compared the results with that obtained on a Sinhalese sample from Sri Lanka. They could confirm, "that the present day gene pool of the Sinhalese of Sri Lanka seems to have originated largely via migration from the northeastern region of India" (p. 13).

STR studies (six loci) on three tribal groups of South India-Andhra Pradesh (Koya, Lambadi, and Chenchu), two caste groups of Western India (Brahmin and Patel-Gujarati) and a tribal group (Kanet) of Himachal Pradesh (North India) revealed, "that the geographically close caste populations show the greatest affinity. However, the tribal populations from the same region each show a distinct gene pool with very little affinity for each other" (Papiha and Mastana, 2000 :p. 16). They concluded. that "these results demonstrate that molecular STR systems are additional and powerful markers for genetic differentiation and evolutionary studies" (p. 17).

The genetic relationships of four Indian subcontinent populations (peoples from Punjab, Gujarat, Andhra Pradesh and Bangladesh) with their neigbouring populations—Iranians, Afghans, Sinhalese in Sri Lanka, Nepalese, Bhutanese, Malays, Bataks in northern Sumatra and Chinese studied by Roychoudhury and Nei (1985) show that the populations of the Indian sub-continent and Sinhalese in Sri Lanka are closer to Iranians and Afghans than to Mongo-loid populations and Iranians are closer to their adjacent neighbours *i.e.* Afghans and Northern Indians (Punjabi) than to their distant neighbours, *i.e.* Western and Southern Indians, the Sinhalese of Sri Lanka and Bangladesh Muslims. Similarly they found that the Southern Indians were closer to their neighbouring populations *i.e.* Western Indians and the Sinhalese and concluded that there is a general tendency of positive correlation between genetic distance and geographic distance. However, they observed that this is not true for the Bangladesh population, which is geographically closer to the Nepalese and Bhutanese, but its genetic distances from these two populations are larger than that from Iranians and Afghans. The Nepalese and Bhutanese are also genetically closer to the Malayan and Chinese than to any Indian subcontinent population.

Roychoudhury and Nei (1985) reported that the values of genetic distances indicate that Southern Indians (Andhra Hindus) and the Sinhalese are slightly closer to the Mongoloid populations than Caucasoid populations, and observed that this was due to gene exchange in the past. In this connection they noted that the Sinhalese, as well as Veddah of Sri Lanka, who are supposed to be an ancient mixture of Caucasoid and Australoid peoples (Coon 1970) have incidences of *TF*Chi* and *HB*E* alleles, which are prevalent in Southeast Asia (Kirk et al. 1962; Wickermasinghe et al. 1963) (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.9. THE DENDROGRAMS

The dendrograms were generated on the basis of biogenetical traits (genetic, dermatoglyphic, anthropometric) and Hiernaux distances for various Indian populations subdivided by

1. Zones/Geographical Regions (North, West, East, Central and South),
2. Ethnic Groups (Caste, Scheduled Caste, Scheduled Tribe, Community),
3. Linguistic Division (Austro-Asiatic, Tibeto-Chinese, Dravidian and Indo-European),
4. Geographical Proximity and Social Ranking Based on Genetic Distances,
5. Dendrograms Generated based on Dermatoglyphic, Anthropometric, and Hiernaux Distances for Indian Population Groups Subdivided by Regions and Social Ranking,
6. Dendrogram of Genetic Markers According to Different Language Families and Ethnic Groups of India,
7. Dendrogram of Dermatoglyphic Traits According to Different Language Families and Ethnic Groups of India,
8. Dendrogram of Anthropometric Traits According to Different Language Families and Ethnic Groups of India, and
9. Dendrogram of Hiernaux Distances

According to Different Language Families and Ethnic Groups of India

5.9.1. Zones/Geographical Regions (North, West, East, Central, and South)

The dendrograms generated based on genetic, dermatoglyphic, anthropometric and Hiernaux distances for various Indian populations subdivided by zones (North, West, East, Central, and South India) are represented in Figure 13. Clustering of various zones based on these distances yields the following picture.

The dendrogram based on genetic distances shows two main clusters—one consisting of North and East India and second consisting of Central and South India. In the first cluster of North and East India zones which is due to geographical proximity, racial and linguistic affinities as majority of the population groups reported from these two zones belong to the Caucasoid group and speak Indo-European languages and also since most of the studies reported are from the Himalayan populations, many of them show Mongoloid admixture in varying degree. Further, it is reported that genetic relationship of the Bengalis is closer to the North Indians (Roychoudhury 1981, 1983b). In the second cluster of Central and South India zones which are closer again due to geographical proximity and further because about 50 per cent of all the studies reported are among the scheduled tribes which may be responsible for their observed closer genetic similarity, since it has been reported that closer the geographical position between populations the closer the genetic or/and morphological similarity between them (Blake et al. 1981; Pingle 1984). Thus, the population groups of Central and South India show smaller amount of gene differentiation among them than those from North, East, and West India.

The single point clusters of West India zone may be due to the distribution of number of studies reported *i.e.* about 60 per cent are among the caste groups and communities as compared to East, Central, and South India zones. The nature of the genetic variation in the people of West India studied by Sanghvi (1978), on the basis of analysis, suggested that the bulk of the population of Maharashtra has been indigenous and has progressed over the last five millennia more under cultural interaction than on large scale immigrations and there is limited inflow of genes into this region through Brahmins and some other small groups. On the other hand, Gujarat is a more complex region mainly due to its geographical location along the western coast of India, and due to its inland connections. Gujarat has been assimilating and absorbing various population and cultural streams, which came into this region in the course of its history. Indraji (1896), Shaw (1964), and Fuchs (1977) have described this in details. These manifold connections and contacts with other populations coming into Gujarat certainly have affected the genetic composition of the present-day inhabitants of the state.

In the dendrogram based on dermatoglyphic distances, it is observed that North, Central, and South India form one main cluster while East India clearly separates out from this cluster. Again, the Central and South India zones show small distance and that this may be due to the maximum number of studies reported among scheduled tribes. North India zone is also showing small distance with these zones and it has been observed that maximum studies reported from this zone are from Western and Central Himalayan Regions, where Mongoloid admixture has been observed among the population groups of inner and middle Himalayas which show somewhat similar pattern of distribution of dermatoglyphic traits as observed among the scheduled tribe groups. Next comes West India, from where almost all the studies are among scheduled tribes. The East India zone is falling apart and it has been observed that about 55 per cent studies are from Eastern Himalayan region and as many studies are from scheduled tribes. It has been found that the distribution of patterns of various dermatoglyphic traits among population groups of East India is quite different from the rest of the zones. However, it is difficult to interpret the present dermatoglyphics results, since as also pointed out by Jantz and Hawkinson (1979), dermatoglyphics when incorporated into population studies along with other types of data, often produces results difficult to interpret. Friedlander (1971) and Neel et al. (1974) who found no agreement between dermatoglyphics variation with anthropometry and/or serology have made similar observations.

The trend observed for dermatoglyphic traits is in sharp contrast to the clustering observed in the dendrogram based on anthropometric distances. Zegura and Jamison (1978) suggested

that anthropometric variables might be more influenced by the environment as compared to dermatoglyphic traits, at least in the case of digital variables, are more affected by random evolutionary processes—notably founder effect and random genetic drift (Meier 1974). Thus, a close correspondence would not necessarily exist between anthropometric and dermatoglyphic traits, since different conditions and processes are responsible for bringing about biological changes and population differences. It is found that West, East, South and Central India together form one major cluster and separating out from them is North India. It is noted that from North India, maximum studies are available among castes and communities and Balakrishnan (1978) that considerable homogeneity has been demonstrated has reported it among populations of North-West India and it has been further pointed out by Balakrishnan (1981) that homogeneity is increased in certain regions by excluding the tribal populations (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

It has been observed that among the North Indians the predominant racial element is the Caucasoid (Aryan) as compared to rest of the

