CHAPTER TWO

METHODODOLOGY

1. CHOICE OF PARAMETERS

The traditional anthropological method of population comparison has been mostly morphological and anatomical and this approach has still continued as one of the most important methods, even though there has been a fundamental change in the outlook of physical anthropology with growing importance of population genetics and emphasis on the process of microevolution rather than taxonomic classification on the basis of typology (Singh, 1978).

According to Driver (1965) a systematic classification of biological characteristics was introduced in 1735 and the broad outline of which is still accepted. Intuitive and impressionistic methods were replaced by quantitative measurements (anthropometry) which occupied the most prominent position in 19th century (Czekanowski, 1962).

In pre-Darwinian times, little was known about the sources of variation and its transmission in man either within the population or between populations (Laughlin and Osborn, 1967). Anthropologists suggested development of
racial variations due to adaptation to particular environments (Hooton, 1946). Variation is a useful theme for both the complex of history of man and man's evolutionary history. It has been established that physical characters are partly influenced by environment (Pearson and Lee, 1903). On the other hand, Boas (1911) and Shapiro (1939) demonstrated environmentally influenced plasticity of physical characters in migrant populations.

Introduction of genetic characters for racial classification of human populations has greatly assisted in understanding the problem of origin and evolution of populations (Sanghvi et al., 1981). The genetic evidence sometimes clashes with morphological and other evidence about the genealogy of races, micro-races or population units. This is partly due to limited number of known Mendelian characters. Later, morphological and genetic evidence collected from carefully selected populations showed regularities and led to the idea of measuring relative proximity or distance (Sanghvi, 1953; Karve and Malhotra, 1968). The importance of anthropometric characters has been re-recognised in the modern approach of population genetics. There have been a number of conjoint studies of morphometric and morphoscopic traits together with purely genetical markers for finding out the relative
degrees of homogeneity between some endogamous populations in India (Malhotra, 1966; Gulati, 1971; Bhamu, 1974; Singh, 1978).

Several scholars have done many works on population variation with regard to the anthropometric characters. Some of them have been cited to show physical variations among different sections of the same population living in different habitats (Thurston, 1909; Sarker, 1935; Oliver and Howells, 1957; Das, 1960; Phookan, 1974; Singh, 1986). Even dermatoglyphics are not free from such intra-population and regional variation (Mukherjee and Chakravortti, 1964) although these characters appear to show a greater stability.

Therefore, it is difficult to select one set of characters on the basis of their stability through generations. Under these circumstances the criteria of total biological comparison of populations to determine their relative proximity or distance should be based on a variety and number of traits (Sokal, 1961).

Das et al. (1985) made an observation on anthropometric and some genetic traits on six Assamese Muslim groups from various parts of Assam and had shown more or
less marked variations among them. Such variations have been pointed out as a microevolutionary process.

For this present work, a number of characters representing morphometric, dermatoglyphic which are polygenic in nature, a few morphoscopic and behavioural characters, determined by inheritance, a few single gene markers other than blood groups have been incorporated with a view to cover a large part of the genome.

A brief account on the genetical significance of the traits selected for the present study now follows.

2. NOTES ON SELECTED CHARACTERS

A. ANTHROPOMETRY

Somatometric measurements: Large hereditary components of stature, maximum head breadth and other physical measurements are established by results of biometrical comparisons between different degrees of consanguineous relatives (Galton, 1889; Pearson, 1903; Newman, 1923; Hilden, 1925; Penrose, 1954, 1963; Osborn and George, 1959). Essentially, the selection of characters is based on the behaviour, function and structure relationship (Campbell, 1964). Most of these traits show no apparent segregation
and are influenced by genes at several loci. Therefore, the main advantage of using these continuous variables for assessing the proximity between two populations is that they represent a large part of the genome (Singh, 1978).

Boas (1911) and Shapiro (1939) have demonstrated that there are sizable environmental components in the variability of these traits and some of them are less influenced by environment than others. The traits selected for the present study are among the traditional racial criteria which are believed to be monadapative and relatively more stable (Haddon, 1929; Hooton, 1946), although, some amount of adaptive value and balanced polymorphism (Penrose, 1955) of these characters have been suggested. These multifactorial traits are likely to remain relatively more stable, in any case, being less sensitive to random genetic drift and other mechanisms of microevolution.

