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Asymmetry and Diversity of Dermatoglyphic Traits: Population Comparison in Five Endogamous Groups of West Bengal, India

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With 4 figures, 6 tables and 3 appendices

Summary: Five different endogamous populations encompassing the main social ranks in the caste hierarchy of West Bengal, India were analyzed. To compare variability in populations with contrasting ethnohistorical backgrounds, analysis of variance, Scheffe's test and cluster analysis were performed, as based on dermatoglyphic variables, namely, 22 quantitative traits and 36 indices of diversity and asymmetry. The present study reveals that: 1. Overall disparities among the 5 populations are expressed only in finger ridge counts on the Ist and Vth digits and PII, in a-b ridge counts, in endings of main lines A and D, and in MLI on the palms; 2. Heterogeneity is greater in fluctuating asymmetry than in directional asymmetry; 3. There is a greater heterogeneity in the 22 quantitative traits than in the 36 indices of diversity and asymmetry, with females contributing more than the males; 4. The highest contribution to population variation is by Lodha among five populations; 5. Inter-group variations are homogeneous in most of the variables, which does not correspond with the relationships to caste hierarchy of these populations; 6. The dendrograms based on dermatoglyphic variables demonstrate that the traditional grouping of Indian populations, based on caste hierarchy, may not be a reflection of their genetic origin, in that the pattern of clustering corresponded best with the known ethnohistorical records of the studied populations; 7. Hence, dermatoglyphic affinities may prove quite useful in tracing the ethnohistorical background of populations.

Key words: Quantitative dermatoglyphics, population variation with contrasting ethnohistorical backgrounds, endogamous groups, West Bengal, India.

Zusammenfassung: Es wurden fünf verschiedene Populationen untersucht, die den wichtigsten sozialen Rängen in der Kastenhierarchie von West-Bengalen, Indien, angehören. Um die Variabilität in Populationen mit unterschiedlichem ethnohistorischen Hintergrund zu vergleichen, wurden die Varianzanalyse, der Scheffe-Test sowie die Clusteranalyse herangezogen, basierend auf 22 quantitativen Merkmalen und 36 Indices der Diversität und Asymmetrie. Die vorliegende Untersuchung ergab: 1. Generelle Verschiedenheiten zwischen den fünf Populationen ergaben sich nur für die Leistenzahlen auf den Fingern I und V sowie auf PII, in den a-b-Leistenzahlen, in den Endigungen der Hauptlinien A und D sowie des MLI auf den Palmae; 2. Die Heterogenität ist hinsichtlich der fluktuierenden Asymmetrie größer als in der direktionalen; 3. Die Heterogenität in den 22 quantitativen Merkmalen ist ausgeprägter als in den 46 Indices der Diversität und Asymmetrie, vor allem bei den Frauen; 4. Den größten Beitrag bezüglich der Variabilität zwischen den fünf Popu-

lationen bewirken die Lodha; 5. Bezüglich der meisten Variablen sind die Intergruppen-Variationen homogen, was nicht mit den Beziehungen zur Kastenhierarchie in diesen Populationen übereinstimmt; 6. Die auf den Hautleistenvariablen basierenden Dendrogramme zeigen, dass die auf der Kastenhierarchie basierende traditionelle Gruppierung der indischen Bevölkerungen nicht ihre genetische Herkunft reflektieren dürfte und dass das Clustermuster besser mit den bekannten ethnohistorischen Kenntnissen der untersuchten Populationen übereinstimmt; 7. Affinitäten in den Hautleistenmerkmalen erweisen sich daher als geeignet, um den ethnohistorischen Hintergrund von Populationen zu erkennen.

Schlüsselwörter: Quantitative Hautleistenmerkmale, Variation in Populationen mit unterschiedlichem bevölkerungsgeschichtlichem Hintergrund, endogame Gruppen, West-Bengalen, Indien.

Introduction

Genetic variation in human populations has been studied through the use of several traits pertaining to morphological, biochemical, serological and polygenic systems such as anthropometrics and dermatoglyphics. Recently, Crawford & Duggirala (1992) found a significant association between dermatoglyphics and geography, and demonstrated that dermatoglyphics is a highly informative polygenic system that can be used to study evolutionary processes and population structure. Dermatoglyphics have been used to investigate interpopulation structuring in a number of human populations (Crawford 1976, Lin et al. 1983, Blangero 1990), because several studies had demonstrated that dermatoglyphics are phylogenetically more stable than other biological traits (Rothhammer et al. 1977, Froehlich & Giles 1981). The fact that dermatoglyphic traits appear to be evolutionarily conservative renders them more reliable for studies of the historical relationships of populational structures. It has also been suggested (Singh 1982) that dermatoglyphic traits are the result of a biogenetic expression, rather than of the physical environment, and this because dermatoglyphic features are formed before the 19th week of gestation (Penrose & Ohara 1973) and thereafter are not amenable to change due to age and/or environmental factors. Dermatoglyphic characteristics thus permanently preserve an earlier stage of fetal development, whereas most other biological characteristics are perforce examined postnatally.

The only possibility of exerting any influence on dermatoglyphic traits is by local disruptions that may sometimes occur during early fetal development (Jantz & Webb 1980). Newman (1960) has suggested that "since dermatoglyphic traits are polygenetically controlled, putatively non-adaptive, and undergo no postnatal modifications, they have distinct methodological advantages over either anthropometry or serology in clarifying the older and more basic relationships between human populations". Ethnic relationships and geographic trends in dermatoglyphic configuration in many human populations (but particularly in Indian populations) have been evinced by numerous studies (Cummins & Midlo 1961, Banerjee & Banerjee 1975, Chakraborty et al. 1982, Singh 1982, Malhotra & Sarkar 1984, Micle & Kobyliansky 1985, Karmakar et al. 1989, Karmakar 1990a, 1990b, Kamali & Mavalwala 1990, Arrieta et al. 1990, 1991, Reddy & Reddy 1992, Gualdi-Russo et al. 1994, Kamali et al. 1994, Krishnan & Reddy 1994, Reddy et al. 2000). Similar geographic trends were observed also in anthropometric traits (Mahalanobis et al. 1949, Karve 1954, Karve &

Malhotra 1968) and in serological data (Majumder & Rao 1958, Singh et al. 1974, Mukherjee et al. 1974, 1987, Chakraborty et al. 1986, 1987, Banerjee et al. 1992).

A review of the literature reveals that most of the studies on dermatoglyphic asymmetry and intraindividual diversity of finger ridge counts in populations are mainly on persons of Indo-European ancestry (Jantz 1975, Kobyliansky et al. 1979, Roche et al. 1979, Chakraborty et al. 1982, Vona & Porcell 1983, Malhotra & Sengupta 1985, Reddy et al. 1985, Malhotra 1987, Malhotra et al. 1987, Micle & Kobyliansky 1987, Karve 1990), African ancestry (Jantz 1974, Salzano & Benevides 1974) or on Amerindians (Dittmar 1998).

There was justification, therefore, to investigate the asymmetry of dermatoglyhic traits in Indian populations as well, and this was done in the present study, albeit preliminary findings have already been reported elsewhere (Karmakar et al. 2001, 2002).

Homologous parts in a living organism, including in humans, often display differences, although the genetic components for both sides are the same. This bilateral difference has been termed asymmetry and is comprised of two main categories, namely, directional (signed) difference and fluctuating (non-signed or random/absolute difference). These two categories differ in their biological significance. The directional asymmetry (DAs) signifies a well-defined constant direction of bilateral differences. Fluctuating asymmetry (FlAs), on the other hand signifies random differences between two values of a bilateral character, and may be derived by subtracting from the value of non-signed bilateral differences in each individual the value of DAs. Thus, the obtained values for both DAs and FlAs can be related to the total values of the examined traits and thereby, naturally, the asymmetry values for different traits become comparable.

The etiology of DAs in a trait may be regarded as developmentally controlled, and perhaps has a genetic basis. FlAs in a trait, on the other hand, is considered to stem from inability of the organism to buffer the negative influences of disturbing developmental factors (see inter-alia, Ludwig 1932, Waddington 1960, van Valen 1962, Doyle & Johnston 1977, Kobyliansky & Livshits 1986, Livshits & Kobyliansky 1987, 1989, 1991). Consequently, FlAs may serve as an indirect measure of developmental stability. In the manifestation of dermatoglyphic FlAs, a principal role is attributed to exogenous factors, but the existence of a genetic component has also been suggested (Jantz 1977, Malhotra 1987, Karmakar 1990a, 1990b). Hence, research on the biological significance of the two kinds of asymmetry in dermatoglyhic traits is much needed, as is also the study of their variation among diverse populations.

