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MORPHOLOGICAL AND GENETIC COMPOSITION OF THE GONDS OF CENTRAL INDIA : A STATISTICAL STUDY

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BY

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CHAPTER I: INTRODUCTION AND SUMMARY

1.1 Background

The racial composition of the people of India is still a riddle and one which is getting increasingly difficult to solve as over a period of time it has been fast changing due to absorption of various populations into the Hindu castefold and the fission and fusion within the caste system as a product of occupational or cultural change in the way of life. Admixture over a long period of time has produced a wide diversity in morphology (as well as skin colour) of Indian people. The waves of migrations of people from the Eurasian steppes into India through its most possible route of least resistance, through the passes in the mountains of North Western India (Afganisthan) and the ultimate absorption and admixture with the local population or populations who had preceded them earlier, produced this diversity. There was in addition infilteration of Mongoloids from the North-east though of much smaller volume. The caste groups though heterogeneous in morphology and skin colour generally belong to the Europoid or Caucasoid type whereas the most primitive element in India is confined to the tribal populations of Central and South India who have to a large extent kept themselves out of the Hindu castefold. But even they are gradually adopting the Hindu way of life by the large scale migrations of these caste groups into the isolated tribal areas due to population pressure and the need to bring more land under cultivation.

he tribe as the definition implies has a fixed erritory, a self-contained subsistence economy and as originally a political association obeying to the Rules of clan exogamy (Weber, 1958). However not all tribes were political associations like in the case of Chenchus, Kolams, Hill Reddis, Konyak Nagas and many others. The caste groups, however, do not have a fixed territory and the way of living is firmly linked with the type of caste and they are formed by purely social and occupational association practising strictly the rules of endogamy. The nature of formation of tribal units therefore preclude the resistance to absorption into the castefold and have thus over centuries of invasions by foreign elements have retained the morphological type and territorial areas to a great extent. The caste groups with their more sophisticated form of agriculture and implements were able to cultivate the valleys consisting of heavy fertile soils which produced surplus and comparatively greater prosperity which in turn increased their population. The tribals, who were isolated and unchanding, retained primitive way of life living on the hilly areas which were *'their food area'*, by *food gathering and hunting, or* progressing a step further into shifting agriculture by cutting forest on gentle slopes, raking the soil with a wooden hoe and broadcasting small millets and pulses. They were sparsely spread over large areas which are necessary for this mode of living andthis did not greatly increase their population, whereas the more sophisticated agriculturists in the valleys and plains represanted by the Europoid group increased in population due to surplus.

The concept of racial purity is a misnomer and in India a continuous admixture has been going on over centuries, with caste endogamy not being as rigid or strict as it is in recent times. However there has been probably less admixture with tribal groups who kept themselves outside the caste system and the plain people, thus retaining distinctively different morphological characters between these two main groups of people. With time, however, some of the tribal groups have changed their mode of economy due to the disturbance in their ecology caused by immigration of economically more advanced and politically powerful populations and the exploitation of these areas by Government and private agencies for raw materials such as timer, minor forest produce and minerals, a source of great wealth from the days of the British Raj. This change in way of life has made the tribal more dependent on the Hindu castes who in turn are dominating and ultimately absorbing them into the lowest rung of the caste hierarchy. Hence, it is imperative to try to solve the riddle of the genetic composition of these tribal groups who with time will be absorbed into the caste system and will be obliterated from history as a separate racial entity.

A few studies in the past have classified the composition of tribal people on the basis of linguistic and morphological evidence (Risley 1910, Eickstedt 1935 and Guha, 1936). Risley has tried to classify the people of India on the basis of linguistic evidence but this proved to be a failure because language and physical anthropology in the Indian context did not correspond and produced physico-anthropological contradictions. He was refuted later by the German anthropologist, Eickstedt (1935), who based his classification on morphology rather than on linguistic data. Though his classification is held with considerable doubt, it is perhaps the most interesting, for in addition, he tried to correlate the distribution of racial types with geographical regions. He found that the people who were distributed in the plains and river valleys practising plough agriculture belonged to the Melanid and Indid types. The Melanid are the progressive type of dark-skinned people of South India who are Dravidian speaking and hetrogeneous within themselves They are generally similar to the Indid or Europoid types except for skin colour which resulted, perhaps due to the earlier immigration and more admixture with the darker local population. These he considers as foreign elements who migrated into India from the North West. He considered the more primitive stratum of people as those who lived on the hill tops (the tribals) practising a primitive mode of economy. The following is his classification:

1	Veddoid		
	a	Malid	South Indian tribals (South of Krishna river)
	b	Gondid	Tribals of Central India
2	a	Kolid	Munda-speaking group in Orissa and Chota Nagpur areas
	b	Melanid	Dravidian caste groups of South India
3	a	Indid	represented by the Europoid people such as Todas, Konkan Brahmins belonging to the West Coast
	b	North Indid	Represented by Pathans etc., of North Western India
4	Palemongoloids		
	a	Progressive	Eastern Indian Mongolian populations
	b	Primitive	

Guha (1936) differed from the above classification, especially of the primitive groups and put forward his own classification, that all the tribal groups of peninsular India belong to one common stock 'The Proto-Australoid' which is the terminology most often used by anthropologists in India. Another anthropologist, Fuchs (1958) also did not agree with Eickstedt's classification of the closeness of Melanids with Kolids who are quite different morphologically from one another. Majumdar (1958) viewed the various tribal groups of Peninsular India as affiliated to the same racial stock and that they did not belong to independent races or even types. However Irawathi Karve, (1965) felt that racial composition of a cultural region was more meaningful than just a haphazard measuring of people in India as a whole. She has found that a linguistic area is a culturally unified area and that

Thus based on this view mostly regional studies in Utter Pradesh (Mahalanobis, Majumdar and Rao, 1949), Bengal (Majumdar and Rao, 1960), Maharashtra (Karve and Dandekar 1951) were done, using more sophisticated statistical analysis. These authors used mostly anthropometric measurements but no biochemical genetic markers except for ABO blood group system, as the techniques for identifying the various biochemical markers had not been fully developed. It is only in recent times that individual studies on various populations have been analysed for various genetic markers. Hence in the present study an attempt has been made to re-open the problem of racial composition of the tribal groups by the use of both morphological and genetic markers using a number of multi-variate statistical techniques.

1.2 Objectives of the Present Study

In the present study, data have been collected on the morphological and genetic traits of five tribal populations belonging to the Gondi speaking groups which is one of the largest tribal group of Central India consisting of four million in 1961 census which amounts to about 13 percent of the total tribal population of India. The area of distribution of the Gondi speaking groups of Madhya Pradesh and Maharashtra states

States

where this group attained a great prominence on the political scene of the past and dominated over people of the whole area named after them by the Mohammadans as 'Gondwana' (Imperial Gazetteer of India, 1906). The Gonds had kingdoms in Deogarh on the foot hills of the Satpura, Mandla (Madhya Pradesh) and Southern kingdoms at Chanda (Maharashtra) from the 14th - 18th centuries A.D. until they were defeated by the Marathas. The Gonds are neither racially, nor culturally, nor linguistically homogenous populations (Furer-Haimendorf, 1979). Haimendorf raises the question of whether the Gonds are of different racial types who under the dominant influence of Gond culture appear today as one homogeneous group. The Gonds of Adilabad district of Andhra Pradesh (who call themselves Koitur) still consider themselves as RajGonds and find pride in considering themselves the true exponents of Gond culture and language and above all in a traditional Gond religion as compared to those belonging to Madhya Pradesh who have come under the influence of Hindi or Marathi speaking caste groups. Indeed, these Rajgonds hold sway even today on the rest of the Gondi-speaking tribal groups of the Southern region. They are relatively less exposed to outside influence and to the influence of the more intolerant exponents of Hinduism. The five largest Gond populations in the Southern areas have been selected for study so as to determine the morphological and genetic composition of these Gondi speaking populations. The study of the racial composition based on morphological and genetic characters would not be sufficient without extending the study by comparing these groups with the neighbouring populations of Central India who have lost their original language and cultural traditions. To summarise, the objectives of the present study are :

1 The study of the morphological and genetic composition of the five Gond populations.

2 The comparison of these Gonds with their immediate neighbours in Central India on the basis of available published data on morphological and genetic characters.

3 To reopen the question of the general classification of tribal populations of **Peninsular** India by comparing some of the representative tribal populations of these areas based on both morphological and genetic characters using multivariate statistical techniques. (TABLE 1)

3 Background of the Gonds

.1 Gondwana - A setting in space and time

Today the Gondi speaking groups are spread over the whole of the Central Provinces-an area which extends from the Godavari gorges in the South to the Vindhya mountains in the North. Gondi with its many local dialects belongs to the Dravidian language of the so called intermediate group and according to Grierson (1906) closer to Tamil and Kanarese than to Telugu.

The majority of the Gonds are found today in the state of Madhya Pradesh. Their main strong holds are the Satpura Plateau including the districts of Betul, Chhindwara and Seoni where the Western type of Gondi is spoken and the district of Mandla in the East where the Gonds adopted the local dialect of Hindi. To the North West, the Gonds extends across the Narbada river and are particularly numerous in Indore. Further South, Gonds are numerous in the districts of Durg, Raipur and Bastar district. The district of Bastar, a princely State until 1947, is the home of three important groups of Gonds, the Marias, Hill Marias, Bisonhorn Marias and Murias, all of whom differ in language and customs very considerably from the Gonds of the former Chhattisgarh states as well as those of Mandla in the north and Chhindwara, Yeotmal and Chanda in the West. The latter two districts are now included in the state of Maharashtra and so are the two taluks of Kinwat and Rajura which formed part of the state of Hyderabad i.e., the Nizam's dominions. The district of Adilabad of the former Hyderabad state, now in Andhra Pradesh, is the home of a substantial group of Gonds including the Raj Gonds who are closely akin to the Gonds of Yeotmal and Chanda. (Map 1)

This vast area of Gonds sprawls across Central India which includes thick forests of Dandakaranya and mountain ranges of Vindhyas and Satpuras and river valleys of Narbada, Tapti and Indravathi and it extends into Pranhita-Godavari valley in the South-East.. Geology of this area differs considerably leading to different geo-morphological features. These areas can be broadly classified as follows :

1 Alluvium

The valley of the Narbada from Jabalpur to Wardha. This valley consisting of heavy black soil, was under the control of the Gond Kings during 14th to 18th century and it is the area of Jowar and Cotton cultivation.

2 **The Deccan Trap** :
The soil is a shallow black soil spread over Wardha, Nimar, West of Nagpur and South of Chhindwara. It is an area of Cotton and Jowar cultivation. The Raj Gonds, Dhurwe Gonds and Kolams are distributed in this area.

3 **The Gondwana Systems** :
Corresponds to mainly older and middle mesozoic and perhaps upper paleozoic formations. The main areas are in the Satpura range, in the basin of the Godavari, in Nagpur, Wardha and parts of Adilabad and Chanda district. These areas consist of light sandy loamy soil which is poor and mainly belongs to tribals. The main food grains of this area are millets.

4 **Vindhyan Series** :
Consists of sand -stone and lime-stone deposits in Raipur, Bilaspur and Bastar. These are rice growing areas.

5 **The Gneissic System** :
They are the metamorphic rocks which are the oldest known formation covering large portions of the plateau districts and in the Nagpur and Chattisgarh plains underlying the more recent formations. It is the sandy soil present in Wainganga and Mahanadi basin which are rice lands of the provinces. The rainfall is heavy and the land though of little natural fertility responds readily to manure or irrigation. It is also the area of Sal forest (Shorea *robusta*).

Historical Perspective of Gond Kingdoms :

Reliable information on the early history of the Gonds is scarce and not until Muslim times do Gond states figure in contemporary chronicles. Furer-Haimendorf (1979) gives a detailed historical information on the Gonds but for the present study, a brief outline need only suffice. Muslim chronicles give information of the Gonds from the 14th century A.D. and call the area of the Gonds as 'Gondwana'. In the 15th century A.D. the Gond dynasty is established at Garha, close to the Narbada river and Jabalpur. The maharajas of Garha exercised overlordship over the local Gond petty chieftains of districts of Jabalpur, Mandla, Seoni, Chhindwara, Balaghat, Damoh and parts of Hoshangabad and Betul and retained their independence until the year 1564 A.D. when a Mughal army under Asaf Khan conquered Garha. After a period of administration by Mohammedan officers as Jagirdars, the Government reverted to the Gond Rajas of the old family who had however to recognise the sovereignty of the Mughal emperors. The end of the dynasty came in [illegible] A.D. when the Marathas imprisoned the last ruler and brought the state under direct control. Another Gond state arose in the south and west of

Garha early in the 17th century, the kingdom of Deogarh whose rulers, previously tributaries of the maharaja of Garha, took advantage of the decline of Garha subsequent to the Mughal conquest and secured for themselves a large part of these territories. The third great Gond dynasty of Madhya Pradesh was that of Chanda and it is the dynasty which is directly concerned in its influence on the population of the southern areas of the Gondwana regions. The Rajas of Chanda ruled over a large part of what is today the Adilabad district and many of the Gonds still recognised their authority in tribal matters. In 1749, Bhonsles of Berar and Nagpur conquered the city of Chanda which was incorporated into the Bhonsle kingdom in 1751.

1.4 Background of Gonds included in the present study

1.4.1 Description of area of study : The area of study lies between 18° 40' and 19° 40' North and 78° 45' and 80° 45' East approximately (Fig. 1). The geology and hence the physical characteristics of the soils differ from east to west as the strike of geological formations is North-west to south-east. The western portion of the field area is mountainous but covered by black cotton soils of Deccan traps. It is almost the eastern end of Marathwada black cotton soils. The tribal populations selected here are the Raj Gonds and Kolams of Utnoor and Asifabad talukas (Andhra Pradesh). East of these trap hills the plains of Gondwana sedimentary soils form the valley of Pranhita and Godavari rivers. The rivers flow almost along the geological strike. The predominant tribal populations of these soils are mostly Koyas along with Manne and Naikpods. For the sample study Koyas and Manne of Chinnur taluka (Andhra Pradesh) were selected. East of river Pranhita valley and mainly in the valley of Indravathi river the main sub-group of Gonds - the Marias, Muria and Bisonhorn Marias live. The geology is mainly of metamorphic and Gneiss rocks. This is a country of dense forests, of plains and hills. The main hilly terrain of Abujhmar hills is a vast area supporting one of the most primitive populations of shifting cultivators. The sample population selected are the Maria Gonds living mainly in the Sironcha tahsil of Chanda district (Maharashtra).

Description of the tribal groups

1 Raj Gonds :

The Raj Gonds of Adilabad district, Andhra Pradesh (tnoor and Asifabad talukas) were selected for the study. A comprehensive account of social and cultural life observed over a period of 38 years in Adilabad district is given in the monograph on the 'Raj Gonds of Andhra Pradesh' by Furer - Haimendorf, 1979. The Gonds of the district describe themselves as Raj Gonds and their territory coincides with the black cotton soils formed by the Deccan [illegible] vation and grow jowar (Sorghum vulgare) and cotton as rainfed crops.

The basis of social structure of the Raj Gonds is a system of four exogamous phratries (Saga) each of which is sub-divided into a number of named clans (Pari). The phratries have no names but are described as seven-wen, six-wen, five-wen and four-wen phratries. In the literature on the Gonds of Madhya Pradesh the clans constituting these phratries are referred to as seven-God, six-God, five-God and four-God clans. The most distinctive feature of the Gond religion is the cult of the phratry and clan deities described by the generic term Persa pen or Great God. The Gonds practise three types of marriages - (a) marriage by negotiations (b) marriage by service and (c) marriage by capture. Cross-cousin type of first cousin marriages are prevalent among the Gonds.

2 Kolams :

Most Kolams speak Kolami which is also a Dravidian language closely related to Gondi. They are distributed in Asifabad and Utnur taluks of Adilabad district, Andhra Pradesh which is the area from which they were sampled for the study. The northern area of their distribution is in the Wun taluk of Yeotmal district, Maharashtra and are the close neighbours of the Gonds. In their own language the Kolams refer to themselves as Kolavar but in Gondi they are called Pujari (Furer-Haimendorf, 1979). The Kolams also speak in Gondi to the Gonds and Pardhans (bards to the Gonds). Until two generations ago most Kolams subsisted on shifting agriculture and food gathering and it was only the enforcement of the Forest Conservancy Act that forced them to adopt a new mode of life. In the 1940's they would still be found felling and burning the jungle on hill slopes, broadcasting small millets, pulses and more rarely jawari millet in the ashes and then raking the seeds over with a primitive hoe. The Kolams, like the Gonds, are organised into exogamous clans and most of these have names identical with those of certain Gond clans. These clans are grouped in phratries corresponding to the Gond system of seven brother clans, six brother clans etc. But among the Kolams these groupings are devoid of any mythological sanction and it is almost certain that they have been formed by the coordination of existing exogamous units withthe Gond clan system. Kolams and Gonds consider themselves related communities and Kolams eat freely in the house of Gonds and many Gonds part take without hesitation of the food of the Kolams (Furer-Haimendorf, 1979).

3 Manne :

These are Telugu speaking tribal group whose territory is small and present in Chennur and Sirpur talukas of Adilabad district, Andhra Pradesh (Fig.1). They were shifting agriculturists some 50 years back and some old people today know the skill of iron smelting with the help of bellows. According to Furer-Haimendorf, (1979), the Manne are Telugu speaking sub-group of the Kolams and have forgotten Kolami under the dominance of Telugu culture, and have now become a separate endogamous group not intermarrying with the Kolams. They practise plough cultivation and grow jowar which forms their staple crop. They have also a seven-brother clan, six-brother clan, five-brother clan and four-brother clan phratry system as practised by the rest of the Gonds. Cross cousin marriage is also prevalent in this group.

4 **Koyas :**

The Koyas living in the northern most extremity of their distribution in Adilabad district (Chennur and Sirpur talukas) of Andhra Pradesh have been selected for the study. Incidentally, East Godavari area is also the southern boundary of Gondi speaking groups of Central Provinces. The Koya area consists of sedimentary soils of the Gondwana formation. The Koyas speak Koye, a language described by Grierson, (1906) as a dialect of Gondi. Most of them have forgotten the language and have adopted Telugu from their neighbours. Reverand J Cain (Thurston, Vol. IV, 1909) writing about the Koyas of the Godavari district states that they have a tradition, that about 200 years ago they may have been driven from the plateau in the Bastar country by famines and disputes and this relationship is also acknowledged by the Gutta Koyas or Hill Koyas who live in the highlands of Bastar. Some fifty years back they used to practise shifting agriculture and have since then adopted settled agriculture growing jowar and rice as rainfed crops. They have a similar phratry system as the Gonds and some of their clan Gods which are still in Bastar are brought down on clan festivals to the East Godavari district.

5 Maria Gonds :

The Maria Gonds also speak Gondi and are distributed in Sironcha taluk of Chanda district (Maharashtra) from which the sample for the study was selected. A supplement on the Maria Gonds of Chanda is included in Grigson, (1949). Their Bastar neighbours are called the Marias who are a separate endogamous group. Most of the Marias were practising shifting agriculture some 50 years ago and some of them still do so on top of the Abujhmar hills (Hill Maria Gonds). Due to the stopping of 'Podu' (cutting and burning the forest for cultivation) by the Government, the Marias have settled down to cultivating rice in low lying areas and have become as expert as their neighbours, the Murias at levelling the land and utilising water by tapping small streams by efficient channelling and bunding. The Marias erect memorial stones like the neighbouring Munda speaking tribals. They had a Gotul system which is a youth club for both unmarried girls and boys, which has now more or less disappeared in Chanda but is still practised among the Marias of Bastar (Elwin, 1947).

The God-grouping similar to the Raj Gonds seems to be a recent importation to the Maria Gonds of Chanda (Grigson, 1949). However, the Bastar Maria and Murias have neither God-grouping nor Chuddur Penk. The Hill Marias of Chanda did not have any God-grouping or Chuddur Penk when Grigson visited them in the 1940's. The Maria Gonds hold allegiance to the Chanda Zamindari, a Raj Gond of the Atram Clan who is related to the former ruling house of Chanda.

1.5 Neighbourhood of the Gonds

.5.1 Immediate Neighbours

In the hilly terrains of Vindhyas and Satpuras(Map 1) the inhabitants are chiefly Bhils, Gonds, Korkus and other tribes who practise a little agriculture on these hill slopes. There appears to be little doubt that in earlier days the prevailing language of Central India belong to the Dravidian or Munda family , the aboriginal tribes who spoke this group of languages having been gradually absorbed into the ranks of the northern invaders or driven as refugees to the fastnesses of the Vindhyan ranges. As is usual in such cases, the mother tongue has been lost and only a small number of Gonds in the hills South of Bhopal still show traces of Dravidian forms in the speech. The Bhils have only a 6°/o non-Aryan words, the rest being a mixture of Gujarathi and Malwi. The forests of this area are mixed deciduous with teak as valuable timber.

5.2 Eastern neighbours

The Eastern neighbours of the Gonds belong to the very distinct cultural and linguistic group of the Munda speaking tribal group. They are distributed throughout this sal (SHOREA robusta) forest area which covers a large tract in the east of Madhya Pradesh commencing in the plateau beneath the Kaimur range in Rewah and extending over Mandla, the northern frontier of Chattisgarh, the hills bounding the valley of the Mahanadi and South to the valley of the Indravathi (Map 1). This forest also extends into the Chota Nagpur plateau up to the Raj Mahal hills which is the eastern extremity of the plateau. This is mainly a rice growing area where efficient bunding and terrace cultivation on hill slopes are built and water channelised from small streams. Chota Nagpur is considered the centre of Munda languages and south of it the languages spoken are mainly Gadaba and Bondo in the south eastern part of Orissa. The racial origin of the Munda speaking groups is still an unsolved problem. Some anthropologist like R. Von Heine Geldern (Fuchs, 1973) attempted to prove that there was a Mongolian admixture in these groups and that this component was brought to India by the Neolithic Austro-Asiatic people who came from the East. This theory was called into question by several people, one of them being the anthropologist D N Majumdar (Fuchs, 1973) who maintained that the general physical make up of these tribes did not suggest a Mongoloid infusion and it was hard to assert a general miscegenation on the basis of a few stray cases of Mongoloid features. The various Munda tribes could easily be affiliated to the same Proto-Australoid stock as the other tribes.

These groups have totemistic divisions and erect memorial stones for their dead. The highest object of veneration of the Mundas is Sing Bonga, the Supreme God represented by sun worship by the whole of the Munda speaking group. The Chota Nagpur area also consists of a number of Dravidian speaking groups living amidst the Munda speaking group like the Oraons and Maler and in southern Orissa by another large Dravidian speaking group, the Khonds. It has been admitted by several anthropologists A.C. Haddon, S.S. Sarkar and T.C. Basu that the Mundas differ racially from these Dravidian speaking groups.

5.3 Tribals of South India :

The northern boundary of the tribals of South India appears to be the Krishna river which cuts through the Nallamalai range which is a part of the Eastern Ghat ranges. The eastern ghats are not a continuous range but are broken up into irregular bits all along its length unlike the Western Ghats which is continuous except for the Palghat gap which separates the Nilgiri hills on the north from the Annamalai hills in the south. The Chenchus are found to reside on the Nallamalai range along the banks of river Krishna and are the northern most tribe of these South Indian tribal group and are separated from the Gondi speaking population by the Godavari delta and plains of granite and black cotton soils which is a formidable barrier, consisting of the agricultural caste groups. The Eastern Ghats in the south consists of a lot of tribal groups who were initially food each of these tribals from one another producing a diverse array of kinship systems. The Veddas of Ceylon (now Sri Lanka) are said to be morphologically similar to the South Indian tribal groups according to some anthropologists (Eickstedt, 1935).

6 Summary of the Findings and extent of Objectives Achieved by this Study

The following are briefly the main findings of the thesis:

1. Morphological and genetic relationship between the Gonds:

Statistical analysis showed that the Gonds are a heterogenous group being morphologically and genetically different from each other, forming separate endogamous entities. The morphological and genetic distances between these five Gond populations when projected graphically revealed that the spatial distribution of these populations generally corresponded to their present geographical distribution. The Manne lie intermediate forming the connecting link between the other four populations. The Raj Gonds and Plains Maria Gonds lie fartherest away from each other at two opposite poles. However, the actual relationship between each of the Gond populations show differences when based on these two different biological variables. The morphological relationship shows a greater variability, the clustering pattern differing between sexes. This variability in morphological relationship between sexes may in part be due to difference in sex morphism and the greater degree of environmental influence on morphological characters. The relationship based on genetic characters closely corresponds to the degree of geographical continuity between the populations. The Raj Gonds and Kolams live in close proximity to each other on highlands forming one cluster, whereas the Manne, Koyas and Maria Gonds form a second cluster and live adjacent to each other in the valley formed by the Pranitha-Godavari and Indravathi rivers.

2. Interpretations based on morphological relationship between tribal groups:

A. The tribals clustered according to the geographical regions they belong and formed three main clusters.

i) Central Indian group (including Gonds of the present study)

ii) Orissa and Chota Nagpur group

iii) South Indian group (south of Krishna river)

The Gonds of this study lie in close proximity to the main Central India cluster showing morphological closeness to Bhils, Korkus and Gonds (Madhya Pradesh). This is substantiated by the fact that there was a contiguous belt of Gond culture extending from Garha (Madhya Pradesh state) in the North to Chanda in the south (Maharashtra state) from at least the 14th century A.D. to the 18th century when the Gond kingdoms were overthrown by the Marathas. The Central Indian group and Orissa and Chotanagpur group are however closer to each other relatively than to the more distant south Indian tribal group. The South Indian group is separated from the rest of the tribal people of Peninsular India by the Krishna and Godavari deltas. These findings do not substantiate the contention made by Russel and Hiralal (1916), that the Gonds who speak a Dravidian language might have migrated from south India to Central India sometime between 9th century to 13th century A.D. This is also criticised by Haimendorf (1979) on the basis that this is not supported by ethnological evidence.

2. The relationship of these populations whose origin was in doubt such as *Korkus*, *Khonds*, *Oraons* and *Andhs* was resolved to some extent by this study.

3. Differences between morphological and genetic relationship of the Gonds with the rest of the tribal populations of India:

   The tribal populations based on both morphological and genetics clustered generally according to the geographical regions they belong. However, the morphological and genetic relationship did not correspond well and this may be due to a) smaller number of groups utilised in the genetic study and b) the populations used for genetic study are not exactly the same as those used in morphological study. The relationship of the Gonds with the rest of the tribal populations also differs in the two studies. The Gonds are morphologically close to the Central Indian group whereas they are far apar from this group genetically.

The emphasis of the present study based on quantitative techniques is on the importance of geographical proximity in producing morphological and genetic similarity between populations. This is revealed in the smaller Gond study as well as in the case of the larger tribal study. Geographical proximity between populations being brought about by closer distance as well as similar geographical factors (such as soil, terrain, flora etc.,) drawing these populations together under a common eco-cultural umbrella. The closer the geographical distance between populations the closer the genetic as well as morphological similarity between them. This is more so in populations such as these who due to having adopted a settled agricultural occupation are less mobile.

CHAPTER - 2 : MATERIALS AND METHODS

.1 Area of distribution of the Gonds

Measurements and analysis for blood samples (serological and bio-chemical characters) was carried out in the five Gond populations belonging to two districts, Adilabad district of Andhra Pradesh and Chanda district of Maharashtra which are adjoining to each other. The enumeration of total number of adult persons(listed in the electoral papers) as well as villages belonging to each of these tribes was carried out by village headmen or Patwaris under the personal supervision of the Revenue Officer (Tahsildar) for the purpose of this work. This tribe-wise data is not available in the Census and hence this data proved to be not only useful but essential for location of the various tribal villages on the map and thus getting a clear picture of their distribution (Fig. 1).

These five Gond populations are located to distinct geo-morphological zones which are suitable to their respective modes of production. The Kolams and Raj Gonds though living in close proximity to each other in Utnoor and Asifabad talukas of Adilabad district (Andhra Pradesh) have their distinct territories which do not overlap. The Kolams who were until recently *shifting* cultivators using a hoe, live on the hill tops where the top soil is thin and suitable only for the cultivation of small millets. The Raj Gonds, however cultivate the valley bottoms near streams where there is a thick layer of black cotton soil suitable for jowar and cotton cultivation where the plough has to be used. This can be clearly seen from the distribution of Kolam and Raj Gond villages in the map (Fig. 1). The total adult Kolam population in both talukas is about 4,000 being three times more numerous in Asifabad than in Utnoor talukas whereas the Raj Gonds have a total adult population of 20,000 being five times more numerous than Kolams with an even distribution in both talukas. The smaller size of Kolam population probably indicating a smaller growth rate in their group and reflecting indirectly the poor economic status of this group of shifting cultivators as compared to the relatively more prosperous and larger group of the Raj Gonds.

The Koyas and Manne like the above two groups are found together in close proximity in Sirpur and Chinnur talukas of Adilabad district. Here again these two groups are located in distinct territories which have determined the different means of production they have adopted. The Koya villages are present in clay soils found along rivers, especially the Pranitha river which necessitates the practice of settled cultivation and the use of plough technology. The Manne are located to sandy soils (Gondwana sandstone) on gently sloping terrains suitable only for shifting cultivation. The mixed Koya and Manne villages (Fig. 1) are located in those areas where there is both clay and sandstone deposited together side by side during ancient times (Gondwana sedementary soils where alternate layers of clay and sand was deposited). In such mixed villages, the Manne occupy the sandy soils whereas the Koyas occupy the clays. Though both groups are at different economic levels, this is not reflected in their population size. The Koyas and Manne population are of similar size being approximately 7,000 each, in both talukas, being more numerous in the northern taluka of Sirpur than in Chinnur where the Telugu speaking non-tribals are more numerous and cultivating the more fertile alluvium laid down by the Godavari river. This similar small population sise of both Koyas and Manne is reflected in an equally backward economic status. The adoption of a cash crop an oil seed (Til) by the Koyas and hence transition into cash economy has not had a beneficial effect but on the contrary has increased the exploitation of this group by non-tribal shopkeepers and money-lenders. The Manne however owning poor soils had no conflicts with any group, tribal or non-tribal, and lived mostly by food-gathering and charcoal burning as the returns from shifting cultivation was very poor. The Manne extend into eastern part of Asifabad Taluka (east of the railway line) from where the area rises up into hills on the west and is the area of Kolams and Raj Gonds. It is here that one encounters mixed Manne and Kolam villages, the railway line laid along the foot hills serving as a boundry between Kolam and Manne territory.

The Maria Gonds are distributed mainly in the Indravathi river basin extending from Sironcha taluka (Maharashtra) into Bastar district (Madhya Pradesh). The Maria Gonds come in contact with the Koyas in the south-western part of Sironcha taluka. The Maria Gonds in Sironcha taluka are divided into two endogamous groups, the Plains Maria Gonds and the Hill Maria Gonds each belonging to a different economic level. The plains Maria Gonds occupy the major portion of the north-eastern area of the taluka and practice settled rice cultivation (rain-fed) whereas the Hill Marias live on the Abhujmar hills which lies on the extreme east of the Sironcha taluka and extends mostly into Bastar district. Here the Hill Marias practice shifting cultivation as the rugged terrain is not suitable for settled cultivation.

2.1.1 Selection of individuals

Data on anthropometric measurements and blood samples were collected on 100 individuals from each group consisting of 50 males and 50 females, of Raj Gonds, Kolams, Koyas, Manne and Plains Maria Gonds. In the case of ll Marias only blood samples were collected on 50 les without measuring them. In addition, extra 50 ls samples for each of the above five groups was llected for the purpose of screening for G6PD defi- iency, haemoglobin and transferrin variants. Villages ere selected to represent as far as possible the ifferent areas of distribution of the tribe. Since most of the villages were situated along the main streams, villages were selected so as to represent each of the main streams thus covering representative proportion of the tribal group in the area which was selected for study. All available adult population in the villages were covered avoiding as far as possible (as consanguinity was high in these groups) relatives and rejecting members of the same family. Information n age, marital status, relatedness of spouse, place of birth of spouses etc., were also collected on each of the individuals. Proformas containing the name of the ndividual, age, village, consanguinity and place of irth of spouse were separately filled up for each roband and coded.

n each selected individual after the measurements were aken, blood samples were collected on each of the individuals measured, by means of finger prick method. Heparished micro-capillary tubes were used for collecting the lood, the tubes being appropriately labelled and sealed ith plasticine at both ends. About 40 to 50 blood samples were collected in a day and kept in the thermos filled with ice. Most of the measurements were carried out between 8 a.m. to 4 p.m. during the day when the light was sufficient.

2.2 Bio-chemical methods followed

Two micro capillary tubes full of blood was collected per each individual. The red cells of one tube were used for screening G6PD deficiency and the red cells of the second tube was used for blood grouping and haemoglobin polymorphism.

The red blood cells were separated from the plasma by breaking the capillary tube at the junction of plasma and red cell layers. The red cells were washed with normal saline (three washings) and then used for blood groupings and haemoglobin analysis and G6PD screening test. These were first carried out so as to prevent any damage to red cells. The plasma analysis was carried out after the red cell analysis, which would take two days for completion after return to the laboratory. It was possible to process 40-50 samples at a time on the average with minimum loss of efficiency.

2.2.1 Blood grouping

1 ABO blood group system

The blood grouping in ABO blood group system was done by using the standard tube technique. This method has many advantages over other techniques like slide or tile methods, since the detection of weaker reaction is possible, drying of the contents is eliminated and less amounts of sera are required. The anti-A, anti-B and anti-AB sera were used, procured from the Haffkine Institute, Bombay.

The blood grouping was performed by mixing one volume of 2 % red cell suspension in saline to one volume of anti-A, anti-B and anti-AB reagents in tubes (4 mm I.d x 50 mm) marked A, B and AB respectively. The contents of the tubes were mixed well by shaking them gently. They were then kept for 30 minutes at room temperature after which they were centrifuged for one minute at 1000 r.p.m. Agglutination in the tubes was observed by gently shaking the sediments in the tubes. The spectrum of agglutination may range from '+' (agglutination with more free cells) to ++++ (complete clumps). Whenever there was weak agglutination it was observed under a microscope for confirmation.

2 Rh_0(D) blood group system

The antisera was purchased from Chemech laboratories, Bombay and proved satisfactory. To detect Rh_0 (D) positive or negative one volume of anti-D serum was added to precipitin tubes containing one volume of red cell suspension. The tubes were mixed and incubated at 37° for 45 minutes and then centrifuged at 1000 r.p.m. for one minute. The results were read after dislodging the red cell button with gentle shaking. Controls of the positive and negative cells were kept with the test simultaneously and read first. The negative cases were reconfirmed by observing under microscope for any evidence of agglutination.

3 MN blood group system

The anti M and anti N antisera was supplied by Haffkine Institute, Bombay. The standard tube technique was followed as advocated by Haffkine Institute. One volume of anti M and anti N sera were added to two tubes containing one volume of red cell suspension to be tested. The tubes were kept for one hour at room temperature and then gently shaken and observed for agglutination. Extra care was taken whenever there was doubt due to weak agglutination by checking under the microscope for presence of clumped cells.

2.2.2 Screening for glucose-6-phosphate dehydrogenese deficiency

Brilliant cresyl blue (BLB) dye decolourization technique of Motulsky and Campbell - Krant (1961) was adopted for screening of G6PD deficiency. This technique is adopted by many investigators because it is more accurate and reliable. Brilliant cresyl blue dye (National Aniline Company) one of the components of the reaction mixtures, both stimulates the activity of the shunt pathway and acts as an indicator of reduced nicotinamide adenine dinucleotide phosphate (NADPH) changing colour from blue to colourless. The time required for decolourisation is a measure of the amount of G6PD activity. The test was performed by using the following reagents.

D-glucose-6phosphate (G 6 P) disodium salt : 825 mg/ 100 ml of glass distilled water.

Nicotinamide adenine dinucleotide phosphate (NADP) : 50 mg/100 ml of distilled water.

Brilliant cresyl blue : 32 mg/100 ml of distilled water.

Tris (hydroxymethyl) methylamine buffer (pH 8.5) : 8.96 gm/97 ml of distilled water and 3 ml of concentrated HCl.

The hemolysate was prepared by adding 20µl of the whole blood to 1 ml of water in a tube. The reaction mixture was prepared in the proportion of 1 part G6P, 1 part of NADP, 2.5 parts of BCB and 2 parts of tris buffer. 0.65 ml of this mixture was added to the haemolysate in the tube and mixed by rolling the tube between the palms. A few drops of liquid paraffin were layered on the surface of the test solution to prevent contact with air. The test solution was then incubated in a water bath at 37°C and initial time was recorded. The tubes were carefully observed at 20 minutes interval after an initial period of 40 minutes for three hours and then after overnight observation of the samples. Decolourisation from blue to the pink colour of haemoglobin normally was completed in 65 minutes. Dye decolourisation time above 100 minutes was considered to indicate G6PD deficiency.

2.2.3 Polyacrylamide gel electropheresis

Separation of serum proteins :

A simplified disc electrophoretic method of Clark (1964) was adopted for separation of the serum proteins. The serum sample was mixed in 40°/. sucrose and directly applied as a thin layer on the top of the separation gel whereas in the procedure of Davis (1964) both a 'spacer gel' and a sample containing 'large pore' gel is superimposed on a working gel. The former procedure was adopted for convenience. 7°/. gel was used for the separation of serum proteins. The following reagents were used for forming the gels :

Acrylamide	:	28 gm/100 ml of distilled H_2O
N, N' - methylene-bisacrylamide	:	759 mgs in the above solution
TEMED (N_4 - tetra-methylethylenediamine)	:	0.28 ml/100 ml of distilled H_2O
Ammonium persulphate	:	0.14 gm/100 ml of distilled H_2O
Glycine-tris buffer	:	0.29 gm of glycine and 0.6 gm of tris/100 ml of distilled H_2O

The gel solution was prepared by mixing 2 volumes of acrylamide, 1 volume of TEMED, 4 volumes of ammonium persulphate and 1 volume of glycine-tris mixture. This mixture was immediately poured into glass tubes (6 mm Id x 75 mm) which were inserted vertically into vaccine bottle stoppers. Routinely 3/4 length of the tubes were filled and immediately the remaining space in the tubes were filled with water by over layering carefully with the aid of a bent hypodermic needle of a small bore size. The tubes were allowed to stand for 30 to 40 minutes for polymerization. The electrode buffer was prepared by dissolving 29 g of glycine and 6 g of tris in 975 ml of distilled water to which 5 ml of 1N HCl (i.e. 10 mol percent) was added and adjusted to get a final pH 8.1. 50 ml of this stock solution was diluted with 450 ml of distilled water and kept in cold until use.

For transferrin and albumin separation, 20 µl of haemoglobin free serum was mixed with 100 ml of 40°/. sucrose and 30 µl of 0.005°/. bromophenol blue solution. The layer of water was removed from the top of the gel and 20 µl of the sample mixture was applied. The remaining space was filled with electrode buffer. The glass tubes with gels were inserted into the apparatus. 250 ml of gel buffer was poured into each electrode vessel. Power regulation of 30 milliamperes and 700 volts capacity was used to draw the current. 2.5 milliamperes current per tube was allowed for the first five minutes and then it was raised to 5 milliamperes for the rest of the run for 30 minutes. Electrophoresis was carried out in a cold room at 4°C.

After the electrophoresis, the gels were removed from the tubes by injecting a jet of water through a long needle and placed in 10·/. Amido black 10 B prepared in 7·/. acetic acid for 5 - 10 minutes. The excess of the stain in the gels was removed by washing with 7·/. acetic acid.

For haptoglobin electrophoresis, samples were prepared by adding 5 µl of fresh haemolysate to 20 µl of serum and incubated at 37°C for 20 - 30 minutes to form Hp-Hb complex. 50 µl of 40·/. sucrose solution and 20 µl of 0.005·/. of bromophenol blue was then added to it. 30 µl of this mixture was applied on the top of the gel and subjected to electrophoresis in a similar way described for transferrin and albumin separation.

To detect the phenotypic patterns of haptoglobin, the staining procedure of Mccombs and Bowman (1969) was adopted. The stain was prepared by dissolving 2 gm of O-dianisidine (dimethoxy benzidine) in 1000 ml of distilled water to which 5 ml of glacial acetic acid was added. The solution was mixed thoroughly and filtered to get a particle free stain. To get the haptoglobin patterns, the gels were immersed in the above fresh stain and then a few drops of 3% hydrogen peroxide were added to it. Within a few minutes green bands of haptoglobin-haemoglobin complex appeared. Hp 0-0 phenotype samples were repeated again for confirmation.

2 Separation of haemoglobins

For routine screening, the haemolysates were electrophoresed in 5.5% polyacrylamide gel using the buffer system of Dietz et al (1971) at pH 8.3.

Reagents of the following composition were used :

Solution A	:	48 ml of 1N HCl, 36.3 g of tris and 0.23 ml of N_4 - tetramethylethylene diamine in water to make 100 ml of solution, pH 8.3.
Solution C	:	30 g of acrylamide and 0.8 g of N,N'-methylenebisacrylamide in water to make 100 ml of solution.
Solution D	:	0.14 g of Ammonium persulphate in 100 ml of distilled water, stable for only a week.

Just before use the gels were prepared by mixing 2 volumes of solution A, 4 volumes of solution C, 8 volumes of Ammonium persulphate and 7.82 volumes of water. Electrode buffer was prepared by mixing 28.8 g of glycine and 6 g of tris in one litre of distilled water and adjusted to final pH 8.3. The electrode buffer is 1:10 dilution of the stock solution.

The samples were prepared by adding 30 µl of haemolysate to 50 µl of 40°/. sucrose solution. 40 µl of this mixture was applied on the top of the gel and subjected to electrophoresis in a similar way as described for the serum proteins. The major fractions of haemoglobin were seen on the transparent gels without using the stain. In each electrophoretic run a known Hb AS sample was run along with the sample. Sickle cell test was performed by using 2°/. sodium metabisulphite. The pH of this solution should be adjusted to 6.0 and above as an acidic pH will inhibit and distort the sickling phenomena of the red cells. Add a drop of this 2°/. Na metabisulphite to one drop of heparinised blood placed on a microscopic slide and then mix by blowing air from a pasteur pipette. A cover slip was overlaid and sealed with vaseline. The red cells were observed under a microscope for sickling after 15-20 minutes and thereafter if negative for an hour. If sickling is still negative, observe for a few more hours.

