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Quantitative Dermatoglyphics and Population Structure in Northwest India

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ABSTRACT The nature and extent of dermatoglyphic variation in northwest India is examined with the help of 28 quantitative variables—20 finger ridge counts and 8 palmar pattern ridge counts—among 12 endogamous populations. These populations represent the entire spectrum of ethnic and socioeconomic variation of the region and are presently distributed in three different states—Rajasthan, Punjab, and Himachal Pradesh. Of a total sample of 1,160 adult males, about 100 from each group were considered. Multiple discriminant analysis and R-matrix analysis were used to derive population relationships and patterns of external gene flow, respectively. Published data on genetic markers were reanalyzed to make the comparative evaluation of the patterns with reference to dermatoglyphs. Both the discriminant analysis and the F_{ST} from R-matrix analysis suggest highly significant discrimination among the northwestern groups, whether one uses only 20 finger ridge count variables or all 28 variables, including the 8 palmar pattern ridge counts. The 8 palmar variables add very little to the variation explained by the 20 finger ridge count variables. F_{ST} values suggest that the populations of Punjab are most homogeneous and those of Himachal Pradesh most heterogeneous. However, the levels of differentiation are similar for dermatoglyphs and genetic markers. The pattern of external gene flow as inferred through R-matrix analysis is consistent with the breeding and population structure of the groups, although genetic markers portray a relatively more realistic picture. Overall, the patterns of variation observed in dermatoglyphs and genetic markers are consistent with different dimensions of population structure; whereas dermatoglyphs conform more to the geographic pattern and less to ethnic resemblance, the reverse is true in the case of genetic markers. Am. J. Hum. Biol. 12:315–326, 2000.

The northwestern region of India is characterized by populations with great diversity in ethnic composition, linguistic background, and geographical affiliation. The Himalayan valleys have acted as access routes for many waves of migrants and for ages have promoted intermingling of many ethnic groups in this region. Its southern peripheral region consists of original autochthonous elements like Dravidians and Proto-Australoids, while the northern parts are inhabited by Indo-Aryans. This ethnic heterogeneity is reflected in the presence of a large number of languages and dialects in the region. However, it has been opined that intermixing in certain states is so much that it is difficult to differentiate populations on

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ethnic grounds (Papiha et al., 1982). The present-day population of northwest India is, therefore, an amalgamation of many streams of ethnic movements and its social structure consists of many hierarchical subpopulations. The overall scenario in northwest India hence poses many interesting problems from the perspective of microevolutionary studies.

As part of a large Indo-Soviet project, three northeastern states of India (Fig. 1)—Rajasthan, Punjab, and Himachal Pradesh—were investigated, among others, for anthropometry, dermatoglyphs, and genetic markers to explore patterns of variation in relation to the population structure. The results of the genetic investigations based on 12 loci—8 blood groups and 4 red cell enzymes—were reported earlier (Papiha et al., 1982). The following salient features emerged:

1) The genetic differentiation as reflected through the F_{ST} values is slightly higher in Rajasthan (0.009), compared to Punjab (0.006) and Himachal Pradesh (0.007). The total F_{ST} for the whole region and for all the populations together was found to be 0.013.
2) Overall, the pattern of clustering indicated that within a geographical area it is the internal structure that regulates genetic differentiation. At the less local level, geographic distance and major ethnic affiliation exert a primary influence.
3) Differences that exist in the genetic constitution of tribal and caste groups of northwest India are particularly apparent from the genetic distance studies; while the tribals and lower castes cluster together, high caste Brahmins and nontribal middle castes form a compact cluster.

In this article, we explore the nature of quantitative dermatoglyphic variation in the populations of northwest India and make a comparative evaluation of the patterns with those based on genetic markers. An attempt is also made to infer the relative extent of gene flow into these populations, using R-matrix analysis of both the quantitative dermatoglyphic variables and the genetic markers at the state and regional levels.

MATERIALS AND METHODS

Finger and palm prints of a total of 1,160 adult males were collected during January–March 1979, using the ink and roller method (Cummins and Midlo, 1961). These prints were scored for a number of qualitative and quantitative finger and palmar dermatoglyphic variables. Only the quantitative variables, 20 finger ridge counts and 8 of 10 palmar pattern ridge counts, were used in this study. Due to the extremely low frequency of patterns in the thenar/I interdigital area, the ridge counts in most cases were zero and are not included. While the 20 finger ridge counts were determined following Cummins and Midlo (1961) and Holt (1968), the palmar pattern ridge counts were determined following Malhotra et al. (1982).

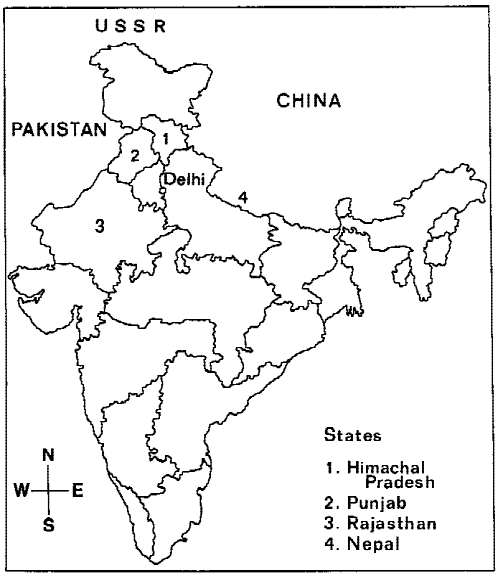

Fig. 1. Map of India showing the sampling locations in northwest India and Nepal.

