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

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CERTIFICATE

*Certified that the thesis entitled " **A Study of Dermatoglyphics, Blood Groups and Other Genetic Traits of the Kochs of Meghalaya**" is the record of the original work done by Shri Murali Kotal. To the best of my knowledge, the contents of this thesis did not form a basis of the award of any previous degree to him, and that the thesis has not been submitted by him for any research degree in any other University, or Institute.*

In habit and character, shri Murali kotal is a fit and proper person for the degree of doctor of philosophy.

7/3/02

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Dated, Shillong, the 18th March, 2002

DECLARATION

I, Shri Murali Kotal, hereby declare that this thesis entitled ***"A Study of Dermatoglyphics, Blood Groups and Other Genetic Traits of the Kochs of Meghalaya"*** *is my bona fide research work, and that the thesis has not been submitted by me for award of any research degree in any other University.*

18-03-02

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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

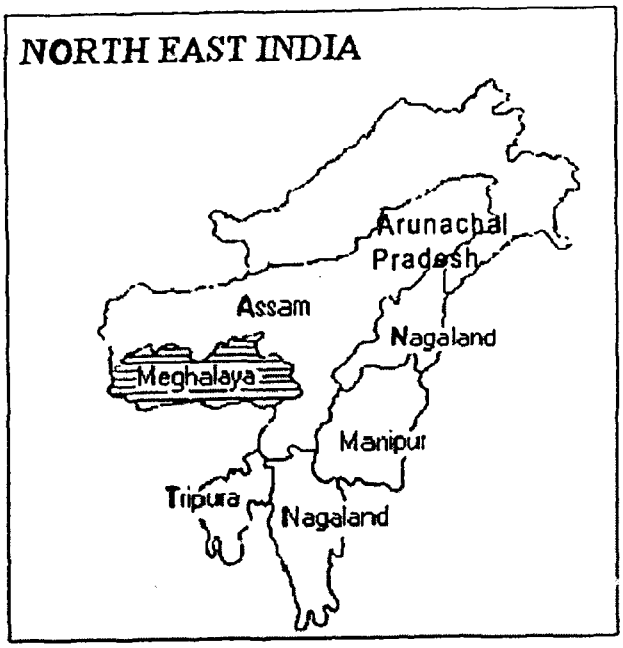
26° 10'N latitude and 89° 45′ and 92° 47′ E. longitude. The state covers an area of about 22,429 square kilometers. It is bounded by Assam on the north, east and north – west, and by Bangladesh on the south and southwest. Meghalaya comprises seven district viz., Jaintia Hills, East Khasi Hills, West 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.

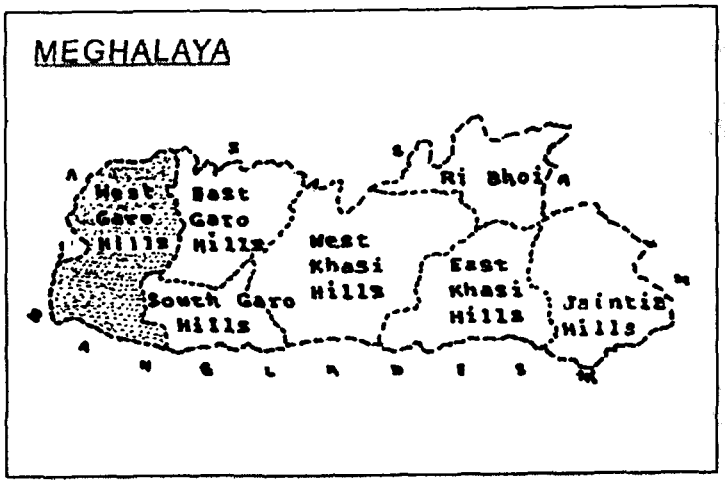
The present study was carried out in five villages of West Garo Hills district. The West Garo Hills district is situated in the North–western part of Meghalaya (Figure 1.1). It lies between 25° 8′ and 26° 1′ N latitude and between 89° 50′ and 90° 59′ E longitude. The district is bounded by Bangladesh 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%.

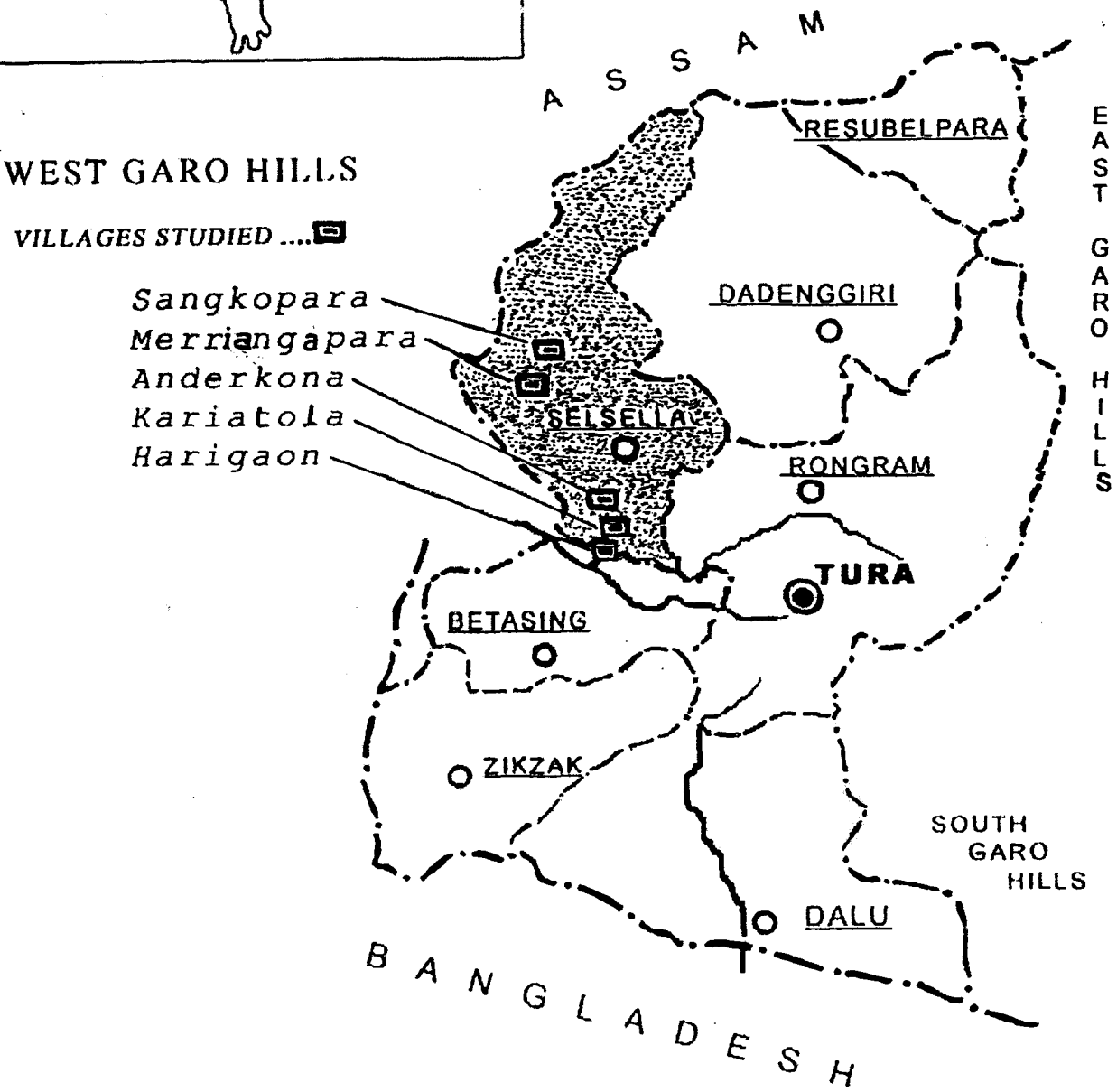
Figure 1.1 also shows the location of five villages belonging to the five subgroups of Koch, namely, Chapras, Sangas, Satparis, Tintikiyas and Wanangs. The villages selected for the present study are *Andherkona* for the Chapras, *Harigaon* for the Sangas, *Kariatola* for the Satparis, *Sangkopara* for 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 min.. 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 II
REVIEW OF LITERATURE

In the present chapter, we shall make a review of related literature with special reference to those works carried out in populations of Northeast India. It may be made it clear that the following review is far from being complete and exhaustive, but its main purpose is to have a glance at those related literature with a view to understanding of the genetic structure of the study population

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Phylogenetic Affinity

Establishing the genetic relationship between and within human populations is one of the major focuses of anthropological population genetics. Along with genetic markers of the blood, morphological (including dermatoglyphic, somatometric, somatoscopic and behavioural traits) characters have been widely used for this purpose. Of course, it is generally believed that morphological and behavioural traits like arm-folding, hand-clasping, earlobe attachment, tongue rolling, mid-phalangeal hair, etc., are not as valuable as genetic markers from the genetic point of view. In the present study, however, we agree with Salzano (1961) that such traits may be useful in population genetic studies for several reasons. One of such reasons is that the findings on the genetic affinity of human populations in respect of known loci are still not as clearly understood as were in the case of these traits. In several cases, the findings on genetic markers corroborate those on anthropometric and other morphological and behavioural traits (Harrison, 1977). Moreover, it is also realized that even the so-called non-adaptive traits like blood groups are completely non-adaptive. According to Boyd (1952 from Crawford, 1973), 'it is doubtful if any hereditary characters are completely non-adaptive, and . . . probably we can deal only with different degrees of adaptive value'.

As mentioned earlier, anthropologists before1950s and even in the late 1960s took great interest in the racial classification of populations. However, after 1950s a new development in anthropological research had emerged because of the advancement in

population genetic research. It has been realized that the use of genetic markers is very helpful in understanding the genetic variation and affinity between populations. Also, the genetic variation does exist not only between races but also within a race. For this reason, genetic relationship of populations within a particular racial group in respect of various genetic markers has attracted a great deal of attention among the physical anthropologists (see review, Dobzhansky *et al.* 1973; Crawford, 1973; Majumder, 1991). The main purpose of this short review is not to mention all those important works in the field of anthropological genetics, but to make a glance at the overall scenario that has developed in this field. In fact, we would like to point out that the population genetic researches in Northeast India have also reflected the overall interest in the field of population genetics all over the world. Therefore, it may be necessary to have a glance at the development in this field with regards to populations of Northeast India.

Like in other parts of the globe, scholars in Northeast India have used the various genetic markers with a view to understanding the evolutionary relationship between populations of the region. Perhaps, Mitra (1938) for the first time reported data on the ABO blood groups for the Plains Assamese, Angami and Lushai populations of this part of the country. It was then followed by two sets of data among the Khasi (Basu, 1938; Macfarlane, 1941), and those data reported by the British Research Association Committee (1939) for the Angami, Konyak and Ao tribes of Nagaland. But a large number of data on the ABO blood groups were published after India's Independence, though most of the works have been carried out in Assam only (see reviews Das, 1974; Phookan, 1975; Chakravarty, 1990).

As just mentioned above, for the purpose of this presentation, an attempt has been made to give a general picture rather than giving a detail of all the works carried out by different scholars. One of the important general characteristics, relating to the gene frequencies of the ABO blood groups in the population of Northeast India, is that the B allele occurs more frequently than the A allele in the tribal populations. While among the Hindu caste populations, the frequency of A allele is higher than that of B. In fact, this is one of the general differences between the Mongoloid (tribal) and Caucasoid (non-tribal) populations in Northeast India. In the case of O allele, there is not much difference between tribal and non-tribal populations. It may be noted that the Hindu and

Muslim populations of Assam are similar in respect of the ABO blood group system, occurring in the pattern of O > B >A > AB (Ahmed Das, 1980), though the Muria Muslims show more resemblance to the tribal population (Danker-Hopfe *et al.*, 1988). According to Das (1984), "No doubt that among the tribal population of Northeast India O gene predominates. The other two genes, i.e. A and B also occur in considerably higher numbers. But among most of the groups like the Khasi, Naga and Lushai- Kuki A (allele) is much more frequent than B. On other hand, among the Boro B (allele) is slightly more frequent than O. The reverse is true in the case of certain Arunachal tribes".

With respect to the phylogenetic position of population, various studies have made a comparison of their findings with those reported for other populations. Some studies try to find out the differences and similarities between the so-called Mongoloid and Caucasoid populations (Das *et al.*, 1987; Sengupta, 1987; Danker-Hopfe *et al.*, 1988); others deal with the genetic variation within these populations (Phookan, 1975; Das, 1978; Das *et al.*, 1985a, 1985b, 1986a, 1986b; Singh *et al.*, 1986), and some others made a comparison of these populations with other populations living outside the region (Flatz *et al.*, 1972; Das, 1978). For comparison within and between populations, some studies have used only ABO blood groups, and others have considered with anthropometric traits and other genetic markers like PTC, colour blindness, and other blood group polymorphisms.

Danker-Hopfe *et al.* (1988) have made an attempt to show the phylogenetic relationship of 13 endogamous Assamese-populations on the basis of certain genetic markers, finger ridge patterns, anthropometric and behavioural traits. It was assumed that the two major population groups, namely, Mongoloids and Caucasoid, would form two distinct clusters as revealed by the distribution of five ABO blood group polymorphisms (Das *et al.*, 1987). The distance analyses of Sanghvi (1953), Hiernaux (1965) and Nei (1972) were taken into consideration. "It appears that distance analyses of data of different natures produce different results. 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" (Danker-Hopfe *et al.*, 1988). In fact, many studies have revealed the existence

of such a difficult situation. For example, Walter *et al.* (1986) have reported the distribution of haptoglobin, transferin (Tf) and Gc sub-types among the Brahmin, Kalita, Kaibarta, Rajbanshi, Muslim, Ahom, Chutia, Kachari and Sonowals. It is evident from this study that the Sonowals belong to one sub-cluster with the Ahom and Chutia. Accordingly, the authors have suggested that the Chutia and Ahom are from the same racial stock and thereby these populations "show a close genetic relationship". It may, however, be noted that these two populations are distant from each other with respect to the distribution of GM and Km allotypes (Walter *et al.*, 1987). Walter *et al.* (1986) have also shown that the Brahmin, Kaibarta and Rajbanshi form another sub-cluster with the Brahmin showing a 'somewhat different position'. They have explained that the Brahmins are different from the Kaibarta and Rajbanshi because of the absence of enough gene flow due to caste marriage system. It is, however, surprising to find that the Brahmin show a close genetic relationship to the Sheik Muslims and the Kalita (Danker-Hopfe *et al.*, 1988), which is difficult to explain. Similarly, according to the Nei's distance analysis of genetic traits carried out by Walter et al. (1987) and Danker-Hopfe *et al.* (1988), the Kaibarta and Kalita are very close to each other. But these two populations are quite different from each other in respect of the distribution of haptoglobin, transferin and Gc polymorphisms (Walter *et al.*, 1986).

Without going into detail of all the contradictory results, it may be pointed out here that different results are shown according to different studies. Consequently, the interpretation of the phylogenetic affinity of the populations in Northeast India has become more complicated. In most cases, the results of the analyses of genetic traits are more or less similar to those of traditional anthropometry. Harrison (1977) has also made such an observation on the over-all picture of population genetic study. In other parts of the world there has been an increasing interest in DNA polymorphisms so as to have a better understanding of the origin of modern humans and the phylogenetic relationship between various human populations. It may be noted that biologists, especially the molecular anthropologists, have recently given more attention to mitochondrial DNA analysis with a view to understanding the origin and divergence of human populations (Johnson *et al.*, 1983; Cann *et al.*, 1987; Stoneking, 1993; Hagelberg, 1996). Human mitochondrial DNA (mtDNA) is a self replicating circular molecule of approximately

16,569 base pairs in length, which is located in the cellular cytoplasm (Anderson et al., 1981). It has only 37 genes, no introns, and codes for 13 polypeptides that are essential to the energy metabolism of the cell (Hagelberg, 1996; Bertranpetit *et al.*, 1996). The mother to her offspring always transmits it. As such, there is no recombination during meiosis and thereby every individual (male or female) receives identical copies of the mother's DNA genome. This is important in constructing the phylogenetic relationship of human populations. Being inherited in maternal fashion, any variation in mtDNA through generations should be due to mutation. Thus, evolution in this sense takes place by the accumulation of mutations from generation to generation. Since mtDNA evolves about 10 times faster than nuclear DNA, it implies that deleterious mtDNAs are important in understanding not only genetic differentiation between and within populations, but human diseases and ageing as well (Wallace, 1995;). Similarly, there are numerous neutral or harmless mutations, which can provide useful genetic information of the human populations. Since each human cell consists of thousands of mtDNA copies, it is possible that mtDNA sequences should persist for a long time in biological samples of archaeological sites, thereby providing useful information concerning paleoanthropological interests (Hagelberg, 1996).

Since the early 1980s, mtDNA analysis has occupied an important position in the study of the evolutionary relationship of human populations. Perhaps, the most notable example of such works is that carried out by the late Allan Wilson and colleagues at the University of California in Berkeley (Cann *et al.*, 1987). Using a high resolution mapping of mtDNA of 147 women from Africa, Asia, Europe, Australia and New Guinea; these scholars (Cann *et al.*, 1987) have found that there is little variation in the mtDNA types of all the women, despite the differences in their geographical origins. Moreover, women with an African ancestry show more variation in the mtDNA types, suggesting that the African origin was the oldest and had more time to accumulate mutations. Therefore, it is suggested that all modern mtDNA types could be traced to a single female ancestor, known as the '**African Eve**', who lived in Africa about 200,000 years age, or between 290,000 and 140,000 years ago. Interestingly, the concept of an African Eve seems to be consistent with the fossil record, which suggests that all modern human populations trace their origin to Africa (Poirer *et al.*,1994). In other words,it has

been interpreted that the finding of Cann *et al.* (1987) is in confirmation with the *SingleReplacement Hypothesis*,which states that all modern humans originated in Africa only, and then replaced the archaic humans throughout the Old world in a recent expansion from Africa. This hypothesis is in contrast to the *Multi-regional Transition Hypothesis*, or *Regional Continuity Model*, which states that although *Homo erectus* originated in Africa, the archaic *Homo sapiens* evolved independently into modern humans in different parts of the world with enough hybridization to produce a single biological species of modern *Homo sapiens* (Stringer and Andrews, 1988; Hagelberg, 1996). Although the present work are not concerned with DNA analysis, we just mention to acknowledge and appreciate the latest development in population genetics, which in future, we hope that such studies would be carried out in this part of the country with a view to having a better understanding the phylogenetic position of populations Khongsdier, 2001).

DEMOGRAPHIC-GENETIC STRUCTURE

According to Roberts (1973), "No is it satisfied with counting genes in populations. Instead, being aware of differences in gene frequency between peoples, human population genetics has endeavoured to understand the processes responsible for these differences and the mechanisms by which the observed frequencies are maintained and regulated". Thus, genetic markers are used not only to understand the genetic composition and population affinity but also to quantify the evolutionary processes of various evolutionary forces. "Following these applications of the concept of genetic constitution, the frequencies of genes in the array that characterises a given population, there came a new concept, that of genetic structure. Where as genetic constitution is concerned essentially with individual loci, genetic structure concerns the way in which genes are distributed and combined within populations. As such it is concerned not with gene frequencies but with measures of gene relationships (linkage disequilibrium coefficients of inbreeding, coefficients of kinship, parameters of the decline of kinship with distance). For all these, factors are of relevance that do not enter the simple concept of genetic constitution – the effective population size, population distribution, population

density, assortative mating, migration. These all affect the evolution and differentiation of populations, and are themselves affected by social, cultural, as well as natural environmental, factors" (Roberts, 1991). Thus, the aim of population genetics is now not only to understand the genetic constitution of a population but also to make out the genetic structure of such a population.

Population structure is characterised by a colossal number of interrelated components or characters that may be arranged in terms of genetic, taxonomic, demographic, social and ecological hierarchical orders of relatedness for the expediency of a given study at a given point of time. Basu (1995) writes, " While (1) in genetics we have the hierarchy of endogamous groups..., (2) in demography we have the hierarchy of segmentation as well as the hierarchy of age groups, (3) in social science we have the hierarchy of social groups arranged in ascending/descending order of social status/economic condition/power (authority) as in the case of caste, class and community; (4) in ecology we have the hierarchy of populations inhabiting niches, subniches, and so forth within the broad range of distribution of the group...; (5) in taxonomy we have the hierarchy of categories, i.e. phylum, class, order, etc. whether or not we accept the existence of infra-specific taxa in the case of humans". Each of these structures is closely interrelated (Harrison and Boyce, 1972; Yablokov, 1986). The relationship between demography and genetic structure, i.e. demographic-genetic structure, has been a focus of attention in population genetics (Neel and Salzano, 1967; Basu, 1969; Roberts, 1968; Salzano, 1972).

From the genetic point of view, endogamous groups are known as Mendelian populations. "A Mendelian population is a community of individuals of a sexually reproducing species within which matings take place. There is a hierarchy of Mendelian populations. The most inclusive Mendelian population is the species. The lowermost member of the hierarchy is a panmictic unit, within which matings take place" (Dobzhansky, 1970). Despite a number of problems, it is believed that an understanding of the concept of the hierarchy of Mendelian populations is a vital requisite to understanding the genetic structure of human population (Harrison and Boyce, 1972; Basu, 1995). Let us have a glance on some of the works carried out in this respect

among the populations of Northeast India, taking into consideration the demographic-genetic structure of a population.

In his book entitled *Microevolution,* Das (1981) has described the micro-variation in the Boro, Chutia and Khasi populations. He has observed that each of these populations is divided into different sub-populations/subgroups, which are different from one another in respect of anthropometric, somatoscopic, dermatoglyphic and genetic traits. Such differences within a given population have also been observed in other populations like the Brahmin (Das *et al.*, 1986a) and Kalita (Das *et al.*, 1986b). All these studies have revealed that scholars in this part of the country have also made an attempt to understand how the genes are maintained and regulated within a population. Of course most of the works have been carried out in the populations of Assam with stray researches in other populations of the different states in the region. It may also be worthwhile to mention that the classification of these populations has been based mostly on the frequencies of certain genes and anthropometric traits in view of the geographical location, linguistic affinity, or ethnohistoric background of the population concerned. For example, the Garo, Rabha and Kachari are known as Boro mainly because of their linguistic affinity (i.e. since they speak the Boro language of the Tibeto-Burman group). On the other hand, the Khasi population consists of five major sub-divisions, namely, Khynriam, Pnar, Bhoi, War and Lyngngam. The question of how the Khasi population is known by different names is not fully understood, though it is likely that these five groups are known according to the names of their geographical locations (Khongsdier, 1996). Das (1981, 1984) has suggested the importance of both hybridization and geographical isolation in bringing about the differences between the Khasi sub-groups. He is of the opinion that the Bhoi, who show the greatest deviation from the other Khasi sub-groups, inhabit in a lower attitude area in the northern part of Meghalaya towards Assam. Therefore, intermarriage with the other groups like Khynriam, who are living in the higher altitude, is infrequent. Instead, there is a possibility of gene flow to the Bhoi from other neighbouring populations in Assam. This sort of speculation has also been given in connection with the micro-variation in anthropological traits within the Boro, Chutia, Brahmin and Kalita (Das, 1981, 1984; Das *et al.*, 1986a, 1986b). So it appears that studies in Northeast India have taken anthropometric, dermatoglyphic and genetic

traits along with geographical and socio-cultural (including linguistic) factors with a view to understanding the hierarchy of Mendelian populations.