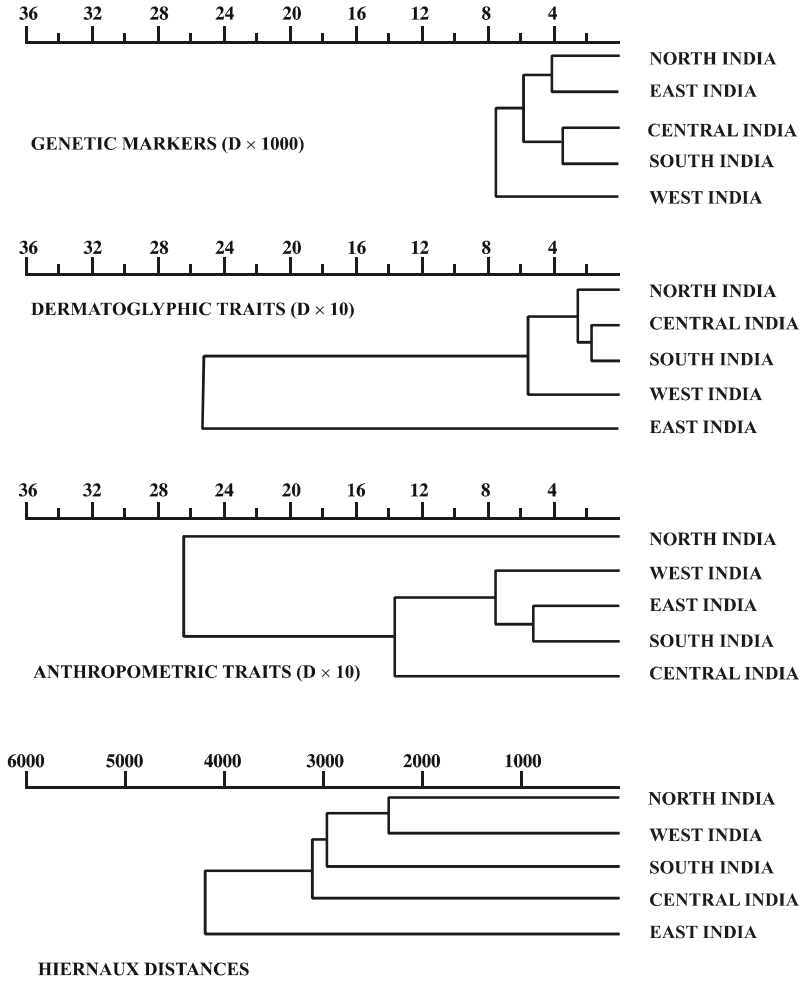

Fig. 13. Dendrograms of Genetic Markers, Dermatoglyphic Traits, Anthropometric Traits and Hiernaux Distances According to Different Zones of India

zones, whereas among the population groups of East India the racial elements present are those of Australoid (Pre-Dravidian), Caucasoid (Aryan, Dravidian) or/and Mongoloid in varying degree. Among the population groups of South India zone the racial elements present are Australoid (Pre-Dravidian), Caucasoid (Dravidian) with some admixture with Caucasoid (Aryan). According to Roychoudhury and Nei (1985) Mongoloid element may be present among some populations of South India and Ceylon (*now* Sri Lanka) due to the presence of *TF*Chi* and *HB*E* alleles which are prevalent in Southeast Asia. The differences observed for West India from where most of the ethnic groups reported are caste and community, as also observed from North India, as compared to Central India where almost all the studies belong to scheduled tribes. Balakrishnan (1978) among others concluded that tribal groups are distinct from the non-tribal groups.

It has been observed that the variations in the clustering pattern for different sets of characters may be due to variation in the heritable nature of various traits. As also observed by Nei and Roychoudhury (1972) that genetic distance between populations is not always correlated with their morphological difference. The evolution at structural gene level and that at the morphological level do not obey the same rule. They noted this when they compared the protein differences with the morphological differences for the three major races of man. From their observation that the structural genes that produce proteins are remarkably similar among the three major races of man compared with the differences in some morphological characters, they concluded that the genes controlling the morphological characters were subject to stronger natural selection than "average genes" in the process of racial differentiation (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

Lastly, in the dendrogram based on Hiernaux distances two clusters have been identified by this analysis, first corresponding to the North, West, South, and Central India, and second to East India. This shows that there is general tendency of positive correlation between genetic distance and geographic distance. As it has been found, that West Indians are closer to their neighbours—North and South Indians are closer to the Central Indians, which in turn is not true for East Indians. This may be due to some biological connections of the East Indians with the people of East Asia and South-East Asia (Flatz 1967; Flatz et al. 1972; Goedde et al. 1972; Blake and Omoto 1975, among others).

5.9.2. Ethnic Groups (Caste, Scheduled Caste, Scheduled Tribe, Community)

Figure 14 shows dendrograms for various Indian populations based on social ranking. Irrespective of various distances, *i.e.* genetic, dermatoglyphic, anthropometric and Hiernaux distances, clustering of different groups classified by social ranking is relatively clear.

It is observed that caste group is invariably clustered with the scheduled caste and the community, while the scheduled tribe is distinct from all. An explanation of this phenomenon can be found in the fact that the scheduled castes may have in them a substantial contribution of gene flow from the higher castes in past generations (Majumdar 1965). Since the communities are grouped based on religion, occupation etc. they represent a heterogeneous group. The distribution of major ethnic components may be present in the proportions similar to those observed in caste groups as the groups forming the communities in one way or the other are the offshoot of the major Indian ethnic stock (mainly the groups based on *Varna* system of Manu) at different periods of time in Indian history. The scheduled tribes, who represent mainly the Australoid (Pre-Dravidian), or Mongoloid strain, understandably are distinct from all the other groups subdivided by social ranking. Similar findings have also been reported by many other investigators (for example Balakrishnan 1978; Bhasin et al. 1986; Chakraborty et al. 1986; Char et al. 1989; Danker-Hopfe et al. 1988; Mukherjee et al. 1979, 1989; Papiha et al. 1982; Roychoudhury 1984; Saha et al. 1976; Walter et al. 1993).

5.9.3. Linguistic Division (Austro-Asiatic, Tibeto-Chinese, Dravidian, and Indo-European)

The dendrograms for different Indian populations subdivided by language families are presented in Figure 15. With the exception of the dendrogram based on anthropometric distances, all other dendrograms show almost similar clustering pattern. It is observed that Indian population groups classified by Austro-Asiatic,

Dravidian, and Indo-European linguistic categories form one major cluster, while those classified by Tibeto-Chinese category stand out from them.

Given the history of Indian populations, it is worthwhile to mention as proposed by Hutton (1981) that Austro-Asiatic speakers represent the earliest inhabitants of the Indian subcontinent and are descendants of two early migrations into South Asia from Central Asia. Dravidian speakers followed these Austro-Asiatic speakers. Though currently concentrated in Southern India south of the Godavari River, recent linguistic analyses suggest that Dravidian languages once occupied a much larger area of Western and Southern India. Glottochronology studies (Gardner 1980) indicate that these languages in South Asia date no earlier than 3000 B.C. Linguistic connections between Dravidian languages of South India, Elamite of Iran, and Uralic in Central Asia suggest that the language family was brought to South Asia from the northwest (Fairservis and Southworth 1989; McAlpin 1975, 1981; Tyler 1967).