2.3 Anthropometric techniques

The techniques followed were according to Human biology, I.B.P. Handbook No.9 (Guide to field method compiled by J.S. Weiner)

1 Stature : The anthropometer was used for measuring height. The subject should stand on a horizontal platform provided alongwith the anthropometer with his heels together, stretching upwards to the fullest extent, aided by gentle traction by the measurer on the mastoid processes and the eyes and ear lobes should be in Frankfurt plane. The subject's back should be as straight as possible. The horizontal arm of the instrument is brought down on to the subject's head. The readings recorded in centimeters.

2 Upper arm length : The external superior border of the head of the radius is marked and the length from this mark to the inferior border of the acromion process is measured with the anthropometer.

3 Fore-arm length : Measured from the marked head of the radius to the tip of the lateral styloid.

4 Bigonial diameter : The spreading calipers is used. The maximum diameter between the angles of the mandible on their external surfaces is measured with pressure exerted to compress the tissues.

5 Morphological face height (Nasion-Gnathion) : The sliding calipers is used for this measurement. One arm of the calipers is held horizontally at the marked nasion, the other arm of the calipers is hooked under the tip of the chin. The teeth should be fully occluded.

Nose height or length : One arm of the sliding calipers is held horizontally at the marked nasion while the other arm of the calipers is brought down to reach the union of the upper lip with the nasal septum.

Nose breadth : Sliding calipers is held horizontally and its arms brought into contact with the outside of the nares without pressure.

Head length : Spreading calipers is used to measure the maximum length in the saggital plane from the glabella to the most salient point on the occiput. Pressure is exerted to compress the tissues.

Head breadth : The maximum breadth in the transverse plane wherever it occurs is measured by the spreading calipers and pressure is exerted to compress the tissues.

10 *Biocromial diameter* : The anthropometer is used to measure the maximum shoulder width. The subject stands with the shoulders relaxed to the point of slumping forward. Standing behind the subject, the measurer feels for the outside edge of the acromial process of the shoulder blade which can be felt at the ridge just above the shoulder joint. He then places the edge of one arm of the anthropometer along the external border of one acromial process and brings the other arm of the anthropometer inwards until its edge rests on the opposite acromial external border.

11 Bi-iliac or bi-iliocristal diameter : The subject stands with his heels together and the anthropometer arms are brought into contact with the iliac crests at the place which gives the maximum diameter. Strong pressure is applied to the anthropometer blades to push aside any fat covering the bone.

12 Right upper arm circumference : This is measured with a tape with the arm relaxed. The subject's arm hangs down just away from his side and the circumference is taken horizontally at the marked level, that is, half-way between the inferior border of the acromial process and the tip of the olecranon process.

Skinfold thicknesses : The skinfold is picked up between thumb and fore-finger and the skinfold calipers jaws applied at exactly the level marked. The measurement is read two seconds after the full pressure of the caliper jaws is applied to the skinfold.

13 Right triceps skinfold : The skinfold is picked up at the back of the arm about 1 cm above the level marked on the skin for the arm circumference and directly in line with the point of the elbow.

14 Right subscapular skinfold : The skinfold is picked up under the angle of the left scapula. The fold should be vertical or pointing slightly downwards and outwards.

5 Weight : Since the tribal people wear very few clothes it was without inconvenience that the weight could be taken.

6 Bizygomatic breadth : The maximum diameter between the zygomatic arches. However in this study the maximum diameter between the zygomatic arches was measured by the investigator with the help of the spreading calipers and hence could not be used for general comparison with other groups. This measure could however be used for comparison between the tribal groups in the study.

CHAPTER 3 : SCRUTINY OF DATA AND ANALYSIS

1 Importance of scrutiny : The problem of scrutinising the primary records assumes paramount importance in investigations where the observations are recorded in the field and the investigator has no chance of repeating his measurements. The magnitude and proportion of recording errors are sometimes extremely large and analysis based on such data may result in wrong conclusions. Scrutiny often helps in discovering some rules to correct serious discrepancies and thus salvaging what might have been thought as lost, a classical example is that of the revision of Risley's anthropometric data for Bengal undertaken by Mahalanobis (1933). He was able to classify the various types of mistakes and find out ways and means of rectifying them using only internal evidence as far as possible. This resulted in the removal of the many inconsistencies in Risley's primary data. The U.P. Anthropometric Survey of 1941 (Mahalanobis, Majumdar and Rao, 1949) and the Bengal Anthropometric Survey (Majumdar and Rao, 1945) give in detail the authors experiences in scrutiny of data and methods that could be applied to ensure greater reliability of the field records.

The scrutiny of raw data for the presence of 'outliers' that is, observations which appear to be inconsistent with the remainder of that set of data, is an important and essential step to valid analysis of data. If these 'outliers' are not genuine members of the population, then their presence is likely to distort the inference rocess. What characterises the 'outliers' is its impact on the observer (it appears extreme in some way). Accordingly, the outlier problem should be tackled in the following way i.e., the data set is examined and outliers are detected. The next stage would be whether there is any justification in rejecting or adjusting these values and the use of appropriate statistical methods for the purpose. Clearly, the answer depends on the form of the population; techniques will be conditioned by and specific to, any postulated model for that population. Thus; methods for the processing of outliers take on an entirely relative form. Outliers can be due to either random or to deterministic reasons. Random occurence of outliers is due to inherent variability, that is, observations very intrinsically over the population; such variation is a natural feature of the population and uncontrollable. Outliers due to deterministic reasons are due to reading, recording or calculating errors in the data. When it is obvious that this is so, the remedy is clear and non-controversial

The error value should be removed from the sample or replaced by corrected values when the method of correction is unambiguously understood. Of course, extreme values must occur in a set of data with some frequency depending on the true distribution of the variables in the population. What is important is whether or not they are so extreme that they could not reasonably have arisen by chance from the adopted model. If the outliers prove to be discordant on an assumed distribution, it is quite likely that we may choose to reject them before proceeding to further study of the data. We cannot of course be sure that this action is entirely proper. Some authors recommend 'trimming of data' i.e., removing some low and some high observations as a routine method, and applying appropriate techniques of statistical analysis on the rest. However, the stricture of Kruskal in 'Outliers in statistical data' (Barnett and Lewis, 1978) can be followed and that is apparent outliers should be reported even when one feels that the causes are known or when one rejects them for whatever good rule or reason.

4.1 Scrutiny of the present material : It is difficult to lay down specific rules for the detection of 'outliers' as the underlying distribution of the observations and the stochastic nature of the outliers may not be known to begin with. As a first step a 'descriptive analysis' of the data should be undertaken. This includes, for each set of observations on a given character and a given tribe:

i) making frequency distribution in narrow class intervals and drawing histograms

ii) computing measures of location like the mean, mode, median and measures of dispersion like the range and standard deviation

iii) recording the maximum and minimum values

iv) computing measures of skewness and kurtosis, and so on

Outliers are suspected if,

a) there are gaps in the histogram and the extreme observations are far removed from the nearest neighbours.

b) if the variation in some samples is larger than in the others for the same character.

c) if there is a general consistency in measures of skewness and kurtosis, but in some cases the values are ~~discarded~~ discordant.

A list of outliers detected in the data and the action taken are given in Table 2. The presence of these outliers produced a deviation in the normal distribution and increased skewness and kurtosis significantly. The increase in positive skewness indicated an outlier which has a low value whereas an increase in negative skewness indicated the presence of a large value. The same was reflected in kurtosis, either leptokurtic or platykurtic shift in distribution indicating the presence of an extremely low or high value in the data set. The significant increase in skewness and kurtosis

Table 2 SCRUTINY OF RAW DATA

Detection of Outliers and Action Taken

Population (Code of Individual and Sex)	Observation as Recorded (in m m)	Action Taken	Basis on Which Action Was Taken
KOLAM (♂) 071	BgB 126	Omitted	**Maximum Was Too Large**
KOLAM (♂) 049	LAL 178	Omitted	**Minimum Was Too Small**
Kolam (♂) 092	BIB 201	Omitted	**Minimum Was Too Small**
KOLAM (♀) 102	BAB 246 BIB 337	Values Where Interchanged	BAB Never Smaller Than BIB In Same Individual
KOLAM (♀) 025	UAL 201	Omitted	Minimum Too Small
KOLAM (♀) 121	LAL 288	Omitted	Maximum Value Too Large
KOLAM (♀)	UAL 368	Omitted	**Maximum Value Too Large**
KOYAS (♂) 028	UAL 247 LAL 282	Upper Arm 282 Lower Arm 247	Interchange Error Upper Arm Cannot Be Larger Than Lower Arm
KOYAS (♂) 048	UAL 280 LAL 295	Upper Arm 295 Lower Arm 280	Interchange Error Upper Arm Cannot Be Larger Than Lower Arm
KOYAS (♂) 083	UAL 203 LAL 271	Upper Arm 271 Lower Arm 203	Interchange Error Upper Arm Cannot Be Larger Than Lower Arm
KOYAS (♂) 076	MAC 326	Omitted	Maximum Too Large. Not consistent With Fat Fold Measurements of Same Individual

TABLE 2 SCRUTINY OF RAW DATA

Detection of Outliers and Action Taken (Continued)

Population (Code of Individual and Sex)	Observation as Recorded (in m m)	Action Taken	Basis on Which Action Was Taken
MANNE (♂) 007	HB 164	Omitted	Maximum Too Large
MANNE (♂) 028	BgB 136	Omitted	Maximum Too Large
MANNE (♀) 015	HB 159	Omitted	Maximum Too Large
MANNE (♀) 001	HL 210	Omitted	Maximum Too Large
MANNE (♀) 001	BgB 116	Omitted	Maximum Too Large
MANNE (♀) 093	UAL 350	Omitted	Maximum Too Large
PLAINS MARIA (♂) 052 GOND	TFF 13.0 SFF 19.0	Omitted	Maximum Values Too Large
PLAINS MARIA (♀) 127 GOND	BgB 119	Omitted	Minimum Values Too Low
PLAINS MARIA (♀) 036 GOND	BAB 236	Omitted	Minimum Values Too Low
PLAINS MARIA (♀) 120	BAB 212	Omitted	Minimum Values Too Low

was tested by looking at the tables of critical values for 5% test of discordancy for one or more outliers in a normal sample (Barnett and Lewis, 1978). The removal of outliers in many cases brought back the distribution to normality (Tables 3 to 6).

3.1.2 Use of indices in detection of recording errors and outliers

The examination of maximum and minimum values of calculated indices on bony measurements also helped in the detection of the presence of outliers (Tables 7 to 10). For example, in the case of Cephalic index which is maximum head breadth/ maximum head length, the ratio is a extremely large value indicating that head breadth is larger than head **length** which is not normally the case. In some cases, values are interchanged, i.e., upper arm for lower arm measurement and this was detected by looking at the lower arm/upper arm ratio which would be a large value, indicating that the lower arm which is not normally longer than upper arm is extremely large. In such cases, when the raw data were examined, it was found that upper arm measurements which were recorded routinely next to lower arm measurements were interchanged one for the other during the process of recording the data. In these cases, the values were corrected (Table 2). Out of a total of 21 outliers detected in the raw data,

TABLE 3 MALE TRIBALS

SKEWNESS (γ_1) AND KURTOSIS (γ_2) BASED ON ORIGINAL MEASUREMENTS (FIRST LINE) AND AFTER ADJUSTING FOR OUTLIERS WHEREEVER FOUND NECESSARY (SECOND LINE)

CHARACTER	KOLAM (52)		KOYA (51)		MANNE (56)		PLAINS MARIA (54)		RAJGOND (54)	
	γ_1	γ_2	γ_1	γ_2	γ_1	γ_2	γ_1	γ_2	γ_1	γ_2
H B	0.154	-0.618	0.393	0.373	1.617*	4.543	-0.266	0.478	-0.297	0.236
					0.709*	0.293				
H L	-0.144	-0.061	0.484	1.120	-0.050	-0.083	0.045	-0.091	-0.320	0.285
Bz B	-0.549*	1.259	0.095	0.154	0.135	-0.359	-0.431	0.406	-0.143	0.335
Bg B	0.832*	2.933	0.170	0.187	1.716*	8.425*	-0.170	-0.633	-0.125	-0.613
	-0.141	-0.029			-0.399	0.270				
T F L	-0.256	-0.067	0.444	0.112	0.657*	0.319	-0.052	-0.096	-0.036	-0.240
N L	0.091	-0.817	-0.270	1.412	0.028	0.042	0.094	-0.412	-0.272	0.148
N B	0.051	0.570	-0.125	-0.366	0.460	-0.443	0.740*	0.250	0.110	0.184
St	-0.118	-0.230	-0.384	0.931	-0.424	-0.408	-0.331	-0.173	-0.381	-0.044
U H L	-0.047	-0.634	-1.946*	6.876*	-0.010	-0.271	0.126	0.765	0.143	-0.396
			-0.300	0.739						
L A L	-2.166*	9.977*	-0.071	0.594	0.195	-0.668	-0.020	0.276	-0.036	[illegible]
	0.078	-0.617	-0.655*	1.605						
B A B	0.046	-0.791	0.181	-0.466	0.211	1.022	-0.016	-0.738	0.160	-0.143
B I B	-0.410	2.614	-0.393	0.566	-0.060	0.469	-0.026	0.877	-0.335	-0.256
	0.556*	0.458								
M A C	-0.106	-0.658	1.794*	9.015*	-0.471	1.395	0.070	0.783	-0.436	0.210
			-0.548*	-0.062						
T F F	0.956*	0.411	1.025*	0.989	1.700*	3.775	1.803*	4.308*	2.369*	7.412*
							1.266*	1.822		
S F F	0.316	-0.227	0.447	-0.141	0.963*	1.425	1.782*	4.938*	0.985*	1.141
							1.457*	3.795		
Wt	0.336	-0.414	0.360	-0.139	-0.385	0.179	0.182	0.416	-0.085	-0.555

TABLE 4 FEMALE TRIBALS

SKEWNESS (γ_1) AND KURTOSIS (γ_2) BASED ON ORIGINAL MEASUREMENTS (FIRST LINE)
AND AFTER ADJUSTING FOR OUTLIERS WHEREEVER FOUND NECESSARY (SECOND LINE)

CHARACTER	KOLAM (50)		KOYA (50)		MANNE (49)		PLAINS MARIA (48)		RAJGOND (37)	
	γ_1	γ_2	γ_1	γ_2	γ_1	γ_2	γ_1	γ_2	γ_1	γ_2
H B	-0.017	-0.381	0.408	-0.579	1.226*	4.166*	-0.349	0.002	-0.446	1.907
					-0.010	-0.457				
H L	0.073	-0.276	0.203	-0.751	2.238*	8.880*	0.015	-0.559	0.758*	0.581
					0.586*	0.869				
Bz B	0.311	-0.035	0.459	-0.367	0.825*	1.668	0.116	1.226	0.110	-1.199
Bg B	-0.051	-0.536	-0.192	0.838	1.136*	2.821	0.984*	4.309*	0.920*	1.256
					0.417	0.486	-0.235	1.449		
T F L	0.158	1.010	0.534*	0.649	-0.134	0.453	0.087	0.376	0.208	-0.550
N L	-0.362	0.309	-0.646*	1.945	-0.212	0.377	-0.325	0.332	0.064	-0.679
N B	0.367	-0.462	0.034	0.410	0.362	-0.533	0.008	0.274	-0.104	-1.021
S St	0.092	0.042	-0.420	-0.122	0.164	0.511	0.113	0.392	-0.044	-0.035
U A L	-0.118	6.899*	-0.428	-0.326	1.025*	3.235	-0.246	-0.423	-0.599*	-0.134
	0.534*	0.133			-0.100	-0.825				
L A L	0.654*	1.540	0.141	-0.713	-0.262	-0.092	-0.583*	0.381	-0.170	-0.482
	-0.035	-0.486								
B A B	-1.495*	4.934*	-0.456	-0.653	0.100	0.698	-2.338*	8.217*	-0.302*	2.575
	- .194	-1.21					-0.040	0.445		
B I B	2.177*	11.823*	0.231	-0.388	-0.190	0.062	0.194	-0.103	0.060	-0.357
	-0.666	1.575								
M A C	0.217	-0.665	0.458	-0.205	0.635*	1.695	0.446	0.433	0.342	0.894
T F F	1.419*	2.859	1.337*	2.448	0.922*	0.648	0.154	-1.051	0.763*	1.051
S F F	1.989*	7.269*	1.467*	4.218*	0.834*	0.046	0.768*	0.186	1.386*	2.364
Wt	0.381	-0.338	0.334	-0.298	0.203	0.482	0.508	0.375	-0.271	-0.057

TABLE 5. MALE TRIBALS

MEAN ($\bar{X}$) AND STANDARD ERROR (± S.E.) OF ANTHROPOMETRIC MEASUREMENTS AFTER OMITTING OUTLIERS (NUMBER INDICATED IN BRACKET)

CHARACTER	KOLAM (52)		KOYA (51)		MANNE (56)		PLAINS MARIA (54)		RAJGOND (54)	
	$\bar{X}$	± S.E.	$\bar{X}$	± S.E.	$\bar{X}$	± S.E.	$\bar{X}$	± S.E.	$\bar{X}$	± S.E.
H B	137.308	0.781	141.843	0.606	141.073 (-1)	0.602	142.185	0.664	139.481	0.491
H L	184.173	0.726	186.922	0.793	184.839	0.889	186.241	0.834	187.148	0.647
Bz B	118.481	0.691	118.647	0.787	120.018	0.767	118.019	0.747	119.259	0.726
Bg B	103.314 (-1)	0.709	101.900	0.871	103.115 (-1)	0.729	104.906	0.698	102.096	0.750
T F L	109.442	0.818	108.843	0.815	111.673	0.819	110.963	0.917	110.736	0.799
N L	49.288	0.620	47.529	0.571	49.607	0.624	47.944	0.419	47.815	0.510
St	1613.038	7.719	1593.118	8.554	1607.607	7.633	1606.648	7.873	1628.278	8.757
U A L	315.058	2.257	306.608	2.354	311.018	2.835	305.778	2.185	313.630	2.126
L A L	262.510 (-1)	1.746	255.961	2.317	264.500	2.226	256.778	1.799	263.241	1.944
B A B	351.615	2.307	357.078	2.313	353.607	2.127	351.111	2.115	355.759	2.067
B I B	252.471 (-1)	1.722	256.569	1.677	258.036	1.934	264.481	2.011	254.333	1.699
M A C	226.308	2.350	236.000	1.978	228.071	2.065	243.741	2.577	238.444	2.282
T F F	46.731	0.970	49.118	1.109	49.286	1.542	58.113 (-1)	2.061	48.148	1.615
S F F	75.481	1.977	75.588	1.983	70.625	1.978	86.226 (-1)	3.230	78.333	2.368
Wt	96.771	1.612	98.708	1.364	94.852	1.362	105.509	1.795	103.170	1.828
NB	39.308	0.442	38.196	0.364	38.054	0.324	39.185	0.401	37.481	0.415

TABLE 6 FEMALE TRIBALS

MEAN ($\bar{X}$) AND STANDARD ERROR (±S.E.) OF ANTHROPOMETRIC MEASUREMENTS AFTER OMITTING OUTLIERS (NUMBER INDICATED IN BRACKET)

CHARACTER	KOLAM (50)		KOYA (50)		MANNE (49)		PLAINS MARIA (48)		RAJGOND (37)	
	$\bar{X}$	±S.E.	$\bar{X}$	±S.E.	$\bar{X}$	±S.E.	$\bar{X}$	±S.E.	$\bar{X}$	±S.E.
H B	135.260	0.763	137.160	0.609	136.479	0.650	135.125	0.725	134.459	0.618
					(-1)					
H B	177.340	0.884	180.660	0.779	177.167	0.745	180.042	0.892	181.054	0.954
					(-1)					
Bz B	113.280	0.682	111.440	0.855	113.204	0.662	111.396	0.725	115.297	0.872
Bg B	96.043	0.696	94.042	0.862	95.596	0.688	96.721	0.728	94.118	0.936
					(-1)		(-1)			
T FL	103.120	0.707	101.553	0.817	105.522	1.014	104.128	0.910	104.056	0.883
N L	44.560	0.476	42.760	0.436	45.878	0.499	43.271	0.471	44.946	0.520
N B	36.580	0.301	35.160	0.369	35.338	0.342	35.875	0.407	36.027	0.424
St	1490.500	6.646	1505.540	8.521	1503.551	6.614	1500.833	9.201	1515.216	7.164
U A L	287.938	2.102	293.840	2.113	289.479	1.848	286.813	1.883	287.784	2.479
	(-2)				(-1)					
L A L	235.959	1.880	240.040	2.073	238.306	2.080	233.958	1.804	238.432	1.684
	(-1)									
B A B	311.330	1.811	321.000	1.727	320.490	1.751	317.478	2.135	312.081	2.923
							(-2)			
B I B	245.420	1.803	247.000	1.929	250.755	2.117	254.688	1.870	247.838	2.168
M A C	210.560	2.195	215.000	2.141	2.3.347	2.281	225.146	2.535	222.622	2.920
T F F	66.400	2.914	62.200	2.997	58.673	2.019	30.000	3.332	75.676	3.520
S F F	70.400	2.511	69.260	2.315	69.898	2.140	87.500	2.600	78.514	4.132
Wt	33.653	1.310	32.531	1.580	31.449	1.483	38.479	1.680	37.943	1.669

TABLE 7 MALE TRIBALS

MEAN ($\bar{X}$) AND STANDARD ERROR (±S.E.) BASED ON INDICES

AFTER OMITTING OUTLIERS (NUMBER INDICATED IN BRACKETS)

INDICES	KOLAM (52)		KOYA (51)		MANNE (56)		PLAINS MARIA (54)		RAJGOND (54)	
	$\bar{X}$	± S.E.	$\bar{X}$	± S.E.	$\bar{X}$	± S.E.	$\bar{X}$	± S.E.	$\bar{X}$	± S.E.
C I	74.585	0.429	75.914	0.430	76.487 (-1)	0.380	76.400	0.413	74.572	0.350
N I	80.346	1.278	80.885	1.159	77.370	1.160	82.097	1.170	78.927	1.267
B I B/B A B	71.851 (-1)	0.494	71.944	0.519	73.049	0.557	75.386	0.540	71.538	0.434
L AL/U A L	83.567 (-1)	0.615	83.523	0.563	85.149	0.483	84.076	0.542	84.597	0.371
B A B/St	21.803	0.118	22.421	0.112	22.005	0.118	21.863	0.117	21.862	0.112
B I B/St	15.675 (-1)	0.086	16.115	0.100	16.049	0.086	16.468	0.114	15.626	0.088
U AL/St	19.531	0.100	19.247	0.110	19.334	0.116	19.031	0.096	19.263	0.087

TABLE 8 FEMALE TRIBALS

MEAN ($\bar{X}$) AND STANDARD ERROR (±S.E.) BASED ON INDICES (FIRST LINE)

AND NUMBER OF OUTLIERS REMOVED (SECOND LINE)

INDICES	KOLAM (50)		KOYA (50)		MANNE (49)		PLAINS MARIA (48)		RAJGOND (37)	
	$\bar{X}$	± S.E.	$\bar{X}$	± S.E.	$\bar{X}$	± S.E.	$\bar{X}$	± S.E.	$\bar{X}$	± S.E.
C I	76.317	0.427	75.979	0.429	77.052	0.380	75.108	0.452	74.306	0.370
					(-2)					
N I	82.483	0.994	82.562	1.071	77.572	1.137	83.282	1.163	80.336	0.915
B IB/B A B	78.921	0.679	76.971	0.512	78.261	0.569	80.152	0.497	79.582	0.812
							(-2)			
L AL/U A L	82.069	0.596	81.744	0.573	82.175	0.526	81.628	0.554	83.002	0.722
	(-2)				(-1)					
B AB/St	20.901	0.123	21.334	0.098	21.230	0.095	21.142	0.110	20.599	0.173
							(-2)			
B IB/St	16.471	0.113	16.411	0.106	16.674	0.110	16.979	0.109	16.364	0.147
U AL/St	19.312	0.108	19.525	0.117	19.286	0.085	19.117	0.088	18.990	0.128
	(-2)				(-1)					

TABLE 9 MALE TRIBALS

SKEWNESS (γ_1) AND KURTOSIS (γ_2) BASED ON INDICES (FIRST LINE) AND AFTER ADJUSTING FOR OUTLIERS WHEREVER FOUND NECESSARY (SECOND LINE).

INDICES	KOLAM (52)		KOYA (51)		MANNE (56)		PLAINS MARIA (54)		RAJGOND (54)	
	γ_1	γ_2	γ_1	γ_2	γ_1	γ_2	γ_1	γ_2	γ_1	γ_2
C I	0.082	0.031	0.026	-0.957	0.451	0.305	0.071	0.551	0.278	0.675
					0.450	0.504				
N I	-0.204	-0.496	0.517	1.465	0.356	-0.063	0.923	0.991	-0.161	-0.774
B IB/B A B	-0.411	0.973	-0.199	0.203	-0.104	-0.502	0.028	1.206	0.049	-0.482
	0.229	-0.795								
L A L/U A L	-2.104	11.252	3.626	15.625	0.111	-0.430	-1.190	4.444	-0.378	1.132
	0.645	0.292	0.498	1.361						
B A B/St	0.142	-0.330	0.151	0.222	0.101	-0.660	0.334	0.694	-0.180	-0.675
B I B/St	-0.939	5.476	-0.326	-0.298	0.201	-0.130	0.488	0.214	0.097	-0.185
	0.811	0.363								
U A L/St	0.035	0.004	-3.167	13.822	-0.229	0.111	1.075	2.553	-0.112	0.679
			-0.671	1.382						

TABLE 10 FEMALE TRIBALS

SKEWNESS (γ_1) AND KURTOSIS (γ_2) BASED ON INDICES (FIRST LINE) AND AFTER ADJUSTING FOR OUTLIERS WHEREVER FOUND NECESSARY (SECOND LINE).

INDICES	KOLAM (50)		KOYA (50)		MANNE (49)		PLAINS MARIA (48)		RAJGOND (37)	
	γ_1	γ_2	γ_1	γ_2	γ_1	γ_2	γ_1	γ_2	γ_1	γ_2
C I	0.006	-0.732	0.006	-0.489	0.192	2.932	-0.157	0.315	-0.170	-0.453
					0.072	0.027				
N I	0.345	1.535	0.155	-0.012	0.842	1.770	-0.163	-0.407	0.153	0.184
B IB/B A B	4.462	27.142	0.349	-0.012	0.132	-0.715	3.571	14.362	0.456	-0.467
	-0.276	1.600					0.063	0.520		
L AL/U A L	1.342	5.011	0.416	-0.175	0.142	-0.345	-0.302	-0.357	0.178	0.776
	-0.141	0.249			0.234	-0.375				
B AB/St	-1.443	5.555	0.222	0.027	-0.165	-0.695	-2.926	10.335	-1.359	4.682
	0.047	-0.537					-0.859	1.830		
B I B/St	2.112	12.124	0.314	1.489	0.428	0.656	0.474	-0.103	0.296	-0.336
	-0.858	2.370								
U AL/St	-0.227	9.948	0.424	0.054	0.676	1.346	-0.349	-0.222	-0.550	0.268
	0.300	0.272			0.188	0.159				

4 were due to interchange errors. When the outliers were due to large or small values, these values were omitted and computation carried out without those values. Out of a total number of outliers the majority were due to such errors. Hence a priori knowledge of the distribution as in this case is important in predicting the presence of outliers. The formula for second (γ_1) and third (γ_2) moments were followed according to those given in SPSS (Statistical Programme for Social Sciences).

The formulae are as follows :-

$$\gamma_1 = \sum \frac{(X_i - \bar{X})^3}{Ns^3} \quad \text{(Skewness)}$$

$$\text{where } s^2 = \sum \frac{(X_i - \bar{X})^2}{N}$$

$$\gamma_2 = \sum \frac{(X_i - \bar{X})^4}{Ns^4} \quad \text{(Kurtosis)}$$

In the case of measurements such as skinfold thickness measurements and weight, the distribution to start with is not normal. Hence, the presence of outliers in such a skewed distribution is due to inherent variability and the action to be taken is controversial, so nothing was done in the case of these measurements (Tables 3 - 10). However, they were not used for multivariate analysis.

.2 Preliminary analysis of data

Anthropometric Measurements

Out of the 16 anthropometric measurements only 11 were selected for further analysis. The five measurements which were rejected were the upper arm length, lower arm length, mid-arm circumference, triceps skinfold, and subscapular skinfold. In the case of upper arm length and lower arm length, these are highly correlated with stature and hence it was decided that they are redundant i.e., would not add any further information in differentiating the populations. In the case of the last three measurements which were soft tissue measurements, the distributions are effected by environmental factors and would not be suitable for comparative purposes.

3.2.1 Variances

Variances within tribes and tests of homogeneity for both females and males were carried out on each of the 16 measurements (Tables 11 and 12). Both χ^2 and the test statistic maximum s^2/minimum s^2 were used to test for homogeneity of variances for each measurement within the female and male tribal group. The alpha percentage points for s^2 max/s^2 min. given by David (1952) were used for testing for statistical significance. The females showed a significant difference in variances for 5 out of 16 measurements, the particular measurements being stature, lower arm length, bi-acromial breadth, triceps fatfold and subscapular fatfold. The males also showed significant difference in variances for 5 out of 16 measurements, these five particular measurements being head breadth, nose length, triceps fatfold, subscapular fatfold and weight. In the case of characters such as triceps fatfold etc subscapular fatfold and weight which are not normally distributed the above tests are not strictly applicable, and the significance indicated may not be due to lack of homogeneity. However, in the case of characters used for further statistical analysis the variances were nearly the same for all the male and female groups.

3.2.2. The test for homogeneity of a set of correlation coefficients was according to Rao (1965) as follows :

Let r_1 ------------ r_k be k correlation coefficients based on samples of sizes n_1 ------------ n_k. By means of the $\tan h^{-1} r$ transformation, the quantities Z_1 ---------- Z_k corresponding to r_1 ------ r_k can be obtained. If the bias in mean Z can be neglected, the test for homogeneity of the correlation coefficient is equivalent to the test of equality of the mean values of Z. The scheme of computation is as follows :

Test for homogeneity of parallel estimate of correlation coefficients

Sample No.	Sample size	Correlation coefficient	$\tan h^{-1} r$	Reciprocal variance		
t	n	r	z	$n-3$	$(n-3)z$	$(n-3)z^2$
1	n_1	r_1	z_1	n_1-3	$(n_1-3)z_1$	$(n_1-3)z_1^2$
⋮	⋮	⋮	⋮	⋮		
k	n_k	r_k	z_k	n_k-3	$(n_k-3)z_k$	$(n_k-3)z^2_k$
Total				N	T_1	T_2

The best estimate of $\tan h^{-1}\rho$, when a common ρ is applicable is T_1/N. The statistic for testing homogeneity is $H = T_2 - \frac{T_1^2}{N}$ which can be used as χ^2 on $(k - 1)$ D.F.

The correlation matrix was found to be homogeneous within the male groups as well as within the female groups. In the males α levels are high in 7/105 correlations. In the rest of the coefficients, the α levels are less than 0.05%. In the females the α levels are high in 4/105 correlation coefficients and the rest have α levels less than 0.05%. The correlation coefficients in the males compared with those of U.P. anthropometric survey (Majumdar and Rao, 1941) were similar (Table 13).

TABLE 15

POOLED WITHIN GROUP STANDARD DEVIATIONS AND CORRELATIONS

MEASUREMENTS	PRESENT DATA			U. P. ANTHROPOMETRIC
	MALES	FEMALES	POOLED	SURVEY
Standard Deviation				
H B	4.616	4.687	4.649	4.500
H L	5.654	5.830	5.736	6.600
Bz B	5.411	5.094	5.266	4.580
Bg B	5.370	5.074	5.234	5.040
T F L	6.180	5.858	6.032	6.160
N L	4.051	3.300	3.721	3.500
N B	2.861	2.519	2.708	2.520
St	59.498	53.230	56.671	57.400
B A B	15.906	13.832	14.978	
B I B	13.267	13.536	13.393	
Wt	11.243	10.568	10.936	
Correlations				
H B x H L	0.255	0.361	0.305	0.3982
H B x Bz B	0.152	0.132	0.143	0.5407
H B x Bg B	0.103	0.020	0.066	0.2295
H B x T F L	0.228	0.111	0.175	0.1825
H B x N L	0.132	0.059	0.101	0.1235
H B x N B	0.092	0.067	0.081	0.1613
H B x St	0.233	0.200	0.218	0.1927
H B x B A B	0.252	0.202	0.230	
H B x B I B	0.179	0.142	0.161	
H B x Wt	0.292	0.263	0.279	
H L x Bz B	0.143	0.316	0.222	0.2292
H L x Bg B	0.052	0.083	0.066	0.2192
H L x T F L	0.338	0.246	0.296	0.3067
H L x N L	0.156	0.112	0.135	0.1758
H L x N B	0.224	0.203	0.214	0.1930
H L x St	0.249	0.170	0.213	0.2698
H L x B A B	0.153	0.207	0.176	
H L x B I B	0.229	0.114	0.174	
H L x Wt	0.306	0.255	0.282	
Bz B x Bg B	0.316	0.312	0.314	0.4360

TABLE 13

POOLED WITHIN GROUP STANDARD DEVIATIONS AND CORRELATIONS (Continued)

MEASUREMENTS	PRESENT DATA			U. P. ANTHROPOMETRIC
	MALES	FEMALES	POOLED	SURVEY
Bz B x T F L	0.326	0.327	0.326	0.2710
Bz B x N L	0.155	0.125	0.143	0.1852
Bz B x N B	0.163	0.260	0.206	0.2729
Bz B x St	0.266	0.284	0.272	0.2891
Bz B x B A B	0.280	0.258	0.271	
Bz B x B I B	0.248	0.273	0.259	
Bg B x Wt	0.313	0.400	0.351	
Bg B x T F L	0.220	0.159	0.193	0.1701
Bg B x N L	0.081	0.080	0.080	0.1108
Bg B x N B	0.146	0.160	0.151	0.1854
Bg B x St	0.165	0.043	0.113	0.2103
Bg B x B A B	0.091	0.064	0.080	
Bg B x B I B	0.184	0.106	0.149	
Bg B x Wt	0.243	0.139	0.198	
T F L x N L	0.341	0.449	0.503	0.5520
T F L x N B	0.048	0.120	0.078	0.0764
T F L x St	0.424	0.308	0.375	0.2500
T F L x B A B	0.317	0.251	0.290	
T F L x B I B	0.336	0.300	0.319	
T F L x Wt	0.420	0.293	0.365	
N L x N B	0.025	0.240	0.108	0.0618
N L x St	0.263	0.194	0.236	0.1974
N L x B A B	0.177	0.142	0.164	
N L x B I B	0.225	0.199	0.213	
N L x Wt	0.200	0.042	0.137	
N B x St	0.039	0.155	0.086	0.1612
N B x B A B	0.033	0.163	0.085	
N B x B I B	0.173	0.1[illegible]	0.171	
N B x Wt	0.197	0.210	0.202	
St x B A B	0.579	0.552	0.568	
St x B I B	0.559	0.505	0.534	
St x Wt	0.671	0.621	0.650	
B A B x B I B	0.437	0.449	0.441	
B A B x Wt	0.607	0.489	0.557	
B I B x Wt	0.700	0.550	0.631	

Equality of variances and co-variances for males and females

The likelihood ratio test for equality of co-variances within males and females was used. The χ^2 approximation used was according to Box (1949).

Wilk's λ was calculated according to

$$= \frac{\left|n_1 W_1\right|^{n_1/2} \left|n_2 W_2\right|^{n_2/2}}{\left|n_1 W_1 + n_2 W_2\right|^{n/2}} \times \frac{n^{pn/2}}{n_1^{pn_1/2} \quad n_2^{pn_2/2}}$$

$n = n_1 + n_2$ (degrees of freedom)

W_1 is within co-variance matrix in males

W_2 is within co-variance matrix in females

Wilk's $\lambda = 0.3891717 \times 10^{-17}$

Wilk's Statistics

$$D_1 = \frac{2p^2 + 3p - 1}{6(p+1)\ (q - 1)} \left[\frac{1}{n_1} + \frac{1}{n_2} \mp \frac{1}{n} \right]$$

$n = n_1 + n_2$ (D.F.)

p = number of variables

q = groups

χ^2 approximation

$$\chi^2 = (-2 \log \lambda_6) \quad (1 - D_1) \text{ with } f_1 = \frac{p(p+1)\ (q-1)}{2}$$

$\chi^2 = 78.8979$ with D.F., 66

The co-variance matrices were found to be equal within male and female tribals.

TABLE 14 ANALYSIS OF VARIANCE

(INDIVIDUAL ANTHROPOMETRIC CHARACTERS)

F. STATISTICS

CHARACTERS	BETWEEN MALE TRIBALS F(4,482)	BETWEEN FEMALE TRIBALS F(4,482)	SEX DIFFERENCE WITHIN TRIBALS F(5,482)	SEXUAL DIMORPHISM F(4,482)
H B	9.3106**	2.5778*	29.0532**	3.3416**
H L	2.5922*	4.3178**	33.4196**	0.2814
Bz B	1.0165	3.8753**	34.4140**	1.6832
Bg B	2.3295*	2.0975	50.4718**	0.2658
T F H	1.6866	2.4057*	32.3000**	0.1042
N L	3.4251**	5.3792**	31.6999**	1.2534
N B	4.5603**	2.0819	25.7829**	1.6448
St	2.6680*	1.3683	39.5933**	1.3948
B A B	1.4555	4.0209**	131.9257**	2.0438
B I B	6.0459**	3.3935**	9.6177**	0.2774
Wt	7.7744**	4.3188**	46.0932**	0.3535

* $P < .05$

** $P < .01$

TABLE 15 : D^2 MATRIX BASED ON ANTHROPOMETRICS IN GONDS (MALES)

	KOLAM	KOYA	MANNE	PLAINS MARIA GOND	RAJ GOND
Kolam	X				
Koya	2.5188	X			
Manne	1.5878	0.3756	X		
Plains Maria Gond	3.0084	1.5379	1.3564	X	
Raj Gond	1.4313	1.3700	1.2776	2.7960	X

TABLE 16 : D^2 MATRIX BASED ON ANTHROPOMETRICS IN GONDS (FEMALES)

	KOLAM	KOYA	MANNE	PLAINS MARIA GOND	RAJ GOND
Kolam	X				
Koya	1.3831	X			
Manne	0.3991	1.5306	X		
Plains Maria Gond	1.5741	1.3567	1.5132	X	
Raj Gond	1.2069	2,2051	2.2286	2.3750	X

LE 17 : X^2 VALUES : HOMOGENEITY OF D^2 VALUES IN MALES

	Kolam (50)	Koya (51)	Manne (54)	Plains Maria Gonds (54)	Raj Gond (54)
	0.00				
	63.59	0.00			
[illegible]	41.22	22.96	0.00		
[illegible]	78.10	40.34	36.62	0.00	
Gond	37.16	35.93	34.49	75.49	0.00

TABLE 18 : X^2 VALUES : HOMOGENEITY OF D^2 VALUES IN FEMALES

	Kolam (50)	Koya (50)	Manne (47)	Plain Maria Gond (45)	Raj Gond (37)
	0.00				
	47.08	0.00			
	21.78	39.50	0.00		
aria	37.38	32.13	34.78	0.00	
	25.66	46.89	46.14	48.22	0.00

Univariate analysis of anthropometric data: Analysis of variance was carried out on each of the 11 measurements between female groups and male groups and for sexual dimorphism (Table-14). The F values were high for 8 of the 11 measurements showing significant differences between the five tribal groups, both for the females as well as for the males. There was also a significant difference between sexes within each tribal group for each of the 11 measurements. Except for the head breadth, which showed a significant difference in sex dimorphism, all other measurements showed no difference in sexual dimorphism between the five tribal groups (Table 14).

.5 Multivariate analysis of Anthropometric data

1 Tests and cluster analysis based on Mahalanobis's D^2 values

D^2 values were calculated as given in Chapter 5 for males (Table 15) and female tribals (Table 16) based on 10 measurements (excluding weight which is environmentally influenced). χ^2 tests for homogeneity within males and females for D^2 values are given in Tables 17 and 18.

$$\chi^2 = \frac{n_1 n_2}{n_1 + n_2} D^2_{12}$$

Degrees of freedom = no. of variables (10)

D^2 values were significantly different in both female as well as male tribal groups. In the males the Raj Gonds and Kolams are significantly different from the Plains Maria Gonds showing that they lie furtherest away from each other. This test indicates that morphologically both female and male tribal groups are heterogeneous within themselves indicating that each of the five tribal groups forms a separate endogamous group.

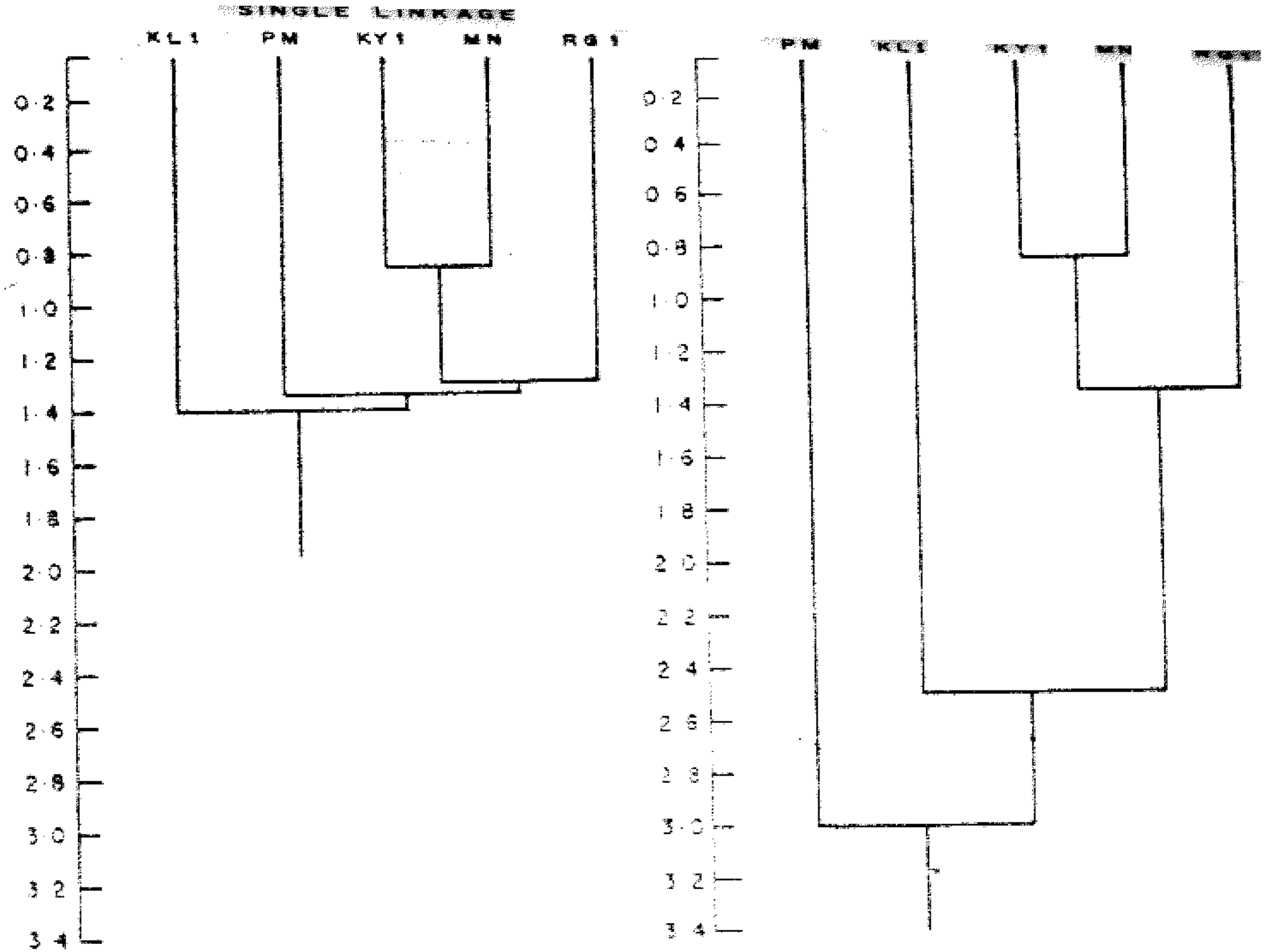
A multivariate test using Wilk's λ for the hypothesis that the means values of all the characters are the same in the male and female groups showed significance corroborating the evidence supplied by univariate analysis.