Recently, demographic data have also been taken into consideration to define the hierarchy of Mendelian populations. Demographic data on marital distance, i.e. the distance between the birth places of spouses, and village endogamy are believed be very important in making out the boundary of endogamous groups and the extent of gene flow into the local populations. A bio-demographic study among the War Khasi has revealed that the Khasi population as a whole is not only divided into four or five sub-groups. Instead, each sub-group, like the War Khasi, is again subdivided into several endogamous units comprising a village, or a group of few villages (Khongsdier, 1994, Khongsdier and Ghosh, 1994, 1996). It is observed that among the War Khasi there is a very high tendency to village endogamy with low admixture rate and marital distance. Accordingly, it is suggested that each village, or a number of few villages, is likely to form a separate *deme*, which is different from one another in respect of anthropometric and genetic traits. The findings on anthropometric characters seem to confirm such a hypothesis (Khongsdier, 1997). It is also suggested that village endogamy is largely responsible for the active operation of natural selection and genetic drift. It may be noted that the rate of village endogamy seems to vary from one population to another in this part of the country (Barua, 1986, 1993). Interestingly, among the Semsa, a sub-group of the Dimasa in North Cachar hills of Assam, the rate of village endogamy is 100 % (Limbu and Khongsdier, 2000).

Besides the study of the hierarchy of Mendelian populations, an attempt has also been made to show how demographic variables like fertility, mortality, population size, mating, etc. are indispensable for understanding the evolutionary mechanisms that are operating in human populations of Northeast India. An overview of the works done in this respect may be summarised under the following headings:

Natural Selection: Natural selection is one of the important evolutionary forces, which brings about changes in gene frequencies of a population from generation to generation. It occurs when individuals of the different genotypes in a population are different from one another in their fitness known as *Darwinian fitness, or genetic fitness*. Darwinian

fitness is defined as the "reproductive capability of an individual or class of individuals, in terms of the number of offspring they contributed to the next generation" (Johnston, 1973). Thus differential fertility and mortality are the fundamental events of natural selection. From the demographic-genetic point of view, "differences in rates of reaching maturity, mating, fecundity, fertility, mortality and emigration are the raw materials of natural selections"(Spuhler, 1973).

Natural selection is believed to operate at four different levels: (i) **Total or individual selection**, which is measured through differential fertility and mortality (Crow, 1958), assuming that some phenotypic variation in reproduction has a genetic basis and fitness is heritable; (ii) **Phenotypic selection**, which is concerned with the selective differential of the optimum set of phenotypes in relation to the overall fitness, e.g. birth weight and survival to 28 days after birth (Haldane, 1954); (iii) **Genotypic selection**, which is concerned with the selective differentials of certain genetic markers, e.g. selective advantage of HbS over HbA; and (iv) **Genic selection**, which is concerned with the selective differential at molecular level (Tanaka and Nei, 1989).

The total selection, which is believed to measure the maximum opportunity for the changes in the genetic composition of a population, has been widely studies in several populations of Northeast India. Many scholars have followed the Crow's (1958) formula, and some others have also taken into consideration its modified version (Johnston and Kensinger, 1971). According to reviews (Sengupta and Gogoi, 1995; Sengupta and Kalita, 1996), the Index of opportunity (I), according to Crow's formula varies between 0.1070 for the Punjabi Sonar of Shillong and 1.0700 for the Gallong of Arunachal Pradesh. It is observed that, in many populations of Northeast India, the mortality component due to selection contributes more towards the Index of opportunity for selection.

Reddy and Chopra (1990) have reported that the mean value of the 'Index of opportunity for selection', according to Crow's formula, for 96 Indian populations is 0.665 with a standard deviation of 0.316. Considering these figures, the population mean was estimated as lying between 0.600 and 0.730, following the 95 % confidence interval suggested by Snedecor and Cochran (1967). Accordingly, Khongsdier (2000) has suggested that the different degrees of the total opportunity for selection for the Indian

populations may be arbitrarily classified as shown in Table **2.1.** It may be noted that when there is no change in the genetic composition of the population, the value of I is zero (Livingstone and Spuhler, 1965).

Table 2.1. Degree of opportunity for selection.

Degree of intensity	Crow's index of opportunity for selection
Low	Below 0.340
Moderate	0.340 - 0.470
Mild	0.470 - 0.600
Average	0.600 - 0.730
High	0.730 - 0.860
Very high	Above 0.860

Source: Khongsdier (2000)

Following the above classification, the intensity of natural selection is observed to be very low in populations like the Ahom (0.2180), Kachari (0.2500) and Khamti (0.3120) of Assam (see review Sengupta and Gogoi, 1995b). Natural selection operates with moderate to average intensity in Sonowal (0.3640) and Kaibarta (0.3360) of Assam, Pnar (0.4012), Christian War Khasi (0.3592), Non-Christian War Khasi (0.4463), Semsa (0.6165) and Hajong (0.6310) of Meghalaya. It is likely that natural selection plays an important role in regulating the genetic composition of the populations of Arunachal Pradesh like the Apatani (0.8890), Gallong (0.1.070) and Khamti (0.9340).

Genetic Drift: Another important factor, which brings about changes in the genetic composition of a population, is genetic drift. Brooks (1899) first gave the idea about genetic drift. Then, it was systematically developed mostly by Wright since 1921. That's why, it is often referred to as the *Sewall Wright effect*. Genetic drift is a random

fluctuation in gene frequencies in a population from one generation to another. It is very effective in small populations because of the greater random sampling error in such populations. Accordingly, one of the basic assumptions of the Hardy-Weinberg law is that a population should be large. In fact, genetic drift largely depends on the effective population size, which is a measure of the actual numbers of breeding individuals in a population (Wright, 1938, 1940; Nei, 1965; Crow and Kimura, 1970; Cavalli-Sforza and Bodmer, 1971). Since the gene pool of each generation represents a sample drawn from the previous generation, the smaller the population the greater the fluctuations will be. Thus, the allele frequencies of the new generation may not be totally representative of the parental population in a small population. For example, if the frequency of allele d is q in a parental population, the probability that q should take a particular value in the next generation is given by

$$\frac{2N\ !}{K\ !(2N-K)\ !}(q)^{K}(1-q)^{2N-K}$$

Where N = total number of individuals, k = expected number of alleles, and q = allele frequency in the parental population. Suppose, the frequency of q in a population of 5 diploid individuals is 0.5, the probability that the same frequency of q (0.5) will occur in the next generation is 24.61 %, whereas in the case of a population with only 2 individuals, it is about 37.50 %.

For simplicity, let us consider the mating between two heterozygotes, i.e. individuals who carry 50 % of allele D and 50 % of allele d. This type of mating would produce three types of genotypes with probabilities: ¼ DD, 1/2Dd, 1/4 dd. Substituting the above formula, we get,

$$\frac{N\ !}{D\ !d\ !x\ !}(1/4)^{D}(1/4)^{d}(1/2)^{x}$$

Where N = total number of individuals, D = expected number of individuals with DD genotypes, d = expected number of individuals with dd genotypes, and x = N – (D + d), i.e. expected number of individuals with Dd genotypes. Assuming these two parents have only two children, the genetic constitution, or gene pool of the next generation would be either one of the six combinations of genotypes (3 x 2), that is, if there are three children, it would be 3 x 3 and so on. It is seen from Table **2.2** that the probability that both the children would be DD genotypes is 6.25 %. Similarly, the probability that the two children of dd genotypes would form the genetic composition of the next generation is 6.25 %. Consequently, in the absence of mutation, selection and migration, either one of the alleles would be lost or fixed in small population due to random sampling process. As a result, the fate of small population is either extinction or fixation of the advantageous allele.

Table 2.2. Probabilities of the two offspring genotypes in the mating between heterozygotes.

Offspring genotype	Allele frequency		Probability (%)
	D	d	
DD, DD	1.00	0.00	6.25
DD, Dd	0.75	0.25	25.00
DD, dd	0.50	0.50	12.50
Dd, Dd	0.50	0.50	25.00
Dd, dd	0.25	0.75	25.00
dd, dd	0.00	1.00	6.25

Thus, it is believed that in small population the role of genetic drift is more important than that of mutation and selection, i.e. an allele may be lost or fixed with little reference to selection and mutation pressures. In the case of the population shown in Table **2.2**, there is a chance of 6.25 % that an allele d will be lost or fixed, though such an allele is favoured by the natural selection. So it means that the intensity of natural

selection will become either zero or 100 % in such a population. However, selection is more effective in large population than the genetic drift. Suppose, for example, the selection coefficient (s) against the allele d is 0.001. In a population with the effective population (N_e) of 100 individual, the product of N_e and s is 100 x 0.001 = 0.1, whereas in the population with the N_e of 10,000, the product is 10. Therefore, the changes in allele frequencies are largely due to genetic drift in small isolated populations, but the situation is just reverse in large populations where selection is more important. Similar phenomenon is in the case of mutation. According to Dobzhansky (1970), the mutation and selection rates may be regarded as small if the product $4N\mu$ and $4N_es$ is less than unity. In fact, the role of genetic drift in regulating the genetic composition of a population is enhanced by the neutral theory of protein evolution postulated by Kimura (1968, 1983) and others. The exponents of this theory have proposed that most of the polymorphisms found in natural populations are neither useful nor harmful to their carriers, but simply neutral so that natural selection has little role to play. The frequency of such neutral mutants in populations largely depends on chance and random sampling.

In Northeast India, there are hardly studies, which are concerned with the effect of genetic drift on the genetic composition of the population. The findings among the War Khasi (Khongsdier and Ghosh, 1994, 1996) and the Semsa (Limbu and Khongsdier, 2000) indicate that genetic drift plays a very important role in regulating the genetic make up of these populations. It is likely that there are still several small and isolated populations in different states of Northeast India where genetic drift plays an active role. Thus, it may be necessary to carry out thorough studies in this field with a view to having a better understanding of the evolutionary effectiveness of genetic drift in natural population.

Gene Flow: According to Johnston (1973), "The process by which genetic variation is introduced into a population is called gene flow, migration, or admixture". It occurs when genes from outside are introduced in the gene pool of a native population, or when a hybrid population is formed owing to the admixture of the gene pools of two or more populations. It is expressed as $m = (q_a - q_n)/(q_a - q_b)$, where m stands for the admixture rate, q is the allele frequency in population *n*, and q_a and q_b are the frequencies of the

same allele in the populations *a* and *b*, respectively. In Northeast India, no report has been published in this respect, though it is always mentioned that gene flow is very important factor for regulating the gene frequencies in the populations. An attempt has, however, been made in some studies (Barua, 1986; Khongsdier, 1994, Khongsdier and Ghosh, 1994, 1996) to estimate the admixture rate on the basis of the number of gamates introduced from outside into the native population. These studies have revealed that the admixture rate in populations of Northeast India varies from zero per cent onwards.

Thus it is obvious from the present review that many studies have been carried out in Northeast India to find out the genetic variation between and within populations, but there are hardly any studies, which deal with the causes of such genetic variation. The speculation that the micro-genetic variation within a given population is due to either mating patterns or geographical isolation is always possible, but hardly meaningful without empirical evidence. Therefore, it warrants further in-depth studies with a view to understanding the causes of genetic variation between and within populations in Northeast India.

CHAPTER III
MATERIALS AND METHODS

In this chapter we shall discuss the materials collected for the present study and the methods that have been applied.

The present research study on population genetics among the Koch of West Garo Hills, district, Meghalaya, has been carried out in two phases. The first phase of the study was carried during April – May 1996, and the second phase was carried out during the period between September and December 1996. Data were collected from five subgroups of the Koch population of Garo Hills, namely, Chapras, Sangas, Satparis, Tintikiyas and Wanangs. No statistical sampling technique was applied for data collection of the present study. Instead, it is considered to be convenient to select one major village from each Koch sub group. The villages selected for the present study are Andherkona for the Chapras, Harigaon for the Sangas, Kariatola for the Satparis, Sangko Para for the Tintikiyas and Mar*riangapara* for the Wanangs.

Data on demographic parameters, adult anthropometry, genetic traits viz, ABO and Rh blood groups, P.T.C. taste blindness, colour blindness, earlobe attachment, middle-phalangeal hair, behaviour traits like hand clasping, arm folding, tongue rolling and tongue folding and dermatoglyphics were collected from each of the above mentioned village. The nature and methods of data collection may be described briefly as follows:

DEMOGRAPHIC DATA

Demographic data were collected from each of the five selected villages 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 Organisation (WHO, 1964, 1968), which are as follows:

Individual Records: Individual records include information on name, age, sex, marital status, occupation, education, religion, community affiliation, place of birth, place of residence, clan, tribe, etc., were collected through structured household schedule.

The reproductive history: Information on reproductive performance of each married woman was collected through fertility schedule and pedigree. Special attention was given to collect data on age at marriage, age at first birth, number of pregnancies, number of live births, number of abortions (spontaneous and induced abortion), still-birth, birth order, age, sex and marital status of each offspring, if death - age at death, etc.

Mating Patterns: Data on mating patterns include number of marriages, marriages within the village, marriages with other subgroups and other populations, marital distance in the case of marriage with other subgroups or populations, i.e., distance between the place of residence and birth place of the spouses, and consanguineous relationship between spouses were also collected.

Age: Age of each member of the household was recorded. But in the present study we also faced certain difficulty in collecting data on age of individuals especially those elderly individuals because they were not aware of their real age. Consequently, we had to estimate the age of individuals in certain cases with reference to some important local events. Consequently some amount of error might have occurred in estimating the age of persons. However, these data were cross-checked on several occasion, at the time of collecting pedigrees from various people, including relations and neighbours. For younger generations, the child's deciduous as well as permanent dentition was also considered for assessing age.

ANTHROPOMETRIC DATA

The anthropometric measurements were taken on 250 adult males aged from 20 years to 60 years. Sixteen measurements were considered for the present study. They are as follows: Height vertex, sitting height, height tragus, height acromion, head length, head height, head breath, upper facial length, total facial length, nasal height, nasal breadth, head circumference, chest girth, minimum frontal breadth, bizygomatic breadth and bigonial breadth, on all the subjects. An effort had been made to take into consideration those methods and techniques of measurements suggested by the International Biological

Programme given in Weiner and Lourie (1981) and Sen (1994). A brief description of the anthropometric measurements may be given as follows:

Height

It means the vertical distance between the floor and the landmark vertex. While taking the measurement, the subject was asked to stand erect a wall with his/her heels joined together and touching the wall, the arms hanging loose on his/her sides, the palms touching the thighs and the head resting on the eye – ear or Frankfurt horizontal plane. The subject was not allowed to wear any kind of foot wear. Standing on the front of the subject, the anthropometer was placed vertically in the mid – sagittal plane. Then the cross – bar fitted to the movable socket was lowered to touch the vertex gently and the reading was noted.

Sitting Height

It measures the vertical distance from the vertex to the plane. The subject was made to sit on a stool keeping the thighs horizontally and the knees unbending. The vertebral column was made to stretch to the maximum and the head resting on the Frankfurt horizontal plane. The anthropometer was held vertically at the back of the subject in the mid – sagittal plane allowing the instrument to rest on the surface where the subject was sitting. The cross – bar on the movable socket was lowered to touch the vertex gently and the reading was recorded.

Height Tragus

It measures the vertical distance from the tragion to the floor. While taking the measurement, the subject was asked to stand erect against a wall with his/her heels joined together and touching the wall, and hands hanging loose on his/her sides, the palms touching the thighs and head resting on Frankfurt horizontal plane. The subject was not allowed to wear any kind of foot-wear. Standing on the front of the subject, the anthropometer was placed vertically in the mid – sagittal plane. Then the cross – bar fitted to the movable socket was lowered to touch the tragion point gently and reading was noted.

Height Acromion

It measures the vertical distance from the acromion to the floor. The arm of the subject was positioned in such a manner beside the body that it was parallel to the anthropometer rod. Anthropometer is placed on the right side with the left hand palpating to locate the

landmark and the right hand sliding the movable cross – bar to touch the acromion. The subject was not allowed to sink or elevate his/her shoulders, while taking the measurement.

Head Length

It measures the straight distance between glabella and opisthocranion, i.e., the most projecting point on the dorsal surface of the head in the mid–sagittal plane. The measurement was taken with a spreading caliper. One tip of the caliper was placed on the glabella point with the help of left hand and the other tip of caliper on the opisthocranion with the right hand. While taking the measurement, less pressure was applied so as not to create discomfort to the subject.

Head Breadth

It measures the straight distance between the two eurya (eu) i.e., maximum breadth taken at right angle to mid–sagittal plane wherever found. The measurement was taken by holding the spreading caliper in such a manner behind of the subject, and that the joint of the caliper was in the mid–sagittal plane of the head. Then, the tips of the caliper was sliding forward and backward to get the maximum breadth.

Head Height

It measures the projective distance between tragion and vertex. It was obtained by substracting the height tragus from the height vertex.

Horizontal Head Circumference

It measures the maximum circumference of the head taken horizontally. The measurement was taken by holding the tape with left hand on glabella and then rotating horizontally over the opisthocranion back to glabella.

Minimum Frontal Breadth

It measures the straight distance between the two fronto-temporalia. Before taking the measurement, the two points were marked and the instrument was placed on the temporal bone to get the accurate measurement.

Bizygomatic Breadth

It measures the straight distance between the two Zygia, i.e., the most lateral points on the zygomatic arch. The greatest breadth of the bizygomatic arch is usually found near the ear and not on the cheek. The spreading caliper was gently moved forwards and

backwards in such a manner that its two ends touched gently the zygomatic arches. The maximum value was recorded.

Bi-gonial Breadth

It measures the straight distance between the two gonia, i.e., the most lateral points on the posterior inferior angle of the lower jaw. The tips of the spreading caliper were placed gently on the two gonion points with the help of the tips of the index finger.

Total Facial Length

It measures the straight distance between nasion and gnathion. The measurement was taken by holding the sliding caliper in such a manner that the upper arm of the caliper fixed the nasion point, while the lower arm touched the gnathion point.

Upper Facial Length

It measures the straight distance between nasion and prosthion. The subject was asked to grin and show his/her teeth. Then the measurement was taken in such a manner that the upper arm of the caliper was fixed on the nasion point and the lower arm on the prosthion landmark.

Nasal Height

It measures the straight distance between nasion and subnasale. The measurement was taken by holding the sliding caliper in such a manner that the lower arm of the caliper touched the sub-nasale point and its upper arm was held between the thumb and first finger on nasion.

Nasal Breadth

It measures the straight distance between two alare points. The measurement was taken from the front side of the subject. The flat surface of the fixed cross–bar was placed in such a manner to touch the alare point of the right side of the nose and then the movable cross–bar was sliding to touch the left alare in order to obtain the measurement.

Chest Girth

It measures circumference of the chest of subject when he is breathing normally. This measurement was taken with a steel tape (Precision–1mm) at the level of the mesosternale, at the right angle to the axis of the body and reading was taken.

GENETIC MARKERS:

ABO Blood Groups: Blood samples on 462 individuals 250 males and 212 females were collected from the five sub groups of Koch. The Chapra sample consisted of 103 individuals, Sangas-75 individuals, Satparis- 75 individuals, Tintikiyas - 105 individuals and Wanangs- 104 individuals. The standard slide method suggested by Lawler and Lawler (1951) and Bhatia (1977) was followed for collection of blood samples in the present study, which may be summarised as follows:

(a) A clean glass slide marked A and B was used for blood testing.

(b) Anti-A and anti-B, supplied by Span Diagnostic Ltd (Surat), were dropped on the glass side which was marked A and B, respectively.

(c) Before taking the blood sample from the subject, his/her finger was cleaned with 90% alcohol. Then, the clean finger was pricked with the help of sterilised disposable lancet, and then squeezing it gently till the blood came out for about two drops or so.

(d) One drop of the blood was then added to the anti-A antisera and another drop of blood to anti-B antisera on the glass slide. The mixture was then stirred thoroughly with a rod stirrer, and allowed it to stand for about 3 to 4 minutes. A drop of saline water was also added as a precaution against coagulation.

(d) The results were noted after five minutes. If agglutination took place at A, a person was treated as belonging to the A blood group, and if agglutination was present at B, a person was treated as belonging to the B blood group. If agglutination did not take place on both A or B, a person was categorized as belonging to O blood group.

Rh(D) Blood Groups

For Rh blood grouping one drop of anti D serum was taken in a glass side and a one drop of packed red cell was mixed thoroughly with the anti sera. If agglutination occurred, it was taken as positive reaction, i.e., Rh-positive and lack of agglutination was taken as negative result, i.e., Rh-negative.

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. Total 462 individuals were tested 250 males and 212 females.

A stock solution containing 0.13% of phenylthiocarbamide (PTC) was prepared with distilled water following Mohr (1951). From this stock solution, 12 additional serial solutions were made by diluting half of the solution with equal quantity of boiled tap water, starting from the first solution to the solution No.13. In this way a serial dilution of PTC was prepared, in which the concentration of the solution in each bottle become half of the previous bottle. In the last bottle i.e., bottle No. 14 contains simple plain water.

The subjects were asked to wash their mouths before tasting the solutions, specially to those who were found chewing tobacco or smoking. First of all a few drops of plain water from the bottle No.14 were dropped into the mouth of the subject, and then the solution No. 13, 12, 11 etc. were given in descending order. When the subject got the taste, the number of the solution was noted as his/her threshold value.

Colour blindness

The Ishihara chart (1959) was used to collect date on 250 male individuals among 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 number of the 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 along with the Ishihara plates.

.Computation of Allele Frequencies and Goodness of Fit

In the present study we have followed the following methods for calculating the gene frequencies in respect of the ABO and Rh(D) blood groups, PTC taste sensitivity, and colour blindness.

ABO Blood Groups: For calculating the allele frequencies of the ABO blood groups, we have followed the method suggested by Bernstein (1930), which is as follows:

$$\left.\begin{array}{l} p = 1-\sqrt{(a_1 - a_3)} \\ p = 1-\sqrt{(a_1 - a_2)} \\ r = 1-\sqrt{a_1} \end{array}\right| \quad \ldots\ldots (1)$$

Where a_1, a_2 and a_3 are the phenotype frequencies of the blood groups O, A, and B, respectively; whereas p, q and r are the allele frequencies of the genes A, B and O, respectively. If the sum of p, q and r are not equal to unity or 1, Bernstein (1930) has suggested a simple method by which the allele frequencies defined by equation (1) can be adjusted as follows:

$$\left.\begin{array}{l} p' = p(1+ D/2) \\ q' = q(1+ D/2) \\ r' = (r + D/2)(1 + D/2) \end{array}\right| \quad \ldots\ldots (2)$$

Where $D = 1 - (p + q + r)$

The *standard errors* of allele frequencies were calculated according to the method suggested by Balakrishnan (1988). In the case of the allele frequencies for the ABO blood groups, the following quantities were first calculated to obtain the variance in p, q and r alleles:

$I_{pp} = \Sigma(A^2/E)$ ..... (3)

$I_{qq} = \Sigma(B^2/E)$ ..... (4)

$I_{pq} = I_{qp} = \Sigma\{(A)(B)/E\}$ .....(5)

Where E, A and B are obtained as follows:

Phenotype	E	A	B
A	$P^2 + 2pr$	2r	-2p
AB	2pq	2q	2p
B	$q^2 + 2qr$	-2q	2r
O	r^2	-2r	-2r

Thus, the variances for p, q and r alleles are calculated as follows:

$V_{(p)} = I_{qq}/IG$ ..... (6)

$V_{(q)} = I_{pp}/IG$ ..... (7)

$V_{(r)} = (I_{qq} + I_{pp} - 2\, I_{pq})/IG$ .... (8)

Where G is the total number of samples, and $I = \{(I_{pp})(I_{qq}) - (I_{pq})^2\}$ ..... (9)

Thus the *standard error* of the allele frequencies are the square root of the variances obtained as per equations (6), (7) and (8).