Both univariate and multivariate analysis of variance (ANOVA) and multiple discriminant analysis were employed in order to study the nature and patterns of dermatoglyphic variation. The patterns were compared with those based on the genetic marker data of these 12 populations (Papiha et al., 1982). For the purpose of studying the patterns of gene flow into the populations of northwestern India, as well as those of different states, the R-matrix analysis was further employed for genetic marker data (Harpending and Ward, 1982) and for different sets of quantitative derma-

TABLE 1. Sample sizes and socioeconomic, ethnic, and geographical backgrounds of the 12 northwestern Indian populations of the present study

Population and geographic background	Socioeconomic status	Sample size	Racial affiliation[a]
Rajasthan, Udaipur District			
Paliwal Brahmins (PB)	Upper caste	98	Caucasoid
Rajaput (RR)	Kshatriya	99	Caucasoid
Oswal Mahajan (OM)	Vyshya/traders	97	Caucasoid
Bhils (BT)	Schedule Tribe	97	Proto-Australoid
Meghwal (MR)	Lower caste	90	Mixed
Punjab State, Patiala			
Jat Sikh (JS)	Kshatriya	97	Caucasoid
Ramdasia Sikh (RS)	Lower Caste	98	Mixed
Mahajan Agarwal (MA)	Vyshya/traders	100	Caucasoid
Himachal Pradesh, Kangra District			
Brahmins (BH)	Upper caste	95	Caucasoid
Chowdhury (CW)	Middle caste	96	Caucasoid
Gaddi Rajput (GR)	Kshatriya tribe	99	Caucasoid + Mongoloid
Nepalis (NH)	Immigrants	94	Mongoloid

[a]Based on physical features.

TABLE 2. Results of the univariate ANOVA for the dermatoglyphic variables among the 12 populations of northwestern India

	Finger ridge counts								
	Radial		Ulnar		Larger		Palmar pattern ridge counts		
	F	*P*	F	*P*	F	*P*	Variable	F	*P*
R1	2.1	0.021	17.4	0.000	4.0	0.000	Hyp. R	2.2	0.012
R2	2.7	0.002	3.0	0.001	5.1	0.000	IIR	2.2	0.012
R3	0.9	0.517	7.1	0.000	5.3	0.000	IIIR	4.7	0.000
R4	1.6	0.100	23.7	0.000	5.4	0.000	IV R	2.3	0.009
R5	2.5	0.005	15.2	0.000	5.9	0.000	Hyp. L	2.2	0.012
L1	0.8	0.667	11.7	0.000	5.0	0.000	IIL	1.5	0.136
L2	2.9	0.001	4.1	0.000	5.6	0.000	IIIL	2.8	0.001
L3	2.0	0.025	8.0	0.000	5.7	0.000	IV L	1.7	0.077
L4	2.0	0.026	24.2	0.000	8.7	0.000			
L5	1.6	0.101	16.2	0.000	9.7	0.000			

D.F.: 11,1070.

toglyphic data (Relethford and Blangero, 1990). The R-matrix analyses of the genetic marker data were done using the POPSTR program in the ANTANA package developed by Harpending and Rogers, whereas the RMET program of Relethford was used in the case of quantitative dermatoglyphics.

Sampled populations, socioeconomic and geographic backgrounds

The name of the populations, their socioeconomic/ethnic affiliation, and geographical backgrounds are provided in Table 1. Altogether, 12 populations were sampled for the purpose of this dermatoglyphic study. These samples were drawn from three different states (Fig. 1), five from Rajasthan, three from Punjab, and four from Himachal Pradesh. Of the four sampled from Himachal Pradesh, Nepalis were migrant settlers, originally from different parts of Nepal. These populations represent the broad spectrum of ethnic and socioeconomic variation of the region under study, as it includes upper caste Brahmins, Kshatriyas, Vyshyas/traders, agricultural middle castes, lower castes, and tribes who represent among them the Mongoloid, Caucasoid, and Australoid racial elements, as depicted through physical features.

RESULTS

Univariate analysis

For the sake of brevity, we are not presenting variable-wise descriptive statistics for the 12 groups; the results can be supplied upon request. Results of the univariate ANOVA are presented in Table 2 for the three different sets of quantitative dermatoglyphic variables. The F-values suggest

TABLE 3. Multivariate test statistic Wilks' λ and associated F-value for the extent of differentiation based on different sets of quantitative dermatoglyphic variables

Variable set	Wilks' λ	F-value	D.F.	*P*
10 finger ridge counts (larger)	0.8025	2.27	110,8365	0.000
20 finger ridge counts	0.4947	3.68	220,10738	0.000
28 variables (finger + palm)	0.4139	3.06	308,10504	0.000

TABLE 4. Eigenvalues and the proportion of variation explained by the significant canonical variates in the multiple discriminant analysis

Variable set	Canonical variate	Eigenvalue	Proportion of variation	Cumulative variation
10 finger ridge	1	0.1165	0.5114	
counts	2	0.0418	0.1837	0.6951
20 finger ridge	1	0.6476	0.7571	
counts	2	0.0536	0.0626	0.8197
28 variables (finger +	1	0.6798	0.6457	
palmar ridge counts)	2	0.0820	0.0779	0.7236
	3	0.0741	0.0704	0.7940

that 6 of the 8 palmar pattern ridge counts and 16 of the 20 finger ridge counts show significant population heterogeneity ($P < 0.05$). When larger finger ridge counts on the 10 fingers are considered, all showed highly significant ($P < 0.001$) population heterogeneity. The palmar pattern ridge counts in the II and IV interdigital areas of the left hand, and the radial ridge counts on 3rd and 4th fingers of the right hand and 1st and 5th fingers of the left hand, did not show significant ($P < 0.05$) differences among the populations.

