A STUDY OF DERMATOGLYPHICS, BLOOD GROUPS AND OTHER GENETIC TRAITS OF THE KOCHS OF MEGHALAYA

By

MURALI KOTAL
DEPARTMENT OF ANTHROPOLOGY

THESIS SUBMITTED
TO
THE NORTH-EASTERN HILL UNIVERSITY
FOR PARTIAL FULFILLMENT OF THE DEGREE OF DOCTOR OF PHILOSOPHY
IN
ANTHROPOLOGY

NORTH-EASTERN HILL UNIVERSITY
SHILLONG - 793 014
MARCH, 2002

CHAPTER I

INTRODUCTION

Traditionally, physical anthropology is primarily concerned with the taxonomic classification of human population at both micro and macro levels with a view to understanding the processes of human evolution in space and time. As such, it deals with the phylogenetic position of human populations in terms of their differences and similarities mainly in respect of morphological or anthropometric characters. Indeed, "ascertaining this history has always been and remains one of the main goals of physical anthropology" (Harrison, 1977). However, it has been realised that most of the anthropometric or morphological characters like height, weight, skin colour, etc., are to great extent influenced by environmental conditions in which the population lives. Thus, attempt to establish the evolutionary phylogenetic affinity of human populations in respect of continuous traits like anthropometric characters may not become so meaningful because of the complexity in their genetic basis. Accordingly, it has been felt necessary to use discrete characters or genetic markers like blood groups, red cell enzymes, serum proteins, etc., for understanding the evolutionary processes of human populations. With this end in view, physical anthropologists have been largely involved in the study of the genetics of human populations since the middle of the present century. In fact, population genetics is now considered the backbone of physical anthropology (Kirk, 1978).

As the term suggests itself, population genetics refers to the genetics of Mendelian population, or a breeding community whose members share in a common gene pool (Dobzhansky, 1951). According to Li (1955), "Population genetics is concerned with the statistical consequences of Mendelism in a group of families, or individuals, it studies the hereditary phenomenon on population level". While doing population genetic studies, physical anthropologist generally look for small endogamous and/or isolated populations since they are likely to represent the Mendelian populations. According to Keith (1950) these population groups are the "evolutionary units" which are very useful for studying all micro-evolutionary processes. Moreover, social or cultural structures are also more integrated in small isolated populations as compared with urban or advanced societies. Thus the WHO scientific Group (1964, 1968) has recommended that there is an urgent need to carry out population genetic studies among these isolated populations since many of them are undergoing cultural disintegration due to increasing contact with more sophisticated peoples.

It is well acknowledged that each population consists of individuals with a different genotype, or genetic constitution. The number of individuals with a particular genetic trait that is controlled by a pair of alleles at a given locus in a chromosome can be counted and thereby the frequency of such a gene can be calculated in a population. The 'array of gene frequencies over all loci' in a population is known as *gene pool*, or genetic constitution. However, understanding of the genetic constitution/composition of a population depends largely on our understanding of the genetic structure of such a population. The genetic structure of a population is concerned with the mechanism in which genes are 'distributed and combined' within a population (Roberts, 1993). The distribution and combination of genes within populations are due to a number of factors or evolutionary forces like mutation, selection, genetic drift, effective population size, migration, fusion-fission process, inbreeding, mating patterns, etc. As such these evolutionary forces are to great extent responsible for the changes in the genetic composition of the population. In fact, population genetics is concerned not only with the counting of genes in a given population, but also with these evolutionary forces. Thus, according to Vogel and Motulsky (1986), "Population genetics deals with the behaviour of genes in large groups and is concerned with the evolutionary forces...." The observable variation or similarities in gene frequencies in human populations 'are the product of the forces of evolution, acting not one at a time but simultaneously' (Crawford, 1973).

If evolution is a 'process of change or movement', a change in the genetic composition of a population is nothing but an evolution. Thus, human evolution may be considered a change in the allele frequencies of human population from one generation to another. If the gene frequencies in a population remain unchanged from generation to generation, such a population is said to be in genetic equilibrium. According to Hardy-Weinberg law, the genetic equilibrium is supposed to take place when the population is large and the mating is at random along with the absence of other evolutionary forces like selection, mutation, drift, migration, etc. For example, in the case of natural selection, it can be assumed that the individuals of the different genotypes have an equal chance of reproduction in such a population of genetic equilibrium. Thus, it is clear that no population, or genetic locus, in the world confirms to the assumptions of this law, but it is astonishing how close most gene frequencies are to those expected in the Hardy-Weinberg equilibrium (Livingstone, 1973). Under these circumstances, it may be said that the Hardy-Weinberg equilibrium depicts a static form of evolution, i.e. "in revealing the conditions under which evolutionary change cannot occur, it brings to light the possible forces that cause a change in the genetic composition of a population" (Volpe, 1985). Therefore, understanding of the Hardy-Weinberg law is a prerequisite for making out the evolutionary forces that are operating in human populations.

The operation of various evolutionary forces mentioned above is undoubtedly responsible for the changes in the genetic composition of a population. In its simplest way of interpretation, whether the change is due to mutation or any other evolutionary forces, the fact is that the genes transmitted by individuals who are better adapted to a particular environment would be increasing from generation to generation. The degree of an individual's ability to adapt to his or her environment can be measured in terms of reproductive performances/differential fertility and mortality. As a matter of fact, individuals of different genetic characters (genotypes) have differential reproductive capacities, thereby contributing their genes differently to individuals of the next generation. Consequently, genes that enhance the ability of an individual to survive and reproduce in his or her environment tend to increase in frequency in a population from one generation to another. For instance, suppose the individuals with too short or tall stature are not favoured in a given environment and thereby they are always eliminated by the natural selection. As a result, their number will be reduced in a population. Similarly, "the relative frequencies of homozygotes and heterozygotes for certain growth genes and for genes located in the same chromosomes would be altered; some genetic factors which were previously eliminated because of their harmfulness might become neutral or even favourable; after some generations the genetic constitution of the whole species may be changed" (Dobzhansky, 1951). "This is the dynamic process that has occurred in the past, occurs today, and will continue to occur as long as inheritable variation and differing reproductive abilities exist. Under these circumstances, the genetic composition of a population can never remain constant" (Volpe, 1985).

Genetic variation is primarily attributable to hereditary characters, or genes, which are transmitted by parents to their offspring through egg and sperm, or sex cells. The outline of the causes of such genetic variation has been well documented since the rediscovery of Mendel's laws of inheritance in 1900. It may however be made it clear that, although we inherit genes from our parents and other ancestors, this does not mean that we inherit our obvious physical and/or mental traits. Our physical and/or mental characters are collectively known as *phenotype*. The phenotype of an individual arises during the long process of growth and development in response to the environmental conditions in which the individual lives. In fact, it is not only the genes carried by the fertilized egg, or *zygote,* but the environments as well, which determine the phenotype of individual. In other words, the phenotype of an individual is attributable to the interplay between genetic and environmental factors. Dobzhansky (1970) writes, "The genotype does not, therefore, determine the phenotype; it determines a range of potentially possible phenotypes. The range of phenotypes that can develop with a given genotype is technically known as the norm of reaction of that genotype. Which potentialities of the norm of reaction will in fact be realised in a given individual at a certain stage of his development is decided by the sequence of the environments in which the development takes place.... The norm of reaction is the entire range, the whole repertoire, of the variant paths of development that may occur in the carriers of a given genotype in all environments, favourable and unfavourable, natural and artificial". For example, it may not be true to say that we inherit a given disease like diabetes. In fact, the disease is due to the interaction between a particular genotype and a given environment, which lacks a particular substance, known as *insulin.* The disease will not be produced, provided insulin is given to the individual with such a genotype. So what we inherit is the result of the self-reproduction of the genes which determines the norm of reaction to the environmental conditions. The varied environments, in which the individual or population lives, modify, to a great extent, the phenotypic expression of the genes. Some genetic variants, or genetic combinations of traits, are more conducive to survival and reproductive success than the others in certain environments, whereas some others are unfavourable, diminishing and become extinct. The end result is that different populations show adaptations to their respective environmental conditions. Adaptation as such may be thought as a process by which a population is becoming better adapted to the environmental pressures so as to maintain itself in a given environment (Johnston, 1973). In fact, the biological study of man has established that the observable differences between and within populations are the evolutionary processes by which populations are able to adapt to the different environmental conditions.