Apart from directional and fluctuating asymmetry, there are two more variables, namely, the indices of asymmetry and interindividual diversity. The index of asymmetry delineates the ridge count variation among homologous fingers, while the index of diversity quantifies ridge differences between non-homologous fingers. Micle & Kobyliansky (1986) emphasized the importance of these two indices and studied them on a set of 66 dermatoglyphic variables. Finger ridge count asymmetry and diversity displaying ethnic variation has been demonstrated by Jantz (1974, 1975) as based on a comparative study between groups of European and African ancestry. Dittmar (1998) suggested that interpopulational comparison not only reveals ethnic differences of asymmetry and diversity, but also shows geographical

variation among populations from Europe, the Middle East, and Africa; she also concluded that these traits are suitable for comparative studies in dermatoglyphics. In a series of studies, Leguebe & Vrydagh (1979, 1981) investigated the diversity of finger ridge counts in males and females across the world and summarized their findings as follows: a) the structure of diversity of ridge counts on separate fingers differs in the population groups; b) there is similarity between males and females; and c) the left hand is more homogeneous than the right. Krishnan & Reddy (1994) found much homogeneity of finger ridge counts (TFRC and ATFRC) in 239 Indian populations as compared to populations from the rest of the world. Therefore, it should prove worthwhile to examine separately the intergroup variations with respect to sex and sides (right and left).

It is already known from several early studies that females exhibit higher correlations for various dimensions and developmental events than do males (Garn et al. 1972, 1975, Burdi et al. 1974, Palti & Adler 1975). It has also been observed that females are more symmetric than males in terms of having both sides (right and left) equal with no bilateral differences (David 1984, Reddy et al. 1985, Reddy 1998, Goodson & Meier 1986, Micle & Kobyliansky 1986, Kobyliansky & Micle 1987, 1988, 1989, Malhotra 1987, Arrieta et al. 1987, 1990, Perez & Porras 1990). The same, and other studies, however, report the reverse, that is that males are more symmetric than females (Holt 1951, Parsons 1964, Reddy et al. 1985, Reddy 1998, Malhotra 1987, Kobyliansky & Micle 1988, Arrieta et al. 1990, Micle & Kobyliansky 1991, Dittmar 1998). It was further observed in several investigations that many populations typically display similar bilateral differences between males and females, e.g. sex differences are absent between the right and left sides (Holt 1959, Mavalwala 1962, Knussmann 1967, Pons 1970, Vrydagh-Laoureux 1971, Ghosh 1982, Arrieta et al. 1995). Clearly then, the study of population variation in both sexes is important.

In view of the above, and because of the well-known ethnic diversity of Indian populations with varied ecosystems, we deem it important to use dermatoglyphic traits and dermatoglyphic asymmetry (DAs and FlAs) as one uses other independent biological criteria for ascertaining ethnic relationships. We reasoned that both should prove helpful in evaluating group relationships and understanding dermatoglyphic homogeneity/heterogeneity among different population groups of the same geographic region – in our case the State of West Bengal, India.

The choice of the five populations used in the present study was advantageous because: (a) their biological structure was already investigated, via biochemical and serological markers (Mukherjee et al. 1974, 1987, Singh et. al. 1974, Chakraborty et al. 1982, 1986, 1987, Chakraborty 1987, Banerjee et al. 1992, Das & Kumar 1997), and (b) their ethnohistorical background was well known.

The aim of the present study was to ascertain: (i) whether five different endogamous population groups (both male and female) from the same State of West Bengal are homogeneous or heterogeneous in nature with respect to dermatoglyphic traits, asymmetry (directional and fluctuating) and intraindividual diversity, and (ii) possible relationships between dermatoglyphic differences and known ethnohistorical backgrounds of these populations. The obtained results are discussed in light of earlier findings on biochemical and serological markers of the same population groups of West Bengal.

Table 1. Sample description.

Population	Abbreviation	Nos. of families	Nos. of individuals
Brahmin (Rarhi)	BR	100	449
Mahisya	MA	100	504
Padmaraj	PA	100	525
Muslim (Sunni)	MU	100	555
Lodha	LO	100	402
Total		500	2435

Material and methods

The five populations used in this study are presented in Table 1, dermatoglyphic traits in Appendix 1, and formulae for calculating various indices in Appendix 2.

Ethnohistorical background

In India the sociometric situation is quite complex due to a very old (approximately 3000 years) and unique caste system, and the presence of a large number of tribal groups with a high degree of inbreeding, as well as of various religious communities. Indian people are characterized as belonging to several endogamous groups and are structured in a system commonly referred to as Hindu caste (derived from the Latin word Casta = pure/unmixed and absolutely based on function and occupation), in which each caste and sub-caste behaves as an endogamous entity. Indian castes belong to quadruple divisions of society and are arranged in a social gradation or a hierarchical order called Jati. In this hierarchy, Brahmins are at the top and beneath, in descending order, are the Kshatriya, Vaisya and Sudra. Endogamous populations represent 3 categories of social stratification based on caste hierarchy to wit: higher caste group; lower caste group and tribes. The low-caste group consists of scheduled and non-scheduled castes. Scheduled caste is a common term used to designate the low-ranking caste groups, while tribes are migrant groups and both these categories are protected by the Government (Census of India 1951, District Gazetters, Bengal, 1909). There is, however, a gradual transformation of tribes into castes all over India (Risley 1891).

Subjects selected for the present study are five Bengali-speaking groups, namely: Brahmin (Rarhi), Mahisya, Padmaraj, Muslim (Sunni) and Lodha. They were sampled from rural communities in the Howrah and Midnapore Districts of West Bengal. Members of these populations practice monogamy and are strictly endogamous. Details for the people and their history may be found in Appendix 3.

Genetic background based on variations in serological and biochemical markers

A number of endogamous castes and tribes from West Bengal, India, has been investigated for serological and biochemical markers which could identify the genetic affinities of the populations (see among others: Mukherjee et al. 1974, Chak-

raborty et al. 1986, 1987, Mukherjee et al. 1987, Banerjee et al. 1992). Chakraborty et al. (1986, 1987) and Mukherjee et al. (1987) have extensively studied the pattern of genetic affinities, employing 12 polymorphic systems on 10 endogamous groups (5 castes and 5 tribes) of West Bengal. Their populations belonged to 3 categories: (i) Brahmins (high castes); (ii) Scheduled Castes (low castes) and (iii) Tribes. These authors obtained a complete consistency of the genetic variability for all markers and for all populations, barring the ABO system in two groups, namely, Jalia Kaibarta (a low caste group) and Munda (a tribal group), with both of them showing significant differences. The authors suggested that the genetic peculiarities in the 10 endogamous groups may stem from their different geographic locations. Be that as it may, the gene diversity in each population was very low (0.024 ± 0.006). Interestingly, the Jalia Kaibartas and Bagdis were found to be closer to the high-caste groups, despite their low social ranking – a relationship evinced in a number of earlier studies. Dutta (1969), for instance, suggested that Rarhi Brahmins are the result of intermixing (inter-marriages) of Brahmin and low-caste groups like the Bagdi and Kaibarta. Mukherjee et al. (1974) also observed homogeneity between Mahisya and Muslim with respect to the distribution of alleles. Roy Choudhury (1984) obtained similar results with two segments of Bagdi (Duley and Tentulia), suggesting a close genetic proximity to Brahmins. Cluster analysis of 10 groups by Chakraborty et al. (1986) also failed to assign together populations of the same social ranks, rather, the scheduled castes were genetically close to the high-caste groups instead of being closer to their cohorts of the same social rank; other scheduled castes and some tribes are most likely deemed the result of a considerable admixture with local tribes. The authors further conjecture that some of the tribal and lower-caste populations may have accumulated genes from the high-caste groups in past generations of gene flow and consequently now present an overall genetic profile somewhat dissimilar to their social class. It follows then, that the genetic profile of any given population does not always correspond exactly to its present social ranking, since some low-caste groups are shown to have stronger genetic affiliation with high-ranking groups, instead of being close to groups of their own rank. The present caste hierarchy in India, therefore, may not be a true reflection of the genetic origin of the populations.

Dermatoglyphic print analysis

Dermatoglyphic prints were collected according to the rolled print (inked) method of Cummins & Midlo (1961). Dermatoglyphic variables used in the present study belonged into two main categories. The first category included the 22 usually studied quantitative traits, to wit: 10 digital ridge counts, 2 total and absolute ridge counts, 2 a-b ridge counts, 3 pattern intensity indices (PII), 4 main line (A&D) endings, and (MLI). The second category included the 36 dermatoglyphic variables that represent the indices of diversity and asymmetry, to wit: 11 intraindividual diversity indices, 12 indices of directional asymmetry, and 13 indices of fluctuating asymmetry.