Multivariate analysis

Multiple discriminant analysis. Results of the multiple discriminant analysis of the different sets of dermatoglyphic data are presented in Tables 3 and 4. The Wilks' λ and associated F-values (Table 3) suggest that the discrimination among the northwestern groups is highly significant ($P = 0.000$) whether all 28 variables (finger and palm) or only 20 finger ridge counts, including ulnar and radial counts, or only the 10 larger counts are considered. However, the Wilks' λ is smallest (0.414), suggesting highest discrimination in the case of the 28 variables, and is only half the value of Wilks' λ obtained using the 10 larger finger ridge counts (0.803). In the case of the 20 finger ridge counts, the Wilks' λ is only marginally higher (0.495) than that obtained using all 28 finger and palmar variables. This suggests that the addition of 8 palmar variables does not increase the power of discrimination. The eigenvalues and the percentage of variance explained (Table 4) by the two canonical variates is highest when 20 finger ridge counts only are used (82%), excluding the palmar variables. When all 28 variables are used for the analysis, three, instead of two, canonical variates are significant, although the amount of variation explained does not exceed the amount explained by the two variates in the case of the 20 finger ridge counts. It is, however, interesting to note that in the case of the 20 finger ridge counts, while the contrast between the radial and ulnar counts is an important contributor for the dispersion of groups on the first canonical variate, radial counts are important in discriminating populations on the second variate. On the other hand, when all 28 variables, both finger and palmar, are included in the analysis, the contrasts between the radial and ulnar counts are still important on the first variate. However, the palmar pattern ridge counts contribute primarily to discrimination on the second variate. It is on the first variate that the geographical separation is primarily evident, while on the second variate the differentiation of populations within each state is seen.

This inference of different sets of variables on the relative power of discrimination is fortified by the magnitude of F_{ST} values obtained through R-matrix analysis (Relethford and Blangero, 1990) of the quantitative dermatoglyphic variables (Table 5). The F_{ST} value which reflects the magnitude of relative extent of intergroup variation is largest and similar in the case

TABLE 5. Values of Wright's F_{ST} for the intergroup differentiation of the northwestern groups as derived through R-matrix analysis of the different sets of dermatoglyphic variables and the genetic markers

Variable set	F_{ST}[a] ± SE
10 finger ridge counts	0.01118 ± 0.00137
20 finger ridge counts	0.02086 ± 0.00131
8 palmar pattern ridge counts	0.01017 ± 0.00133
28 dermatoglyphic variables (finger + palm)	0.01867 ± 0.00110
Genetic markers	0.01405

[a]The heritability of dermatoglyphs is assumed to be 1, hence the estimates are minimal.

of 20 or 28 variables. The F_{ST} values are much smaller and similar in the case of the 10 larger finger ridge counts, and when the 8 palmar pattern ridge counts are used, the magnitude is only half that of the 20 finger ridge counts.

The plots of group centroids on the two canonical variates (Figs. 2,3,4) suggest that when the 28 variables are used there is a clear clustering of groups (Fig. 2) from different states. Those from Rajasthan are clearly separated from the populations of Punjab and Himachal Pradesh. However, the higher-caste Brahmins from Himachal are closely placed to the Vyshya (traders) group known as Mahajan Agarwal (MA) from Punjab, far removed from the other local groups of Himachal Pradesh that are included in the study. Similarly, the RS which is categorized as belonging to lower caste from Punjab are placed in close affinity to the agricultural caste Chowdhury from the neighboring Himachal Pradesh, rather than to the other groups from the same geographical region. The ethnic resemblance is not very apparent in the way the populations were placed in the multivariate space, although the upper castes—Brahmins from Himachal Pradesh (BH), traders (MA), and the JS from Punjab—are placed closely together and are far removed from the tribal GR and Mongoloid NH from Nepal. In the case of Rajasthan, although the three socially higher groups are separated from each other and somewhat scattered, the tribal group BT and lower caste MR are clustered together, but in close affinity to the Paliwal Brahmins (PB). When the palmar variables are excluded and only 20 finger ridge counts are used (Fig. 3), although Rajasthan groups are clearly separated from the Punjab and Himachal groups, the separation between the groups of Punjab and Himachal Pradesh is relatively less clear. The ethnic affiliations are also less apparent, as in the case of 28 variables. With the 10 larger counts on the fingers, neither the ethnic resemblance nor the geographical affiliations are as clearly depicted (Fig. 4), as in the case of the former two sets of data.

Using the published data of allele frequencies for the 8 common loci (Papiha et al., 1982) for these 12 groups, we computed Nei's standard distance. The principal coordinate analysis of the distance matrix (Fig. 5) suggests grouping of populations more on ethnic criteria and less on geographical backgrounds; the tribes and lower castes from different states are closely clustered on one side, whereas the upper castes together are on the other side. The migrant Nepalis are separated from both clusters. However, two of the high-ranking castes—Rajputs from Rajasthan (RR) and Jat Sikhs (JS) from Punjab—are placed in close proximity to the cluster of tribals and lower castes. Assuming that the lower castes are mostly derived from the tribal stocks, and there is a certain degree of gene flow expected from upper castes into the lower castes, this pattern can be easily explained. However, the geographical backgrounds are not apparent in this principal coordinate plot. This lack of congruence between the two sets of data is reflected in the low value of correlation observed between the interpopulation distances based on dermatoglyphics and genetic markers ($r = 0.13 \pm 0.12$; d.f. 60, $P > 0.10$).