In view of the above circumstances, knowledge of genetics particularly of population genetics is of considerable importance in understanding the processes of ongoing human evolution and variation. Besides, population genetics contributes to a great extent in "removing misunderstanding among various population groups" as it explains the facts and nature of population variation (Das, 1997). Population genetics is also very useful in the field of medical sciences. Population genetics contributes to our knowledge of the health and disease problems as it is concerned with the genetic constitution of the populations and the factors responsible for the incidence of certain genetic traits in such populations. For example, it is commonly cited that the frequency of the sickle cell trait in Africa is higher in the agricultural communities than in those communities, which depend largely on hunting or animal husbandry. It has been observed that the clearing of forests for cultivation has created the new breeding areas for the mosquitoes (*anopheles gambae*), the vectors of *plasmodium falciparum* (malarial parasite). As a result, there is a wide spread of malaria in those populations, which depend on agriculture. The question is that how these populations are maintaining themselves? It is found that the spread of malaria due to agricultural practices in these populations is responsible for the selective advantage of the heterozygotes for the sickling gene, i.e. the heterozygous individuals (HbAHbS) are more resistant to malarial parasites than the normal homozygotes (HbAHbA) and homozygous affected individuals (HbSHbS). Accordingly, the frequency of the sickle cell trait is very high in these populations of malarial prone areas. So although the sickle cell gene is harmful, if it is expressed in homozygous condition, it is also beneficial to the carriers of the trait (heterozygotes) since they have better resistance to malarial parasites. Under these circumstances, the population geneticists and anthropologists have suggested that the frequency of the sickle cell gene will be declined, if malaria is eradicated. Similarly, if the sickle cell disease could be completely cured by means of medical aids, the selective advantage of the heterozygotes would be thwarted, thereby increasing the frequency of the gene in both heterozygous and homozygous conditions.

What we would like to point out here is that the incidence of hereditary diseases and their modes of inheritance in populations can be better understood with a knowledge of population genetics. As in the case of example cited above, population genetics is of considerable importance in understanding the health hazards due to the interplay between genetic and environmental factors, despite certain limitations. In fact, an individual, or a population is constantly subject to the interplay of these influences. There should be always a 'delicate balance' between genetic and environmental influences. Nowadays, the rapid change in environment is likely to affect the genetic make up of different populations. Knowledge of population genetics is essential for estimating the genetic consequences of such changes concerning the health aspects of populations. For example, population geneticists may be interested in knowing the genetic consequences of modern family planning programme. If the genetic composition of a population also depends on differential fertility and mortality, the control of such differentials is likely to have genetic consequences. It is already suggested that natural selection is relaxed to a great extent through the adoption of modern family planning method (Matsunaga, 1966). Similarly, it is observed that the frequency of certain genetic disorders like Down's syndrome, Klinefelter syndrome, haemolytic diseases, etc. increases with the increasing age groups of mothers. In such cases, adoption of family planning methods may be of considerable importance in avoiding the risks of having children with such genetic disorders. Moreover, population geneticists are also interested in knowing the association/relationship between certain diseases and genetic markers. For instance, it is generally reported that persons of blood types A and AB are more susceptible to small pox, and those with O type are more susceptible to duodenal ulcer and so on.

Accordingly, like other branches of genetics, population genetics is also occupying an important position in researches that are of special interest to the health and family welfare programmes. Basu (1994) writes, "Population genetic studies play an important role in the health and family welfare programmes by providing vital information on the incidence of various hereditary disorders... genetic aspects of fertility, effects of radiation on the genetic endowment of the population, genetic effects of contraceptives, optimal age for child bearing, empirical risks of having defective children, which may be utilised for the prevention of various genetic and genetico-environmental disorders through pre- and post-marital genetic counselling".

Another important field of population genetic research is concerned with the genetic and health aspect of inbreeding. According to Reid (1973), "Inbreeding is the genetic consequences of biologically consanguineous matings, and the offspring of biologically consanguineous matings are said to be inbred". The incidence of genetic anomalies or congenital malformations is known to be associated with the high frequency of consanguineous marriages (Schull and Neel, 1962, 1965; in India see review Basu, 1994). Among the Hopi Indians in the United States, the high frequency of albinism is commonly cited as a result of the high rate of consanguineous marriages. Similarly, infant mortality rate is reported to be associated with consanguineous marriages (see reviews Reid, 1973, Basu, 1994). Knowledge of population genetics may be essential to have a better understanding of these problems in human populations. It has been suggested that the adoption of family planning methods is required for reducing the frequency of consanguineous marriages. "For small size of sibships in a family means fewer relatives or fewer cousins. The frequency of hereditary diseases due to recessive genes is likely to be reduced by the decrease in the frequency of consanguineous marriages. Thus family planning is helpful in reducing the frequency of hereditary defects and diseases" (Roychoudhury, 1988).

OBJECTIVES OF THE PRESENT STUDY

It is obvious from the above that the scope and importance of population genetics is very vast, and it is hardly possible for an individual researcher to master all the areas of population genetics. Therefore, it may be very important for us to limit our area of study, taking into consideration the main objective of physical anthropology as mentioned at the outset. As such, we propose to undertake a genetic study among the Kochs of Garo Hills entitled *A Study of Dermatoglyphics, Blood Groups and Other Genetic Traits of the Kochs of Meghalaya,* taking into consideration the following objectives of study:

1. To describe the demographic structure the Koch population, taking into consideration all the five subgroups, namely, Chapras, Sangas, Satparis, Tintikiyas and Wanangs.
2. To describe the genetic composition of each of the subgroups of the Koch population with the help of some genetic markers like ABO and Rh(D) blood groups, PTC taste blindness and colour blindness.
3. To study the morphological characteristics of the study population with the help of somatometric, dermatoglyphic, and some somatoscopic and behavioural traits.
4. To find out how evolutionary forces like selection and drift are operating in all the subgroups of the Koch population.
5. To find out the phylogenetic position of the study population in relation to other neighbouring populations including the Kochs of Assam.

The present study is concerned mainly with dermatoglyphic, anthropometric and morphological characters with few genetic markers as what generally done in anthropological genetic study of populations. As such, it may be more appropriate to mention these characters in the title rather than to use a broad title, say, a study of population genetics in the Koch population.

AREA OF STUDY

Location

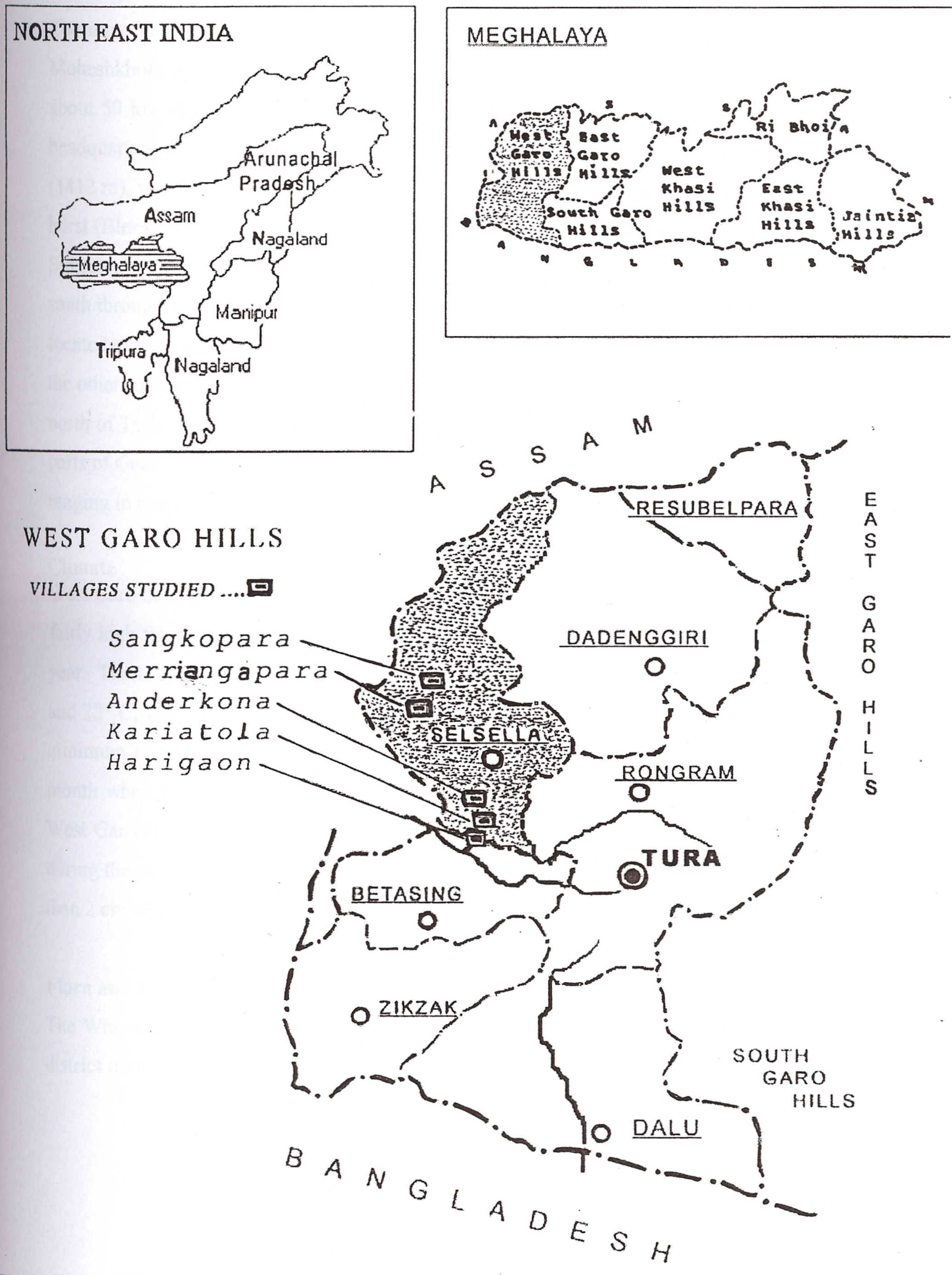
Meghalaya is essentially a small tribal state in the north – eastern region of India. It was officially created as a full-fledged state on January 21, 1972. It lies between 25° 45′ and