Indo-European languages are spoken by the vast majority of South Asians and are primarily concentrated in Northern and Western India. They represent a relatively recent introduction from the West, not earlier than the latter half of the second millennium B.C. This date has been established based on archaeological, linguistico-textual, and

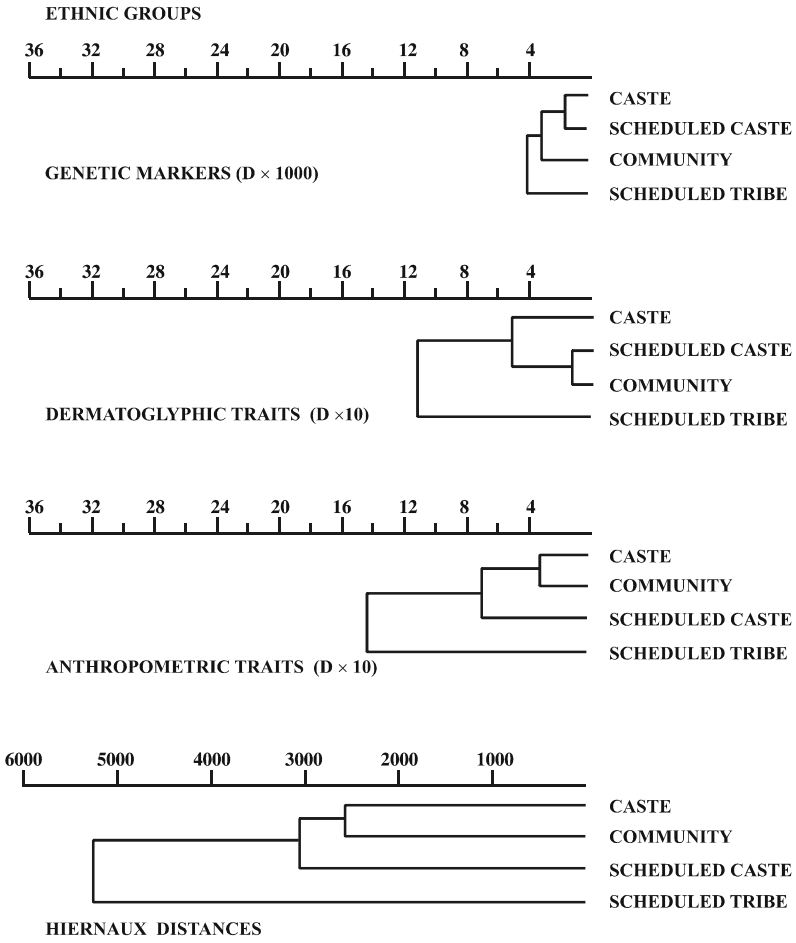

Fig. 14. Dendrograms of Genetic Markers, Dermatoglyphic Traits, Anthropometric Traits and Hiernaux Distances According to Different Ethnic Groups of India

glottochronological evidences (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

Quintana-Murci et al. (2001) reported genetic evidence for the occurrence of two major population movements, supporting a model of demic (of the people) diffusion of early farmers from South Western Iran - and the pastoral nomads from Western and Central Asia-into India with Dravidian and Indo-European-language dispersals, respectively. Farming and animal domestication are recent phenomena in human history occurring from 10,000 years before present onward. Farming arose independently in several parts of the world, including in the Middle East known as the "Fertile Crescent". Which extends from Israel through Northern Syria to Western Iran? From this region, agriculture expanded in both western and eastern directions. The spread of farming economy toward the east into the area from Iran to India started between sixth and fifth millennia B.C. Pastoral nomadism developed in the grasslands of Central Asia east of the Volga-Don region, as well as in Southeastern Europe, opening up the possibility of rapid movements of large population groups (Zvelebil 1980). The spread of these new technologies has been associated with the dispersal of Dravidian and Indo-Iranian languages in Southern Asia (Renfrew 1987; Cavalli-Sforza et al. 1988). Specifically Elanio-Dravidian languages (Ruhlen 1991), which may have originated in the Elam Province (Zagros Mountains, Southwestern Iran), and now confined to southeastern India and to some isolated groups in Pakistan and Northern India. It is hypothesized that the proto-Elamo-Dravidian language, spoken by the Elamites in Southwestern Iran, spread eastward with the movement of farmers from this region (Cavalli-Sforza et al. 1994; Renfrew 1996). A later episode, the arrival of pastoral nomads from the Central Asia steppes to the Iranian plateau, about 4000 years before present, brought with it the Indo-Iranian branch of the Indo-European language family, which eventually replaced Dravidian languages in Iran and most of Pakistan and Northern India, perhaps by an elite-dominance process (Renfrew 1987, 1996; Cavalli-Sforza et al. 1998). The incursion of these "Aryan" people coincided with the decadence of important Neolithic cultures such as the Harppan civilization, by about 3000-4000 years before present. To evaluate these linguistic and archaeological observations, and the genetic impact of these events, Quintana-Murci et al. (2001) studied 459 Y-CHROMOSOMES from several populations located in a key geographical position between the Fertile Cresent, Central Asia, the Indus Valley, and Northern India and the results were compared with data from neighbouring Pakistani populations. They have defined Y-Chromosome haplogroups (HGs) by the analysis of 11 biallelic markers. They reported that the geographical distribution, observed clines, and estimated ages of HG-9 and HG-3 chromosomes in Southwestern Asia all support a model of demic diffusion of early farmers from Southwestern Iran - and nomads from Western and Central Asia into India, bringing the spread of genes and culture (including language) to Southwestern Asia. However, they added that although alternative, explanations that are more complex are possible, the analysis of the modern male-specific gene pools in these populations suggest that major demographic events, involving migration and admixture, accompanied these historical and linguistic events. Reddy et al. (2005) based on autosomal Short Tandem Repeat (STR) loci have shown that populations of India have their own linguistic and geographic clusters while Kumar et al. (2007) based on Y-chromosome have suggested a separate genetic identity of the Austro-Asiatic groups**,** implying that these linguistic groups have their own genetic characteristics. Kumar et al. (2008) analysed Y-SNPs and STRs and suggest that the Indo-European transitional groups are genetically Mudari and have acquired the present language through the process of cultural diffusion, while in the case of Dravidian transitional groups, the spread of language seems to be due to the process of both, the demic and cultural diffusion. Trivedi et al. (2008) proposed that the present day Dravidian speaking populations of South India are the descendants of earliest Pleistocene settlers while Austro-Asiatic speakers came from South East Asia in a later migration event

The distribution of language families in the subcontinent suggests that Indian populations are the product of interaction between at least three different population substrates as also suggested by Hutton (1981).

The Tibeto-Chinese languages are spoken by the Indian populations along the northern and northeastern (Himalayan region) periphery of the subcontinent and these populations are the product of differential admixtures between northern Mongoloids and three distinct

populations, namely speakers of Austro-Asiatic, Dravidian, and Indo-European languages.

As observed, from the dendrograms, the speakers of Tibeto-Chinese languages stand separately from the speakers of rest of the languages except in the anthropometric dendrogram, where Tibeto-Chinese linguistic group shows small differences with the Indo-European linguistic group and they are closer to Austro-Asiatic and Dravidian linguistic groups. From these dendrograms, it is reasonable to believe that the current population of Indian Region is the product of differential admixture of Austro-Asiatic with Dravidian, Dravidian with Indo-Aryan and Tibeto-Chinese with Indo-European and with Dravidian and Austro-Asiatic (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

Roychoudhury et al. (2001) studied eight tribal groups representing Austro-Asiatic (Santal, Munda, Lodha), Dravidian (Muria, Kota, Kurumba and Irula) and Tibeto-Burman (Tipperah) linguistic groups by using a set of autosomal DNA markers, mtDNA restriction-site polymorphisms (RSPs) and mtDNA hyper variable segment-1(HVS-1) sequence polymor-phisms to find out correspondence between linguistic and genomic affinities among them. They observed that the Austro-Asiatic tribal groups (Lodha and Santal) form one cluster, the Tibeto-Burman speaking Tipperah forms a separate cluster, and the Dravidian tribal groups (Irula, Kurumba, Kota, and Muria) although not forming a tight cluster, are positioned in between the Austro-Asiatic and Tibeto-Burman clusters. They further observed