The *Goodness of Fit Chi-square* is obtained as follows:

Chi-square (χ^2) = $G\{a_1^2/ r^2 + a_2^2/(P^2 + 2pr) + a_3^2/(q^2 + 2qr) + a_3^2/2pq\}$ - 1

Where the observed and expected frequencies are worked out as follows:

Phenotype	Observed frequency (O)	Expected frequency (E)
O	a_1	r^2
A	a_2	$P^2 + 2pr$
B	a_3	$q^2 + 2qr$
AB	a_4	$2pq$

Rh(D) Blood Groups: The allele frequencies for the Rh(D) blood groups were obtained by the following formula:

$d = \sqrt{Rh^-}$

$D = 1 - d$

Where Rh^- is the proportion of individuals with Rh-negative and d stands for the allele frequency Rh-negative factor. The *standard of error* (SE) the d allele is obtained as

$SE = \sqrt{(1- d^2/4G)}$, where G is the total number of sample individuals.

PTC Taste Sensitivity: The allele frequencies for PTC Taste Sensitivity were obtained by the following formula:

$t = \sqrt{Nt}$

$T = 1 - t$

Where Nt is the proportion of non-tasters to PTC and t stands for the allele frequency. The *standard of error* (SE) for t allele is obtained as

$SE = \sqrt{(1- t^2/4G)}$, where G is the total number of sample individuals.

DATA ON MORPHOLOGICAL AND BEHAVIOURAL TRAITS

Data on morphological and behavioural traits like earlobe attachment, hand clasping, hand folding, tongue rolling, tongue folding, digital formulae of fingers and toes and mid-phalangeal hair were collected from a sample of 462 individuals. The sample comprises 103 Chapras (51 males and 52 females), 75 Sangas (41 males and 34 females), 75

Satparis (41 males and 34 females), 105 Tintikiyas (61 males and 44 females), and 104 Wanangs (56 males and 48 females). Individuals of close blood relation were excluded from the sample. The methods of data collection for morphological and behavioural traits may be briefly described as follows:

Hand Clasping: Data on hand clasping was collected following the technique suggested by Lutz (1908). The subjects were asked to clasp their hands in natural way. The subjects were classified as R>L (right over left) and L >R (left over right), depending on how they clasped their hands. The phenomena were repeated at least thrice to ascertain the observations.

Arm folding: The type of arm folding were categorised following Weiner (1932). The subjects were asked to fold their arms in a natural way. The subjects were classified as R>L (right over left) or L>R (left over right), depending on how they folded their arms naturally. The subjects were asked to do it least three times so as to make sure of their behavioural habit of folding their arms.

Tongue Rolling: Standard methods (Sturtevant, 1940) were adopted in recording the ability for 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" (Montagu, 1945). The observation was recorded as positive and negative respectively for those individuals who were able and not able to roll their tongue.

Tongue Folding: The subjects were asked to extend the tongue to fold in without touching the lips. 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: Information on manual middle phalangeal hair was collected after the subjects had cleaned their hands with soap and dried them carefully with a cloth. 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.

DERMATOGLYPHIC DATA

Fingers ball (Digital) and Palmar Dermatoglyphics: The standard methods suggested by Cummins and Midlo (1961) were followed to collect finger ball and Palmar prints.

The materials, required for taking prints were white paper, printing ink, a plate of spreading ink, pencil, soap, thin piece of cloth, cotton and rectified spirit.

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, grease, etc., 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 view to making a thin film by a cotton pad (Das and Deka, 1993).

Digital prints: To make a rolled impression, the bulb of the fingers was smeared evenly by the inked cotton pad. The finger was then placed upon the paper with the nail at right angel to the plane of the paper, and it was slowly turned over until the bulb surface (which was originally facing to the left) turned to the right. In this way a clear rolled impression of the finger surface was obtained.

Palmar Prints: The subjects palm was smeared with the inked cotton pad in such a way that all the ridges of the palmar surface would be properly inked. In this process, the palmar surface from first bracelet area to the first phalangeal crease was properly inked and then the palm was placed on the paper. To transfer the print on the paper, a little pressure was exerted on the ulnar and radial borders, inter digital areas and mid-palmar region.

Precautions: Following precautions were taken on order to avoid the errors in printing: (a) Care was taken not to press the finger to hard on the paper, (b) the plate used for spreading ink was made clean to make it free from dust, hair or any other foreign bodies,

(c) a very thin film of ink was applied with a view to getting a clean and sharp print, and (d) the persons with depression or severe cuts were not included in the present sample.

In the subsequent chapters we shall present the results of our findings on demographic, anthropometric measurements, genetic markers, behavioural traits and dermatoglyphics characters among the Koch.

STATISTICAL METHODS

The statistical analyses, which are adopted in the present study, may be briefly described as follows:

Mean: The mean is also known as arithmetic average. It is defined as the value which can be obtained by dividing the total values of various items in a series by the total number of items. It is worked out as under:

Mean ($\bar{X}$) = $\Sigma X_i/N = (x_1 + x_1 + \ldots + x_n)/N$, where is the value of the i-th item X_I, i =1, 2, ..., n, and N stands for the total number of items.

In the case of frequency distribution, the mean is obtained as follows:

Mean ($\bar{X}$) = $\Sigma f_i x_i/f_i N = (f_1x_1/f_1 + f_2x_2/f_2 + \ldots + f_nx_n/f_n)/N$, where f_ix_i is the product of the mid value (x_i) of i-th class-interval and the frequency (f_i) of the i-th item.

Standard Deviation (SD): Standard deviation is defined as the square root of the mean of the squares of the deviation of observations from their arithmetic mean. It is computed as follows:

$SD = \sqrt{\{(X_i - \bar{X})^2/N - 1\}}$

Where X_i is the value of the i-th item, $\bar{X}$ stands for the mean, and N is the total number of cases. In the case of frequency distribution, the SD is obtained as follows:

$$SD = \sqrt{\{(\Sigma fd^2/N - 1) - (\Sigma fd/N-1)^2\}} \times C$$

Where fd is the product of the deviation from the assumed mean (d) and the frequency (f) of item in the i-th class-interval; while C stands for class interval.

The divisor was taken as (N – 1) but not as N because we did not know the true mean and standard deviation of the population. So the mean and standard deviation were estimated through samples collected for the present study, and in doing so we lost what is known as a degree of freedom (Parker, 1973).

Standard Error of Mean (SE): It is calculated as SD/√N-1.

Differences between two means: In the present study, the number of observations in two sample means are almost more than 50. Therefore, the statistical difference between two means is worked out according to standard t-test given as follows:

$$t = (\bar{X}_1 - \bar{X}_2) \div \sqrt{\{(SE_1)^2 + (SE_2)^2\}}$$

where $\bar{X}_1$ and SE_1 are the mean and standard error of a given variable for the first sample, while $\bar{X}_1$ and SE_2 are the mean and standard error of the same variable for the second sample of the same population or different populations.

Differences between proportions: In the present study, the differences between proportions were tested by using the chi-square (χ^2). It is obtained as follows:

$\chi^2 = \Sigma(O_i - E_i)^2/E_i = (O_1 - E_1)^2/E_1 + (O_1 - E_1)^2/E_1 + \ldots + (O_n - E_n)^2/E_n$

where O_i and E_i are the observed and expected frequencies of the i-th character in each class.

The value obtained is then compared with that given in the Table of Chi-square distribution with (N –1) degree of freedom (d.f.). In the case of 2 × C contingency Table, the number of d.f. is (Row –1)(Column – 1). The expected frequency is calculated as (Row Total)(Column Total)/(Grand Total) OR (Column Total)/(Grand Total) multiplied by Row Total.

Analysis of Variance (ANOVA): One way analysis of variance was used for testing the differences between the means of more than two samples (Snedecor and Cochran, 1967). The basic procedure consists in examining the amount of variance "Within Samples" in relation to the amount of variance "Between Samples". Following are the steps followed for computing this test:

1. Correction factor (C) = $(\Sigma X_i)^2/N$, where X_i is the total number of ith item in all the samples, and N is the total number of items in all the samples.
2. Total sum of squares (TSS) = ΣX_i^2 - C, where X_i^2 is the square of each ith item in all the samples.
3. Sum of squares for variance between samples (SSB) = $n_1(\bar{X}_1 - \bar{X}) + n_2(\bar{X}_2 - \bar{X}) + \ldots + n_k(\bar{X}_k - \bar{X})$,

where $\bar{X}$ = Overall mean for all items in all samples

$\bar{X}_1$, $\bar{X}_2$, . . . , $\bar{X}_k$ = Sample means 1, 2, . . . , k

$n_1, n_2, \ldots, n_k$ = Number of items in samples 1, 2, . . . , k.

4. Sum of squares for variance within samples (SSW) = (TSS – SSB)
5. Mean squares for variance between samples (MSB) = SSB/(K- 1), where (K – 1) is the degree of freedom between samples, i.e., K = Number of samples compared.
6. Mean square for variance within samples (MSW) = SSW/(N- K), where (N – K) is the degree of freedom for all individual items for all samples, i.e., N = Number of individual items for all samples.
7. F- ratio = MSB/MSW

The value obtained is then compared with that in the Table of F-distribution with (K – 1) as larger variance and (N – K) as smaller variance, taking 95% confidence interval.

Correlation and Regression Analysis: Regression analysis has many applications. The main purpose is the regression analysis is to know if Y (dependent variable) does depend on X (independent variable), or to make a prediction of Y from X. In the present study, we are also concerned with with the error in Y-variable after adjustments were made for the effects of X-variable. The regression coefficient (b) of Y on X is worked out as follows:

$$b = \Sigma xy/\Sigma x^2$$
where $\Sigma xy = \Sigma XY - (\Sigma X)(\Sigma Y)/N$
$\Sigma x^2 = \Sigma X^2 - (\Sigma X)^2/N$

The regression of Y on X is expressed as

$\bar{Y} = a + bX$, where $a = \bar{Y} - \bar{X}b$, and $\bar{Y}$ = Estimated value

Correlation coefficient(**r**)**:** The correlation coefficient was computed as follows:

$$r = \Sigma xy \div \sqrt{\{(\Sigma x^2)(\Sigma y^2)\}}, \text{ where } y^2 = Y^2 - (Y)^2/N$$

The correlation coefficient is usually taken when there is no reason to think of one variable as dependent variable and the other as the independent variable. It is taken as a simple measure of the degree of relationship, but not to make out the nature of relationship between two or more variables.

CHAPTER IV
DEMOGRAPHIC CHARACTERISTICS

In this chapter we shall describe the results of data on demographic parameters collected from all the five subgroups of the Koch population of Garo Hills in Meghalaya.

Age and Sex Structure

According to Sundbarg's classification of population, a population is said to be *progressive* when the number of persons in relation to the total population are 40.00%, 50.00% and 10.00% in the age groups 0-14, 15-49 and 50 + years, respectively. The population is referred to as *stationary* if these frequencies are 33.00%, 50.00% and 17.00%, respectively; while the frequencies of 20.00%, 50.00% and 30.00%, respectively, are the characteristics of *regressive* population (Khongsdier, 2001). Thus according to this classification of population, Table 4.1 shows that the Chapra population tends to be *regressive* in which the base of the population pyramid constricted (Figure 4.1) indicating the low fertility rates in the population. On the other hand, the Sanga, Satpari and Tintikiya populations are of *stationary* types of population (Figures 4.2, 4.3, and 4.4), which are by and large an indication 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 approaches to be of *progressive type*, which is characterized by high fertility rates. The population pyramid (Figure 4.5) shows that the base is broad, although it tends to be constricted in the case of females, i.e., it indicates to a certain extent that infant and child mortality rates are higher in males than in females among the Wanangs.

Table 4.1 also shows that the overall sex ratio (i.e., the 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), though it is not significant ($\chi^2 = 0.32$, DF = 1, P >0.05). Among the Sangas (81.65), Satparis (96.75)

and Tintikiyas (93.84), the sex ratio is low, especially in the former. However, the Chi-square values indicate the sex ratios do not deviate significantly from the ideal sex ratio of 1:1 in all the three populations, namely, the Sangas (χ^2 = 2.93, DF = 1, P > 0.05) Satparis (χ^2= 0.07, DF = 1, P > 0.05) and Tintikiyas (χ^2 = 0.41, DF = 1, P > 0.05). Also, the differences in sex ratio between populations are found to be statistically insignificant (χ^2 = 3.04 DF = 4, P > 0.05). In comparison with the sex ratio among the War Khasi (109) of Meghalaya (Khongsdier and Ghosh, 1994), the overall sex ratio is lower in each of these Koch subgroups. In fact, it indicates that male mortality is higher than female mortality in the Sangas (81.65), Satparis (96.75) and Tintikiyas (93.84).

In the age group 0-14 years, the sex ratio is high among the Chapras (108.33), but it is lower in the Wanangs (97.47), Tintikiyas (90.28), Satparis (92.50) and Sangas (66.07), although the chi-square values indicate that the deviation from the ideal sex ratio of 1:1 is not statistically significant for all populations (P >0.05), except for the Sangas where the sex ratio is significantly low (χ^2 = 3.88, DF = 1, P < 0.05). It is also found that the differences in sex ratio between populations are not statistically significant (χ^2 = 3.05, DF = 4, P> 0.05).

In the middle age group 15-49 years, the sex ratio among the Wanangs (101) and Chapras (103) is more or less according to the ideal sex ratio, but it is again lower in the Sangas (89), Satparis (95) and Tintikiyas (94), although it is not significant (P > 0.05).

Table 4.2 shows the marital status of individuals in all the subgroups of the Koch population. It is found that in the Sangas, Satparis and Tintikiyas none of the male individuals get married at the age of 24 years and below. On the other hand, about 16.67%, 18.60% and 14.93% of the married females have got married by the age of 24 years and below, in the Sangas, Satparis and Tintikiyas, respectively. Among the Chapras and Wanangs, about 4.62% and 7.06% of the married males get married at the age of ≤ 24 years, respectively. In the case of married females, about 18.46% of them in the Chapras and 28.00% in the Wanangs are married by the age of 24 years and below. Thus, it indicates that the marriage is much more delayed in males than in females as generally observed in many India populations (Khongsdier, 2001).

Table 4.1. Total population of the five Koch subgroups by age and sex

Age group (years)	Chapras		Sangas		Satparis		Tintikiyas		Wanangs	
	Male	Female	Male	Female	Male	Female	Male	Female	Male	Female
0 - 4	11	14	7	17	11	16	26	25	22	29
5 - 9	11	12	15	20	18	13	25	26	31	29
10 -14	17	10	15	19	8	11	14	21	24	21
0-14	75		93		77		137		156	
%	24.19		32.40		31.82		33.50		39.39	
SR	108.33		66.07		92.50		90.28		97.47	
χ^2	0.12		3.88*		0.12		0.36		0.03	
15 - 19	16	18	18	13	15	13	25	26	21	26
20 - 24	16	20	11	15	6	17	21	24	12	18
25 - 29	19	12	14	17	16	13	18	22	22	15
30 - 34	18	13	12	10	10	10	9	16	12	16
35 - 39	18	13	8	15	7	6	21	13	18	14
40 - 44	8	8	9	7	6	8	9	11	8	6
45 - 49	5	13	6	11	10	7	9	7	12	9
15 - 49	197		166		144		231		209	
%	63.55		57.84		59.50		56.48		52.78	
SR	103.09		88.64		94.59		94.12		100.96	
χ^2	0.05		0.60		0.11		0.21		0.01	
50 - 54	8	6	2	4	3	5	6	7	7	3
55 - 59	4	7	6	5	4	3	7	8	3	7
60 +	9	4	6	5	5	1	8	5	7	4
50 +	38		28		21		41		31	
%	12.26		9.76		8.68		10.02		7.83	
SR	123.53		100.00		133.33		105.00		121.43	
χ^2	0.42		2.29		0.43		0.03		0.29	
Total	160	150	129	158	119	123	198	211	199	197
Persons	310		287		242		409		396	
%	100.00		100.00		100.00		100.00		100.00	
SR	106.67		81.65		96.75		93.84		101.02	
χ^2	0.32		2.93		0.07		0.41		0.01	