The dermatoglyphic traits were evaluated for the most part by the methods of Cummins & Midlo (1961) and Penrose (1968). The indices of intraindividual variability and asymmetry in ten finger ridge counts, S^2 , $S\sqrt{5}$, $S\sqrt{10}$ and AI were

calculated according to Holt (1968), Jantz (1975) and Kobyliansky et al. (1979). In addition, indices analogous to S^2 and $S\sqrt{10}$ were separately calculated for the left and right fingers and were designated as S^2L, S^2R, IIDL and IIDR. The Shannon information measure was adapted for illustrating the diversity of pattern types on the ten fingers (Kobyliansky & Micle 1987). It should be noted that all possible combinations of arch patterns, namely, A-A, A-R, A-U and A-W were excluded from the computation of asymmetry values (DAs and FlAs). Our justification for this was that A-R combinations of right/left fingers comprised merely 0.1 % A-U combinations, merely 1.5 % and A-W combinations merely 0.2 % of the total sample, whereas by excluding these arch combinations, we obviated possible technical errors in the computation of asymmetry values.

Procedure applied for caste comparisons basing on family

Data

We used family data, not only parental data, because preliminary trials revealed that differences between parental samples and total family samples were negligible. This became clear to us after undertaking the following steps. First we computed family correlations for two types of dermatoglyphic traits, namely 22 commonly used quantitative traits and 36 traits of asymmetry and diversity indices. We found high correlation between father-offspring, mother-offspring and offspring-offspring for the 22 quantitative traits and negligible correlation between father-mother, as was expected. As for the remaining 36 traits, correlations were all negligible for all of the relative combinations. In the wake of these results, we decided to assess the effect of using the total family sample in caste comparison for the 22 quantitative traits only, and to this end computed all condescriptive statistics, including cluster analysis that was based only on parental populations. Following this procedure, we estimated differences within the total family sample only, and found that average differences for the 22 traits amounted to about 2.5 percent for each of the castes separately. These findings encouraged us to include both parents and children (total sample) in caste comparisons, thereby affording us a five-fold increase in sample size. Regrettably, space limitations prohibit us to present all the relevant data here (i.e., tables, dendrograms, etc.). These, however, will readily be supplied, upon request, to the interested reader.

Statistical tests

One-way Analysis of Variance (ANOVA) was used for assessing the significance of the group differences between quantitative traits and directional asymmetry variables. ANOVA generates a set of transformed variables that enable testing between and within subject effects (through the proportion of group-means) and the obtained F-value may then indicate that the population means are probably unequal.

For assessing the significance of the differences in intraindividual diversity indices and fluctuating asymmetry, variables used the Kruskal-Wallis test of one-way analysis of variance. It ranked all the variables from the original set of data in a single series, then computed the Mean rank for each group, and finally computed the 'H' statistic which approximates a distribution.

Table 2. Comparison of 22 quantitative traits and indices in males of 5 castes, by ANOVA method.

	Brahmin		Mahisya		Padmaraj		Muslim		Lodha			
Trait	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**F ratio**	**Sig. (P)**
Finger RC, I-r	15.75	5.78	16.14	5.74	15.21	5.51	15.54	5.64	18.10	5.15	9.18	0.000
Finger RC, II-r	10.03	6.20	11.17	6.13	9.95	5.45	10.77	6.12	11.67	5.02	3.75	0.005
Finger RC, III-r	11.47	5.43	11.48	5.43	11.25	5.12	11.37	5.34	12.92	3.83	3.86	0.004
Finger RC, IV-r	14.83	5.70	14.96	5.12	14.04	4.90	14.11	5.11	13.91	4.46	2.24	0.062
Finger RC, V-r	12.20	5.34	13.06	4.67	12.20	4.33	11.93	4.63	11.61	4.01	3.33	0.010
Finger RC, I-l	13.87	5.38	14.55	5.57	13.31	5.42	13.93	5.92	15.59	4.59	5.78	0.000
Finger RC, II-l	9.65	6.05	10.53	5.84	9.92	5.44	10.33	5.86	10.68	5.06	1.32	0.262
Finger RC, III-l	12.11	5.71	11.78	5.67	11.29	5.36	11.68	5.30	12.35	4.37	1.41	0.227
Finger RC, IV-l	14.46	5.41	14.59	5.01	13.91	5.18	14.22	5.08	13.21	4.20	2.62	0.034
Finger RC, V-l	11.47	5.03	12.35	4.20	12.03	4.42	11.82	4.25	11.21	4.18	2.39	0.049
TRC	124.89	44.67	129.87	41.71	122.85	38.95	125.66	42.79	131.26	34.17	1.81	0.125
AbsRC	162.70	79.94	178.63	82.78	164.75	75.17	171.86	79.81	172.89	64.93	1.76	0.134
PII, lh	6.35	1.90	6.92	2.02	6.68	1.98	6.89	1.98	6.86	1.71	3.62	0.006
PII, rh	6.63	1.79	7.07	1.92	6.85	1.91	7.03	1.84	6.98	1.59	2.28	0.058
PII, both h	12.98	3.51	13.99	3.79	13.53	3.72	13.91	3.62	13.84	3.12	3.23	0.012
a-b RC, rh	36.66	6.50	37.10	5.28	38.22	5.29	36.98	5.28	38.78	5.13	6.23	0.000
a-b RC, lh	37.66	5.86	37.77	5.69	38.40	5.85	36.69	5.32	38.20	5.61	3.76	0.005
A-line exit, l	3.01	0.97	3.05	0.82	3.00	0.68	2.76	1.14	2.97	0.76	4.44	0.001
A-line exit, r	3.21	0.97	3.26	0.90	3.87	1.04	3.93	1.14	4.03	1.02	35.61	0.000
D-line exit, l	3.98	1.47	3.90	1.34	3.84	1.37	3.94	1.51	3.73	1.40	1.04	0.386
D-line exit, r	4.78	1.49	4.51	1.47	4.51	1.57	4.76	1.53	4.44	1.53	2.62	0.034
MLI	7.50	1.80	7.36	1.63	7.61	1.72	7.69	1.96	7.60	1.70	1.35	0.249

Table 3. Comparison of 22 quantitative traits and indices in females of 5 castes, by ANOVA method.

	Brahmin		Mahisya		Padmaraj		Muslim		Lodha			
Trait	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**F ratio**	**Sig. (P)**
Finger RC, I-r	14.06	6.55	14.32	5.45	12.88	6.00	13.76	5.29	15.45	4.41	6.10	0.000
Finger RC, II-r	10.00	6.14	10.23	5.52	9.98	5.63	10.85	6.07	11.25	4.53	2.17	0.071
Finger RC, III-r	11.12	5.01	11.28	5.22	10.26	4.87	11.27	5.22	12.02	3.99	3.63	0.006
Finger RC, IV-r	14.23	5.93	14.20	5.40	13.02	5.87	14.06	5.36	13.76	4.31	2.06	0.085
Finger RC, V-r	11.37	4.93	12.07	4.56	11.09	4.71	11.49	4.51	10.63	3.95	3.00	0.018
Finger RC, I-l	12.13	5.81	13.12	5.11	11.70	5.53	12.41	5.14	13.55	4.59	4.50	0.001
Finger RC, II-l	9.57	5.97	10.18	5.92	8.73	5.83	10.17	5.96	10.28	4.61	3.12	0.015
Finger RC, III-l	10.94	5.75	10.86	5.85	10.22	5.64	11.27	5.87	11.58	4.15	1.93	0.103
Finger RC, IV-l	13.50	5.89	13.62	5.29	12.52	5.80	13.80	5.51	12.91	3.98	2.39	0.049
Finger RC, V-l	10.18	4.75	11.41	4.54	10.84	4.59	11.51	4.36	10.02	3.84	5.38	0.000
TRC	116.43	44.69	121.01	42.31	111.24	43.56	120.45	43.14	121.08	30.98	2.51	0.040
AbsRC	148.79	76.63	162.70	78.39	148.82	78.06	163.81	77.50	156.54	58.33	2.26	0.060
PII, lh	6.18	2.06	6.74	2.13	6.43	2.26	6.88	2.07	6.81	1.61	4.68	0.001
PII, rh	6.24	1.87	6.64	1.96	6.45	2.11	6.86	1.92	6.71	1.52	3.69	0.005
PII, both h	12.42	3.67	13.39	3.89	12.89	4.20	13.74	3.77	13.52	2.90	4.68	0.001
a-b RC, rh	36.86	5.66	36.32	5.15	38.39	5.31	37.38	5.44	38.70	5.79	7.59	0.000
a-b RC, lh	37.41	5.64	36.57	5.08	37.69	5.66	37.13	5.44	38.06	5.34	2.42	0.047
A-line exit, l	3.13	0.87	3.03	0.72	2.94	0.86	2.73	1.12	3.00	0.72	6.75	0.000
A-line exit, r	3.23	0.86	3.19	0.83	3.96	1.08	3.86	1.12	3.93	1.06	34.27	0.000
D-line exit, l	3.81	1.44	3.67	1.46	3.91	1.52	3.92	1.57	3.56	1.42	2.54	0.038
D-line exit, r	4.56	1.53	4.30	1.59	4.74	1.50	4.52	1.56	4.31	1.62	3.23	0.012
MLI	7.37	1.71	7.08	1.66	7.77	1.87	7.52	2.11	7.40	1.73	4.48	0.001

Table 4. Comparison of 36 traits (indices of intraindividual diversity and asymmetry) in males of 5 castes, by ANOVA method.