Indices: The indices for measurements have the advantage of physical measurements themselves as they are also largely influenced by the multifactorial genetical background. In addition to this, the indices are relatively more independent from environmental influence and of one another (Hardy, 1908).
B. MORPHOSCOPIC AND BEHAVIOURAL CHARACTERS

Certain morphological characters have great genetical importance although they could not be assessed by means of metrical values. Selection of a trait or a set of traits depend on the nature and scheme of the study. As the present study looks for a mosaic of genes, it has been desirable to incorporate as many as types and numbers of characters which have different genetic background. Under these circumstances a brief discussion on the genetical significance of the selected traits may be attempted.

Hair form (HF): Hair form is believed to be responsible due to a number of genes and that there is one pair of alleles which can produce the difference between curly and straight hair, with the heterozygote showing wavy hair (Winchester, 1966). Winchester further stated that the form of hair is dependent primarily upon its shape in cross-section — say straight hair being rounded, while wavy, curly and kinky hair showing progressive degrees of flattening.

Forehead height (FH), Forehead breadth (FB) and Forehead slope (FS): Variability in the degree of forehead height, breadth and slope is believed to have multifactorial genetic basis (Singh, 1978) but so far no
systematic studies have been reported. The traits have been considered as important racial criteria.

**Skin colour (SC)**: Skin colour is one of the most commonly observed characters because of its obviousness and genetical significance. It has been reported that a number of genes in conjunction with environmental agents such as sunlight control variations in human skin pigmentation (Winchester, 1966).

**Eye colour (EC) and Eye-fold (EF)**: The colour of the iris of the eye is a clearly defined character and it was one of the first human characters which was suggested as an example of Mendelian inheritance in man (Winchester, 1966).

Studies on a number of family pedigrees suggested that brown eyes are dominant over blue eyes in the white race (Davenport, 1907). Winchester (1966) suggested that eye-fold to be a single gene variation (Fortuyn, 1932) and inherited as a simple dominant.

**Nasal bridge (NB), Nasal root (NR) and Nasal septum (NS)**: Nasal bridge is suggested to be inherited (Gate, 1952) and a prominent convex bridge is suggested to be dominant over a straight bridge or a concave bridge (Winchester, 1966) which are further suggested to be possibly
determined by three allelic genes (Whitney, 1942). The exact hereditary mechanism of nasal root has not yet been established although suggestions have been made that high root is dominant over low root (Winchester, 1966). No systematic genetical studies on the nasal septum have been reported so far, although it is believed to be due to multiple gene (Singh, 1978).

**Lip form (LF) and Lip Eversion (LE):** Numerous multiple genes are said to determine the shape and size of the lip with full lip being dominant over thin lip (Winchester, 1966). Suggestions are also made that certain environmental agents induced the condition. Winchester (1966) also stated that at least a recessive gene is involved for greater penetration in the male.

**Baldness (BN):** It is an inherited character which can be influenced by environment although it is determined by a sex-influenced gene which is dominant in man and recessive in woman under age consideration (Winchester, 1966).

**Colour blindness (CB):** Colour blindness in man is a well known X-linked recessive trait (Gates, 1952; Winchester, 1966). Colour blindness has been classified into four subtypes such as Deuteronomia (green blindness), Deuteronomomaly (green weakness), Protonopia (red blindness) and Protonomaly (red weakness). Two different loci for protan and deutan
series of colour blindness have been proposed (Carter, 1969; Adam, 1969). The role of relaxation of selection for colour blindness in the incidence of this trait in different populations depending mostly on different economic groups have been postulated by Post (1962) and Pickford (1963).


**Darwin's tubercle (DT):** Darwin's tubercle is said to be inherited as a dominant trait with variable penetrance (Winchester, 1966). It has been reported that the trait occurs more often in males (Hilden, 1928) and it generally increases with age in males and decreases in females (Quelprud, 1934). The right ear is more frequently affected (Quelprud, 1934; Gates, 1952).

