Population Structure and the Patterns of Dermatoglyphic Variation in Andhra Pradesh, India

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ABSTRACT Patterns of dermatoglyphic variation have been studied among the Telugu populations of Andhra Pradesh, India, applying R-matrix analysis and the Relethford and Blangero (1990) extension of the Harpending and Ward (1982) model to the 22 quantitative finger dermatoglyphic variables- 20 finger ridge counts and total number of whorls and total number of loops on the fingers. The studied populations represent entire spectrum of socioeconomic variation in the state of Andhra Pradesh, including upper, middle and lower castes, and migrant alien population as well. The plots of group centroids on the first two scaled eigen vectors derived from the principal coordinate analysis of the R-matrix produce population configurations conforming with known ethnohistorical backgrounds. There is a high degree of consistency in the pattern of population relationships based on male and female samples, probably implying biological validity of the observed pattern. Plots of observed mean phenotypic variance versus the distance from the centroid of the populations suggest greater degree of external gene flow into the migrant population and relatively greater isolation of the upper caste.

INTRODUCTION

The primary goal of anthropological genetics is the assessment of the effect of different evolutionary forces on the genetic structure and composition of the populations, hence their role in shaping contemporary human variation, be it local, regional or global. The local genetic structure is supposed to be almost exclusively driven by migration and drift, and Harpending and Ward (1982) developed a model that aids in understanding the role of these forces in the evolution of the genetic structures. This model has been extended to quantitative variables by Relethford and Blangero (1990) and is now possible to derive estimates of F_{ST} based on these variables, suggesting the relative degree of differentiation of the substructured populations, besides getting insight into the patterns of gene flow into different populations. According to this model, the expected heterozygosity within a population (H_i) is a function of the total heterozygosity (H_T) of the entire region, and the distance of a population from the regional mean centroid of the allele frequencies (R_{ii}). If the gene flow from outside varies in amount from population to population, this linear relationship no longer holds. Very 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 useful insights by examining the outliers, above and below the expected regression line, in the plot of observed phenotypic variance/heterozygosity versus the distance from the centroid of the populations. The above authors have found useful endorsement of the model in its application to several case studies in the sense that the results generally concurred with known patterns of gene flow. Subsequently several other investigators used the model to study genetic structure of the local populations from different regions (Devor et al. 1984; Relethford 1985; Jantz and Meadows 1995; Puppala and Crawford 1996), using different sets of variables.

Indian subcontinent is known for its enormous linguistic, cultural, ethnic, religious and geographic heterogeneity. Its population is divided into hierarchical castes, tribes and religious communities with strictly defined rules governing the mating/marriage practices within each of them and prohibiting marriages outside ones own group. Thus, India offers innumerable situations where one can find populations sub-

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structured with different levels of hierarchy and antiquity , hence most suited for investigations on the micro-evolutionary questions. This complexity is a result of different waves of migration, hence an amalgamation of heterogeneous religious, ethnic, linguistic, and cultural elements which may reflect in their genetic structure as well. Although this aspect of population structure is uniformly true to all regions, the degree to which different populations had undergone admixture process varies vastly from region to region. Further, most of the regional population clusters have a relatively recent history of subdivision, yet are reproductively isolated almost completely. Nevertheless, some of these processes of sub-division were known to be due to violation of endogamous rules, suggesting role of gene flow in the contemporary structure of the populations. Many of these populations, so formed, had maintained as small units during the history of their evolution. This coupled with the preference for consanguineous marriages and village endogamy and restriction of marriages to a small radius in many regions provide interesting situations to apply the model of Harpending and Ward (1982) and Relethford and Blangero (1990). We have recently applied this model to a cluster of groups of marine fishermen on the east coast of India and could explain the pattern of divergence of migrant groups from the parental stocks as due to external gene flow, consistently in each of the three sets of data- genetic markers, dermatoglyphics and anthropometry (Reddy and Chopra 1999). In an another study we found that the patterns of dermatoglyphic and genetic heterogeneity conform to known ethnohistorical, migration and

admixture patterns of the populations in the northwestern region of the country (Reddy et al. 1999).

In the present study we shall examine the population structure of the Telugu populations from Andhra Pradesh, India, applying the above model to the quantitative finger dermatoglyphic variables.

MATERIALS AND METHODS

Rolled finger prints of 1334 individuals, 736 males and 598 females, from the 5 endogamous groups were collected during 1977 - 1984 using ink and roller method (Cummins and Midlo 1961). A total of 22 quantitative dermatoglyphic variables- 20 finger ridge counts, radial and ulnar counts on each of the 10 fingers, and total number of loops and total number of whorls on the fingers- were scored and utilised for the present study. Population and sex-wise sample sizes, socioeconomic status, occupational background etc. are furnished in table 1.

The analytical procedures outlined by Williams-Blangero and Blangero (1989) and Relethford and Blangero (1990) were followed, and the computations were done using *RMET* computer program of John Relethford.