26° 10′N latitude and 89° 45′ and 92° 47′ E. longitude. The state covers an area of about 22,429 square kilometers. It is bounded by Assam on the north, east and north – west, and by Bangladesh on the south and southwest. Meghalaya comprises seven district viz., Jaintia Hills, East Khasi Hills, West Khasi Hills, Ri-Bhoi, East Garo Hills, West Garo Hills and South Garo Hills districts. According to 2001 census, the total population of Meghalaya is 2, 306, 069. The density of population is approximately 103 persons per square kilometer. The overall sex ratio is 975 females per 1000 males. Literacy rate is 63.31. It is a tribal state with several major tribes, although the Garos and Khasis are the major tribal populations of the state.

The present study was carried out in five villages of West Garo Hills district. The West Garo Hills district is situated in the North–western part of Meghalaya (Figure 1.1). It lies between 25° 8′ and 26° 1′ N latitude and between 89° 50′ and 90° 59′ E longitude. The district is bounded by Bangladesh on the south and southwest, Goalpara district of Assam on the north and northwest, and by South and East Garo Hills districts on the east. The West Garo Hills district covers an area of 3,715 sq. km with a total population of 5,15,813 of which 2,59,440 are males and 2,56,373 females (Census of India, 2001). Thus, the density of population per square km is 139 persons with the sex ratio of 988 females per 1000 males. The total literary rate is 51.03%.

Figure 1.1 also shows the location of five villages belonging to the five subgroups of Koch, namely, Chapras, Sangas, Satparis, Tintikiyas and Wanangs. The villages selected for the present study are *Andherkona* for the Chapras, *Harigaon* for the Sangas, *Kariatola* for the Satparis, *Sangkopara* for the Tintikiyas and *Merriangapara* for the Wanangs. Andherkona and Kariatola are situated on the foothill of Ronggira range about 5 to 6 kilometers away from Garobadha Police Station. Harigaon village is situated on the right side of the Ganol river about 30 km to the west of Tura, while Sangkopara is situated on the left side of Garobadha about 5km away from Selsella. On the other hand, Merriangapara village is located on the right side of the river bank of Singwil – Galwang river about 8 km away from Selsella.

FIG. 1.1. LOCATION OF STUDIED VILLAGES IN WEST GARO HILLS DISTRICT OF MEGHALAYA



Topography

The entire Garo Hills is hilly terrain which constitutes an extension of the famous "Shillong Plateau." The altitude varies from 15 metres to 1,412 metres above sea level. The important physiographic features in this part of Meghalaya are the Tura range, the Moheshkhola-Adaguri range and the Simsang valley (Bhakta, 1992). The Tura range is about 50 km above sea level and extends in east-west direction from Siju to Tura, the headquarters of the West Garo Hills district. The highest peak of this range is Nokrek (1412 m), which is about 13 km southeast of Tura. The Tura range is known as a typical horst (Block mountain) bounded by two faults and it is along the northern faults that the Simsang river flows towards the east for about 45 km and thereafter it flows towards south through a gorge that separates the Tura and Kylas ranges. The Kylas range which is located to the east of Simsang river rises abruptly as a hog-back mass and it is higher than the other surrounding hills of the area. The Arbela peak (999 m) and the hills lying to the north of Tura range are low but gradually increase in height in the south. The remaining parts of Garo hills are composed of hill ranges, which run from north to south with peaks ranging in height between 450 and 600 metres.

Climate

West Garo hills district which is relatively lower in altitude than Khasi hills experiences a fairly high temperature from February to October with April as the hottest month of the year. The average maximum and minimum temperatures during this period are about 33° C and 22° C, respectively. May is the next hottest month with the average maximum and minimum temperatures of 31° C and 23° C, respectively, while January is the coldest month when the temperature drops to as low as 12° C. The average annual rainfall in West Garo Hills district is 330 cm (Bhakta, 1992) of which more than two-third occurs during the period between May and August. Winter is practically dry with little or more than 2 cm of rainfall.

Flora and Fauna

The West Garo Hills district is very rich in flora and fauna. The important flora of the district include sal (*Shorea robusta*), teak (*Tectona grandis*), gamari (*Gmelina arborea*), simul tree (*Bombax malabaricum*), jackfruit (*Atrocarpus integrifolia*), champa (*Michelia champa*), pine (*Khasiya pinus*), different types of bamboo, mushrooms, ferns and orchids.

Different species of mammals are found in the district. Some imporatnt fauna include hoolock gibbon (*Hylobates hoolock*) stump-tailed macaque (*Macaca specisosa*), loris (*Myeticebus coucang*), tiger (*Panthera tigris*), leopard (*Panthera pardus*), golden cat (*Felis tenmincki*), deer (*Cercuus*), bear (*Ursus*), fox (*Galeopithecus*) squirrel (*Hylopetes alboniger*), bamboo rat (*Cannonmys bodius bodius*), wild pig (*Sus*), elephant, etc. Different types of reptiles and snakes are also found in the district.

THE PEOPLE

The people of Meghalaya are mostly tribals, among which the Khasis and Garos are the major tribal groups. Other tribal populations like the Kochs, Hajongs, Dalus, Rabhas, Manns, Biates, Naga and Mizo tribes, etc., have also settled in the state along with Nepalis and some Hindu caste populations. The Koch population consists of seven major sub-groups, namely, the Chapras, Sangas, Satparis, Tintikiyas, Wanangs, Banais or Dashgaiyas and Shankars. Their main concentration in the state is in West Garo hills.

According to Waddell (1901) the term "Kochs" has become more of a "caste title than a tribal appellation, so that individuals of the Kachari, Garo, Rabha, Lalung and allied Indo-Chinese tribes are admitted as members . . . (and) anyone of these tribes can become a Koch by establishing a Brahmanical priest and giving up eating beef, though he need not necessarily adjure animal food altogether. In this stage he called "Saraniya" usually pronounced in the Assmese fashion "Horoniya" which means a "refugee" implying that he has taken refuge in Hinduism. The more advance stage can be gained by leaving off beef and swine's flesh, strong drink together, when he assumes the full eternal status of Hindu." Thus in Assam, the term "Kochs" is applied in various senses to indicate various groups of Assam as well as the members of the Hindu caste society (Majumdar, 1972). They are also known as Rajbanshis (Sengupta, 1990).

From the physical anthropological point of view, the physical features of the Kochs may be described as having flat faces of square type with prominent cheek-bone. Their eyes are black and oblique. Their hair is black and straight to curly, their noses are flat and short. They have scantly beards and moustache and dark brown complexion (Dalton, 1872).

Different scholars are different in opinion regarding the ethnic affinity of the Kochs. Some scholars hold that they are the Dravidians (Dalton, 1872), while others are of the opinion that they are the Mongoloid origin (Haddon, 1924; Das, 1962; Sengupta, 1982). For the Kochs of Garo hills, there are two stories regarding their original homeland. Some sections of the Kochs of Garo hills believe that their original home was in Arabela range of the central part of Garo hills, and thereby they are much older than the Garos who believe to have come from Tibet. Another legend says that the Kochs came from Kamrup district of Assam. According to this legend, the Kochs of Garo hills are the descendants of two daughters of the sun, namely, Hira nad Jhira, who were married to a man named Hojo in Kamrup district of Assam (Bhattacharya, 1994).