2 Cluster Analysis

Two types of hierarchial clustering methods, the single linkage or connectedness method and complete linkage or diameter method were followed based on the D^2 matrix of the males and female tribals. The clustering programme used was according to Hclust programme written by Stephen, C Johnson of the Bell Telephone Laboratory, Murray Hill, New Jersey (detail in Chapter 5). The two clustering techniqu

FIGURE 2

D^2 among Gond males (cluster analysis)



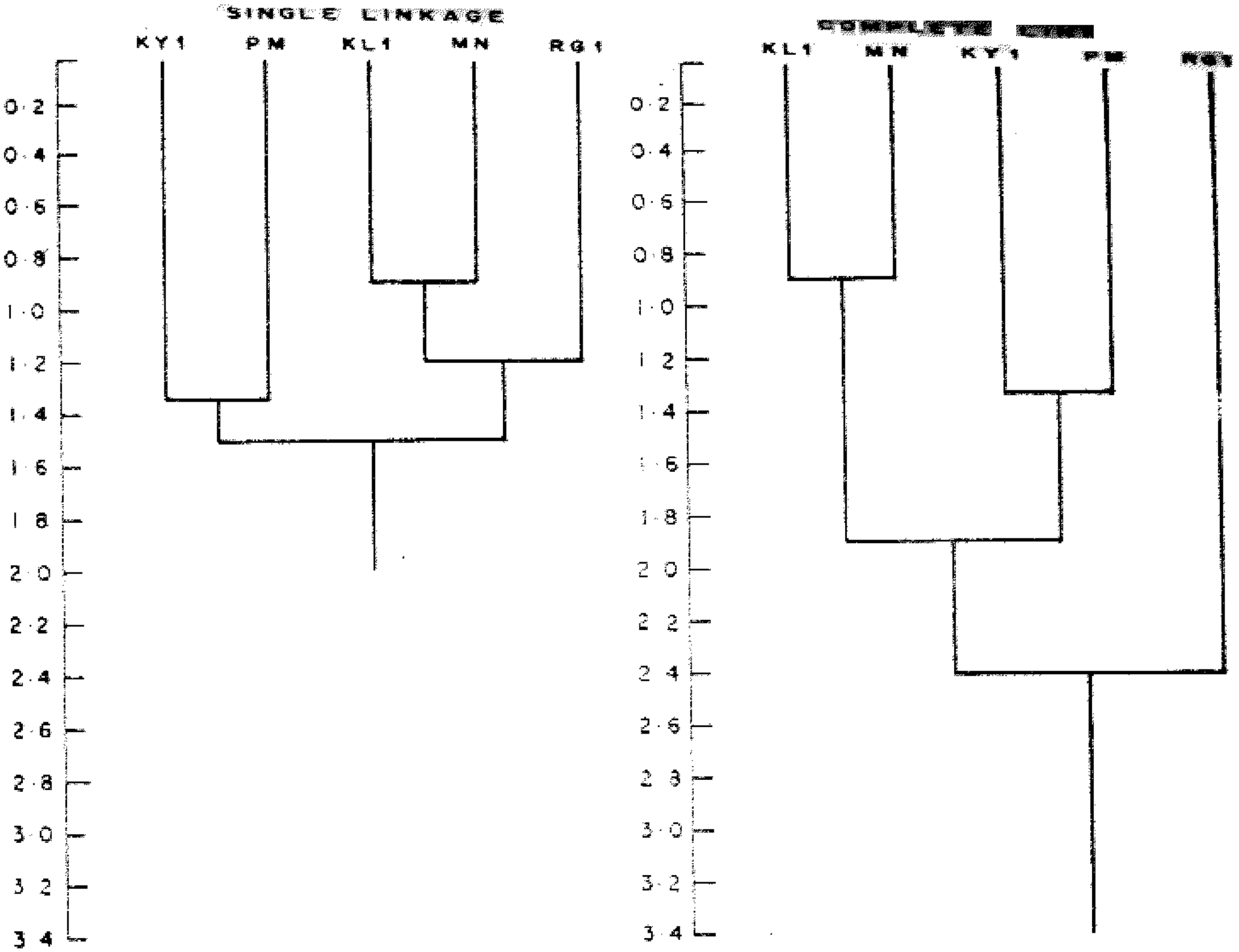
SINGLE LINKAGE

D^2 AMONG GOND MALES (CLUSTER ANALYSIS)

FIG-2.

FIGURE 3

D^2 among Gond females (cluster analysis)



D^2 AMONG FEMALE GONDS (CLUSTER ANALYSIS)

FIG-3.

showed a near correspondence in relationship for both males and females (Figs. 2 and 3). However, the relationship between males and females did not show close correspondence or consistency when either of the clustering techniques were followed. In the males by complete linkage method, the Koyas cluster with Manne and Raj Gonds, the Kolams and plains Maria Gonds joining separately in that order. However, in the females

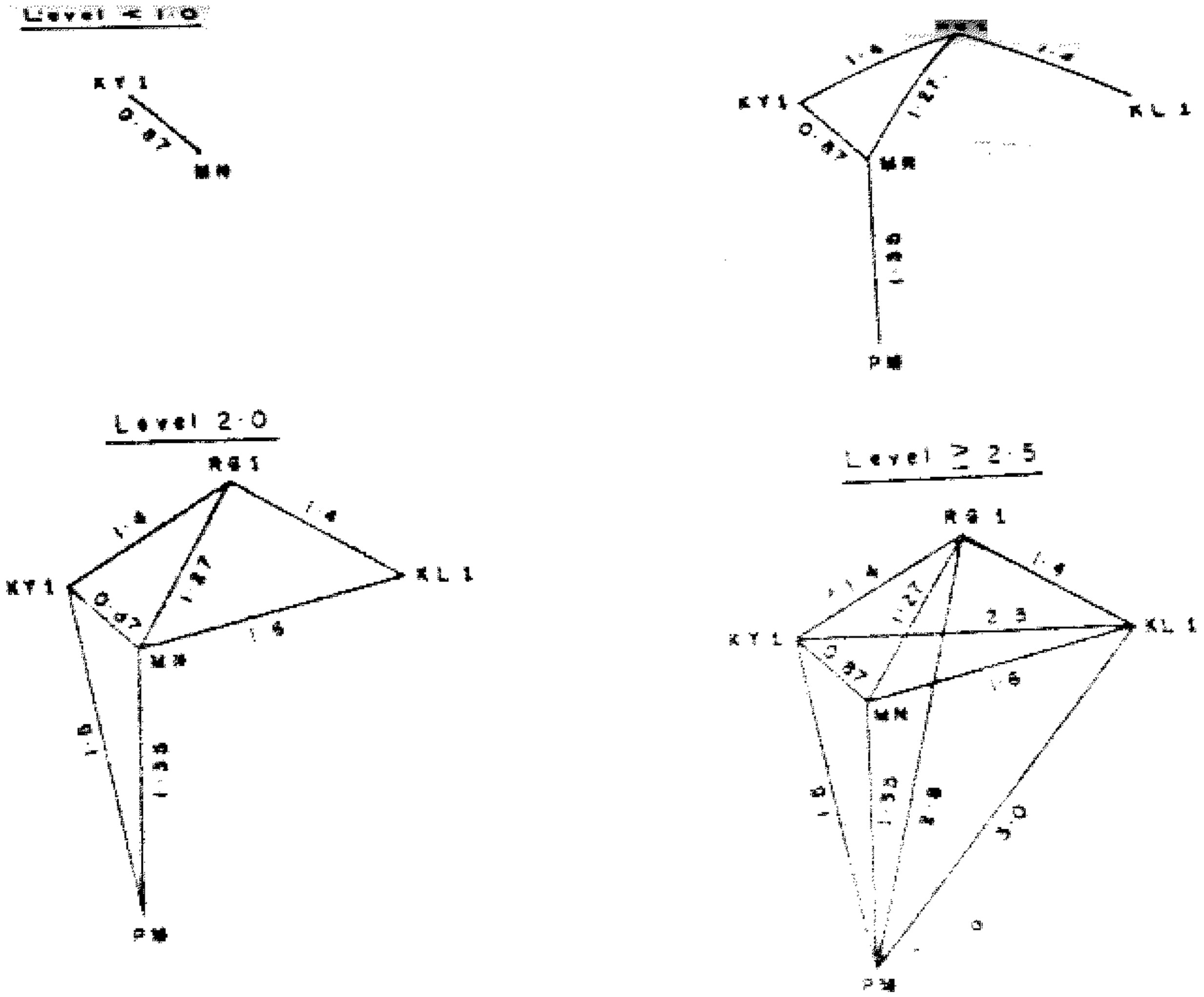
by the same clustering method two clusters are formed, one consisting of Kolams and Manne and the other of Koyas with Plain Maria Gonds. After these two clusters join each other, the Raj Gonds join separately.

3 Complete subgraphs

Subgraphs at various levels of clustering based on complete linkage method were drawn for both males and females separately (Figs. 4 and 5). These help in showing the spatial distribution of these groups. The graphs for males and females generally corresponded with each other with some differences. In the males the Manne (MN) and Koyas (KY 1) get connected first and then the Raj Gonds (RG 1) join with these two to form a sub-graph. Kolams (KL 1) connecting with RG 1 at one extremity and Plains Maria Gonds (PM) join with MN at the opposite

FIGURE 4

D^2 among Gond males (complete subgraph)

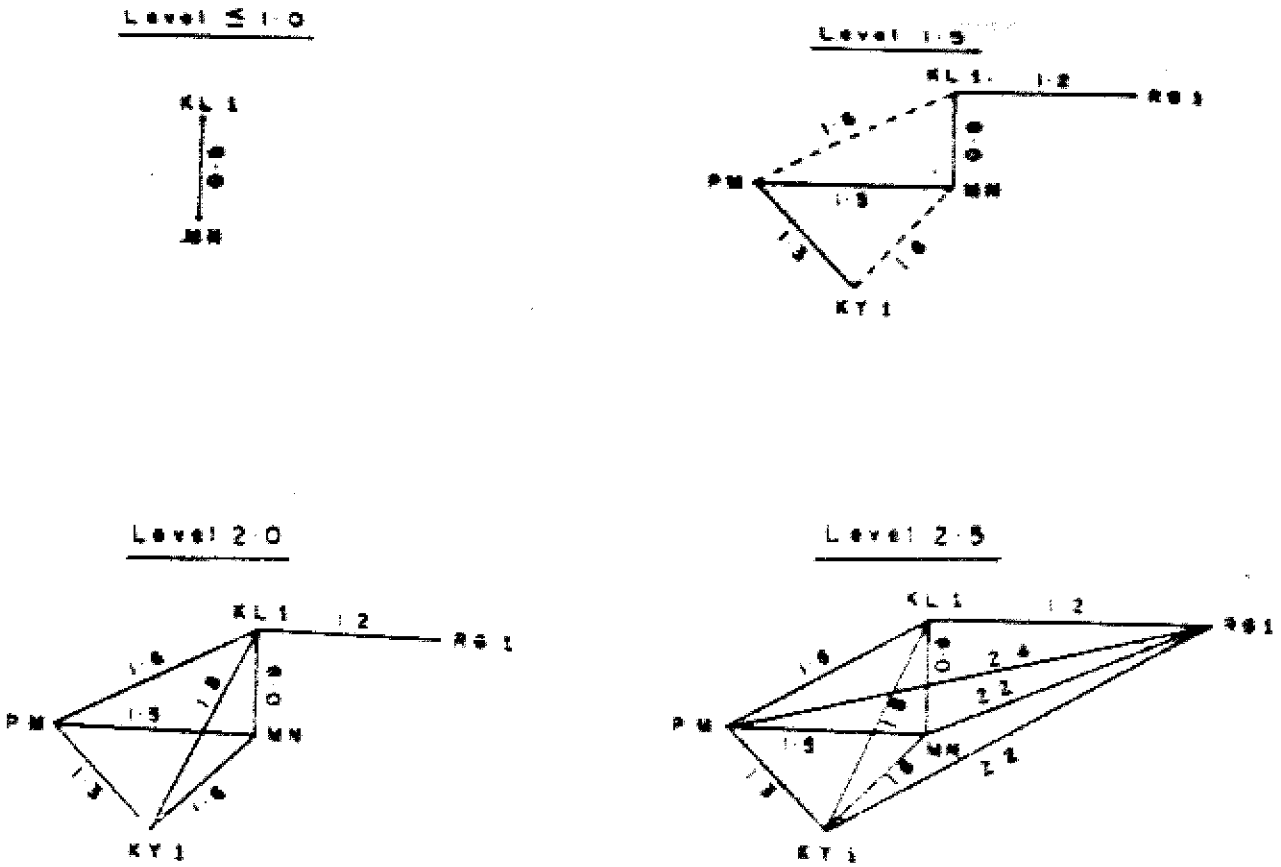

Level < 1.0
KY1
0.87
MN
1.6
1.4
1.27
KY1
KL1
0.87
MN
1.35
PM
Level 2.0
RG1
1.6
1.4
1.27
KY1
KL1
0.87
1.6
MN
1.5
1.35
PM
Level ≥ 2.5
RG1
1.6
1.4
1.27
2.5
KY1
KL1
0.87
1.6
MN
1.5
1.35
2.8
3.0
PM

D^2 AMONG MALE GONDS (COMPLETE SUBGRAPHS)

FIG - 4.

FIGURE 5

D^2 among Gond females (complete subgraph)



Level ≤ 1·0
KL 1
0·8
MN
Level 1·5
KL 1
1·2
RG 1
1·6
0·8
PM
1·5
MN
1·3
1·6
KY 1
Level 2·0
KL 1
1·2
RG 1
1·6
1·8
0·8
PM
1·5
MN
1·3
1·6
KY 1
Level 2·5
KL 1
1·2
RG 1
1·6
0·8
2·4
2·2
1·8
PM
1·5
MN
1·3
1·6
2·1
KY 1

D^2 AMONG FEMALE GONDS (COMPLETE SUBGRAPH)

FIG-5

extremity. The Manne lie intermediate forming the connecting link with other groups. In the females however, KL 1 connects with MN instead of with RG 1. RG 1 joins MN at one extremity and TM and KY 1 connecting with MN at the opposite extremity. Here again, the Manne form a connecting link between the four groups. When complete sub-graphs of both males and females are observed, there is a general correspondence to the present geographical distribution of the groups. The Manne lie intermediate, connecting the Kolams and Raj Gonds with Koyas and plains Maria Gonds. The position of Koyas, however, is different in the two sexes shifting nearer to Manne in the males and away from Manne towards plains Maria Gonds in the females (Figs. 4 and 5).

.3 Analysis of Genetic Data

.3.1 Gene frequency and applications of tests of homogeneity and consistency

1 Blood groups :

a) A B O System : The gene frequency was estimated by maximum likelihood method as given by Rao (1965) (Appendix-I). The test for departure from Hardy-Weinberg and test

TABLE 19

O, A, B BLOOD GROUPS: OBSERVED FREQUENCIES,
M.L. ESTIMATES AND CONSISTENCY AND HETEROGENEITY TESTS

HILL MARIA

CLASS	PROB.	OBS.	E1	E2
A	.279	16	13.68	14.23
B	.322	21	18.77	16.44
O	.294	10	11.79	15.02
AB	.104	4	6.76	5.31
TOTAL		51	x^2= 2.05	

DF=1

KOLAMS

CLASS	PROB.	OBS.	E1	E2
A	.279	17	19.97	[illegible]
B	.322	44	46.69	[illegible]
O	.294	25	22.77	[illegible]
AB	.104	16	12.58	[illegible]
TOTAL		102	x^2= 1.74	

DF=1

KOYA

CLASS	PROB.	OBS.	E1	E2
A	.279	56	57.58	47.14
B	.322	59	42.72	54.49
O	.294	37	55.57	49.76
AB	.104	17	13.03	17.61
TOTAL		169	x^2= 0.41	

DF=1

MANNE

CLASS	PROB.	OBS.	E1	E2
A	.279	32	29.11	[illegible]
B	.322	36	33.16	[illegible]
O	.294	30	32.39	[illegible]
AB	.104	7	10.35	[illegible]
TOTAL		105	x^2= 1.79	

DF=1

PLAINS MARIA GONDS

CLASS	PROB.	OBS.	E1	E2
A	.279	28	29.21	28.73
B	.322	26	27.21	33.21
O	.294	40	38.96	30.32
AB	.104	9	7.63	13.73
TOTAL		103	x^2= 0.38	

DF=1

RAJGONDS

CLASS	PROB.	OBS.	E1	
A	.279	24	23.98	[illegible]
B	.322	34	33.38	[illegible]
O	.294	21	21.02	[illegible]
AB	.104	12	12.72	[illegible]
TOTAL		91	x^2= 0.00	

DF=1

TABLE 20 Gene Frequencies for Biochemical Markers In the Tribal Populations

	Hill Maria Gond	Kolams	Koyas	Manne	Plains Maria Gond	Rajgond
ABO						
A	0.2259	0.1748	0.2452	0.2099	0.1985	0.2226
B	0.2932	0.3527	0.1814	0.2347	0.1865	0.2968
O	0.4809	0.4725	0.5734	0.5554	0.6150	0.4806
Rh						
D	1.0000	0.7575	0.9231	0.8620	0.8606	0.7211
d	0.0000	0.2425	0.0769	0.1380	0.1393	0.2789
MN						
M	0.7549	0.7857	0.8211	0.8812	0.8981	0.8187
N	0.2451	0.2143	0.1789	0.1188	0.1091	0.181
Hb						
A	0.9216	0.9648	0.9671	0.9870	0.9191	0.9286
S	0.0784	0.0352	0.0329	0.0130	0.0808	0.0714
Hp						
Hp1	0.1341	0.0730	0.0645	0.0573	0.0937	0.0909
Hp2	0.8609	0.9270	0.9355	0.9427	0.9063	0.9091
Transferrin						
C	1.0000	0.9597	0.9895	0.9789	0.9907	0.9720
D	0.0000	0.0403	0.0105	0.0211	0.0093	0.0280
G6PD						
Deficient	0.1567	0.0000	0.0076	0.0000	0.0619	0.0659

of heterogeneity were also carried out according to Rao (1965) in Appendix II. The results show (Table 19) that there is no significant departure from Hardy-Weinberg equilibrium in the six groups. The six tribal groups are significantly different from each other in the A B O gene frequency distribution.

The B gene frequency (Table 20) is highest in Kolams, Raj Gonds, Hill Maria Gonds and Manne.

b) Rh (D) blood group system :

The Rh gene frequency was calculated according to the method given in Appendix III. The Rh negative allele is highest in Raj Gonds and Kolams (Tables 20 and 21) and lowest in Koyas with complete absence of the gene in Hill Maria Gonds. χ^2 test for heterogeneity could not be carried out in this case because of the small frequency and absence of Rh negative allele in some of the groups as this would bias the χ^2 estimate.

c) MN Blood Group System :

The gene frequency was estimated by gene counting method since the heterozygote can be identified by immunological tests. The test for consistency and homogeneity was carried out according to Rao, (1965) in Appendix II. There is a significant departure from Hardy-Weinberg equilibrium in the case of Hill Maria Gonds and the Plains Maria Gonds (Table 22). The rest of the groups are

Table 21

Frequency Distribution of Rh Types

Rh Types	Hill Maria Gond	Kolam	Koya	Manne	Plains Maria Gond	Rajgond
D	51	96	168	103	101	83
d	0	6	1	2	2	7
Total	51	102	169	105	103	90

Table 22

MN Blood Groups

Estimation of Gene Frequencies and Tests of Consistency (Hardy-Weinberg) and Homogenity

Pheno-Types	Hill Marias			Kolams			Koyas			Manne			Plains Maria Gond			Raj Gond			Total
	Obs. No.	E_1	E_2	Obs. No.	E_1	E_2	Obs. No.	E_1	E_2	Obs. No.	E_1	E_2	Obs. No.	E_1	E_2	Obs. No.	E_1	E_2	Obs. No.
M	27	23.365	28.490	62	60.498	68.399	75	73.488	75.743	80	78.428	70.134	76	75.012	64.625	61	60.994	63.235	**391**
MN	23	15.172	11.374	30	33.002	27.287	29	32.023	30.239	18	21.147	28.020	13	17.002	25.800	27	27.014	25.245	**140**
N	1	2.463	1.135	6	4.501	2.713	5	3.488	3.018	3	1.425	2.796	4	0.966	2.575	3	2.991	2.520	**22**
	41	$x^2 = 5.4733^*$ D.F. = 1		98	$x^2 = 0.8095$ D.F. = 1		109	$x^2 = 0.9713$ D.F. = 1		101	$x^2 = 2.2406$ D.F. = 1		93	$x^2 = 12.137^{**}$ D.F. = 1		91	$x^2 = 0.00003$ D.F. = 1		553
m:		0.7549			0.7857			0.8211			0.8812			0.8981			0.8187		**0.8336**
n:		0.2451			0.2143			0.1789			0.1188			0.1019			0.1813		**0.1664**

$$\text{Homogenity } (X^2) = \Sigma \frac{(E_2 - E_1)^2}{E_2} = 13.5693^*$$

D.F. = 5

consistent with Hardy-Weinberg's equilibrium. All six groups show heterogeneity between each other ($P < 0.05$ level). The N gene frequency is lowest in the Manne and Plains Maria Gonds (Table 20).

2 Haemoglobin System :

χ^2 test for homogeneity showed significant heterogeneity between the six tribal groups at $P < 0.05$ level (Table 23). The haemoglobin S gene frequency was highest in Plains Maria Gonds, hill Maria Gonds and Raj Gonds (Table 20). This frequency is directly related to the high incidence of Falciparum malaria in the areas in which these groups are residing. The lower haemoglobin S gene frequency among the Manne and Koyas is also directly correlated with the low incidence of malaria in the area in which both these groups are residing.

3 G 6 P D System

The screening for G 6 P D enzyme deficiency was analysed only on male blood samples. This being a linked gene, the proportion of the deficient gene in the males was the actual gene frequency of the abnormal gene. The χ^2 test for homogenity (Table 24) showed significant heterogeneity between these tribal groups ($P < 0.05$). The deficient gene is absent in Kolams and Manne (Table 20) and since

Table 23

Test of Homogenity for Haemaglobin Types

Haemoglobin Types	Hill Maria Gonds	Kolams	Koyas	Manne	Plains Maria Gonds	Rajgonds	Total
AA	43 (46.1)	132 (128.5)	213 (206;3)	151 (140.2)	140 (151.1)	120 (126.7)	799
AS	8 (4.8)	10 (13.5)	15 (21.7)	4 (14.7)	27 (15.9)	20 (13.3)	84
Total	51	142	228	155	167	140	883

$$\text{Homogenity } (X^2) = \frac{\Sigma\,(O-E)^2}{E} = 26.538^*$$

(D.F. = 5)

Table 24

Homogenity Test for G6PD Types

Types	Hill Marias	Koyas	Plains Maria Gonds	Rajgonds	Total
Normal	45 (49.3)	125 (119.6)	106 (103.2)	92 (95.9)	368
Deficient	9 (4.7)	6 (11.4)	7 (9.8)	13 (9.1)	35
Total	54	131	113	105	403

Homogenity $(\chi^2) = \frac{\sum (O-E)^2}{E} = 10.133^*$

(D.F. = 3)

FIGURE 14

D^2 on Anthropometric measurements (all tribal populations): cluster analysis:single linkage method the sample is small and the frequency of G 6 P D is small, the probability of detection is small. It is difficult to decide without a larger study. However, this is a plausible hypothesis that the absence of G 6 P D deficiency in these two areas probably indicates a common origin as postulated by Haimendorf, 1979. It is also possible that these two groups lived under similar habitat on hill tops, practising shifting agriculture some 50 years ago, where the absence of wells and the long distance of alternate water supply (such as streams) prevented the population from exposure to mosquitos biting since the mosquito breeding sites were far away thus lessening exposure to malarial infection. However, this is only a speculation and evidence of low malarial infection among these populations would confirm the reason for the absence of G 6 P D deficiency and also a lower haemoglobin S frequency. The highest G 6 P D deficiency is found among the Hill Maria Gonds, the Raj Gonds and Plains Maria Gonds. These three groups also have a high haemoglobin S gene frequency which is consistent with the fact that these groups were and are in areas hyperendemic for Falciparum malarial infection.

TABLE 25

HAPTOGLOBIN TYPES

ESTIMATION OF GENE FREQUENCIES AND TESTS OF HOMOGENITY

PHENOTYPES	HILL MARIAS	KOLAM	KOYA	MANNE	PLAINS MARIA GONDS	RAJGOND	TOTAL
2 - 1	11 (6.71)	13 (14.56)	20 (25.37)	15 (16.04)	18 (15.71)	14 (12.60)	91
2 - 2	30 (34.29)	76 (74.43)	135 (129.63)	83 (81.96)	78 (80.29)	63 (64.39)	465
TOTAL	41	89	155	98	96	77	556

HOMOGENITY $(X^2) = \Sigma \frac{(O-E)^2}{E} = 5.5006$

(D.F = 5)

Haptoglobin System

The gene frequency was calculated by gene counting method because the heterozygote could be identified by electrophoresis. The χ^2 test for homogeneity shows that the six groups are homogeneous for this protein (Table 25). The haptoglobin 1 gene frequency is low in these populations ranging from 0.06 - 0.13 comparable to most Indian populations where it is very low. (Table 20).

5 Transferrin System

Gene frequency was calculated by gene counting. The χ^2 test showed significant heterogeneity between all the six groups (Table 26) at $P < 0.05$ level. The highest gene frequency of the slow variant gene which is rare in other populations in India is present in Kolams, Manne, Raj Gonds and Koyas (Table 20). However, in the Plains Maria Gonds and Hill Maria Gonds the D gene is low or absent. This is an interesting finding as it differentiates these two groups from the rest of the other Gondi-speaking groups. Another Dravidian-speaking group, the Oraons have also been found to have a high D gene frequency (Kirk Lai, Vyas and Vidyarthi, 1962; Mukherjee, Das and Sharma, 1975). This group now reside amidst the Munda-speaking group living in Orissa and Chota Nagpur areas of India. Hence, this D gene

Table 26

Homogenity Test for Transferrin Types

Types	Kolams	Kovas	Manne	Plains Maria Gond	Rajgond	Total
Normal	137 (142.7)	187 (182.9)	136 (136.0)	159 (155.2)	135 (137.0)	754
Variant	12 (6.2)	4 (8.0)	6 (5.9)	3 (6.8)	8 (5.9)	33
Total	149	191	142	162	143	787

Homogenity $(X^2) = \frac{\Sigma (O-E)^2}{E} = 10.588^*$

(D.F. = 4)

prove to be a useful marker in differentiating the vidian-speaking Central Indian tribal group from the nda-speaking tribes as well as from the South Indian ibal group where the frequency of D gene is found to e very low (Kirk, Lai, Vyas, Vickrama Singhe and Pereira).

lti-variate Analysis

ei's and Sanghvi's distance measures were computed based gene frequencies of 7 biochemical characters (Tables 27 nd 28). Methods of computation are given in Chapter 5.

1. Cluster Analysis

Single linkage and complete linkage clustering was done on both Nei's and Sanghvi's distance matrices. Both these clustering techniques based on two different distance matrices showed close correspondence in the relationship between the five tribal groups (Figs 6 and 7). The Raj Gonds and Kolams cluster together whereas the other three, the Plain Maria Gonds, Manne and Koya form a separate cluster.

2. Sub-graphs

Complete sub-graphs were projected at different clusterin levels with Nei's and Sanghvi's distance matrices based on the complete linkage method. The sub-graphs based on both these measures showed a close correspondence in the relationship and spatial distribution of the five groups. The Manne are an intermediate group connecting the Koyas and Plains Maria Gonds with Kolams and Raj Gonds (Figs. 8 and 9). The Manne being closer to Koyas and Plains Maria Gonds than to Kolams and Raj Gonds.

Degree of Correspondence of Anthropometric with Genetic Relationship

Though the clustering based on both morphological as well as genetic relationship show a spatial distribution corresponding generally to the present geographical distribution of these groups, the actual relationship between each of the Gond populations show differences when based on these different biological variables.

TABLE 27 : NEI'S GENETIC DISTANCE IN GONDS

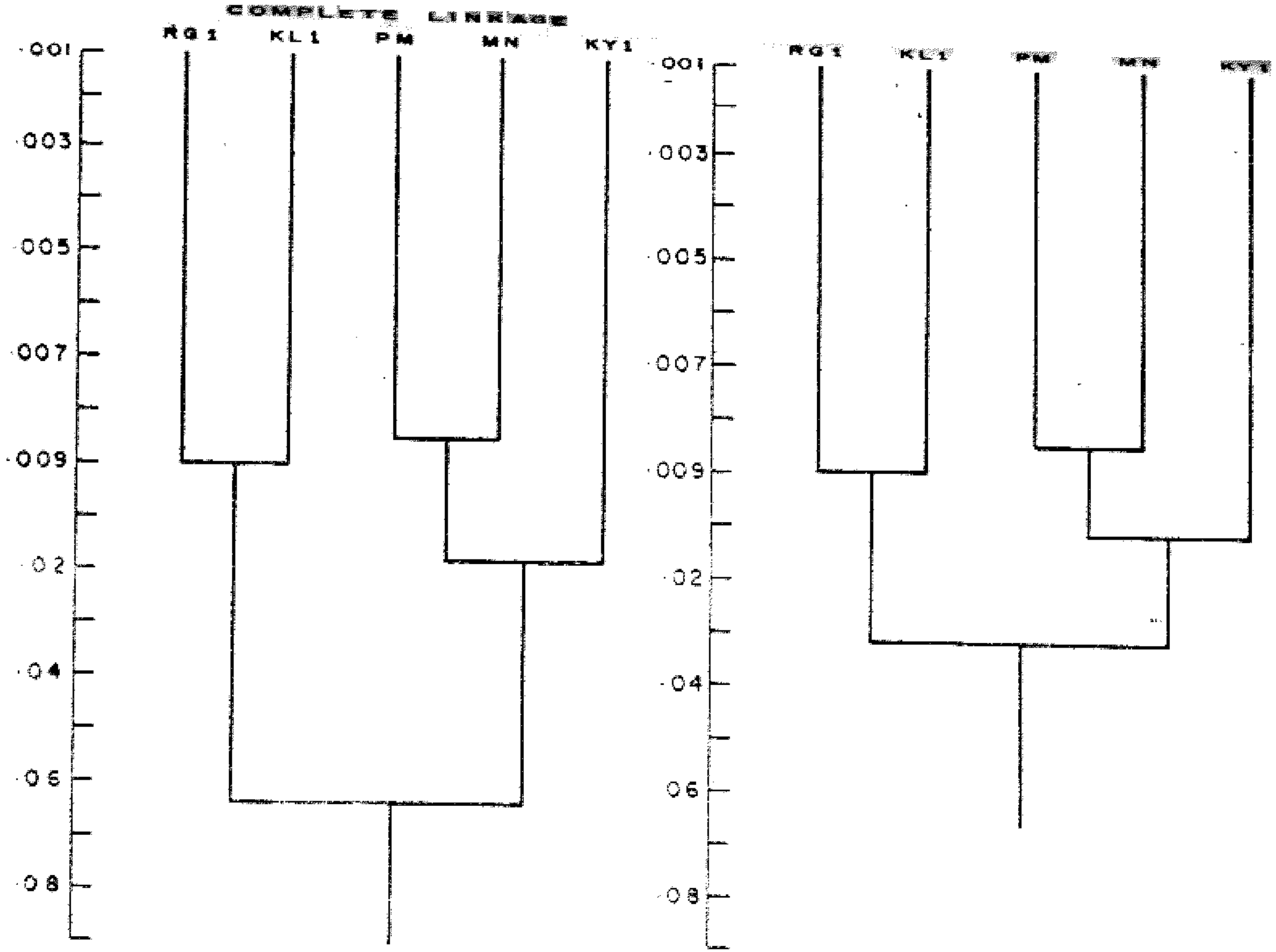
	KOLAM	KOYA	MANNE	PLAINS MARIA GOND	RAJ GOND
Kolam	X				
Koya	0 0641	X			
Manne	0.0365	0.0119	X		
Plains Maria Gond	0.0548	0.0182	0.0088	X	
Raj Gond	0.0095	0.0604	0.0325	0.0368	X

TABLE 28 : SANGHVI'S GENETIC DISTANCE IN GONDS

	KOLAM	KOYA	MANNE	PLAINS MARIA GOND	RAJGOND
Kolam	X				
Koya	0.5375	X			
Manne	0.2837	0.0956	X		
Plains Maria Gond	0.4559	0.1877	0.1457	X	
Raj Gond	0.0886	0.6238	0.3536	0.3537	X

FIGURE 6

Nei's Genetic Distance among Gonds (cluster analysis)

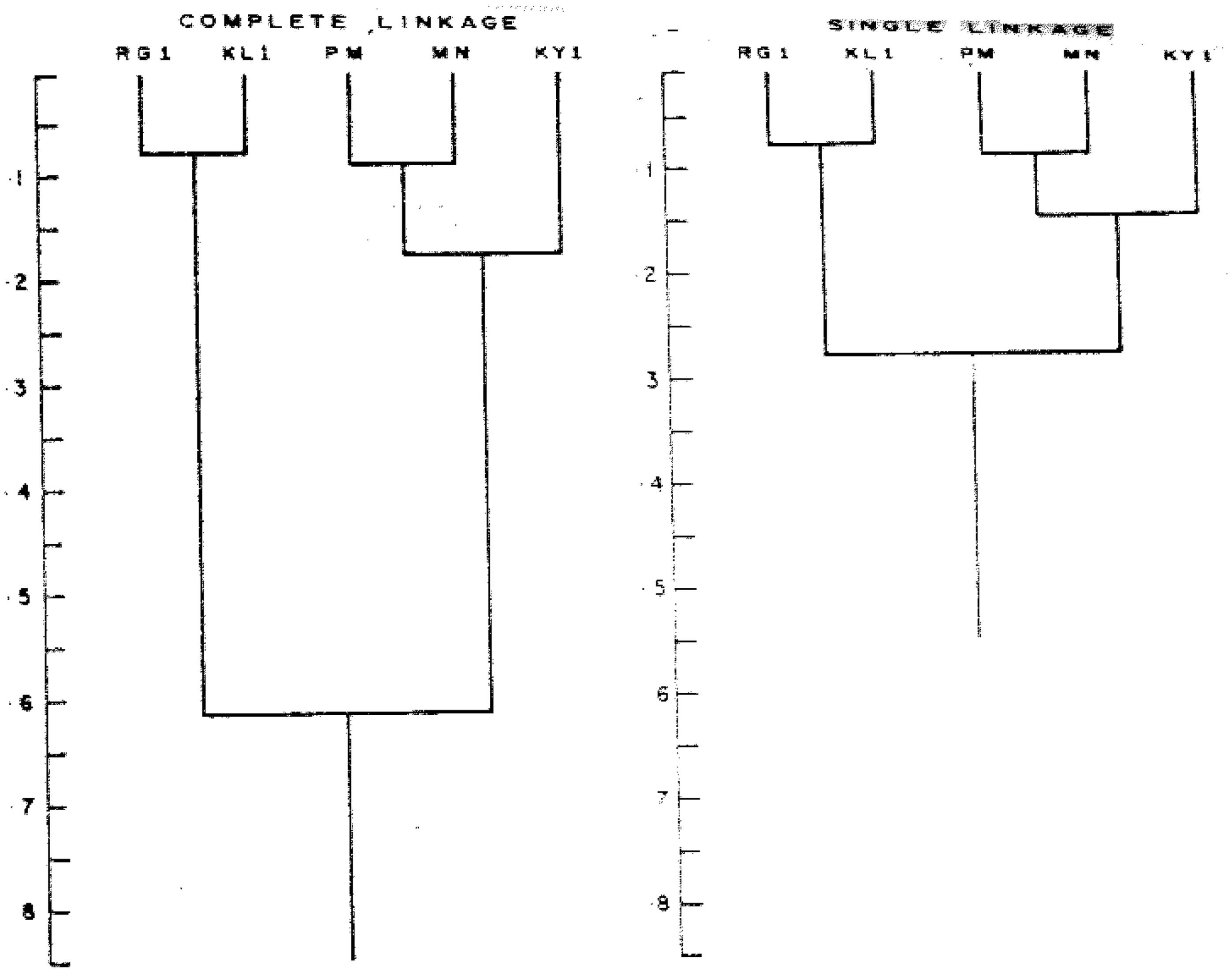


NEI'S GENETIC DISTANCE AMONG GONDS (CLUSTER ANALYSIS)

FIG-6.

FIGURE 7

Sanghvi's Genetic Distance among Gonds(Cluster analysis)



SANGHVI'S GENETIC DISTANCE AMONG GONDS (CLUSTER ANALYSIS)

FIG - 7.