R-matrix analysis: patterns of external gene flow. One of the ways to visualize the extent of isolation of or gene flow into different groups is through the model of Harpending and Ward (1982) for genetic markers and its extension to quantitative traits by Relethford and Blangero (1990). One indicator that is useful in examining the problem of gene flow is the regression of average heterozygosity on the genetic distance from the centroid. As per the model, the average heterozygosity (H_i) or phenotypic (genetic) variance ($V_{Hi}G$) of the i_{th} population should be equal to overall mean heterozygosity of the entire population, H_T (in this case, all study populations) multiplied by $1\text{-}r_{ii}$, where r_{ii} is the genetic distance of a particular population from the gene frequency centroid. If the gene flow from outside the region varies in amount from population to population, this linear relationship no longer holds. Very

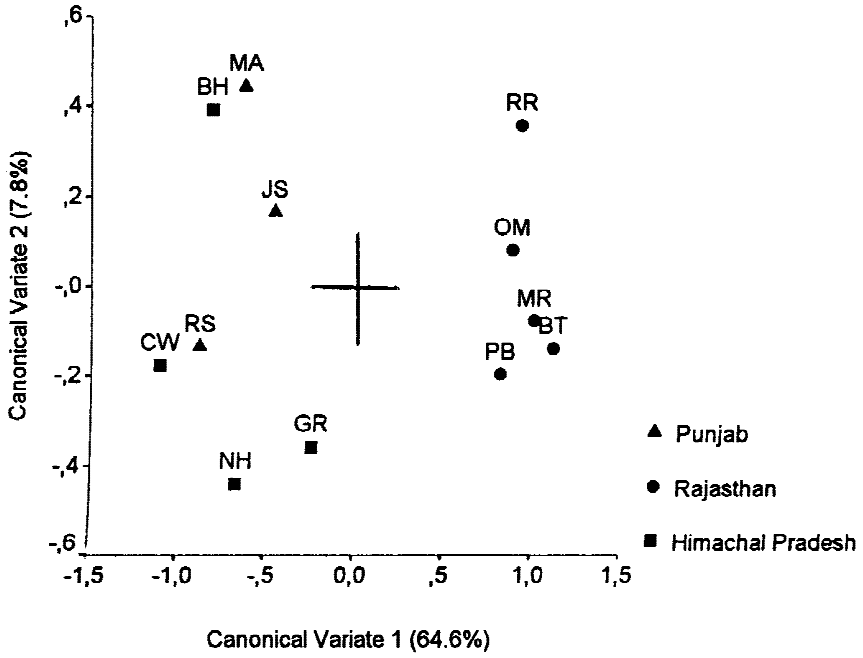

Fig. 2. Plots of group centroids of the 12 northwestern Indian populations, based on multiple discriminant analysis of the 28 dermatoglyphic variables.

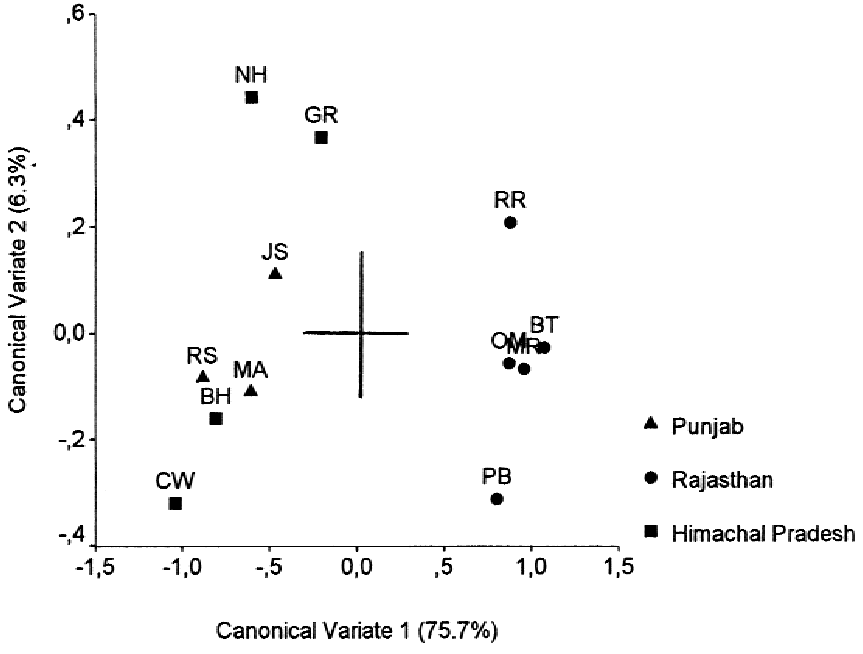

Fig. 3. Plots of group centroids of the 12 populations based on the discriminant analysis of the 20 finger ridge count variables.