Beisdes Assam and Meghalaya, the Kochs are also found in Manipur, Tripura, North Bengal, Chittagong and Naokhali districts in Bangladesh. In Meghalaya, they are mainly distributed in western and south-western parts of West Garo hills district. Their total population has not been available for the last two national censuses, but according to 1971 Census it is about 13,520 of which 6,712 are males and 6,808 are females. They speak a language which belongs to the Tibeto-Burman Origin (Gait, 1905). The influence of both Bangali and Assamese languages is reflected in their dialect.

The Kochs of West Garo hills district are divided into seven endogamous subgroups, namely, Chapras, Sangas, Satparis, Tintikiyas, Wanangs, Banais and Shankars. Each subgroup lives in a separate village or a group of villages. The Sangas or Harigavas are named after their village Harigoan, while the Satparis and Banais are known as the inhabitants of seven and ten villages, respectively (Bhattacharya, 1994). On the other hand, the Chapras are known as the inhabitants of lowland areas, while the Wanangs are named after the clan-name, i.e., Wanang, and the Tintikiyas are so named on the basis of the dress that the women of the clan use to wear, viz., *lufan* (cloth covering the waist), *kambang* (cloth covering the body) and *paga* (cloth covering the head). The Shankars are known as those Koch people who were excommunicated for committing social offences such as practice of group exogamy.

Each subgroup of the Kochs in Garo hills consists of several exogamous clans known as *nikiny.* The clan is very strong and united. Widows, orphans, aged and disabled persons are taken care by the clan members. Monogamy is the general practice among the Kochs of Meghalaya. Divorce and re-marriage are permitted but the remarriage of the widow is not favoured by the people. Unlike the Kochs of Assam, the Kochs of Garo hills follow the matrilineal system of society, in which the line of descent is traced through females. With the exception of Banais, parental property is also inherited by the daughters only. The youngest daughter or the daughter who looks after the aged parents gets the lion's share of property.

Koch religion is believed to be a blend of tribal and Hindu religion (Bhattacharya, 1994). They worship *Siva, Kamakhya, Kali* and *Pagla* and each clan has its own deity known as *nikiniya. Kamakhya* is believed to be the most sacred goddess and *Padma* is a family goddess, which is worshipped on the *Sraban Sankriti* day. They also perform different types of *pujas* like *Bastu Puja* and *Lakshmi puja.* Their important festivals include *Holi, Asthapraha, Saraswati Puja, Kiti–Bihu, Katigasa. Magh–Bihu and Pushna.*

Agriculture is the mainstay of the people and land is owned individually. Their major agricultural produce include rice, jute, pulses, mustard seeds, etc. Many also are engaged in labour work. Besides working as daily labourers, weaving and fishing are the subsidiary occupations practiced by many of them. Some Kochs also work in government and private organizations. A few of them have joined the military services. Some are teaching and others are employed in other private jobs.

CHAPTER X
SUMMARY

Population genetics is now considered the backbone of physical anthropology (Kirk, 1978). As the term suggests itself, population genetics refers to the genetics of Mendelian population, or a breeding community whose members share in a common gene pool (Dobzhansky, 1951). According to Li (1955), "Population genetics is concerned with the statistical consequences of Mendelism in a group of families, or individuals, it studies the hereditary phenomenon on population level". While doing population genetic studies, physical anthropologists generally look for small endogamous and/or isolated populations which are likely to represent the Mendelian populations. According to Keith (1950) these population groups are the "evolutionary units" which are important for studying all micro-evolutionary processes. Moreover, social or cultural structures are also more integrated in small isolated populations as compared with urban or advanced societies. Thus, the WHO scientific Group (1964, 1968) has recommended that there is an urgent need to carry out demographic and population genetic studies among these isolated populations since many of them are undergoing cultural disintegration due to increasing contact with more sophisticated peoples.

From the physical anthropological point of view, the main interest in studying population genetics is to understand the processes of human microevolution and variation. In doing so, physical anthropologists have used genetic markers, demographic and anthropometric data with a view to understanding the phylogenetic (evolutionary) position of human populations. The differences or dissimilarities between generations within a population, or between populations within a major racial group in respect of genetic and anthropometric traits are considered the on-going process of human evolution. On the other hand, the on-going process of human evolution is subject to a number of evolutionary forces like mutation, natural selection, genetic drift and gene flow, which act differently in different populations. Understanding of the operation of these evolutionary forces in human populations is of great importance to the human evolutionists, biologists and physical anthropologists. Thus, a large number of studies have been carried out in different human populations all over the globe in order to understand the phylogenetic position of human populations and the evolutionary mechanisms operating in human populations. In such studies, different demographic, morphological and genetic traits have been used extensively by many scholars (Crowford, 1973; Harisson, 1977).

With this end in view, we have undertaken a genetic study among the Kochs of Garo Hills entitled *A Study of Dermatoglyphics, Blood Groups and Other Genetic Traits of the Kochs of Meghalaya,* taking into consideration the following objectives of study:

1. To describe the demographic structure of the Koch population, taking into consideration all the five subgroups, namely, Chapras, Sangas, Satparis, Tintikiyas and Wanangs.
2. To describe the genetic composition of each of the subgroups of the Koch population with the help of some genetic markers like ABO and Rh(D) blood groups, PTC taste blindness and colour blindness.
3. To study the morphological characteristics of the study population with the help of somatometric, dermatoglyphic, and some somatoscopic and behavioural traits.
4. To find out how evolutionary forces like selection and drift are operating in all the subgroups of the Koch population.
5. To assess the phylogenetic position of the study population in relation to other neighbouring populations including the Kochs of Assam.

STUDY POPULATION

The Koch population of Meghalaya consists of seven major sub-groups, namely, the Chapras, Sangas, Satparis, Tintikiyas, Wanangs, Banais or Dashgaiyas and Shankars. In the present study we are dealing with the Chapras, Sangas, Satparis, Tintikiyas and Wanangs. They are mainly distributed in West Garo hills, and they are believed to be one of the oldest inhabitants of Garo hills, i.e., older than the Garos (Koch, 1984). Some section of the Kochs of Garo hills claim that their original place of residence is Arbela hill in the central Garo Hills, but many scholars believe they have migrated from Kamrup district of Assam. They peak a language which belongs to the Tebeto-Burman family. The influence of both Bangali and Assamese languages is reflected in their dialect. They can also speak Bengali, Assamese, Garo and Hindi. Unlike the Kochs of Assam, the Kochs of Garo hills follow the matrilineal system of society in which the line of descent is through females. Monogamy is the general practice among the Kochs of Meghalaya, and residence is also matrilocal. Divorce and re-marriage are permitted, but re-marriage of the widow is not favoured by the people. Agriculture is their mainstay of livelihood.

MATERIALS AND METHODS

The present study was carried out in two phases among the Kochs of West Garo Hills district, Meghalaya. The first phase of the study was carried during April – May 1996, and the second phase was conducted during September and December 1996. Data were collected from five subgroups of the Koch population, namely, Chapras, Sangas, Satparis, Tintikiyas and Wanangs. No statistical sampling technique was applied for data collection of the present study. Instead, it was considered convenient to select one major village from each Koch sub-group. The villages selected for the present study are *Andherkona* for the Chapras, *Harig aon* for the Sangas, *Kariatola* for the Satparis, *Sangkopara* for the Tintikiyas and *Merriangapara* for the Wanangs.

Data on demographic parameters, anthropometry, genetic markers, morphological and dermatoglyphic traits were collected from each of the above mentioned villages. Demographic data were collected through in-depth interview with each of the married woman or head of the household, using household and fertility schedules, taking into consideration those demographic data as suggested by the World Health Organization (WHO, 1964, 1968). Special attention was also given in collecting information on the mating patterns including marital distance and consanguineous marriages.

Anthropometric Data: The anthropometric measurements were taken on 250 adult males aged from 20 years to 60 years. These adult males were mostly the heads of households. Sixteen measurements were considered for the present study. These are:

Height vertex, sitting height, height tragus, height acromion, head length, head height, head breadth, upper facial length, total facial length, minimum frontal breadth, bizygomatic breadth, bigonial breadth, nasal height, nasal breadth, head circumference and chest girth on all the subjects. An effort was made to take into consideration those methods and techniques of taking measurements suggested by the International Biological Programme given in Weiner and Lourie (1981) and Sen (1994).

ABO Blood Groups: Blood samples on 462 individuals 250 males and 212 females were collected from the five sub-groups of Koch, following the standard slide methods suggested by Lawler and Lawler (1951) and Bhatia (1977). The Chapra sample consisted of 103 individuals, Sangas-75 individuals, Satparis- 75 individuals, Tintikiyas - 105 individuals and Wanangs- 104 individuals. The allele frequencies of the ABO blood groups were calculated following the method suggested by Bernstein (1930), and the variances in allele frequencies were computed according to the method suggested by Balakrishnan (1988).