FIGURE 8

Nei's Genetic Distance among Gonds(complete subgraph)

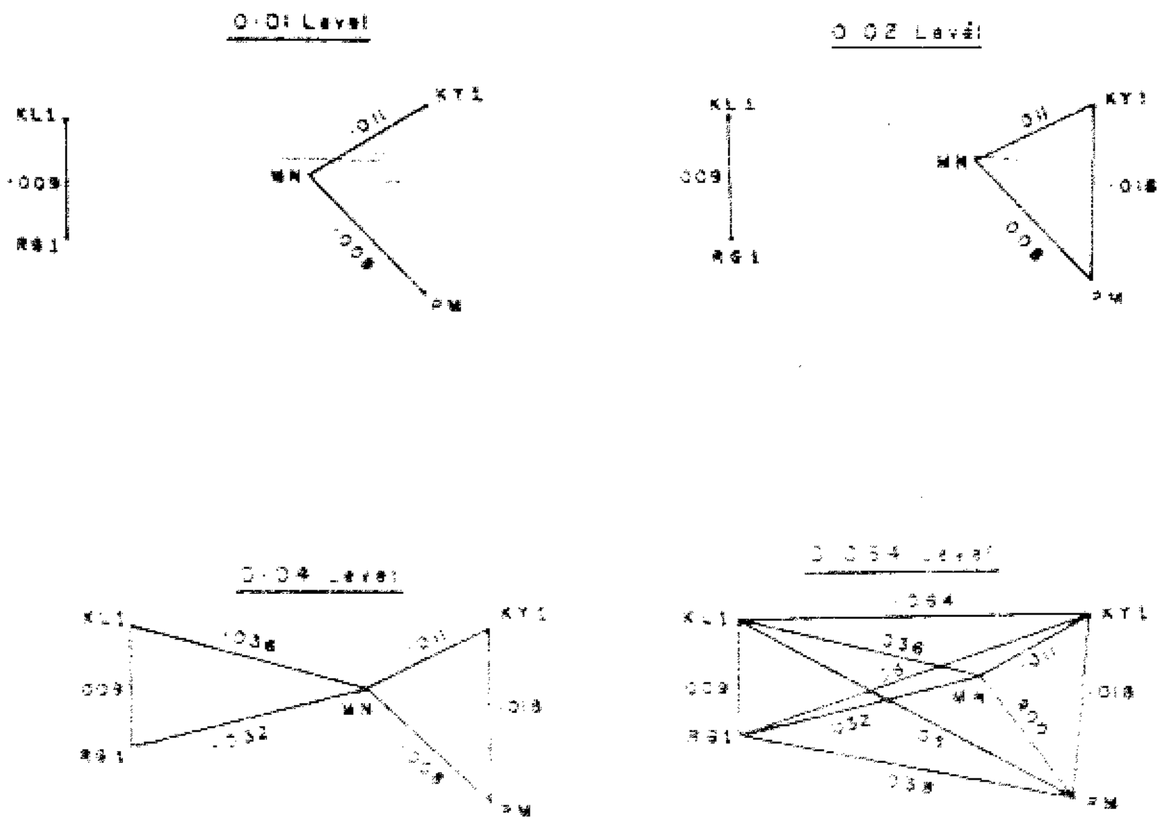
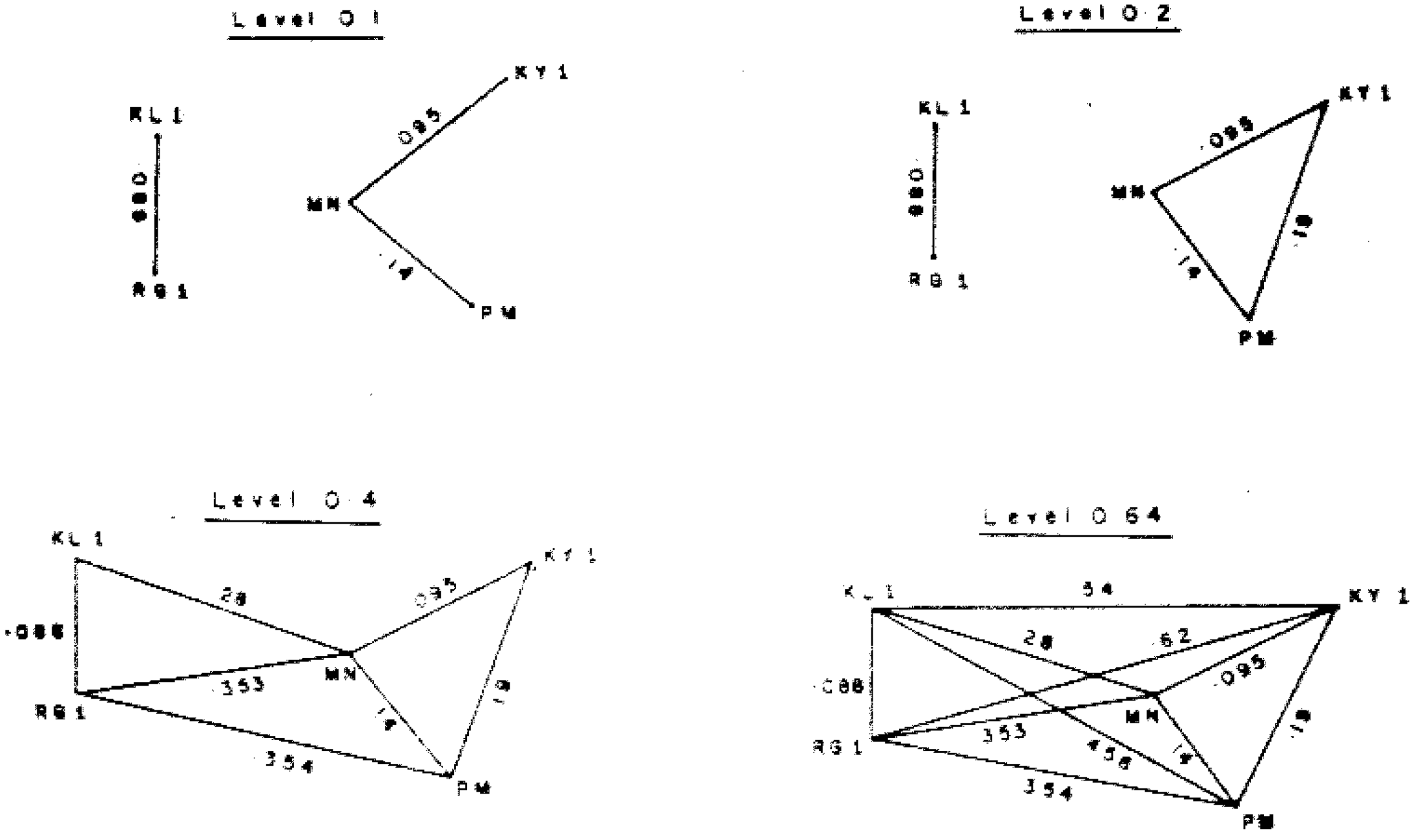

0·01 Level
KL1
·009
RG1
MN
·011
KY1
·008
PM
0·02 Level
KL1
·009
RG1
MN
·011
KY1
·018
·008
PM
0·04 Level
KL1
·036
·009
RG1
·032
MN
·011
KY1
·018
·008
PM
0·054 Level
KL1
·054
KY1
·036
·009
·011
MN
·018
·032
·008
RG1
·038
PM

FIG-8. NEI'S GENETIC DISTANCE AMONG GONDS (COMPLETE SUBGRAPHS)

FIGURE 9

Sanghvi's Genetic Distance among Gonds(complete subgraph)


Level 0.1
KL 1
RG 1
.088
MN
KY 1
PM
.095
.14
Level 0.2
KL 1
RG 1
.088
MN
KY 1
PM
.095
.14
.19
Level 0.4
KL 1
KY 1
MN
RG 1
PM
.088
.28
.095
.353
.14
.19
.354
Level 0.64
KL 1
KY 1
MN
RG 1
PM
.54
.088
.28
.62
.095
.353
.456
.14
.19
.354

SANGHVI'S GENETIC DISTANCE AMONG GONDS (COMPLETE SUBGRAPH)

FIG - 9.

The morphological relationship shows a greater variability, the clustering pattern differing between male and female Gond populations. Generally the spatial distribution of the tribes corresponds in both sexes, the Manne forming the intermediate link with Raj Gonds and Kolams lying on its west and the Koyas and Plain Maria Gonds lying on its east. However ,the relative position of the some of the groups shifts significantly in both sexes. The Koyas move nearer the Manne and Raj Gonds and away from the plains Maria Gonds in the males but shift closer to the plains Maria Gonds and away from the rest in the females. The Kolams too show a variability in their position between sexes being far removed from all the groups in the males but moving very close to the Manne in the females. This variability between sexes in the relationship between these five populations is difficult to interpret and may in part be due to differences in sex dimorphism as well as environmental influence on morphological characters.

The genetic relationship between these groups however shows a clustering corresponding closely to the degree of geographical contiguity. Since there were not enough samples to study the male and females separately the combined sample was used for the analysis. The Raj Gonds and Kolams cluster closely with Manne, Koyas and Plains Maria Gonds forming a second cluster. The Manne form an intermediate link between the Raj Gonds and Kolams lying on their west and Koyas and Plains Maria Gonds on their east. The Raj Gonds and Kolams though occupying each a distinct geomorphological area (Fig. 1) live in close proximity on high lands which are covered with volcanic trap material (the black cotton soil) which is contiguous with Marathwada area. These hills rise up on the west of Asifabad taluka and occupy almost the whole of Utnoor taluka of Adilabad district and form the area of distribution of Raj Gonds and Kolams. This area being contiguous with Marathwada is also influenced by Marathi culture.

The eastern part of Asifabad taluka (east of railway track going to Baladshah) becomes less hilly and dips down into the Pranitha-Godavari valley, the area of Mannes and Koyas. The region is dominated by Telugu-speaking plains people and their culture, as a result of which the Koyas and Manne have forgotten their mother tongue and speak mostly Telugu. The valley is contiguous with Indravathi river basin (extending into Chanda District and Bastar District in Madhya Pradesh) further east and is the area of the Maria Gonds. The Maria Gonds in the south-west of Sironcha taluka, Chanda district are in contact with Koyas. However, the Maria Gonds being isolated have retained their own culture and language. The

Manne stop short on the west in Asifabad taluka where the hills rise up and are in contact with the Kolams. Both these groups are located each to a different geo-morphological territories suitable for shifting cultivation.

The genetic characters unlike morphology are purely heritable and not influenced by environment and hence perhaps reflect more closely the effect of geographical proximity in producing a greater genetic similarity within these two clusters of Gond populations. Geographical proximity between populations is produced by a closer distance as well as similar geographical factors (such as soil, terrain, flora etc) which has brought these populations in close contiguity with each other under a common eco-cultural zone of influence. The greater the geographical proximity between populations the closer the genetic as well as morphological similarity between them. This is more so in populations such as these who due to having adopted a settled agricultural occupation are less mobile. This low mobility in turn produces a smaller marriage distance (distance between place of birth of spouses) thus restricting the spatial distribution of genes to a small area.

In conclusion, all these five Gond populations have been found to be heterogenous both in morphology and genetic characters and this is further substantiated by evidence of linguistic and cultural differences among them (Haimendorf, 1979). However, relatively speaking the Kolams and Raj Gonds are closer to each other genetically whereas the Manne, Koyas and Maria Gonds together form another cluster and this relationship closely corresponds to the degree of geographical contiguity between them.

CHAPTER 4 : CONSANGUINITY AND MARRIAGE DISTANCE PATTERN AMONG THE GONDS

ntroduction

ta on frequency of consanguinous marriages as well marriage distance was collected on the same individuals whom blood samples and physical measurements were taken. f the spouse was also included in the study, the code umber of the respective spouse was entered on their proforma at the time of the interview. The marriage distance is the distance between the places of birth of spouses and was measured along the travel route and not the map distance. The distances between places was entered after cross checking in the field by verifying with other people who were familiar with that area. The study of marriage distance pattern indicates the movement of husband and wife prior to marriage. This matrimonial migration may be an important component of total migration since occupational mobility in these primitive tribal groups is very low. Hence, this migration distribution may be important in regulating to a large extent the spatial distribution of genes in these groups. The type and degree of consanguinity also plays an important role in the distribution of genes. There is very little data on these parameters in these tribal populations, and it is not clear to what extent geographical and socio-religious factors influence these marriage patterns.

Consanguinity

1) Among the Gonds in the present study

The frequency of consanguinous marriages was high in all the groups ranging from 27'/. to 68'/. (Table 29). The average inbreeding co-efficient α was calculated as follows

$$\alpha = \sum P_i F_i$$

where P_i is the proportion of each type of consanguinous marriage, F_i = the inbreeding co-efficient i.e., the probability that two genes in the offspring are identical by descent from one common ancestor. The average inbreeding co-efficient is highest in Kolams being 0.0426. In the other four groups the inbreeding co-efficient ranges over a narrow interval of 0.017 - 0.022 (Table 29).

The most frequent type of consanguinous marriage was the first cousin marriage of cross cousin type. There was a total absence of parallel first cousin and uncle-niece marriages in these groups. The two types of cross-cousin marriages that occur are matrilateral (mother's brother's daughter) and patrilateral (father's sister's daughter) types in these groups. The matrilateral type is the most frequent in these groups (Table 29).

TABLE 29 : FREQUENCY OF VARIOUS TYPES OF MARRIAGES AND AVERAGE INBREEDING CO-EFFICIENT IN GOND GROUPS

TRIBES	TOTAL MARRIAGES	NOT RELATED (%)	FIRST COUSIN TYPE		TOTAL CONSANGUINOUS MARRIAGES (%)	AVERAGE INBREEDING COEFFICIENT
			MATRILATERIAL CROSS COUSIN MARRIAGES (%)	PATRILATERIAL CROSS COUSIN (%)		
Hill Maria Gond	42	27 (64.28)	15 (100.0)	0 (0)	15 (35.71)	0.0223
Kolam	129	41 (31.78)	85 (96.60)	3 (3.40)	88 (68.22)	0.0426
Koya	180	128 (71.11)	45 (86.54)	7 (13.46)	52 (28.89)	0.0180
Manne	136	97 (71.32)	39 (100.0)	0 (0)	39 (28.68)	0.0179
Plains Maria Gond	116	84 (72.41)	16 (50.0)	16 (50.0)	32 (27.59)	0.0172
Raj Gond	131	92 (70.23)	33 (84.62)	6 (15.38)	39 (29.77)	0.0186

2) Comparison of marriage patterns of Gonds with other neighbouring groups

Among all the States surveyed in India, the co-efficient of inbreeding is found to be highest in Andhra Pradesh. Sanghvi (1966), after surveying 6,945 marriages in 14 districts of Andhra Pradesh found that the highest inbreeding co-efficient in the Hindus was 0.033 while the values for the Muslims and the Christians the value was 0.025 and 0.029 respectively. Of the rural Andhra Pradesh villages, the coastal areas of Vishakapatnam and East Godavari had the highest inbreeding co-efficient due to the prevalence of uncle-niece marriages ranging from 0.045 - 0.48 (Sanghvi 1966). The inbreeding co-efficient in the Gonds are comparable to the non-Hindu groups like the Muslims and the Christians of Andhra Pradesh, though the Muslim and Gond cousin marriages are of different kind. The Muslims favour the marriage of parallel cousins whereas the Gonds strictly forbid the marriage of the children of brothers as these would be of the same clan. The inbreeding co-efficient in the Gonds is lower than the Hindus of Andhra Pradesh. The co-efficient is higher in the south and diminishes as one goes north with Maharashtra as the culture contact between north and the south. A consanguinous regulation has been enforced with great rigidity in the north.

In the south, it had to be relaxed to conform with the prevailing custom of great preference for consanguinous marriages at the time of entry of the Brahmin influence in the first millinium B.C. Baudhyana recorded that cross cousin marriage was a peculiar custom of southerners and as such it was a valid marriage in that part of the country and characteristic feature of the Dravidian people (Kapadia, 1968). In the kinship terminology of all the three main languages of this family, there is a clear indication of cross cousin marriages. This term of marriage is a general feature of the kinship systems of most South Indian populations including the tribal people. The preference of cross cousin marriages in the Gonds is due to the fact that these strengthen the cohesion of the existing kin groups (Haimendorf, 1979). Besides the Gonds, another Central Indian tribe the Bhils also practise cross cousin marriage and Karve's (1957) survey of 1,350 Bhil marriages (of West Khandesh) showed that 59.3°/. of these marriages were consanguinous. The marriages with mother's brother's daughter are more frequent than those with father's sister's daughter with a mean coefficient of inbreeding being 0.025 comparable to Gonds. There is not much data on inbreeding in tribal populations of other States such as Madhya Pradesh and Northern States. The Dhangars are a semi-nomadic tribe of Maharashtra who comprise of 23 endogamous sub-groups and have been surveyed by Malhotra (1976). In a survey of 5,282 marriages among the Dhangars the inbreeding co-efficient (F) for autosomal genes varies between 0.008 - 0.039 with an average of 0.017. These values are lower than southern Dravidian speaking groups or Central Indian Gondi speaking tribal groups. Parallel cousin marriages and uncle-niece marriages were absent among the Dhangars, the most frequent type of marriages being the matrilaterial type of cross cousin marriages. Another tribe the Mathuras, a North Indian nomadic group who has now settled in Adilabad district of Andhra Pradesh have a low inbreeding co-efficient of 0.0047 (Pingle, 1975).

It appears that a tradition of cross-cousin marriage is widely prevalent among the tribal populations of South India as well as Central Indian tribal populations. The North-Eastern tribes like the Nagas (except Angamas), the Bodo groups consisting of Galongs, Daflas and Miris also practice cross cousin marriages. However the Apa Tanis and Khasis do not have the institution of cross-cousin marriages. Marriages with the mother's brother's daughter were the standard type of union between eastern people among whom Pali literature mostly developed (Kapadia, 1968) and occurred for two generations in the princely family of Sakyas.

3 Marriage distance patterns

1) Among the Gonds :

The mean marriage distance was very low in all the six tribal groups ranging from 5.39 - 11 miles indicating a low mobility. The range of mobility varied from a minimum to within village marriages to a maximum value ranging from 27 - 100 miles (Table 30). The distribution of marriage distances in all the groups showed a positive skewness (Figures 10, 11 and 12) which was statistically significant in all the groups (Table 30). The degree of leptokurtosis was statistically significant in Hill Marias and Raj Gonds (Table 30). The range of mobility was highest in the Roj Gonds. Marriages within villages occurred frequently and were a reason for the positive skewness The frequency ranged from 16°/. to 45°/. in the six groups (Table 31). The lowest village endogamy occured in Maria Gonds both those living on the hills as well as well as in the plains. Most of their marriages occurred within 20 miles range in all the groups.

2) Comparison with other populations

The positive skewness and leptokurtosis of marriage distances observed in the Gonds is in agreement with those recorded among Dhangars of Maharastra (Majumdar and Malhotra, 1971) and in Santals of Bihar (Basu, 1971). The mean marriage distance in Santals is 6.7 miles comparable to the Gonds. In the Dhangars the mean

TABLE 30 : DESCRIPTIVE ANALYSIS OF MARRIAGE DISTANCE PATTERN IN GONDS

MARRIAGE DISTANCE (MILES)	HILL MARIA GOND	KOLAM	KOYA	MANNE	PLAINS MARIA GOND	RAJ GOND
MEAN ± S.E	10.48 ± 2.16	11.03 ± 0.92	6.01 ± 0.48	5.39 ± 0.57	8.54 ± 0.85	9.01 ± 1.23
MEDIAN	8.33	8.39	4.29	2.75	5.90	3.31
RANGE	0 - 50.00	0 - 50.00	0 - 27.00	0 - 30.00	0 - 50.00	0 - 104.00
SKEWNESS	2.35**	0.89**	1.04**	1.49**	1.72**	3.34**
KURTOSIS	6.88**	0.55	0.29	2.28	3.15	16.63**

** Critical value for 5°/. test of discordancy

** Critical value for 1°/. test of discordancy

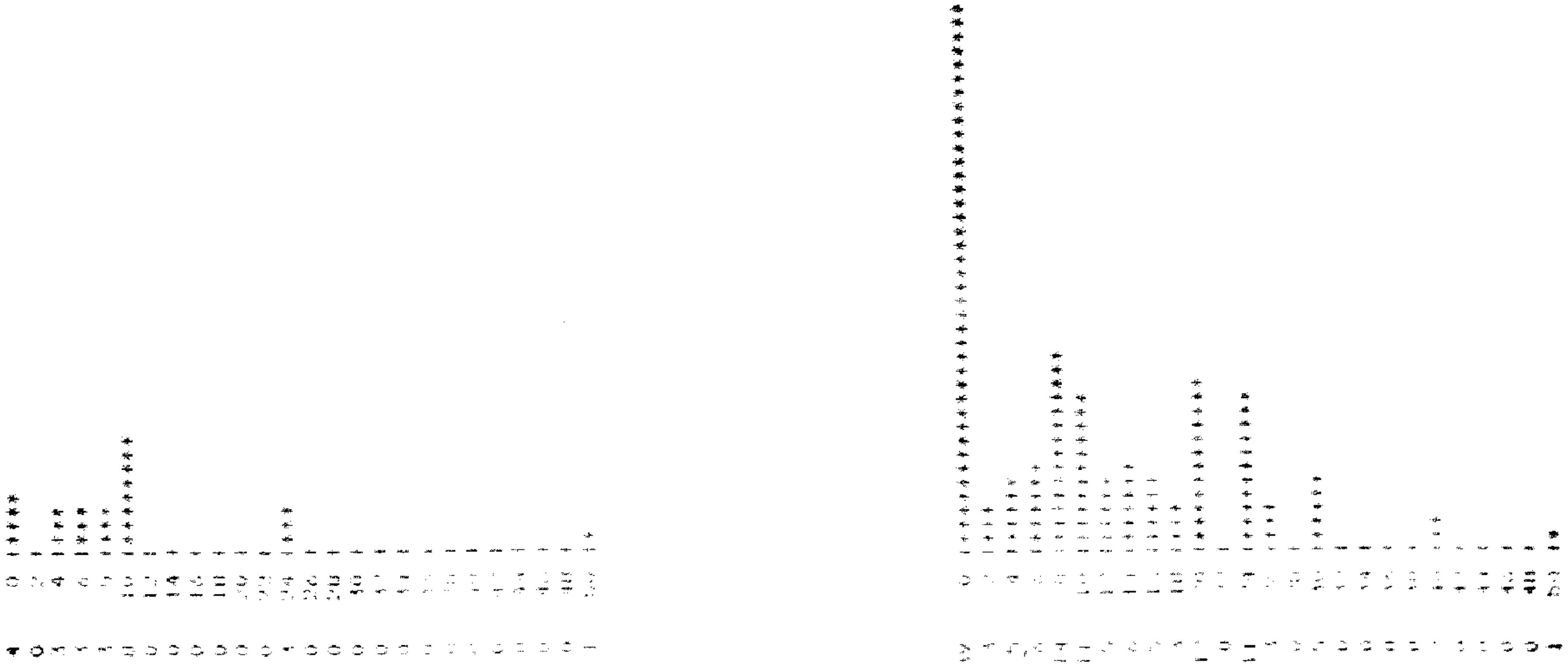
TABLE - 31 : CUMULATIVE FREQUENCY (%) OF MARRIAGE DISTANCE DISTRIBUTION

Marriage Distance (Miles)	Hill Maria Gond	Kolam	Koya	Manne	Plain Maria Gond	RajGond
0	16.0	29.8	36.7	45.1	27.2	39.1
5	28.0	35.9	55.9	59.2	45.6	55.6
10	84.0	59.5	78.2	79.6	73.5	69.2
15	--	67.9	87.2	93.0	85.3	78.9
20	--	83.2	98.4	96.5	89.0	87.2
25	96.0	91.6	--	97.2	94.1	91.7
27	--	--	100.0	--	--	--
30	--	--	--	100.0	--	--
50	100.0	100.0	--	--	100.0	--
104	--	--	--	--	--	100.0

F I G U R E 10

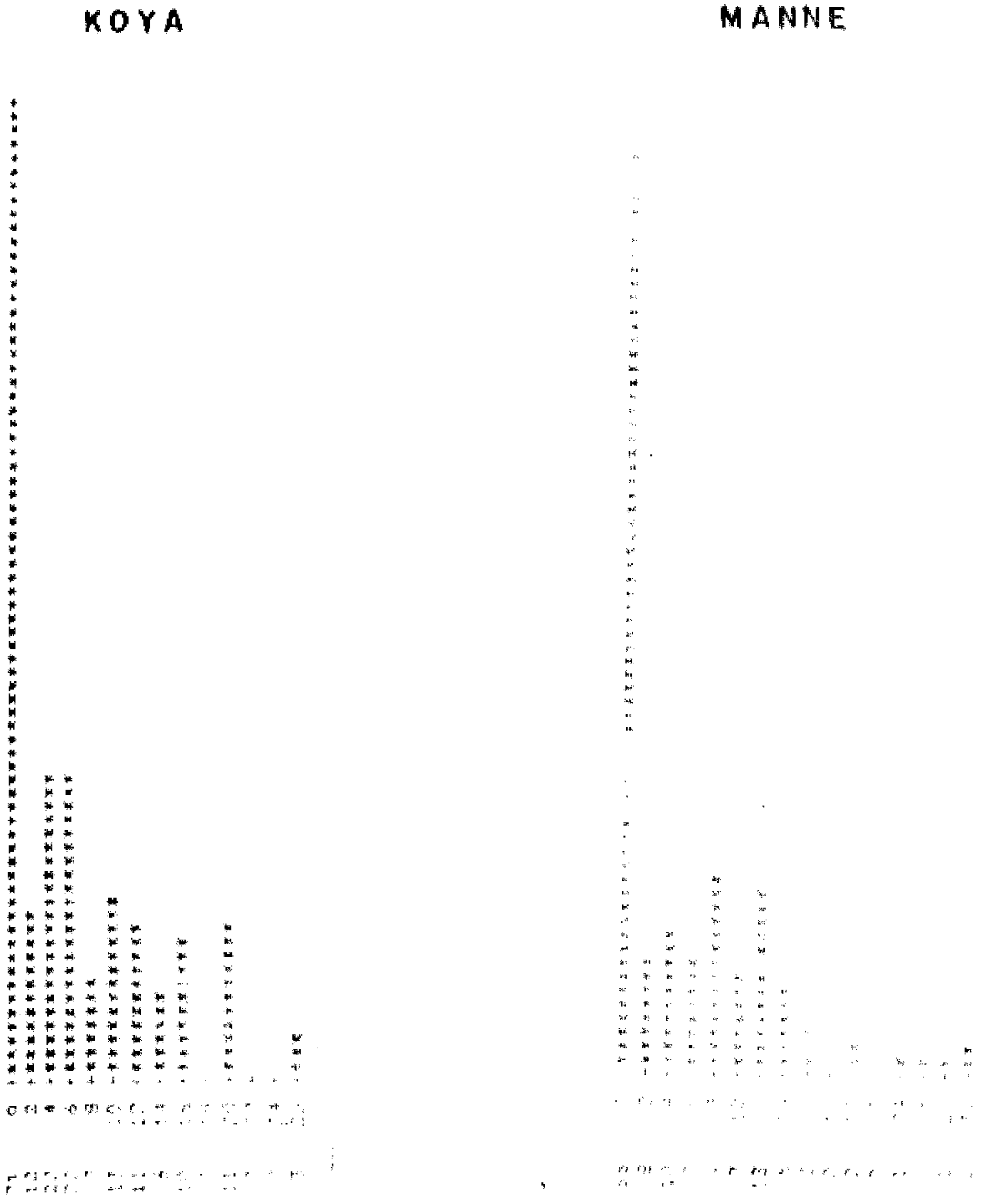
Marriage Distance distribution in Gonds: Hill Maria Gonds and Kolams

FIG.10. MARRIAGE DISTANCE DISTRIBUTION IN GONDS



HILL MARIA GOND

KOLAM

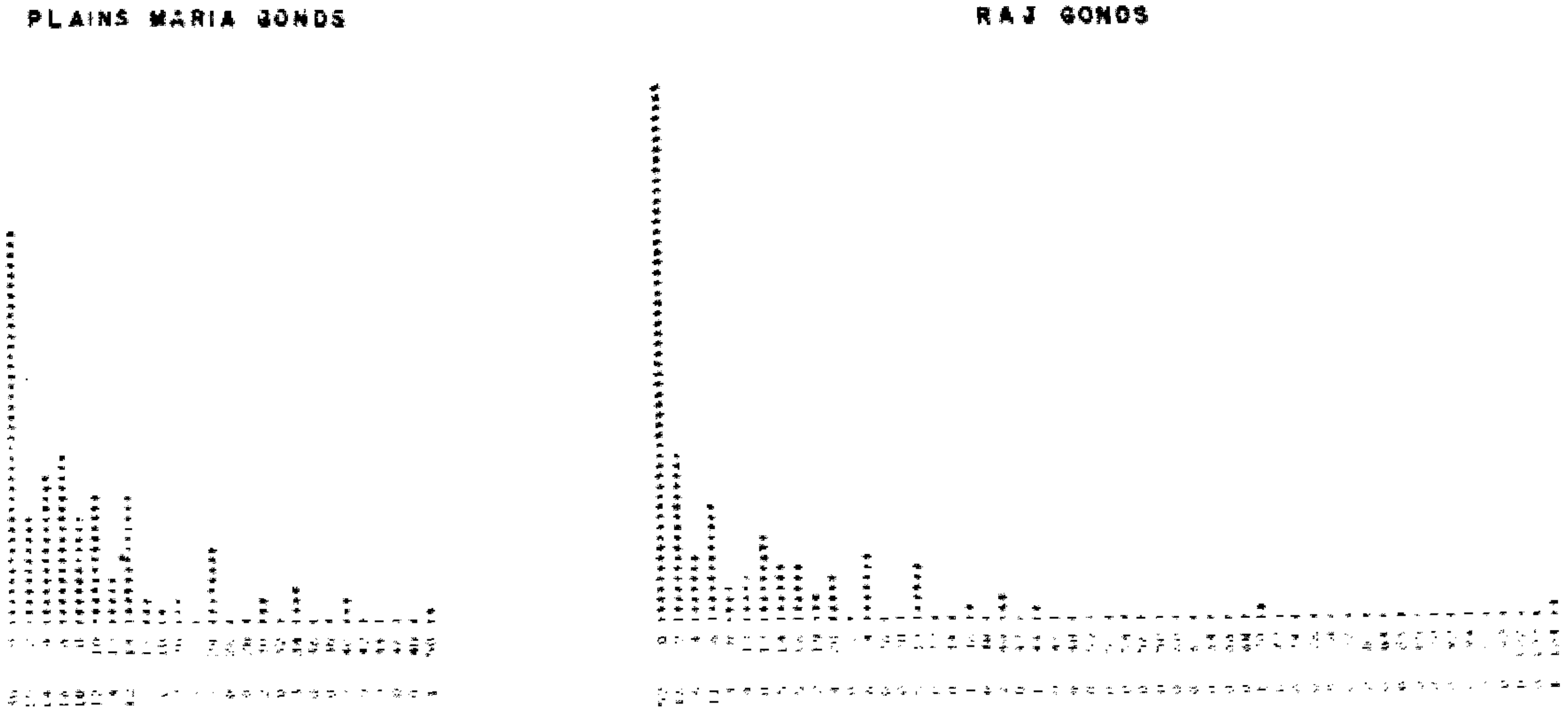


IG.11. MARRIAGE DISTANCE DISTRIBUTION IN GONDS

KOYA

MANNE

FIG. 12. MARRIAGE DISTANCE DISTRIBUTION IN GONDS



PLAINS MARIA GONDS

RAJ GONDS

marriage distance ranges from 6.42 - 50.3 miles in 22 endogamous groups increasing as one goes north. The Gonds and Santals are a settled agricultural tribal group unlike the Dhangars who are a semi-nomadic shepherd group. The Dhangars of south Maharashtra are comparable in the mean marriage distance to those of the Gonds. The frequency of intra-village marriages is high in the Gonds varying from 15°/. to 45°/.. In the Dhangars, there is a considerable variation, varying from 2°/. - 47.2 °/. with an average of 25.4°/.. Generally speaking, there appears to be a decrease in frequency of intra-village marriages as one moves towards north. This higher frequency of village endogamy in Gonds and Dhangars of south Maharashtra are comparable to groups living in the adjacent southern states of Andhra Pradesh and Karnataka where it reaches a frequency of 40 to 50°/. (Karve, 1965) and where consanguinity is also preferred. In contrast, this practice of village endogamy and consanguinity in the adjacent northern state of Madhya Pradesh is tabooed.

4.4 Relationship between consanguinity and marriage distance

1) Among the Gonds

Except in the case of Kolams and Koyas, there appeared to be no relationship between frequency of consanguinity and the marriage distance as indicated by χ^2 test (Table 32). In the case

TABLE 32 : RELATIONSHIP BETWEEN MARRIAGE DISTANCE AND CONSANGUINITY IN GONDS

	HILL MARIA GOND		KOLAM		KOYA	
	MARRIAGE DISTANCE (MILES)		MARRIAGE DISTANCE (MILES)		MARRIAGE DISTANCE (MILES)	
	≤ 5	> 5	≤ 5	> 5	≤ 5	> 5
NOT RELATED	4	9	7	38	71	70
RELATED	1	7	40	46	35	12
TOTAL	5	16	47	84	106	82

$X^2 = 0.911$, D.F, 1　　$X^2 = 9.629^{**}$, D.F, 1　　$X^2 = 8.334^{**}$, D.F, 1

	MANNE		PLAINS MARIA GOND		RAJ GOND	
	MARRIAGE DISTANCE (MILES)		MARRIAGE DISTANCE (MILES)		MARRIAGE DISTANCE (MILES)	
	≤ 5	> 5	≤ 5	> 5	≤ 5	> 5
NOT RELATED	61	42	46	55	51	41
RELATED	23	15	15	15	23	16
TOTAL	84	57	61	70	74	57

$X^2 = 0.019$, D.F, 1　　$X^2 = 0.1822$, D.F, 1　　$X^2 = 0.1396$, D.F, 1 of Kolams and Koyas, however, marriage distance and frequency of consanguinous marriages are inversely related, showing that the frequency of related marriages decreases with increasing marriage distance. In the case of the other four groups, it appears that distance is not a major criteria for selection of suitable mates, especially when most marriages related or unrelated occur within a narrow radius of 15 miles which involves only a day's journey.

2) Comparison with other groups

The negative correlation between consanguinity and marriage distance was observed in the Dhangar study (Majumdar and Malhotra, 1979). The southern Dhangars showing a lower matrimonial distance and higher inbreeding co-efficient whereas the Dhangars of northern Maharashtra showed a higher matrimonial distance with a lower inbreeding co-efficient. Further data should be collected on other groups in India to see whether the predicted theoretical distribution that inbreeding co-efficient decreases with increase in matrimonial distance (Malecot, 1967) occurs in other populations.

.5 Conclusions

The Gonds have a low mean matrimonial distance comparable to Santals and southern Dhangars of Maharashtra. Since there is scanty data on other tribal groups of India, a comparative picture cannot be obtained until more data becomes available in the future. The inbreeding co-efficient in the Gonds is comparable to other tribal groups of Andhra and is lower than that given for the Hindu caste group of rural Andhra Pradesh. The cross-cousin type of consanguinous marriages occurring commonly among the Gonds is also preferred by other Central Indian tribe such as Bhils of West Khandesh, (Maharashtra) as well as the Gonds of Madhya Pradesh and also in the eastern tribals such as the Nagas and the Bodo groups belonging to the Mongoloid physical type. The cross cousin type of marriage is preferred throughout the south among the Dravidian speaking populations and it appears from this that at least at one time cross cousin type of marriages were widely prevalent in India and were in fact mentioned as occurring in the Yadavas and Pandavas and the royal houses of Kosalas and Sakyas as mentioned in the ancient literature (Kapadia, 1968). However, today in the western and northern India, there is a strict prohibition of marriages between two individuals related through a common male ancestor up to the seventh generation on the father's side and a fifth generation on the mother's side.

PTER 5 : COMPARISON OF THE GONDS WITH OTHER TRIBAL GROUPS BASED ON ANTHROPOMETRIC DATA

Selection of published data on various tribal groups :

Different distance measures and clustering algorithms stress different aspects of the similarity or dissimilarity of groups. There is nothing like which is an appropriate measure of distance and a method of cluster analysis unless the problem is posed in a narrow but a definite way. For exploratory studies, it would be useful to try different methods and interpret the results and also to see whether different methods give nearly consistent results.

Data were collected from published sources on anthropometric and biochemical genetic markers which were common to those of the Gond groups in the study (Table 1). As can be seen from the table, there are a lot of gaps in the data from published sources with very few populations having in common both biochemical as well as anthropometric data. Hence a multivariate analysis was carried out separately on all populations having data available on the seven anthropometric measurements which were common to the Gond populationsin the study, regardless of whether they had common biochemical information (Table 33). The populations selected were mostly tribal groups with some non-tribal agriculturists and scheduled caste groups of Maharashtra like the Marathas and Mahars who form a large proportion of the population of Maharashtra. The area from which each of the populations was selected by each investigator has been noted in the table and three main geographical regions have been identified. The areas consisted of the following :

TABLE 33

MEAN VALUES OF ANTHROPOMETRIC CHARACTERS OF SOME MALE TRIBAL GROUPS FROM PUBLISHED SOURCES

MEASURE-MENTS (mm)	MARATHA C. P. & BERAR (17)	2 MARATHA W. KANDESH (121)	3 MARATHA E. KANDESH (113)	4 MARATHA HYD. DST. (44)	5 . BOS. (150)	6 KOLI-MALHAR (30)
ST	[illegible]	1626.49	1626.77	1623.18	1600.00	1603.30
HL	[illegible]	182.32	181.87	181.18	186.41	179.76
HB	[illegible]	144.39	143.23	142.32	140.56	136.63
TFL	[illegible]	114.32	114.30	110.68	-	108.33
BZB	[illegible]	135.09	133.85	133.50	131.90	129.50
BGB	[illegible]	103.51	103.22	104.59	-	102.33
NL	[illegible]	50.59	50.06	47.04	45.72	42.33
NB	[illegible]	36.34	36.38	35.38	40.67	36.30
SOURCE	[illegible] 1951	KARVE & DANDEKAR, 1951	KARVE & DANDEKAR, 1951	KARVE & DANDEKAR, 1951	GHOSH, 1965	KARVE & DANDEKAR, 1951

*[illegible] IN BRACKETS ARE [illegible] (DETAILS ARE GIVEN IN THE TEXT)

MEAN VALUES OF ANTHROPOMETRIC CHARACTERS OF SOME
MALE TRIBAL GROUPS FROM PUBLISHED SOURCES
(continued)

	7	8	9	10	11	12
MEASURE-MENTS (mm)	KORAKU (26)	KUMBI MANA (26)	KUMBI TIRALE (49)	MAHAR (102)	WARLI (31)	DHANGAR HATKAR (70)
ST	1627.61	1598.61	1637.47	1622.00	1610.10	1636.33
HL	180.92	182.65	185.22	183.66	178.90	185.30
HB	140.00	138.38	142.73	143.20	137.22	145.20
TFL	108.73	108.73	110.06	108.69	108.31	110.53
BzB	131.77	131.11	135.28	134.50	127.67	134.13
BgB	103.30	99.38	103.55	105.19	99.57	103.16
NL	44.73	44.30	47.08	45.57	43.38	46.93
NB	39.92	36.00	36.43	36.24	36.77	35.30
SOURCE	KARVE & DANDEKAR, 1951	KARVE & DANDEKAR, 1951	KARVE & DANDEKAR, 1951	KARVE & DANDEKAR, 1951	KARVE & DANDEKAR, 1951	KARVE & DANDEKAR, 1951

*FIGURES IN BRACKETS : ESTIMATED VALUES (DETAILS ARE GIVEN IN THE TEXT)

MEAN VALUES OF ANTHROPOMETRIC CHARACTERS OF SOME
MALE TRIBAL GROUPS FROM PUBLISHED SOURCES.
(continued)

MEASUREMENTS (mm)	13 DANGAR KHUTEKAR (33)	14 GOND (26)	15 GUJAR (44)	16 HALBI (33)	17 KOLAM (30)	18 JENU KURUBA (63)
ST	1611.32	1610.26	1653.18	1584.97	1627.16	1581.17
HL	180.48	183.38	186.29	184.27	182.40	179.44
HB	141.30	140.04	142.34	140.03	138.86	135.60
TFL	109.66	107.65	111.43	106.82	108.96	102.97
BzB	131.21	133.80	133.16	131.18	133.10	127.25
BgB	101.21	101.54	103.27	101.42	101.40	97.39
NL	45.51	44.92	47.29	44.03	44.16	39.98
NB	35.69	37.65	36.00	37.75	38.16	37.03
SOURCE	KARVE & DANDEKAR, 1951	KARVE & DANDEKAR, 1951	KARVE & DANDEKAR, 1951	KARVE & DANDEKAR, 1951	KARVE & DANDEKAR, 1951	KARVE & DANDEKAR, 1951

*FIGURES IN BRACKETS ARE ESTIMATED VALUES (DETAILS ARE GIVEN IN THE TEXT)

MEAN VALUES OF ANTHROPOMETRIC CHARACTERS OF SOME
MALE TRIBAL GROUPS FROM PUBLISHED SOURCES
(continued)

*	19	20	21	22	23	24
MEASUREMENTS (mm)	BETTE KURUBA (35)	SHOLEGA (40)	ANDHS (55)	BHILS MAVACHI (58)	BHILS TADVI (36)	GOND (51)
ST	1531.31	1609.70	1609.29	1601.60	1625.27	1607.17
HL	177.94	182.32	180.00	179.77	179.36	186.04
HB	136.66	134.67	141.35	139.72	139.05	140.08
TFL	103.80	110.47	109.23	105.01	109.83	110.31
BzB	127.03	130.00	133.23	129.60	131.05	131.47
BgB	100.86	100.70	103.29	101.69	101.08	104.[illegible]6
NL	40.57	42.75	46.40	42.27	45.02	42.96
NB	35.74	36.70	37.00	36.67	36.83	38.35
SOURCE	KARVE & DANDEKAR, 1951	KARVE & DANDEKAR, 1951	KARVE & DANDEKAR, 1951	KARVE & DANDEKAR, 1951	KARVE & DANDEKAR, 1951	KARVE, 1954

*FIGURES IN BRACKETS ARE ESTIMATED VALUES (DETAILS ARE GIVEN IN THE TEXT)

MEAN VALUES OF ANTHROPOMETRIC CHARACTERS OF SOME MALE TRIBAL GROUPS FROM PUBLISHED SOURCES

(continued)

	25	26	27	28	29	30
MEASUREMENTS (mm)	JUANG (40)	KHOND (51)	KOYA (51)	SAVARA (29)	ORAONS (1) (100)	ORAONS (2) (39)
ST	1536.35	1566.74	1588.67	1604.34	1614.50	1587.87
HL	185.97	187.16	182.06	189.34	**189.43**	183.56
HB	137.80	139.98	139.29	129.62	136.86	129.13
TFL	110.80	110.80	107.76	109.14	113.38	105.69
ZB	131.52	132.09	130.34	132.89	130.14	129.10
B_gB	101.77	101.84	101.80	103.69	97.70	101.72
NL	43.22	44.59	42.14	42.17	47.34	41.46
NB	37.95	37.12	38.69	37.93	37.56	36.95
SOURCE	KARVE, 1954	KARVE, 1954	KARVE, 1954	KARVE, 1954	MAJUMDAR & RAO, 1949	KARVE, 1954

*FIGURES IN BRACKETS ARE ESTIMATED VALUES (DETAILS GIVEN IN THE TEXT)

MEAN VALUES OF ANTHROPOMETRIC CHARACTERS OF SOME
MALE TRIBAL GROUPS FROM PUBLISHED SOURCES
(continued)

	31	32	33	34	35	36
MEASUREMENTS (mm)	BHILS (137)	BONDOS (46)	GODABA (52)	KORKUS (51)	MUNDAS (1) (32)	MUNDAS (2)
T	1629.20	1573.52	1594.67	1636.44	1623.69	1582.00
HL	181.87	184.15	186.92	180.58	189.25	186.95
HB	137.62	140.04	139.90	137.82	139.00	138.00
TFL	112.22	111.65	110.96	111.36	106.47	111.75
BzB	131.18	132.13	131.94	130.16	131.34	131.70
BgB	98.42	103.25	103.73	95.44	101.56	99.32
NL	48.60	43.17	44.00	48.08	41.40	48.40
NB	37.49	38.50	38.54	39.80	36.34	40.13
SOURCE	MAJUMDAR & RAO, 1949	KARVE, 1954	KARVE, 1954	CHATTAPADHYAY, 1952	KARVE, 1954	SARKAR, 1954

*FIGURES IN BRACKETS ARE ESTIMATED VALUES (DETAILS ARE GIVEN IN THE TEXT)

MEAN VALUES OF ANTHROPOMETRIC CHARACTERS OF SOME MALE TRIBAL GROUPS FROM PUBLISHED SOURCES

(continued)

	37	38	39	40	41	42
MEASUREMENTS (mm)	BHATRA (100)	KODAKUS (100)	PARDHANS (101)	KORWA (102)	KORKU (50)	MURIA (100)
ST	1603.58	1579.50	1628.90	1574.00	1620.60	1617.98
HL	182.42	187.80	189.60	185.80	182.68	187.31
HB	139.56	139.20	138.10	137.50	141.42	137.99
TFL	111.59	116.00	117.40	111.20	114.40	111.66
BzB	132.04	131.70	131.10	131.00	133.58	131.19
BgB	100.85	100.30	101.10	102.90	103.36	100.63
NL	47.43	49.20	50.30	46.20	45.98	48.22
NB	40.11	39.90	37.90	39.70	38.30	40.46
SOURCE	RAKSHIT, 1963	AHMED, 1976	AHMED, 1972	AHMED, 1973	BASU, 1970	RAKSHIT, 1963

*FIGURES IN BRACKETS ARE ESTIMATED VALUES (DETAILS ARE GIVEN IN TEXT)

MEAN VALUES OF ANTHROPOMETRIC CHARACTERS OF SOME
MALE TRIBAL GROUPS FROM PUBLISHED SOURCES
(continued)

	43	44	45	46	47	48
MEASURE-MENTS	HILLMARIA (1)	BISON HILL MARIAS	DORLA	DHURWAS	KADAR	SANTALS
N	(100)	(50)	(100)	(100)	(43)	(100)
ST	1627.00	1617.00	1600.10	1612.00	1557.50	1593.00
HL	185.40	181.40	181.00	182.00	178.90	185.00
HB	138.70	138.50	138.20	140.10	132.70	137.00
TFL	113.12	110.40	104.80	111.60	110.12	113.00
BzB	111.20	131.72	130.40	132.00	124.93	-
BgB	*(101.24)	*(99.93)	*(101.43)	*(102.49)	96.18	-
NL	49.20	49.00	44.40	46.60	48.00	48.00
NB	38.70	39.30	39.20	39.70	39.30	37.00
SOURCE	ROY, 1938	ROY, 1938	RAKSHIT, 1960	RAKSHIT, 1960	SARKAR, 1939	BISWAS, 1956

*FIGURES IN BRACKETS ARE ESTIMATED VALUES (DETAILS ARE GIVEN IN TEXT)

MEAN VALUES OF ANTHROPOMETRIC CHARACTERS OF SOME MALE TRIBAL GROUPS FROM PUBLISHED SOURCES

(continued)

MEASUREMENTS (mm)	DANDAMI MARIAS (49)	HILL MARIAS (2) (50)
ST	1594.80	1620.60
HL	180.50	184.57
HB	137.12	136.96
TFL	115.88	117.69
BzB	• 128.92	130.63
BgB	95.20	96.57
NL	45.30	46.16
NB	37.88	38.33
SOURCE	MAJUMDAR, 1941	MAJUMDAR, 1941

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*FIGURES IN BRACKETS ARE ESTIMATED VALUES (DETAILS ARE GIVEN IN TEXT)

1) The tribal belt of Central India.
2) Orissa and Chota Nagpur.
3) South India (The area of eastern and western ghats lying south of the Krishna river).