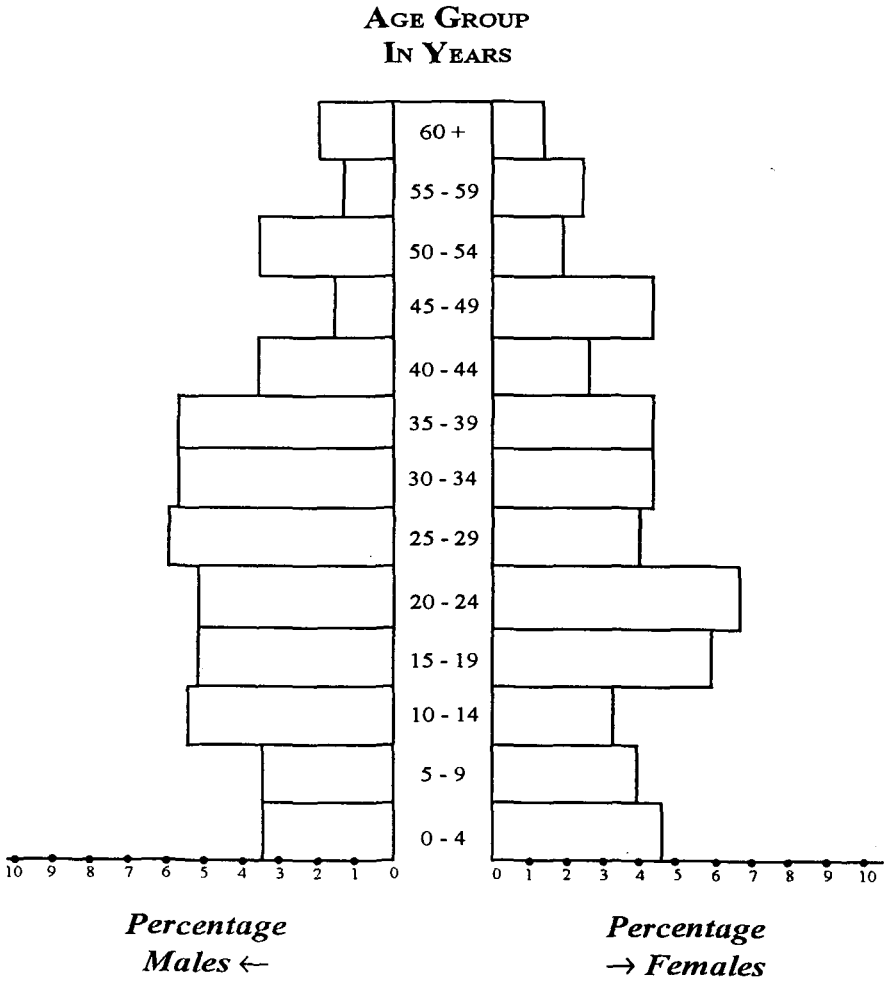


Fig.-4.1. Population Pyramid of Chapras

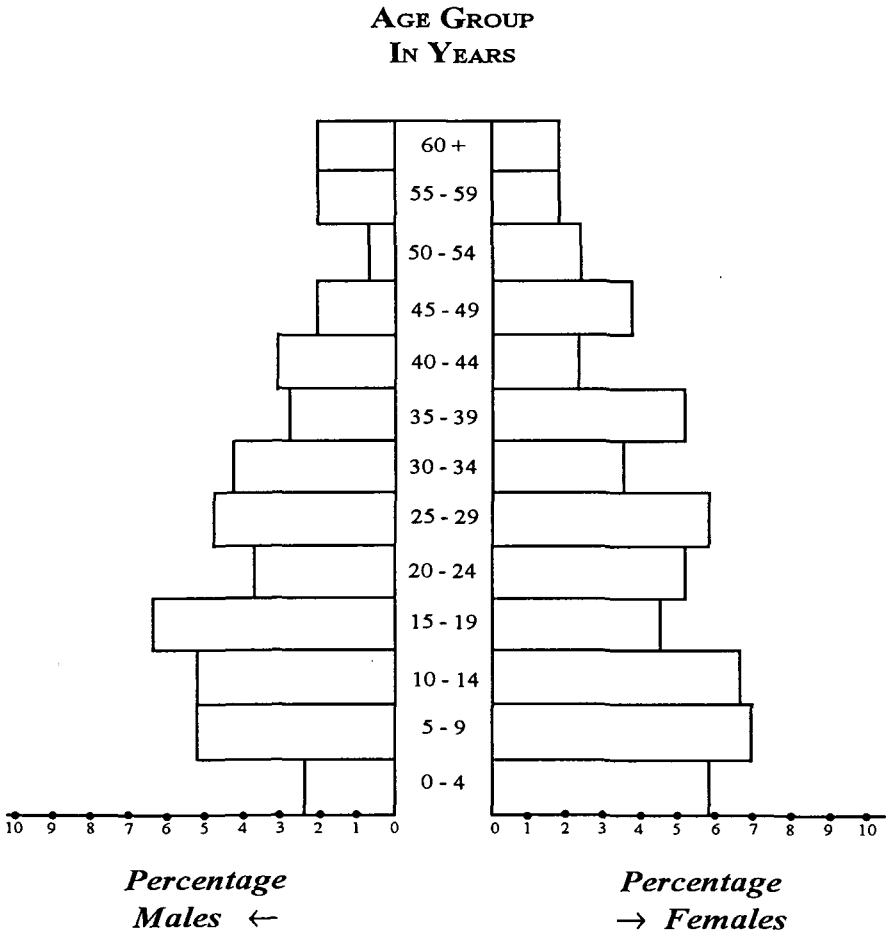


Fig.-4.2. Population Pyramid of Sangas

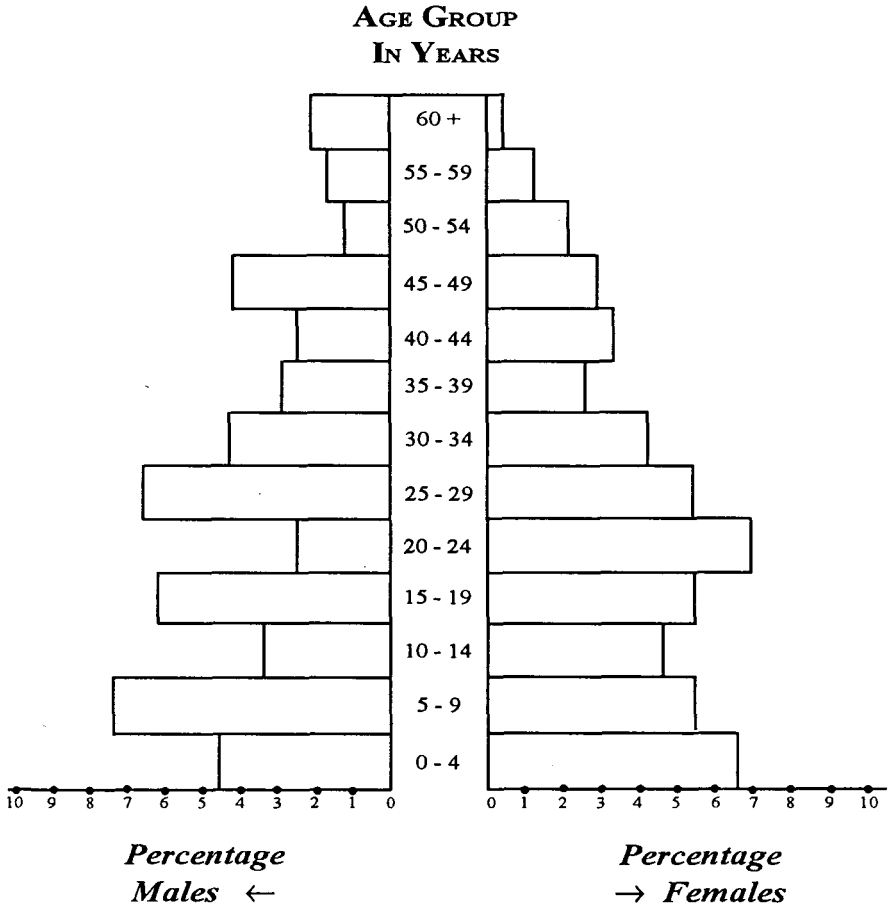


Fig.-4.3. Population Pyramid of Satparis

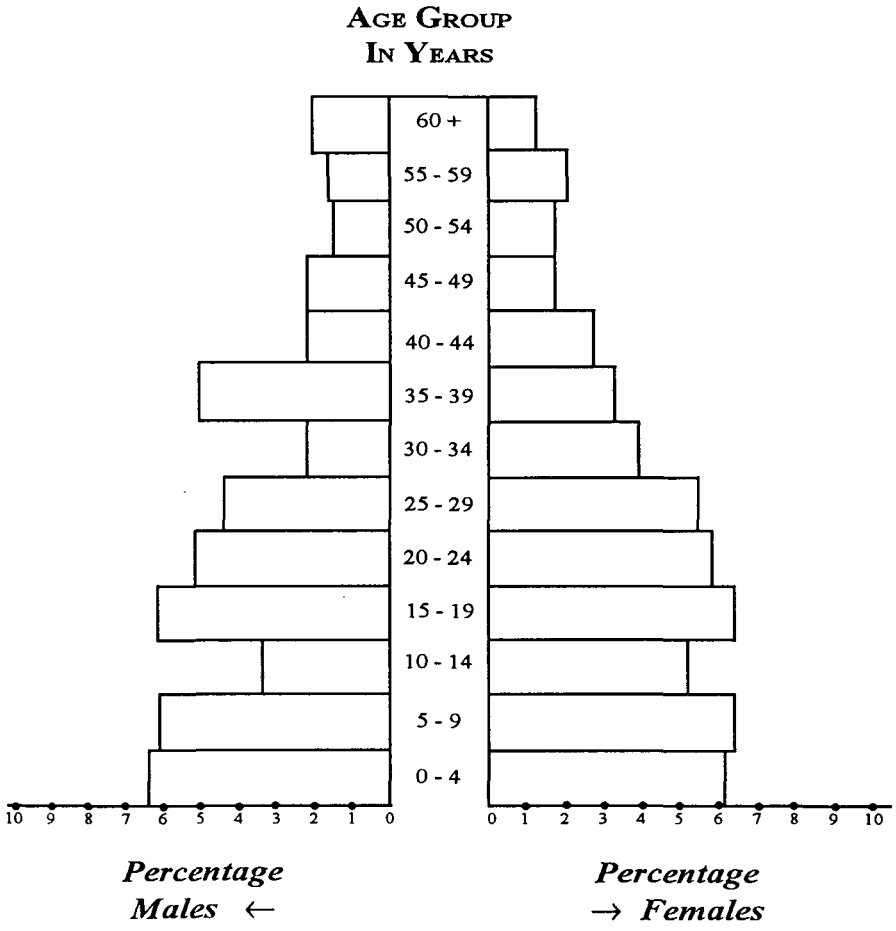


Fig.-4.4. Population Pyramid of Tintikiyas

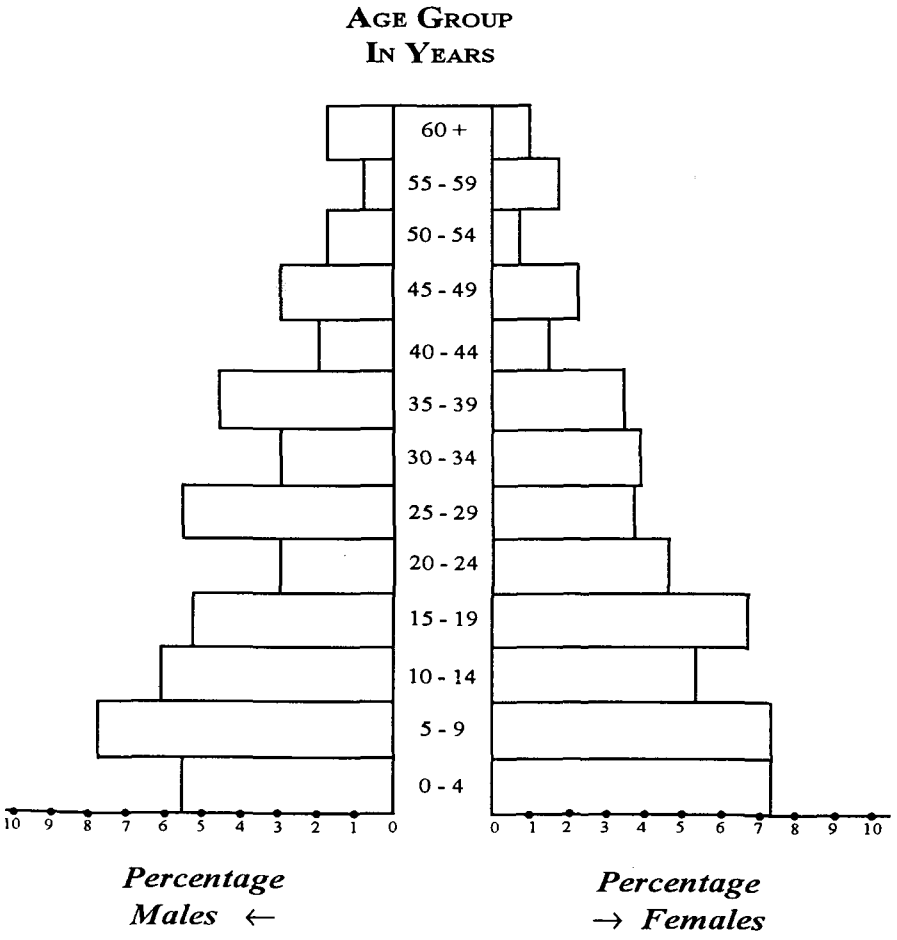


Fig.-4.5. Population Pyramid of Wanangs

Table 4. 2. Marital status of individuals by age groups

Population	≤ 24 years		25-29 years		30-34 years		≥ 35 years	
	Male	Female	Male	Female	Male	Female	Male	Female
Chapras:								
Married	3	12	6	11	8	12	48	30
Unmarried	68	62	13	1	9	1	2	2
DSW	0	0	0	0	1	0	2	19
Total	71	74	19	12	18	13	52	51
Sangas:								
Married	0	8	7	7	10	7	30	26
Unmarried	66	66	7	9	2	2	2	4
DSW	0	0	0	1	0	1	5	17
Total	66	74	14	17	12	10	37	47
Satparis:								
Married	0	8	7	10	9	8	27	17
Unmarried	58	62	9	3	0	1	1	2
DSW	0	0	0	0	1	1	7	11
Total	58	70	16	13	10	10	35	30
Tintikiyas:								
Married	0	10	6	14	7	12	54	31
Unmarried	111	112	12	8	2	2	4	1
DSW	0	0	0	0	0	2	2	19
Total	111	122	18	22	9	16	60	51
Wanangs:								
Married	6	24	16	13	11	15	52	33
Unmarried	104	99	5	1	1	0	2	0
DSW	0	0	1	1	0	1	1	10
Total	110	123	22	15	12	16	55	43

Table 4.3. Mean age at marriage (years)

Population	Male			Female		
	Number	Mean	SE	Number	Mean	SE
Chapras	68	25.03	0.47	84	18.12	0.36
Sangas	52	24.98	0.56	67	19.27	0.43
Satparis	50	23.18	0.59	56	17.43	0.50
Tintikiyas	68	25.21	0.57	89	17.42	0.43
Wanangs	87	23.41	0.46	94	16.97	0.33
F-ratio	3.41, $P < 0.05$			4.65, $P < 0.05$		

Mean age at Marriage

The mean age at marriage for both males and females are shown in Table 4.3. It indicates that there are significant differences between the subgroups of the population in mean age at marriage for both males ($F = 3.41$, $P < 0.05$) and females ($F= 4.65$, $P < 0.05$). In the case of males, the mean age at marriage among the Chapras (25.03 ± 0.47 years), Sangas (24.98 ± 0.56 years) and Tintikiyas (25.21 ± 0.57 years) is more or less same, but it is higher in these subgroups when compared with the Satparis (23.18 ± 0.59 years) and Wanangs (23.41 ± 0.46 years). In other words, the mean age at marriage among the Satparis males is significantly different from those in the Chapras ($t = 2.48$, $P < 0.01$), Sangas ($t = 2.21$, $P < 0.03$) and Tintikiyas ($t = 2.43$, $P < 0.02$). Also, the Wanangs males deviate significantly in mean age at marriage from their counterparts in the Chapras ($t = 2.43$, $P < 0.02$), Sangas ($t = 2.13$, $P < 0.03$) and Tintikiyas ($t = 2.49$, $P < 0.01$). Among the females, the mean age at marriage is highest among the Sangas (19.27 ± 0.43 years) followed by the Chapras (18.12 ± 0.36 years). But among the Tintikiyas (17.42 ± 0.43 years), Wanangs (16.97± 0.33 years) and Satparis (17.43 ± 0.50 years) women, the mean age at marriage is more or less similar, and it is significantly different from the Sangas and Chapras ($P < 0.05$). The one way analysis of variance (ANOVA) also shows that the population differences in mean age at marriage are statistically significant ($F = 4.65$, $P < 0.05$).

According to the review made by Sengupta and Gogoi (1995a), the mean values (±SE) of age at marriage in women of the populations of Assam like the Lalungs, Morans, Deuris, Mishings, Chutias, Ahoms, Kalitas, and Brahmins are 14.59±0.18, 18.51±0.23, 18.47±0.27, 18.43, 18.06 ± 0.16, 17.98 ± 0.29, 16.44 ± 0.15 and 16.51 ± 0.25 years, respectively. Khongsdier (2001) has reported that the mean age at marriage among the Christian and Non-Christian females of the War Khasi is 20.04 ± 0.32 and 19.44 ± 0.25 years, respectively. Thus, the mean age at marriage among the Chapras is more less similar to that among the Morans, Deuris, Mishings and Chutias, but higher than that among the Lalungs, Ahoms, Kalitas and Brahmins, and it is lower than that reported for the Christian and Non-Christian War Khasis. The mean age at marriage among the Sangas is, however, higher than all the above mentioned populations of Assam, but it is lower than that reported for the Christian and Non-Christian War Khasis. With regard to the Satparis and Tintikiyas, it is observed that the mean age at marriage is similar to the Ahoms, but lower than that reported for many populations, except the Lalungs. On the other hand, the Wanangs are similar to the Brahmins and Kalitas in mean age at marriage, although they are lower than many populations.

Mean age at first childbirth

The mean age at first childbirth is given in Table 4.4. Like in the case of the mean age at first marriage, the differences in mean age at first birth between the different divisions of the Koch subgroups are found to be significant for both males ($F = 4.59$, $P < 0.05$) and females ($F = 5.72$ $P < 0.05$). Among males, the mean age at first child birth is highest in the Tintikiyas (27.60 ± 0.61 years) followed by the Chapras (27.34 ± 0.57 years) and the Sangas (26.60 ± 0.50 years), whereas the Satpari (25.37 ± 0.69 years) and Wanang males (25.03 ± 0.43 years) are more or less similar in mean age at child birth. Both Satpari and Wanang males differ significantly from the other subgroups except the Sangas and Satparis ($t = 1.46$, $P > 0.05$).

In the case of females, the ANOVA indicates that there are significant differences between the Koch subgroups in mean age at first child birth ($F = 5.72$, $P < 0.05$). The mean age at first child birth is highest in the Sangas (21.02 ± 0.41 years) followed by the Chapras (20.08 ± 0.40 years) and Tintikiyas (19.40 ± 0.42 years). The Satpari and Wanang females are found to be more or less similar in mean age at first childbirth.

Table 4.4. Mean age at first child birth (years)

Population	Male			Female		
	Number	Mean	SE	Number	Mean	SE
Chapras	56	27.34	0.57	71	20.08	0.40
Sangas	47	26.60	0.50	62	21.02	0.41
Satparis	43	25.37	0.69	50	18.70	0.50
Tintikiyas	65	27.60	0.61	85	19.40	0.42
Wanangs	72	25.03	0.43	85	18.68	0.34
F-ratio	4.59, $P < 0.05$			5.72, $P < 0.05$		

Table 4.5. Ever-pregnant and never pregnant women by age groups.

Pregnancy status	Age groups of married women				Total
	< 24 years	24-33 years	34-43 years	≥ 44 years	
Chapras					
Ever-pregnant	4	20	19	28	71
Never pregnant	6	4	1	2	13
Total	10	24	20	30	84
% of never pregnant	60.00	16.67	5.00	6.67	15.48
Sangas					
Ever-pregnant	6	14	18	23	61
Never pregnant	0	2	1	2	5
Total	6	16	19	25	66
% of never pregnant	0.00	12.50	5.26	8.00	7.85
Satparis					
Ever-pregnant	6	13	14	18	51
Never pregnant	2	3	0	1	6
Total	8	16	14	19	57
% of never pregnant	25.00	18.75	0.00	5.26	10.53
Tintikiyas					
Ever-pregnant	9	24	22	30	85
Never pregnant	1	1	2	0	4
Total	10	25	24	30	89
% of never pregnant	10.00	4.00	8.33	0.00	4.49
Wanangs					
Ever-pregnant	12	27	23	24	86
Never pregnant	10	2	0	0	12
Total	22	29	23	24	98
% of never pregnant	45.45	6.90	0.00	0.00	12.24

Frequency of Never-pregnant women

Table 4.5 shows the frequency of never-pregnant women at the time of survey in all the subgroups of the Koch population. It is seen that about 15.48%, 7.58%, 10.53%, 4.49% and 12.24% of the married women are never pregnant in the Chapras, Sangas, Satparis, Tintikiyas, and Wanangs, respectively. Although it shows that there are variations between subgroups, the chi-square value indicates that the differences are not statistically significant ($\chi^2 = 5.74$ $P > 0.05$). Moreover, most of the never-pregnant women are in the lower age groups, who may still have the chance to reproduce. The Table shows that among the Tintikiyas and Wanangs, there are no women who are never pregnant in the age group 44 years and above. But in the Chapras, Sangas and Satparis, the frequency of never-pregnant women in the age group 44 years and above is found to be 6.67%, 8.00% and 5.26%, respectively. Thus from this point of view, it may be suggested that the number of never-pregnant women is more in the Chapras, Sangas and Satparis when compared with the Tintikiyas and Wanangs.

Fertility

Table 4.6 shows the number of live births and surviving children by age groups of mothers living in wedlock up to 45 years of age for all the Koch populations. 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 both live births ($F = 3.11$, $P < 0.05$) and surviving children ($F = 4.06$, $P < 0.05$). Since the present study is not concerned with the determinants of fertility rates, data on socio-economic factors of the present populations were not collected. Considering the findings on other populations, it may be suggested that the differences in number of live births to the women living in wedlock may be associated with the variation between populations in respect of socio-economic conditions, or adoption of family planning methods.

Among the War Khasi, Khongsdier (2001) has reported that the mean number of live births per mother living continuously in wedlock is 4.08 among the Christians and 3.99 among the Non-Christians. Thus, it indicates that the Koch subgroups of the present study have lower mean live births when compared with the Christian and Non-Christian War Khasis.

Table 4.6. Live births and surviving children by age groups of mothers living continuously in wedlock

Population	≤ 24 years	25-29 years	30-34 years	35-39 years	40-44 years	Total
Chapras						
No. mothers	12	11	11	12	5	51
Live births	11	23	25	36	11	106
Mean ± SE	0.92 ± 0.30	2.09 ± 0.49	2.27 ± 0.53	3.00 ± 0.49	2.20 ± 0.44	2.08 ± 0.24
Surviving	9	14	20	20	9	72
Mean ± SE	0.75 ± 0.24	1.27 ± 0.29	1.82 ± 0.48	1.67 ± 0.30	1.80 ± 0.33	1.41 ± 0.17
Sangas						
No. mothers	8	7	7	10	4	36
Live births	15	11	13	39	18	92
Mean ± SE	1.88 ± 0.28	1.57 ± 0.40	1.86 ± 0.24	3.90 ± 0.70	4.50 ±1.82	2.56 ± 0.37
Surviving	8	8	13	32	16	77
Mean ± SE	1.00 ± 0.25	1.14 ± 0.24	1.86 ± 0.24	3.20 ± 0.69	4.00 ± 1.46	2.14 ± 0.33
Satparis						
No. mothers	9	9	8	6	5	37
Live births	8	18	32	33	26	117
Mean ± SE	0.89 ± 0.25	2.00 ± 0.63	4.00 ± 0.68	5.50 ±1.02	5.20 ± 1.03	3.16 ± 0.43
Surviving	7	17	24	26	20	94
Mean ± SE	0.78 ± 0.26	1.89 ± 0.60	3.00 ± 0.50	4.33 ± 0.90	4.00 ± 0.89	2.54 ± 0.35
Tintikiyas						
No. mothers	11	13	12	11	8	55
Live births	20	29	49	56	32	186
Mean ± SE	1.82 ± 0.40	2.23 ± 0.39	4.08 ± 0.64	5.09 ± 0.62	4.00 ± 1.00	3.38 ± 0.32
Surviving	17	25	40	42	27	151
Mean ± SE	1.55 ± 0.32	1.92 ± 0.30	3.33 ± 0.51	3.82 ± 0.53	3.38 ± 1.01	2.75 ± 0.26
Wanangs						
No. mothers	24	13	14	14	6	71
Live births	22	44	53	87	37	243
Mean ± SE	0.92 ± 0.24	3.38 ± 0.56	3.79 ± 0.66	6.21 ± 0.53	6.17 ± 0.80	3.42 ± 0.33
Surviving	15	36	43	57	34	185
Mean ± SE	0.63 ± 0.16	2.77 ± 0.44	3.07 ± 0.49	4.07 ± 0.40	5.67 ± 0.93	2.61 ± 0.26

F-ratio: Live births = 3.11, $P < 0.05$; Surviving children = $F = 4.06$, $P < 0.05$.

Table 4.7. Live births and surviving children by age groups of all married mothers

Population	≤ 24 y	25-29 y	30-34 y	35-39 y	40-44 y	≥ 45 y	Total
Chapras							
No. mothers	12	11	11	13	9	28	84
Live births	11	23	25	42	30	146	277
Mean ± SE	0.92±0.30	2.09±0.49	2.27±0.53	3.23±0.50	3.33±0.70	5.21±0.50	3.30±0.28
Surviving	9	14	20	24	23	105	195
Mean ± SE	0.75±0.24	1.27±0.29	1.82±0.48	1.85±0.32	2.56±0.42	3.75±0.41	2.32±0.21
Sangas							
No. mothers	8	8	8	12	6	25	67
Live births	11	12	14	50	24	128	239
Mean ± SE	1.38±0.30	1.50±0.35	1.75±0.23	4.17±0.68	4.00±1.33	5.12±0.48	3.57±0.32
Surviving	8	9	14	41	20	99	191
Mean ± SE	1.00±0.25	1.13±0.21	1.75±0.23	3.42±0.72	3.33±1.07	3.96±0.39	2.85±0.27
Satparis							
No. mothers	9	9	9	6	6	18	57
Live births	8	18	34	33	31	88	212
Mean ± SE	0.89±0.25	2.00±0.63	3.78±0.64	5.50±1.02	5.17±0.86	4.89±0.52	3.72±0.34
Surviving	7	17	26	26	24	63	163
Mean ± SE	0.78±0.26	1.89±0.60	2.89±0.46	4.33±0.90	4.00±0.75	3.50±0.58	2.86±0.30
Tintikiyas							
No. mothers	11	13	14	12	11	27	88
Live births	20	29	53	61	46	164	373
Mean ± SE	1.82±0.40	2.23±0.39	3.79±0.59	5.08±0.57	4.18±0.76	6.07±0.50	4.24±0.29
Surviving	17	25	43	46	36	131	298
Mean ± SE	1.55±0.32	1.92±0.30	3.07±0.47	3.83±0.48	3.27±0.78	4.85±0.50	3.39±0.25
Wanangs							
No. mothers	24	14	15	15	6	23	97
Live births	22	45	57	93	37	137	391
Mean ± SE	0.92±0.24	3.21±0.55	3.80±0.61	6.20±0.49	6.17±0.80	5.96±0.48	4.03±0.29
Surviving	15	37	47	62	34	100	295
Mean ± SE	0.63±0.16	2.64±0.42	3.13±0.46	4.13±0.38	5.67±0.93	4.35±0.45	3.04±0.23

F-ratio = 3.11, $P < 0.05$ for live births; F-ratio = 2.59, $P < 0.05$ for surviving children

Table 4.8. Age specific fertility rates

Population	Age groups of mothers at the time of birth (years)						TFR
	15-19	20-24	25-29	30-34	35-39	40 +	
Chapras	0.52	1.12	0.97	0.74	0.39	0.11	3.85
Sangas	0.42	1.01	1.07	0.82	0.53	0.26	4.11
Satparis	0.84	1.15	1.04	0.82	050	0.10	4.45
Tintikiyas	0.82	1.22	1.18	0.98	0.58	0.20	4.98
Wanangs	0.87	1.31	1.22	1.05	0.74	0.22	5.43

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 for all populations. Table 4.7 shows 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. The mean number of surviving children is also found to be lowest among the Chapras (2.32 ± 0.21) and highest among the Tintikiyas (3.39 ± 0.25). The ANOVA test indicates that the differences are statistically significant for both the 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 among the Pnars (6.04) of Jaintia hills (Khongsdier, 1992), Christian (4.81) and Non-Christian (4.66) War Khasis (Khongsdier (2001), Dalus (5.83) of West Garo hills (Patra and Kapoor, 1996), Hajongs (4.94) of West Garo hills (Barua, 1983), Brahmins (4.86), Kalitas (5.11), Kaibartas (4.39) and Ahoms (4.47) of Assam (Das and Das, 1992).