Phenylthiocarbamide Test Sensitivity (PTC) : The serial dilution method suggested by Harris and Kalmus (1949) was followed to collect data on P.T.C. taste sensitivity.

Colour blindness : The Ishihara Chart (1959) was used to collect data on 250 male individuals of the five sub-groups. The subjects were examined in adequate day-light. The chart was kept open and plates were held at a distance, approximately two and half feet from the subjects. The subjects were asked to read the number of plates numbering 1 – 25 within three seconds for each plate. Illiterate subjects were asked to trace the snake like figure or **X**' of the plates 26 to 38 by means of a brush supplied to each of the subjects. The test was made utilising the instructions attached with the Ishihara plates.

Morphological Data : Data on hand clasping were collected following the method suggested by Lutz (1908), and the types of arm folding were categorized following Weiner (1932). Standard methods suggested by Sturtevant (1940) were adopted in recording data on tongue rolling. The subjects were asked to roll their tongue so that the left side is upward and the right remains either stationary, or is lowered and vice versa.

The observation was recorded as positive and negative respectively for those individuals who were able and not able to fold their tongue without touching the lips (Liu and Hsu, 1949).

Earlobe Attachment : The twofold classification of earlobe attachment of Powell and Whiteney (1937) was followed in the present study. Left and right ears of all the subjects covered under the present investigation were examined. The observation was recorded as attached or free. The individuals with an earlobe attached towards the gonion region of the zygomatic arch were classified as having attached earlobe.

Middle Phalangeal hair: All fingers of both the hands of subjects were examined with the help of a hand lens of low manifestation (10-X) in a bright day light, whether the hair was present or not in the middle phalangeal region of the fingers. In some cases, the hair was missing but the follicle was present and these fingers were classified as having hair. The thumb is excluded as it is devoid of middle phalanges.

Dermatoglyphics: The ink printing method, as suggested by Cummins and Midlo (1961), was adopted. The subjects were asked to wash their hand with soap and water in order to remove all dust, hairs and grease from hands and in the case of stubborn grease the hands were cleaned with a piece of cotton dipped in rectified spirit. The palm and fingers were allowed to dry for some time. A small quantity of ink was placed on the inking plate and spread evenly all over it with a cotton pad, making it a thin film (Das and Deka, 1993).

FINDINGS OF THE PRESENT STUDY

The present thesis consists of ten chapters. The first and second chapters deal with the introduction and review of related literature, respectively. In the third Chapter, we have described the materials and methods of data collection adopted in the present study. The findings of the study are presented in five chapters. Demographic characteristics including mating patterns are presented in Chapter IV and results on genetic markers are described in Chapter V. The findings on anthropometry, morphological characters and dermatoglyphics are presented in Chapters VI, VII and VIII, respectively. The discussion and implications of the present findings are given in Chapter IX, and the summary of the study is presented in Chapter X.

The findings on demography, genetic markers, anthropometric, morphological and dermatoglyphic traits may be briefly given as follows:

Demographic Characteristics:

Age and sex composition

(1) Of the five Koch subgroups, the Chapra population tends to be *regressive* in which the base of the population pyramid is constricted indicating the low fertility rates in the population. On the other hand, the Sanga, Satpari and Tintikiya populations are of *stationary* types, which are by and large indicative of low fertility rates that may be due to either adoption of family planning methods or high infant and child mortality rates. On the other hand, the Wanang population tends to be *progressive*, which is characterized by high fertility rates.

(2) The over all sex ratio (i.e., number of males per 100 females) is more or less according to the ideal sex ratio of 1:1 among the Wanangs (101.02), and it is tilt in favour of males in the case of the Chapras (106.67). Among the Sangas (81.65), Satparis (96.75) and Tintikiyas (93.84), the sex ratio is low, especially in the former. In comparison with the sex ratio among the War Khasi (109) of Meghalaya (Khongsdier, 2001), the overall sex ratio is lower in each of these Koch subgroups. In fact, it indicates that mortality is higher in males than in females among the Sangas, Satparis and Tintikiyas.

(3) The mean age at marriage is found to significantly different among the Koch subgroups ($F= 4.65, P < 0.05$). It is found to be 18.12 ± 0.36, 19.27 ± 0.43, 17.43 ± 0.50, 17.42 ± 0.43 and 16.97 ± 0.33 years in the Chapra, Sanga, Satpari, Tintikiya and Wanang women, respectively. The subgroups like the Chapras and Sangas have more or less similar mean age at marriage with the populations of Assam, like the Morans, Deuris, Mishings and Chutias (Sengupta and Gogoi, 1995a), although it is not as high as that among the Christian War Khasis (Khongsdier 2001). On the other hand, the subgroups like the Satparis, Tintikiyas and Wanangs have a lower

mean age at marriage when compared with other populations of Assam and Meghalaya.

Fertility: Three parameters were taken into consideration while measuring the fertility rates in all the Koch subgroups of the present study. These include:(i) mean number of live births and surviving children per mother living continuously in wedlock till attainment of the age 45 years, (ii) mean number of live births and surviving children per married woman of all ages and (iii) total fertility rate (TFR). With the exception of few cases, the mean number of live births and surviving children tends to increase with the increasing age groups of the mothers for all the populations covered under the present study. It is found that the mean number of live births to women of all ages living in wedlock varies between 2.08 ± 0.24 for the Chapras and 3.42 ± 0.33 for the Wanangs, and the mean number of surviving children varies from 1.41±0.17 among the Chapras to 2.75 ±0.26 among the Tintikiyas. The ANOVA test indicates that these differences between the Koch populations are statistically significant for live births ($F = 3.11$, $P < 0.05$) and surviving children ($F = 4.06$, $P < 0.05$).

Like in the case of married women living in wedlock, the mean number of live births and surviving children to all married women also increases with the rise in age group of the mothers. It is found that the mean number of live births per married woman varies from 3.30 ± 0.28 in the Chapras to 4.24 ± 0.29 in the Tintikiyas, and the mean number of surviving children ranges from 2.32 ± 0.21 for the Chapras to 3.39 ± 0.25 for the Tintikiyas. The ANOVA test indicates that the differences are statistically significant for both live births ($F = 3.11$, $P < 0.05$) and surviving children ($F = 2.59$, $P < 0.05$). In comparison with other populations of Assam and Meghalaya, the mean number of live births per married woman of all ages in each of these Koch subgroups is lower than that reported for some populations of Northeast India (Patra and Kapoor, 1996; Khongsdier, 2001).

In order to have a better understanding of the fertility rate in the present populations, an attempt has also been made to show the age-specific fertility rate (ASFR) and total fertility rate (TFR). With the exception of Sangas, the ASFR reaches its peak when the mothers are aged 20-24 years. In the case of the Sangas, the highest ASFR is found to take place when the mothers are in the age group 25-29 years. Further, the highest TFR is observed in the Wanangs (5.43), and the lowest in the Chapras (3.85). Thus, this measure of fertility rate (i.e., TFR) is also similar to that number of live births to women living continuously in wedlock, which indicates that the fertility rate is higher among the Wanangs when compared with the other subgroups. The TFR in other subgroups varies from 4.11 in the Sangas to 4.98 in the Tintikiyas. In comparison with other populations of Meghalaya, the TFR in the Koch subgroups are lower than that reported for the Dalus (Patra and Kapoor, 1996) and War Khasis(Khongsdier, 2001).

Since the present study is not concerned with the determinants of fertility, data on socio-economic factors of the present populations were not collected. Considering the findings on other populations, it may be suggested that the inter-group differences in fertility rates may be associated with the inter-group variation in respect of socio-economic conditions, or adoption of family planning methods.

Infant, Child and juvenile Mortality

It is found that the infant mortality rates, that is, the number of deaths before 1 year of life per 100 live births, are 10.83%, 5.44%, 3.77%, 4.02% and 7.16% in the Chapras, Sangas, Satparis, Tintikiyas and Wanangs, respectively. Thus, it indicates that the infant mortality rates are high especially among the Chapras and Wanangs, although it is not as high as that reported for the Dalus (Patra and Kapoor, 1996). It is more or less similar to that reported in the War Khasis(Khongsdier, 2001), but much lower than that reported for the Muslim Khasis of Shillong (Langstieh, 2001). The differences between subgroups in respect of infant mortality rates are also significant ($\chi^2 = 13.86$, DF = 4, $P < 0.01$), which may be associated with the differences in socio-economic conditions of the populations as has been pointed out in the case of the differences in fertility rates. Of course, it warrants further studies to understand the determinants of infant mortality in all the Koch subgroups of Garo hills.