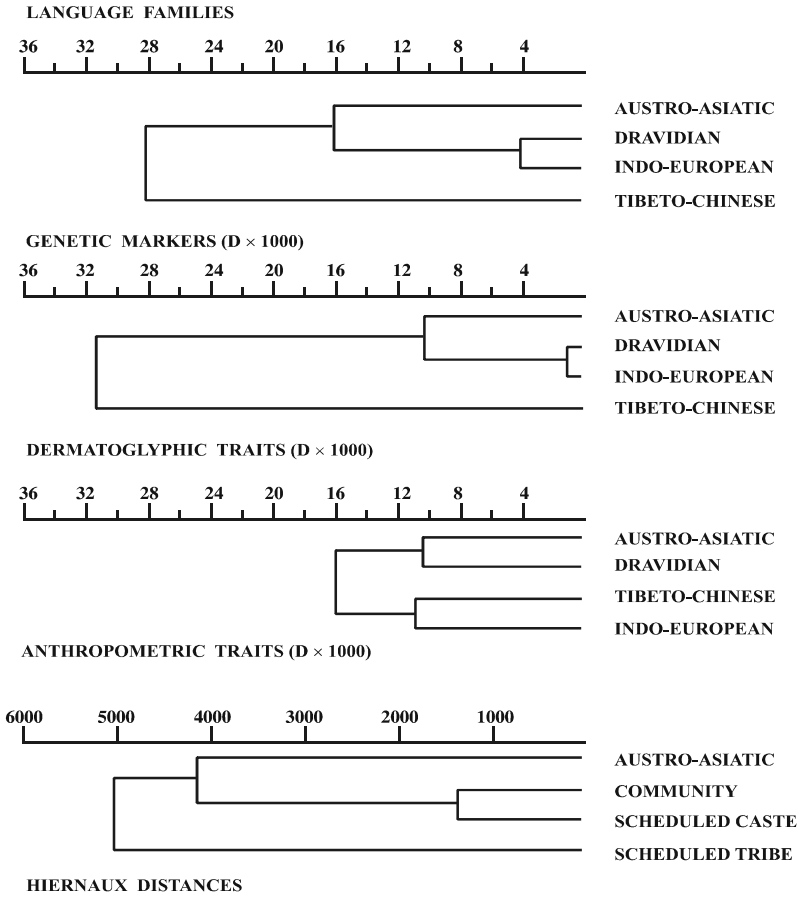

Fig. 15. Dendrograms of Genetic Markers, Dermatoglyphic Traits, Anthropometric Traits and Hiernaux Distances According to Different Language Families of India

that the different language groups in India represent distinct founding groups, and that the Austro-Asiatic speakers are likely to have been the most ancient inhabitants of India (Majumdar et al. 1999; Basu et al. 2000, 2001).

5.9.4. Geographical Proximity and Social Ranking Based on Genetic Distances

Clustering of the population groups of India subdivided by geographical proximity and social ranking based on genetic distances is clearly seen in the dendrogram presented in Figure 16.

In aggregate, one observes three main clusters: first consisting of the North and the West zones, the second consisting of the East zone and the third consisting of the North and the South zones. In the first cluster, it is also observed that the populations classified according to their social ranking cluster together in a way that is anticipated based on their traditional ranking. This affiliation between populations is also equally true for the other two clusters.

First cluster reveals a close relationship between caste, scheduled caste, and community of North, West, and South India. Since most of the scheduled caste groups and communities in India are heterogeneous and represent Caucasoid (Dravidian and/or Aryan) components (except for those in Eastern India) in different proportions, their closeness with the higher groups especially caste groups, is not unwarranted.

The scheduled caste groups of West India clustering with the scheduled tribes once again stress the fact that the chanelisation of gene flow between the two cannot be overlooked.

The salient feature of the dendrogram is that all the population groups of Eastern India form a single cluster, irrespective of their division by social ranking. This is reasonably so, because Eastern India is represented by people with Mongoloid ethnic strain from the Northeastern region, non-tribals of Caucasoid origin from the Northwestern region and tribals from the Southern and Southwestern regions. Therefore, the clustering of the scheduled tribes of South India with those of Eastern India is not incidental. The historical evidence indicates a very strong, viable, and close contact between the people of the Eastern and South India. The spread of Buddhism made deep inroads into the life style of the people of South India even before the beginning of Christian era. Further, it has been observed that the scheduled tribes of East India

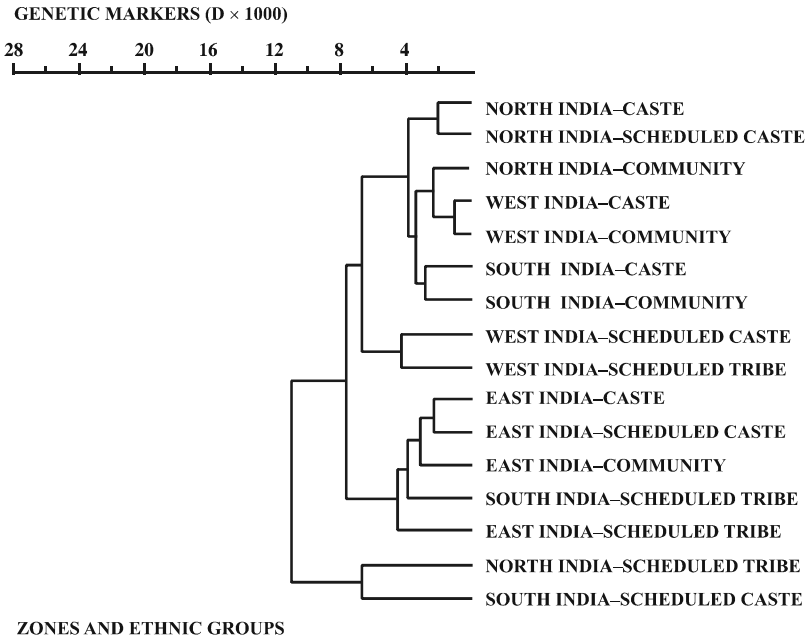

Fig. 16. Dendrogram of Genetic Markers According to Different Zones and Ethnic Groups of India

are having predominantly Australoid (Pre-Dravidian) racial element and admixture with Caucasoids (Dravidians) and Mongoloids in varying degrees; South Indian tribes are also predominantly Australoid (Pre-Dravidian) and having admixture with Caucasoids (Dravidians).

Lastly, the Scheduled tribes of North India clustering with the Scheduled caste of South India may be attributed to the fact that scheduled tribes of the North may still be harbouring the remanent of Caucasoid (Dravidian) strain in them through their early contact in North India (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.9.5. Dendrograms Generated based on Dermatoglyphic, Anthropometric and Hiernaux Distances for Indian Population Groups Subdivided by Regions and Social Ranking

The dendrograms generated based on dermatoglyphic, anthropometric and Hiernaux distances for Indian population groups subdivided by regions and social ranking are presented in Figures 17, 18 and 19, respectively.

From the dendrogram of dermatoglyphics (Fig. 17), in general, it is rather difficult to evaluate the position of the ethnic groups according to their social ranks and their distribution into various zones. Rothhammer et al. (1977) reported that even though no significant correlation existed between genetic and dermatoglyphic distances at the two lower levels it was nevertheless found at the tribal and racial levels. From these results, they concluded that "polygenic (dermatoglyphic) traits evolve at a slower rate than monogenic systems, and are thus less susceptible to evolutionary forces, particularly genetic drift". However, in general, it has been observed that the ethnic groups from North India show small distances while scheduled caste of North India are nearer to the scheduled caste of South India. This may be due to contacts with Caucasoid (Dravidians) who came from North-West and moved Southward. With the arrival of the Aryans, and between caste and scheduled caste of East

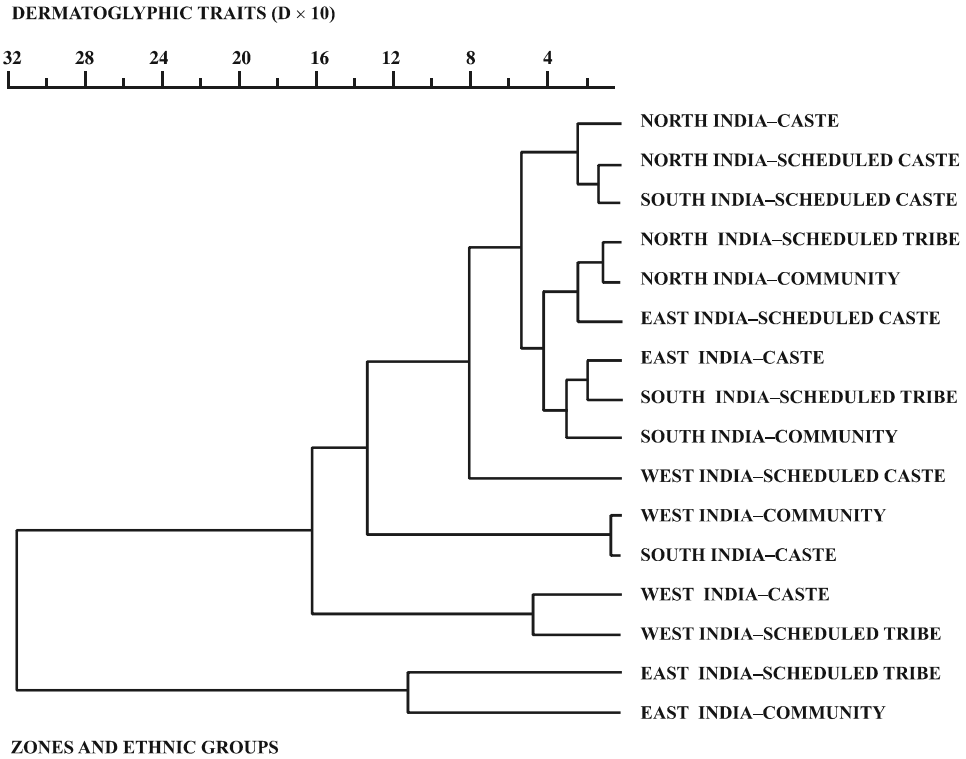

Fig. 17. Dendrogram of Dermatoglyphic Traits According to Different Zones and Ethnic Groups of India