The selection of these areas was based on geographical and cultural differences. The area of Central India is one of the largest tribal area in India extending from the hilly ranges of Rajasthan, foot hills of Vindhyas and Satpura ranges in Madhya Pradesh State consisting of dense teak forest. Many of the Gonds of Madhya Pradesh do not speak Gondi but various dialects of Hindi such as Chattisgarhi. The forest area of Bastar (Madhya Pradesh), Andhra Pradesh and Chanda (Maharastra) is also a Gondi speaking area contiguous with Central India. It has been kept as a separate area because it is the area of the present study. Orissa and Chota Nagpur consisting of a predominantly Sal forest (Shorea robusta) was historically in contact mostly with eastern India but to some extent with the Gondi-speaking area of Central India. This area consists of the Munda-speaking groups (Mundari, Ho, Santali, Saora, Bondo, Korku, Gadaba and many others) who are morphologically different from the Gondi-speaking group and are said to belong to the Kolid racial type (Eickstedt, 1935). The hilly area of South India consisting of the eastern and western ghats south of the Krishna river is inhabited by the Malid group of Veddoid stock of tribal population (Eickstedt, 1935). The tribes of north-eastern India were not included in this study because they are distinct culturally and morphologically from the populations of peninsular India and belong to the Mongoloid physical type.

Out of the total 53 populations which were initially selected for comparison, 7 populations were rejected as the data were not found to be comparable with those in the present study.

The following were the groups rejected

1) Oraons (O1), Mazumdar and Rao, 1949.
2) Bhils (B1), Mazumdar and Rao, 1949.
3) Mundas (MD2), Sarkar, 1954.
4) Korkus (KR3), Basu, 1970.
5) Kadar (KA), Sarkar, 1959.
6) Dandami Marias (DM), Mazumdar, 1941.
7) Hill Marias (HM2), Mazumdar, 1941.

The investigators Mazumdar, Sarkar and Basu have used different techniques for taking measurements from the other investigators like Iravathi Karve and Dandekar who used techniques similar to that followed in the present study. Hence these populations could not be used for the purpose of comparison with other groups.

All the selected populations were given code names for convenience and the first alphabet in the code represented the first letter of the population and the second code alphabet represents the third letter of the population. In some cases where the same population was studied by different scientific workers, a third code letter was used to represent the different samples 1, 2 ... etc. In a few cases where the set of rules could not be strictly adhered to because the first and second code letters would have already represented another group, a different alphabet was used. These rules were adhered to because it would be easy for anyone to immediately identify the population by looking at the code name. In some of the populations, data on one measurement out of the seven had not been collected and since these populations were important for comparison, the missing data was estimated and this was indicated by an asterisk in the table. Missing value of one measurement was estimated as follows :

Suppose one measurement (x_1) is missing for one group say A

Choose groups B, C, D .... which are close to A.
Compute the canonical variates based on B, C, D ....
Using the original variables x_1, x_2 ... x_p

Let the last canonical variate be

$$a_1x_1 + \text{------} \; a_px_p$$

Substitute the values for x_2^A, ... x_p^A for group A

Then solve for $x_1^A = \dfrac{- a_2x_2^A - \dots - a_p x_p^A + \alpha}{a_1}$ Where

α is the average value of $(a_1x_1 + \dots a_px_p)$ for the groups B, C, D ... x_1^A thus computed is the estimate of x_1 for group A.

Use of various multivariate techniques on anthropometric data

Genetic Distance Measures

For metric data the best distance measure is Mahalanobis's D^2 provided that some assumptions are satisfied, the two most important being homogeneity of the variances and correlations and normality of the multivariate distributions. Simpler distance measures like co-efficient of racial likeness (CFL) which was shown by Penrose to be linearly related to Mahalanobis's D^2 when all inter-correlations are constant. The formulae of these two distance measures are as follows :

Let $\bar{x}_{ij}$ represent the mean of the ith variate in j^{th} population and $\bar{x}$; the column vector of the means for the jth population. Then :

$$\sum_{i=1}^{j} (\bar{x}_{ij} - \bar{x}_{ik})^2 = C(\bar{x}_j - \bar{x}_k)^1 (\bar{x}_j - \bar{x}_k) = CRL_{jk}$$

(Co-efficient of racial likeness)

$$(\bar{x}_j - \bar{x}_k)^1 W^{-1} (\bar{x}_j - \bar{x}_k) = D^2_{jk} \text{(Mahalanobis } D^2\text{)}$$

where W is the pooled within population dispersion matrix. CRL and D^2 are actually squared distances. Though Mahalanobis's D^2 is more difficult to compute than CRL, it has some advantages over the CRL. D^2 is not unduly effected by addition of highly correlated variables. Whereas CRL increases when adding a variate that is completely correlated with those already included, D^2 remains unaltered. D^2 is a measure of overlap between populations (see Rao, 1954) and is thus more appropriate to study affinities or dissimilarities between individuals in different populations. In this study Mahalanobis's D^2 was computed between the 46 groups selected for comparison (Appendix -IV).

Cluster Analysis

In many empirical fields, there is an increasing interest in identifying the groupings or clusterings of the object under study that best represent certain empirically measured relation of similarity. For example, large arrays of data are often collected without strong theoretical structures. The problem then is discovering if there is any structures (i.e., natural arrangement of the object into homogenous groups) inherent in the data. Recent work along these lines in the biological sciences goes under the name CLUSTER ANALYSIS. The few empirically validated clustering methods of early numerical taxonomy have mutiplied to form a vast and complex field nearly impossible to survey.

The most commonly used clustering techniques on biological material are the combination of the following four criteria :

1) Sequential;
2) Agglomerative;
3) Hierarchic;
4) Non-overlapping

Sequential : Most clustering methods are sequential i.e., a recursive sequence of operations is applied to the set of operational taxonomic units. In contradiction to this is simultaneous clustering which is an instant division into parts in a non-hierarchic system which has only one rank level.

Agglomerative : Starting with a set of separate entity, agglomerative techniques group these into successively fewer than t sets arriving eventually at a single set containing all t operational taxonomic units. These are most frequently employed especially when limited to sequential, hierarchic and non-overlapping procedures, that a great variety of methods has been developed.

Hierarchic : Clustering method is defined as hierarchic (Sneath and Sokal, 1973) if it consists of a sequence of W + 1 clusterings, C_0, C_1 ... C_w, in which C_o is the disjoint partition of all t OTU (operation taxonomic units) and C_W is the conjoint partition. ~~The number of parts k_r in partition~~ . The number of parts k_i in partition C_i must obey the constraint $k_i \geqslant k_i + 1$, where $k_i + 1$ is the number of parts in partition C_{i+1}. Consequently in such a clustering there are successively fewer taxa. Sneath's definition of hierarchic is that there can be either overlapping or non-overlapping of taxa. Non-overlapping creates mutually exclusive taxa whereas overlapping implies that there is no limitation on the degree of overlap of taxa, i.e., one OTU may be simultaneously a member of two or or more taxa. However Johnson (1967) and Jardine and Sibson (1971) consider as non-overlapping hierarchic classification of Sneath and Sokal as a hierarchic classification. Classifications that are non-hierarchic are those that do not exhibit ranks in which subsidiary taxa become members of larger and more inclusive taxa.

The relative merits of hierarchic versus non-hierarchic classifications are difficult to evaluate. For traditional biological taxonomy, hierarchic classifications are required and even in related fields such as phyto-sociology it seems desirable to have higher ranking taxa that summarise common information about the majority of the members of the taxons. Non-hierarchic representation is prepared when emphasis is placed on faithful representation of the relationships among the OTU's rather than on a summarisation of these relationships.

4) Non-overlapping : In a non-overlapping method, taxa at any one rank are mutually exclusive, that is, OTU's contained within one taxon may not also be members of a second taxon of the same rank. However, these quite frequently distort the finitic relationship among OTU's. For this reason some workers have preferred to relax the criterion of mutual exclusiveness in taxonomy and prefer to permit overlapping in membership at a given rank. In overlapping clustering techniques, the more OTUs are permitted to overlap at any given rank, the closer the resulting hierarchy resembles the original dissimilarity matrix. However, it becomes increasingly more difficult to draw and interpret the resulting dendogram.

The two methods used in this study are

A Single linkage or minimum or connectedness method.

B Complete linkage or maximum or diameter method.

They belong to the hierarchic, agglomerative, sequential, and non-overlapping clustering techniques.

Single linkage clustering

This method was introduced into taxonomy by Flore et al, (1951) and Sneath, (1957). This method has also been called the minimum method by Johnson, (1967). An OTU, that is a candidate for an extant cluster has similarity to that cluster equal to its similarity to the closest member within the cluster. Thus connections between OTU's and clusters and between two clusters are established by single links between pairs of OTU's. This procedure frequently leads to long straggly clusters. Jardine and Sibson, (1968) have attempted a mathematical axiomatic approach, in which they set up a series of self-contained axioms that they think any acceptable hierarchial classification scheme should satisfy. They show that single linkage cluster analysis is the only hierarchic method that satisfy their axiom. The axiom that seems to cause most difficulty is referred to as the concept termed continuity. That is, when a particular method is followed with a particular set of data, and one population is dropped, the relationship should not differ much from the original analysis. Though this is not a general property of most cluster analysis, it is true of single linkage method.

Complete linkage clustering

It is known as the maximum method (Johnson, 1967) and is the direct antithesis of the single linkage technique discussed above. An OTU that is a candidate for admission to an extant cluster has similarity to that cluster equal to its similarity to the furtherest member within the cluster. When two clusters join, their similarity is that existing between the furtherest pair of members, one in each cluster. The method will generally lead to tight, hyperspherical, discreet clusters that join others only with difficulty and at related low overall similarity values. Clusters by this method are compact and more structured, showing more taxa and more ranks. This method is space dilating whereas the single linkage method is space contracting.

H Clust a hierarchical clustering programme written by Stephen C. Johnson of the Bell Telephone Laboratories, Murray Hill, New Jersey and was used on the distance matrix of the 46 populations to give clustering based on the maximum and minimum methods of clustering. The representation of these analysis in the form of dendograms or trees have the advantage that they are readily interpretable as conventional taxonomic hierarchies.

Ordination methods

Suppose that on each individual, we have taken p measurements. In such a case the mean values of the tribes under study can be represented as points in a p-dimensional Euclidean space. If $p = 3$, we can have a physical representation of the points using three space co-ordinates. The configuration of the points (tribes) can then be easily studied. If $p > 3$, it may be possible to represent the points approximately in a 3 dimensional space. The method of obtaining the co-ordinates in three dimensions is as follows

Let $x_1 \ldots, x_p$ the original measurements. Then we define the first canonical variate as a linear function.

$$y_1 = a_1 x_1 + \ldots + a_p x_p$$

The co-efficient $a_1, \ldots, a_p$ are obtained in such a way that the sum of all possible D^2 values based on y_1 alone is maximised. The second variate

$$y_2 = b_1 x_1 + \ldots + b_p x_p$$

is obtained in such a way that the sum of all possible D^2's based on y_1 and y_2 is maximised. The basis for obtaining a third variate, fourth variate etc., is now clear. Theoretically, we can have p canonical variates $y_1, \ldots, y_p$ which are obtained by a linear transformation of the original variates $x_1, \ldots, x_p$. The best one dimensional representation is provided by y_1, two dimensional by y_1, y_2 and so on. For further details, reference may be made to Chapter 9 of Rao's, 'Advanced Statistical Methods for Biometric Research', 1971.

The computational technique for obtaining the canonical variates is as follows : First, we obtain the variance co-variance matrices between (B) and within (W) tribes based on the p = 7 characters as in this study. Then eigen values of B with respect to W and the corresponding

Eigen vectors are computed. If $\lambda_1, \ldots, \lambda_p$ or the eigen values, then

$$\frac{\lambda_1 + \ldots + \lambda_t}{\lambda_1 + \text{——} , \lambda_p}$$

denotes the ratio of variance explained by t canonical variates (co-ordinates). If this ratio is large for $t = 3$, then three dimensional representation will suffice. The standardised eigen vector provides the co-efficients of the canonical variates.

In this case (Table 34)
$\lambda_1 = 0.6329$, $\lambda_2 = 0.5719$, $\lambda_3 = 0.3302$, $\lambda_4 = 0.1830$
$\lambda_5 = 0.1775$, $\lambda_6 = 0.1072$, $\lambda_7 = 0.0534$.
and the variance explained by 3 variates is

$$\frac{\lambda_1 + \ldots + \lambda_3}{\lambda_1 + \ldots \lambda_7} \doteq 75\%.$$

The canonical variates are

$y_1 = 30.78$
$y_2 = 27.81$
$y_3 = 16.06$

Compute the mean values of y_1, y_2, y_3 for each tribe and represent it as a point in space of y_1, y_2, y_3. Thus the three dimensional model whose photograph is given in Plate 1 has been obtained.

It is also possible to obtain canonical co-ordinates directly from D^2 values using a technique explained by Torgerson, (1958); Rao (1965) and Gower (1966 a and b). This was done in the case of biochemical data using Sanghvi's and Nei's distances.

TABLE 34 CANONICAL COORDINATES BASED ON 7 ANTHROPOMETRIC MEASUREMENTS

Populations	λ_1 = 0.6329	λ_2 = 0.5719	λ_3 = 0.3302	λ_4 = 0.1930	λ_5 = 0.1775	λ_6 = 0.1072	λ_7 = 0.0534
M1	25.2352	10.7752	22.2870	6.9892	0.8703	29.2169	4.2703
M2	25.1898	11.2112	21.7492	6.5691	0.4134	28.8122	4.4715
M3	24.7327	11.0915	21.7245	6.7794	1.2746	28.7894	4.1447
MA	24.9795	10.4764	21.8414	6.6724	1.0315	28.3609	4.0552
KI	23.4790	9.2263	21.7330	6.9660	0.8164	28.9397	3.8362
KR1	23.7236	10.0307	21.7504	6.1760	0.2379	29.8283	4.2494
KM	23.6162	9.8109	22.2816	7.1720	0.8128	28.5483	4.4816
KT	24.8923	10.3034	22.1889	7.0342	0.6423	28.9675	4.4096
MB	25.0393	9.8267	22.3311	6.6599	0.8038	28.9775	4.3134
WB	23.3776	9.5932	21.4165	6.9763	0.6843	28.9754	4.2175
DH	25.1497	10.2608	22.3115	6.9154	0.9352	29.0806	4.3044
DK	24.3871	9.9521	21.6135	6.9013	1.0490	28.7432	4.4981
G1	23.9709	9.9764	22.2204	6.6905	0.3851	28.7762	4.4965
GJ	24.3607	10.2433	22.4531	7.4538	0.6457	29.0331	4.3268
RL	23.7813	9.7961	22.3491	6.4529	0.5250	28.7974	4.6282
KL2	23.6008	9.8446	21.9525	6.8735	0.3966	29.3389	4.3109
JK	22.5843	9.9453	21.7599	6.8411	1.1127	28.7123	4.5776
BK	23.3019	9.7914	21.9215	6.2633	0.4418	28.5787	4.2747
SO	22.8525	9.4736	22.1944	7.1238	0.8110	28.9921	3.7404
A	24.5496	10.1834	21.5516	6.3309	0.8509	28.9127	4.3314
BM	24.0454	9.1796	21.7331	6.3349	0.4438	28.9201	4.4655
BT	23.8677	9.9379	21.3901	6.3201	0.7413	29.1041	4.2144
G2	23.6754	9.4952	22.8460	6.6041	0.9170	29.3364	4.1434
JA	22.7819	9.7531	23.2068	6.2480	1.5220	28.4070	4.3277
KN	23.5232	9.9637	22.2433	6.6314	1.3175	28.6090	4.5164
KY2	23.2974	9.4223	22.1293	6.2709	0.7057	29.3672	4.4941

TABLE 34 CANONICAL COORDINATES BASED ON 7 ANTHROPOMETRIC MEASUREMENTS (continued)

Populations	$\lambda_1 = 0.6329$	$\lambda_2 = 0.5719$	$\lambda_3 = 0.3302$	$\lambda_4 = 0.1830$	$\lambda_5 = 0.1775$	$\lambda_6 = 0.1072$	$\lambda_7 = 0.0534$
SV	23.5575	9.3197	23.4340	6.9774	0.7247	29.1249	4.3313
O1	23.4222	10.9492	22.9727	7.7072	0.4604	28.6868	4.4625
O2	23.6683	9.0668	22.5050	6.7076	0.5817	28.3697	4.5026
B	23.4808	11.0501	21.5993	7.0298	0.5219	28.8006	4.2947
BN	23.2509	9.6599	22.5782	6.3928	1.4799	29.3152	4.3399
GD1	23.5096	9.8513	22.3930	6.3419	0.9891	29.3176	4.2187
KR2	22.8729	11.2269	21.1503	6.9136	0.1146	29.3606	4.5036
MD1	23.7087	9.0707	23.2954	7.3620	0.2133	29.1254	4.5353
MD2	22.9082	11.2751	22.7983	6.3756	0.4980	28.8572	4.3316
BA	23.3057	10.9023	21.9259	6.1457	1.6068	29.3696	4.4612
KD	22.8815	11.4795	22.5545	6.3932	1.1811	28.4441	4.4808
PR	23.3954	11.5229	22.3651	7.9341	1.0515	28.9054	3.9990
KH	23.0211	10.9473	22.3853	6.1693	0.7478	29.1088	4.3401
KR3	23.8472	12.2629	21.9472	6.3150	1.4155	29.5420	4.1756
MR	23.1220	11.1719	22.7243	6.6750	0.1176	29.7015	4.1393
BM1	23.3256	11.9023	22.2674	6.1915	0.4213	29.0345	4.3421
SH	23.1819	11.1612	21.5645	5.5573	0.1174	29.0179	4.7938
DR	23.3993	9.9564	22.4637	5.1334	0.2103	29.0774	4.3759
DU	23.5641	10.3718	21.8970	6.2770	0.7125	29.3065	4.2745
KA	21.9759	11.2747	21.5032	6.2297	0.3432	28.1679	4.1558
DH	22.2642	12.4757	21.3542	7.0736	1.7255	29.1704	4.5220
BM2	22.1561	12.7257	21.9149	7.5550	1.5250	29.4353	4.4955
KL1	23.3260	12.1978	22.4610	5.4263	0.1347	28.8504	3.7740
KY1	24.2113	10.7905	22.4674	5.4028	0.4580	28.9831	4.7231
MN	24.3232	11.1422	22.3815	6.1500	0.6708	28.7561	3.2951
PM	24.3017	12.7618	22.7579	5.1288	1.6389	29.2145	4.3219
BG1	24.1312	12.7024	22.7443	6.1321	0.3176	28.8142	4.2452

Representation of the relationship in three dimensional model

Attempts at representing taxonomic relationships in one or two dimensions is unsatisfactory because of the higher dimensionality when based on many characters. This is because it is difficult to gain an overall view of relationships from two dimensional representations that are the projections of the other dimensions on the plane formed by the two axes being considered. A second disadvantage of this approach is that as the number of dimensions to be considered increases, the number of combinations taken two at a time becomes quite large. Therefore, a three dimensional model which represents at least 75 percent of variation between populations gives a better picture of the relationships. Labelling of sticks representing each population can be done by means of label stickers labelled with the population code name such that they project out like a flag. Since the model cannot be carried around, coloured photographs from various suitable angles could be taken and slides prepared for the purpose of projection.

2.5 Clustering versus ordination

Both methods may differ greatly in the taxonomic results to which they lead. Cluster methods will yield clusters of some kind, whatever the structure of the data, even if the populations are randomly distributed. Attempts are being made to put them on firmer scientific basis (Gower 1967). The relationship between major clusters is said to be not very clear by clustering techniques (Rohlf, 1970). Ordination also has disadvantages with many populations and clusters, the ordination may give no simple low-dimensional result (Williams and Lance, 1968). Clearly one might have clusters that overlap in two or three space though they are quite distinct in hyperspace. Also final differences between populations within a cluster may not be accurate. There is also danger with ordination diagrams if one depends on it alone and that is the worker may examine these for clusters and decide on their limits by visual inspection alone. Interpretation based on visual inspection alone is counter to the aims of objectivity and hence in this study a combination of both methods of clustering as well as ordination have been used to get a clearer picture of the relationship between the populations. Since no one method is ideal, a combination of two or more methods is better for interpretation than any one method alone.

Results and discussion of multivariate analysis

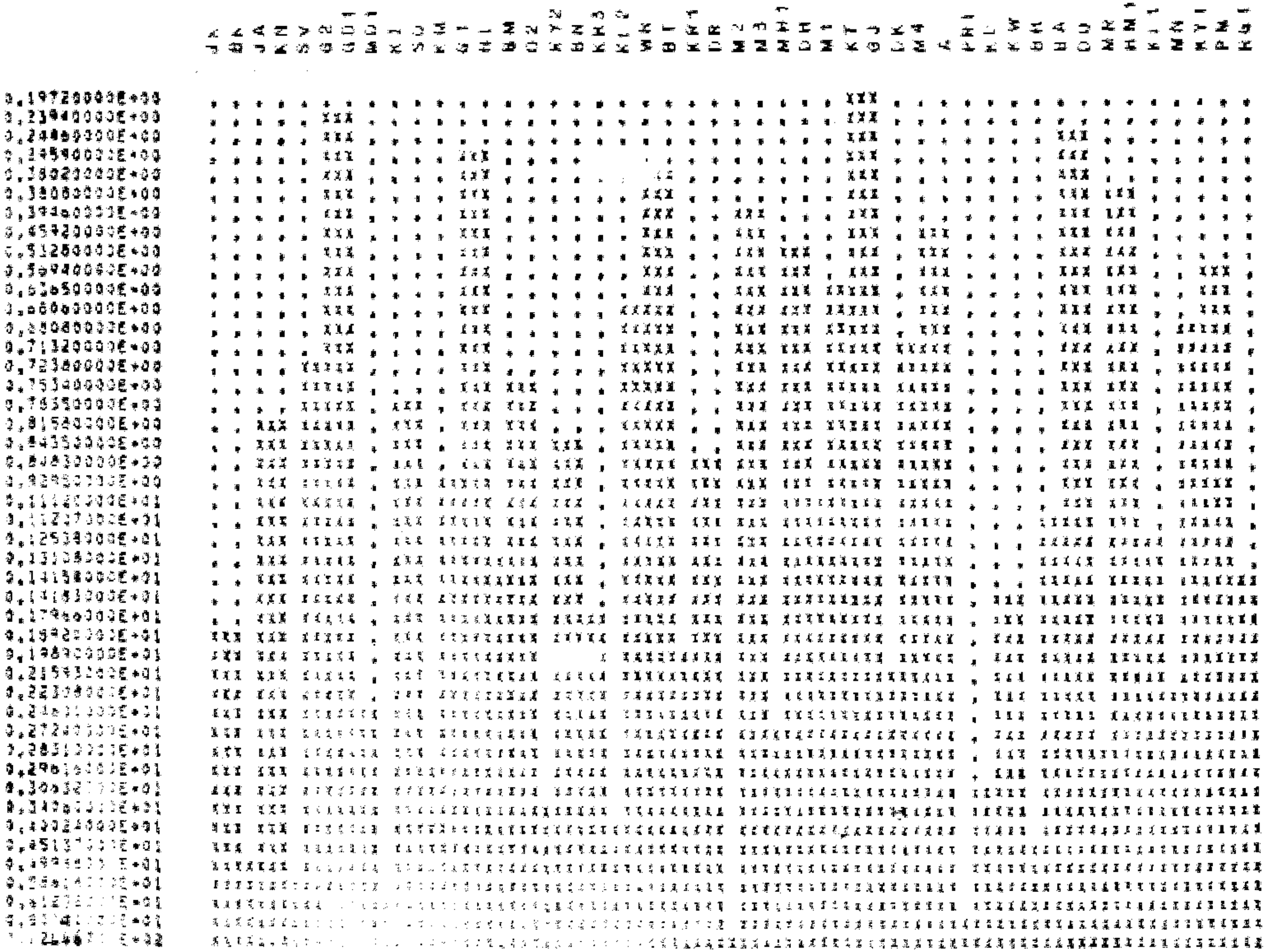
3.1 Cluster analysis : The complete linkage method gave more compact and biologically meaningful clusters separating out according to geographical regions (Figs. 13 and 14). The single linkage method also produced clustering according to geographical

FIGURE 13

D^2 on Anthropometric measurements (all tribal populations) : cluster analysis: complete linkage method

Cluster analysis

COMPLETE LINKAGE METHOD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0,23940000E+00
0,24060000E+00
0,24590000E+00
0,28020000E+00
0,38000000E+00
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0,45420000E+00
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0,56940000E+00
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0,66060000E+00
0,68080000E+00
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0,84350000E+00
0,84830000E+00
0,92950000E+00
0,11120000E+01
0,11270000E+01
0,12530000E+01
0,13130000E+01
0,14130000E+01
0,14183000E+01
0,17960000E+01
0,19820000E+01
0,19890000E+01
0,21593000E+01
0,22300000E+01
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0,27240000E+01
0,28310000E+01
0,29610000E+01
0,30632000E+01
0,34760000E+01
0,40024000E+01
0,45130000E+01
0,49960000E+01
0,58610000E+01
0,61270000E+01
0,65740000E+01
0,21460000E+02

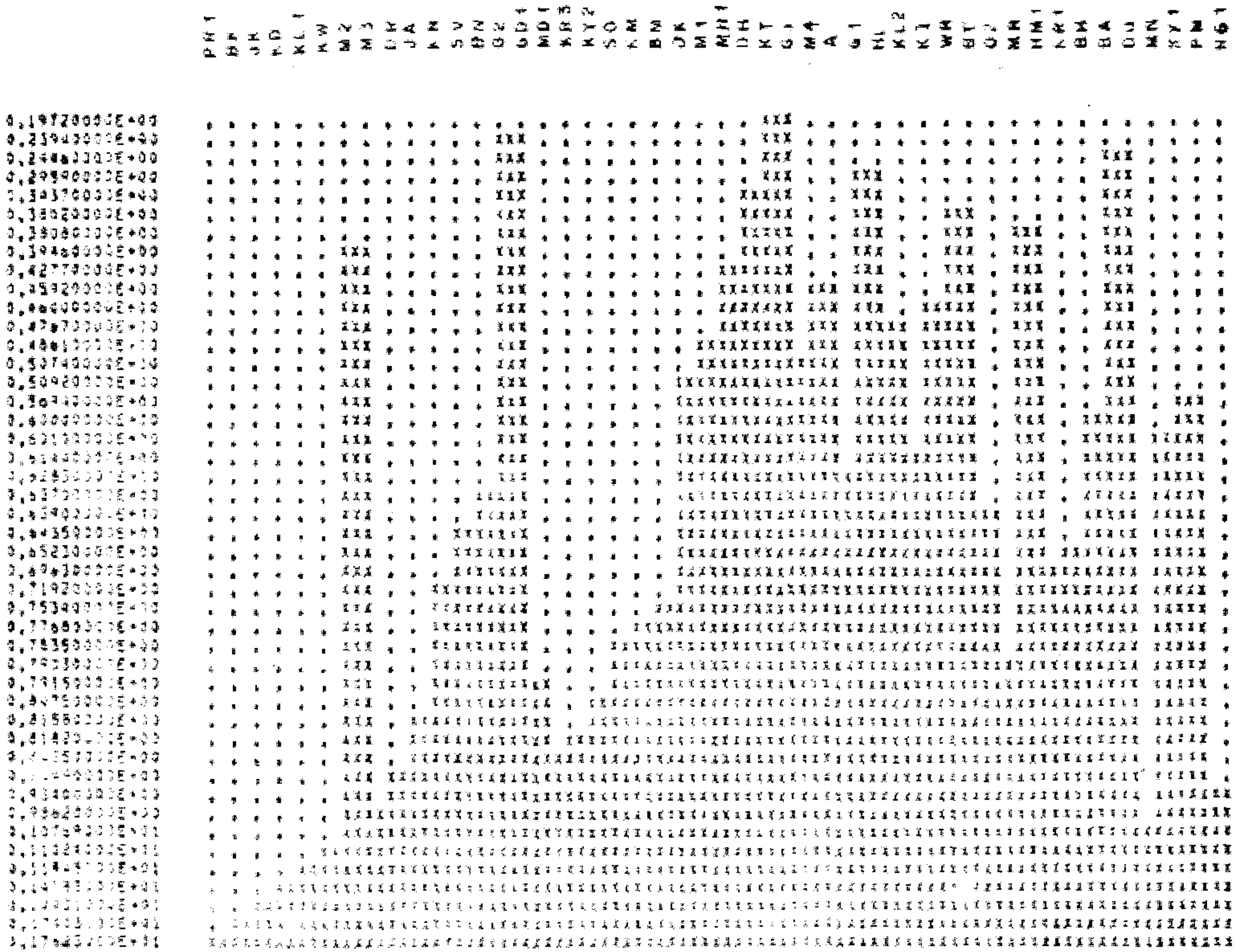
FIGURE 14

D^2 on Anthropometric measurements (all tribal populations): cluster analysis: single linkage method

Fig. 14. D² On Anthropometric Measurements

Cluster analysis

SINGLE LINKAGE METHOD



regions; but unlike the complete linkage method, formed long straggly clusters which included morphologically diverse groups within the same clusters (Table 35). Complete linkage method clearly separates out at level 5.8 the following clusters:

1 Southern Gond group (red)
2 Central Indian, non-tribal groups (green)
3 Central Indian, tribal group (green)
4 Orissa and Chota Nagpur group including South Indian populations within the same cluster (yellow and blue).

The use of colours, each representing a region in Table 35 brought out clearly the clustering based on geographical distribution adding a new dimension to the picture.

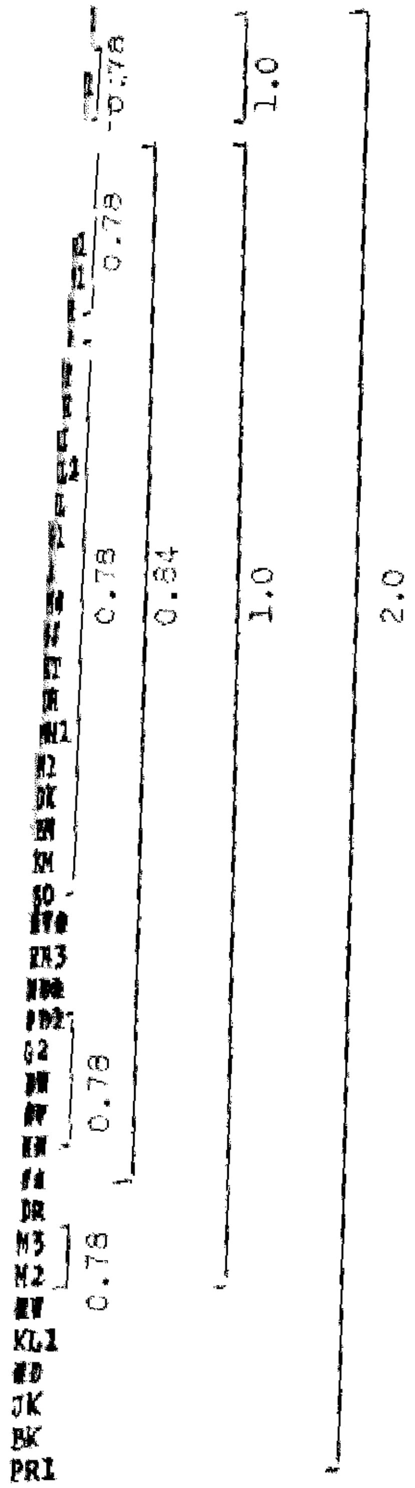
.2 Results based on canonical co-ordinate analysis

A three dimensional model based on the first three canonical co-ordinates giving about 75°/. of the variation between populations was constructed. The sticks representing the populations were painted with respective colours representing the geographical area from which they are sampled. The model brought out clearly a clustering of groups according to geographical areas (see Plate 1). The clustering in three dimensional space also helped to separate more clearly the overlapping populations between any two main clusters. The presence of outliers like PR 1, and KD were easily observed in three dimensional space.

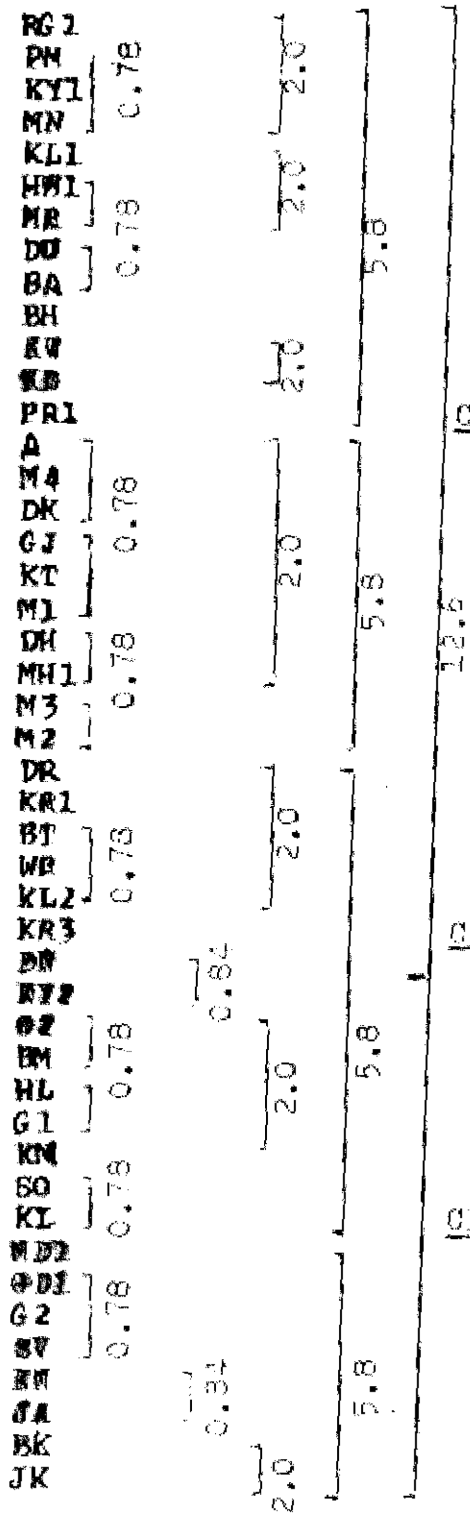
T A B L E - 35

CLUSTERS DERIVED FROM VARIOUS MULTIVARIATE TECHNIQUES (ANTHROPOMETRIC MEASUREMENTS)

le Linkage
od


0.78
1.0
2.0
0.78
1.0
0.78
0.84
1.0
2.0
WN1
M2
DK
KM
SO
KR3
G2
0.78
JA
DR
M3
M2
0.78
KL1
JK
BK
PR1

Complete
Linkage
Method


RG2
PN
KY1
MN
0.78
KL1
HW1
MR
DU
BA
0.78
BH
KD
PR1
2.0
2.0
2.0
5.8
A
M4
DK
GJ
KT
M1
0.78
DH
MH1
M3
M2
0.78
2.0
5.8
DR
KR1
BT
WR
KL2
0.78
KR3
KY2
2.0
0.84
OZ
BM
HL
G1
0.78
KN
SO
KL
0.78
MD2
GD1
G2
SV
0.78
KN
JA
BK
JK
0.84
2.0
5.8
5.8
5.8
12.6

Visualised from three dimensional model (Canonical co-ordinate analysis)

Cluster - I

RG1
KY1
PN
MN
PR1
KL1
BH
BA
HW1
MR
DU
KD

Cluster - II

KR3
G1
BT
KL2
HL
KR1
DR
KM
G2
KY2
OZ
WR
BM
K1

Cluster - III

MD1
SV
BN
GD1
KN
JA
KW

Cluster - IV

A
DK
MN1
M4
GJ
KT
DH
M1
M3
M2

Cluster - V

SO
BK

PLATE 1

Distribution of tribal populations in 3-dimensional space based on anthropometric measurements

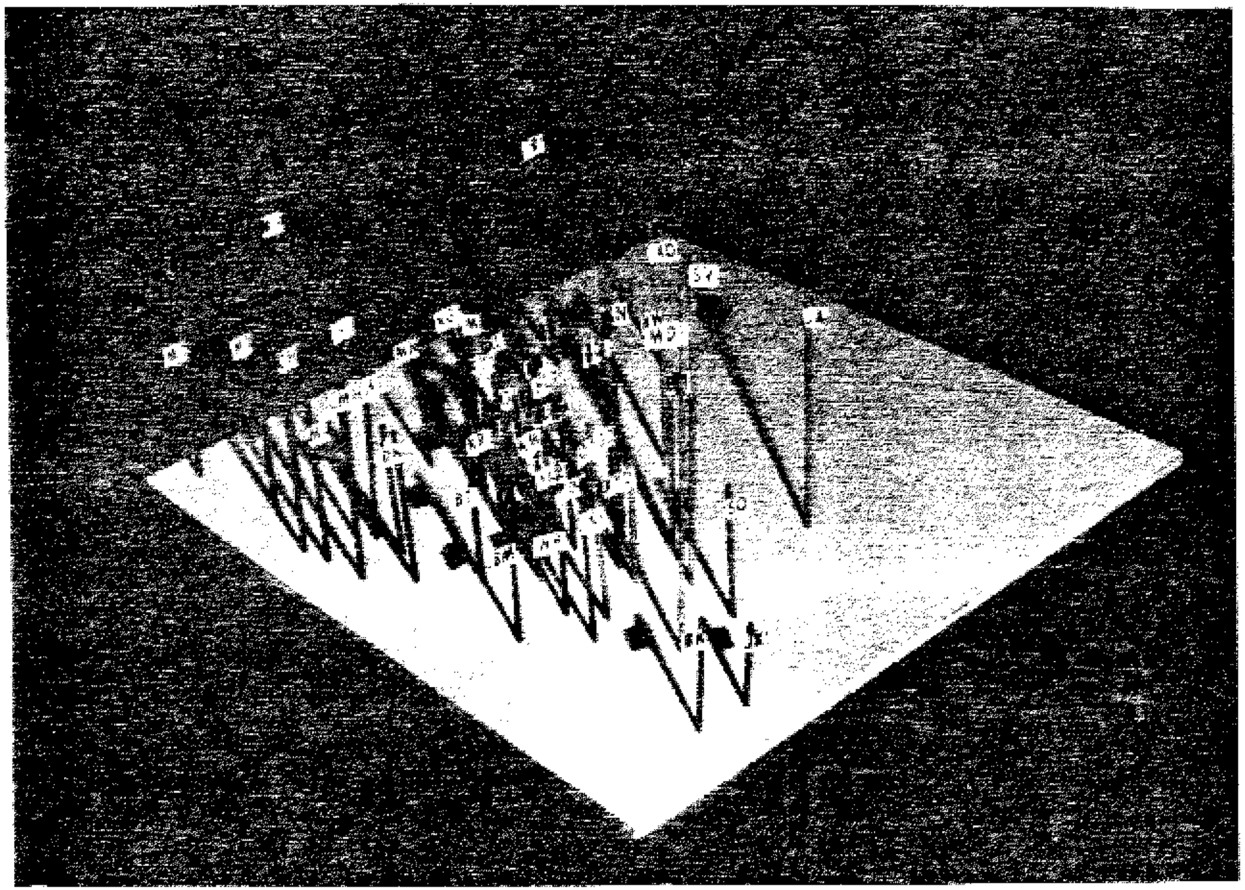


PLATE 1

The relationship of those population whose origin s doubtful because of the lack of correspondence tween morphological and linguistic data were resolved o some extent in the study. The following are the pulations.

A Korkus Munda speaking group found in Central India amidst the Gondi speaking groups. They have been found to belong morphologically to the Central India group (Plate 1).

B Khonds : Dravidian speaking group (Kui dialect) who reside amidst the Munda-speaking group in Orissa and Chota Nagpur areas and are found to be closely related to that group.

C Oraons They are a large Dravidian speaking group (Kurukh dialect) in the Chota Nagpur area and have been found to be morphologically close to the Gondi speaking groups of Central India and in fact are found on the periphery of the Central Indian cluster lying between the Orissa and Central Indian group. Though Khonds and Oraons are both Dravidian speaking groups they are morphologically distant from each other, the Khonds being closer to the Munda-speaking people and the Oraons to the Central Indian tribals.

D Bhils They live in the western part of India along the northern foothills of Vindhyas, speaking Gujarati and Malwi and have been found to be closely related to the Central Indian populations in this study.

E **Halbi** : They are an agricultural group living in southern Maharashtra and who speak Chattisgarhi Hindi and have been found to belong in the study morphologically to the Central Indian group.

F **Andhs** : There were some speculations as to whether this group belong to the tribal or non-tribal population. This group lives in Maharashtra practising agriculture, speaking Marati and Hindi. They have been classified as tribals in Maharashtra but have been found to be closer morphologically to the non-tribal Central Indian group in the study (Plate 1). This is further confirmed by Haimendorf's assesment that the Andhs were mistakenly classified as a tribe (personal communication, 1981).