Like in the case of infant mortality rate, the child mortality rate, i.e., number of child deaths aged between 1 and 4 years of life per 100 live births, is found to be very high among the Wanangs (13.81%) and Chapras (13.72%), followed by the Sangas (8.37%), Satparis (7.55%) and Tintikiyas (8.58%). The chi-square value indicates that the these inter-group differences in child mortality rates are significant ($\chi^2 = 9.56$, DF = 4, $P < 0.05$).

With regard to juvenile mortality rate i.e., number of child deaths aged between 4 and 14 years of life per 100 live births, the highest frequency was found among the Satparis (9.91%) and the lowest among the Wanangs (3.58%). Thus, it indicates that there is a wide variation between populations in juvenile mortality as well, although it is not significant ($\chi^2 = 8.91$, DF = 4, $P > 0.05$).

Reproductive wastage

It is found that the rate of reproductive wastage (abortions and still births) is fairly high in the Kochs of Garo hills, although it is lower in the Wanangs (4.00%) and Sangas (4.05%). It is relatively high among the Chapras (8.42%), followed by the Satparis (6.19%) and Tintikiyas (5.57%). These differences in reproductive wastage is found to be insignificant ($\chi^2 = 6.83$, DF = 4, $P > 0.05$). The abortion rates are found to be 4.71%, 1.21%, 4.87%, 3.54% and 2.00% in the Chapras, Sangas, Satparis, Tintikiyas and Wanangs, respectively, and the frequencies of still births are about 3.70%, 2.83%, 1.33%, 2.03% and 2.00%, respectively. Thus, it indicates that the still birth rate is higher than the abortion rate in the Sangas, and it is more or less same in the case of the Wanangs. In other subgroups, the abortion rate is higher than the still birth rate.

The Koch subgroups of the present study have lower rate of reproductive wastage when compared with the War Khasis (Khongsdier, 2001), but they are more or less similar to the Dalus (Patra and Kapoor, 1996).

Mating Pattern

It has been observed that all the Koch subgroups of the present study are characterised by high tendency to village exogamy. In other words, the village endogamy in the present populations is not as high as that reported for the War Khasis(Khongsdier and Ghosh, 1994, 1996) and Semsaspopulation (Limbu and Khongsdier, 2000). Besides, it is found that about 94% of the marriages took place within the Koch subgroups only, i.e., only about 6% of the total marriages took place with other populations like the Garos, Hajongs, Dalus, Bengalis, etc. Also, the mean marital distance is high in these population groups, except the Satparis, when compared with those reported for the War Khasisof Meghalaya (Khongsdier, 2001). This clearly shows that the Koch population of Garo hills as a whole is highly endogamous in relation to other populations. In other words, it may be assumed that the Koch population of Garo hills is divided into a number of sub-populations like the Chapras, Sangas, Satparis, Tintikiyas, Wanangs, Banais and Sankars, which may exchange genes with one another with little effect of distance. This may also be associated with low frequency of consanguineous marriages (except two cases-one among the Sangas and the other among the Tintikiyas). However, such a contention is based mainly on the marriage pattern observed in the Chapras, Sangas, Satparis, Tintikiyas and Wanangs. Unfortunately, data on mating pattern of the Banais and Sankars are not available to support our suggestion here.

Genetic Markers

It is found that the blood types A and B are more common in all the populations. In the case of Sangas and Satparis, the frequency of blood type A is more than B, while blood type B is higher than A among the other subgroups. The frequency of O blood type is more or less similar in all the Koch subgroups covered under the present study, although it is lower in the Wanangs (18.27%). With respect to blood type AB, the frequency is very low in the Sangas (8%) in comparison with the other subgroups. These inter-group differences in ABO blood groups are, however, not statistically significant ($\chi^2 = 10.97$, D.F. = 12, $P > 0.05$). Following the methods suggested by Balakrishnan (1988), the allele frequencies of p (A), q (B) and r (O) are also not statistically significant in all the subgroups. Thus, it indicates that all the Koch subgroups of the present study are in genetic equilibrium in respect of the ABO blood group system.

With respect to the Rh (D) blood groups, it is found that Rh-negative blood type is absent in the Chapras and Tintikiyas, and it is very low in other subgroups. Thus, the present findings seem to support the general observation that Rh-negative allele is almost absent in Mongoloid populations, or it presents in a very low dose in Mongoloid populations of Northeast India (Das, 1974). In the case of colour blindness, no colour blind individual was detected in the Sangas. Among the Chapras, Satparis, Tintikiyas and Wanangs, the frequencies of colour blindness are found to be 5.88%, 2.44%, 3.28%

and 5.36%, respectively. Although it is higher in the Chapras and Wanangs, the frequency of colour blindness does not vary significantly between the Koch subgroups of the present study.

With respect to PTC taste sensitivity, the lowest frequency of non-tasters is found among the Satparis (10.67%) and the highest among the Wanangs (37.50%). The Chi-square value indicates that the inter-population differences are statistically significant ($\chi^2 = 22.56$, DF = 4, $P < 0.05$), but such differences are mainly due to the differences between the Satparis and other subgroups like the Sangas, Tintikiyas and Wanangs. Thus, data on PTC taste sensitivity are to a certain extent different from other genetic markers, since the Satparis deviate significantly from the other Koch subgroups of the present study.

On the basis of the data presented above, it indicates that the Koch subgroups of the present study are by and large similar in respect of ABO and Rh(D) blood groups, and colour blindness, although a subgroup like the Satparis deviate significantly from the other subgroups in respect of PTC taste sensitivity.

In order to have a better understanding of the genetic relationship of the present populations with other neighbouring populations, an attempt has been made to calculate the genetic distance according to the method suggested by Nei (1972). For calculating Nei's genetic distance, we have taken into consideration two genetic loci, namely, ABO blood groups and PTC taste ability because data on other genetic loci were not available for all the populations taken for comparison. The dendrogram based on the method suggested by Sokal and Sneath (1963) shows that the Tintikiyas and Sangas are close to each other, forming a cluster with the Lyngngams and Wanangs. On the other hand, the Satparis and Chapras are distant from each other, and both of them differ from the other subgroups. The dendrogram also shows that the Koch subgroups of the present study stand far apart from the Kochs of Assam.

Anthropometric Measurements

On the average, these subgroups of the Kochs of Meghalaya are similar in anthropometric characters, although there are certain differences between them in respect of some measurements. With respect to stature, the Sangas are the tallest, whereas the Satparis are the shortest. As regards the other groups, the Tintikiyas are taller than the Chapras and Wanangs, and the Wanangs are shorter than the Chapras. However, the ANOVA test indicates that the ineter-group differences in respect of anthropometric measurements - like height vertex, sitting height, height tragus, height acromion, head breadth, bizygomatic breadth, bigonial breadth, upper facial length, nasal height and chest girth - are not statistically significant. The only significant differences between these groups are found in respect of head length, head height, head circumference, minimum frontal breadth, total facial length, and nasal breadth. But it is also observed that the differences among the groups in respect of anthropometric measurements, as indicated by ANOVA test, are mainly attributed by the differences between two groups, except in the case of minimum frontal breadth and total facial length. Therefore, these Koch subgroups are by and large similar in anthropometric measurements. Similar observation is made in the case of the anthropometric indices. It is found that they are by and large similar in respect of nasal index, total facial index and length-height index, although there are significant differences between them in respect of cephalic index and breadth-height index. However, the differences in cephalic index among them are mainly attributed by the difference between Tintikiyas and Wanangs. In fact, the Tintikiyas seem to differ significantly from the Wanangs in respect of head height, head circumference and bread-height index.

On the basis of the anthropometric characters, the Koch subgroups of the present study are by and large similar. However, it is likely that the Tintikiyas deviate significantly from the other subgroups especially the Sangas and Wanangs and the Satparis.

In order to have a better understanding of the ethnic affinity of these Koch subgroups of Garo hills with other neighbouring populations, we have also calculated the coefficient of diversity (CD) as suggested by Najjar (1978). The dendrogram, derived as per the method suggested by Sokal and Sneath (1963), shows that all the Koch subgroups belong to the same cluster, and the Tintikiyas and Chapras stand closer to each other. Thus, the dendrogram also shows that the present populations are on the average similar in anthropometric characters, and they are distant themselves from the Kochs of Assam.

Dermatoglyphic Traits

In the present study, we have taken into consideration five dermatoglyphic traits, namely, finger patterns, finger pattern indices, finger ridge counts, main line formulae and C-line termination. The highest frequency of whorls is observed among the Satparis (45%) and the lowest among the Chapras (34%). The Sangas and Chapras are more or less similar in respect of loops. So are the Satparis and Tintikiyas. The homogeneity test indicates that the Tintikiyas are closer to the Satparis and Wanangs, and the Sangas are similar to the Wanangs in respect of finger patterns, although the differences between any other subgroups are highly significant.