**Hypertrichosis (HT):** According to Winchester (1966) this trait is determined by dominant gene of the Y-chromosome in man. It is expressed after the attainment of adulthood (Stern, 1960).
Ear lobe attachment (EL): The mode of inheritance of the variations in the ear lobe attachment is not well established although it is claimed to be due to the influence of heredity (Hilden, 1922; Carriere, 1937; Quelprud, 1934; 1941; Powell and Whitney, 1937; Weiner, 1937; Suzuki, 1950; Gates, 1954; Gabel, 1958; Saldanha, 1962). Dutta and Ganguly (1965) suggested that the effect of isolation and genetical drift on the traits.

Three categories of variations such as complete, intermediate and free lobe attachment have been suggested (Dutta, 1963; Dutta and Ganguly, 1965; Basu, 1966; Chattopadhyay, 1968) while some others recognised only two classifications — the attached lobe and free lobe (Singh and Malhotra, 1970; Mohanraju and Mukherjee, 1973).

Tongue folding (TF): Ability of tongue folding is said to be influenced by dominant genes (Winchester, 1966). Hirschhorn (1970) has pointed out that a possible source of error due to the lack of practice or tendency to imitate, so that there should be careful recording of the trait.

Arm folding (AF): The genetics of this trait has not been fully established so far (Singh, 1978). It has been suggested that the incidence of arm folding of right
arm over left arm (R-type) is almost the same in different populations of the world (Sarkar and Devis, 1975) except among a few populations (Freire-Maia et al., 1960). Association of age with the trait has been pointed out by Freire-Maia and Almeida (1966), Rhoads and Damon (1973), Mahapatra (1970), and Singh and Gulati (1973) observed a different trend among the females. But, many have failed to find any significant sex difference (Weiner, 1932; Singh and Malhotra, 1971, Guha, 1975).

**Hand clasping (HC):** This trait was first observed as a genetical variation by Lutz (1908) and afterwards studied by many (Downey, 1926; Yamaura, 1940; Kawabe, 1949; Freire-Maia, Quelce-Salgado and Freire-Maia, 1958; Pons, 1961; Chakravortty, 1974) who could not establish the mode of inheritance.

Guha (1975) in her studies on twins concluded that the trait depends on a pair of autosomal alleles which do not maintain a dominant - recessive relationship (Singh, 1978). Rhoads and Damon (1973) pointed out that hand clasping does not show sex and age differences. The trait has been recommended as a racial characteristic (Downey, 1926) and later as a population marker (Malhotra, 1968; Singh and Malhotra, 1971).
Handedness (HN): Handedness was first studied by Francis Ramaley (1913), who concluded that left handedness is inherited as a Mendelian recessive trait (Trankell, 1955). But, Chamberlain's (1928) data did not conform to this hypothesis (Singh, 1978).

Dohlberg (1926), Newman (1928) and Hirsch (1930) have studied this trait on twins and suggested that there was a higher percentage of left handers among the identical twins than in non-identical twins. Rife (1940) observed that left handers are more likely to have left handed children than those of the right handed parents. It has been stated that the use of one hand in preference to the other is determined not by the greater development of the hand itself (Singh, 1978) but by the functional dominance of one side of the brain over the other (Winchester, 1966).

The role of environment has been pointed out that the differences in the type of this trait are primarily culturally determined and have association with sex and age (Falek, 1959; Curt Stern, 1960; Hardyek, et al, 1975). According to Critchley (1927), it is a combination of physiological and psychological conditions (Sarkar and Davis, 1975).
C. GENETICAL TRAITS

**ABO Blood group:** The blood group - A, B, AB and 0 is claimed to be the best established series of multiple alleles in man (McKusick, 1968) and it has special significance for putting Hardy Weinberg principle into test. After the discovery of human ABO blood group by Landsteiner in 1900, Bernstein (1924) showed genetic behaviour of the ABO blood type genes, based on a series of three alleles. Afterwards Hirszfeld and Hirszfeld (1918, 1919) demonstrated the existence of systematic and significant difference in blood group frequencies between different populations of the world. Several million tests of blood groups covering almost all countries of the world have now been published (Boyd, 1950; Mourant et al, 1976). Existence of polymorphism in blood group system has been agreed upon (Ford, 1940).