G **Kumbi Mane** : This group was measured by Karve, (1951) in Maharashtra and is mentioned in her monograph as being perhaps a mixture of Kumbi with Gond as they were quite different from the larger group of Kumbi Tiriole. In this study they have been found to be morphologically closer to the tribal groups of Central India rather than to the Kumbi Tiriole who along with Marathas belong to the non-tribal cluster of Central India.

conclusion it has been found that the Gonds of the sent study (southern Gond area) belong to the larger tral Indian tribal group with whom they overlap considerably. This is further substantiated by the fact that they are geographically and culturally contiguous with each other. The Central Indian and Orissa and Chotanagpur clusters form distinct clusters with only a small degree of overlap between the clusters. This difference between the two clusters may indicate the intrusion of the Mongoloid element into a people who had common origin from the Central Indian tribal groups. This Munda-speaking group reside on the high plateau of Chotanagpur which is 3,000 - 4,000 feet above sea level, being steepest on the western side. Hence the contact of this group is more with the people on the eastern side and admixture probably occurred in historical times with Mongoloid population living near the Himalayan foothills in the DUAR area near Bhutan. This area is geographically most accessible and closest to the eastern extremity of the hills of Chotanagpur (Rajmahal Hills) across the southern banks of the Ganges The hills of Assam and Nagaland are far too remote from this area because of the large intervening region of the Gangetic delta of Bengal.

The Southern Indian groups has been represented by only three populations in the study due to the paucity of comparable data available and hence firm conclusions cannot be arrived at this juncture. However, it appears that these three populations are morphologically close to each other and differ from the Central Indian and Orissa tribal groups from whom they are separated by large tracts of fertile delta land formed by the Krishna and Godavari rivers.

CHAPTER - 6 : COMPARISON OF GONDS WITH OTHER TRIBAL GROUPS BASED ON GENETIC CHARACTERS

Collection of published data

Data on genetic markers (blood groups, serological and biochemical) on various tribal populations of India was collected from published sources. Those populations having data of one or more of the 7 genetic markers in common with those included in the present study on the Gonds were collected and noted in the Table 1 with the code names and area of sampling. This collage of data shows a lot of gaps revealing the lack of systematic work done on this group which makes any general comparative analysis difficult. All 43 of these groups had information on only ABO blood group. The populations that had information on four common genetic markers (ABO, MN, Rh and Haemoglobin) were 23 in number and of which only 9 had all the seven biochemical markers in common, indicating the paucity of data. The gene frequencies of the various genetic markers is given in the Table 36. The ABO gene frequency of the various groups was recalculated by maximum likelihood method from phenotypic frequency so as to be comparable with that of the Gond study.

Genetic diversity between tribal groups

In the case of studying diversity within a population based on discretely transmitted Mendelian traits it only suffices to estimate the gene frequency

Table 36

Data on blood groups and biochemical markers used for analysis

Populations	Symbol region	ABO			Rh		MN		Hb		Hp		Tf		G6PD	
		A	B	O	D	d	M	N	A	S	Hp1	Hp2	C	Not C	Deficient	Normal
A	●	0.2173	0.2173	0.5654												
B2	●	0.2440	0.2210	0.5350	0.8730	0.1270	0.5660	0.4340	0.9140	0.0860	0.1030	0.8970	0.9890	0.0110	0.0660	0.9340
B3	●	0.2044	0.2505	0.5451	0.8302	0.1698	0.5854	0.4146	0.9190	0.0810						
BT	●	0.2192	0.2746	[illegible]												
BA	●	0.3837	0.2796	0.3367												
DH	●	0.4270	0.1548	0.3883												
DK	●	0.3262	0.2826	0.3911												
G1	●	0.2465	0.2176	0.5359												
GD2	●	[illegible]	0.2601	0.5492	0.8958	0.1042	0.7594	0.2406	1.0000	0.0000						
GD3	●	0.1715	0.3065	0.5219	0.9955	0.0045	0.8289	0.1711	0.9357	0.0643						
GD4	●	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.7844	0.2156	0.9866	0.0134						
GJ	●	[illegible]	0.2239	0.5143												
HL	●	0.2204	0.1876	[illegible]												
HM3	●	0.2239	0.2932	0.4829	1.0000	0.0000	0.7549	0.2451	0.9216	0.0784	0.1341	0.8659	1.0000	0.0000	0.1667	0.8333
HS2	●	0.3136	0.2501	[illegible]	0.9573	0.0427	0.6975	0.3025	0.9980	0.0020						
IU	●	0.2182	0.2373	0.4257	0.8821	0.1180	0.6460	0.3542	0.8570	0.1430	0.1590	0.8410	1.0000	0.0000		
K	●	0.0111	0.2359	0.7530	1.0000	0.0000	0.8186	0.1814	1.0000	0.0000	0.1472	0.8528	1.0000	0.0000		

Table 56

Data on blood groups and biochemical markers used for analysis

(continued)

Populations	Symbol region	ABO			Rh		MN		Hb		Hp		Tf		G6PD	
		A	B	O	D	d	M	N	A	S	Hp1	Hp2	C	Not C	Deficient	Normal
KA	●	0.117	0.1701	0.7182	0.9411	0.0589	0.8108	0.1892	0.9953	0.0047	0.3028	0.6972	1.0000	0.0000	0.0000	1.0000
KI	●	0.1995	0.1793	0.6213												
KL1	●	0.1748	0.3527	0.4725	0.7575	0.2425	0.7857	0.2143	0.9648	0.0352	0.0730	0.9270	0.9597	0.0403	0.0000	1.0000
KL2	●	0.2738	0.1863	0.5399												
KM	●	0.3499	0.1681	0.4819												
KO	●	0.118	0.1980	0.6840	0.7657	0.2343	0.6364	0.3636	0.9778	0.0222						
KR1	●	0.2282	0.2282	0.5437												
KT	●	0.2606	0.2069	0.5325												
KU	●	0.2812	0.1292	0.5896	0.8790	0.1210	0.7590	0.2410	0.8950	0.1050	0.1340	0.8660	1.0000	0.0000		
KY1	●	0.2452	0.1814	0.5734	0.9231	0.0769	0.8211	0.1789	0.9671	0.0329	0.0645	0.9355	0.9895	0.0105	0.0076	0.9924
KY3	●	0.2274	0.1946	0.5780	0.8771	0.1229	-	-	0.9599	0.0401	0.0889	0.9111	0.9707	0.0293	0.1887	0.8113
M	●	0.2190	0.1846	0.5964	0.8775	0.1225	0.6000	0.4000								
MD1	●	0.2420	0.1310	0.4770												
MH1	●	0.2254	0.2981	0.4785												
MH2	●	0.2185	0.2150	0.5366	0.7879	0.2121	0.5775	0.4225	1.0000	0.0000	0.0966	0.9034	-	-	0.0500	0.9500
MN	●	0.2099	0.2347	0.5554	0.8620	0.1380	0.8812	0.1188	0.9870	0.0130	0.0573	0.9427	0.9789	0.0211	0.0000	1.0000

Table 36

Data on blood groups and biochemical markers used for analysis (cont'd)

Population	Symbol region	ABO			Rh		MN		Hb		Hp		Tf		G6PD	
		A	B	O	D	d	M	N	A	S	Hp1	Hp2	C	Not C	Deficient	Normal
MR	●	0.0904	0.2651	0.6445												
N	●	0.1040	0.2127	0.6833	1.0000	0.0000	-	-	0.9767	0.0233	0.1585	0.8415	0.9667	0.0333	[illegible]	0.9922
NT	●	0.2104	0.2212	0.5684	0.9118	0.0882	0.4942	0.5058	0.9160	0.0840						
03	●	0.2000	0.2700	0.5300	1.0000	0.0000	0.6160	0.3840	1.0000	0.0000	0.1500	0.8500	0.9680	0.0320		
PB	●	0.2026	0.2754	0.5220	0.9367	0.0633	0.7079	0.1903	1.0000	0.0000						
PK	●	0.2250	0.2711	0.5064	0.9954	0.0046	0.7711	0.2289	0.9309	0.0691						
PM	●	0.1985	0.1865	0.6150	0.8606	0.1393	0.8981	0.1019	0.9191	0.0808	0.0937	0.9063	0.9907	0.0093	0.0619	0.9381
PR2	●	0.1268	0.2834	0.5898	1.0000	0.0000	-	-	0.8264	0.1726	0.1471	0.8529	1.0000	0.0000	[illegible]	1.0000
RG1	●	0.2226	0.2968	0.4806	0.7211	0.2789	0.8187	0.1813	0.9286	0.0714	0.0909	0.9091	0.9720	0.0280	0.0659	0.9341
RG2	●	0.2559	0.2587	0.4854	0.7288	0.2712	-	-	0.9416	0.0584	[illegible]	[illegible]	[illegible]	[illegible]	0.2253	0.7747
SN	●	0.2130	0.2680	0.5190	1.0000	0.0000	-	-	0.9940	0.0060	0.1401	0.8599	-	-	0.1402	0.8598
TD	●	0.1720	0.3720	0.4560	0.7320	0.2680	0.8750	0.1250	0.9950	0.0050	0.2800	0.7200	1.0000	0.0000		
WR	●	0.2711	0.1395	0.5894												

in the population from which all relevant inference can be made. The quantity of importance in such traits is the proportion of heterozygous individuals, which under random mating, is mathematically equivalent to the compliment of the sum of squares of gene frequencies. This is defined as the heterozygosity or co-efficient of gene diversity (Nei, 1973). Lewontin (1972) proposed another index for such Mendelian traits following the concept 'entropy' used in information theory. The following are the indices of diversity used

1. Lewontin (log) diversity

For 3 allelic system (ABO)
Groups

$$\begin{array}{llll} 1. & p_1 & q_1 & r_1 \\ \vdots & \vdots & \vdots & \vdots \\ n & p_n & q_n & r_n \end{array} \qquad \begin{array}{l} \dfrac{-p_1 \log p_1 - q_1 \log q_1 - r_1 \log r_1}{-\log 1/3} \\ \dfrac{-p_n \log p_n - q_n \log q_n - r_n \log r_n}{T_1 \text{ (within)}} \end{array}$$

$$\bar{p} \quad \bar{q} \quad \bar{r} \qquad -\bar{p} \log \bar{p} - \bar{q} \log \bar{q} - \bar{r} \log \bar{r} = T_2 \text{ (Total diversity)}$$

$$G = T_2 - \frac{T_1}{n}$$

(Between group diversity)

For 2 allelic system

$$\frac{-p \log p - q \log q}{-\log \frac{1}{2}}$$

the rest as carried out for 3 allelic system.

. Nei's index of diversity

For 3 allelic system

$$\frac{1 - p^2 - q^2 - r^2}{2/3}$$

Table 37

Index of diversity between populations for various biochemical markers and blood groups

Locus	No. of populations	Diversity 1		Diversity 2	
		Total	G	Total	G
Blood groups					
1. ABO	46	0.9011	.0219	0.8911	0.0203
2. Rh	29	0.4788	0.1648	0.3699	0.0962
3. MN	24	0.8429	0.0539	0.7903	0.0625
Biochemical					
4. Hb	28	0.2696	0.1365	0.1759	0.04718
5. Hp	19	0.5523	0.0433	0.4469	0.0371
6. Tf	17	0.1915	0.1241	0.0522	0.0134
7. G6PD	14	0.3922	0.1652	0.2350	0.0781

roups

1 p_1 q_1 r_1 $\left(\frac{1 - p_1^2 - q_1^2 - r_1^2}{2/3} \right)$

2 p_2 q_2 r_2 . . . .

n p_n q_n r_n $(1 - p_n^2 - q_n^2 - r_n^2)/2/3$

T_1' (within)

erage $\bar{p}$ $\bar{q}$ $\bar{r}$ $\frac{1 - \bar{p}^2 - \bar{q}^2 - \bar{r}^2}{2/3} = T_2$

G' (between diversity) $= T_2' - \frac{1}{r} T_1' / T_2'$

or 2 allelic System

$$\frac{1 - p^2 - q^2}{\frac{1}{2}}$$

... the rest as carried out for 3 allelic system.

th these indices of diversity were calculated between he tribal groups for each of the seven genetic markers. ble 37)

he index of diversity G and G' between groups for the ghly polymorphic traits showed only a 6 percent versity. However, in the case of these genetic aits which had allelic frequencies with extreme lues like for G6PD and Rh, the index G (Lewontin) owed more diversity than Nei's index G' as would be pected from the structure of the formulas. Nei's dex would suppress the diversity in the case of treme allelic values whereas Lewontin's would aggerate the diversity. The question would arise to which would be a more suitable measure of versity to use, especially when dealing with rarer netic traits. In such cases, if Lewontin's versity was small between the groups it would all more confirm that the genetic diversity as such tween these groups is extremely small. This problem selection between the two indices would not arise the case of those genetic traits such as ABO etc. ich have intermediate allelic values. The small netic diversity seen between these tribal groups comparable to the diversity seen in other racial oups such as between Caucasians, Mongoloid and groid races (Chakraborti, 1980 and Nei 1975). A nparison of the 'between' versus 'within' race riation of the three types of characters (biochemical, rmatoglyphic and anthroponetric) suggest that while e average V_B / V_W ratio for the pure Mendelian traits d the highly heritable one (dermatoglyphic) is only 13 the imperfectly heritable anthropometric variables eld an average V_B / V_W ratio of 1.11 which is almost 6 times of the variance ratio of the biochemical and rmatoglyphic traits (Chakraborti, 1980). The rrespondence between the variance ratios and the gree of genetic determination is poor which again stifies Nei's conclusion that the dynamics of racial fferentiation at the morphological level do not obably obey the rule that can be postulated for the namics of differentiation at the structural gene vel. A number of studies (King and Wilson, 1975;

herry, Case, Wilson, 1978) give support to the proposal that morphological evolution and biochemical volution in structural genes can proceed at independent ates. Biochemical comparisons made with proteins nd nucleic acids indicates that humans are remarkably milar to Chimpanzees at the gene level. The structural genes of this pair of species are more imilar than the structural genes of most pairs of pecies within a genus, regardless of whether the pecies compared are vertebrates or invertebrates. is biochemical picture however, contrasts with that ovided by morphologist who assign Chimpanzees and mans not just to separate species but to separate onomic families. Thus the morphological difference tween these two species appears large, whereas the ochemical difference is small. It is also possible at the effect of random genetic drift is more on ese qualitative Mendelian traits which increases e diversity within groups thus reducing diversity tween groups. Nei, (1975) suggested that the genes trolling these morphological characters were bject to stronger natural selection than 'average es' in the process of racial differentiation.

parison of tribal groups based on ABO gene frequencies

ious measures of distance were used to compare 43 bal groups for the ABO blood group system. The owing distance measures were used

TABLE 38 COORDINATES FOR TWO DIMENSIONAL PLOTS OF A B O GENE FREQUENCIES WITH DISTANCES OF SANGHVI, NEI AND BHATTACHARYA TYPES

Populations	P	Q	R	SANGHVI X	SANGHVI Y	NEI X	NEI Y	BHATTACHARYA (STEREOGRAPHIC) X	BHATTACHARYA (STEREOGRAPHIC) Y
A	.2173	.2273	.5554	.5347	.4914	.3264	.2173	.4508	.8727
B2	.2440	.2210	.5350	.6004	.7203	.3961	.2440	.5254	.8475
B3	.2044	.2505	.5451	.5030	.7626	.4073	.2044	.4645	.8811
BT	.2192	.2746	.5062	.5394	.8324	.4436	.2192	.4768	.8979
BA	.0837	.2796	.6367	.2260	.7437	.3712	.0837	.3193	.8092
DB	.2270	.1348	.6383	.5586	.6194	.3444	.2270	.4946	.8020
DK	.3262	.2826	.3911	.9027	.9316	.5147	.3262	.3724	.9416
GI	.1465	.2176	.6359	.3605	.6394	.3358	.1465	.4070	.8041
GD2	.2304	.2601	.5095	.5670	.5054	.4334	.2304	.4888	.8815
GD3	.1826	.3065	.5109	.4493	.8229	.4593	.1826	.4180	.9060
GD4	.2032	.3136	.4832	.5000	.9155	.4794	.2032	.4186	.9214
GJ	.2555	.2259	.5186	.5287	.7408	.4084	.2555	.4133	.9774
HL	.2264	.1376	.6360	.5371	.6238	.3473	.2264	.4916	.9049
HM3	.2259	.2932	.4809	.5339	.5827	.4640	.2259	.4625	.7517
HS2	.2136	.0901	.6963	.7727	.3161	.3045	.2136	.3379	.8968
IU	.2050	.3570	.4380	.5045	.9739	.3175	.2050	.4394	.9441
K	.2111	.2339	.5550	.3273	.5831	.2788	.2111	.1618	.7603
KA	.2117	.1701	.6182	.2749	.4977	.2609	.2117	.3720	.7384
KI	.1995	.2793	.5213	.4909	.3955	.3222	.1995	.4689	.7848
KL1	.1748	.2527	.5725	.4302	.9896	.3082	.1748	.4276	.9433
KL2	.2738	.1863	.5399	.6738	.4579	.3732	.2738	.5369	.8228
KM	.3499	.1682	.4819	.4610	.5702	.3461	.3499	.4039	.8342
KO	.1130	.3980	.4890	.2924	.3704	.1968	.1130	.3756	.7727
KR1	.2282	.2282	.5437	.5916	.7160	.2953	.2282	.4898	.8484

TABLE 38 COORDINATES FOR TWO DIMENSIONAL PLOTS OF A B O GENE FREQUENCIES WITH DISTANCES OF SANGHVI, NEI AND BHATTACHARYA TYPES

(Continued)

Populations	P	Q	R	SANGHVI X	SANGHVI Y	NEI X	NEI Y	BHATTACHARYA (STEREOGRAPHIC) X	BHATTACHARYA (STEREOGRAPHIC) Y
KT	.1606	.1154	.5305	.6413	.4933	.3494	.2406	.5222	.8196
KU	.1812	[illegible]	.5396	.6920	.5243	.3115	.2812	.3546	.7590
KY1	.1452	.1514	.5734	.6634	.5247	.3510	[illegible]	.5121	.8057
M	.2190	.1448	.5961	.5389	.6129	.3096	.2190	.4871	.7956
KT3	[illegible]	[illegible]	.5780	.5596	.6436	.3560	.2274	.4935	.8128
KO1	.1420	[illegible]	.4770	.5935	.5650	.4642	.2420	.4979	.9068
MH1	[illegible]	[illegible]	.4765	.5547	.5943	[illegible]	[illegible]	.4812	.9162
MH2	.1183	[illegible]	.5588	.5277	.7110	[illegible]	.1960	.4809	.8411
MN	[illegible]	[illegible]	[illegible]	.5165	.7282	[illegible]	[illegible]	.4715	.8475
MR	[illegible]	[illegible]	.6445	.2225	.7153	.3383	.2404	.3305	.8281
N	[illegible]	[illegible]	.6633	.5554	.5498	.3056	.1340	.3553	.7813
NT	[illegible]	[illegible]	.5534	.5178	[illegible]	.2759	.2174	.4736	.8339
[illegible]	[illegible]	[illegible]	[illegible]	.4422	.5168	[illegible]	[illegible]	.4383	.8784
[illegible]	[illegible]	[illegible]	[illegible]	.4536	.8420	.4330	.2026	.4605	.8847
[illegible]	[illegible]	[illegible]	[illegible]	.5537	.8282	.4429	.2250	.4821	.8689
PM	[illegible]	[illegible]	[illegible]	.4855	.7323	.3300	.1945	.4668	.7923
[illegible]	[illegible]	[illegible]	[illegible]	.3120	.7850	.4005	.1259	.3769	.8609
[illegible]	[illegible]	[illegible]	.4026	.5478	.4690	[illegible]	.2226	.4786	.9137
[illegible]	[illegible]	[illegible]	[illegible]	.6297	.6213	.4465	.2599	.5124	.8908
[illegible]	[illegible]	[illegible]	[illegible]	.7242	.5117	[illegible]	.3120	.4713	.8818
TD	[illegible]	[illegible]	[illegible]	.4233	1.0345	.3289	[illegible]	.3629	.4240
WR	[illegible]	[illegible]	[illegible]	[illegible]	.4637	.3753	[illegible]	.3340	.8232
Average	[illegible]	[illegible]	[illegible]	0.5315	[illegible]	0.4038	0.2287	0.4643	0.8522

Sanghvis distance

The co-ordinates were plotted for 43 populations on a two dimensional plot (Table 38).

$$x = \frac{p}{\sqrt{\bar{p}\,(1 - \bar{p})}}$$

$$y = \sqrt{\frac{\bar{q} + \bar{r}}{\bar{q}\;\bar{r}}}\;q + \sqrt{\frac{\bar{5}}{\bar{r}\,(\bar{q} + \bar{r})}}\;p$$

Bhattacharya's (sterographic) distance

The following are the co-ordinates

$$x = \frac{2(\sqrt{p} + \sqrt{1/3}}{1 + \sqrt{1/3}\,(\sqrt{p} + \sqrt{q} + \sqrt{r})} - \frac{1}{\sqrt{3}}$$

$$y = \frac{2z + x}{\sqrt{3}}$$

$$z = \frac{2(\sqrt{q} + \sqrt{1/3}}{1 + \frac{1}{\sqrt{3}}\,(\sqrt{p} + \sqrt{q} + \sqrt{r})} - \frac{1}{\sqrt{3}}$$

Nei's distance

Points were plotted in an equilaterial triangle, the distance between points representing Nei's genetic distance (Table 38). The following are the co-ordinates :

$$x = p$$

$$y = \frac{2q + p}{\sqrt{3}}$$

3 distance measures show a similar distribution populations based on ABO gene frequencies. All populations though belonging to different

geographical areas showed no diversity, clustering together in the centre (Figs **15, 16** and **17**) of the two dimensional plots. It appears that ABO alone does not seem to differentiate these different populations and this was also found to be the case *in the Bengal study (Mazumdar and Rao, 1945).*

In the Bengal study 14 populations representing Hindu higher castes and lower castes, Muslims and tribals showed a χ^2 value of 6.27 which is not very high for 6 *degrees of freedom. Differences between the caste* groups and tribals seem to exist the tribals having a low frequency for the O gene and somewhat higher for B, which seems to be a significant finding. However, caution is necessary because of the paucity of the material and that the information on the tribals is based solely on D.N. Mazumdar's data (Rao, 1945). The study of Mazumdar (Ph D thesis, 1980) who based his work on an examination of 899 published data sets on ABO blood group indicated wide variability in all geographical zones and most socio-religious categories in India. When χ^2 tests of homogeneity within 32 geographical and socio-religious sub-sects were carried out, only 13 sub-sects were found homogenous in respect for ABO gene frequencies. However, the study of Balakrishna, (1978) who based his study on both ABO as well as Rh blood groups from published studies showed the tribal

FIGURE 15

Distribution of ABO gene frequencies of tribal populations based on Sanghvi's Distance

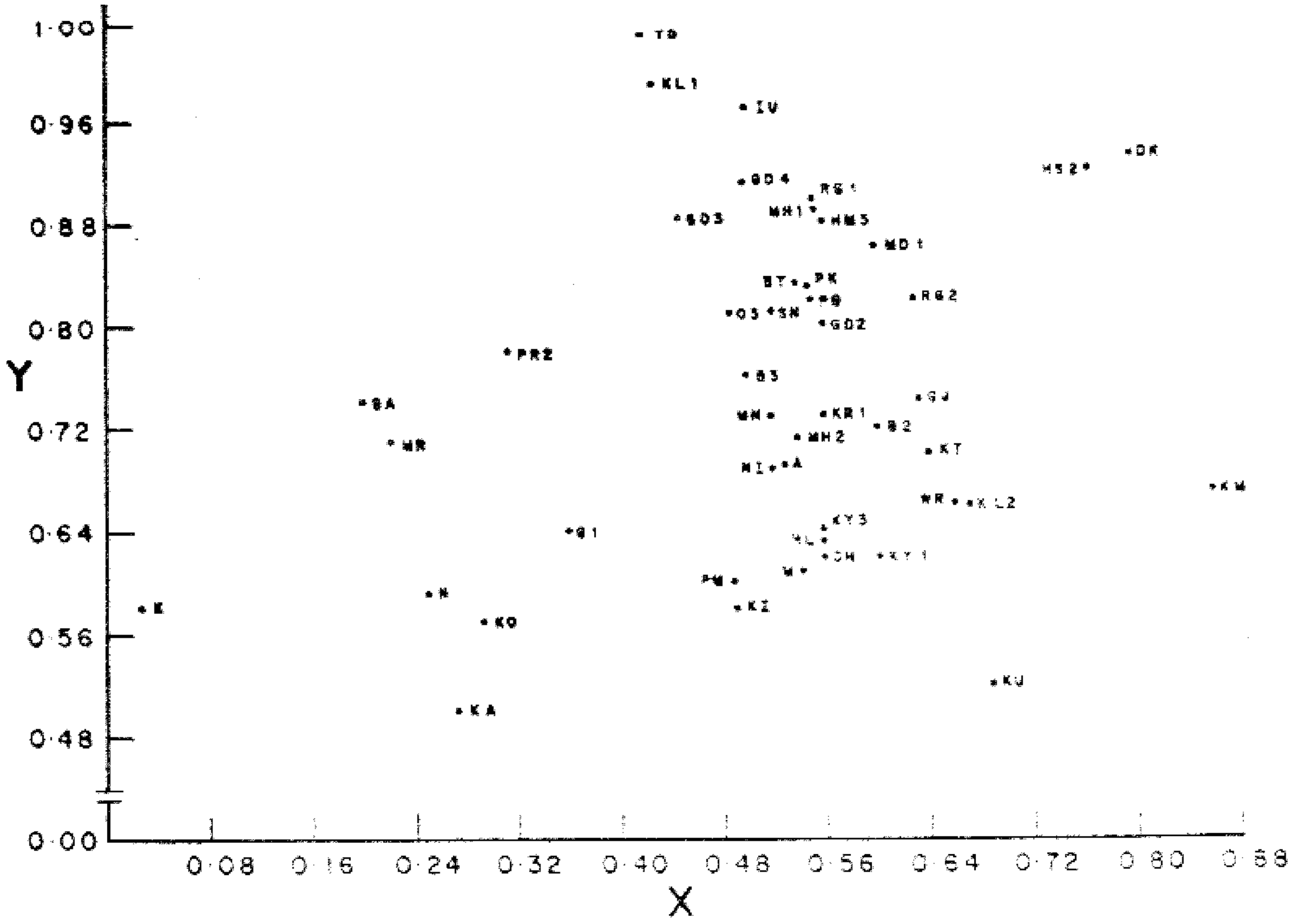
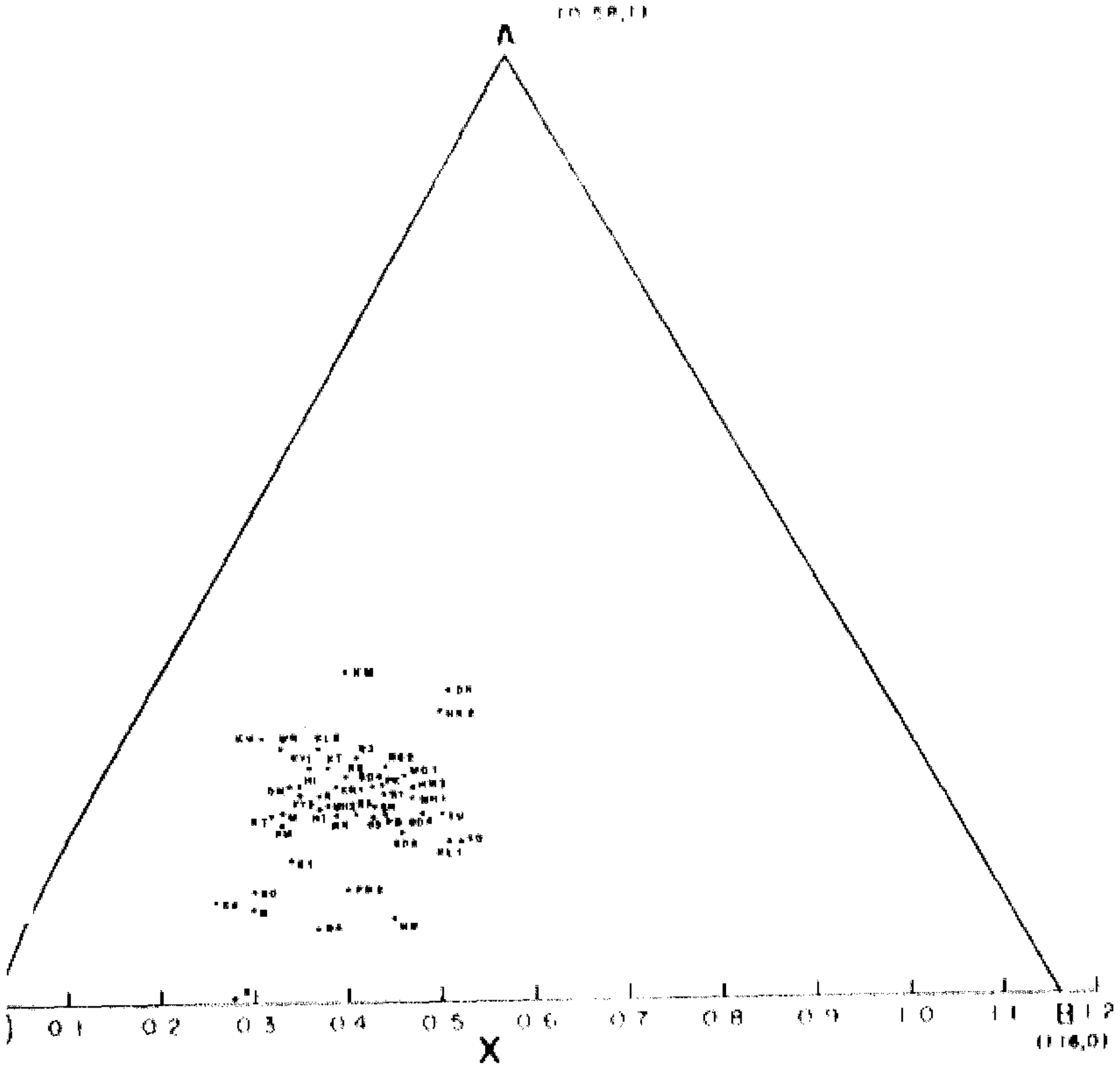


FIG.15. DISTRIBUTION OF ABO GENE FREQUENCIES OF TRIBAL POPULATIONS BASED ON SANGVI'S DISTANCE



DISTRIBUTION OF **ABO** GENE FREQUENCIES OF TRIBAL POPULATIONS BASED ON NEI'S DISTANCE

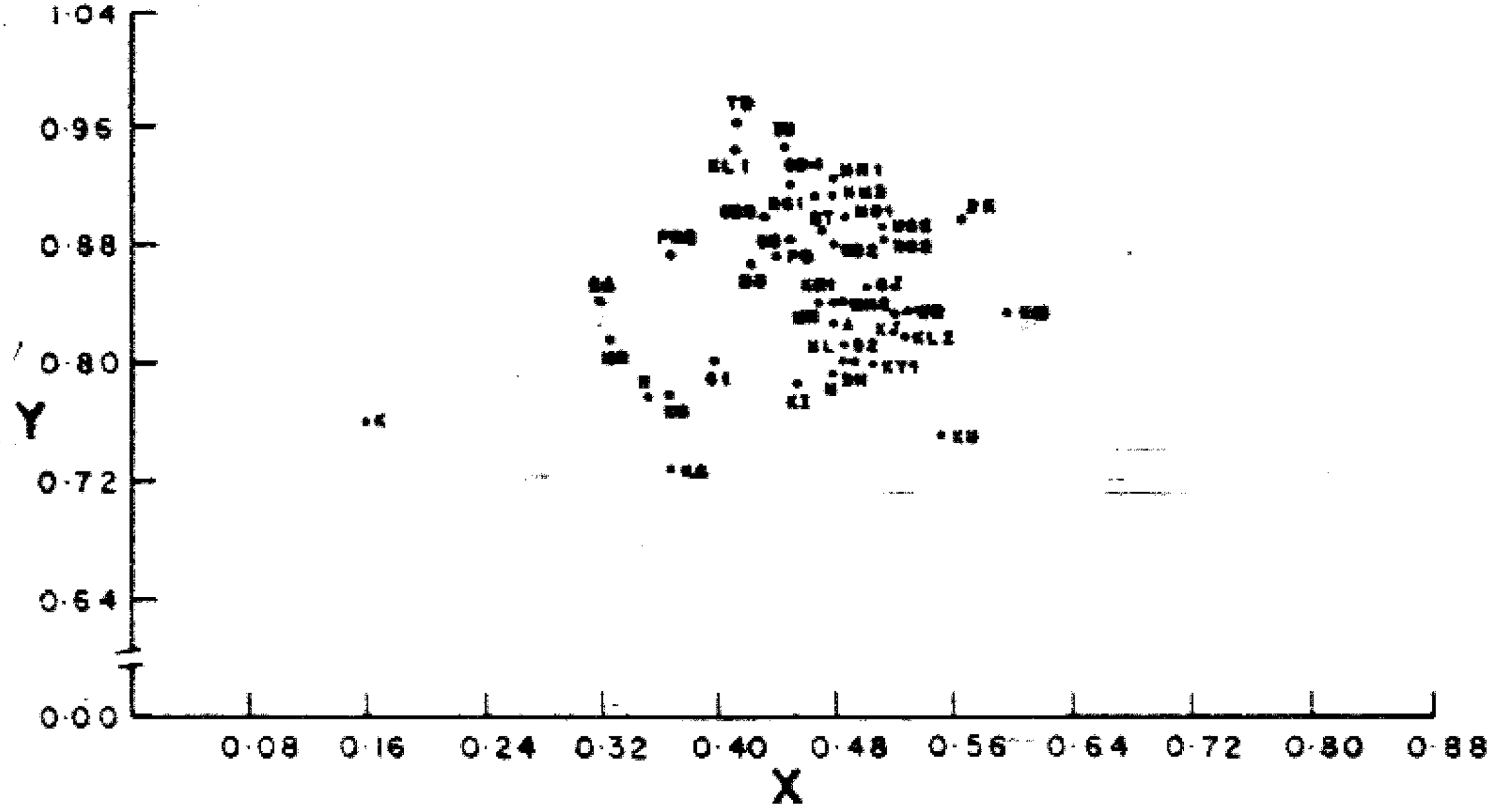


FIG. 17. DISTRIBUTION OF ABO GENE FREQUENCIES OF TRIBAL POPULATIONS BASED ON BHATTACHARYA'S DISTANCE

groups were distinct from non-tribal groups. The addition of another genetic marker like Rh to ABO probably helped in bringing out more clearly the differences between tribal and non-tribal groups.

Selection and use of multivariate methods to determine genetic relationship between tribal groups of India

3 populations having in common at least four genetic markers (ABO, Rh, MN and Haemoglobin) were selected for the analysis. They also belonged as in the case of those populations used for anthropometric study to the same three geographical regions.

Genetic distance : Genetic distance based on attribute data is an attempt to express by a single number how much difference there is in genetic constitution between two populations. The greater the difference between two gene frequencies, the greater the distance (instead of gene frequency, phenotype frequencies may be used for DNA sequences). The motives for considering genetic distance are of two kinds

1. To reduce a complicated mass of data to easily visualisable form.
2. In general, to reconstruct the evolutionary history of the populations concerned.

Thus two populations may be similar, with small genetic distance apart if they are recently descended from a common ancestral population which split up or as a result of selective forces bringing heir gene frequencies nearer together. A review f various genetic distance measures is given by mith, 1977.

he measures of genetic distance most often used n practice are those based essentially on the idea f Mahalanobis's D^2. One such measure used in the present analysis is :

1. G_c^2 (Sanghvi and Balakrishnan)

   The same fundamental assumption in Mahalonobis's D^2 is followed, that is, while the populations may differ in their mean gene frequencies, all of them have the same dispersion matrices. In actual practice, such a situation is rare, but this assumption is at least theoretically possible in the case of normally distributed quantitative characters. When we come to multinominal distributions, there is no longer so, since the variances and co-variances are dependent on the means. However, when this point was examined by Sanghvi and Balakrishnan, this defect was found to be not really serious in practice. The distance measured is calculated as follows :

   G^2_c (between populations i and j) == due to ABO

$$\frac{(p_i - p_j)^2}{\bar{p}} + \frac{(q_i - q_j)^2}{\bar{q}} + \frac{(r_i}{}$$

where $\bar{p}$ is the average gene freque

p^{th} allele over all populations co

G^2_c (populations i and j due to MN system) =

$$\frac{(m_i - m_j)^2}{\bar{m}} + \frac{(n_i - n_j)^2}{\bar{n}} = X_2$$

where $\bar{m}$ is the average m allele frequency over all populations concerned.

Total $G^2_c = X_1 + X_2$

Nei's genetic distance or Euclidean distance

In a study of the number of gene differences between related species, Nei developed a statistical method for estimating the number of codon differences per gene and the divergence time between closely related species. This method utilises electro-phoretic data on protein identity between different species. However, this method is not very useful for a study of gene differences between races of closely related local populations within a species, since the gene differences are not large enough for the effect of polymorphism within populations to be neglected. Recently, Nei (1972) modified his method taking into account the effect of polymorphism within populations. He defined the normalised identity of genes between populations, which is equivalent to protein identity. He then related it to the accumulated number of gene differences per locus which was now called genetic distance. This measure of genetic distance according to Nei has several advantages over those proposed by Cavalli Sforza and Edwards (1967), Balakrishnan and Sanghvi (1968) and others.

(A) It is related to Malecot's co-efficient of kinship in a simple way.

(B) It measures the accumulated number of gene substitutions per locus.

(C) If the rate of gene substitutions per year is constant, it is linearly related to evolutionary time.

(D) In some migration models it is linearly related to geographical distance or areas.

$$\text{Nei's } D_{ij} \text{ (for ABO)} = (p_i - p_j)^2 + (q_i - q_j)^2 + (r_i - r_j)^2 = Y_1$$

$$D_{ij} \text{ (for MN system)} = (m_i - m_j)^2 + (n_i - n_j)^2 = Y_2$$

$$\text{Total } D_{ij} = Y_1 + Y_2$$

Nei's and G^2_c distance matrices for the 23 populations are given in the APPENDICES V and VI. The two methods of cluster analysis (single linkage and complete linkage) and canonical coordinate analysis has been carried out on these two measures of distances as in the case of Mahalanobis's D^2 given in the preceding chapter.

Three dimensional models were made using canonical coordinates (Tables 39 and 40) based on both Nei's and Sanghvi's distances matrices with populations

TABLE 39

Canonical coordinates based on Nei's distance computed from ABO, MN, Rh and Hb data

Population	1	2	3	4
B2	1.009	0.359	0.037	0.013
B3	0.918	0.074	-0.028	-0.010
GD2	-0.309	0.459	-0.020	0.065
GD3	-0.708	0.333	-0.069	0.189
GD4	-0.312	0.078	-0.086	0.084
HM3	-0.273	0.462	-0.017	0.178
HS2	0.193	0.326	0.091	0.180
IU	1.180	-1.136	-0.057	0.078
K	-1.383	0.747	-0.063	-0.203
KA	-0.755	0.297	-0.040	-0.282
KL1	-0.081	-0.882	-0.157	0.047
KO	0.847	-0.358	-0.161	-0.340
KU	-0.010	0.102	0.673	-0.120
KY1	-0.490	0.101	0.229	-0.035
MH2	1.134	-0.056	-0.047	-0.087
MN	-0.735	-0.305	0.080	-0.005
NT	1.499	0.762	-0.027	-0.003
O3	0.364	0.838	-0.127	0.069
PR	-0.007	0.244	-0.069	0.028
PK	-0.339	0.405	0.015	[illegible]
PM	-0.922	-0.346	0.261	[illegible]
RG1	-0.131	-1.077	0.042	-0.020
TD	-0.690	-1.430	-0.162	0.076

TABLE 40

Canonical coordinates based on Sanghvi's Distance computed from ABO, MN, Rh and Hb Data

Population	1	2	3	4
B2	-0.283	-0.705	-0.045	-0.011
B3	-0.508	-0.505	0.014	-0.011
GD2	0.812	-0.053	0.046	0.071
GD3	0.795	0.110	-0.278	0.054
GD4	0.375	0.109	0.036	0.076
HM3	0.699	-0.203	-0.308	0.057
HS2	0.236	-0.289	-0.119	0.076
IU	-2.151	-0.285	-0.251	-0.003
K	1.566	0.493	0.291	-0.090
KA	0.764	0.408	0.253	-0.127
KL1	-0.798	0.439	0.066	0.066
KO	-0.823	-0.118	0.555	-0.134
KU	-0.111	-0.135	-0.508	-0.172
KY1	0.357	0.208	-0.081	-0.038
MH2	-0.699	-0.418	0.501	0.032
MN	0.111	0.546	0.018	0.011
NI	-0.101	-1.171	0.032	-0.019
O1	0.838	-0.542	0.200	0.035
PB	0.395	-0.083	0.135	0.048
PE	0.673	-0.112	0.248	0.037
PM	0.003	0.603	-0.329	-0.117
RG1	-1.153	0.532	-0.124	0.016
TD	-0.997	1.131	0.146	0.118

of three geographical areas represented by different colours similar to those used in the model on anthropometric measurement.