	Brahmin		Mahisya		Padmaraj		Muslim		Lodha			
Trait	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**Mean**	**S.D.**	**F ratio**	**Sig. (P)**
Div I	8.93	4.28	8.60	4.17	8.62	3.87	8.53	4.11	8.17	4.05	0.93	0.445
Div II	9.80	4.92	9.65	4.50	9.11	4.26	9.01	3.85	9.51	4.40	1.58	0.176
Div III	12.13	4.67	11.65	4.54	11.34	4.19	11.00	4.07	11.61	4.56	2.28	0.059
Div IV	64.39	61.00	60.73	60.55	59.42	54.87	59.48	61.99	53.04	50.58	1.05	0.380
Div V	78.72	80.64	75.19	74.19	68.64	64.10	62.79	55.67	68.48	60.81	2.18	0.069
Div VI	152.86	117.29	146.96	119.90	136.89	105.10	130.15	105.87	132.14	98.42	1.90	0.108
Div VII	3.26	1.51	3.14	1.52	3.14	1.42	3.11	1.49	2.95	1.39	1.21	0.303
Div VIII	3.56	1.76	3.51	1.66	3.36	1.57	3.25	1.40	3.39	1.50	1.51	0.197
Div IX	3.67	1.36	3.57	1.39	3.47	1.30	3.37	1.28	3.42	1.25	1.97	0.097
Div X	13.75	6.16	13.25	6.25	12.94	5.88	12.61	5.93	12.63	5.71	1.46	0.211
Div XI	0.57	0.25	0.55	0.31	0.52	0.29	0.56	0.27	0.54	0.25	1.02	0.396
DAs I	0.86	5.34	1.01	4.50	0.54	4.36	0.47	3.93	1.34	4.51	1.47	0.208
DAs II	0.28	1.16	0.15	1.09	0.17	1.15	0.14	1.23	0.12	1.11	0.70	0.590
DAs III	-0.98	5.21	-0.67	4.10	-0.18	4.57	0.29	4.87	0.58	4.33	4.51	0.001
DAs IV	3.62	9.24	3.18	9.63	2.54	9.35	1.74	8.67	5.16	8.94	4.57	0.001
DAs V	14.39	85.58	13.97	70.57	10.16	60.40	3.23	55.35	15.44	62.22	1.48	0.206
DAs VI	0.30	1.87	0.36	1.62	0.24	1.54	0.14	1.37	0.44	1.55	1.30	0.267
DAs VII	-0.03	7.73	-0.08	6.59	0.87	6.90	0.62	7.46	0.33	6.41	0.90	0.463
DAs X	0.72	3.42	0.73	3.63	0.24	3.01	0.11	2.88	0.40	2.99	2.04	0.087
DAs XI	0.39	3.81	0.35	3.61	0.15	3.45	-0.10	3.37	0.70	3.10	1.78	0.131
DAs XII	-0.62	3.89	-0.27	3.75	-0.04	3.76	-0.31	3.45	0.56	3.38	3.11	0.015
DAs XIII	0.41	4.35	0.69	4.27	0.03	4.33	0.44	3.96	0.99	3.75	1.76	0.134
DAs XIV	1.83	4.77	1.63	4.31	1.90	4.08	1.61	4.11	2.52	4.52	1.58	0.176
FlAs I	4.06	3.46	3.48	2.85	3.41	2.71	3.05	2.47	3.56	2.76	4.04	0.003
FlAs II	0.89	0.73	0.79	0.75	0.86	0.77	0.91	0.83	0.83	0.74	0.97	0.421
FlAs III	3.92	3.42	3.28	2.46	3.50	2.94	3.80	3.04	3.51	2.52	2.00	0.092
FlAs IV	7.04	5.96	7.35	6.21	7.08	6.09	6.63	5.58	7.05	5.47	0.54	0.708
FlAs V	54.53	65.86	46.71	52.81	42.82	42.52	37.99	40.19	42.92	44.94	3.77	0.005

Table 4 (continued).

	Brahmin		Mahisya		Padmaraj		Muslim		Lodha			
Trait	Mean	S.D.	Mean	S.D.	Mean	S.D.	Mean	S.D.	Mean	S.D.	F ratio	Sig. (P)
FlAs VI	1.44	1.19	1.25	1.02	1.21	0.95	1.08	0.83	1.22	0.96	4.18	0.002
FlAs VII	4.73	6.10	3.56	5.54	4.17	5.49	4.37	6.04	3.83	5.13	1.56	0.183
FlAs X	2.53	2.30	2.75	2.36	2.30	1.93	2.16	1.90	2.18	2.04	3.71	0.005
FlAs XI	2.99	2.36	2.70	2.39	2.62	2.24	2.60	2.13	2.37	1.99	2.14	0.074
FlAs XII	2.94	2.55	2.76	2.54	2.80	2.50	2.65	2.20	2.66	2.09	0.58	0.676
FlAs XIII	3.14	3.01	3.20	2.83	3.20	2.90	2.95	2.64	2.87	2.41	0.74	0.565
FlAs XIV	3.58	3.15	3.30	2.77	3.20	2.54	3.09	2.70	3.33	3.04	1.03	0.393
FlAs XVI	8.17	3.50	8.15	3.62	7.80	3.32	7.52	3.11	7.87	3.26	1.68	0.152

Table 5. Comparison of 36 traits (indices of individual diversity and asymmetry) in females of 5 castes, by ANOVA method.

	Brahmin		Mahisya		Padmaraj		Muslim		Lodha			
Trait	Mean	S.D.	Mean	S.D.	Mean	S.D.	Mean	S.D.	Mean	S.D.	F ratio	Sig. (P)
Div I	9.01	4.00	8.29	3.67	8.61	4.24	8.03	4.14	8.18	3.46	2.27	0.060
Div II	8.87	4.60	8.64	4.20	8.39	4.01	8.41	3.78	8.12	3.32	1.04	0.387
Div III	11.73	4.47	10.93	3.94	11.04	4.28	10.54	4.03	10.60	3.48	2.97	0.019
Div IV	64.36	53.72	54.56	48.13	60.08	56.29	54.06	55.76	51.36	42.76	2.22	0.065
Div V	65.58	68.76	59.02	53.30	57.10	58.39	55.92	55.09	49.95	42.01	2.07	0.082
Div VI	147.02	107.12	124.22	86.60	126.67	98.12	118.74	102.59	113.35	74.04	3.84	0.004
Div VII	3.29	1.43	3.02	1.34	3.13	1.48	2.93	1.49	2.96	1.23	2.45	0.045
Div VIII	3.23	1.64	3.11	1.46	3.05	1.46	3.05	1.39	2.94	1.18	1.15	0.330
Div IX	3.60	1.33	3.32	1.18	3.33	1.27	3.20	1.29	3.21	1.02	3.69	0.005
Div X	12.92	5.86	11.91	5.45	12.17	5.69	11.89	5.41	11.45	4.85	2.04	0.087
Div XI	0.54	0.25	0.56	0.29	0.54	0.28	0.56	0.28	0.56	0.23	0.42	0.795
DAs I	-0.16	4.82	0.34	4.67	-0.22	4.72	0.38	4.38	-0.06	3.78	0.96	0.431
DAs II	0.06	1.40	-0.10	1.30	0.02	1.24	-0.03	1.33	-0.11	1.20	0.67	0.612
DAs III	-0.56	5.32	-0.25	4.08	0.70	4.98	0.28	4.81	0.64	4.70	2.97	0.019
DAs IV	4.94	11.94	3.20	10.02	3.23	9.21	2.28	9.08	4.89	9.85	3.08	0.016
DAs V	0.77	72.07	4.04	59.02	-2.98	65.45	1.82	56.59	-1.42	45.87	0.48	0.747
DAs VI	-0.07	1.70	0.08	1.60	-0.09	1.65	0.11	1.50	-0.03	1.29	0.80	0.527
DAs VII	-1.30	7.77	-1.20	6.26	-0.55	6.50	-1.22	7.21	0.18	5.49	1.89	0.110
DAs X	1.19	4.01	0.69	3.59	0.25	3.12	-0.02	2.88	0.62	3.27	4.36	0.002
DAs XI	0.77	4.11	0.58	3.54	0.50	3.71	0.27	3.30	0.86	3.34	0.98	0.418
DAs XII	0.27	4.31	0.42	3.63	0.04	3.32	0.00	3.58	0.47	3.53	0.81	0.519
DAs XIII	0.45	4.27	0.09	4.06	1.26	4.24	0.67	4.19	0.96	3.60	2.86	0.023
DAs XIV	1.95	4.39	1.23	4.46	1.18	4.18	1.34	3.89	1.97	4.37	1.87	0.113
FlAs I	3.83	2.93	3.61	2.96	3.53	3.13	3.43	2.73	2.93	2.37	2.78	0.026
FlAs II	0.99	0.99	0.92	0.91	0.88	0.87	0.99	0.90	0.93	0.75	0.65	0.629
FlAs III	3.79	3.73	3.20	2.52	3.96	3.01	3.85	2.88	3.71	2.88	2.28	0.058
FlAs IV	8.45	8.41	7.43	6.70	7.05	5.90	6.94	5.84	7.55	6.30	1.80	0.127
FlAs V	48.37	53.32	41.41	41.97	43.25	49.04	38.86	41.07	32.28	32.51	3.69	0.005

Table 5 (continued).