India it has been observed that the non-tribal population of East India, who speak Indo-European languages are closer to the people of Northwestern India (also speakers of Indo-European languages). In turn, it has also been observed that caste groups of East India show small differences with South Indian community and scheduled tribe, which may be due to variable number of studies reported in the literature from these divisions. Another cluster shows close relationships between different ethnic groups of West India with South India (Caste and Community). Based on odontometric analysis also, Hemphill et al. (1992) observed that Maharashtrians bear affinities with South Indian groups. Therefore, the closeness of the West Indians and the South Indians is not surprising as noted by Malhotra (1984) and Malhotra et al. (1978) and the unique position of Maharashtra as the boundary between Indo-European and Dravidian speaking regions of India results in wide variations in marital patterns and village endogamy. It has been suggested by Hemphill et al. (1992) that this may simply reflect Maharashtra's position as the 'gate way' between Dravidian and Indo-European India. Lastly, the scheduled tribe and community groups of India fall closer to each other (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

From the anthropometric and Hiernaux distances (Figs. 18 and 19) it has been observed that except for North India, where all the four ethnic groups fall nearer to each other in social rank—caste, community or/and scheduled caste and scheduled tribe while for the rest of the zones it is generally observed that caste, scheduled caste and community groups are closer to each other, whereas scheduled tribe groups are nearer to one another. The ethnic groups of West India are closer to South India as observed before and scheduled tribes of East India and South India show small differences as observed in dendrogram of genetic markers.

Thus, overall the various ethnic groups of North India are showing less differences, different ethnic groups of West India and South India are falling nearer to each other and scheduled tribes of East India and South India

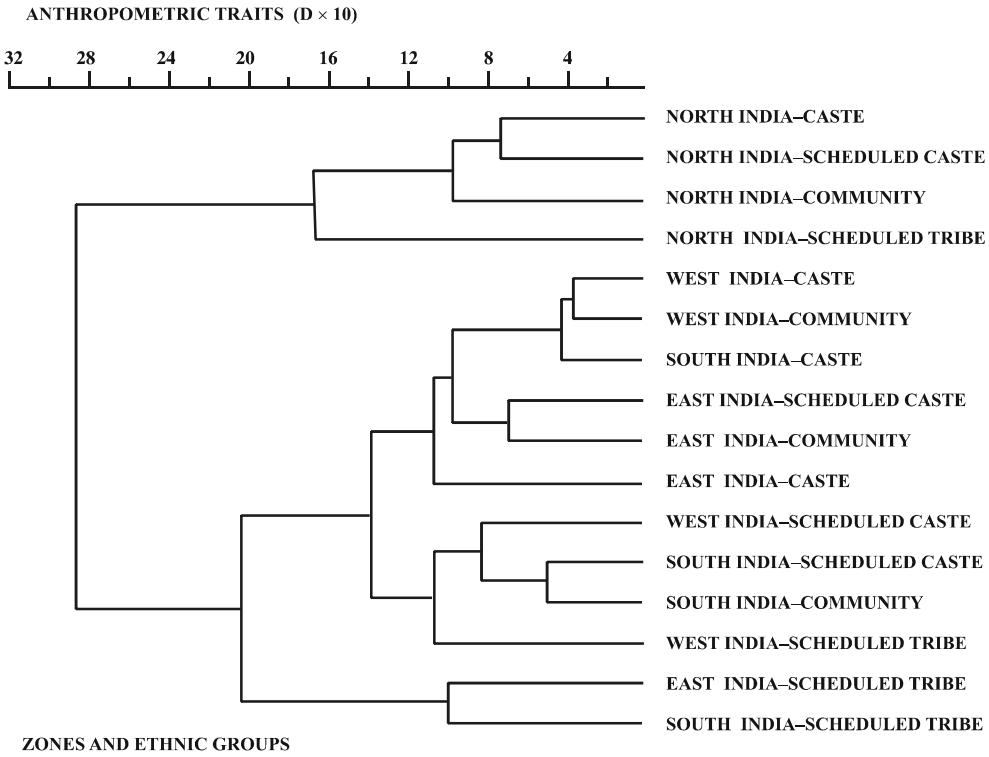

Fig. 18. Dendrogram of Anthropometric Traits According to Different Zones and Ethnic Groups of India

are showing small distances and, in general, scheduled tribes are falling apart from the other ethnic groups as observed from the dendrograms of genetic markers (Fig. 16), anthropometric traits (Fig. 18) and Hiernaux distances (Fig. 19).

5.9.6. Dendrogram of Genetic Markers According to Different Language Families and Ethnic Groups of India

Figure 20 shows the dendrogram constituted based on genetic distance for Indian population groups classified by language families and social ranking.

In aggregate, two main clusters are observed-one consisting of Dravidian and Indo-European populations with different social rankings, and a second consisting of Tibeto-Chinese population groups with scheduled tribe associating with community, Austro-Asiatic scheduled tribes stand distinct from all.

Given the history of Indian populations, it is reasonable to believe that considerable genetic admixture has taken place. It can be inferred that the original nucleus of Indian populations was probably Dravidian, which may have been refined to some extent by infusion of Aryan blood. Further, the associations of caste, community, scheduled caste, and scheduled tribe as observed in the present study under each linguistic group conform to the overall social ranking of the traditional groups. Thus, the clustering of Dravidian and Indo-European linguistic groups is in qualitative agreement with the ethnohistory of Indian populations. Similarly, clustering of Tibeto-Chinese scheduled tribes and community is in harmony with their ethnic background being preponderantly of a

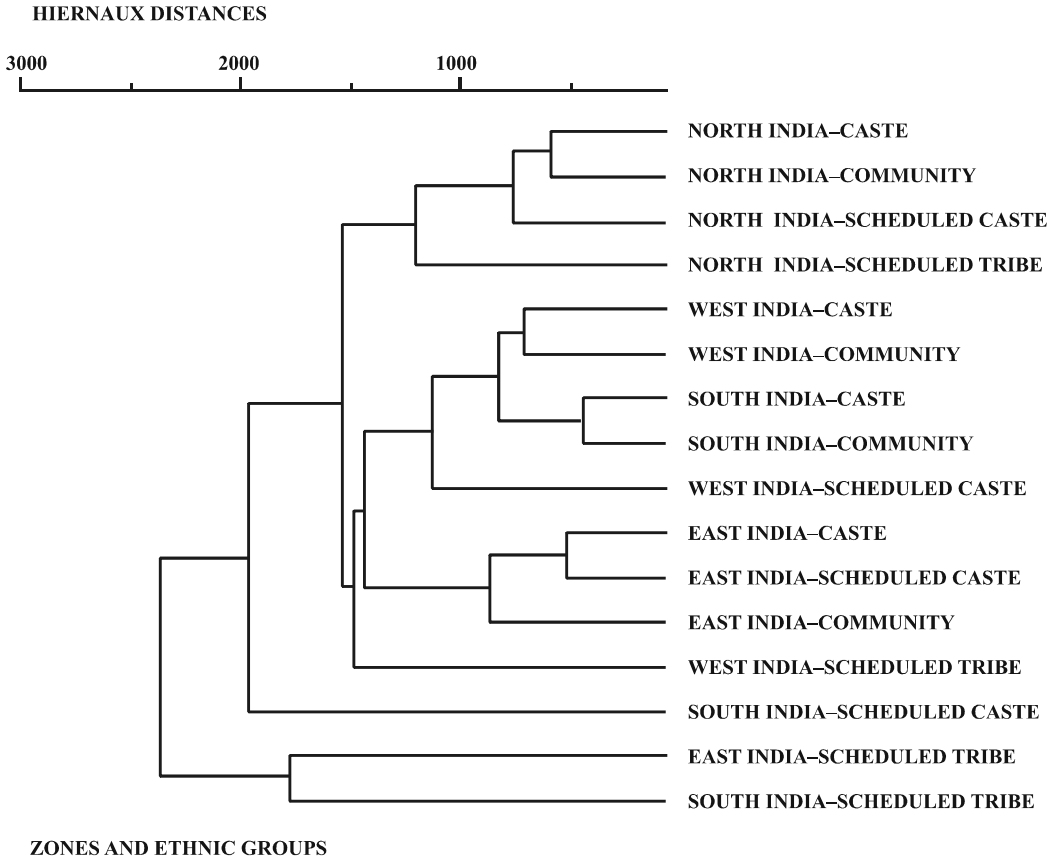

Fig. 19. Dendrogram of Hiernaux Distances According to Different Zones and Ethnic Groups of India