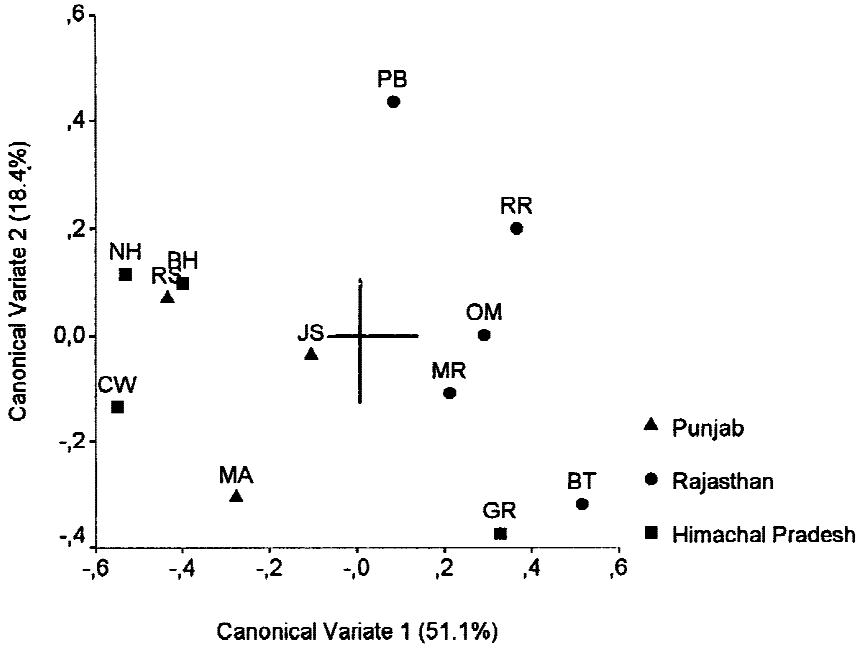

Fig. 4. Plots of group centroids of the 12 populations based the discriminant analysis of the 10 larger finger ridge count variables.

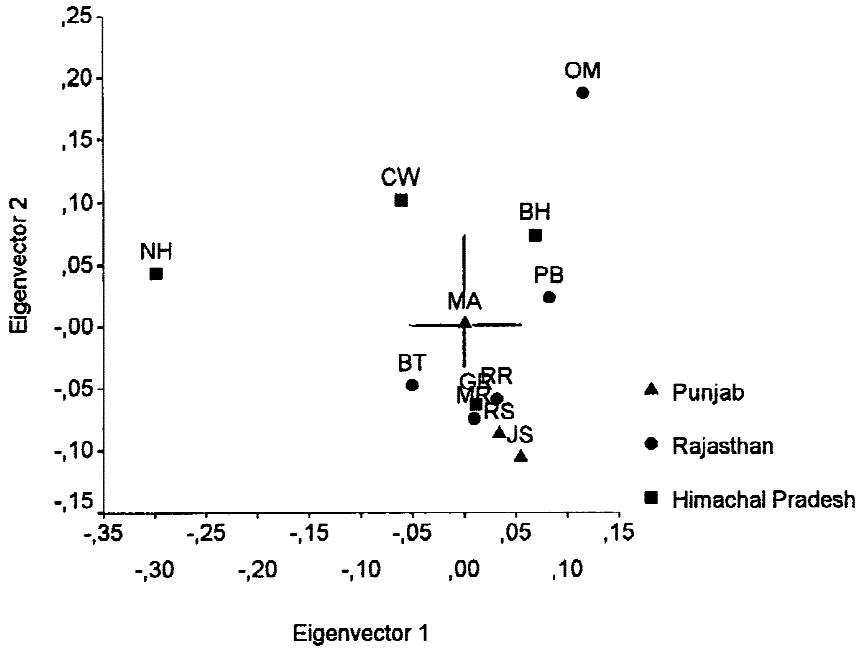

Fig. 5. Principal coordinate plots of the 12 northwestern Indian populations based on the genetic distances.

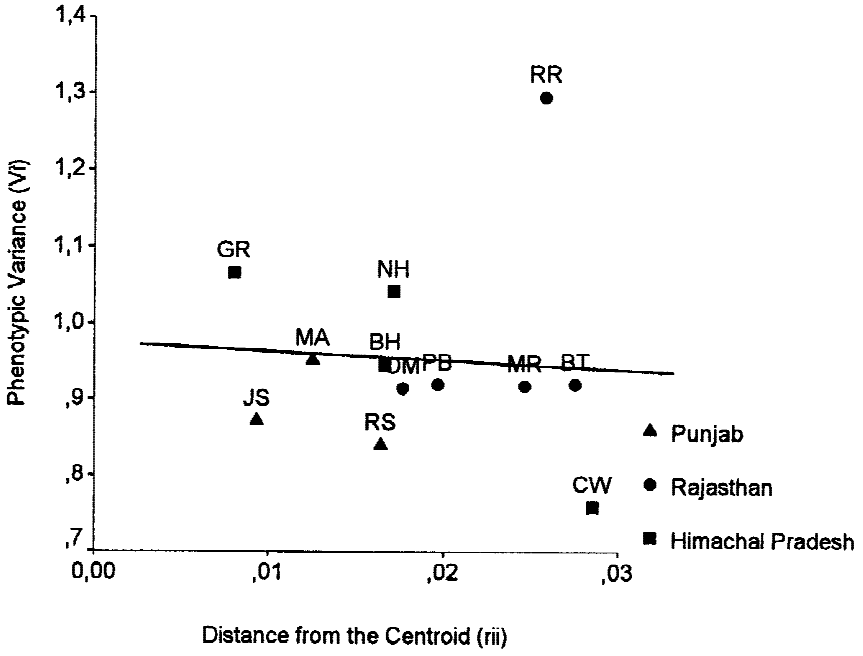

Fig. 6. Plots of mean phenotypic variance versus the dermatoglyphic distance from the centroid of the 12 populations and the theoretical regression line. All 28 variables were used.