	Brahmin		Mahisya		Padmaraj		Muslim		Lodha			
FIAs VI	1.32	1.07	1.25	1.00	1.26	1.06	1.17	0.94	1.01	0.80	3.08	0.015
FIAs VII	4.99	5.95	4.00	4.80	4.37	4.81	4.34	5.75	3.66	4.09	1.93	0.103
FIAs X	2.99	2.66	2.78	2.28	2.41	1.97	2.29	1.74	2.51	2.08	4.06	0.003
FIAs XI	3.10	2.69	2.64	2.35	2.77	2.46	2.52	2.13	2.50	2.20	2.33	0.054
FIAs XII	3.07	3.01	2.73	2.38	2.39	2.29	2.56	2.50	2.64	2.33	2.25	0.062
FIAs XIII	3.20	2.82	3.02	2.71	3.13	2.85	2.99	2.92	2.72	2.34	0.91	0.457
FIAs XIV	3.29	2.89	3.39	2.89	3.25	2.62	2.93	2.55	3.34	2.82	1.10	0.357
FIAs XVI	8.74	4.07	8.06	3.49	7.81	3.45	7.43	3.45	7.88	3.17	4.22	0.002

Scheffe's test was used for multiple comparisons between all groups. In this analysis procedure, group means are sorted in an ascending order, and then a matrix indicates significant difference between group means (pairwise mean comparisons) is established.

The above statistical analyses were performed with BMDP statistical software (Dixon 1983). Data were processed both at the Tel Aviv University Computer Center, Israel, and at the Indian Statistical Institute, Calcutta, India.

Results

Analysis of variance

The results of the univariate ANOVA are presented in Tables 2 to 4 for the two different sets of dermatoglyphic variables, namely, the 22 quantitative dermatoglyphic traits and the 36 indices of diversity and asymmetry, in males and females separately.

22 quantitative traits (Tables 2–3). The F-values suggest that 4 variables (fingers I, II, III and V) for the right hand out of 5 finger ridge counts in males and 3 variables (fingers I, III and V) in females show significant population heterogeneity ($P < 0.05$). Correspondingly, for the left hand in males there are 3 (I, IV and V) and in females there are 4 (I, II, IV and V) significant variables. Pattern intensity index (PII) for right, left and both hands; a-b ridge counts; main line endings of A for right and left – all show significant heterogeneity in both sexes. Significant heterogeneity is also evident for endings of main line D but in males only on the right whereas in females they are on both sides. Main line index (MLI), and total finger ridge counts (TRC) show significant heterogeneity in females. It appears that males show marginally higher heterogeneity in populations (4*) for the right finger ridge counts than females (3*) and females for the left (4*). However, both sexes are equally heterogeneous when considering 10 finger ridge count variables (7* out of 10). Both sexes are also comparable in showing significant heterogeneity in the case of PII, a-b ridge counts, A-line endings and D-line endings (except on left in males). In the overall picture, females show higher population heterogeneity (18*) than do males (15*).

36 dermatoglyphic traits of diversity and asymmetry (Tables 4–5). Some sex-differences may be observed in population heterogeneity with respect to diversity indices of finger ridge counts. Thus, males are significantly different between castes for only one index out of 11, namely, finger ridge counts of both hands (Div III), whereas in females there are 4 such indices: finger ridge counts of both hands, S^2 of both hands, IIDL and $S\sqrt{10}$ (Div III, VI, VII and IX). Div III is common in both sexes for caste comparison. Males and females contribute almost equally (3* and 4*, respectively, out of 12) to significant population heterogeneity in regard to directional asymmetry (DAs) and somewhat less so in regard to fluctuating asymmetry (FlAs). For DAs, the common indices between sexes are a-b ridge counts (DAs III). Total finger ridge counts (DAs IV), IIIrd finger ridge counts (DAs XII), are found significant in males and the Vth finger ridge counts (DAs X), IInd finger ridge counts (DAs XIII) in females.

Some interpopulation heterogeneity is observable between sexes insofar as the 13

Table 6. Summary of significant population pairs in Scheffe's test of 22 quantitative traits and 36 indices of asymmetry in males and females.

Variables	Population pairs*	Variables	Population pairs
Male			
1R (fRC)	1×5, 2×5, 3×5, 4×5	1L (fRC)	1×5, 3×5, 4×5
2R (fRC)	3×5	5R (fRC)	3×5
AB-R (a-b RC)	2×5	AB-L (a-b RC)	1×3, 1×5, 2×5, 1×3,
A-R (MLTA)	1×3, 1×4, 1×5, 2×3,		4×5, 1×4, 2×4, 3×4
	2×4, 2×5	DAs III (a-b RC)	1×4, 1×5
FlAs VI (Div VIII–Div VII)	1×4	FlAs I (Div I–Div II)	1×4
FlAs XII (fRC IIIr–IIIl)	3×5	FlAsX (fRC Vr–Vl)	1×4
Female			
1R (fRC)	3×5, 4×5	3R (fRC)	3×5
5R (fRC)	2×5	1L (fRC)	3×5
5L (fRC)	1×4, 2×5, 4×5	PIIl	1×4, 1×5
PIIr	1×4	PIIb	1×4
AB-R (a-b RC)	2×3, 1×5, 2×5	AL (MLTA)	1×4, 2×4, 4×5
A-R (MLTA)	1×3, 2×3, 1×4, 1×5,	MLI	2×3,
Div VIII (fRC both hands)	1×4	Div VI (S^2)	1×4, 1×5
Div IX ($S\sqrt{10}$)	1×4, 1×5	DAs X (fRC Vr–Vl)	1×4
		FlAs IV (hRC)	1×2, 1×4, 1×5
FlAs (fRC Vr–Vl)	1×4	FlAs XIII (fRC IIr–IIl)	3×5
		FlAs XVI (AI)	1×4

*Abbreviation of populations: 1 = BR, 2 = MA, 3 = PA, 4 = MU, 5 = LO.

indices of FlAs, with 4 out of 6 common indices proving significant namely: FlAs I, V, VI and X. In females FlAs XI, and XVI, are significant to population heterogeneity but these are negligible in males. The overall heterogeneity in the studied 5 populations is higher in females (15*) than in males (8*) when the 36 variables are considered together. Our findings show very clearly that the category of 22 quantitative variables contributes more to significant population heterogeneity than do the 36 indices of diversity and asymmetry in both sexes.

Scheffe's test

The Scheffe's test for inter-population comparison was applied to all the selected dermatoglyphic traits among our 5 populations. However, for the sake of brevity, only the results for significant population pairs are incorporated in Table 6. For each variable the number of population pairs was 10.

22 quantitative traits (Table 6). In males finger ridge counts (LO) differ significantly among 4 populations for the 1st digit on the right and among 3 populations (except MA) on the left. LO also differ from PA on the IInd and Vth digits for the right side. Finger ridge counts on the IInd to Vth digits for the left hand do not show any significant difference between populations. In females, LO differ from PA and MU on the Ist digit, from PA on the IIIrd digit, and from MA on the Vth digit for the

right hand. The left hand shows significant differences only for two digits, namely, between PA – LO on the Ist digit, and between BR – MU, MA – LO, and MU – LO on the Vth digit. The largest contribution to population heterogeneity among the 5 groups is that by LO. Pattern intensity indices (3 indices) contributing to population heterogeneity are found only in females between BR – MU and BR – LO (only for PII-L). Palmar a-b ridge counts are significant in 3 population pairs out of 10, namely MA – PA, BR – LO and MA – LO for the right, and in 7 population pairs for the left hand only in males. Main line endings of A are interesting in that both males and females have an equal number of significant population pairs (R = 6*, in males; R = 6*, in females). Endings of main line D fail to show any significant differences. Main line index (MLI) differs significantly only in females between MA PA.