In India, although many studies have been reported so far from different parts of the country (Fandit, 1933; Majumdar, 1942, 1943; Sanghvi, 1945; Majumdar and Kishan, 1949; Chaudhuri, et al, 1952; Sirsat, 1956; Singh and Singh, 1961; Gosh, 1964; Srivastava, 1965, 1970; Malhotra, 1966; Seth, 1968; and Rizvi and Roy, 1984; etc.), still many populations have not

D. DERMATOGLYPHS

Dermatoglyphic traits are undoubtedly the most strongly heritable among all known multifactorial human variations (Galton, 1892; Farg, 1950; Bonnevie, 1954; Penrose, 1954; Holt, 1955; Weninger, 1965; Mukherjee, 1966, 1967, 1968, 1971, 1972; Barnicot, et al, 1972) and others. The characters are relatively stable and less influenced by random genetic drift (Rife, 1953, 1954). Newman (1960) observed that the complex nature of dermatoglyphic variations have been very rarely used for assessment of genetic distance (Chai, 1972), they appear to be an useful tool for the purpose.

3. CHOICE OF STATISTICAL METHODS

Common statistical constants basically necessary for understanding the meaningful centralised values and their standard dispersions have essentially found unavoidable in such kind of research like the present one.
The present study of bioanthropological variations between three Muslim male populations has required to incorporate a number of quantitative and qualitative characters which are largely heritable and controlled by single or multiple genes. This has required careful selection of particular statistical methods for treating the morphometric and morphoscopic characters for the purpose of finding test for significance between pairs of such traits.

Statistical methods such as t-test and chi-square tests have been developed in response to the problem for comparing variations in single characters represented by quantitative and qualitative traits respectively. These tests for significance have essentially adopted to evaluate the probabilities of certain magnitudes of differences of the frequencies or means of the characters in the two populations and to assess the level of significance of the differences between two populations. Such univariate techniques helped us to understand the degree and directions of differences between the two populations in respect of variability (Kowalski, 1972).

An idea about the similarities and differences in the gene pools of the various populations can be got only by considering a large number of loci simultaneously.
(Balakrishnan, 1988). These characters are usually considered to be measures of proximity or distance. Genetic distance, according to Balakrishnan (1988) is simply a tool to investigate the relationship among set of populations. Sophisticated measures of multivariate distance have rapidly evolved to assess the overall proximity or distance between populations when a whole set of variable is used for this purpose.

Among various simple to generalized measures, the Coefficient of Racial Likeness (C.R.L) devised by Heinke as early as 1898 is one of the earliest methods which is followed by that of Pearson (1926), Zorapkin (1934), Clark (1952), Penrose (1954), Sokal (1961) etc. In India Mahalanobis (1936) devised an excellent distance coefficient ($D^2$) which requires lengthy computations.

Later on, Sanghvi's $T^2$ and $X^2$ (Sanghvi, 1953) methods have been found quite appropriate and profitably applied for the analyses of morphological and genetical distance by Karve and Malhotra (1968) and also by Gulati (1971), Bhamu (1974) and Sanghvi, Balakrishnan and Karve (1981) etc. for testing the homogeneity of populations within a caste cluster or otherwise. Sanghvi's methods required
a simple property of the 't' values in order to arrive at
a measure of differences based on the morphological
measurements and \( x^2 \) values for measures of genetical
differences. The two methods of Sanghvi's \( t^2 \) and \( x^2 \)
are comparatively simpler in computation and the only
important condition is to adjust for uniform sample
size (Sanghvi, 1953). Singh (1978) for the first time
used Sanghvi's \( x^2 \) method for finding relative proximity
of populations based on dermatoglyph distances \( (x^2_d) \)
between three populations of Manipur valley and have
proved to be quite effective for this category of traits.

The data and procedure now follows in the next
chapter.