isolated populations will be less heterozygous than the linear prediction, while the populations receiving more gene flow from outside will be more heterozygous. The theory thus indicates that we might gain some insight by examining the outliers. In fact, in a recent study (Reddy and Chopra, 1998), this analysis was quite useful in explaining the divergence of migrant fishermen from the parental counterparts through the patterns of external gene flow shown consistently in each of the three types of variables—genetic markers, dermatoglyphs, and anthropometrics.

The results of the application of the above model to the 28 quantitative dermatoglyphic variables are presented in Figures 6–9. When all northwestern groups are considered in the analysis (Fig. 6), it is RR, the warrior caste from Rajasthan, that is an outlier, above the regression line, suggesting much greater gene flow into them from outside. The migrant group NH from neighboring Nepal, who live currently in Himachal Pradesh, along with the tribal group Gaddi Rajput from Himachal, are also above the regression line, suggesting some degree of external gene flow. Below the regression line and indicating the greatest degree of isolation are the Chowdhuries from Himachal Pradesh. The remaining six groups, four from Rajasthan and one each from Punjab and Himachal, fall on the regression line.

Because of the linguistic and geographical barriers between populations of different states, it may be pertinent to consider populations of each state separately for this analysis. The analysis for Rajasthan (Fig. 7) suggests greater external gene flow into Rajputs, and relatively more isolation of the rest of the groups. Similarly, the greater isolation of Chowdhuries of Himachal Pradesh (Fig. 8) is very evident, and the indication of greater external gene flow into NH and GR is also apparent. Although the position of JS and RS from Punjab below the regression line (Fig. 9) is similar to that observed in the pooled analysis of the northwestern groups, the much greater external gene flow into the Mahajan Agarwals (MA) is brought out very clearly by considering each state separately; in fact, the MA is placed on the regression line when all 12 populations are considered.

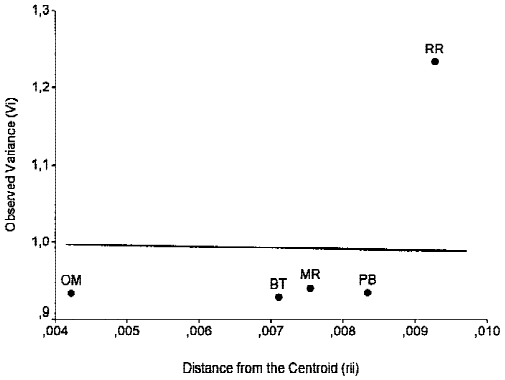

Fig. 7. Plots of mean phenotypic variance versus the dermatoglyphic distance from the centroid of the five populations from Rajasthan and the theoretical regression line.

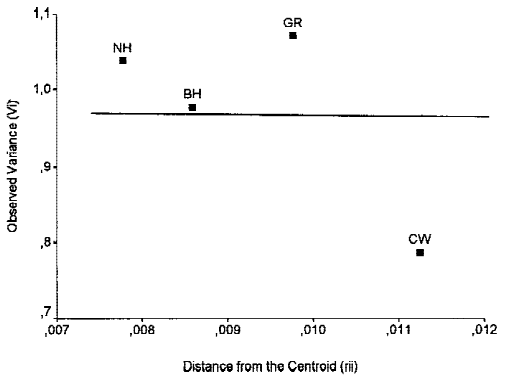

Fig. 8. Plots of mean phenotypic variance versus the dermatoglyphic distance from the centroid of the four populations from Himachal and the theoretical regression line.

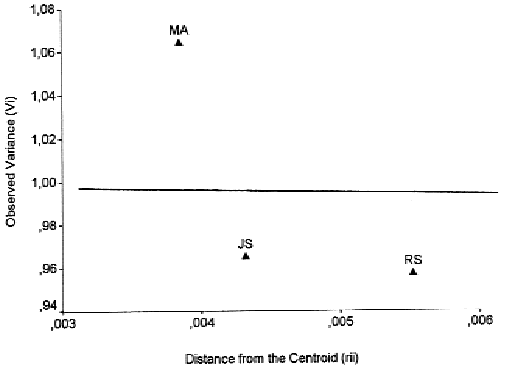

Fig. 9. Plots of mean phenotypic variance versus the dermatoglyphic distance from the centroid of the three groups from Punjab and the theoretical regression line.

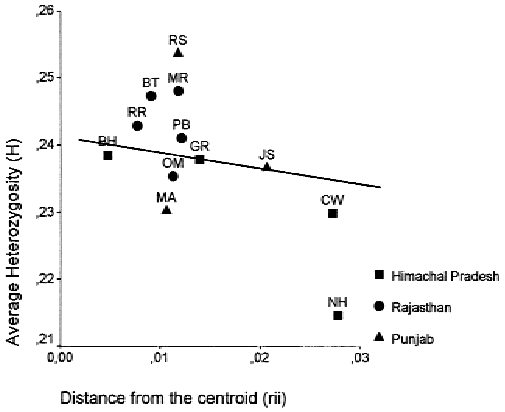

Fig. 10. Plots of observed mean heterozygosity versus genetic distance from the gene frequency centroid of the 12 northwestern groups and the theoretical regression line.