In order to have a better understanding 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) in Table 4.8. The Table shows that the ASFR tends to increase till it reaches its peak, and thereafter it declines with the increase in age of the mothers. With the exception of Sangas, the ASFR reaches it 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. The Table further shows that the TFR is highest among the Wanangs (5.43), and lowest among 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 fertility rate is highest among the Wanangs and lowest among the Chapras. The TFR in other populations varies from 4.11 in the Sangas to 4.98 in the Tintikiyas.

Table 4.9. Infant, child and juvenile mortality rates

Parameters	Chapras	Sangas	Satparis	Tintikiyas	Wanangs
Number of mothers	84	67	57	88	97
Number of live births	277	239	212	373	391
Number of infant deaths (death < 1 year of life)	30	13	8	15	28
Number of child deaths (death between 1 and 4 years of life)	38	20	16	32	54
Juvenile deaths (death between 5 and 14 years of life)	17	15	21	27	14
Infant mortality rate (%)	10.83	5.44	3.77	4.02	7.16
Child mortality rate (%)	13.72	8.37	7.55	8.58	13.81
Juvenile mortality rate (%)	6.14	6.28	9.91	7.24	3.58

Mortality

Table 4.9 shows that the infant, child and juvenile mortality rates in the populations covered under the present study are fairly high. 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 in the present populations are high especially among the Chapras and Wanangs. The differences between populations in respect of infant mortality rates are also found to be 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 these populations.

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%), and it is followed the Sangas (8.37%), Satparis (7.55%) and Tintikiyas (8.58%). The chi-square value indicates that the these inter-population 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, it is found to be highest among the Satparis (9.91%) and 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, $P > 0.05$).

Table 4.10. Reproductive wastage

Parameters	Chapras	Sangas	Satparis	Tintikiyas	Wanangs
Number of mothers	84	67	57	88	97
Number of pregnancies	297	247	226	395	400
Number of live births	277	239	212	373	391
Number of abortions	14	3	11	14	8
Number of still births	11	7	3	8	8
Abortion rate (%)	4.71	1.21	4.87	3.54	2.00
Still birth Rate (%)	3.70	2.83	1.33	2.03	2.00
Reproductive wastage (%)	8.42	4.05	6.19	5.57	4.00

Reproductive wastage

The reproductive wastage (abortions and still births) for the Koch populations of the present study is given in Table 4.10. It is seen that the rate of reproductive wastage is fairly high in the present populations, although it is lower in the Wanangs (4.00%) and Sangas (4.05%). It is highest 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. The frequencies of still births to these populations are found to be 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 populations, the abortion rate is higher than the still birth rate.

Table 4.11. Marriage within and outside the village

Marriage	Chapras	Sangas	Satparis	Tintikiyas	Wanangs
Within village	23	25	27	39	28
%	27.06	37.31	47.37	43.33	28.28
Outside village	62	42	30	51	71
%	72.94	62.69	52.63	56.67	71.72
Total	85	67	57	90	99
Chi-square value	17.89**	4.31*	0.16	1.60	18.68**
Mean marital distance ±SD (km)	28.99±43.56	21.60±33.74	7.75 ± 15.75	40.39±47.02	22.61±45.09

Chi-square value = 10.88, DF = 4, $P < 0.03$
*$P < 0.05$, **$P < 0.001$

Village Endogamy

Table 4.11 shows the frequency of village endogamy in terms of the number of marriages taking place within the village and outside the village. The Table shows that the frequency of marriage outside the village, i.e., one of the spouses is from outside the village, is more than 50% in all the subgroups, and it is very high among the Chapras (72.94%), Wanangs (71.72%) and Tintikiyas (55.67%). This variation in village exogamy between the subgroups is highly significant ($\chi^2 = 10.88$, DF = 4, $P < 0.001$), i.e., it varies from 53% for the Satparis to 73% for the Chapras. The Chi-square values for each subgroup indicate that village exogamy is significantly higher than village endogamy in the Chapras ($\chi^2 = 17.89$, DF = 1, $P < 0.001$), Sangas ($\chi^2 = 4.31$, DF = 1, $P < 0.05$) and Wanangs ($\chi^2 = 18.68$, DF = 1, $P < 0.001$). In the case of the Satparis and Tintikiyas, there is no difference between village endogamy and village exogamy, i.e., about 50 % of the marriages in these two groups may be considered as taking place within the village, although village exogamy is higher than village endogamy. Nevertheless, it is obvious from the present findings that village endogamy is very low in comparison with other populations of Meghalaya like the War Khasi (Khongsdier, 2001). As such it is expected that the genetic variation between these populations should be low as there should be a continuous gene flow among themselves.

In fact, Table 4.12 shows that the admixture rate, calculated according to Lasker (1952), is very high in all the Koch subgroups of the present study. It varies from 28.72% among the Satparis to 45.20% among the Wanangs. It may be mentioned that the high admixture rate (Table 4.12) was based on the number of individuals migrated from one village to another village within and between the Koch subgroups through marital relationship. The marital relationship with other populations like the Garos, Hajongs, Rabhas, Dalus, Manns, etc., is found to be 11.76%, 7.46%, 3.51%, 4.44% and 4.04% in the Chapras, Sangas, Satparis, Tintikiyas and Wanangs, respectively. Thus, it clearly indicate that most of the marriages take place within and between the Koch subgroups only.

Table 4.12. Admixture rate between villages

Marriage	Chapras	Sangas	Satparis	Tintikiyas	Wanangs
Both parents from the same village	128	133	133	206	109
One of the parents from another village	120	112	79	152	216
Both of the parents from another village	62	42	30	51	71
Total number of persons	310	287	242	409	396
Admixture rate (%)	39.35	34.15	28.72	31.05	45.20

Genetic Drift

From an evolutionary point of view, changes in gene frequencies due to random genetic drift or random sampling are considered to be important in small isolated population. In the present study we have calculated the variance due to genetic drift according to Wright (1931, 1943), which is as follows:

$$v^2_{dq} = \{q(1 - q)\}/2N_e$$

Where v^2_{dq} is the variance due to drift, q stands for the gene frequency (here taken as 0.5), and N_e is the effective population size.

Following the above method, the results are presented in Table 4.13. It may however be noted that variances shown in Table 4.13 are based on the assumption that all the Koch subgroups of the present study are endogamous. But we have already seen that the admixture rates between and within the Koch subgroups are fairly high. Thus, drift may not play much role in these Koch subgroups of Garo hills. In fact, Wright (1931) has clearly pointed out the importance of migration in neutralizing the effect of genetic drift in human populations. According to Wright (1940), the differentiation in gene frequency

due to genetic drift depends on the coefficient of breeding isolation, i.e. the product of effective population size and admixture rate. 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_e M is greater than 50. In the present study, Table 4.13 shows that the coefficient of breeding isolation varies from 16 among the Satparis to 44 among the Wanangs. Thus, it suggests that differentiation in allele frequency due to genetic drift is not so important in all the Koch subgroups of the present study, although it may still important in the Satpari population.

Table 4.13. Breeding size, effective population size, coefficient of breeding isolation and variance due to genetic drift.

Population	Breeding size (N)	Effective population size (N_e)	Coefficient of breeding isolation (N_{em})	Variance due to genetic drift (where q = 0.5)
Chapras	121	100.10	39.3894	0.001249
Sangas	105	75.70	25.8524	0.001651
Satparis	86	55.20	15.8530	0.002265
Tintikiyas	149	94.33	29.2887	0.001325
Wanangs	151	97.26	43.6903	0.001285

Selection Intensity

Natural selection is one of the most powerful evolutionary forces, which brings about changes in the genetic composition of a population. It is operating in human populations through differential fertility and mortality. Assuming that some phenotypic variation in reproduction has a genetic basis and fitness is heritable, Crow (1958) has proposed an index which is known as Index of Total Selection Intensity (now called the Index of Opportunity for Selection), taking into consideration the differential fertility and mortality. In the present study, we have followed the method suggested by Crow (1958) for calculating the total selection intensity. We have also followed the modified version suggested by Johnston and Kensinger (1971).

Table 4.14 shows the parameters used in calculating the index of selection intensity. It may be noted that for calculating this index, we have taken into

consideration only those mothers who are aged 40 years and above since fertility declines drastically when the mothers reach this age. It may be noted that this has been observed in other populations as well (Das and Ghosh, 1988; Khongsdier, 2001). Table 4.14 shows that the mean number of live births per mother varies from 4.76 among the Chapras to 6.00 among the Wannags, whereas the proportion of child deaths (i.e., deaths before reproductive age) varies from 0.2048 for the Tintikiyas to 0.2727 among the Chapras. The proportion of embryonic deaths is found to vary from 0.0318 among the Sangas to 0.0708 among the Tintikiyas.

On the basis of these parameters, we have calculated the selection intensity according to the methods suggested by Crow (1958) and Johnston and Kensinger (1971). Table 4.15 shows that the index of total selection intensity (I), calculated according to Crow's formula, varies from 0.4776 among the Wanangs to 0.7999 among the Chapras. It indicates that the differential mortality contributes more towards the total selection intensity among the Chapras (0.3749), Satparis (0.3678), Tintikiyas (0.2575) and Wohangs (0.2985), but in the case of Sangas it is differential fertility which contributes more towards total selection intensity. Nevertheless, it indicates by and large that differential mortality contributes more towards selection intensity in the Koch population as generally observed in other Indian populations (Reddy and Chopra, 1990).

Table 4.15 also shows the index of total selection intensity calculated according to the method suggested by Johnston and Kensinger (1971). It is seen that, like in the case of Crow's formula, the value of I varies from 0.5284 among the Wanangs to 0.9022 among the Chapras. It indicates that the I values according to Johnston and Kensinger's method are higher than those calculated according to Crow's formula for all the Koch subgroups of the present study. This may be due to the fact that in the modified version of Johnston and Kensinger, we have taken into account the embryonic deaths, i.e., reproductive wastage which include abortions and still-births.

Having reviewed the values of I calculated according to Crow's formula for various Indian populations, Khongsdier (2000) has suggested different degrees of the intensity of opportunity for natural selection, viz., low - < 0.340, moderate - 0.340 to 0.470, mild - 0.470 to 0.600, average - 0.600 to 0.730, high - 0.730 to 0.860, and very high - > 0.860. Taking into consideration these suggested degrees of I, it is likely that

opportunity for natural selection is very high among the Chapras, and it is in moderate intensity in the Sangas and Satparis. On the other hand, the opportunity for natural selection seems to be mild in the case of Tintikiyas and Wanangs. In comparison with populations of Northeast India, the total selection intensity in the Koch subgroups of the present study are found to be higher than the Christian (0.3592) and Non-Christian (0.4463) War Khasis (Khongsdier, 2001), Ahoms (0.2180), Kacharis (0.2500) Khamtis (0.3120), Sonowals (o.3640) and Kaibartas (0.3360) of Assam, but it is lower than that reported for the Apatanis (0.8890) and Khamtis (0.9340) of Arunachal Pradesh (Sengupta and Gogoi, 1995b).

Table 4.14. Parameters used in calculating index of selection intensity

Parameters	Chapras	Sangas	Satparis	Tintikiyas	Wanangs
Number of mothers aged 40 years and above	37	31	24	38	29
Number of conceptions	186	157	126	226	180
Number of live births	176	152	119	210	174
Number of embryonic deaths	10	5	7	16	6
Mean number of live births per woman aged 40 years and above ($\bar{X}$)	4.7568	4.9032	4.9583	5.5263	6.0000
Variance in number of live births due to fertility (V_f)	6.9949	6.9261	4.7899	7.4072	4.9655
Proportion of child deaths (i.e. deaths before 15 years of age) P_d	0.2727	0.2171	0.2689	0.2048	0.2299
Proportion of survivors, birth to reproductive age ($P_s = 1 - P_d$)	0.7273	0.7829	0.7311	0.7952	0.7701
Proportion of embryonic deaths (P_{ed})	0.0538	0.0318	0.0556	0.0708	0.0333
Proportion of survivors, birth to reproductive age ($P_b = 1 - P_{ed}$)	0.9462	0.9682	0.9444	0.9292	0.9667

Table 4.15. Indices of opportunity for selection.

Population	According to Crow (1958)			According to Johnston and Kensinger (1971)			
	I_m	I_f	I	I_{mc}	I_{mc}	I_f	I
Chapras	0.3749	0.3091	0.7999	0.0569	0.3749	0.3091	0.9022
Sangas	0.2773	0.2881	0.6453	0.0328	0.2773	0.2881	0.6993
Satparis	0.3678	0.1948	0.6343	0.0589	0.3678	0.1948	0.7305
Tintikiyas	0.2575	0.2425	0.5625	0.0762	0.2575	0.2425	0.6815
Wanangs	0.2985	0.1379	0.4776	0.0344	0.2985	0.1379	0.5284

CHAPTER V
GENETIC MARKERS

In the present chapter, we shall deal with four genetic markers, namely, ABO and Rh (D) blood groups, PTC taste sensitivity and colour blindness. The first three traits are autosomal characters, while the last one is an X-linked trait.

ABO Blood Groups

The percentage distribution of the ABO blood groups is given in Table 5.1. It is seen 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, whereas in other populations the blood type B is higher than A. The frequency of O blood type is more or less similar in all populations covered under the present study, although it is lower in the Wanangs (1827%). With respect to blood type AB, it is seen from the Table that the frequency is very low in the Sangas (8%) in comparison with the other populations of the present study. It may however be noted that these differences between populations in respect of the phenotype distribution of ABO blood groups are not statistically significant (χ^2 = 10.97, D.F. = 12, P > 0.05).

The allele frequencies of the ABO blood groups given in Table 5.2 are shown in Table 5.2. Following the methods suggested by Balakrishnan (1988), it is found that the allele frequencies of p (A), q (B) and r (O) are not statistically significant in all populations. Thus, it indicates that all populations covered under the present study are in genetic equilibrium in respect of the ABO blood group system. It is also observed that the differences between these populations are not statistically significant (χ^2 = 10.97, DF = 12, P > 0.05). We shall discuss this subject matter in the chapter of discussion.

Rh (D) blood groups

The distribution of the Rh (D) blood groups is shown in Table 5.3. It is found that Rh-negative blood type is absent in the Chapras and Tintikiyas, and it is very low in other populations. 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).

Table 5.1. Phenotype frequencies of the ABO blood groups

Population	O	A	B	AB
Chapras (n = 103)	24	26	38	15
%	23.30	25.24	36.89	14.56
Sangas (n = 75)	17	31	21	6
%	22.67	41.33	28.00	8.00
Satparis (n = 75)	18	29	19	9
%	24.00	38.67	25.33	12.00
Tintikiyas (n = 105)	24	33	34	14
%	22.86	31.43	32.38	13.33
Wanangs (n = 104)	19	31	36	18
%	18.27	29.81	34.62	17.30

$\chi^2 = 10.97$, DF = 12, $P > 0.05$.

Table 5.2. Allele frequencies of ABO blood groups

Population	Allele frequencies			χ^2- value
	p ± SE	q ± SE	r ± SE	(DF=1)
Chapras	0.2231 ± 0.0312	0.3018 ± 0.0354	0.4751 ± 0.0390	0.1723
Sangas	0.2934 ± 0.0407	0.2036 ± 0.0348	0.5030 ± 0.0457	1.7324
Satparis	0.2982 ± 0.0409	0.2088 ± 0.0352	0.4930 ± 0.0459	0.0296
Tintikiyas	0.2571 ± 0.0325	0.2635 ± 0.0328	0.4794 ± 0.0389	0.0063
Wanangs	0.2718 ± 0.0319	0.3056 ± 0.0349	0.4226 ± 0.0349	2.0000

Table 5.3. Phenotype and allele frequencies of the Rh- blood groups.

Population	Phenotype frequency		Allele frequencies	
	Rh^-	Per cent	D	d
Chapras (n = 103)	0	0.00	1.0000	0.0000
Sangas (n =75)	1	1.33	0.8845	0.1155
Satparis (n = 75)	1	1.33	0.8845	0.1155
Tintikiyas (n = 105)	0	0.00	1.0000	0.0000
Wanangs (n = 104)	2	1.92	0.8613	0.1387

Table 5.4. Phenylthiocarbmide (PTC) taste sensitivity

Population	No	PTC solution number													
		0	1	2	3	4	5	6	7	8	9	10	11	12	13
Chapras	103	9	5	2	3	8	13	12	21	26	2	1	0	0	1
Sangas	75	14	2	2	1	6	12	15	14	5	3	0	1	0	0
Satparis	75	6	2	3	10	12	9	11	12	8	2	0	0	0	0
Tintikiyas	105	28	1	6	5	12	8	21	17	5	1	0	1	0	0
Wanangs	104	33	6	8	8	10	8	14	10	6	1	0	0	0	0

PTC Taste Sensitivity

Table 5.4 shows the distribution of individuals who have the taste sensitivity to PTC, which follows a binomial distribution for all the populations. The graph (Figure 5.1) shows that the anti-mode (which demarcates the non-tasters and tasters) varies for different populations. Among the Satparis, Tintikiyas and Wanangs, the anti-mode falls on 1, whereas among the Chapras and Sangas it falls on 2 and 3, respectively. Following the method suggested by Harris and Kalmus (1949), the individuals were divided into tasters and non-tasters on the basis of anti-mode (i.e., the anti-mode was considered the cut-off point for determining the tasters and non-tasters). The percentage distribution of tasters and non-tasters is given in Table 5.5. It is found that the frequency of non-tasters is lowest among the Satparis (10.67%) and highest among the Wanangs (37.50%). The Chi-square value indicates that the inter-population differences are statistically significant

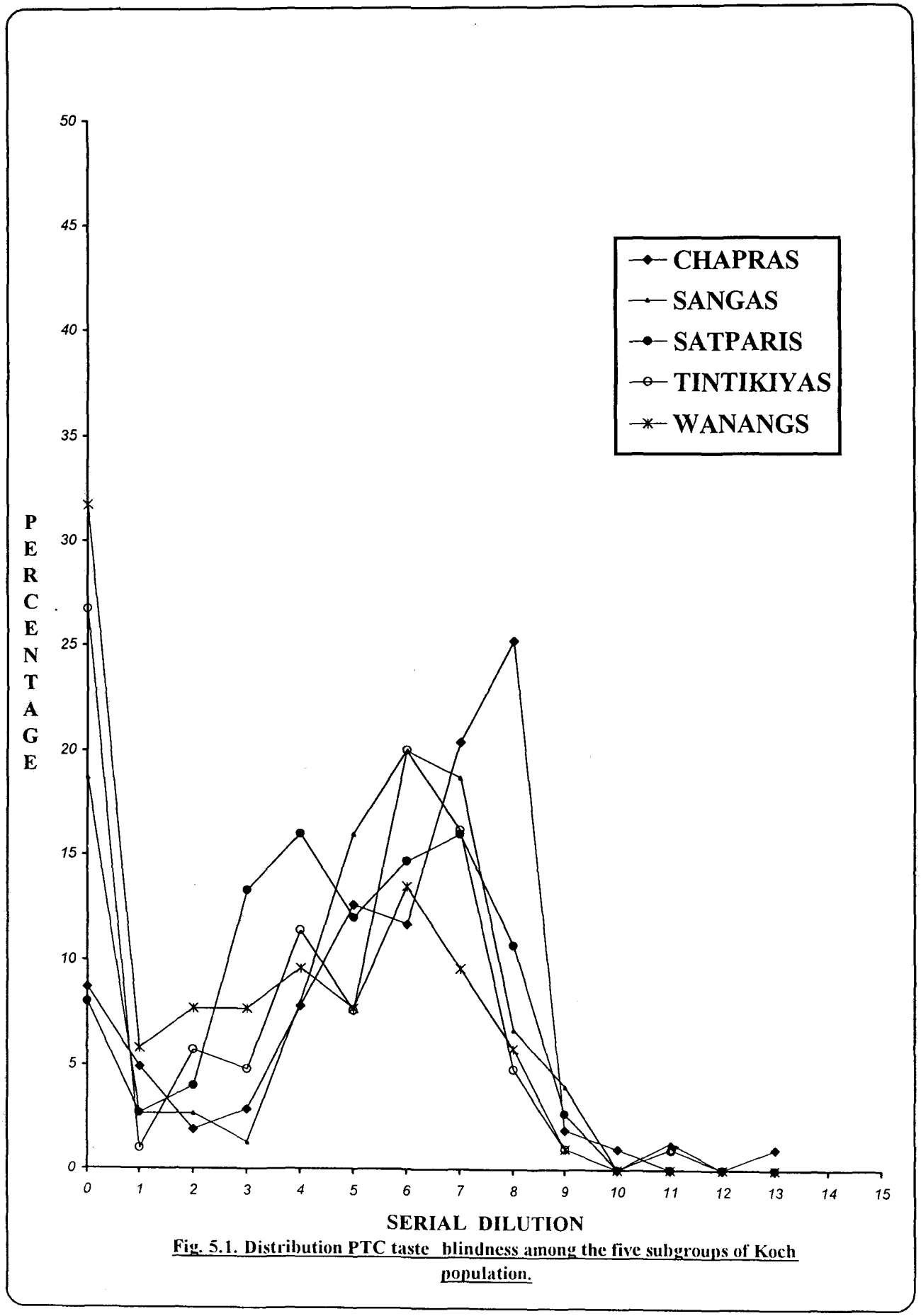


Fig. 5.1. Distribution PTC taste blindness among the five subgroups of Koch population.

(χ^2 = 22.56, DF = 4, P < 0.05), but the differences between two populations shows that the Koch subgroups of the present study are by and large similar in respect of PTC taste sensitivity, although the Satparis deviate significantly from all the other subgroups except the Chapras (Table 5.6). Thus, data on PTC taste sensitivity are to a certain extent different from those on the ABO blood group, which indicate that all the subgroups are similar in ABO allele frequencies. However, it may be noted that PTC taste sensitivity is rather a weak genetic marker in comparison with the ABO blood groups.

Table 5.5. PTC phenotypes and allele frequencies

Population	Phenotypes		Allele frequencies	
	Tasters	Non-tasters	T	t
Chapras (n = 103)	87 (84.47)	16 (15.53)	0.6059	0.3941
Sangas (n = 75)	56 (74.67)	19 (25.33)	0.4967	0.5033
Satparis (n = 75)	67 (89.33)	8 (10.67)	0.6734	0.3266
Tintikiyas (n = 105)	76 (72.38)	29 (27.67)	0.4745	0.5255
Wanangs (n =104)	65 (62.50)	39 (37.50)	0.3876	0.6124

Figures within parentheses indicate percentage
χ^2 = 22.56, DF = 4, P < 0.05.

Table 5.6. Chi-square (χ^2) tests between populations in respect of PTC taste sensitivity

	Chapras	Sangas	Satparis	Tintikiyas
Chapras	0.00			
Sangas	1.75, P = 0.19	0.00		
Satparis	0.68, P = 0.41	3.81, P = 0.05*	0.00	
Tintikiyas	2.90, P = 0.09	0.07, P = 0.79	5.22, P = 0.02*	0.00
Wanangs	7.49, P = 0.006*	1.53, P = 0.22	9.91, P = 0.002*	1.18, P = 0.28

*Significant.

Table 5.7. Phenotypes and allele frequencies of colour blindness

Population	Phenotypes		Allele frequencies	
	Normal	Colour blind	C	c
Chapras (n = 51)	48 (94.12)	3 (5.88)	0.9412	0.0588
Sangas (n= 41)	41 (100.00)	0	1.0000	0.0000
Satparis (n= 41)	40 (97.56)	1 (2.44)	0.9756	0.0244
Tintikiyas (n = 61)	59 (96.72)	2 (3.28)	0.9672	0.0328
Wanangs (n = 56)	53 (94.64)	3 (5.36)	0.9464	0.0536

Figures within parentheses indicate percentage.