With respect to finger pattern indices, the pattern intensity index is more or less similar in all the subgroups, but the frequency of Dankmeijer's index and Furuhata's index is different from one group to another. The Furuhata's index varies from 119.40 for the Chapras to 188.53 for the Satparis, whereas Dankmeijer's index ranges from 19.49 among the Satparis to 54.41 among the Chapras. In the case of finger ridge count, the lowest mean value is among the Chapras (133.60 ± 25.50) and the highest among the Satparis (158.40 ± 23.15). The t- test indicates that each subgroup deviates significantly from the other, except the Chapras and the Wanangs and the Sangas and Tintikiyas who are closer to each other. Nevertheless, it indicates that the present subgroups of the Koch population are different from one another in respect of finger ridge count. Of course, such differences between these subgroups in respect of finger ridge count may also be attributed to large amount of individual variation in finger ridge count.

As regards mainline formulae, it is observed that the percentage distribution of the formula-11.9.7 ranges from 13% among the Satparis to 21% among the Tintikiyas. On the other hand, the percentage distribution of mainline formula- 9.7.5 varies from 35% among the Sangas to 40% among the Wanangs, while the frequency of mainline formula- 7.5.5 ranges between 33% for the Tintikiyas and 46% for the Chapras and Satparis. However, these differences between the Koch subgroups are not statistically significant

($\chi^2 = 9.16$, DF = 8, $P > 0.05$). In other words, it indicates that the Koch subgroups of the present study are by and large similar in frequency of three mainline formulae, except the differences between the Satparis and the Tintikiyas, which is statistically significant ($\chi^2 = 6.16$, DF = 2, $P < 0.05$).

With respect to C-line termination, it is found that C-line termination towards ulnar side is very common in all the subgroups of the Koch population. The percentage distribution of C-line termination towards ulnar side varies from 70% among the Tintikiyas to 84% among the Satparis. In the case of radial side, the frequency varies from 13% among the Satparis to 21% among the Tintikiyas. The highest frequency of C-line termination towards proximal is found among the Tintikiyas (6%) and the lowest among the Wanangs (0.96%), while the proportion of individuals without C-line termination varies from 6% among the Sangas to 0.49% among the Chapras. The homogeneity test, however, indicates that the Koch subgroups of this study are by and large similar to one another in respect of C-line termination towards ulnar and radial sides, although the Tintikiyas deviate significantly from the Wanangs and Satparis.

In comparison with other populations, the Koch subgroups differ significantly from other populations in respect of finger patterns. With respect to finger pattern intensity, they are by and large similar to the Kochs of Assam, Garos and Hajongs rather than to the Khasi subgroups like the Khynriams, Pnars, Bhois and Wars. On the other hand, they show a different degree of affinity to other populations with respect to finger ridge counts. Such a trend is indeed expected because these Koch subgroups of Garo hills are different from one another in respect of finger ridge count. For example, it is observed that the Chapras and Wanangs are different from the Kochs of Assam and Garos, but they are similar to the Khasi subgroups like the Khynriams, Pnars, Bhois and Wars. On the other hand, the Satparis are similar to the Kochs and Garos but deviate significantly from the Khasi subgroups. Again the Tintikiyas are similar to the other groups except the Kochs, Khynriams and Bhois. This clearly indicates that the Koch subgroups of the present study are different from one another in respect of finger ridge count, thereby showing a different pattern of relationship with other neighbouring populations.

With respect to the frequency of mainline formulae, all the Koch subgroups are similar to the Hajongs despite the difference between the Tintikiyas and the Hajongs. They also show a similar pattern of significant variation from the Kochs of Assam and the Khasi subgroups of Meghalaya, except the Tintikiyas who are by and large similar to all neighbouring populations in respect of mainline formulae.

On the basis of the dermatoglyphic traits presented above, it indicates that the Koch subgroups of the present study are by and large similar to one another in respect of pattern intensity index, mainline formulae and C-line termination towards ulnar and radial sides. However, they differ from one another in respect of finger patterns and total finger ridge count. When compared with other neighbouring populations, all the subgroups differ from other populations in respect of finger patterns, and they show a different pattern of relationship with respect to finger ridge counts. On the other hand, data on pattern intensity index and mainline formulae indicate that they are by and large closer to the Kochs of Assam, Garos and Hajongs.

Morphological Traits

In all the sub-groups under consideration, the right types of hand clasping are very common in both the sexes. It is also found that the inter-group differences are not statistically significant in respect of hand clasping ($\chi^2 = 0.84$, DF = 4, $P > 0.05$). With respect to arm folding, the left type of arm folding is more common than the right type in all the subgroups. Left type of arm folding is more common among the Chapras and Sangas. Like in the case of hand clasping, the inter-group differences are not statistically significant despite the presence of significant difference between the Sangas and Tintikiyas. In the case of tongue rolling, it is observed that most of males and females are unable to roll their tongue in all the subgroups. The highest frequency of tongue rolling is observed among the Wanangs (31%) and the lowest among the Sangas and Satparis (13%). The inter-group variation is highly significant in respect of tongue rolling ($\chi^2 = 11.66$, DF = 4, $P< 0.02$) due to the significant deviation of the Wanangs from the Sangas ($\chi^2 = 7.38$, DF = 1, $P < 0.02$) and Satparis ($\chi^2 = 7.38$, DF = 1, $P < 0.01$).

With respect to tongue folding, the Sangas have the highest frequency (40%), while the lowest frequency is observed among the Wanangs (31%). In the case of Chapras, Satparis and Tintikiyas, it is found to be 38%, 33% and 35%, respectively.

However, this inter-group variation in respect of tongue folding is not statistically significant ($\chi^2 = 2.0835$, DF = 4, $P > 0.05$), thereby suggesting that these Koch subgroups of Meghalaya are by and large similar in respect of this trait. Also, the Koch subgroups of the present study stand closer to one another in respect of the frequency of earlobe attachment.

As for the distribution of mid-phalangeal hair, most of the individuals in the present study do not possess mid-phalangeal hair on any of the finger digits. It holds true for all the divisions of the Koch population. The Chi-square value indicate that the inter-group differences in respect of mid-phalangeal hair is not statistically significant ($\chi^2 = 2.62$; DF =4, $P > 0.05$). Thus, all the Koch subgroups of the present study are similar in respect of mid-phalangeal hair.

When compared with other populations, the Koch subgroups of the present study are by and large different from other populations of Assam and Meghalaya, but they are similar to the Dalus in frequency of hand clasping, earlobe attachment and tongue rolling. With respect to arm folding, they stand closer to the Lalungs, but in respect of hand clasping they are similar to the Kochs of Assam, Khasis and Dalus.

IMPLICATIONS OF THE PRESENT FINDINGS

In view of the present findings on Koch subgroups of Garo hills, it may be necessary to look into three important aspects. The first aspect is related to inter-subgroup variation or the differences within the Koch population of Garo hills, the second is concerned with the relationship of all the Koch subgroups with other neighbouring populations, and the third is related to the possible role of evolutionary forces like selection and genetic drift in all the Koch subgroups. These may be briefly pointed out as follows:

Inter-Group Variation

On the basis of the genetic data presented in the previous chapters, the Koch subgroups of the present study, i.e., Chapras, Sangas, Satparis, Tintikiyas and Wanangs, are by and large similar in respect of the ABO and Rh(D) blood groups, and colour blindness, despite few exceptions like the Satparis who deviate significantly from the other subgroups in respect of PTC taste sensitivity. It has also been observed that all the subgroups of the Koch population are by and large similar in anthropometric, morphological and dermatoglyphic traits. In other words, regardless of certain differences in respect of few traits, the Koch subgroups of Garo hills are by and large similar in genetic, anthropometric, morphological, behavioural and dermatoglyphic traits considered for the present study. Thus, these results are according to our expectation on the basis of the findings on the mating pattern, which indicate that most of the marriages took place within Koch subgroups only. As mentioned earlier, data on mating patterns suggest that village exogamy is fairly high in all the subgroups, but marriages with other populations like the Garos, Dalus, Hajongs, Rabhas, etc., were not taking place frequently. Further, with the exception of Satparis, mean marital distance is also fairly high in all the subgroups. Thus, the Island Model of population proposed by Wright (1943) seems to be applicable to the Koch population of Garo hills. "In Island Model every population exchanges gene equally with every other and there is no effect of distance between populations" (Cavalli-Sforza and Bodmer, 1971). In other words, it may be assumed that the Koch population of Garo hills is divided into a number of sub-populations like the Chapras, Sangas, Satparis, Tintikiyas, Wanangs, Banais and Sankars, which may exchange genes with one another with little effect of distance. The absence of significant inter-group differences in respect of many genetic, anthropometric, morphological, behavioural and dermatoglyphic traits is likely to support such a contention. Nevertheless, even if this population does not follow the Island Model, it is obvious that there is a continuous gene flow between the Koch subgroups of the present study. Of course, the influence of physical- environmental factors on the present qualitative and quantitative traits may not be so significant because these Koch subgroups of the present study are by and large living in a similar ecological condition.