36 indices of diversity and asymmetry (Table 6). Of these, the 11 indices of diversity are homogeneous in males, none of them showing any significant differences. Females have only 5 significant population pairs for 3 indices: Div III on both hands between BR – MU, Div VI (S^2 on both hands) between BR – MU and BR – LO, and Div IX ($S\sqrt{}/10$) between BR – MU, and between BR – LO. Females are thus more heterogeneous compared to males.

12 indices of DAs (Table 6). Significant differences are found only in a-b ridge counts (DAs III) for BR-MU and BR-LO in males. In females they are on the Vth finger ridge counts (DAs X) for BR-MU. Males and females thus contribute equally to the populations heterogeneity.

13 indices of FlAs (Table 6). Population pair BR-MU was significant in males for 3 indices: FlAsI (Div I – Div II), FlAs VI (Div VIII – Div VII) and FlAs X (finger ridge counts on Vr –Vl). PA-LO pair was likewise significant for FlAs XII (finger ridge counts on III r – III l) in males. In females BR also contributed considerably and were significant in the case of FlAs IV, FlAs X and FlAs XVI. FlAs XIII (finger ridge counts on IIr – IIl) was significant in pair PA-LO. Both sexes have contributed equally to population heterogeneity. Among the 3 categories of indices, namely, Div, DAs and FlAs, population heterogeneity was more pronounced for FlAs (M = 11*, F = 12*) than for Div (M = O, F = 5*) on DAs (M = 7*, F = 7*).

Cluster analysis

The results here are presented as dendrograms for males and females (Fig. 1a, 1b and 2a, 2b). Mainly two clusters were formed with respect to 22 traits in both sexes. One cluster comprised 3 groups (LO, MU, MA) while the other comprised 2 (PA, BR). In males MU, and in females LO showed some deviation from the remaining groups, whereas, in males LO, and in females BR were clearly apart from the other groups in respect to 36 traits. MU and PA and also MA and BR were close to one another in males. In females PA, MU and MA were mutually close but LO belonged to the same cluster, although it was at some time removed from the others.

Discussion

From the F-values in Tables 2–3, it seems that of 22 studied indices, 10 indices of finger ridge counts, pertaining to both sides and sexes contribute similarly to our

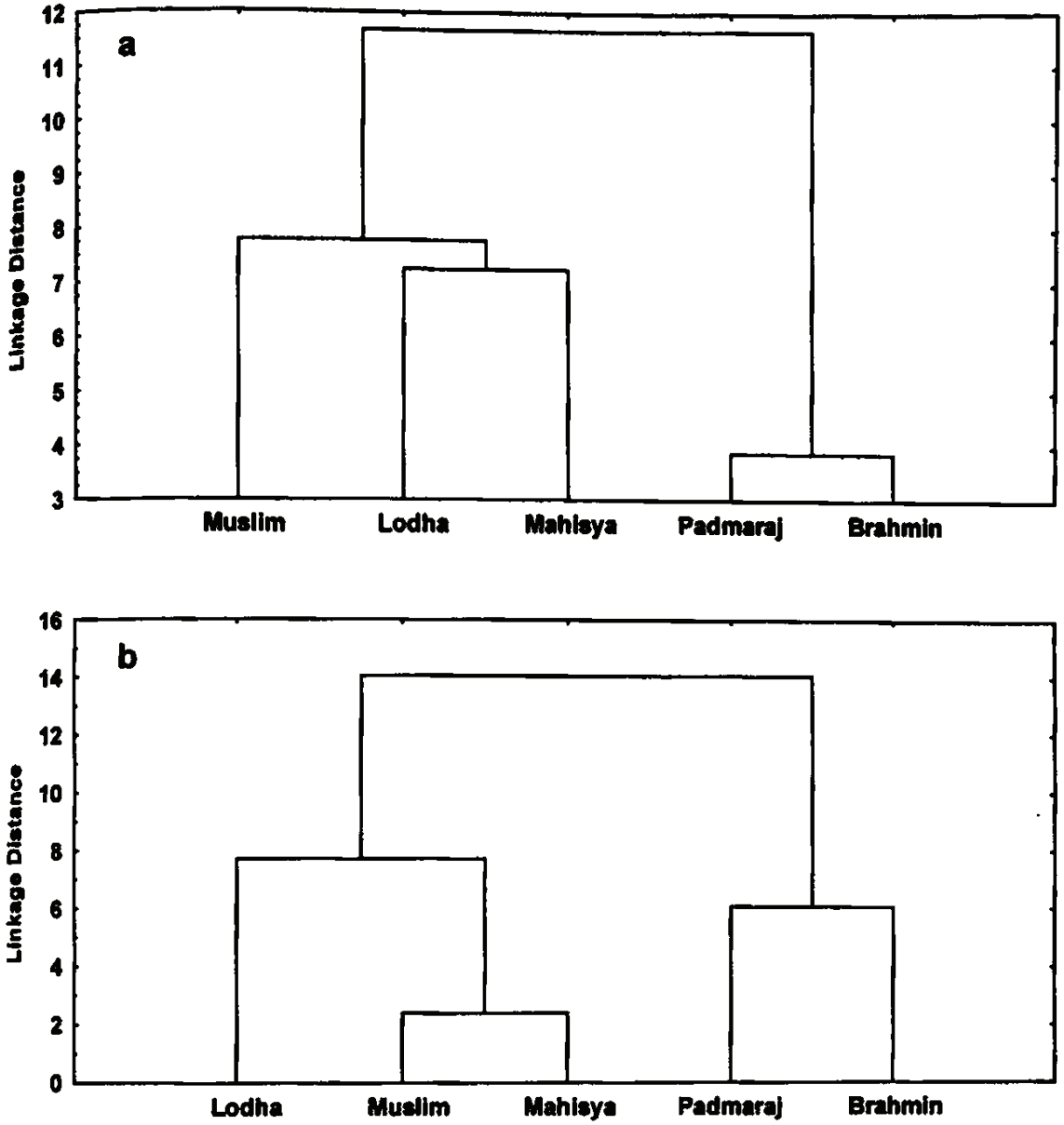

Fig. 1. a) Tree diagram for 5 populations (males, 22 traits). Weighted pair-group average – Euclidean distances. b) Tree diagram for 5 populations (females, 22 traits). Weighted pair-group average – Euclidean distances.

Indian populations heterogeneity. Heterogeneity here is more well pronounced for the Ist and Vth digits in both sexes than for the other digits, which is in agreement with the earlier findings of Micle & Kobyliansky (1991) in Jewish populations. The underlying reason may be different pattern types, which in different digits occur in varying frequencies, with each digit displaying a characteristic frequency for each pattern type (Holt 1961). Significant population heterogeneity is associated with PII, a-b ridge-counts and endings of main lines A and D, and with MLI. It is rather difficult to interpret the overall pattern of variation because different variables vary in different ways, be it sex, sides, or a number of significant traits. The general tendency for greater heterogeneity in the right hand is in concord with the findings of