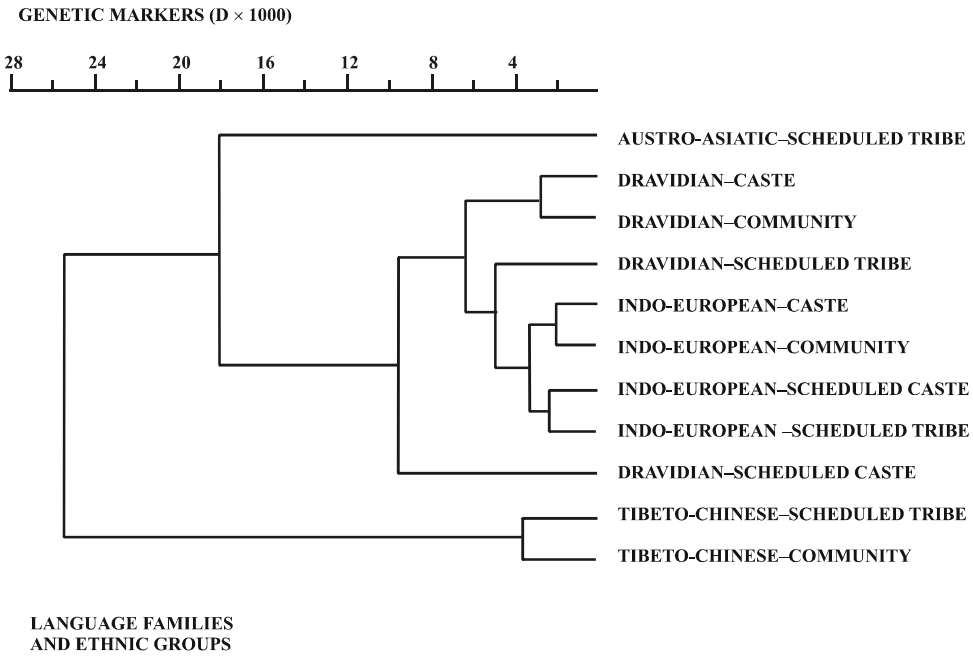

Fig. 20. Dendrogram of Genetic Markers According to Different Language Families and Ethnic Groups of India

Mongoloid gene pool (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.9.7. Dendrogram of Dermatoglyphic Traits According to Different Language Families and Ethnic Groups of India

The dendrogram obtained based on dermatoglyphic distance for population groups classified by language families and social ranking is presented in Figure 21.

Here, too, it is observed that the distinct clusters conform to the one observed in the dendrogram based on genetic distances. The results are almost similar and clustering of Dravidian speaking people with those of Indo-European speaking people further substantiates the ethnohistory of Indian population that Dravidian has received certain amount of Aryan blood in their veins while Tibeto-Chinese who show Mongoloid affinities are comparatively more distinct. Clustering of groups by their social ranking in a broad sense, confirm traditional social groupings (For details see Bhasin et al. 1994; Bhasin and Walter 2001).

5.9.8. Dendrogram of Anthropometric Traits According to Different Language Families and Ethnic Groups of India

The dendrogram generated based on anthropometric traits for Indian populations classified by language families and social ranking is presented in Figure 22. It has been observed that Tibeto-Chinese join the main cluster, which consists of Indo-European, and Dravidian speaking people and Austro-Asiatic (Scheduled Tribe) make a cluster with Dravidian (Scheduled Tribe) and Indo-European (Scheduled Tribe). This is understandable, since as reported earlier the Tibeto-Chinese speakers are dominating Eastern Himalayan region in Eastern India and this zone is the meeting ground of three ethnic groups: people with Mongoloid elements from the Northeastern region, non-tribals of Caucasoid origin from Northwestern region and tribals from the Southern and Southwestern regions. Whereas Austro-Asiatic (Scheduled Tribe) make a cluster with Dravidian (Scheduled Tribe) and Indo-European (Scheduled Tribe) and these are showing small differences with the Tibeto-

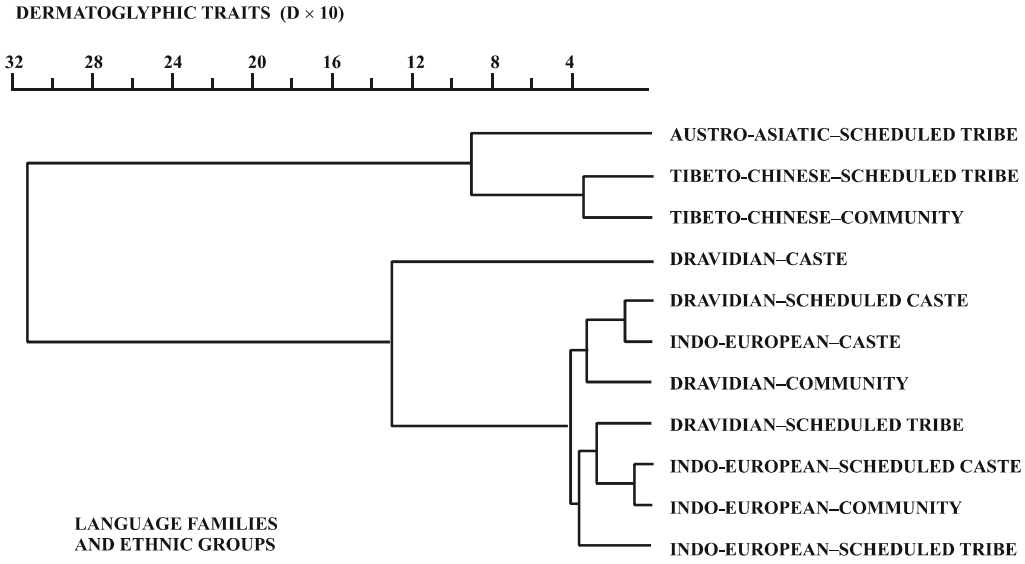

Fig. 21. Dendrogram of Dermatoglyphic Traits According to Different Language Families and Ethnic Groups of India