Relationship with other populations

In comparison with neighbouring populations of Assam and Meghalaya, the Koch subgroups of the present study show in general a different degree of affinity to the neighbouring populations with respect to the ABO blood groups and PTC taste sensitivity. There are also contradictory results, which indicate that populations, which are related to one another in respect of the ABO blood groups, are different with respect to PTC taste sensitivity. For example, the Chapras are similar to the Lyngngams and different from the other populations like the Kochs of Assam, Khynriams, Pnars, Bhois, Wars and Hajongs of Meghalaya in respect of the ABO blood groups. But in the case of PTC taste sensitivity, they deviate significantly from the Lyngngams, and stand closer to all other populations mentioned above. Similarly, the Tintikiyas are significantly different from the Kochs of Assam, Bhois, and Dalus in respect of the ABO blood groups, but they stand closer to these populations with respect to PTC taste ability. A similar observation is made with regard to anthropometric, dermatoglyphic and morphological traits. It may be mentioned here that this is the common observation in many population genetic studies (Danker-Hopfe *et al.*, 1988; Khongsdier, 2000). Different models of distance analysis have been proposed to solve this problem in the study of population affinity (Mahalanobis, 1936; Nei, 1972, and others). Then, the dendrogram has been drawn on the basis of the calculated distances, i.e., the closer populations are grouped into clusters. Various methods have been used to obtain such clusters (Sokal and Sneath, 1963; Balakrishnan, 1988). In fact, these different distance and cluster analyses proposed by various authors have been used extensively in population genetic studies. The results are very helpful in certain studies, but they are also contradictory in others. There are two major types of such contradictory results as pointed out earlier. One is related to a different picture of relationship as shown by the dendrograms according to morphological/anthropometric and genetic characters, like in the case of the present study, and the other is the different patterns of relationship which may not be related to history, even when one uses only genetic markers. In this connection, Danker-Hopfe *et al.* (1988) write, "The population exhibits differences and similarities among themselves in different manners with regard to different traits.... With regard to genetic traits the populations present a dendrogram which is difficult to explain." Also, the data collected by one study are in many cases contradict those collected by others from the same population(s). For example, Walter *et al.* (1986) have shown that the Brahmins, Kaibartas, and Rajbanshis belong to one sub-cluster with the Brahmins showing somewhat a different position. They have explained that the Brahmins are different from the Kaibartas and Rajbanshis because of the absence of enough gene flow, i.e., absence of intermarriage between them. It is, however, surprising to find that the Brahmins show a close genetic relationship to the Sheik Muslims and the Kalitas according to the study conducted by Danker-Hopfe *et al.* (1988). In the present study, we have observed that the dendrogram according to genetic markers is not consistent with the dendrogram based on the anthropometric characters. But the Koch subgroups of the present study deviate from the Kochs of Assam in respect of both genetic and anthropometric characters.

The question arises, therefore, whether to depend on genetic markers like the ABO blood groups and PTC taste ability, or on the anthropometric and morphological characters which are polygenic in nature for the study of population affinity. This is also a subject of debate among various scholars. Geneticists have emphasized to use genetic markers as they are less affected by environmental factors. However, other evolutionists and anthropologists have claimed that quantitative characters such as anthropometric and dermatoglyphic, and morphological characters are more useful for the assessment of evolutionary relationship of human populations than a few genetic traits because they represent a large part of the genome of human populations (Rife, 1954; Sokal, 1959; Hiernaux, 1972). It may also be noted that even the hypothesis of African Eve, which is based recently on mtDNA analysis that man originated in Africa, is in confirmation with the fossil records and earlier studies on morphological characters (see review Khongsdier, 2000). Therefore, the point that we would like to make it clear is that both genetic and anthropometric/morphological characters are very helpful in understanding the evolutionary relationship of human populations. But the methods or models of using them may still need for further modifications. Of course, this is beyond the scope of the present study. We hope that future studies of population genetics will throw much more light in this regard with the device of more appropriate and systematic approaches or techniques of international standard. This is particularly important in the field of physical anthropology, which is concerned with the study of evolutionary relationship of human populations. In the present study, we are also concerned with only the weak genetic markers like the ABO blood groups and PTC taste ability. It has been suggested that strong genetic markers like serum proteins, red cell enzymes and DNA polymorphisms may be more helpful to have a better understanding of the phylogenetic position of populations in this part of the country (Khongsdier, 2000).

Despite the various limitations, it is obvious that the Koch subgroups of the present study are by and large similar in genetic and other quantitative and qualitative characters due to enough gene flow between them. However, when compared with the Kochs of Assam and other populations, the present populations are by and large unique in their demographic, genetic, somatometric, dermatoglyphic and morphological characteristics. This is true if we take into consideration that each individual is genetically unique, and a group of individuals or population is likely to follow the same pattern when such a population is compared with other populations. When the populations are genetically unique, it has been suggested that the role of chance factors is very important in bringing about similarities and differences between populations. Besides the sampling error during data collection may also contribute to such contradictory results. In such cases, interpretation of the genetic relationship between populations may not be as simple as expected.

The another point to make it clear here is that when a population is genetically unique, its variation from other populations is likely to be similar to that of individual variation. The only difference is that we ignore the individual variation while studying population variation by assuming that the individual variation would be neutralized by the number of individuals included in our sample. This may not always be possible, and it is, of course, a subject of debate in anthropological researches that always lack of appropriate sampling technique. The same is true with the present study, which considers each village of each subgroup of the Kochs in Garo hills as representative sample of the population. Nevertheless, we consider the sample of the present study as representative ones because data on genetic markers as well as anthropometric, dermatoglyphic and morphological characters are to a great extent consistent with the demographic data on mating patterns of each of the subgroups. In other words, the Koch subgroups of the present study are by and large similar in genetic, anthropometric, dermatoglyphic and morphological traits/characters due to an exchange of genes between them through inter-marriage.

Evolutionary Mechanisms

As mentioned earlier, evolutionists, population geneticists and physical anthropologists have recognised the role of many evolutionary forces like mutation, selection, genetic drift and gene flow in bringing about human variation. In the present study, we are concerned mainly with total selection intensity, genetic drift and gene flow.

With respect to genetic drift, it is found that the coefficient of breeding isolation is relatively high in all the subgroups, except the Satparis. This is due to the fact that the migration rates are relatively high in all the subgroups. It is observed that the migration rates vary between 29% for the Satparis and 45% for the Wanangs. The importance of migration is that even a very small admixture rate may produce an important effect on genetic drift. Wright (1931) has clearly suggested that migration neutralises to a great extent the effect of genetic drift in a population. Wright (1943) has shown that the changes in a given allele frequency due to genetic drift depends on the product of the effective population size and admixture rate. Such a product is known as the coefficient of breeding isolation (N_eM). In a population with an allele frequency of 0.5, genetic differentiation due to drift is very great where N_eM is less than 0.5, genetic differentiation is still important where N_eM is less than 5, but differentiation due to genetic drift is slight where N_eM is greater than 50. Thus, in view of the present findings on the Koch subgroups of Garo hills, one may suggest that the action of genetic drift may not be so significant because of the high migration rate among themselves. In the case of Satparis, it may be worthwhile to mention that they have lower rate of village exogamy and lower mean marital distance in comparison with the other subgroups. It has also been observed that they deviate significantly from the other groups, except the Chapras, in respect of PTC taste sensitivity. Therefore, the role of genetic drift may not be totally ruled out in this Koch subgroup.

But the differences and similarities between these Koch subgroups and other populations are subjected to speculation. It is clear that they are by and large different from the Kochs of Assam, but stand closer to the neigbouring populations like the Garos, Lyngngams, Dalus and Hajongs. It may be speculated that the Koch subgroups of the present study are different from the Kochs of Assam because of the action of genetic drift, and their intermixture with the neighbouring populations may also be attributable to their deviation from the Kochs of Assam.

Last but not least, the role of natural selection in these Koch subgroups may be equally important. It is found that the total selection intensity calculated according to Crow's formula is likely to operate with moderate intensity in the Wanangs, while it is mild in intensity among the Tintikiyas. The average intensity of natural selection is observed in the Sangas and Satparis, and the intensity is fairly high in the Chapras. It is also observed that the mortality component due to selection contributes more towards the Index of opportunity for selection, which is in confirmation with earlier studies in many populations in Northeast India. Thus, it is likely that natural selection plays a very important role in bringing about changes in gene frequencies of the present populations.