Results of multivariate analysis

1 Nei's genetic distance

A Cluster analysis

Both techniques of clustering, the single linkage and complete linkage methods based on Nei's distance matrix, cluster the populations according to geographical regions (Table 41). However, the single linkage method gives long and straggly clusters very early in the clustering process unlike the complete linkage method (Fig 18). At 0.002 level of clustering (Table 41) the single linkage method clusters almost all the populations together into one group whereas clustering continues to differentiate groups at even 0.015 level in complete linkage method. Though the clustering by geographical regions is evident in both methods, complete linkage method maintains a clear geographical diversity even as the clustering process progresses towards completion. The geographical clusters produced are the following

1 Southern Gond group (in red) is split into two groups .

2 Orissa and Chota Nagpur group (in yellow).

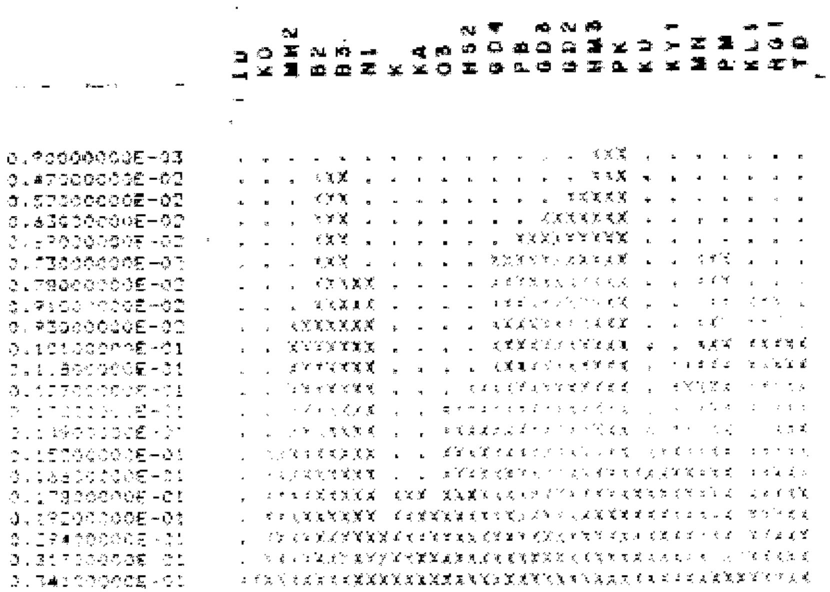
3 Central Indian Group (in green).

FIGURE 13

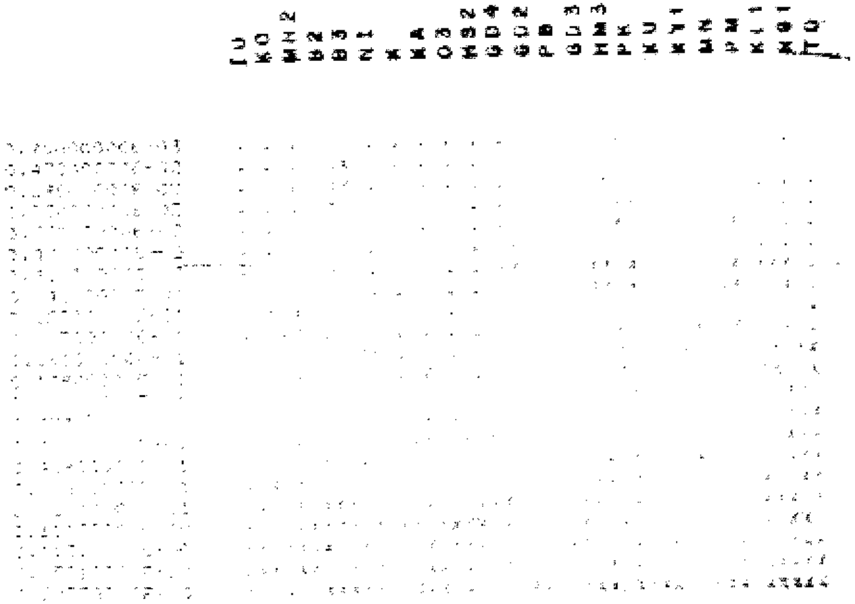
Nei's Genetic Distance(all tribal populations) : Cluster analysis

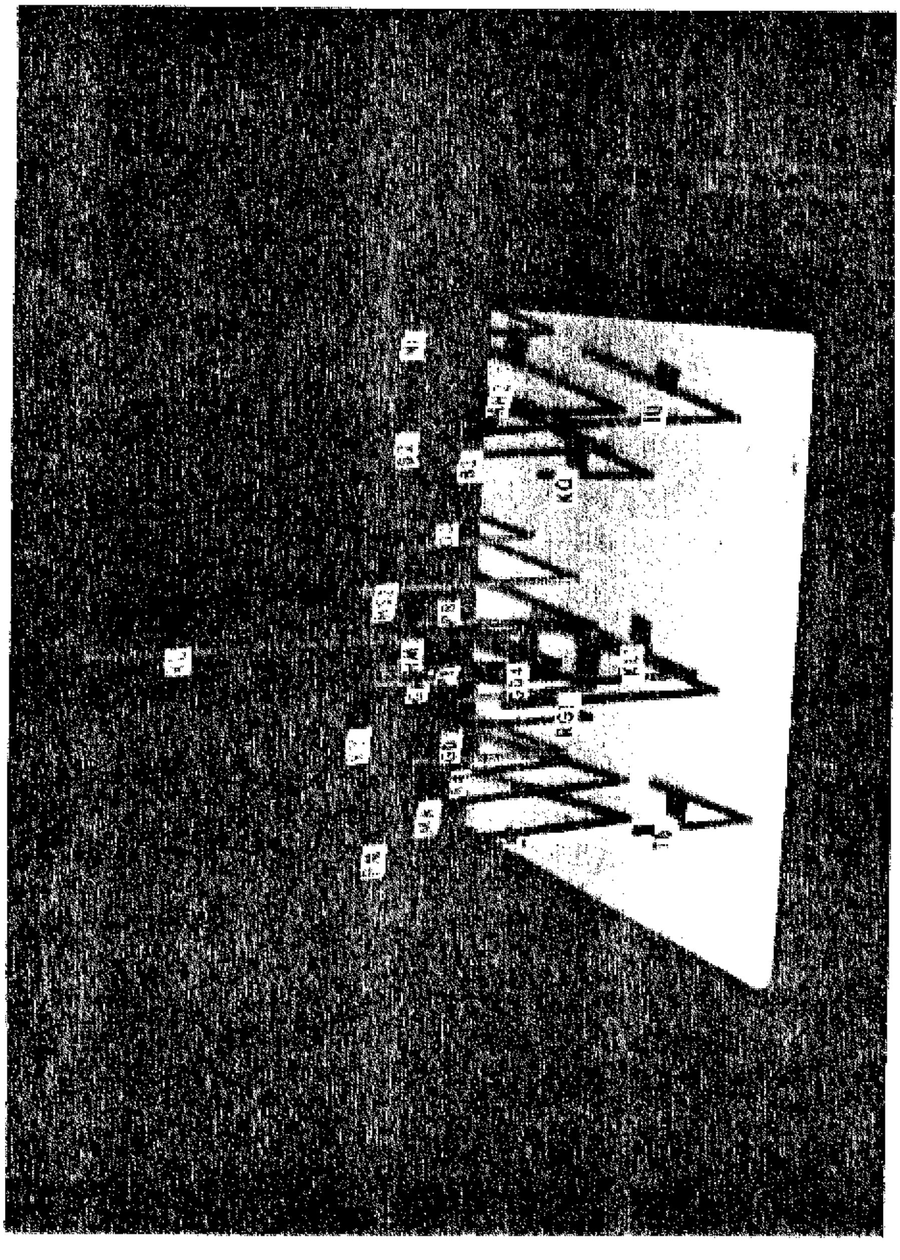
FIG. 18. Nei's Genetic distance (All tribal populations)
Cluster analysis

SINGLE LINKAGE METHOD



COMPLETE LINKAGE METHOD





However, the South Indian populations [illegible] [illegible] as a heterogeneous group, randomly interspersed among the various populations. The relationship of the various groups differs very slightly by the two methods of clustering. Both show that four of the six Gond populations of the present study (HM_3, PM, MM and KY1) are closer to Orissa group than to Central Indian group. The other two populations, the Raj Gonds and Kolams are neither close to the Orissa or to the Central Indian group.

B Canonical co-ordinate analysis

This was carried out directly from Nei's distance matrix as described in the methods. A three dimensional model was built based on the first three co-ordinates (Plate 2). The clustering of populations according to geographical regions was visualised quite clearly and showed a similar relationship between populations as seen by complete linkage method of clustering. Here too, four of the six Gond populations are closer to the Orissa and Chota Nagpur group with the Raj Gonds and Kolams being far apart from Orissa as well as Central Indian group. The heterogeneity of south Indian populations is seen very clearly when depicted in a three dimensional space.

Sanghvi's genetic distance

A Cluster analysis

Though the clustering appears to be generally similar by both methods (Fig 19) there appear to be some obvious inconsistencies between the two methods. (TABLE 42)

1 IU, a South Indian population found to be an outlier in single linkage method is shown to cluster closely with TD, KL1 and RG1 in complete linkage method.

2 KU which is a Central Indian population clusters with its own group in single linkage method and is placed between the Gonds of the present study and Orissa group in complete linkage method.

These inconsistencies are not found when based on Nei's distance matrices.

B Canonical analysis

The three dimensional model depicts the same general geographical clustering as seen by the clustering techniques and is most similar to single linkage method in the position of IU which is seen as outlier by both methods. However, K and KA which are both South Indian populations and which cluster together by both single linkage method and complete linkage method are seen to be quite diverse in three dimensional space. When all three methods are compared there is inconsistency in clustering based on Sanghvi's genetic distance.

TABLE 42 : SANGHVI'S GENETIC DISTANCE

linkage
thod

Complete linkage
Method

Visualised from three dimensional model (Canonical co-ordinate analysis)

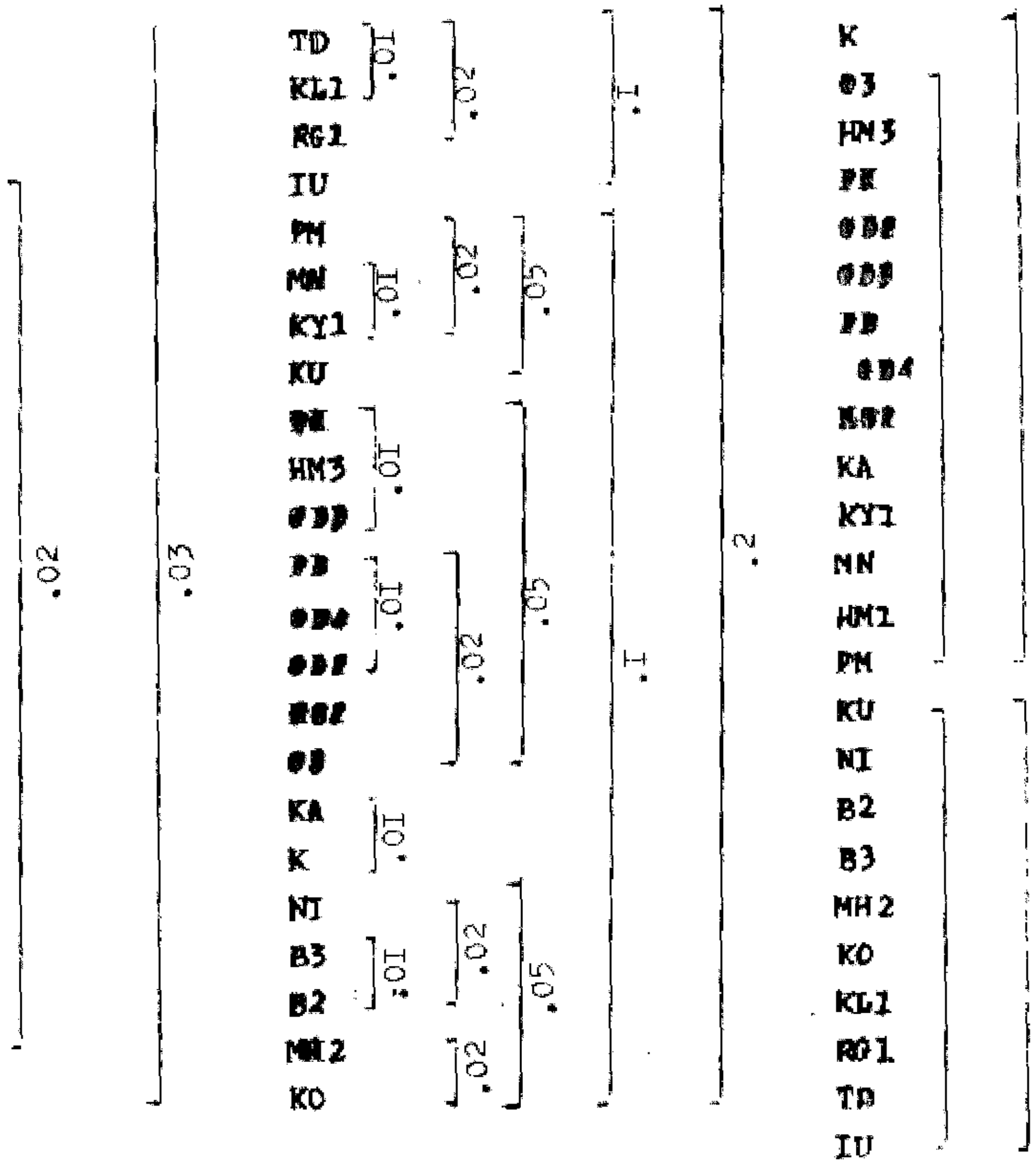
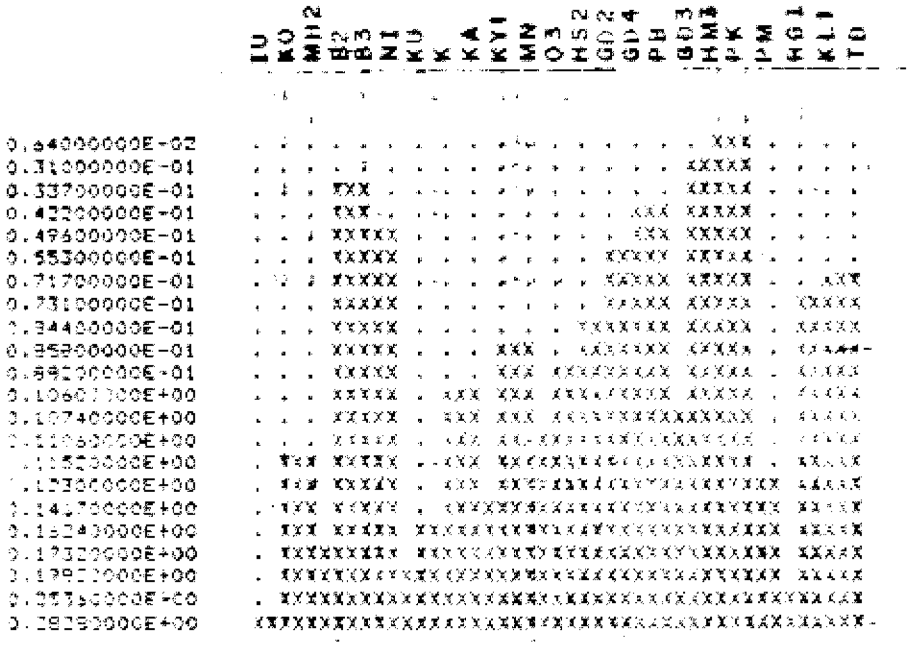

.02
.03
TD
KL1
RG1
IU
PM
MN
KY1
KU
PK
HM3
OD3
PB
OD4
OD2
MO2
O3
KA
K
NI
B3
B2
MH2
KO
.01
.02
.05
.1
.2
K
O3
HM3
PK
OD2
OD3
PB
OD4
MO2
KA
KY1
NN
HM1
PM
KU
NI
B2
B3
MH2
KO
KL1
RG1
TD
IU

FIGURE 19

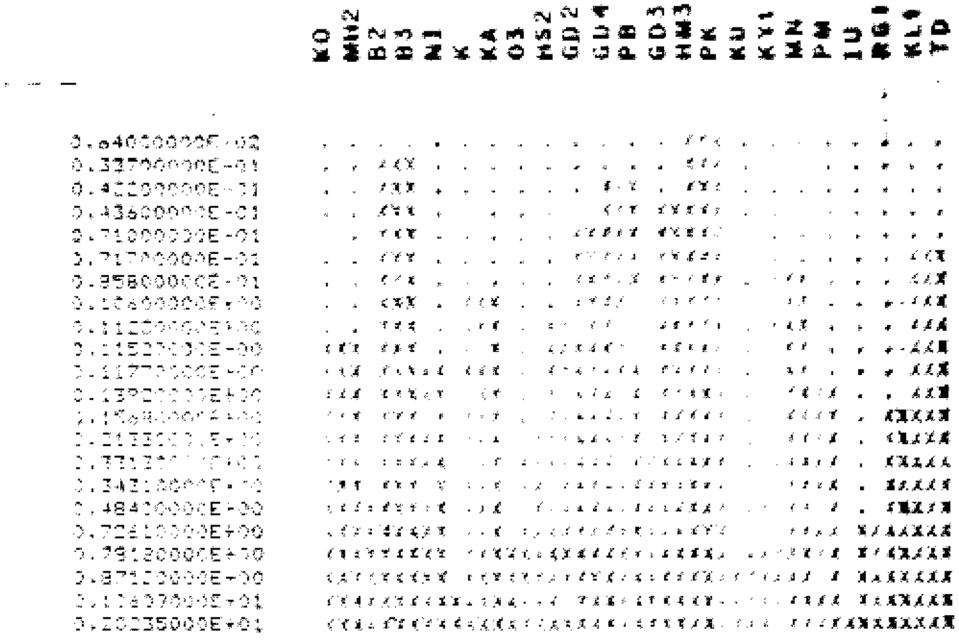
Sanghvi's Genetic Distance(all tribal populations) : Cluster analysis

FIG.19. SANGVI'S GENETIC DISTANCE (ALL TRIBAL POPULATIONS) CLUSTER ANALYSIS

SINGLE LINKAGE METHOD



COMPLETE LINKAGE METHOD



C Comparison of Nei's distance with Sanghvi's genetic distance

Though clustering based on both Nei's and Sanghvi's genetic distance show an overall similarity, some unexplained inconsistencies appear in all three methods of clustering based on Sanghvi's distance. Hence for the purpose of discussion of the results the interpretation based on Nei's genetic distance will be adhered to.

.5 Discussion

.5.1 GENETIC RELATIONSHIP BETWEEN TRIBAL POPULATIONS

The results based on the combination of these multivariate techniques shows clearly that the Orissa group (the Munda-speaking populations) and Central Indian group (Bhils, Mahars, Naikadas and Koli) each form a separate homogenous group. The Gonds of the present study however are split up into two groups, the Plains Maria Gonds (PM), the Manne (MN), Koyas (KY1) and Hill Maria Gonds (HM3) being closer to the Orissa cluster and the remaining two populations, the RajGonds and Kolams lying at a distance from both Orissa and Central Indian cluster. An interesting finding is that the South Indian group appear to be heterogenous within itself and the four populations representing it are distributed randomly in three dimensional space.
The Irulas and Kurumbas who live on the slopes of Nilgiri hills (Tamil Nadu) and who are morphologically

classified by anthropologists as belonging to a common group lie apart from each other. The Kotas and Todas who lived together in Symbiosis on the high plateau of the Nilgiri hills and who are more alike morphologically (Caucasiod) than with the Irulas and Kurumbas also showed divergence between each other. Since all these four populations have been analysed by the same group of workers (Saha, Kirk, Shanbhas, Joshi and Bhatia 1976) and using similar techniques, the only other explanation for this would be that they being small populations and living in geographically isolated areas were probably subject to considerable random genetic drift, resulting in diversity within the South Indian group. The Todas are a pastorolist group and the Kotas an artisan group who may have migrated later from the North to these Nilgiri hills and are linguistically and culturally different from the Irulas and Kurumbas who are primitive groups more indigenous to these areas. Besides, the Irulas and Kurumbas live on the hill slopes which are highly malarious as compared to the high plateau of the Todas and the Kotas which are highly malarious as compared to the high plateau of the Todas and the Kotas which is relatively free from Malaria. Hence the difference in geographical terrain can also make a difference to the micro-environment of these tribal groups producing a diversity between each other. The mountainous terrain of South India is a smaller area than that compared to Central India or Orissa and seems to produce more genetic diversity among its groups than within the Central Indian and Orissa tribal populations which show more genetic homogeneity within their geographical areas. The genetic markers used in this study are single gene markers which appear to be more subject to the effects of random genetic drift than the anthropometric measurements. The genetic diversity between the South Indian groups has been probably accentuated because of the micro-ecological diversity produced by the mountainous terrain of the Eastern and Western Ghats.

2 DIFFERENCE BETWEEN MORPHOLOGICAL AND GENETIC RELATIONSHIP BETWEEN THE TRIBAL POPULATIONS

The tribal populations based on both morphology and genetics clustered generally according to the geographical regions they belong. However, the relationship between the populations based on both these biological variables, did not correspond very well. This lack of correspondence is probably due to :

A) Smaller number of groups utilised in the genetic study due to lack of availability of data.

B) The populations used for genetic study are not exactly the same as those used in the morphological study.

The main differences seen between the two studies are:

1 Greater diversity within the south Indian populations in genetic characters as compared to morphology.

2 The relationship between the Gonds of the present study is different in both the studies. The Gonds are morphologically close to the Central Indian group whereas they are far apart from this group genetically. Four of the six Gond populations (Plains Maria Gonds, Hill Maria Gonds, Koya and Manne) are genetically closer to the Orissa group to whom they are geographically contiguous with whereas the other two consisting of Raj Gonds and Kolams are further apart from both Orissa and Central Indian group.

Some studies have shown the lack of correspondence between morphology and genetics may be due to the fact that morphological evolution and biochemical evolution in structural genes can proceed at independent rates (King and Wilson, 1975, Cherry, Case, Wilson, 1978). It is also possible that the effect of random genetic drift is more on these qualitative Mendelian traits which increases the diversity within groups thus decreasing diversity between groups.

6.6 A note on the techniques used in the present study

Tree structure is more appropriate for evolutionary studies, when one is tracing the time sequence for separation of species, families etc. It may not be appropriate for studying intra specific differences where the effects of separation at some point and later mixture due to migration and contacts cannot be isolated. In problems like that in the present study, it is more appropriate to study inter-relationships and explain similarities and dis-similarities between populations which may be in part due to environment, nutrition, and other factors.

CHAPTER 7 CONCLUSIONS AND GENERAL DISCUSSION

NCLUSIONS

Morphological and genetic relationship between the Gonds

Statistical analysis showed that the Gonds are a heterogenous group being morphologically and genetically different from each other, forming separate endogamous entities. In addition, this tribal endogamy has a territorial basis, each of these populations being located to distinct geomorphological areas.(Fig. 1)

The morphological and genetic distances between these groups when projected graphically revealed that the spatial distribution of these Gond populations generally corresponded to their present geographical distribution. The Manne lie intermediate forming the connecting link between the other four populations. The Raj Gonds and Plains Maria Gonds lie fartherest away from each other at two opposite poles. However, the actual relationship between each of the Gond populations show differences when based on these two different biological variables. The morphological relationship shows a greater variability, the clustering pattern differing between male and female Gonds. The Koyas move nearer the Manne and Raj Gonds and away from the Plains Maria Gonds in the males and away from the rest but nearer the Plains Maria Gonds in the females. The Kolams too show a variability in their position between sexes being far removed from all the groups in the males but moving very close to the Manne in the females. This variability in morphological relationship between sexes is difficult to interpret and may be in part due to differences in sex dimorphism and the greater degree of environmental influence on morphological characters.

The relationship based on genetic characters however is different from the morphological relationship and closely corresponds to the degree of geographical contiguity between the populations. The Raj Gonds and Kolams form a close cluster with Manne, Koyas and Plains Maria Gonds forming a second cluster. The Raj Gonds and Kolams live in close proximity to each other on the highlands consisting of black cotton soil which are contiguous with Marathwada, whereas the Manne, Koyas and Plains Maria Gonds lie on the east in the valley of Pranitha-Godavari and Indravathi rivers which is predominantly influenced by Telugu culture. The genetic characters unlike morphology are purely heritable and not influenced by environment and hence perhaps reflect more closely the effect of geographical proximity in producing a greater genetic similarity within these two clusters of Gond populations.

Interpretations based on morphological relationship between tribal groups

The tribals clustered according to the geographical gions they belong (Plate 1) and formed three main clusters :

1) Central Indian group (including Gonds of the present study).
2) Orissa and Chota Nagpur group.
3) South Indian group (south of Krishna river).

The Gonds of this study fall very close to the main ntral Indian cluster showing morphological closeness to those populations such as Bhils, Korkus and Gonds (of Madhya Pradesh). This is substantiated by the fact that there was a contiguous belt of Gond culture extending from Garha (Madhya Pradesh State) in the North to Chanda in the South (Maharashtra State) from at least the 14th century A.D to the 18th century when the Gond kingdoms were overthrown by the Marathas.

The Central Indian group and Orissa and Chota-Nagpur group form each a distinct cluster with a small degree of overlap between them. The eastern area consists of Munda-speaking tribal populations and is ecologically different from Central India in consisting of Sal forests (Shorea *robusta*) with an extensive rice cultivation in contrast to the Teak forests, Jowar (Sorghum *vulgare*) and cotton cultivation of Central Indian tribes. The difference between these two clusters may be also due to the possibility of inclusion of Mongoloid element due to admixture in the past, geographical factors having helped in cultural and probably genetic diffusion from eastern India into the Chota-Nagpur plateau, the centre of Munda culture. The plateau is steep and inaccessible on the west and south whereas it slopes down to the east becoming accessible for easy communication. This is also substantiated by linguistis who consider Munda languages to be distantly related to Mon-Khmer languages (which include Khasi) spoken by the Mongoloid populations of eastern India, both belonging to Austro-Asiatic branch of Austric language family.

The Central Indian group and Orissa and Chota-Nagpur group are however closer to each other relatively than to the more distant South Indian tribal group. The South Indian group is separated from the rest of the tribal people of peninsular India by the Krishna and Godavari deltas occupied by economically better off and politically powerful plains people. The South Indian tribal populations are mostly food-gatherers, a mode of living which is determined by the rugged and hilly terrain of western and eastern Ghats which they inhabit, whereas the Central Indian and Orissa and Chota-Nagpur tribals have adopted agriculture due to greater availability of cultivable lands. These findings do not substantiate the contention made by Russel and Hiralal, 1916 that the Gonds who speak a Dravidian language might have migrated from South dia to Central India sometime between 9th century & 13th century A.D. This is also criticised by imendorf, (1979) on the basis that this is not pported by ethnological evidence. It is perhaps re reasonable to postulate that the Dravidian ture and languages were wide-spread even among ibes of Central India who may have been in the st speaking their own languages.

e relationship of those populations whose origin s in doubt because of the lack of correspondence tween morphological and linguistic data was resolved some extent by this study. The following are some the populations :

Korkus : Munda-speaking group found in Central India living amidst the Gondi-speaking group. They have been found to belong morphologically to the Central Indian group.

Khonds : Dravidian speaking group (Kui dialect) who are located amidst the Munda-speaking group in Orissa and Chota-Nagpur areas have been found to be closely related to that group.(Map 1)

Oraons : They are a large Dravidian speaking group (Kurukh dialect) in the Chota-Nagpur area (Map 1) and have been found to belong morphologically to the Central India cluster lying on its periphery. Though Khonds and Oraons are both Dravidian speaking groups they are morphologically distant from each other, the Khonds being close to the Munda-speaking people and the Oraons to the Central Indian group.

. Andhs : This group lives in Maharashtra practising agriculture. They speak both Marati and Hindi. They have been classified as tribals in Maharashtra but have been found to belong morphologically to the non-tribal Central Indian group in the study.

nother interesting finding that comes out of the study is the distinct separation of Central Indian tribal cluster from the non-tribal cluster which confirms the orphological distinctness of tribals from non-tribals inspite of the fact that they may belong to the same eographical area.

fferences between morphological and genetic relationship the Gonds with the rest of the tribal populationsof dia

tribal populations based on both morphology and netics clustered generally according to the geographical gions they belong. However, the actual relationship ween these populations based on both these biological riables did not correspond very well. This lack of rrespondence may partly be due to

) Smaller number of groups utilised in the genetic study due to lack of availability of data.

) The populations used for genetic study are not exactly the same as those used in the morphological study.

The relationship of the Gonds with the rest of the tribal populations also differs in the two studies. The Gonds are morphologically close to the Central Indian group, whereas they are far apart from this group genetically. The Gonds of this study are genetically more heterogenous (Plate 2) and break up into two groups, one consisting of the Plains Maria Gonds, Hill Maria Gonds, Koyas and Manne and being genetically closer to the Orissa and Chota-Nagpur group with whom they are geographically contiguous. The second group consisting of the remaining two Gond populations, the Raj Gonds and Kolams who are placed far apart from Orissa and Central Indian groups. Some studies have shown that the lack of correspondence between morphology and genetics may be due to the fact that the morphological evolution and biochemical evolution in structural genes can proceed at independent rates.

7.2 General discussion

The emphasis of the present study based on quantitative techniques is on the importance of geographical proximity in producing morphological and genetic similarity between populations. This is revealed in the smaller Gond study as well as in the case of the larger tribal study. Geographical proximity between populations being brought about by a closer distance as well as similar geographical factors (such as soil, terrain, flora etc), drawing these populations together under a common eco-cultural umbrella. The closer the geographical distance between populations the closer the genetic as well as morphological similarity between them. This is more so in populations such as these who due to having adopted a settled agricultural occupation are less mobile. This low mobility in turn produces a smaller marriage distance (distance between place of birth of spouses) thus restricting the spatial distribution of genes to a smaller area.

The old concept that a community is 'pure bred' from a single physical race is hence misleading and Eickstedt's classification (1935) of tribal groups of India is based on this concept. He classified the Gondi-speaking groups (Gondid) as a sub-type of Veddoid race to which the South Indian group (Malid) also belong. The Munda-speaking groups are classified as belonging to the Kolid race and is according to him closer to Dravidian Hindu caste groups of Tamil Nadu who are morphologically very different from them. This hypothesis has been viewed with considerable doubt by anthropologists. The present study however classifies the tribal populations of peninsular India into three main geographical clusters, the Central Indian group (consisting of Gonds, Bhils, Korkus etc), the Munda-speaking groups in the east and the South Indian tribal groups lying south of Krishna river. The Central Indian group is relatively closer morphologically to the Munda-speaking group than to the more distant South Indian tribal group which is separated from the rest of the tribal populations by the Krishna and Godavari deltas.

Scope for future work :

1 A systematic and regional study on tribal populations should be carried out in depth and data collected on both morphological and genetic characters on populations belonging to the same area. It is imperative to use standard techniques for taking anthropometric measurements for the purpose of comparative analysis. When sufficient data of this kind becomes available, it would be interesting to find out how much correspondence there is between morphological and genetic relationship between groups.

2 The collection of data on rare variants of proteins and enzymes will help in a more clear demarcation of the boundaries of overlapping population clusters in a qualitative way.

3 The use of new molecular techniques such as the use of DNA restriction enzymes pattern for the purpose of differentiating populations will throw more light on the dynamics of population evolution

A beginning in that direction has been made by the detection of Haemoglobin S polymorphism as seen by the presence of two different size DNA fragments associated with the haemoglobin S gene. The two fragments with which haemoglobin S is associated are 7.6 K.B and 13 K.B fragments, the 13 K.B present in East Africa, India and Asia (Kan and Dozy, 1978; Feldenzer, Mears, Burns, Natta and Bank, 1979). This is an important finding and indicates that probably haemoglobin S of West Africa arose out of an independent mutation to that found in East Africa and India.

APPENDIX II

ESTIMATION OF GENE FREQUENCIES OF BLOOD GROUPS

(Rao, 1965)

ABO SYSTEM :

Every human being can be classified into one of four blood groups O, A, B, AB. The inheritance of these blood groups is controlled by three allelomorphic genes O, A, B of which O is recessive to A and B.

If r, p and q are gene frequences of O, A and B then the expected probabilities of the six genotypes (four phenotypes) in random mating are as follows :

Phenotype	Gene type	Probabilities	
O	O O	r^2	
A	A A A O	p^2 $2pr$	$p^2 + 2pr$
B	B B B O	q^2 $2qr$	$q^2 + 2qr$
AB	A B	$2\ pq$	

Given $\bar{O}$, $\bar{A}$, $\bar{B}$ and $\overline{AB}$ are observed frequencies adding to N, the problem is to estimate the gene frequencies p, q, and r. A rough estimate is supplied by

$$r' = \sqrt{\frac{\bar{O}}{N}}$$

$$p' = 1 - \sqrt{\frac{\bar{O} + \bar{B}}{N}}$$

$$q' = 1 - \sqrt{\frac{\bar{O} + \bar{A}}{N}}$$

These may not necessarily add to unity, whereas the true values should. Let D denote the deviation

$$- D = p' + q' + r' - 1$$

Better estimates due to Berstein are obtained

$$r = (1 + \tfrac{1}{2} D) \quad (r' + \tfrac{1}{2} D)$$

$$p = (1 + \tfrac{1}{2} D) \; p'$$

$$q = (1 + \tfrac{1}{2} D) \; q'$$

There is still some deviation, $(1 - p - q - r) = 1/4 \; D^2$. If this is small, then Bernstein's method supplies fairly good estimates. We shall now show how these estimates can be improved by the method of maximum likelihood using the frequency $\bar{O} = 176$, $\bar{A} = 182$, $\bar{B} = 60$ and $\overline{AB} = 17$. Approximate solutions obtained by Bernstein's method are

$$P_o = 0.26449, \; q_o = 0.09317, \; r_o = 0.644234$$

In general the probabilities and derivatives with respect to the independent parameters p and q are as follows :

	Probabilities	Derivatives	
	π	$\frac{\partial \pi}{\partial p}$	$\frac{\partial \pi}{\partial q}$
O	r^2	$-2r$	$-2r$
A	$p(p + 2r)$	$2r$	$-2p$
B	$q(q + 2r)$	$-2q$	$2r$
AB	$2pq$	$2q$	$2p$

There is another algorithm which yields maximum likelihood estimates which is suitable for desk electronic calculators and which avoids the repeated computation of the information matrix and its inverse.

Let p_o, q_o, r_o be provisional estimates and compute $P_0 = p_0/r_0$ and $Q_o = q_o/r_o$. Let us represent by P_K and Q_K the Kth approximation of p/r and q/r. The $(K + 1)^{th}$ approximation found from the formulas

$$\frac{\bar{A} + \bar{A}\bar{B}}{P_{k+1}} = 2\,(\bar{O}) + \frac{\bar{A}}{2 + P_k} + \frac{2\bar{B}}{2 + Q_k}$$

$$\frac{\bar{B} + \bar{A}\bar{B}}{Q_{k+1}} = 2\,(\bar{O}) + \frac{2\bar{A}}{2 + P_{k+1}} + \frac{\bar{B}}{2 + Q_k}$$

The iteration may be repeated until stable values of Q are obtained from which the estimates of p, q and r are computed as

$$r = \frac{1}{P + Q + 1}, \quad \hat{p} = \hat{r}\,p, \; \hat{q} = \hat{r}Q$$

By adopting the provisional estimates

$$p_o = 0.26449, \; q_o = 0.09317, \; r_o = 0.64234$$

with $p_o = 0.41176$, $q_o = 0.14505$, the first round of computation yields $P_1 = 0.41167$, $Q_1 = 0.14503$ indicating stability. The m.l estimates of p, q, r are $\hat{r} = 0.64238$, $\hat{p} = 0.26445$, $\hat{q} = 0.09316$, which agree closely with the estimates obtained by the iterative procedure using the information matrix. With the estimates so obtained, the expected probabilities of the phenotype classes and the information matrix may be obtained as before to compute the standard errors of the estimates.

APPENDIX II

FOR DEPARTURE FROM HARDY-WEINBERG AND TESTS OF HOMOGENEITY (RAO, 1965)

istribution in four blood group classes O, A, B, AB 53 individuals belonging to community C and 364 viduals of community D are given in Table below. test is applied to examine the equality of the thetical proportions of the blood group classes he two communities. The χ^2 = 11.77 on 3 D.F puted in the table is significant at the 5°/. level icating differences between communities.

	O	A	B	AB	Total
munity C	121	120	79	33	353
munity D	118	95	121	30	364
tal	239	215	200	63	717
Community tal =	0.5063	0.5581	0.3950	0.5238	0.4923

$P_i - n_i p =$ 121(0.5063) + 120(0.5581) + ... −353(0.4923)

= 2.9428

- p) = 0.24994 χ^2 = 2.9428/0.24994 = 11.7 on 3 D.F.

χ^2 test on 3 D.F is not however the best for the lable data if the object is to establish differences ween communities. The intrinsic (or genetic) differences any, between the communities, is in the relative quencies of the O, A, B genes. A test of the hyposis of equality of gene frequencies is more fundamental n that of the equality of frequencies of the phenotypes ithout recognising that the latter are known functions f the former. Only when such functional dependence on ore intrinsic characters like the gene frequencies is known or is in doubt, is a test of the type involving ne phenotypical frequencies valid.

sing maximum likelihood estimates (gene frequencies), he expected values (E_1 and E_2) on the basis of ndividual estimates and combined estimates are btained for each community as shown below

	Maximum likelihood estimates		
	$\hat{p}$	$\hat{q}$	$\hat{r} = (1 - \hat{p} - \hat{q})$
ommunity C	0.24649	0.17317	0.58034
ommunity D	0.19025	0.23573	0.57401
ombined sample	0.21762	0.20435	0.57803

Expected values under the two hypothesis

		Community C			Community D		
lasses	Probabilities	Observation	E_1	E_2	Observation	E_1	E_2
O	r^2	121	118.89	117.94	118	119.93	121.62
A	$p^2 + 2pr$	120	122.44	105.52	95	92.68	108.81
B	$q^2 + 2qr$	79	81.54	98.14	121	118.74	101.19
AB	$2\,pq$	33	30.13	31.40	30	32.65	32.34
otal	1	353	353	353	364	364	364

χ^2 (goodness of fit)

or Community C $= \sum \frac{(O - E_1)^2}{E_1} = 0.44$ I D.F.

or Community D $= \sum \frac{(O \pm E_1)^2}{E_1} = 0.35$, I D.F.

^{2} for homogeneity of ommunities $= \sum\sum \frac{(E_1 - E_2)^2}{E_2} = 11.04$, 2 D.F.

values of χ^2 for the individual communities are
ll, which indicates that the specification of cell
abilities in terms of gene frequencies are valid.
last χ^2 establishes the difference between
unities in a better way than the χ^2 of 11.77 on
F obtained from a direct comparison of phenotypic
uencies. The two χ^2 are nearly of the same magnitude,
the χ^2 based on a comparison of gene frequency
1 D.F less giving a lower probability in favour of
null hypothesis. The test can be extended to
ne difference between several communities
ltaneously.