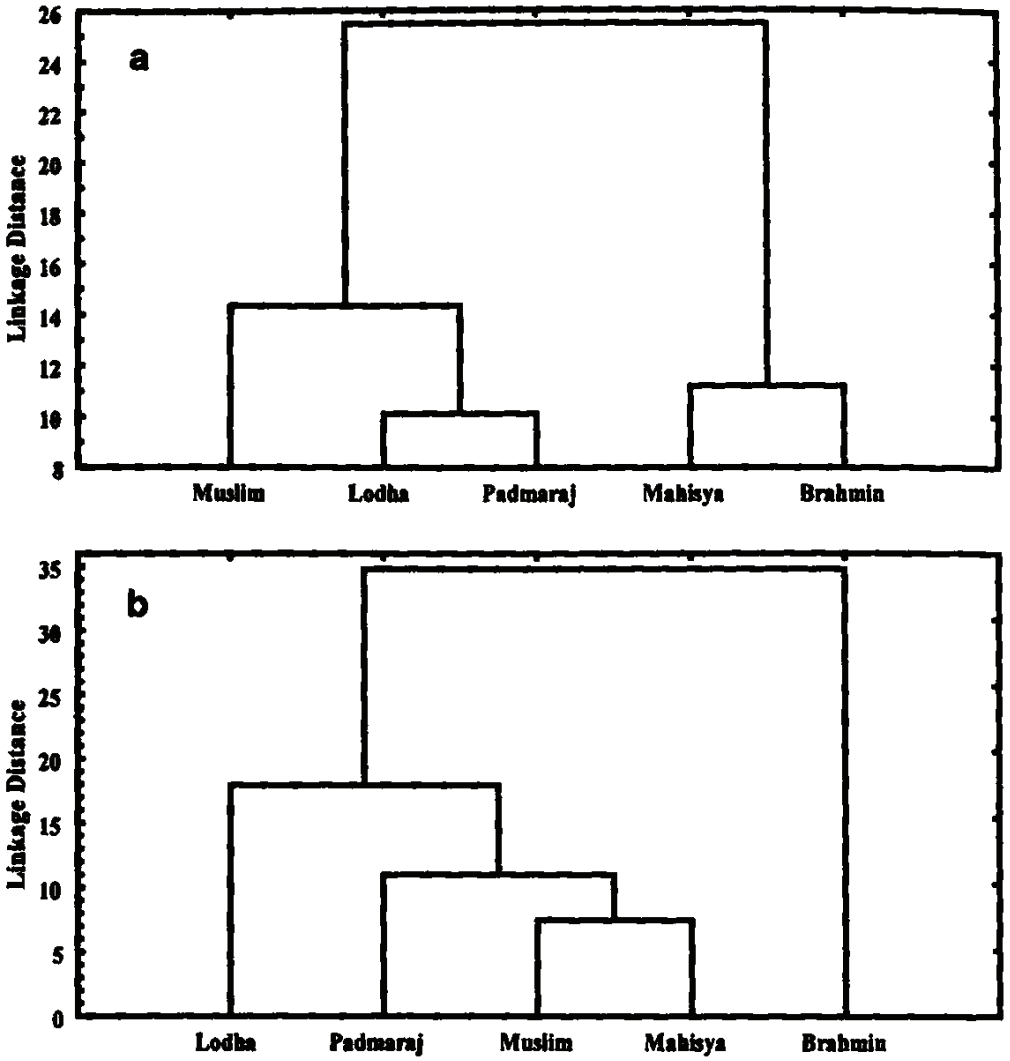

Fig. 2. a) Tree diagram for 5 populations (males, 36 traits). Weighted pair-group average – Euclidean distances. **b)** Tree diagram for 5 populations (females, 36 traits). Weighted pair-group average – Euclidean distances.

Singh (1982). The sex differences in most of the variables rank equally insofar as population heterogeneity which corroborates the findings of Reddy et al. (1985), Mavalwala (1963), and Reddy & Reddy (1992).

In the present study some sex differences were observed in 11 indices of diversity of finger ridge counts for which females were more heterogeneous than males, a finding which is consistent with the earlier findings of Micle & Kobyliansky (1991) in Jewish populations. A strong heterogeneity was detected in 13 indices of FlAs, with higher heterogeneity in females than in males, which conforms with the findings of Reddy et al. (1985), Malhotra (1987), and Micle & Kobyliansky (1991).

Use of the Scheffe's test (Table 6) showed that low heterogeneity exists in the 5 studied populations with regard to the 22 quantitative traits, which suggests that these populations are almost homogeneous in nature. Note that only 25 out of 220 population pairs were significantly heterogeneous.

Of the significant population pair differences (10 pairs for each variable), LO made the largest contribution (28* pairs: M = 16, F = 12) to population heterogeneity. Our Indian population pairs differed significantly from those in other populations, particularly BR for some of the variables in both sexes, which indicates that the differentiation between castes and tribes cannot in fact be denied. Next, after LO, in decreasing order of population heterogeneity were: MU for 21* pairs (M = 10, F = 11); BR for 18* pairs (M = 8, F = 10); and in a tie for fourth place, with 16 pairs each: PA (M = 9, F = 7) and MA (M = 7, F = 9). Male-female differences were also evinced in our study, with females showing greater contributions than males. The intergroup differences were rather small, in that out of a total of 380 population pairs, only 18 pairs in males and 24 pairs in females were significantly different. This observation reaffirms the homogeneity among our 5 populations banning a few exceptions for some of the traits, e.g. MLI, main line endings of A, PII and a-b ridge counts.

Our findings are generally similar to those of Mukherjee & Saha (1970) among endogamous castes and communities from West Bengal. The latter authors found a strong similarity among their groups, as, for example that Hindu caste groups and Muslims are homogeneous with respect to dermatoglyphic traits. They also noted a greater homogeneity among Bengalee caste populations than among ones from other parts of India. Additionally, they suggested, on the basis of the found similarities, that a better picture of populations in West Bengal could be gleaned by pooling several endogamous groups from different parts of West Bengal. Mukherjee et al. (1974) also observed homogeneity between MA and MU with respect to the distribution of the alleles "of some serum group systems".

Gene diversity based on caste ranking among populations of West Bengal was investigated in detail by Chakraborty et al. (1986, 1987), who observed a rather confused picture of genetic differences between the studied populations. Some low-caste groups were found by them to have stronger genetic affiliation with high-ranking groups, instead of being closer to groups of their own rank. Not surprisingly, therefore, they failed to congruity between the genetic profile of any given population and its current social rank. They concluded that the present caste hierarchy might not truly reflect the genetic origin of the populations. In the present study, likewise, trends were well evident in the clustering patterns among our 5 populations, and also in the dendrograms presented in Figs. 1a-1b and 2a-2b, pertaining to dermatoglyphic variables.

Our male and female samples also broadly reflect the same pattern of population configurations in that low ranked scheduled caste PA and MA are close to high-ranked caste BR; MU and MA groups are in the same cluster; LO close to MA, and so on. The observed clustering patterns based on dermatoglyphic traits are in congruity with the known ethno-historic background of our subjects and fully support earlier conclusions regarding other studied groups to wit: (i) low-caste groups are close to the high-caste groups, because of their ethno-historic ties with the latter (Dutta 1969); (ii) some of the tribal and lower-caste populations may have accumulated genes from the high-caste groups through past generations of gene flow (Chakraborty et al. 1986); (iii) considerable variation exists in the admixture of Bengali populations and such admixture is neither restricted to a specific social class nor is it uniform over endogamous groups of all social ranks. Rather such variation demon-

strates that the traditional grouping of Indian populations, as based on caste hierarchy, may not genuinely reflect the genetic origin of the populations (Chakraborty et al. 1986, 1987).

Our endogamous groups may have their identity as a population, but in the clustering patterns and dendrograms the caste identity is not pronounced. The mutual proximity of our 5 populations could be related to their ethnohistorical commonness, in which case, our findings would corroborate the findings of Singh (1982) on populations of Uttar Pradesh, those of Kamali et al. (1986, 1994), and Kamali & Mavalwala (1990) on Iranian populations, those of Reddy & Reddy (1992) on Telugu populations of Andhra Pradesh, those of Malhotra et al. (1986) on 19 populations from Western India and those of Karmakar et al. (1989, 1996), Karmakar (1990a, 1990b) on 20 Dhangar castes of Maharashtra.

In the last-mentioned 20 Dhangar castes a comparison was made between dermatoglyphs, genetic markers and anthropometry. The results showed best congruence between dermatoglyphic (particularly palmar) distances and such distances as are based on geographic proximity and revealed by anthropometry. Thus, dermatoglyphs are beneficial polygenic markers that aid in tracing prehistoric affinities of populations, as suggested by Rife (1953) and by Froehlich & Giles (1981). The benefits of dermatoglyphs purportadly stem from their phylogenetically more stable characteristics rather than from any other biological attribute. Moreover, dermatoglyhic traits are more impervious to evolutionary and environmental forces than are genetic markers or body measurements. Indeed the close resemblances between Jewish populations in different countries of the world after 2000 years of diaspora (Sachs & Bat-Miriam 1957, Kobyliansky 1990) are a classical example of the temporal stability of dermatoglyphic traits. Dermatoglyphics, therefore, is a study that may enable the biological reconstruction of human prehistory and is certainly quite useful in tracing the ethnohistorical background of human populations (Reddy & Reddy 1992).