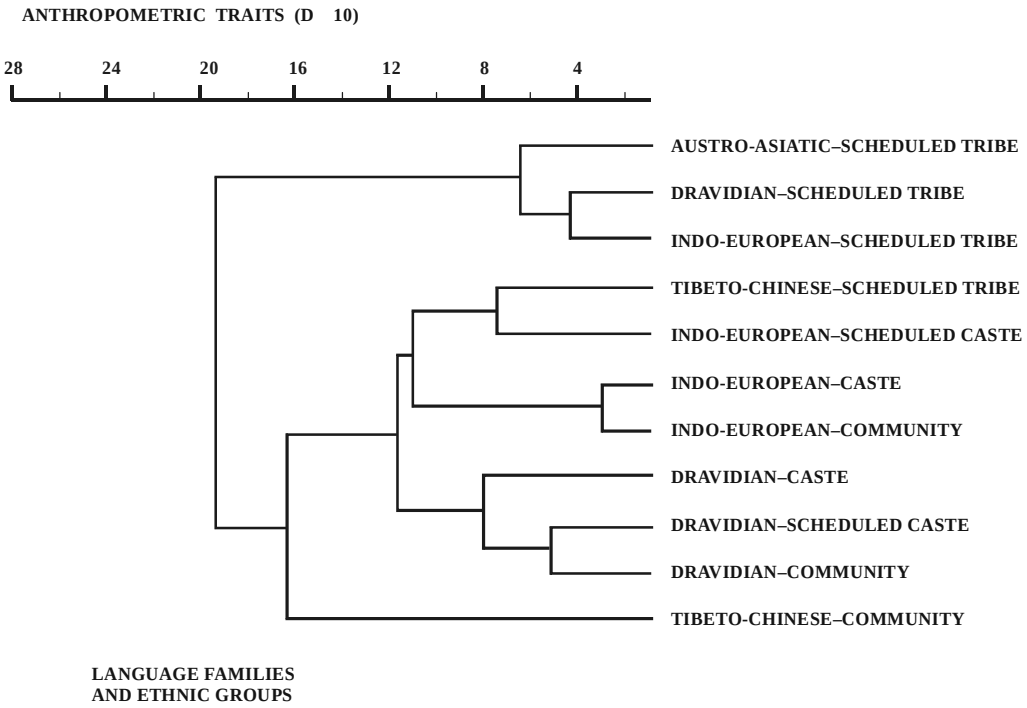

Fig. 22. Dendrogram of Anthropometric Traits According to Different Language Families and Ethnic Groups of India

Chinese (Scheduled Tribe) speakers. It has already been established that Austro-Asiatic speaking tribals are predominating in Bihar, Orissa, as well as also in Central India, Assam and Nicobar Islands, and admixture has taken place among them and other linguistic groups—Dravidian, Indo-European and Tibeto-Chinese, as well as between these groups in varying degrees. The Indo-European and Dravidian speakers are showing small distances and it has been suggested that the Dravidians who entered Indian region early and moved southward with the arrival of Aryans have had admixture with them.

5.9.9. Dendrogram of Hiernaux Distances According to Different Language Families and Ethnic Groups of India

A similar trend is observed from the clustering of the population groups in the dendrogram (Fig. 23) generated based on Hiernaux distances. Nevertheless, it can be said that clustering observed based on various biogenetics distances is more justified for the Indian population classified by language families and social ranking as it goes well with their ethnohistory.

The above discussion was based on the dendrograms generated from various biogenetic (genetic, dermatoglyphics and anthropometric) traits and different Indian populations subdivided by geographical regions, social status and linguistic division that have been considered separately as well as in combination *viz.*, geographical regions/zones with social ranks and social ranks with linguistic groups.

1. From the dendrograms derived from various geographical regions/zones (North, West, East, Central and South India) with morphogenetic traits, it has been observed that there is a general tendency of correlation between morphogenetic distance with geographic distance.
2. The dendrograms based on social ranking and morphological traits show that the scheduled tribes are distant from all the other groups and

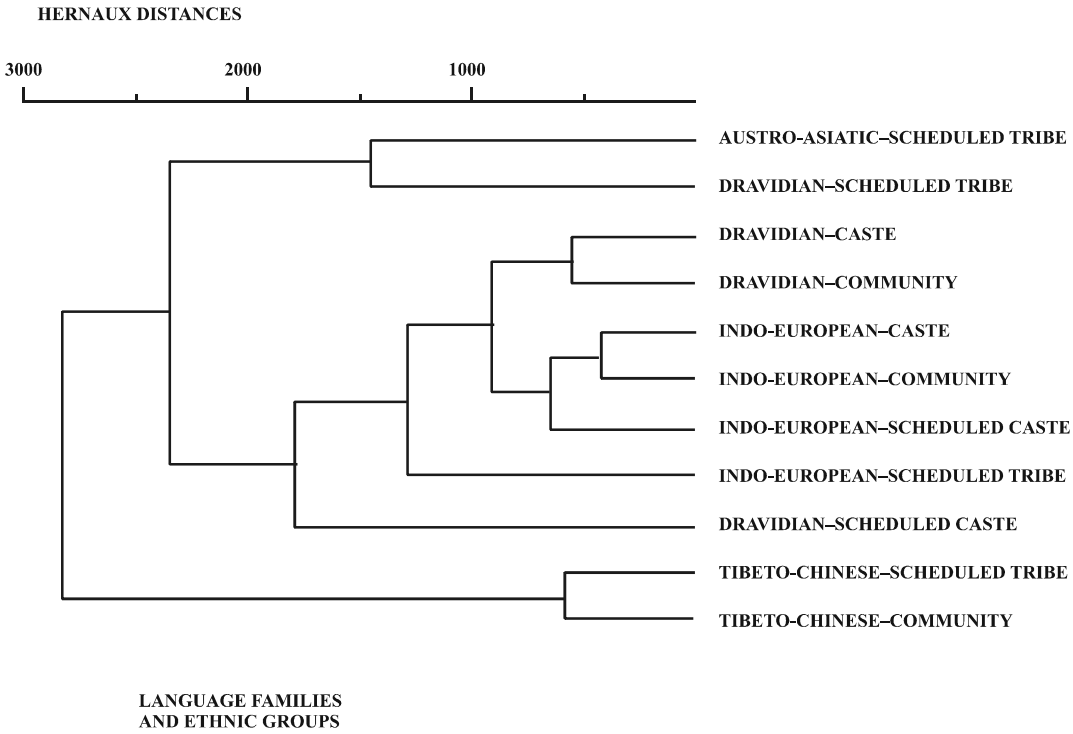

Fig. 23. Dendrogram of Hiernaux Distances According to Different Language Families and Ethnic Groups of India

caste group is invariably clustered with the scheduled caste and the community, which shows that scheduled caste population may have in them a substantial trace of gene flow from upper castes or/and from communities, who are grouped on the basis of religion, occupation, and region, etc.

Considering now India as a whole, the biological trait distribution is seen to follow a simpler pattern than that might have been expected from the complex history of its people. The scheduled tribe groups stand out as a uniform and unique population, showing less similarity with the neighbouring peoples and certainly much less when compared to the caste groups of India.

3. From the dendrograms based on different linguistic groups, it has been observed that Austro-Asiatic, Dravidian, and Indo-European linguistic categories form one cluster and Tibeto-Chinese category stand out separately.

It may be concluded that the current population of India is the product of differential admixture between three distinct population entities *viz.*, Austro-Asiatic (Australoid or Pre-Dravidian), Dravidian and Indo-European (Caucasoid) linguistic groups, whereas the Tibeto-Chinese linguistic group along the Northeastern and Northern peripheries of the subcontinent is the product of admixture between Mongoloids and Australoid and Caucasoid populations in varying degrees (For details see Bhasin et al. 1994; Bhasin and Walter 2001)

6. END NOTE

It may be concluded that there are differences in the occurrence of the frequencies of various biogenetical traits (genetic markers of blood, other genetic markers like colour blindness and tasting ability, different dermatoglyphic and somatometric traits) among the population groups inhabiting different geographical zones of India *viz.* North, West, East, Central, South and Islands. From the Himalayan region, some differences in the frequencies and mean values of distribution of various genetic markers and morphological traits have been observed among population groups of Western and Eastern Himalayan regions. Since sufficient studies are not available on the population groups of Central Himalayan region, it has not been possible to observe a differential trend regarding the occurrence of various traits, but it has been observed that the population groups in this area show more similarities with those of Western than Eastern Himalayan region.

About the four groups *i.e.*, caste, scheduled caste, scheduled tribe, and community from India, various zones of India and Himalayan regions, conspicuous differences are observed among the scheduled tribes as compared to castes, scheduled castes, and communities. It has been further observed that the range in the occurrence of the frequencies of the various genetic markers and morphological traits among scheduled tribes is sufficiently wide as compared to other groups. This may be because the scheduled tribes are small in numbers.