APPENDIX III

Rh (D) GENE FREQUENCY ESTIMATION

gene frequency was calculated by estimating the
s frequency of the recessive allele and then
mating from it the frequency of the dominant
le by 1-d;

$$\text{allele frequency} = \frac{\text{Observed Rh negative cases X 2}}{\text{Total number of individuals.}}$$

[illegible]	0.0000	[illegible]								
[illegible]			[illegible]	[illegible]						
[illegible]	[illegible]	[illegible]				[illegible]				
[illegible]	0.	[illegible]	[illegible]		[illegible]	[illegible]	1.0000	[illegible]		
[illegible]		[illegible]				[illegible]	[illegible]	[illegible]	1.0000	1.0000

	[illegible]		[illegible]		[illegible]		[illegible]		[illegible]	
	D^2	D^2 (JPTC)	D^2	D^2 (JPTC)	D^2	D^2 (JPTC)	D^2	D^2 (JPTC)	D^2	D^2 (JPTC)
[illegible]	0.0000	0.0000								
[illegible]	[illegible]	[illegible]	0.0000	0.0000						
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.0000	0.0000				
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.0000	0.0000		
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.0000	0.0000
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.7405
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
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[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1.4074
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1.0357
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
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[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]

(CONT)

	DM		DK		G1		GJ		HL	
	D^2	D^2 (3PPC)	D^2	D^2 (3PPC)	D^2	D^2 (3PPC)	D^2	D^2 (3PPC)	D^2	D^2 (3PPC)
DM	0.0000	0.0000								
DK	[illegible]	[illegible]	0.0000	0.0000						
G1	[illegible]	1.4770	[illegible]	[illegible]	0.0000	0.0000				
GJ	[illegible]	[illegible]	[illegible]	[illegible]	1.6090	0.9708	0.0000	0.0000		
HL	[illegible]	[illegible]	[illegible]	[illegible]	0.2559	0.1625	2.0503	1.1716	0.0000	0.0000
HL2	[illegible]	[illegible]	[illegible]	0.7414	0.4707	0.2316	2.0461	4.0066	1.0405	0.5507
JA	[illegible]	7.6401	[illegible]	[illegible]	2.0440	2.6815	7.4008	6.5507	2.6095	2.3353
AA	[illegible]	5.7427	[illegible]	[illegible]	3.1032	1.9527	7.8005	5.1384	2.5561	1.6497
SO	[illegible]	[illegible]	[illegible]	[illegible]	2.7583	1.5171	5.2230	4.4942	2.5616	1.1714
A	[illegible]	[illegible]	[illegible]	[illegible]	1.8903	0.7128	2.0595	0.7046	1.7717	1.5442
BP	[illegible]	[illegible]	[illegible]	[illegible]	0.6603	0.5054	3.3571	2.5062	1.1491	1.0427
BI	[illegible]	[illegible]	[illegible]	[illegible]	0.1994	0.7404	[illegible]	2.2234	[illegible]	[illegible]
G2	[illegible]	[illegible]	[illegible]	[illegible]	1.4393	0.7075	3.3510	2.1930	[illegible]	0.1573
JA	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	2.2321	7.4167	5.7583	2.4745	1.3119
KN	[illegible]	[illegible]	[illegible]	[illegible]	1.5771	0.9451	3.6332	2.3413	1.1147	0.3509
KY2	[illegible]	4.1911	[illegible]	[illegible]	1.4431	0.7652	4.5548	3.4154	0.9524	0.5424
SM	[illegible]	[illegible]	[illegible]	[illegible]	1.3544	2.0540	4.8100	3.7063	[illegible]	1.0620
O1	[illegible]	[illegible]	[illegible]	[illegible]	3.7021	2.5097	[illegible]	[illegible]	[illegible]	[illegible]
C2	[illegible]	[illegible]	[illegible]	[illegible]	1.4383	0.9907	[illegible]	[illegible]	0.6250	0.2466
S1	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1.7913	[illegible]	[illegible]	[illegible]	2.5599
BW	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.3913
GU1	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.5014	[illegible]
HW2	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
HU1	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	2.0021	[illegible]	[illegible]	[illegible]	[illegible]
HU2	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	4.7997	[illegible]	[illegible]
BA	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1.3080	[illegible]	[illegible]	[illegible]	[illegible]
KB	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PM1	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	3.2599	4.0544	[illegible]	[illegible]	3.2930
KW	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1.7747	[illegible]
KR3	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.1057	[illegible]	[illegible]	[illegible]	0.5597
MR	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
MM1	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	2.0044	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
UM	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.2100	[illegible]	[illegible]	[illegible]	[illegible]
CU	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
AA	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	12.0319	[illegible]	[illegible]
LM	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
MM2	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
AL1	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1.5068	[illegible]	[illegible]	[illegible]	[illegible]
KY1	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
MM	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
PM	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1.0215	[illegible]	[illegible]	[illegible]	1.2557
MG1	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1.0759	[illegible]	[illegible]	0.9555

(CONT)

	AL2		JA		BA		SO		A	
	D^2	D^2 (3PTC)	D^2	D^2 (3PTC)	D^2	D^2 (3PTC)	D^2	D^2 (3PTC)	D^2	D^2 (3PTC)
AL2	0.0000	0.0000								
JA	[illegible]	[illegible]	0.0000	0.0000						
BA	[illegible]	[illegible]	[illegible]	0.2000	0.0000	0.0000				
SO	[illegible]	0.7140	2.0211	0.5140	3.4153	0.7072	0.0000	0.0000		
A	[illegible]	1.1059	[illegible]	[illegible]	4.6449	3.5602	5.8869	3.3730	0.0000	0.0000
[illegible]	[illegible]	[illegible]	[illegible]	1.4549	1.5502	0.7273	2.5484	1.6215	1.5210	1.2725
[illegible]	[illegible]	[illegible]	[illegible]	2.1375	3.6108	1.5046	2.1924	1.1276	1.0076	0.5936
G2	[illegible]	[illegible]	[illegible]	2.2149	3.0304	1.4546	2.3629	1.2441	3.1571	2.6783
[illegible]	[illegible]	2.0116	[illegible]	[illegible]	7.1534	2.6225	3.4508	1.1047	5.9919	5.4264
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	3.4926	2.6451	3.2745	1.5849	3.6255	3.1794
KY2	[illegible]	[illegible]	[illegible]	[illegible]	2.2273	0.4340	2.2075	0.2030	2.6711	2.4764
SY	[illegible]	[illegible]	[illegible]	[illegible]	4.3549	2.0049	2.5944	2.3166	5.4551	4.5072
O1	[illegible]	[illegible]	[illegible]	[illegible]	8.5070	5.7014	3.6058	2.9216	6.5910	4.9775
O2	[illegible]	[illegible]	[illegible]	[illegible]	1.7402	0.5640	2.1065	1.0041	2.5930	2.7473
Z1	[illegible]	[illegible]	5.4370	[illegible]	7.4344	5.2245	3.5242	3.1955	4.8494	1.6462
SN	[illegible]	[illegible]	[illegible]	[illegible]	2.5009	1.2014	2.8182	0.4257	3.3943	2.8753
CO1	[illegible]	[illegible]	[illegible]	[illegible]	3.3733	2.7907	2.5164	1.3643	3.2217	3.0040
BW2	[illegible]	[illegible]	[illegible]	[illegible]	10.0155	5.5910	5.9416	3.9463	5.4536	4.1515
MO1	[illegible]	[illegible]	[illegible]	[illegible]	5.6019	2.1327	3.2812	2.3177	6.5135	4.5145
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	4.3672	7.1049	5.5154	3.7250	5.3736	2.1039
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	4.4496	4.5570	2.7120	1.4250	4.4105
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	3.3419	3.3240	5.3649	4.4012	5.1612	5.9457
PH1	[illegible]	[illegible]	[illegible]	[illegible]	11.1125	4.7717	5.3518	5.7233	5.4430	4.2451
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	5.0415	4.1095	3.4544	1.7461	4.1177	3.5904
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	5.2197	2.9044	3.4460	1.5207	1.4628	0.5593
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	9.3016	5.3593	4.5040	[illegible]	4.9756	4.4716
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	4.6259	6.4149	4.5037	1.5773	3.5556	3.1708
SM	[illegible]	[illegible]	[illegible]	[illegible]	4.3027	7.1954	5.7532	[illegible]	2.6640	2.3045
UR	[illegible]	[illegible]	[illegible]	[illegible]	7.5120	1.1470	3.7610	0.4023	2.2235	1.9420
LU	[illegible]	[illegible]	[illegible]	[illegible]	7.7449	3.4570	3.0795	1.7404	1.5511	1.4423
SA	[illegible]	[illegible]	[illegible]	[illegible]	3.6157	3.3067	5.5465	[illegible]	5.4046	7.5209
LM	[illegible]	[illegible]	[illegible]	[illegible]	5.6400	4.1113	1.5914	[illegible]	6.8545	5.1469
PM2	[illegible]	[illegible]	[illegible]	[illegible]	2.5617	4.9449	5.1426	[illegible]	7.6445	5.0262
KL1	[illegible]	[illegible]	[illegible]	[illegible]	4.5705	4.1652	5.9550	4.0417	5.5404	4.4077
KY1	[illegible]	[illegible]	[illegible]	[illegible]	1.4504	7.1555	5.1048	[illegible]	1.4441	1.6497
MN	[illegible]	[illegible]	[illegible]	[illegible]	7.4055	5.7055	5.3103	[illegible]	1.7612	1.5033
PA	[illegible]	[illegible]	[illegible]	[illegible]	7.0374	7.6095	4.2713	4.2107	1.6095	1.6495
A41	[illegible]	[illegible]	[illegible]	[illegible]	7.0175	[illegible]	4.0022	[illegible]	2.7046	1.6757

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	[illegible]		[illegible]		[illegible]		[illegible]		[illegible]	
	D	D (JPEC)	D^2	D^2 (JPEC)	D^2	D^2 (JPEC)	D^2	D^2 (JPEC)	D	D (JPEC)
[illegible]	0.0000	0.0000								
[illegible]	1.1433	0.7398	0.0000	0.0000						
[illegible]	2.1245	1.4204	2.0904	2.3616	0.0000	0.0000				
[illegible]	5.2401	3.7513	5.4951	4.1025	2.2282	0.9376	0.0000	0.0000		
[illegible]	3.5657	2.0014	3.7894	3.2203	1.4530	0.3152	0.8158	0.5553	0.0000	0.4707
[illegible]	1.2491	0.7229	1.7808	1.2045	0.7178	0.0230	2.5252	1.2549	2.3074	1.1390
[illegible]	3.4075	3.0704	4.7209	4.0559	0.9435	0.3877	2.5787	0.2550	1.3843	3.3346
U1	7.2213	5.3589	5.2093	4.4130	4.2314	2.7121	4.3577	1.4558	2.9430	1.3337
L2	2.7534	2.7168	2.2420	2.3381	3.9024	3.2697	2.8207	1.5140	1.8127	1.1716
[illegible]	4.3212	3.8418	1.6732	1.4384	3.1037	4.5410	5.4697	4.4450	4.5151	3.4755
[illegible]	2.3342	1.5394	3.0172	1.7843	3.0549	3.2824	1.2345	3.5274	1.1701	0.4310
[illegible]	2.7424	2.2448	2.9083	2.7088	3.2394	0.1092	1.4290	0.5408	0.7194	0.9202
[illegible]	9.4905	5.9320	3.5584	2.7737	7.0144	5.5529	9.2067	6.3112	8.3192	5.7808
[illegible]	3.5228	2.4670	5.1539	4.3045	2.4043	0.3860	5.1061	1.1552	3.2497	0.4721
[illegible]	0.8287	0.7720	5.2219	4.5910	4.6337	3.7946	3.5579	2.4327	2.5531	2.1795
[illegible]	3.9501	3.5371	2.2959	1.5291	3.4233	2.9856	4.4356	2.9873	3.0622	2.2430
[illegible]	8.0285	7.0501	5.1972	5.5377	5.2874	4.6081	3.3064	[illegible]	2.5031	2.7535
PH1	8.3037	7.3734	5.7595	5.2131	3.2940	4.2411	5.0020	[illegible]	3.7021	2.4548
[illegible]	4.0095	4.1959	4.9418	3.3215	2.2543	1.5576	1.5865	3.7257	1.5093	1.0135
[illegible]	2.4137	1.2578	1.2338	[illegible]	1.5732	1.4600	3.3710	2.5545	2.6666	1.4614
[illegible]	6.2442	5.7050	4.2626	[illegible]	3.2150	3.1094	4.5302	2.2755	3.7492	1.7538
[illegible]	5.4717	5.2743	3.0083	2.4129	4.4032	3.7671	5.4161	3.4151	3.6736	2.3193
[illegible]	4.8075	4.0030	2.7251	1.9779	3.3345	4.7911	7.1062	4.4505	5.5507	3.7241
[illegible]	1.4648	1.3464	1.3930	1.4017	2.7212	1.7604	5.2478	4.3137	4.2594	1.2818
UU	2.0343	2.1909	1.5122	0.7509	2.3497	2.4937	4.2727	2.7424	4.2942	1.6942
[illegible]	9.2701	8.7337	5.3734	5.2757	5.7260	7.6937	7.0103	5.5395	7.5545	6.5360
[illegible]	6.9804	6.1133	4.0215	2.4017	6.4331	5.1950	4.9904	3.4032	5.5301	4.8097
[illegible]	7.9037	5.0200	4.0048	3.3947	5.6214	4.4277	5.6217	2.5548	5.1192	3.5763
[illegible]	5.4068	4.5156	4.0240	2.7209	4.3334	3.1039	6.7304	3.5973	4.5140	2.0795
[illegible]	3.7452	3.5780	4.3750	2.6974	1.6714	1.7651	4.2069	3.3014	1.8767	1.4051
[illegible]	4.4463	4.0213	3.0039	2.5407	4.4971	3.3911	5.5224	4.3247	3.4057	1.5346
[illegible]	3.4558	3.0975	3.4470	3.7722	2.4063	2.4483	4.0603	3.4552	2.4702	1.3521
[illegible]	3. 300	3.3356	2.7933	2.4713	1.5794	1.0098	5.1303	2.7523	2.4357	1.3953

(CONT)

	KY2		SV		O1		O2		#1	
	D^2	D^2 (3PTC)	D^2	D^2 (3PTC)	D^2	D^2 (3PTC)	D^2	D^2 (3PTC)	D^2	D^2 (3PTC)
KY2	0.0000	0 0000								
SV	2.2255	1.0981	0.0000	0.0000						
O1	5.3079	3.1775	[illegible]	3.2567	0.0000	0.0000				
O2	0.2075	0.3060	1.1516	0.9283	5.3307	4.2910	0.0000	0.0000		
#1	4.4046	3.0630	5.3213	6.3095	2.4978	2.2119	5.1154	4.7810	0.0000	0.0000
#H	0.6435	0.2436	2.1267	0.9421	5.2561	1.9119	1.8655	0.5290	5.2220	2.5458
GO1	1.1245	0.9237	0.7256	0.4590	3.4909	1.5630	1.2815	0.3455	4.4016	3.4275
AR2	5.4356	4.5285	4.3594	9.2214	4.6590	3.4039	7.7251	7.1253	1.4751	0.6624
MU1	3.5359	1.5406	0.7915	0.1069	4.5417	4.2254	1.5336	0.5147	7.1753	5.8129
MU2	4.3458	4.0005	5.2233	4.5493	1.5704	0.1407	5.6511	5.5115	2.6226	1.6161
BA	2.3295	2.3488	5.1025	4.5061	4.1539	1.2462	4.3693	3.9212	1.7170	0.1593
KU	5.4515	4.9924	6.2217	5.5404	2.6034	0.2598	7.1624	6.5034	3.5206	2.1578
PH1	7.3112	6.1512	3.7455	5.0553	1.0240	0.5609	7.4515	6.3044	2.5601	2.0504
KW	2.2590	1.4137	3.9343	2.0557	2.6456	0.1746	3.2951	2.7459	3.4232	2.1179
AR3	1.7466	1.0600	3.9231	4.1251	5.4456	2.3332	3.1575	1.7871	2.5436	0.6591
MH	4.0530	7.4526	4.3551	4.1257	1.5212	0.1259	5.1522	4.7715	2.1526	1.4136
GK1	4.0217	3.0209	[illegible]	5.5025	2.4571	0.4007	5.5545	5.1655	3.5051	3.5747
BH	4.2065	3.7340	[illegible]	6.4102	4.4424	2.1087	5.3615	5.5522	2.0374	3.3492
OR	1.4208	0.4363	[illegible]	1.2239	5.6560	2.4524	2.0406	1.0527	2.0750	1.2424
GU	1.3854	1.5079	4.2171	3.4302	1.6111	1.7097	3.3999	2.5425	2.0219	2.3243
KA	6.9440	3.0034	11.7027	10.0510	5.6531	3.1610	9.4117	6.7329	3.5631	2.3244
OM	4.5680	2.8697	6.4515	7.3345	5.0578	3.2654	6.6105	5.2762	3.5505	1.6741
OM2	5.1617	1.9036	4.6910	5.9225	2.3610	1.5060	6.7591	5.0978	3.2596	1.7528
KL1	5.1521	3.5940	8.2217	9.5651	3.5570	1.1471	5.6916	4.5594	2.2506	0.6535
KY1	3.5237	3.0221	7.6153	2.6209	3.5347	1.7282	3.2652	3.0532	3.1770	.2047
AM	4.3769	4.1267	5.5124	5.0159	3.3778	2.3575	4.5750	4.7431	1.5780	1.2308
PM	3.3201	2.2375	2.3295	3.0557	4.7716	1.9320	3.6225	3.5591	3.2357	.1203
RU1	4.0234	2.6671	3.1444	2.5778	1.4510	1.4602	3.2774	2.9117	1.6518	1.6930

	SM		GD1		KR2		MO1		MO2	
	D^2	D^2 (3PrC)	D^2	D^2 (3PrC	D^2	D^2 (3PrC)	D^2	D^2 (3PrC)	D^2	D^2 (3PrC)
SM	0.0000	0.0000								
GD1	0.6370	0.2685	0.0000	0.0000						
KR2	7.2433	4.6373	7.6028	5.7472	0.0000	0.0000				
MO1	4.6074	1.0509	2.4601	0.7044	10.4643	9.9064	0.0000	0.0000		
MO2	4.5205	2.7740	3.0418	2.4027	3.5256	2.7195	7.3001	5.7374	0.0000	0.0000
SA	2.7455	1.5071	2.6700	2.3220	1.6527	0.8555	7.5834	5.2561	1.3953	[illegible]
KD	3.7324	3.5323	[illegible]	3.1247	4.5256	3.0195	9.1401	0.5595	0.6447	[illegible]
PR1	[illegible]	3.6526	4.0953	2.5706	5.2089	3.6530	7.2474	6.7096	2.2599	[illegible]
KW	1.3534	0.9346	[illegible]	0.7621	5.2559	3.4541	5.2979	2.8151	0.9207	[illegible]
KR3	1.3335	1.0925	1.5494	1.3521	4.9379	2.5459	6.1232	3.1782	4.2124	[illegible]
MR	4.4324	[illegible]	2.2150	2.0144	2.6605	2.5416	5.9936	5.0764	0.5314	[illegible]
MM1	4.3105	2.8041	3.1404	2.7329	1.3017	1.4429	6.8038	0.1774	0.2716	[illegible]
BM	5.3477	3.4556	4.5716	1.8117	1.2537	0.5465	6.4714	7.4154	1.4517	[illegible]
DR	3.5014	0.5066	2.7239	1.0529	3.7612	2.6027	4.6541	2.5434	[illegible]	[illegible]
DU	2.0323	1.3937	2.0108	1.7513	2.7165	1.4645	6.9963	4.7019	[illegible]	[illegible]
KA	7.6114	5.3050	[illegible]	[illegible]	2.9264	0.3314	14.5459	11.3104	2.9604	[illegible]
OM	4.0744	3.1473	[illegible]	4.6513	1.6756	0.5764	10.3250	7.7901	[illegible]	[illegible]
MM2	4.4152	2.5715	4.4925	3.5350	3.7215	1.2133	6.5025	6.7373	4.2640	[illegible]
KL1	5.2195	2.7090	3.9594	2.2441	4.3406	2.6272	7.2874	5.2179	1.9472	[illegible]
KY1	3.6740	2.0859	2.1054	1.2535	5.5046	5.0182	4.7402	3.0841	2.1908	[illegible]
MM	4.4157	3.3457	3.2774	2.7530	4.3277	3.6264	7.1250	5.4659	2.7544	[illegible]
PM	3.0846	2.3632	1.6597	1.5574	5.6780	4.5787	5.7984	3.4429	[illegible]	[illegible]
RG1	4.4025	1.8245	2.2559	[illegible]	5.0504	4.2979	2.4409	1.1049	2.4467	[illegible]

	SA		KD		PR1		KW		KR3	
	D^2	D^2 (3PrC)	D^2	D^2 (3PrC)	D^2	D^2 (3PrC)	D^2	D^2 (3PrC)	D^2	D^2 (3PrC)
SA	0.0000	0.0000								
KD	2.3607	1.4058	0.0000	0.0000						
PR1	4.0316	1.4745	1.3662	0.2750	0.0000	0.0000				
KW	1.4570	1.1250	1.4133	0.5558	3.5632	1.0954	0.0000	0.0000		
KR3	1.6542	0.7012	3.7674	3.2263	4.5330	2.7658	2.6945	1.5961	0.0000	[illegible]
MR	1.2936	0.7457	1.7352	0.1725	1.1524	4.2564	1.2534	0.4253	[illegible]	[illegible]
MM1	0.7594	0.2729	[illegible]	0.5996	1.1623	0.7491	1.7182	1.3532	[illegible]	[illegible]
SM	0.6000	0.2403	[illegible]	1.3597	4.2070	1.7602	2.7652	1.2137	[illegible]	[illegible]
DR	1.7423	0.9742	[illegible]	3.6544	7.2834	3.4753	2.5636	1.5321	[illegible]	[illegible]
DU	0.2446	0.1755	[illegible]	2.2356	4.5137	2.0722	1.0165	1.2721	7.0922	[illegible]
KA	3.2626	2.0872	[illegible]	2.7239	4.7288	4.2133	4.1233	1.5125	[illegible]	[illegible]
OM	1.7686	1.5510	[illegible]	3.6344	5.0957	4.9654	5.0607	2.5224	[illegible]	[illegible]
MM2	3.9284	1.1312	[illegible]	1.7561	3.7925	3.0402	4.4342	1.4699	[illegible]	[illegible]
KL1	2.9251	0.6456	3.6772	1.1243	3.2422	0.5446	1.2003	1.3509	[illegible]	[illegible]
KY1	2.3734	1.7474	3.1711	2.3705	3.5429	1.3509	1.1566	1.4413	[illegible]	[illegible]
MM	1.8033	1.3014	[illegible]	3.4204	2.7749	1.3456	2.5164	2.3529	[illegible]	[illegible]
PM	1.7665	1.7191	[illegible]	2.5267	3.7126	1.4321	1.6541	1.2012	[illegible]	[illegible]
RG1	2.3310	1.3250	3.7155	2.0716	[illegible]	1.1012	2.5744	1.1792	[illegible]	[illegible]

(CONT)

	HR		HH1		BH		DR		DW	
	D^2	D^2 (3PrC)	D^2	D^2 (3PrC)	D^2	D^2 (3PrC)	D^2	D^2 (3PrC)	D^2	D^2 (3PrC)
HR	0.0000	0.0000								
HH1	0.3808	0.2745	0.0000	0.0000						
BH	1.4008	1.2623	0.6963	0.3811	0.0000	0.0000				
DR	2.6814	2.2852	2.7830	1.9741	1.9435	1.8083	0.0000	0.0000		
DW	1.9106	1.2418	1.2642	0.7226	1.1227	0.5375	1.4565	0.3844	0.0000	0.0000
KA	3.9684	2.8106	3.5975	2.1958	2.9552	2.2943	5.4449	4.5838	4.6956	1.1715
DM	5.9616	3.0943	4.5258	2.6310	5.3873	1.1977	7.3352	2.4223	4.0649	1.7936
HH2	4.4115	1.5979	3.4452	1.5922	5.3882	1.8499	7.4208	2.4017	4.3010	1.7358
KL1	1.2147	0.5684	1.2538	0.3016	1.2383	0.7570	2.3176	1.4400	2.3[illegible]81	0.7786
KY1	2.1938	1.4347	2.1962	1.5160	2.7599	2.2952	2.5699	1.7461	2.4043	1.1775
HH	2.2106	1.5661	1.5049	1.0355	1.6837	1.2363	3.3642	2.1054	1.6217	1.1103
PW	2.1507	1.5632	2.0034	1.4982	2.4791	2.1360	2.5418	1.7959	1.4563	1.1402
RG1	1.7082	1.1626	1.5568	1.1776	2.6662	1.8482	2.7709	1.4112	2.4899	1.0132

	KA		DM		HH2		KL1		KY1	
	D^2	D^2 (3PrC)	D^2	D^2 (3PrC)	D^2	D^2 (3PrC)	D^2	D^2 (3PrC)	D^2	D^2 (3PrC)
KA	0.0000	.0000								
DM	1.2281	0.7437	0.0000	0.0000						
HH2	4.9254	0.9461	0.7139	0.3795	0.0000	0.0000				
KL1	1.9965	4.3462	9.7246	4.1857	7.8791	2.7829	0.0000	0.0000		
KY1	7.6793	7.1900	8.325[illegible]	6.1335	7.1356	4.7328	1.9136	0.5613	0.0000	0.0000
HH	6.6247	6.2988	7.5291	5.7390	7.0874	4.6616	1.1945	0.2566	0.6608	0.4435
PW	8.0997	7.2678	8.3591	5.2341	7.7757	4.9135	1.6199	0.5071	0.5690	0.0222
RG1	7.4628	6.3396	7.5621	5.3222	5.1012	4.0567	1.3925	0.3940	0.9348	0.0297

	HH		PW		RG1	
	D^2	D^2 (3PrC)	D^2	D^2 (3PrC)	D^2	D^2 (3PrC)
HH	0.0000	0.0000				
PW	0.6010	0.2914	0.0000	0.0000		
RG1	1.0495	0.3772	1.4158	0.0487	0.0000	0.0000

APPENDIX .V. NEI'S GENETIC DISTANCE MATRIX (ALL TRIBALS)

	B2	B3	GD2	GD3	GD4	HR3	HS2	IR	K	Ka
B2	0.0000									
B3	0.0047	0.0000								
GD2	0.0612	0.0648	0.0000							
GD3	0.0956	0.0901	0.0134	0.0000						
GD4	0.0659	0.0578	0.0067	0.0094	0.0000					
HR3	0.0569	0.0597	0.0074	0.0077	0.0112	0.0000				
HS2	0.0294	0.0368	0.0149	[illegible]	[illegible]	0.0151	0.0000			
IR	0.0573	0.0341	0.1318	[illegible]	[illegible]	0.1129	0.0775	0.0000		
K	0.1415	0.1272	0.0521	[illegible]	0.1495	0.0594	0.1116	0.1928	0.0000	
Ka	0.0909	[illegible]	0.0278	[illegible]	[illegible]	[illegible]	0.0036	0.1440	0.0178	0.0000
KL1	0.0859	[illegible]	0.0792	[illegible]	[illegible]	[illegible]	0.0649	0.0361	0.1016	0.0724
KG	0.0369	0.0203	0.0149	0.1073	0.0693	0.0427	0.0768	0.0467	0.1017	0.0624
KU	0.0474	0.0518	0.0442	[illegible]	[illegible]	[illegible]	0.0310	0.0442	0.1131	0.0470
KT1	0.0714	0.0731	0.0166	[illegible]	[illegible]	[illegible]	0.0239	0.1220	0.0647	0.0192
MR2	[illegible]	[illegible]	0.0777	[illegible]	[illegible]	[illegible]	0.0469	0.0468	0.1463	0.0925
MN	[illegible]	0.0535	0.0338	[illegible]	[illegible]	[illegible]	0.0524	0.1116	0.0623	0.0249
ML	[illegible]	0.0157	0.0862	[illegible]	[illegible]	[illegible]	0.0559	0.0300	0.1597	0.1194
O3	[illegible]	[illegible]	0.0264	[illegible]	[illegible]	[illegible]	0.0234	0.1286	0.0777	0.0598
PG	[illegible]	0.0335	0.0069	[illegible]	[illegible]	[illegible]	0.0125	0.0478	0.0548	0.0196
PK	0.0600	0.1528	0.0052	[illegible]	[illegible]	[illegible]	0.0166	0.1175	0.0541	0.0318
PM	[illegible]	0.1036	0.0904	[illegible]	[illegible]	[illegible]	0.0683	0.1183	0.0649	0.0278
KG1	[illegible]	[illegible]	0.0351	[illegible]	[illegible]	[illegible]	0.0698	0.0373	0.1313	0.0810
TD	[illegible]	0.1154	0.0985	[illegible]	[illegible]	[illegible]	0.1026	0.0753	0.1197	0.0923

	KL1	KD	KU	KT1	MR2	MN	ML	O3	PG	PK
KL1	[illegible]									
KG	0.0493	[illegible]								
KU	[illegible]	[illegible]	[illegible]							
KT1	[illegible]	[illegible]	[illegible]	[illegible]						
MR2	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]					
MN	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]				
ML	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]			
O3	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]		
PG	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	
PK	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.0129	[illegible]
PM	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.0559	0.0429
KG1	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.0941	0.0779
TD	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	0.0775	0.0972

	PM	KG1	TD
PM	0.0000		
KG1	[illegible]	0.0000	
TD	[illegible]	0.0161	0.0000

APPENDIX.VI. SANGVI'S GENETIC DISTANCE MATRIX (ALL TRIBALS)

	B2	B3	GD2	GD3	GD4	MR3	MS2	JU	K	KA
B2	0.0000									
B3	0.0337	0.0000								
GD2	0.5208	0.0629	0.0000							
GD3	0.5676	0.6165	0.1399	0.0000						
GD4	0.4400	0.4319	0.0718	0.1148	0.0000					
MR3	0.3626	0.4744	0.1463	0.0436	0.1591	0.0000				
MS2	0.1982	0.2551	0.1195	0.2293	0.1123	0.1074	0.0000			
JU	0.5342	0.3575	1.5548	1.2177	1.0356	1.1004	0.7383	0.0000		
K	1.0120	0.9448	0.1558	0.3544	0.1994	0.5307	0.7816	2.2235	0.0000	
KA	0.6577	0.6432	0.2201	0.2935	0.2124	0.4056	0.4876	1.5214	0.1966	0.0000
KL1	0.5461	0.3628	0.6477	0.6527	0.3414	0.7123	0.5117	0.4995	1.0901	0.6537
KO	0.3594	0.2156	0.7416	0.9274	0.3456	0.5654	0.6665	0.7946	0.8461	0.5071
KU	0.2442	0.2546	0.6411	0.0932	0.4777	0.3210	0.2150	0.7133	0.6714	0.4979
KY1	0.4274	0.4570	0.1345	0.1705	0.2106	0.2039	0.1933	1.1357	0.4222	0.1461
MA2	0.2524	0.1732	0.4473	0.9158	0.4321	0.8206	0.4129	0.6571	1.2609	0.6499
MA	0.6321	0.5011	0.1794	0.2455	0.1316	0.4124	0.2237	1.1379	0.4864	.2671
MI	0.0490	0.1177	0.6067	0.0838	0.5559	0.4646	0.3289	0.7928	1.7504	.1578
U3	0.3744	0.4068	0.1042	0.3313	0.2133	0.2477	0.1652	1.2714	2.4741	.3719
PO	0.3351	0.3521	0.0553	0.2215	0.7522	0.2234	0.8044	1.1525	0.3836	.4436
PR	0.3933	0.4794	0.1128	0.8310	0.1298	0.3504	0.1187	1.2150	0.4012	0.3217
PB	0.5674	0.3316	0.4423	0.3008	0.3177	0.4003	0.4460	0.6537	0.6456	0.4742
RG1	0.6062	0.4229	0.3045	0.0152	0.3331	[illegible]047	2.0298	1.2425	1.2221	.6308
TO	0.3776	0.7419	[illegible]	0.0682	0.4420	[illegible]157	2.1493	0.7261	1.1571	.9609

	KL1	KO	KU	KY1	MA2	MA	MI	U3	PO	PR
KL1	0.0000									
KO	0.3101	0.0000								
KU	0.5559	0.5331	0.0000							
KY1	0.4675	0.5490	0.1765	0.2222						
MA2	0.3403	0.1152	0.5665	0.3352	0.2702					
MA	0.2526	0.4623	0.3451	0.1758	0.3121	0.0000				
MI	0.5209	0.4649	0.4104	0.2144	0.3144	0.6947	0.0000			
U3	0.5441	0.7033	0.5024	0.3474	0.2192	1.5721	0.3346	0.2145		
PO	0.4374	0.4637	0.4245	0.1471	0.3429	0.2241	0.4173	0.1774	0.2500	
PR	0.5510	0.3594	0.3557	0.2441	0.7857	0.2384	0.4862	0.2175	0.1710	1.0052
PB	0.3754	0.5012	0.1624	0.1332	0.7449	0.1250	1.0842	0.4781	0.4469	.2376
RG1	0.0731	0.4089	0.3551	0.5403	0.4920	0.2461	0.9627	1.4755	1.0847	0.2259
TO	0.0717	0.5418	[illegible]3	0.6263	0.2235	0.2879	1.2474	1.1714	0.6424	0.5385

	PB	RG1	TO
PB	0.0000		
RG1	0.3234	0.0000	
TO	0.4037	0.1568	0.1068

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TABLE - 1

SOURCE DATA ON POPULATIONS USED FOR ANALYSIS

(Regions surveyed and types of data available)

s	Code Name	Region	Region (Colour Code)	Measurements	ABO	MN	Rh	Hb	Hp	Tf	G6PD
	A	Bombay, M H	●	7	+						
undar)	B1	Tarvi Mountains, Rajasthan	●	7							
ls(Pagiba' al)	B2	Jhabua, M P	●	–	+	+	+	+	+	+	
ls (Vyas l)	B3	Panchmahal hills, Gujarat	●	–	+	+	+				
ils nchi	BM	West Khandesh, MH	●	7							
ils Tadvi	BT	West Khandesh, M H	●	7	+						
tra	B'	Bastar, M P	●	7	+						
te Kuruba	BK	Coorg, Karnataka	●	7							
son Hill rias	BH	Bastar, M P	●	7							
ndos	BN	Koraput, South Orissa	●	7							
hangar atkar	DH	Des, M H	●	7	+						
Dhangar Futekar	DK	Des, MH	●	7	+						
Dandami Marias	DM	Bastar, M P	●	7							
Dorla	DR	Bastar, M P	●	7							

TABLE 1(Contd.)

me	Code Name	Region	Region (Colour Code)	Measurements	ABO	MN	Rh	Hb	Hp	Tf	G6PD
e	DU	Baster, M P	●	7							
e and ker)	G1	CP & Berar, M H	●	7	+						
e)	G2	CP & Berar, M H	●	7							
ba	GD1	Joypore, Orissa	●	7							
ba	GD2	Koraput, Orissa	●	–	+	+					
eng aba	GD3	Koraput, Orissa	●	–	+	+	+	+			
aro aba	GD4	Koraput, Orissa	●	–	+	+	+	+			
ar	GJ	East Khandesh, M H	●	7							
lbi	HL	CP & Berar, M H	●	7	+						
ll rias oy)	HM1	Baster, M P	●	7							
ill arias ajumdars)	HM2	Baster, M P	●	7							
ill arias Pingle)	HM3	Chanda, MH	●	–	+	+	+	+	+	+	+
Hos (Ghosh)	HS1	Singhbhum, Bihar	●								
Hos Kumar etal)	HS2	Singhbum, Bihar	●	–	+	+	+	+			
Irula	IR	Nilgiris, Tamil Nadu	●	–	+	+	+	+	+	+	
Juang	JA	Keonjghar, Orissa	●	7							

TABLE I (Contd)

s	Code Name	Region	Region (Colour Code)	Measure-ments	ABO	MN	Rh	Hb	Hp	Tf	G6PD
raba	JK	Coorg, Karnataka	●	7							
	K	Nilgiris, Tamil Nadu	●	-	+	+	+				
	KA	Annamalai Hills, Kerala	●	7	+	+	+	+	+	+	+
us	KD	Surguja, Chota Nagpur, M P	●	7							
Malhar	KI	Thana dt., M H	●	7	+						
m gle)	KL1	Adilabad dt, A P	●	7	+	+	+	+	+	+	+
am rve)	KL2	C P and Berar, M H	●	7	+						
bi Mana	KM	C P and Berar, MH	●	7	+						
d	KN	Koraput, Orissa	●	7							
i	KO	Surat dt., Gujarat	●	-		+	+	+			
ku arve)	KR1	CP and Berar, MH	●	7							
raku tto- dhyaya	KR2	Amraoti dt, MH	●	7							
oraku nsu)	KR3	Amraoti dt, MH	●	7							
nbi irole	KT	CP and Berar	●	7	+						
urumba	KU	Nilgiris Tamil Nadu	●	-	+	+	+	+		+	

TABLE 1 (contd.)

	Code Name	Region	Region (Colour Code)	Measurements	ABO	MN	Rh	Hb	Hp	Tf	G6PD
	KW	Surguja dt., MP	●	7							
s	KY1	Adilabad dt., A P	●	7	+	+	+	+	+	+	+
	KY2	Koraput Orissa	●	7							
	KY3	Khammam & Warangal dts., A P	●	–	+		+	+	+	+	+
ha hvi)	M	Bombay Presidency, M H	●	–	+	+	+				
tha ve)	M1	C P and Berar, MH	●	7							
tha ve)	M2	W. Kandesh M H	●	7							
tha ve)	M3	East Khandesh, MH	●	7							
tha ve)	M4	Nizam's Dominions M H	●	7							
des rve)	MD1	Sundergarh, Orissa	●	7	+						
ades arkar)	MD2	Orissa	●	7							
har arve)	MH1	Dos, M H	●	7	+						
har Parikh tal)	MH2	Bombay dt. M H	●	–	+	+	+	+	+	+	+
anne Pirele)	MN	Adilabad dt., AP	●	7	+	+	+	+	+	+	+
aria	MR	Bastar, MP	●	7	+						
aikpod	F	Adilabad dt., A P	●	–	+		+	+	+	+	+

TABLE 1 (Contd)

	Code Name	Region	Region (Colour Code)	Measurements	ABO	MN	Rh	Hb	Hp	Tf	G6PD
	NI	Surat dt, Gujarat	●	–	+	+	+	+			
dar)	O1	Southern U P	●	7							
e)	O2	Sundergarh Orissa	●	7							
)	O3	Chota Nagpur, Bihar	●	–	+	+	+	+	+	+	
ng ja	PB	Koraput, Orissa	●	–	+	+	+	+			
a oja	PK	Koraput, Orissa	●	–	+	+	+	+			
ins ia ds ngle)	PM	Chanda dt, M P	●	7	+	+	+	+	+	+	
yans	PN	Kerala	●	5							
dhans	PR1	Mandla dt, M P	●	7							
dhans oud)	PR2	Adilabad dt, AP	●	–	+		+	+	+	+	+
jgonds ingle)	RG1	Adilabad dt, AP	●		+	+	+	+	+	+	+
ajgonds Goud)	RG2	Adilabad dt, AP	●	–	+		+	+	+	+	+
antals	SN	Santal Parganas, Bengal	●	5	+		+	+	+		+
Sholega	SO	Biligiri Rangan hills, Mysore	●	7							
Savara	SV	Sambalpur and Cuttack, Orissa	●	7							
Toda	TD	Nilgiris, Tamil Nadu	●	–	+	+	+	+	+	+	
Warli	WR	Thane dt, M S	●	7	+						

M A P 1

Distribution of tribal populations of peninsular India

GREEN BOUNDARY – CENTRAL INDIAN TRIBALS
YELLOW BOUNDARY – ORISSA AND CHOTANAGPUR TRIBALS
RED BOUNDARY – GONDS OF PRESENT STUDY
BLUE BOUNDARY – SOUTH INDIAN TRIBALS

INDIA - PHYSICAL

TAKLA MAKAN DESERT
KISTAN
DELHI
BANGLADESH
ARABIAN SEA
B E N G A
SRI LANKA
COLOMBO
MALDIVE ISLANDS
O C E A

FIGURE 1

Map showing distribution of all Gond villages (Tribe wise)

FIG. 1 MAP SHOWING DISTRIBUTION OF ALL GOND VILLAGES (TRIBEWISE)

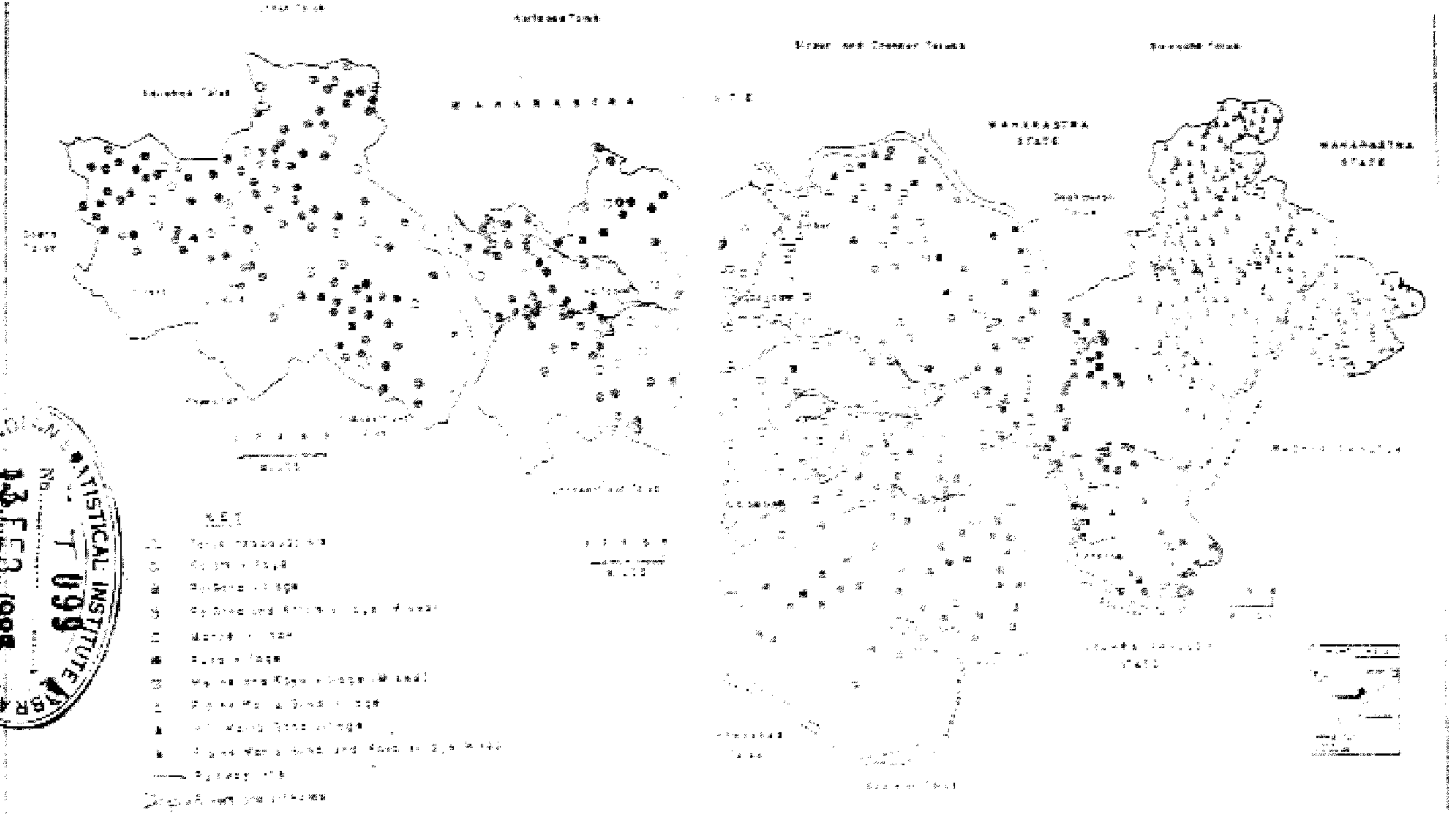
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Table 2 SCRUTINY OF RAW DATA

Detection of Outliers and Action Taken

Population (Code of Individual and Sex)	Observation as Recorded (in m m)	Action Taken	Basis on Which Action Was Taken
KOLAM (♂) 071	3gB 126	Omitted	Maximum Was Too Large
KOLAM (♂) 049	LAL 178	Omitted	Minimum Was Too Small
Kolam (♂) 092	SIB 201	Omitted	Minimum Was Too Small
KOLAM (♀) 102	BAB 246 SIB 337	Values Where Interchanged	BAB Never Smaller Than SIB In Same Individual
KOLAM (♀) 025	UAL 201	Omitted	Minimum Too Small
KOLAM (♀) 121	LAL 188	Omitted	Maximum Value Too Large
KOLAM (♀)	UAL 368	Omitted	Maximum Value Too Large
KOYAS (♂) 028	UAL 247 LAL 282	Upper Arm 282 Lower Arm 247	Interchange Error Upper Arm Cannot Be Larger Than Lower Arm
KOYAS (♂) 048	UAL 180 LAL 295	Upper Arm 295 Lower Arm 180	Interchange Error Upper Arm Cannot Be Larger Than Lower Arm
KOYAS (♂) 083	UAL 303 LAL 271	Upper Arm 271 Lower Arm 303	Interchange Error Upper Arm Cannot Be Larger Than Lower Arm
KOYAS (♂) 076	UAL 325	Omitted	Maximum Too Large. Not consistent With Fat Fold Measurements of Same Individual

TABLE 2 SCRUTINY OF RAW DATA

Detection of Outliers and Action Taken (Continued)

Population (Code of Individual and Sex)	Observation as Recorded (in m m)	Action Taken	Basis on Which Action Was Taken
MANNE (♂) 007	HB 164	Omitted	Maximum Too Large
MANNE (♂) 028	BzB 136	Omitted	Maximum Too Large
MANNE (♀) 015	HB 159	Omitted	Maximum Too Large
MANNE (♀) 001	HL 210	Omitted	Maximum Too Large
MANNE (♀) 001	BzB 116	Omitted	Maximum Too Large
MANNE (♀) 093	[illegible] 130	Omitted	Maximum Too Large
PLAINS MARIA (♂) 052 GOND	IFF 13.0 SFF 19.0	Omitted	Maximum Values Too Large
PLAINS MARIA (♀) 127 GOND	BzB 114	Omitted	Minimum Values Too Low
PLAINS MARIA (♀) 036 GOND	BAB 115	Omitted	Minimum Values Too Low
PLAINS MARIA (♀) 120	BAB 112	Omitted	Minimum Values Too Low