Colour Blindness

Table 5.7 shows the frequency 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 seems to be low in all the populations covered under 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. We shall discuss this in Chapter IX.

COMPARISON WITH OTHER NEIGHBOURING POPULATIONS

Table 5.8 shows the Percentage distribution of the ABO blood groups and PTC taste sensitivity in the present populations and other populations of Assam and Meghalaya. The homogeneity test for the differences between two populations are given in Tables 5.9 and 5.10 for the ABO blood groups and PTC taste ability, respectively. It can be seen from Table 5.9 that the present populations differ significantly from the Khynriams, Pnars and Wars, but they are similar to the Lyngngams, Garos and Hajongs (although the Chapras differ from the Hajongs) in respect of the ABO blood groups. Except the Sangas, the present population groups also differ significantly from Kochs of Assam. On the other hand, the Koch subgroups of the present study are by and large similar to the other neighbouring populations, except the Wanangs, in respect of PTC taste sensitivity. Table

5.10 shows that the Chapras, Sangas and Tintikiyas are not statistically different from the Kochs of Assam, and they are also similar to the Garos and Dalus of Meghalaya. So unlike in the case of ABO blood groups, the Chapras, Sangas and Tintikiyas are similar to the Kochs of Assam with respect PTC taste sensitivity. But the Satparis and Wanangs deviate significantly from the Kochs of Assam in respect of both PTC taste sensitivity and ABO blood groups.

Under the above circumstances, the Koch subgroups of the present study show, in general, a different degree of affinity to the different populations of Assam and Meghalaya with respect to the ABO blood groups and PTC taste sensitivity. In other words, although data on ABO blood groups are to a certain extent relevant to those on 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. It may be noted that this is the common observation when one deals with 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). Besides, such contradictory results may also be attributed to sampling error that might have taken place during data collection.

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 groups and PTC taste ability (Table 5.11) because data on other genetic loci are not available for all the populations taken for comparison. The results are summarized in Table 5.12. The dendrogram based according to method suggested by Sokal and Sneath (1963) is shown and Figure 5.2. It 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.

Table 5.8. Percentage distribution of the ABO blood groups and PTC taste sensitivity in the Koch subgroups of Garo hills and other populations

Population	ABO blood groups					PTC taste sensitivity		
	N	O	A	B	AB	N	Tasters	Non-tasters
Chapras[1]	103	23.30	25.24	36.89	14.56	103	84.47	15.53
Sangas[1]	75	22.67	41.33	28.00	8.00	75	74.67	25.33
Satparis[1]	75	24.00	38.67	25.33	12.00	75	89.33	10.67
Tintikiyas[1]	105	22.86	31.43	32.38	13.33	105	72.38	27.62
Wanangs[1]	104	18.27	29.81	34.62	17.30	104	62.50	37.50
Kochs[2]	527	37.38	30.36	26.76	5.50	551	77.50	22.50
Lyngngams[3]	120	20.00	39.17	28.33	12.50	120	70.00	30.00
Khynriams[4]	222	49.00	29.20	18.70	2.09	222	88.74	11.26
Pnars[4]	197	52.97	33.50	11.61	2.10	170	82.94	17.06
Bhois[4]	192	38.69	30.43	23.04	7.84	210	78.09	21.90
Wars[4]	230	55.72	28.64	11.97	3.67	236	87.71	12.29
Garos[5]	144	25.69	29.86	32.64	11.81	125[7]	78.40	21.60
Dalus[6]	145	35.86	17.24	35.17	11.72	132	82.58	17.42
Hajongs[5]	125	17.60	43.20	24.08	14.40			

Sources: [1]Present study, [2]Sengupta (1993), [3]Ahmed et al. (1997), [4]Das (1978), [5]Das *et al.* (1978), [7]Deka (1978), [6]Borthakur *et al.* (1997).

Table 5.9. Chi-square values (DF=3) between the Koch subgroups and other populations in respect of ABO blood groups

Population	Chapras	Sangas	Satparis	Tintikiyas	Wanangs
Kochs	18.88***	7.23	9.18*	14.21**	27.44***
Lyngngams	4.99	1.08	0.51	1.49	3.06
Khynriams	33.83***	16.90***	19.10***	28.72***	41.89***
Pnars	53.25***	26.22***	28.34***	44.79***	58.97***
Bhois	13.11***	6.36	5.52	8.69*	17.53***
Wars	51.25***	27.13***	27.36***	43.82***	59.14***
Garos	1.27	3.13	2.04	0.12	2.17
Dalus	5.40	15.50***	12.93**	8.94*	12.17**
Hajongs	8.83*	2.44	1.40	4.09	4.93

*P < 0.05, **P < 0.01, ***P < 0.001

Table 5.10. Chi-square values (DF=1) between the Koch subgroups and other populations in respect of PTC taste sensitivity

Population	Chapras	Sangas	Satparis	Tintikiyas	Wanangs
Kochs	2.51	0.30	5.56*	1.29	10.52**
Lyngngams	6.47*	0.49	9.87**	0.15	1.41
Khynriams	1.17	8.80**	0.02	13.83***	30.89***
Pnars	0.11	2.27	1.66	4.34*	14.45***
Bhois	1.76	0.37	4.54*	1.26	8.57**
Wars	0.66	7.41**	0.14	12.10***	28.68***
Garos	1.36	0.37	3.88*	1.12	7.00**
Dalus	0.15	1.85	1.71	3.55	12.11***

*P < 0.05, **P < 0.01, ***P < 0.001

Table 5.11. Allele frequencies of the ABO and Rh blood groups, PTC taste blindness in populations of Meghalaya and Assam

Population	ABO blood groups				Rh (D) blood groups		PTC taste sensitivity	
	N	p (A)	q (B)	r (O)	N	d (Rh^-)	N	t
Chapras[1]	103	0.2231	0.3018	0.4751	103	0.0000	103	0.3941
Sangas[1]	75	0.2934	0.2036	0.5030	75	0.1155	75	0.5033
Satparis[1]	75	0.2982	0.2088	0.4930	75	0.1155	75	0.3266
Tintikiyas[1]	105	0.2571	0.2635	0.4794	105	0.0000	105	0.5255
Wanangs[1]	104	0.2718	0.3056	0.4226	104	0.1387	104	0.6124
Kochs	527	0.2004	0.1781	0.6215	511	0.1466	551	0.4743
Lyngngams[3]	120	0.3193	0.2459	0.4348	120	0.1292	120	0.5477
Khynriams[4]	202	0.1772	0.1161	0.7067	202	0.0000	222	0.3355
Pnars[4]	197	0.1976	0.0713	0.7311	197	0.0000	170	0.4130
Bhois[4]	192	0.2155	0.1673	0.6172	192	0.0000	210	0.4679
Wars[4]	230	0.1761	0.0814	0.7425	230	0.0000	236	0.3506
Garos[5]	144	0.2364	0.2557	0.5078	144	0.0000	125	0.4647
Dalus[6]	145	0.1550	0.2676	0.5774	145	0.1176	132	0.4174
Hajongs[5]	125	0.2300	0.2440	0.4120	125	0.0889		0.4080

Sources: [1]Present study, [2]Sengupta (1993), [3]Ahmed et al. (1997), [4]Das (1978), [5]Das *et al.* (1978), [6]Borthakur *et al.* (1997)

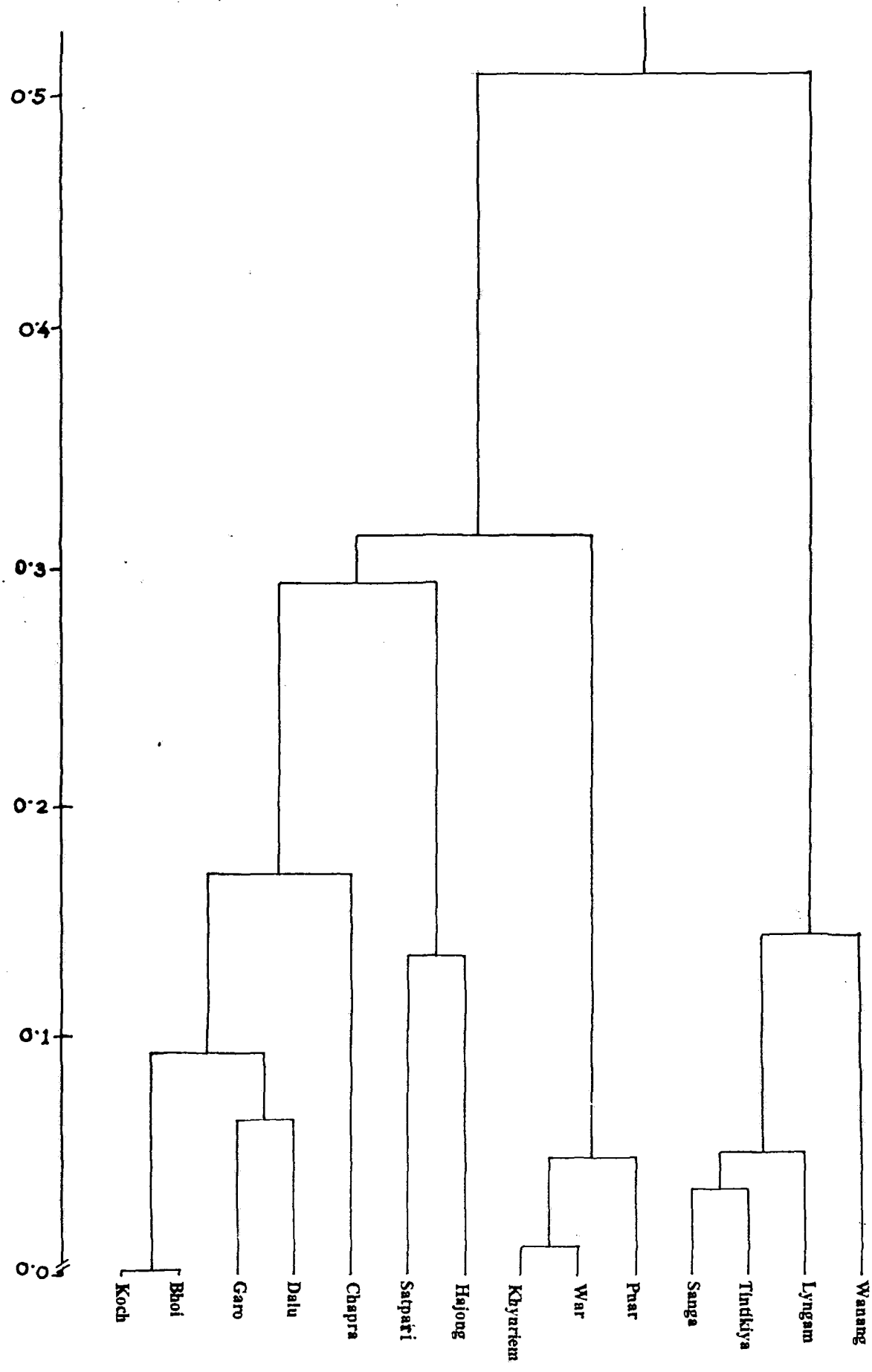
Table 5.12. Nei'standard genetic distance (D× 10) on the basis of the ABO blood groups, ~~Rh factors~~ and PTC taste sensitivity

Population	Chapras	Sangas	Satparis	Tintiki-yas	Wa-nangs	Kochs	Lyng-ngams
Chapras	-						
Sangas	0.223	-					
Satparis	0.136	0.356	-				
Tintikiyas	0.214	0.037	0.482	-			
Wanangs	0.587	0.236	1.044	0.119	-		
Kochs	0.268	0.127	0.390	0.189	0.546	-	
Lyngngams	0.355	0.062	0.591	0.042	0.084	0.346	-
Khynriams	0.445	0.453	0.323	0.736	1.460	0.224	1.007
Pnars	0.570	0.433	0.488	0.616	1.211	0.133	0.834
Bhois	0.264	0.116	0.352	0.192	0.562	0.002	0.337
Wars	0.568	0.602	0.432	0.799	1.529	0.234	1.073
Garos	0.059	0.032	0.235	0.032	0.298	0.086	0.132
Dalus	0.092	0.238	0.267	0.235	0.648	0.099	0.454
Hajongs	0.158	0.180	0.136	0.253	0.573	0.438	0.242

Table 5. 12 Cond/

Population	Khyn-riams	Pnars	Bhois	Wars	Garos	Dalus
Khynriams	-					
Pnars	0.068	-				
Bhois	0.208	0.132	-			
Wars	0.012	0.032	0.217	-		
Garos	0.419	0.396	0.085	0.493	-	
Dalus	0.237	0.292	0.108	0.307	0.067	-
Hajongs	0.687	0.743	0.398	0.804	0.162	0.389

Fig. 5.2 **Genetic Distance (DX10) on the basis of the ABO blood groups and PTC taste** sensitivity **among 14 populations.**



CHAPTER VI
SOMATOMETRIC CHARACTERS

In this Chapter, we shall describe the somatometric characters collected from all the Koch subgroups of the present study.

Anthropometric Measurements

Table 6.1 shows the means and standard deviations of anthropometric measurements for the adult males of Chapras, Sangas, Satparis, Tintikiyas and Wanangs. 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 Table shows that 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. The one-way analysis of variance (ANOVA), however, shows that the differences between these subgroups are not statistically significant in respect of stature.

Unlike the case of stature, the Wanangs have the highest mean value of sitting height, while the lowest mean value is observed among the Tintikiyas. The Wanangs are followed by the Satparis (81.40 ± 3.42), Sangas (80.90 ± 5.03) and Wanangs (80.49 ± 3.77). These differences in sitting height are however not statistically significant ($F = 1.37$, $P > 0.05$). In fact, the ANOVA test indicates that the differences between the Koch subgroups of the present study 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. However, the differences between these groups are significant in respect of

head length, head height, head circumference, minimum frontal breadth, total facial length, and nasal breadth.

Table 6.1. Means and standard deviations of anthropometric measurements and indices (Males)

Character	Chapras (n=51)	Sangas (n=41)	Satparis (41)	Tintikiyas (n=61)	Wanangs (n=56)	F-ratio
HV	159.41 ± 5.45	160.53 ± 5.69	158.04 ± 6.55	159.55 ± 5.29	158.77 ± 5.30	1.17
SHV	80.49 ± 3.77	80.90 ± 5.03	81.40 ± 3.42	80.34 ± 4.01	82.06 ± 5.68	1.37
HT	145.95 ± 5.41	147.26 ± 5.41	144.60 ± 6.29	145.57 ± 5.52	146.02 ± 5.22	1.24
HA	128.05 ± 5.14	130.67 ± 5.35	129.08 ± 5.84	128.44 ± 5.31	128.32 ± 4.53	1.80
HL	18.71 ± 0.69	18.43 ± 0.85	18.65 ± 0.53	18.96 ± 0.59	18.69 ± 0.49	4.59*
HB	14.16 ± 0.58	14.22 ± 0.53	14.05 ± 0.37	14.13 ± 0.52	13.99 ± 0.49	1.66
HH	13.46 ± 0.87	13.27 ± 1.08	13.45 ± 1.17	13.81 ± 1.50	12.80 ± 0.96	5.79*
HC	53.24 ± 1.65	53.05 ± 1.41	53.33 ± 1.30	53.88 ± 1.30	53.01 ± 1.42	3.38*
MFB	10.16 ± 0.41	10.55 ± 0.54	10.34 ± 0.39	10.52 ± 0.52	10.54 ± 0.81	4.49*
BGB	10.55 ± 0.67	10.56 ± 0.70	10.51 ± 0.48	10.69 ± 0.66	10.64 ± 0.51	0.87
BB	13.33 ± 0.53	13.34 ± 0.44	13.25 ± 0.40	13.44 ± 0.69	13.36 ± 0.42	0.86
TFL	12.45 ± 0.63	12.77 ± 0.81	12.21 ± 0.67	12.76 ± 0.79	12.67 ± 0.53	5.43*
UFL	7.87 ± 0.56	7.99 ± 0.71	7.63 ± 0.46	8.08 ± 1.36	7.84 ± 0.50	2.05
NH	6.02 ± 0.39	6.03 ± 0.57	5.94 ± 0.48	6.09 ± 0.34	6.10 ± 0.45	0.98
NB	3.72 ± 0.33	3.67 ± 0.30	3.56 ± 0.18	3.71 ± 0.27	3.77 ± 0.28	3.37*
CG	82.17 ± 3.22	83.40 ± 3.98	83.26 ± 4.12	82.56 ± 3.80	81.58 ± 3.58	1.98
Indices						
CI	75.59 ± 2.54	77.33 ± 4.18	75.48 ± 2.77	74.58 ± 3.03	74.87 ± 3.01	5.45*
NI	61.98 ± 5.95	61.44 ± 7.78	60.34 ± 5.64	60.89 ± 5.44	62.02 ± 5.94	0.67
TFI	93.59 ± 5.75	95.76 ± 6.47	92.24 ±5.48	95.20 ± 5.90	94.91 ± 4.44	0.96
LHI	72.01 ± 5.04	72.14 ± 6.23	72.20 ± 5.94	72.95 ± 8.33	68.52 ± 5.40	0.98
BHI	95.31 ± 7.09	92.89 ± 6.84	95.78 ± 8.65	96.85 ± 8.86	91.93 ± 7.23	3.73*

With respect to head length the differences between the subgroups are found to be statistically significant at 0.01% (F = 4.59). The Scheffe's multiple range test of the differences between two populations, however, shows that it is only the difference

between the Sangas and the Tintikiyas, which is statistically significant (Difference standard error of difference = 0.5338 ± 0.1273, $P < 0.001$). In other words, the differences in head length between the Koch subgroups of the present study are mainly due to the difference between the Sangas and the Tintikiyas, otherwise all other groups are by and large similar. Similarly, the significant differences between the Koch subgroups of the present study in respect of head height ($F = 5.79$, $P < 0.000$) and head circumference ($F = 3.38$, $P < 0.01$) are mainly attributed by the differences between the Tintikiyas and the Wanangs (1.0048 ± 0.2134, $P < 0.000$). According to Scheffe's multiple range test, the difference in head height and head circumference between the Tintikiyas and the Wanangs are found to be 1.0048 ± 0.2134 ($P < 0.000$) and 0.8601 ± 0.2632 ($P < 0.033$), respectively. With respect to minimum frontal breadth, it is found that the Chapras deviate significantly from the Sangas (0.3900 ± 0.1191, $P < 0.032$), Tintikiyas (0.3608 ± 0.1077, $P < 0.026$) and Wanangs (0.3769 ± 0.1099, $P < 0.021$). On the other hand, the Satparis deviate significantly from the Tintikiyas (0. 5435 ± 0.1392, $P < 0.005$) and Wanangs (0.4592 ± 0.1417) in respect of total facial length. As regards the differences in nasal breadth among the five subgroups ($F = 3.37$, $P < 0.01$), it is found that the multiple range test is significant only the difference between the Sangas and the Wanangs (0.2044 ± 0.0580, $P < 0.02$). Thus, it is obvious 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, it may be concluded that the Koch subgroups of the present study are by and large similar in anthropometric measurements.

Anthropometric Indices

In order to have a better understanding of the relationship between the Koch subgroups of the present study, an attempt has also been made to calculate some indices which are generally used for finding out the ethnic affinity of a population. The means and standard deviations of such indices are given in Table 6.1. Of the five indices, the ANOVA test shows that there are significant differences between the subgroups only in respect of cephalic index and breadth-height index. According to Scheffe's multiple range test, it is found that the Sangas deviate significantly from the Tintikiyas (2.7571± 0.6292, $P < 0.001$) and Wanangs (2.4617 ± 0.6404, $P < 0.006$) in cephalic index. Thus,

the Sangas deviate significantly from the Tintikiyas in both head length and cephalic index. With respect to breadth-height index, the multiple-range test is found to be significant only in the case of the difference between Tintikiyas and Wanangs (4.9270 ± 1.4463, $P < 0.023$). In other words, the differences in cephalic index among the Koch subgroups of the present study 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 data used for calculating CD are given in Table 6.2 and the results are shown in Table 6.3. The dendrogram (Figure 6.1), derived as per the method suggested by Sokal and Sneath (1963), shows that all the Koch subgroups of the present study belong to the same cluster, and the Tintikiyas and Chapras stand closer to each other. Thus, the dendrogram (Figure 6.1) also shows that the present populations are by and large similar in anthropometric characters, and they are distant themselves from the Kochs of Assam. All the five Koch subgroups belong to one major cluster in which the Tintikiyas and Chapras belong to one sub-cluster, and the Sangas, Satparis and Wanangs belong to another sub-cluster. Thus, unlike the case of genetic markers, i.e., ABO blood groups and PTC taste sensitivity, the dendrogram based on the anthropometric traits shows that all the Koch subgroups of the present study are closer to one another. However, in the case of genetic markers, only Tintikiyas, Sangas and Wanangs belong to one major cluster along with the Lyngngams. Nevertheless, it is obvious that the Koch of Garo hills deviate significantly from the Kochs of Assam. The same is true in the case of genetic markers.

Table 6.2. Anthropometric Characteristics (Mean) of adult males for seven Populations of Meghalaya and Assam.