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Appendix 1

List of the utilized traits and indices:

(A) 22 quantitative traits	(B) 36 traits, representing indices of intraindividual diversity and asymmetry			
Finger RC, Ir	Div I	= max – min fRC (lh)	FlAs I	= [Div I – Div II]
Finger RC, IIr	Div II	= max – min fRC (rh)	FlAs II	= PII, [rh – lh]
Finger RC, IIIr	Div III	= max – min fRC (both h)	FlAs III	= a-b, RC, [rh – lh]
Finger RC, IVr	Div IV	= S^2 for lh, (or S^2L)	FlAs IV	= hRC, [rh – lh]
Finger RC, Vr	Div V	= S^2 for rh, (or S^2R)	FlAs V	= [Div V – Div IV]
Finger RC, Il	Div VI	= S^2 (both h)	FlAs VI	= [Div VIII – Div VII]
Finger RC, II1	Div VII	= IIDL (for lh)	FlAs VII	= atd angle, [r – l]
Finger RC, III1	Div VIII	= IIDR (for rh)	FlAs X	= fRC, [Vr – Vl]
Finger RC, IV1	Div IX	= $S\sqrt{10}$, (both h)	FlAs XI	= fRC, [IVr – IVl]
Finger RC, V1	Div X	= $S\sqrt{5}$, (both h)	FlAs XII	= fRC, [IIIr – IIIl]
Total RC (TRC)	Div XI	= Shannon's index	FlAs XIII	= fRC, [IIr – IIl]
AbsRC	DAs I	= Div II – Div I	FlAs XIV	= fRC, [Ir – Il]
PII, lh	DAs II	= PII, rh – lh	FlAs XVI	= AI, asymmetry index
PII, rh	DAs III	= a-b RC, r – l	For technical reasons DAs VIII, IX, XV, and FlAs VIII, IX, XV were excluded from the analysis. Numeration of other traits were left as originally for comparison with our findings in previous relevant publications.	
PII, both h	DAs IV	= hRC, rh – lh		
a-b RC, rh	DAs V	= S^2, rh – lh		
a-b RC, lh	DAs VI	= Div VIII – Div VII		
A-line exit, lh	DAs VII	= atd angle, r – l		
A-line exit, rh	DAs X	= fRC, Vr –Vl		
D-line exit, lh	DAs XI	= fRC, Ivr – IVl		
D-line exit, rh	DAs XII	= fRC, IIIr – IIIl		
MLI	DAs XIII	= fRC, IIr – IIl		
	DAs XIV	= fRC, Ir – Il		

Abbreviations: RC = ridge count; r = right; l = left; h = hand; PII – Pattern Intensity Index; MLI = main line index; Div I to Div XI = indices of intraindividual diversity of finger ridge counts; DAs I to DAs XIV = indices of directional asymmetry; FlAs I to FlAs XVI = indices of fluctuating asymmetry.

Appendix 2

Formulae for some indices of dermatoglyphic diversity and asymmetry

Computation of the directional asymmetry (DA) was effected by the following equation:

$$DAij = X_{iR} - X_{iL}$$

Computation of the fluctuating asymmetry (FlA) was done by using the absolute differences between the bilateral measurements. In order to avoid additional influences of the directional asymmetry, the values of the non-absolute differences for each individual were corrected (Livshits et al. 1988) so as to yield the following equation for computing FA:

$$FlA_{ij} = |(X_{iR} - X_{iL}) - 1/n \sum_{i=1}^{n}(X_{iR} - X_{iL})|$$

where X_i = trait (X) of individual (i); R,L = right and left, n = size of the sample and FlA_{ij} is the value of FlA of trait (j) in the i-th individual.

Div I, Div II, Div III. Maximal minus minimal finger ridge counts in the five left (Div I), five right (Div II), or in all the ten finger ridge counts (Div III). Div IV, Div V = $\sum_{i=1}^{5} q_i^2 - Q^2/5$, for the left (Div IV, S^2L), or right fingers (Div V, S^2R); Div VI, $S^2 = \sum_{i=1}^{n} q_i^2 - Q^2/10$; Div VII, Div VIII = $\sqrt{\sum_{i=1}^{5} q_i^2 - Q^2/5}$, for the left (Div VII, IIDL), or right finger (Div VIII, IIDR); Div IX, $S\sqrt{10} = \sqrt{\sum_{i=1}^{10} q_i^2 - Q^2/10)/10}$; Div X, $S\sqrt{5} = \sqrt{\sum_{i=1}^{5} k_i^2 - Q^2/5)/5}$;

In these formulae, q_i is the ridge count for the i^{th} finger, Q is the sum of the five finger ridge counts of a hand (Div IV,V,VII,VIII) or of all the ten fingers (Div VI,IX,X), and k is the sum of ridge counts of the i^{th} pairs of homologous right and left fingers.

Div.XI. Shannon's index, $D = -\sum_{i=1}^{4} P_i \log P_i$ where P_i is the frequency of each of the four basic finger pattern types on the ten fingers; FlAs XVI, $AI = \sqrt{\sum_{i=1}^{5}(R_i - L_i)^2}$, where R_i and L_i are the ridge counts for the i^{th} finger of the right and left hand.

Appendix 3

The people and their history

Brahmins (Rarhi): In Indian caste hierarchy the Brahmins stand at the top of society. In the *Rigveda* the function and occupation in life assigned to Brahmins are priesthood, knowledge, and the teaching of things divine; simple living is the rule and they are divided into five main sub-castes: Rarhi, Barendra, Vaidiki, Saptasati and Madhyasreni. That said, there are some accounts in the Pauranic literature suggesting that several families of Rarhi Brahmin Gotra may actually be the progeny of an intermixing of Brahmin and non Brahmin (e.g. Bagdi and Kaibarta) ancestors (Dutta 1969). The likelihood of such gene admixtures is affirmed by Chakraborty et al. (1986) and Mukherjee et al. (1987), as based on serological and biochemical markers. Rarhi Brahmins do not practice consanguineous marriage and at present intersubcaste marriages are not prohibited among them, nor are intercaste marriages uncommon. Rarhi Brahmins are predominant in West Bengal and their mother tongue is Bengali. Our Rarhi Brahmin group was sampled from the Howrah District of West Bengal.

Mahisya: The Mahisya is a Bengali-speaking endogamous caste group belonging to the middle caste status (Jal Chal) according to Hindu caste hierarchy in India. The Mahisya is a large Hindu caste, indigenous to the deltaic districts of West Bengal (Risley 1891, District Gazetteers 1909). In some places the Mahisyas are known as Halia Kaivartas or Chasi Kaivartas – an appellation deriving from the Kaivarta caste group whose main occupation is agriculture and is thus distinguished from the Jalia Kaivartas (fishermen). At some point, the Halia Kaivartas separated entirely, banning all intermarriages with Jalia Kaivartas, and ultimately succeeded in obtaining recognition as a distinct caste under the name of Mahisya. According to ancient sources, such as Vajna-valkya' and 'Gautama', the Mahisyas descended from a Ksatriya father and Vaisya mother. The population was sampled by us from the Howrah District of West Bengal.

Padmaraj: Padmaraj (Pod) comprises a scheduled caste (non-Jalchal) whose origin is uncertain. Its members may be descendants of a Vaisya father and Napit mother, if to judge by ancient lore. The social status of pod is very low. They are a fishing, cultivating group who have also taken jobs as carpenters, thatchers, etc. This population was sampled from the Howrah district of West Bengal. Both the afore-mentioned groups belong to Jati Sudra, the low and servile caste in the quadruple grouping of Hindu caste system. This population was sampled by us from the Howrah District of West Bengal.

Muslim (Sunni): Muslim belongs to religious communities. The early phase in the historical development of the Muslim society of Islam involved only the Arabs, but in the later phase, the Arabs came in contact with Iranians, Africans, Tibetans, Chinese, etc. In West Bengal, however, the diversity of Indian Muslims suggests their derivation from various segments of the populace, including higher castes of the Hindu community, but particularly several lower-caste groups that had converted to Islam (Siddiqui 1979). Languages or dialects of the local Muslims conform invariably to the regional pattern, so that Bengali-speaking Muslims predominate over the Urdu-speaking ones. There are two sectarian groups among Muslims in West Bengal, namely, Shia and Sunni, and each group is endogamous. The Sunni group was selected for the present study because it is one of the largest sect in West Bengal, where its members engage in various activities such as architectural work, trade, tailoring, bookbinding, agriculture, etc. This population was sampled from the Howrah District of West Bengal.

Lodha: The Lodhas are a small tribal group mostly found in jungle tracts in the western part of the Midnapore district but a few also in the Hoogly district. Risley (1908) described them as allied to the *Savara* or the *Savar* tribe of Mayurbhanja of the Orissa district. The Lodhas, too, prefer to declare themselves as "Savar", (which is mentioned as Savari in the legend of *Ramayana*), but an Oriya affiliation is also encountered in their language. They speak a corrupt form of Bengali with some Oriya influence. The name Lodha was derived from the Sanskrit word "*Lubdhak*", meaning the people who are experts in making traps to capture birds. Both males and females participate in different economic activities, but mainly cultivation and farming. Yet, even today, the Lodhas still ply their traditional pursuit collecting of jungle produce like firewood, as well as, honey, edible roots, fruits, tubers, birds, snakes, fishes, etc. Fishing is an important occupation of the Lodha (Bhowmick 1963). They have bows and arrows and a variety of traps and snares for catching birds, hares, snakes, etc. Lodhas regard themselves as Hindus of low rank, divided on the basis of totems into nine endogamous clans that do not allow consanguineous marriage. This population was sampled from the Midnapore District of West Bengal.