Results of a similar analysis of genetic marker data (Fig. 10) among these populations is not quite similar to that of the dermatoglyphic data. For example, instead of RR, it is Ramdasia Sikhs from Punjab, scheduled caste group called Meghwals, and a tribal group, namely Bhils, from Rajasthan that show a relatively greater degree of external gene flow, and the migrants from Nepal that show the greatest degree of isolation. These patterns are not complementary, but somewhat contradictory between the two sets, dermatoglyphs and genetic markers. When genetic marker data are analyzed separately for each state (Figs, 11–13), the patterns implicit in the combined analysis are more vividly brought out. For example, that there is greater external gene flow into MR and BT and greater isolation of OM from Rajasthan is clearly depicted. Further, relatively greater isolation of JS and MA from Punjab, lying below the regression line, and relatively greater magnitude of external gene flow into the Brahmins and Gaddi Rajputs of Himachal Pradesh are also brought out in the separate analysis.

Relative patterns of heterogeneity in different states. The F_{ST} values obtained through R-matrix analysis of the dermatoglyphs and genetic markers at the state level and for the pooled data are presented in Table 6.

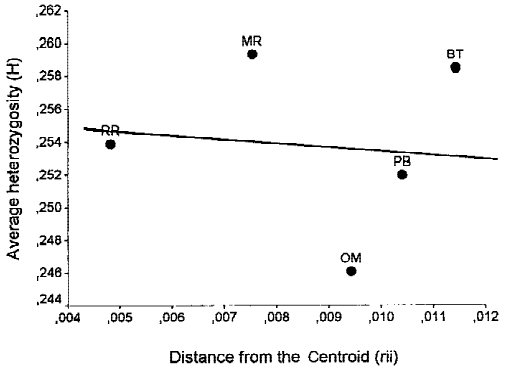

Fig. 11. Plots of observed mean heterozygosity versus the genetic distance from the gene frequency centroid of the five Rajasthan populations and the theoretical regression line.

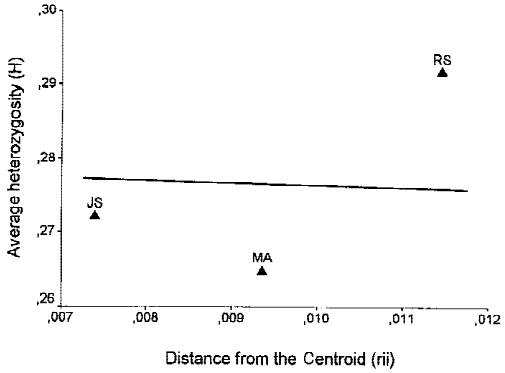

Fig. 12. Plots of observed mean heterozygosity versus the genetic distance from the gene frequency centroid of the three Punjab groups and the theoretical regression line.

For dermatoglyphic variables and genetic markers, the highest F_{ST}, hence the greatest heterogeneity, is observed in the case of Himachal Pradesh. The lowest value, however, is found for Punjab in the case of dermatoglyphs, while it is almost equal in magnitude for Rajasthan and Punjab in the case of genetic markers. Although the intergroup heterogeneity is relatively larger in the case of genetic markers, especially for Punjab and Himachal, for the whole region the intergroup heterogeneity is marginally greater in dermatoglyphs.

DISCUSSION

Quantitative dermatoglyphic variables suggest highly significant variation among the 12 northwestern Indian groups, broadly

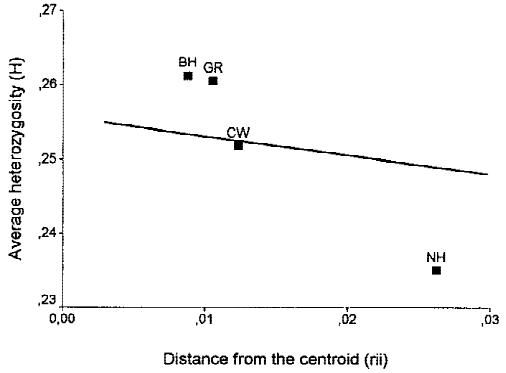

Fig. 13. Plots of observed mean heterozygosity versus the genetic distance from the gene frequency centroid of the four Himachal populations and the theoretical regression line.

TABLE 6. F_{ST} values for different state populations based on the 28 quantitative dermatoglyphic variables and the genetic markers

State	Quantitative dermatoglyphs F_{ST}[a] ± SE	Genetic markers
Rajasthan	0.00730 ± 0.00108	0.00872
Punjab	0.00456 ± 0.00109	0.00940
Himachal	0.00935 ± 0.00138	0.01448
Pradesh	(0.00945 ± 0.00161)[b]	(0.00735)[b]
Northwest India	0.01867 ± 0.00110	0.01405

[a]The heritability of dermatoglyphs is assumed to be 1, hence the estimates are minimal.
[b]Values in parentheses are obtained by excluding Nepali migrants from the computation.