Population	No.	Stature	Sitting Height Vertex	Head Length	Head Breadth	Head Height	Head Circum-ference	M.F.B.
Chapras	51	159.41	80.49	18.71	14.16	13.46	53.24	10.16
Sangas	41	160.53	80.90	18.43	14.22	13.27	53.05	10.55
Satparis	41	158.04	81.40	18.65	14.05	13.45	53.33	10.34
Tintikiyas	61	159.55	80.34	18.96	14.13	13.81	53.88	10.52
Wanangs	56	158.77	82.06	18.69	13.99	12.80	53.02	10.54
Kochs[3]	256	164.43	84.34	18.33	14.56	13.57	54.92	-
Hajongs[2]	100	159.03	81.41	17.81	13.96	12.67	54.53	11.13
Garos[1]	200	160.70	83.50	18.75	14.14	12.03	54.90	10.55
Khynriams[1]	100	156.62	82.36	18.82	14.64	12.29	54.60	10.41
Pnars[1]	100	157.35	81.12	19.10	14.53	11.92	54.59	10.05
Bhois[1]	100	157.00	82.36	18.34	14.24	12.77	51.79	10.46
Wars[1]	100	155.68	81.57	18.67	14.43	11.90	54.16	10.51

Cond/ Table 6.2

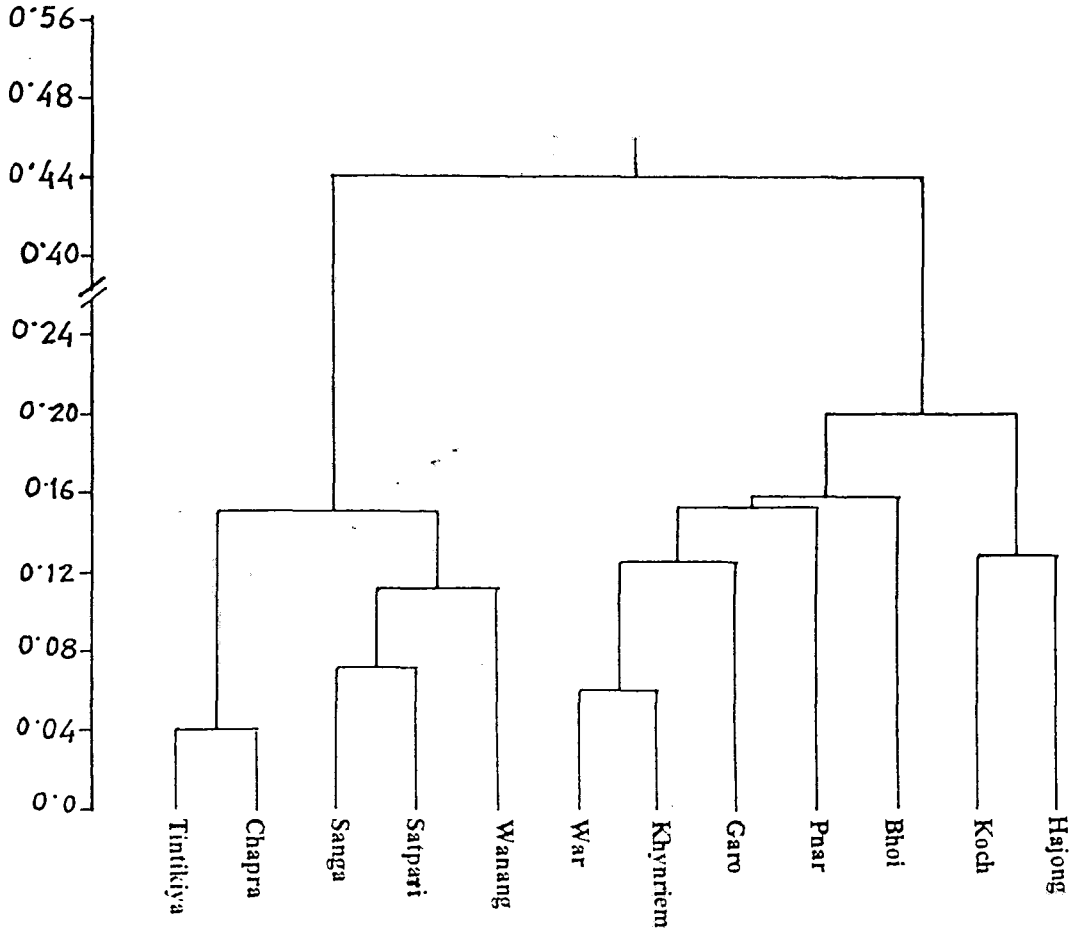
Population	No.	Bizygo-matric breadth	Bigo-nial breadth	Total Facial length	Upper facial length	Nasal height	Nasal breadth
Chapras	51	13.33	10.55	12.45	7.87	6.02	3.72
Sangas	41	13.34	10.56	12.77	7.99	6.03	3.67
Satparis	41	13.25	10.51	12.21	7.63	5.94	3.56
Tintikiyas	61	13.44	10.69	12.76	8.08	6.09	3.71
Wanangs	56	13.36	10.64	12.67	7.84	6.10	3.77
Kochs[3]	256	13.39	-	11.30	6.48	4.84	3.60
Hajongs[2]	100	13.41	10.46	10.66	6.69	4.82	3.56
Garos[1]	200	13.82	10.09	11.39	6.64	4.73	3.97
Khynriams[1]	100	13.51	10.16	11.07	6.36	4.54	3.92
Pnars[1]	100	13.51	10.22	11.40	6.56	4.79	3.72
Bhois[1]	100	13.45	9.95	11.33	6.64	4.87	3.95
Wars[1]	100	13.47	10.05	11.05	6.34	4.58	3.80

Sources : Das (1960, 1967); Phookan & Das (1973); Sengupta (1993).

Table 6.3. Anthropometric distance/Coefficient of relationship between populations

Population	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)
Chapras (1)	-										
Sangas (2)	0.126	-									
Satparis (3)	0.272	0.074	-								
Tintikiyas (4)	0.044	0.067	0.098	-							
Wanangs (5)	0.263	0.095	0.127	0.079	-						
Kochs (6)	0.409	0.405	0.384	0.425	0.432	-					
Hajongs (7)	0.412	0.407	0.379	0.433	0.441	0.127	-				
Garos (8)	0.452	0.462	0.457	0.467	0.465	0.202	0.229	-			
Khynriams (9)	0.512	0.521	0.511	0.530	0.534	0.217	0.241	0.118	-		
Pnars (10)	0.410	0.418	0.398	0.437	0.441	0.142	0.164	0.151	0.138	-	
Bhois (11)	0.396	0.404	0.402	0.421	0.412	0.219	0.217	0.140	0.170	0.167	-
Wars (12)	0.487	0.493	0.476	0.506	0.512	0.183	0.183	0.134	0.069	0.167	0.157

Fig. 6.1 Dendogram based on Anthropometric measurements of 12 populations.



CHAPTER VII
MORPHOLOGICAL AND BEHAVIOURAL TRAITS

In this chapter, we shall deal with the morphological and behavioural traits like hand clasping, arm folding, tongue rolling, tongue folding, earlobe attachment and middle phalangeal hair.

It may be noted that morphological and behavioural traits are not as reliable as genetic markers from the genetic point of view. In the present study, however, we agree with Salzano (1961) that these traits may be useful in population genetics studies for several reasons. One such reason is that the findings on the genetic affinity of human populations in respect of known loci are still not as clearly understood as were in the case of these traits. In several cases, the findings on genetic markers corroborate those on anthropometric and other morphological and behavioural traits (Harrison, 1977). Moreover, there are also certain morphological characters, which are considered to be strongly determined by genetic factors rather than by environmental factors like dermatoglyphic and some other traits. For example, it was Lutz (1908) who for the first time draws our attention that when an individual clasps his hands with finger interlocking, the right thumb remains uppermost in some individuals, while the left thumbs in others. Lutz has considered that the manner of hand clasping was heritable, but he was not able to state the exact mode of its inheritance. Weiner (1932) has supported that hand clasping is genetically determined and the trait is not associated with sex or handedness. Other investigations on hand clasping carried out by Kawabe (1949), Trankell (1955), Freire-*Maia et al.* (1958), Pons (1961) and Quelce-Salgado *et al.* (1961) have all supported Lutz's hypothesis that this functional asymmetry is genetically controlled, although no simple Mendelian mechanism has been offered to explain its mode of inheritance.

With regard to earlobe attachment, individuals can be classified into different categories. Hilden (1922) was the first to study the earlobe types in man. Attachment of earlobe in man is influenced by heredity, although the mode of its inheritance is not established (Carriere, 1937; Quelprud, 1934, 1941). Hilden (1922) is of the opinion that the inheritance of free earlobe is determined by an autosomal dominant gene. Powell and Whitney (1937) also supported the

hypotheses of autosomal dominance of the free type. With respect to mid-phalangeal hair, Danforth (1921) has suggested that complete absence of middle phalangeal hair in man is a simple recessive trait. Chopra (1953), Matsunaga (1956), Beckman and Book (1959) have supported the hypothesis stated by Danforth with a few exceptions.

Thus, we have also taken into consideration some of the morphological traits that are likely to be less influenced by the environmental factors for better understanding of the population genetics of the Koch subgroups of the present study.

Hand Clasping

In the present study, the distribution of the hand clasping among the five sub-groups of Koch population are presented in Table 7.1. In all the sub-groups under consideration, the right types of hand clasping are very common in both the sexes. The right type of hand clasping occurs in higher frequency among the males of Satparis (58.54%), Tintikiyas (68.85%), and Wanangs (71.43%) when compared with those among the Chapras (54.90%) and Sangas (56.10%). In the case of females, the right type of hand clasping occurs more among the Chapras (65.38%), and Sangas (73.53%), when compared with the Satparis (55.88%), Tintikiyas (45.45%), and Wanangs (50%). However, the Chi-square test shows a significant bi-sexual variation only among the Tintikiyas ($\chi^2 = 5.7853$, DF=1, $P < 0.05$) and Wanangs ($\chi^2 = 5.0171$, DF =1, $P < 0.05$). It is also found that the differences between the sub-groups of Koch are not statistically significant in respect of hand clasping ($\chi^2 = 0.84$, DF = 4, $P > 0.05$).

Table 7. 1. Percentage distribution of hand clasping

Sex	Chapras	Sangas	Satparis	Tintikiyas	Wanangs
Male					
R > L	28	23	34	42	40
%	54.90	56.10	58.54	68.85	71.43
L > R	23	18	17	19	16
%	45.10	43.90	41.46	31.15	28.57
Female					
R > L	34	25	19	20	24
%	65.38	73.53	55.88	45.45	50.00
L > R	18	9	15	24	24
%	34.62	26.47	44.12	54.55	50.00
χ^2 (DF=1)	1.18	2.45	0.05	5.79*	5.02*
Persons					
R > L	62	48	43	62	64
%	60.19	64.00	57.33	59.05	61.54
L > R	41	27	32	43	40
%	39.81	36.00	42.67	40.95	38.46

$\chi^2 = 0.84$, DF = 4, $P > 0.05$

Table 7.2. Percentage distribution of arm folding

Sex	Chapras	Sangas	Satparis	Tintikiyas	Wanangs
Male					
R > L	25	17	21	34	31
%	49.02	41.46	51.22	55.74	55.36
L > R	26	24	20	27	25
%	50.98	58.54	48.78	44.26	44.64
Female					
R > L	25	14	18	29	23
%	48.08	41.18	52.94	65.91	47.92
L > R	27	20	16	15	25
%	51.92	58.82	47.06	34.09	52.08
χ^2 (DF=1)	0.001	0.001	0.02	1.10	0.057
Persons					
R > L	50	31	39	63	54
%	48.54	41.33	52.00	60.00	51.92
L > R	53	44	36	42	50
%	51.46	58.67	48.00	40.00	48.08

$\chi^2 = 6.51$, DF = 4, P > 0.05

Arm Folding

The percentage distribution of arm folding is presented in the table 7.2. In all the groups, the left type of arm folding is more common than the right type. Left type of arm folding is more common among the Chapras (male = 50.98%, female = 51.92%) and Sangas Koch (male = 58.54%, female = 58.82%) and only in females for the Wanangs (52.08%). The reverse (R>L) is true among the Satparis (male = 51.22%, female 52.94%), Tintikiyas (male = 55.74%, female = 65.91%) and only in males for the Wanangs (55.36%). The lowest incidence of left type is found in Tintikiya females (34.09%) while the highest frequency in Sanga females (58.82%). The Chi-square however, shows that there is no significantly bi-sexual variation in this trait (Table 7.2). Also, the inter-group differences are not statistically significant except the difference between the Sangas and Tintikiyas, which is significant ($\chi^2 = 6.1149$, DF =1, P< 0.05).

Tongue Rolling

The percentage distribution of tongue rolling among the Koch subgroups of the present study is given in Table 7.3. The persons who are able to roll their tongue are categorized as positive, while those unable are grouped as negative. It is observed that most of males and females are unable to roll their tongue. It is true for all the population groups. In males, the frequency of tongue rolling varies from 12.20% among the Sangas to 30.36% among the Wanangs, whereas in

females it varies from 8.82% for the Satparis to 31.25% for the Wanangs. Except in the case of Chapras, these sex differences are not statistically significant, but it is obvious that the frequency of tongue rolling is higher in both males and females of the Wanangs when compared with the other groups. Pooling the data for both the sexes, the Chi-square value indicates that the inter-group variation is highly significant in respect of tongue rolling (χ^2 = 11.66, DF = 4, P< 0.02). It may, however, noted that this inter-group variation is mainly attributed by the differences between the Wanangs and the Sangas (χ^2 = 7.38, DF = 1, P < 0.01) as well as between the Wanangs and the Satparis (χ^2 = 7.38, DF = 1, P < 0.01), since the differences between any other groups are not statistically significant.

Tongue Folding

Table 7.4 shows the distribution of tongue folding. In the present study, positive individuals are those who are able to fold their tongue, whereas those persons unable to fold their tongue are categorized as negative. It is found that the incidence of tongue folding (positive) is more in males than in females among the Satparis (34.15%), Tintikiyas (36.07%) and Wanangs (33.93%). On the other hand, the frequency of tongue folding is higher in females than in males among the Chapras (40.38%) and Sangas (44.12%). However, these sex differences are not statistically significant for all the population groups. Likewise, the inter-group variation in respect of tongue folding is not statistically significant (χ^2 = 2.0835, DF = 4, P > 0.05), which indicates that these Koch subgroups of Meghalaya are by and large similar in this trait.

Table 7.3. Percentage distribution of tongue rolling

Sex/character	Chapras	Sangas	Satparis	Tintikiyas	Wanangs
Male					
Positive	14	5	7	10	17
%	27.45	12.20	17.07	16.39	30.36
Negative	37	36	34	51	39
%	72.55	87.80	82.93	83.61	69.64
Female					
Positive	6	5	3	11	15
%	11.54	14.71	8.82	25.00	31.25
Negative	46	29	31	33	33
%	88.46	85.29	91.18	75.00	68.75
χ^2 (DF =1)	4.1725*	0.1029	1.0901	1.1834	0.0097
Persons					
Positive	20	10	10	21	32
%	19.42	13.33	13.33	20.00	30.77
Negative	83	65	65	84	72
%	80.58	86.67	86.67	80.00	69.23

χ^2 = 11.6612; DF.=4, P < 0.05; *Significant at 5% level.

Table 7.4. Percentage distribution of tongue folding

Sex/character	Chapras	Sangas	Satparis	Tintikiyas	Wanangs
Male					
Positive	18	15	14	22	19
%	35.29	36.59	34.15	36.07	33.93
Negative	33	26	27	39	37
%	64.71	63.41	65.85	63.93	66.07
Female					
Positive	21	15	11	15	13
%	40.38	44.12	32.35	34.09	27.08
Negative	31	19	23	29	35
%	59.62	55.88	67.65	65.91	72.92
χ^2 (DF = 1)	0.2834	0.4394	0.0264	0.0429	0.5690
Persons					
Positive	39	30	25	37	32
%	37.86	40.00	33.33	35.24	30.77
Negative	64	45	50	68	72
%	62.14	60.00	66.67	64.76	69.23

χ^2 = 2.0835, DF = 4, P > 0.05

Table 7.5. Percentage distribution of earlobe attachment

Sex/character	Chapras	Sangas	Satparis	Tintikiyas	Wanangs
Males					
Free	15	14	12	15	15
%	29.41	34.15	29.27	24.59	26.79
Attached	36	27	29	46	41
%	70.59	65.85	70.73	75.41	73.41
Females					
Free	15	9	12	16	13
%	28.85	26.47	35.29	36.36	27.08
Attached	37	25	22	28	35
%	71.15	73.53	64.71	63.64	72.92
χ^2 (DF =1)	0.0042	0.5175	0.3102	1.7035	0.0013
Persons					
Free	30	23	24	31	28
%	29.13	30.67	32.00	29.52	26.92
Attached	73	52	51	74	76
%	70.87	69.33	68.00	70.48	73.08

χ^2 = 0.6116, DF =4, P>0.05

Earlobe Attachment

Table 7.5 shows the percentage of earlobe attachment in five sub-groups of the Kochs of the present study. The frequency of attached earlobe, irrespective of the sexes, predominates over free earlobe in all the sub-groups. It varies from 68% for the Satparis to 73% for the Wanangs. It is found that there is no significant difference between sexes as well as between the subgroups in respect of the distribution of earlobe attachment. In other words, the present findings indicate that the present subgroups of the Koch population are by and large similar in earlobe attachment.

Mid-Phalangeal Hair

Table 7.6 shows the percentage distribution of persons with mid-phalangeal hair on any of the fingers. It is found that the mid-phalangeal hair is present more in males than in females among the Chapras and Wanangs. In the case of Sangas, Satparis and Tintikiyas, the frequency is higher in females than in males. However, these sex differences are found to be statistically insignificant

for all the subgroups. Pooling the data for both males and females, it is found that the 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.

Table 7.6. Percentage distribution of individuals with mid-phalangeal hair

Sex/character	Chapras	Sangas	Satparis	Tintikiyas	Wanangs
Male					
Present	28	18	15	36	24
%	54.90	48.90	36.59	59.02	42.86
Absent	23	23	26	25	32
%	45.10	56.10	69.41	40.98	57.14
Female					
Present	23	19	14	15	25
%	44.23	55.88	41.18	34.09	52.08
Absent	29	15	20	29	23
%	55.77	44.12	58.82	65.91	47.92
χ^2 (DF = 1)	1.17	1.07	0.16	6.35*	0.88
Persons					
Present	51	37	29	51	49
%	49.51	49.33	38.67	48.57	47.12
Absent	52	38	46	54	55
%	50.49	50.67	61.33	51.43	52.88

$\chi^2 = 2.62$, DF = 4, P > 0.05

COMPARISON WITH OTHER POPULATIONS

For comparison with other populations, we have taken into consideration only hand clasping, arm folding, tongue rolling and earlobe attachment as data on other characters are not available for other neighbouring populations including populations of Assam.

Table 7.7 shows the percentage frequency of hand clasping, arm folding and tongue rolling in the populations of the present study and other populations of Assam and Meghalaya. In the case of hand clasping, the Chi-square values indicate that all population groups of the present study stand closer to the Chutias, Khasis and Dalus (Table 7.8). They are also similar to the

Kochs of Assam, but differ significantly from the Ahoms, Deuris, Mishings, Morans and Lalungs of Assam.

Table 7.7. Hand clasping, arm folding and tongue rolling in the Kochs and other populations

Population	Hand clasping			Arm folding			Tongue rolling		
	N	R>L(%)	L>R(%)	N	R>L(%)	L>R(%)	N	Positive (%)	Negative (%)
Chapras[1]	103	60.19	39.81	103	48.54	51.46	103	19.42	80.58
Sangas[1]	75	64.00	36.00	75	41.33	58.67	75	13.33	86.67
Satparis[1]	75	57.33	42.67	75	52.00	48.00	75	13.33	86.67
Tintikiyas[1]	105	59.05	40.95	105	60.00	40.00	105	20.00	80.00
Wanangs[1]	104	61.54	38.46	104	51.92	48.08	104	30.77	69.23
Ahoms[2]	204	86.30	13.70	204	31.40	68.60	204	76.80	23.20
Deuris[2]	201	92.00	8.00	201	21.90	78.10	201	52.40	47.60
Mishings[2]	201	87.60	12.40	201	31.80	68.20	201	43.30	56.70
Chutias[2]	190	62.30	37.70	190	25.80	74.20	190	40.50	59.50
Morans[2]	206	74.80	25.20	206	17.00	83.00	206	42.30	57.70
Lalungs[3]	94	98.94	1.06	94	56.38	43.62	94	72.34	27.66
Khasis[4]	201	69.16	30.84	67	37.85	62.15	NA	NA	NA
Kochs[5]	561	63.46	36.54	561	40.29	59.71	NA	NA	NA
Dalus[6]	145	69.66	30.34	145	68.28	31.72	145	20.69	79.31

NA = Not available

Sources: [1]Present study; [2, 3]Das et al.(1980,1985); [4]Das and Barua (1974); [5]Sengupta (1993); [6]Borthakur et al. (1997).

Table 7.8. Chi-square values between the Koch subgroups and other populations in respect of hand clasping, arm folding and tongue rolling.

Chi-square for hand clasping(DF = 1)

Population	Chapras	Sangas	Satparis	Tintikiyas	Wanangs
Ahoms	26.72***	17.21***	27.21***	29.02***	24.50***
Deuris	45.35***	32.68***	45.82***	48.21***	42.51***
Mishings	30.02***	19.83***	30.45***	32.46***	27.69***
Chutias	0.10	0.08	0.52	0.27	0.01
Morans	6.92**	3.14	7.96**	8.10**	5.79*
Lalungs	43.97***	36.81***	45.98***	45.81***	42.04***
Khasis	2.44	0.67	3.40	3.13	1.79
Kochs	0.40	0.01	1.06	0.74	0.14
Dalus	2.39	0.73	3.32	3.02	1.79

Chi-square for arm folding(DF = 1)

Population	Chapras	Sangas	Satparis	Tintikiyas	Wanangs
Ahoms	8.64**	2.42	10.02**	23.46***	12.32***
Deuris	22.65***	10.43**	23.56***	44.03***	28.34***
Mishings	8.11**	2.18	9.49**	22.52***	11.65***
Chutias	15.46***	6.17*	16.64***	33.62***	20.16***
Morans	34.30***	18.12***	34.74***	59.60***	41.20***
Lalungs	1.21	3.78	0.32	0.27	0.39
Khasis	1.91	0.16	2.93	8.42**	3.34
Kochs	2.45	0.03	3.74	14.00***	4.87*
Dalus	9.77**	14.85***	5.61*	1.83	6.83**

Chi-square for tongue rolling (DF = 1)

Population	Chapras	Sangas	Satparis	Tintikiyas	Wanangs
Ahoms	92.81***	92.38***	92.38***	92.12***	62.00***
Deuris	31.15***	34.80***	34.80***	30.45***	13.36***
Mishings	17.00***	21.50***	21.52***	16.37***	3.93*
Chutias	13.44***	18.03***	18.03***	12.84***	2.74
Morans	15.80***	20.32***	20.32***	15.16***	3.84*
Lalungs	55.69***	58.47***	58.47***	54.96***	34.15***
Dalus	0.06	1.80	1.80	0.02	3.29

*P < 0.05, **P < 0.01, ***P < 0.001

With respect to arm folding, the five subgroups of the Kochs of present study deviate significantly from the Deuris Chutias and Morans. With regard to the relationship with other populations, each subgroup does not follow the same pattern of relationship. Table 7.8 shows that the Chapras and Satparis are similar to the Lalungs, Khasis and Kochs, but they differ significantly from the other populations like the Ahoms, Deuris, Mishings, Chutias, Morans and Dalus. On the other hand, the Sangas stand closer to many other Mongoloid populations, although they deviate significantly from the Deuris, Chutias, Morans and Dalus. Like in the case of Chapras and Satparis, the Tintikiyas and Wanangs differ significantly from the Ahoms, Deuris, Mishings, Chutias and Morans, but show a different pattern of relationship with other populations, namely, Kochs of Assam, Lalungs, Dalus and Khasis. It is observed that the Tintikiyas are similar to the Lalungs and Dalus, but different from the Kochs of Assam and Khasis; whereas the Wanangs stand closer to the Lalungs and Khasis, but deviate significantly from the Kochs and Dalus. To sum up, the populations of the present study are by and large different from the Ahoms, Deuris, Mishings, Chutias, Morans and Dalus in respect of arm folding, but almost all stand closer to the Lalungs and Khasis.

Unlike the case of arm folding, the present populations are similar to the Dalus in respect of tongue rolling, but they differ significantly from the other populations like the Ahoms, Deuris, Mishings, Chutias, Morans and Lalungs. Of course, the Wanangs are also similar to the Chutias with respect to tongue rolling.