Most present day tribal populations (except Mongoloids) are inhabiting the "Area of Isolation or cul-de-sac" which is defined by the Aravali, the Central Indian highlands and forest comprising of Vindhyan complex, from the west coast to the Bengal Delta, the western belt from Aravali, Sahyadris and the long chain of western ghats up to the southern tip of the peninsula and in the east down from eastern end of the Vindhyas through Nallamalai hills and the chain of eastern ghats culminating in the Nilgiris. The "Areas of Isolation" are connected with the "Areas of Attraction or Nuclear Region" and "Areas of Relative Isolation" as defined by Subbarao (1958) by famous *Z* pattern line of communication for the migration of people and culture dermonstrated by Richards (1933) based on archaeology and historical geography. It is along this line of communication that the present day tribal populations may first have receded to their present habitat. From the size of these populations, it appears that only segments of larger populations receded into the "Areas of Isolation" and not the entire populations (Negi 1976a).

v. Fürer-Haimendorf (1948) stated that it is a phenomenon peculiar to India that throughout the ages great civilizations have arisen without obliterating or absorbing all that has gone before; the older and more static cultures that gave way not by disintegrating but by seeking refuse in remote areas, uncongenial to civilisation based as it was on advanced agricultural economy. There can be no doubt that the so-called aboriginals inhabiting such refuge areas represent comparatively old and primitive life.

The data available on scheduled castes are too few to observe any specific trend. However, reports available on castes and communities

indicate a similar trend of the allele/haplotype frequencies and mean values distribution. It may be because the data on the various population groups have not been classified into specific groups and instead have been lumped and placed in the category of community which distort the peculiarity of the population. It is therefore desirable that some more data should be analysed from the different population groups from various zones to make the evaluation for genetic markers and morphological traits more clear.

It has been observed that the distributions of various allele/haplotype frequencies and mean values in the different language families *i.e.* Austro-Asiatic, Tibeto-Chinese, Dravidian and Indo-European show almost similar patterns in the various zones of India, regions of Himalayas and ethnic groups in the zones and regions.

The correlations of frequencies of genetic markers and mean values of morphological trait with various climatic factors and altitude by different ethnic groups although showing significant differences, in general are not high.

Nevertheless, it can be concluded that the variations in the frequencies of genetic markers and mean values of morphological traits distribution in the Himalayan region may be due to contacts between the various population groups of Western and Central Himalayas with population groups of Central Asia, and that of Eastern Himalayas with the Northern Mongoloid populations. However, isolation effects due to lack of communications have to be considered in the Himalayan region.

In West India, the distribution pattern in frequencies and mean values may have had an impact of the sea coast, which might have drawn strangers both as conquerors and refugees from other geographic areas, particularly from the Mediterranean region and Middle East, and who might have had contacts with the local people. In Central India admixture with the population groups of West India can be assumed. In South India, a different pattern of allele/haplotype frequencies and mean values is generally observed among the tribal population groups, for which one of the main causes might be seen in small population sizes. Inbreeding is prevalent among certain communities like Muslims, Parsis etc. and in most of the different population groups particularly from South India, which might have also resulted in the marked variation in distribution of frequencies and mean values of different genetic markers and morphological traits.

The present study identifies various sources (ecological, social, and linguistic criteria etc.) as influencing patterns of biological relationships among contemporary Indians. This stands in dramatic contrast to several recent studies based upon anthropometrics (Majumdar et al. 1990), ABO blood type frequencies (Majumdar and Roy 1982) and craniometric measurements (Kennedy et al. 1984) which suggest that either no large scale biologically meaningful ethnic groups exist in India or that South Asians represent a basically homogeneous population which varies along both temporal and geographic lines.

The variations observed for the various morphogenetic traits in the distribution of allele/haplotype frequencies and mean values among the Indian population are due to racial elements present among them in varying degree due to migrations and admixture from time to time.

The 'Veddoids' (Proto-Australoids/Australoids) are considered to have lived in India for a long time and they are supposed to be the ones who originally went to Australia and the differences observed in the gene frequencies between these two groups (Indian and Australian) could be due to their numbers now being small. They must have undergone considerable genetic drift. It may be noted that they in their turn do not resemble Veddas of Sri Lanka either physically or in their blood groups. The latter resemble the aboriginal 'Senoi of Malaya' as the Veddas are the only population outside Southeast Asia known to possess haemoglobin E.

The Andaman Islanders who are considered to have Negrito racial strain bear a certain physical resemblance to pygmies of Central Africa and it has for long been argued as to whether or not there is any genetic relationship between them. The Andaman Islanders, who are probably less mixed, having certain unique frequencies like absence of *RH*cDe* which might have been lost due to genetic drift and presence of high *RH*CDe* and *RH*cDE* which suggests a relationship to the Melanesians to their east rather than to Africans to their west.

There are indications that people of the Caucasoid human type and perhaps more specifically something near that special type which is at present associated with the Mediterranean area entered India from the north-west (*i.e.* the Near East of Europeans) and came into contact with the hunting and gathering Australoid peoples, who were the ancestors of the many present day tribal populations. These

people who came from north-west belonged to the Dravidian language family. This based on evidence of persistence to the present time of a Dravidian language spoken by the Brahmi of Baluchistan, since at present the Dravidian languages are confined to the southern states of India. The Dravidian-speaking peoples of south of India who are considered to be one of the earliest differentiated branches of the Caucasoid 'race' show resemblance to the peoples of Southwest Asia and the Mediterranean region.

Next came the Aryans who are identified with Aryan or Indo-European group of languages and are best known from their great ancient scripture, the *Rig Veda* transmitted orally for over 2500 years and not reduced to writing until the fourteenth century A.D. The North Indians fall broadly in the category of Aryans. There have been, of course, many subsequent invasions but the numbers of invaders who were added to the general population have been relatively small.

Differences between the Mongoloid and Caucasoid appear to be sharp on the northern boundary of the Indian subcontinent where Mongoloid from Southeast Asia and East Asia mixed with the Caucasoids and/or Australoids.

In India, the differences in various biological traits due to diversity of ethnic composition of the Indian population, consisting as it does of elements of autochthonous, Caucasoid, and Mongoloid origin, are well documented. The Indian populations have interbred among themselves in varying degrees to give mixtures, which are difficult to unravel. Some of the processes of change—mutation, genetic drift, and linkage equilibrium are almost totally uninfluenced by environment but one of these processes—natural selection—is so dependent. To some extent, the pattern of frequencies distribution of various biological traits is to be regarded as the result of natural selection related to the harmful effects of particular climatic and other local features of the environment. However, one still cannot know at all precisely which environmental features are involved, but these almost certainly express themselves by tending to cause particular diseases, to which people of certain genetic marker group are more susceptible than another.

In addition to mutation, genetic drift, and natural selection, severe epidemics, floods and famine have at various times over the centuries reduced the populations of different zones, and of India as a whole at various times over the centuries, to levels where great accidental fluctuations of gene frequencies were possible. Such fluctuations seem indeed to have occurred, as the frequencies observed at present bear less relationship to those of the original migrants and/or invaders.

It is needless to say that there is still a need for assimilation of the new results, and for further studies on similar lines. There are still important gaps in our knowledge of the frequencies of genetic markers of key populations (for details *see* Bhasin et al. 1992). Gap-filling tests on selected populations would make it possible to use the existing observations much more effici-ently in working out the relationships between the various peoples. As observed above, the available results relating biology, linguistic and social structure variables have given a good and clarified picture of the Indian population.

The variations observed for the various morphogenetic traits in the distribution of allele/haplotype frequencies and mean values among the Indian population are due to racial elements present among them in varying degrees, migrations and admixture from time to time and other factors of evolutionary changes like mating patterns, genetic drift, mutation and selection under different environments. Therefore, it may be concluded that to understand the population variation of the heterogeneous Indian society, there is a need for a holistic approach-involving environment, socio-cultural integrations, and biological traits.

However, such a holistic approach should not only consider the so far less investigated serum protein and red cell enzyme polymorphisms, but should analyze especially the regional and ethnic distribution of the numerous nuclear and mitochondrial DNA polymorphisms, which turned out to be of highest importance to population genetics. This could be shown e.g. recently by Reddy (2008), who studied the genomic diversity mainly in and among different populations of India.

It is hoped that in future the Molecular Biologists may follow this. The motto should not be either … or but as well as! The Molecular Biologist should consider more than now the results of the numerous population studies concerning the morphological traits, so-called classical genetic markers of the human blood. The combination of the results of all the types of research would enable us to understand the

effectiveness of the manifold processes, which resulted in the biological variability of the modern man.

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