representing the socioeconomic and ethnic heterogeneity of the region. This is true with each of the three sets of dermatoglyphic variables, although the geographical affiliations and/or ethnic backgrounds are most clearly portrayed when all 28 variables are used. This is implicit in the magnitude of Wilks' λ, being the smallest for this set of 28 variables. The F_{ST} value, which is a measure of intergroup differentiation, obtained through R-matrix analysis reiterates this inference; this value is largest and almost equal in the case of the largest two sets of variables, 20 finger ridge counts and the 28 including the 8 palmar pattern ridge counts; it is just half that magnitude in case of the 10 larger finger ridge counts or with the 8 palmar pattern counts. It is noteworthy that the distance configurations based on the dermatoglyphic variables suggest clear separation of populations of Rajasthan from those of Punjab and Himachal Pradesh. Populations of the latter

two states are not only geographically more proximate to each other than to those of Rajasthan, but also are recent settlers. In fact, two of the four Himachal populations were known to have migrated mostly from Punjab and to a lesser extent from Rajasthan. The GR is the only autochthonous group among the studied populations from this state. These observations provide sufficient explanation for the lack of clear separation between the groups of Punjab and Himachal Pradesh.

It is also interesting to note that the Gaddi Rajputs with some degree of Mongoloid physical features are placed together with the Mongoloid NH, migrants of neighboring Nepal. Further, the dermatoglyphic variables fail to depict the known socioeconomic or caste affiliations of the studied populations. In contrast, the population configurations as shown by genetic marker analysis are consistent with the known caste/ethnic affiliations of the populations; the tribals and the lower castes on one side are clearly separated from the upper castes, while the geographical affiliations are somewhat masked. Discordance in the pattern of population relationships based on dermatoglyphics and other biological variables, particularly serological and anthropometric, appears to be, however, a rule rather than exception (see, Plato, 1970; Chai, 1972; Neel et al., 1974; Crawford et al., 1976; Jantz and Chopra, 1983; Reddy et al., 1987). Dermatoglyphic variables are considered to undergo slow rate of evolutionary change, and are presumably less useful in depicting local level (caste/tribal) variations (Plato, 1970; Rothhammer et al., 1977; Rudan, 1978; Froehlich and Giles, 1981a,b; Reddy and Reddy, 1992). The close resemblance between Jewish populations of different countries after 2000 years of separation (Sachs and Bat-Miriam, 1957) is a classic example of the temporal stability of dermatoglyphics. However, these variables may be useful in depicting broader, macro-level variations. For example, Krishnan and Reddy (1994) found the results of multivariate graphical analysis of about 200 Indian populations consistent with this observation; the populations cluster on major ethnic/geographical criteria, while local-level variations are submerged.

The pattern of dermatoglyphic configuration observed in the present study confirms the above observations in the sense that local level caste structures are not discernible, while the broad geographical and/or linguistic affiliations are apparent in the way the populations are placed in the multivariate space. At the local level, the genetic differences between populations may be too small and environmental variation too overwhelming, hence the subtle population relationships may be blurred. That the contrasts between radial and ulnar counts are important for discriminating populations at broader levels, while the palmar variables discriminate populations within the state, may be plausible because the palmar variables are apparently more prone to intrauterine environmental factors (Reddy et al., 1991). Further, applying principal component analysis to the finger ridge count data, Krishnan and Reddy (1992) observed that the components that discriminate populations at different levels of hierarchy may be different.

Large-scale anthropometric surveys (Risley, 1908; Guha, 1935) suggested that the populations from Punjab, compared to the populations of the other states in the region, are least variable in body dimensions. The F_{ST} values obtained for different states result in a similar pattern both for dermatoglyphs and genetic markers. This may suggest the greater degree of admixture among the populations of Punjab. Patterns of gene flow as inferred by R-matrix analysis of the dermatoglyphs is also consistent with the breeding and population structure of the groups concerned. For example, the RR from Rajasthan, which is placed as an outlier, above the regression line, suggesting higher degree of external gene flow, is in fact an aggregate of smaller breeding units with some degree of marital exchanges, hence likely to reflect a situation quite akin to what would happen if there was external gene flow into a single unit. However, against the expected pattern the lower caste group MR (Fig. 7), which was expected to have received some gene flow from outside, particularly from the upper castes, is placed below the regression line. Similar exception is apparent in lower caste RS from Punjab (Fig. 8). However, that the trader group MA from Punjab who are distributed in clusters in the urban areas, hence with high mean marriage distance, are placed above the regression line, and the isolated small group of Chowdhuries from Himachal Pradesh below the regression line is expected and can be easily explained.

Patterns of gene flow observed in genetic markers seem to be more consistent with the known patterns of admixture and/or population structure in the sense that the lower castes and tribes, who are expected to have received gene flow from the upper castes and middle caste agriculturists, are seen as outliers above the line, while the upper castes lie on or in close proximity to the line. The outliers below the line are represented by the Nepali migrants. Migrants are known to be usually kin groups from the parental areas, hence a homogeneous collection of individuals or families. Therefore, the observed pattern is on the expected lines. Nevertheless, in the absence of empirical data on the marriage patterns, these inferences remain at best tentative, although it is known that all the subjects in the present study had both parents derived from the same ethnic groups. Therefore, collection of data on marriage patterns among these groups is imminent in order to validate the conjectures made here.

In conclusion, we may say that the patterns of variation observed in dermatoglyphs and genetic markers are both relevant, but consistent with different dimensions of their population structure—whereas dermatoglyphs conform more emphatically to the geographical pattern and less to ethnic resemblance, the reverse is true in the case of genetic markers. The answers to this may lie in the genetic background of the two sets of traits on which the evolutionary forces and the environmental factors may act differentially, as outlined earlier.

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