Table 7.9. Earlobe attachment among the Kochs of Garo hills and other populations

Population	Number	Free	Attached	Sources
Chapras	103	29.13	70.87	Present study
Sangas	75	30.67	69.33	Present study
Satparis	75	32.00	68.00	Present study
Tintikiyas	105	29.52	70.48	Present study
Wanangs	104	26.92	73.08	Present study
Kochs[2]	561	65.25	34.76	Sengupta (1993)
Garos[3]	200	27.00	73.00	Das (1967)
Rabhas[3]	300	18.00	82.00	Das (1967)
Hajongs[4]	298	44.97	55.03	Barua (1985)
Dalus[5]	145	22.76	77.24	Borthakur *et al.* (1997)

Chi-square values (DF =1)

Population	Chapras	Sangas	Satparis	Tintikiyas	Wanangs
Kochs	47.16***	33.28***	30.82***	46.86***	53.36***
Garos	0.15	0.36	0.67	0.22	0.001
Rabhas	5.75*	5.90*	7.14**	6.22*	3.80
Hajongs	7.94**	5.03*	4.13*	7.66**	10.43**
Dalus	1.29	1.63	2.20	1.46	0.57

In the case of earlobe attachment, Table 7.9 shows that the Koch subgroups of the present study are all related to the Garos and Dalus, but they deviate significantly from the Kochs of Assam, Rabhas (except with the Wanangs) and Hajongs.

Thus, 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 the case of 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.

CHAPTER - VIII
DERMATOGLYPHIC TRAITS

In this Chapter we shall describe some of the important dermatoglyphic traits collected for the present study. We shall restrict our presentation on the frequency of finger patterns, finger pattern indices, finger ridge counts, main line formulae and C-line termination taking into consideration the whole population rather than finding out the bimanual and sex differences in these traits within populations. Moreover, such a restriction has also been done in accordance with the objectives of the present study, that is, to see how the Koch subgroups of Garo hills are different or similar to one another, and to understand the relationship of these subgroups with other Koch subgroups or other neighbouring populations of Assam and Meghalaya in respect of dermatoglyphic traits.

Finger Patterns

Table 8.1 shows the percentage distribution of finger patterns among the five subgroups of the Koch populations. It is seen that the frequency of whorls is highest among the Satparis (45%) and lowest among the Chapras (34%). The Sangas and Chapras are more or less similar in respect of loops. So are the Satparis and Tintikiyas. But the Wanangs are in the middle of the Chapra-Sanga group and the Satpari-Tintikiya group. With respect to the frequency of arches, Table 8.1 shows that it is highest among the Chapras (9%) and lowest among the Satparis (4%). The overall differences between these Koch subgroups are found to be highly significant in respect of finger patterns ($\chi^2 = 44.33$, DF = 8, P < 0.000). The Table also shows that the differences between any two subgroups are highly significant, except the differences between the Sangas and Wanangs and between the Tintikiyas and Satparis and Wanangs. In other words, the homogeneity test indicates that the Tintikiyas are clôser 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.

Table 8.1. Percentage distribution of finger patterns

Population	Num-ber	Whorls	Loops			Arches
			Ulnar	Radial	Total	
Chapras	102	33.92	54.51	2.35	56.86	9.22
Sangas	75	37.47	55.60	1.60	57.20	5.33
Satparis	75	45.07	49.47	1.60	51.07	3.87
Tintikiyas	104	42.50	50.19	0.96	51.15	6.35
Wanangs	104	39.62	52.60	1.54	54.13	6.25

Chi-square-values for the differences between any two subgroups

Population	Chapras	Sangas	Satparis	Tintikiyas
Chapras	-			
Sangas	10.14**	-		
Satparis	34.36***	9.61**	-	
Tintikiyas	18.47**	6.46*	5.71	-
Wanangs	11.10**	1.88	8.58**	1.94

*P < 0.05, **P < 0.01, ***P < 0.001

Table 8.2. Finger pattern indices

Population	Dankmeijer's index	Furuhata's index	Pattern intensity index
Chapras	54.41	119.40	12.47
Sangas	28.46	135.80	13.21
Satparis	19.49	188.53	14.12
Tintikiyas	34.11	163.67	13.62
Wanangs	37.16	145.83	13.34

Finger Pattern Indices

Table 8.2 shows the frequency of finger pattern indices in all the sub-groups of the Koch population covered under the present study. It is found that the pattern intensity index is more or less similar in all the subgroups, but the Dankmeijer's index and Furuhata's index are different from one subgroup 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.

Table 8.3. Total finger ridge count

Population	Number	Finger ridge count	
		Mean	Standard deviation (SD)
Chapras	102	133.60	25.50
Sangas	75	144.95	21.42
Satparis	75	158.40	23.15
Tintikiyas	104	142.53	21.19
Wanangs	104	134.06	22.01

t-test for the differences between any two subgroups

Population	Chapras	Sangas	Satparis	Tintikiyas
Chapras	-			
Sangas	3.12*	-		
Satparis	6.65**	3.87*	-	
Tintikiyas	2.73*	0.75	4.75**	-
Wanangs	0.14	3.30*	7.14**	2.83*

*P < 0.01, **P< 0.000

Finger Ridge Count

The means and standard deviations of total finger ridge count are presented in Table 8.3. It is found that the mean finger ridge count is lowest among the Chapras (133.60 ± 25.50) and 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.

Table 8.4. Percentage distribution of mainline formulae

Population	Number	11.9.7	9.7.5	7.5.5
Chapras	102	33 (16.18)	73 (35.78)	94 (46.08)
Sangas	75	22 (14.67)	52 (34.67)	60 (40.00)
Satparis	75	20 (13.33)	57 (38.00)	69 (46.00)
Tintikiyas	104	43 (20.67)	76 (36.54)	68 (32.69)
Wanangs	104	31 (14.90)	83 (39.90)	86 (41.35)

Chi-square-values (DF=2) for the differences between any two subgroups

Population	Chapras	Sangas	Satparis	Tintikiyas
Chapras	-			
Sangas	0.20	-		
Satparis	0.24	0.35	-	
Tintikiyas	5.12	3.12	6.16*	-
Wanangs	1.06	0.24	0.65	3.93

$\chi^2 = 9.16$, D.F. = 8, P = 0.33

Mainline Formulae

Table 8.4 shows the percentage distribution of mainline formulae. It can be observed that the percentage distribution of the mainline formula-11.9.7 is highest among the Tintikiyas (21%) and lowest among the Satparis (13%). On the other hand, the percentage distribution of mainline formula- 9.7.5 varies from 35% among the Sangas to 40% among the Wanangs, whereas the frequency of mainline formula-7.5.5 ranges from 33% for the Tintikiyas to 46% for the Chapras and Satparis. These differences between the Koch subgroups of the present study are however 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).

Table 8.5. C-line termination

Population	Number	Ulnar	Radial	Proximal	Absent
Chapras	102	167 (81.86)	33 (16.18)	3 (1.47)	1 (0.49)
Sangas	75	114 (76.00)	21 (14.00)	6 (4.00)	9 (6.00)
Satparis	75	126 (84.00)	20 (13.33)	3 (2.00)	1 (0.67)
Tintikiyas	104	146 (70.19)	43 (20.67)	12 (5.77)	7 (3.37)
Wanangs	104	170 (81.73)	29 (13.94)	2 (0.96)	7 (3.37)

Chi-square-values for the differences between any two subgroups

Population	Chapras	Sangas	Satparis	Tintikiyas
Chapras	-			
Sangas	0.05	-		
Satparis	0.51	0.19	-	
Tintikiyas	2.41	2.57	4.42*	-
Wanangs	0.28	0.06	0.05	4.29*

*$P < 0.05$,

C-Line Termination

The percentage distribution of C-line termination is summarized in Table 8.5. It is found that C-line termination towards ulnar side is very common in all the subgroups of the Koch population of the present study. The Table shows that 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 Table further shows that the C-line termination towards proximal is highest among the Tintikiyas (6%) and lowest among the Wanangs (0.96%), and the proportion of individuals without C-termination is highest among the Sangas (6%) and lowest among the Chapras (0.49%). Taking into consideration these differences in distribution of C-line termination towards ulnar, radial and proximal sides, it is found that the Chi-square value is significant ($\chi^2 = 16.34$, DF = 8, $P < 0.04$). However, it can be noticed that the number of samples is very small in the case of proximal side, thus the differences may still be due to chance fluctuation. This can be justified if we take into consideration the differences in C-line termination towards ulnar and radial sides only, which indicates that the Chi-square is not significant ($\chi^2 = 6.60$, DF = 4, $P > 0.05$). The homogeneity test for the differences between any two subgroups also indicate that the Koch subgroups of the present

study are by and large similar to one another in respect of the percentage distribution of C-line termination towards ulnar and radial sides, although the Tintikiyas deviate significantly from the Wanangs and Satparis (Table 8.5).

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.

COMPARISON WITH OTHER POPULATIONS

Table 8.6 shows the dermatoglyphic traits among the Chapras, Sangas, Satparis, Tintikiyas and Wanangs in comparison with other populations of Assam and Meghalaya. Table 8.7 indicates that these five subgroups of the Koch of Garo hills are different significantly from the other populations in respect of finger patterns. However, although there are inter-group differences, the Tintikiyas are closer to the Satparis and Wanangs, and the Sangas are similar to the Wanangs in respect of finger patterns (Table 8.1) rather than to the populations of Assam and Meghalaya (Table 8.7). Therefore, it may be concluded that although there are differences between the Koch subgroups, other groups like the Tintikiyas and the Satparis, and the Sangas and Wanangs are similar in finger patterns rather than to the other populations of Assam and Meghalaya (Sengupta, 1993).

With respect to finger pattern intensity, Table 8.7 shows that the Koch subgroups of the present study 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, the Koch subgroups of the present study show a different degree of affinity to other populations with respect to finger ridge counts. Such a trend is indeed expected because the subgroups are different from one another in respect of finger ridge count. For example, Table 8.7 shows that the Chapras and Wanangs are different from the Kochs of Assam and Garos, but they are similar to the Khasi subgroups like the Lyngngams, 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. Table 8.7 shows that almost all the Koch subgroups are similar to the Hajongs despite the difference between the Tintikiyas and the Hajongs. Also, they 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.

Table 8.6. Dermatoglyphic traits among the Koch subgroups and other populations

Population	N	Finger pattern (%)			P.I.I.	T.F.R.C	Mainline formulae (%)		
		Whorl	Loop	Arch		(Mean ± SE)	11.9.7	9.7.5	7.5.5
Chapras	102	33.92	56.86	9.22	12.47	133.60± 2.52	16.18	35.78	46.08
Sangas	75	37.47	57.20	5.33	13.21	144.95±2.47	14.67	34.67	40.00
Satparis	75	45.07	51.07	3.87	14.12	158.40±2.67	13.33	38.00	46.00
Tintikiyas	104	42.50	51.15	6.35	13.62	142.53±2.08	20.67	36.54	32.69
Wanangs	104	39.62	54.13	6.25	13.34	134.06±2.16	14.90	39.90	41.35
Kochs	281	45.87	52.17	1.96	14.39	157.41±2.98	20.67	21.65	25.20
Garos	170	49.35	48.24	2.41	14.67	152.53±5.25	NA	NA	NA
Hajongs	75	44.67	53.73	1.60	14.30	NA	9.23	27.69	44.61
Khynriams	164	37.38	59.82	2.80	62.57	128.30±6.11	26.60	38.46	34.94
Pnars	187	38.77	58.88	2.35	66.67	132.06±5.20	31.10	33.54	35.37
Wars	165	38.91	58.24	2.85	66.92	131.51±5.41	22.67	43.17	34.16
Bhois	71	45.63	53.38	0.99	91.82	139.78±6.13	22.73	43.94	33.33

Sources: Das (1959,1963, 1978) and Sengupta (1993)
NA- Not available; P.I.I. = Pattern Intensity Index; T.F.R.C =Total finger ridge count

Table 8.7. Test of differences between the Koch subgroups and other populations

Finger patterns (Chi-square test for homogeneity, DF= 2):					
Population	Chapras	Sangas	Satparis	Tintikiyas	Wanangs
Kochs	129.46***	37.58***	9.37*	48.59***	52.16***
Garos	103.52***	37.71***	15.84***	33.18***	42.43***
Hajongs	55.52***	20.62***	14.21***	28.55***	24.58***
Khynriams	52.14***	9.74**	16.40***	31.80***	22.65***
Pnars	69.73***	15.32***	23.04***	37.62***	29.84***
Wars	52.82***	9.15*	11.23**	26.39***	19.71***
Bhois	64.31***	28.26***	12.64**	30.42***	32.09***
Total finger ridge count (t-test):					
Population	Chapras	Sangas	Satparis	Tintikiyas	Wanangs
Kochs	4.88***	2.25*	0.18	3.13**	4.89***
Garos	2.99**	1.21	0.91	1.66	2.97**
Khynriams	0.75	2.37*	4.19***	2.09*	0.84
Pnars	0.24	2.06*	4.10***	1.75	0.33
Wars	0.32	2.14*	4.07***	1.78	0.41
Bhois	0.87	0.73	2.59**	2.75**	0.84
Mainline formula(Chi-square test for homogeneity):					
Population	Chapras	Sangas	Satparis	Tintikiyas	Wanangs
Kochs	8.97*	8.44*	13.10**	3.91	12.63**
Hajongs	2.22	2.66	1.38	11.01**	3.90
Khynriams	10.08**	6.53*	11.26**	0.76	9.11**
Pnars	14.90***	10.61**	9.99**	4.47	16.05***
Wars	8.87*	5.07	8.98*	0.35	8.15*
Bhois	6.32*	4.01	6.85*	0.40	4.27

* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$

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 all the Koch subgroups of the present study are by and large closer to the Kochs, Garos and Hajongs.

CHAPTER IX

DISCUSSION

It has long been suggested that the biological variation between and within human populations is due to the cumulative effect of various evolutionary forces like mutation, selection, genetic drift and gene flow over a period of time. This is also the subject that has become the main focus in the field of physical anthropology since the middle of the twentieth century. Physical anthropologists are interested in this type of study with a view to understanding the processes of human evolution, and a large number of demographic, anthropometric, morphological, dermatoglyphic and genetic traits have been used for this purpose. Their studies have revealed both positive and negative results. The positive results are related to the fact that human populations are highly polymorphic, thereby indicating that they are basically the unit of ongoing process of evolution. Various studies especially those carried out by population geneticists and molecular geneticists have documented that polymorphic traits are increasing in human populations (Crawford, 1973). The hypothesis that human evolution is the ongoing process of mutation, selection, genetic drift, gene flow, etc., has become more indisputable. On the other hand, from the negative point of view, various population genetic studies carried out by physical anthropologists are also of repetive in nature. This is particularly so in developing countries because of the lack of infrastructure. In Chapter I, we have mentioned that ascertaining the phylogenetic relationship of human populations has remained the main objective of physical anthropology. Various mathematical models and distance analyses have been suggested for this purpose. But the results of various studies in this regard are still highly controversial and debatable. In Northeast India, the study carried out by Danker-Hopfe *et al.* (1988), as already mentioned in Chapter II, is a good example how distance analyses of data of different natures produce different results. The authors have rightly pointed out that "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" (Danker-Hopfe *et al.*, 1988). In fact, many studies have revealed the existence of such a difficult situation in the interpretation of the phylogenetic position of human populations. We have stressed this point in this discussion because our present study has also indicated the same trend while trying to find out the genetic relationship of the Koch subgroups, namely, Chapras, Sangas, Satparis, Tintikiyas and Wanangs, of Garo hills with other neighbouring populations. Thus, it is likely that the study of phylogenetic relationship of human populations still needs more systematic methods or models, especially in the case of study like the present one which deals with limited and weak genetic markers. Unfortunately, this is not the purpose of the present study, and no attempt has been made to develop such a method or techniques-- instead we have also used the methods that are generally adopted for finding out the phylogenetic affinity of the present populations.

In order to have a better understanding of what has been hinted above, it may be necessary to take into consideration the findings of the present study on the Kochs of Garo hills. The Kochs of Meghalaya are mainly concentrated in West Garo Hills district. Historically, they migrated from Kamrup district of Assam, although some section of them believe that their original homeland is in Arabela range of Central Garo hills.

Demographic Characteristics

On the basis of demographic data presented in Chapter IV, 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 of population, 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 approaches to be of *progressive type*, which is characterized by high fertility rates. The over all sex, i.e., the 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 and Ghosh, 1994), 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.

The mean age at marriage is found to significantly different among the Koch subgroups. 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, although it is not as high as that among the Christian War Khasis. 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.

With respect to 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. It is found that these differences in live births and surviving children between the Koch populations are statistically significant. The same is trend is observed in the case of married women of all ages, indicating perhaps the differences in socioeconomic status between these subgroups. Since we are not concerned with socioeconomic determinants of fertility, we are however not able to give proper explanation regarding the factors affecting fertility rate in the Koch of the present study. We hope that further research will throw much more light in this respect. However, it is observed that 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).

Infant, Child and juvenile Mortality

It is observed 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 and child mortality rates are also statistically significant, 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.

With respect to reproductive wastage, the frequency in the Koch subgroups of the present is found to be lower 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 characterized 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 Khasi (Khongsdier and Ghosh, 1994, 1996) and Semsa population (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 Khasi of Meghalaya (Khongsdier, 2001). This clearly shows that the Koch population of Garo hills as 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 subpopulations like the Chapras, Sangas, Satparis, Tintikiyas, Wanangs, Banais and Sankars, which may exchange genes with one another with little effect of distance. Of course, 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 seen 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, whereas in

other populations the blood type B is higher than A. The frequency of O blood type is more or less similar in all populations covered under the present study, although it is lower in the Wanangs (18. 27%). With respect to blood type AB, it is found that the frequency is very low in the Sangas (8%) in comparison with the other subgroups. These differences between populations in respect of the phenotype distribution of ABO blood groups are, however, not statistically significant (χ^2 = 10.97, D.F. = 12, P > 0.05). In other words, it indicates that the present Koch sub groups are by and large similar in the percentage distribution of the ABO blood group system. Following the methods suggested by Balakrishnan (1988), it is found that the allele frequencies of p (A), q (B) and r (O) are not statistically significant in all populations, thereby indicating 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 clour 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, it is found that the frequency of non-tasters is lowest among the Satparis (10.67%) and highest among the Wanangs (37.50%). The Chi-square value indicates that the inter-population differences are statistically significant (χ^2 = 22.56, DF = 4, P < 0.05), but the differences between two populations shows that the differences between the Koch subgroups of the present study 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.

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 differences between the Koch subgroups of the present study 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, it may be concluded that the Koch subgroups of the present study are by and large similar in anthropometric measurements. Similar observation is made in the case of the anthropometric indices. It is found that the Koch subgroups of the present study 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. Like in the case of anthropometric measurements, it is also found that the differences in cephalic index among the Koch subgroups of the present study 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 data used for calculating CD are given in Table 6.2 and the results are shown in Table 6.3. The dendrogram (Figure 6.1), derived as per the method suggested by Sokal and Sneath (1963), shows that all the Koch subgroups of the present study 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 by and large 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 results on these traits are presented in Chapter VII. It is observed that the frequency of whorls is highest among the Satparis (45%) and 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, it is found that the pattern intensity index is more or less similar in all the subgroups, but the Dankmeijer's index and Furuhata's index are different from one subgroup 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 54.51 among the Chapras. In the case of finger ridge count, it is found that the mean finger ridge count is lowest among the Chapras (133.60 ± 25.50) and 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.

With regard to mainline formulae, it is observed that the percentage distribution of the mainline formula-11.9.7 is highest among the Tintikiyas (21%) and lowest among the Satparis (13%). On the other hand, the percentage distribution of mainline formula-9.7.5 varies from 35% among the Sangas to 40% among the Wanangs, whereas the frequency of mainline formula-7.5.5 ranges from 33% for the Tintikiyas to 46% for the Chapras and Satparis. These differences between the Koch subgroups of the present study are however not statistically significant ($\chi^2 = 9.16$, DF = 8, P = 0.33). 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 of the present study. 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 C-line termination towards proximal is highest among the Tintikiyas (6%) and lowest among the Wanangs (0.96%), and the proportion of individuals without C-line termination is highest among the Sangas (6%) and lowest among the Chapras (0.49%). The homogeneity test for the differences between any two subgroups also indicate that the Koch subgroups of the present study are by and large similar to one another in respect of the percentage distribution of C-line termination towards ulnar and radial sides, although the Tintikiyas deviate significantly from the Wanangs and Satparis (Table 8.5).

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.

In comparison with other populations, these five subgroups of the Koch of Garo hills are different significantly from the other populations in respect of finger patterns. With respect to finger pattern intensity, the Koch subgroups of the present study 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 the subgroups 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 ~~Lyngngams~~, 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. Also, they 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 all the Koch subgroups of the present study are by and large closer to the Kochs, 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 differences between the sub-groups of Koch are not statistically significant in respect of hand clasping (χ^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 groups. 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 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 Koch subgroups of the present study. The frequency of tongue rolling is highest in the Wanangs (31%) and lowest among the Sangas and Satparis (13%). The inter-group variation is highly significant in respect of tongue rolling (χ^2 = 11.66, DF = 4, P< 0.02) due to the significant deviation of the Wanangs from the Sangas (χ^2 = 7.38, DF = 1, P < 0.01) and Satparis (χ^2 = 7.38, DF = 1, P < 0.01).

With respect to the distribution of tongue folding, it is found be highest among the Sangas (40%) and lowest 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 (χ^2 = 2.0835, DF = 4, P > 0.05), which indicates that these Koch subgroups of Meghalaya are by and large similar in 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, it is found that 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 (χ^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 the case of 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 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. It has also been observed that the populations of the present study are by and large similar in anthropometric, morphological and dermatoglyphic traits. In other words, despite 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 the present study 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 differences between the Koch subgroups of Garo hills 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 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 environmental 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 the these populations with respect to PTC taste ability. The same observation is made with regard to anthropometric dermatoglyphic and morphological traits. It may be worthwhile to mention here that this is the common observation in many population genetic studies (Danker-Hopfe *et al.*, 1988; Khongsdier, 2000). Different models of distance analyses have been proposed to solve this problem in the study of population affinity (Mahalanobis, 1936; Bhattacharya, 1946; Hiernaux, 1965; Sanghvi, 1953; Edwards and Cavali-Sofrza, 1964; Balakrishnan and Sanghvi, 1968; Morton *et. al.*, 1971; 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 the different picture of relationship as shown by the dendrograms according to morphological 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. 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 due to the case marriage system. 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 is 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 of 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 and uniformity. 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 have also dealt 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. In their study of the genetics of the Dibongiya Deurisof Assam, Khongsdier and Murry (1999) writes, "sampling error in allele frequency do not only differentiate the populations of the same ethnic group, but also bring about similarity between populations of a different ethnic group." Besides the sampling error during data collection may also contribute to such contradictory results. In such cases, interpretation of the genetic relationship between populations is likely to be difficult.

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, we have shown in Chapter IV that the coefficient of breeding isolation is relative 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 neutralizes to a great extent the effect of genetic drift in a population. He has suggested that if the migration rate is $1/4N_e$, many fixations would take place; the fixation of alleles would slow down where the migration rate is $½ N_e$; but genetic drift is not so important when migration is $4/N_e$. According to Dobzhansky (1970), $4/N_e$ is equivalent to four immigrant individuals per generation, and $1/4N_e$ to one immigrant for every two

generations, and $1/4N_e$ to one immigrant for four generations. In his later publications, Wright (1940, 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. In Chapter IV, we have observed 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.

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 (χ^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 (χ^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 (χ^2 = 11.66, DF = 4, P< 0.02) due to the significant deviation of the Wanangs from the Sangas (χ^2 = 7.38, DF = 1, P < 0.02) and Satparis (χ^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 (χ^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.

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