Sampled Populations and Socioeconomic and Geographic Backgrounds

Broadly speaking the studied populations represent entire spectrum of socioeconomic variation in Andhra Pradesh. Of the five, *Vyshya*, a tradesman caste locally known as *Komati*, occupy the highest and the untouchable caste, *Mala*, the lowest social ranks. The *Kamma* and

Table 1: Sample sizes, socioeconomic, geographic and occupational backgrounds of the studied populations from Andhra Pradesh (A.P.)

Population	Sex	Abbrevation	Sample Size	Socioecono-mic status	Occupation	Sampling location
Vyshya	Male	VY	195	Upper castes	Trade & business.	Chirala town, A.P.
	Female	VYF	182			
Kamma	Male	KM	130	Middle	Land-owning agriculturiests	Puttur taluk, Chittoor dist., A.P.
	Female	KMF	145			
Settybalija	Male	SB	96	Lower	Petty tradesmen	Kodur taluk, Cuddapah dist. A.P.
Mala	Male	ML	182	Pancham	Scavenging & agri. labour	Chittoor taluk, Chittoor dist., A.P.
	Female	MLF	112			
Pattusali	Male	PS	133	Lower	Silk thread weavers	Chandragiri & Puttur taluks, A.P.
	Female	PSF	159			

Settybalija occupy the intermediate positions in the descending order. The *Pattusalis* who were immigrants from Gujarat, a northwestern state of India, in the 18th century, are comparable to the *Settybalijas* in the social hierarchy. The primary occupation of the *pattusalis* is weaving silk thread (sacred) that is sold to pilgrims in the temple towns. They are distributed in different temple towns of Andhra Pradesh and Tamil Nadu. They speak a dialect called "Patnuli" or "Khatri", although currently they are fluent in the local languages, depending on where they are settled. The size of this population is small and is highly inbred (Reddy and Rao 1978).

The *Kammas* are land-owning agriculturists. The *Settybalijas* traditionally were petty tradesmen, selling bangles and other items of ornamental nature to the agricultural groups. They have now taken up agriculture. The *Mala* is a scheduled caste population with traditional roles like carrying death messages, clearing dead cattle from the agriculturist villages and digging graves, besides working as farm labourers to the land-owning castes like *Kamma*. These three groups have been mostly distributed in the rural areas with frequent day-to-day interaction. The *Vyshyas* live mostly in towns and cities, having limited interaction with the agricultural groups.

The *Malas*, *Settybalijas* and *Kammas* have overlapping geographical distributions throughout Andhra Pradesh and the present samples of these populations and of Pattusalis were drawn from the contiguous taluks in the Chittoor and Cuddapah districts of southern Andhra Pradesh. The sample for *Vyshyas* is drawn from Chirala town in Prakasam district, about 200 km away from any of the three other local groups. All these groups are strictly endogamous, and prefer consanguineous marriages, hence highly inbred.

RESULTS

Reddy and Reddy (1992) applying ANOVA to these 22 dermatoglyphic variables observed that 19 of the 22 variables in males and 17 in females show significant heterogeneity in mean values among the groups, and the Wilks' λ and associated F- values from the multiple discriminant analysis were highly significant (p<

0.000). This had suggested a high degree of overall discrimination among the groups, in the male, female and pooled samples. However, although the sex difference was significant, the population-sex interaction was not significant, suggesting that there is consistency in the pattern of intergroup heterogeneity in male and female samples.

The Extent of Differentiation and the Pattern of Relationships Among the Populations

The F_{ST} values that reflect the extent of differentiation in the quantitative dermatoglyphic variables, are obtained from the R-matrix analysis as outlined by Blangero and Blangero (1989) and through the *RMET* program written by John Relethford. The results are given in Table 2. The F_{ST} values suggest relatively greater differentiation among the populations in females, when compared to males. Further the extent of differentiation is found to be larger when compared to that in a cluster of marine fishermen populations from the eastern coast of India (Reddy and Chopra 1999), but similar in magnitude when compared to the northwestern Indian groups (Reddy et al. 1999). It is interesting to note that the F_{ST} values estimated by using 9 of the 22 most discriminating variables which are selected through the step-wise discriminant analysis are substantially larger than those based on all the studied variables. The differences in

Table 2: Genetic F_{ST} values for inter group differentiation estimated through R-matrix analysis of the quantitative dermatoglyphic variables**

Sample	No. of groups	All 22 variables	9 most discriminating variables*
Males + females	9	0.02801±0.00141	0.05051±0.00274
Males	5	0.02339±0.00180	0.03959±0.00341
Females	4	0.02838±0.00205	0.05690±0.00420

* the 9 most discriminating variables selected through stepwise discriminant analysis are ulnar finger ridge counts on L2, L4, L5 and R4 and radial ridge counts on L1, L2 and R5 along with the number of loops and number of whorls on the fingers.

** average heritability for these variables is taken as 0.60, which was an estimate derived for some Telugu populations from Andhra Pradesh, hence considered to be close approximation to the population specific value.
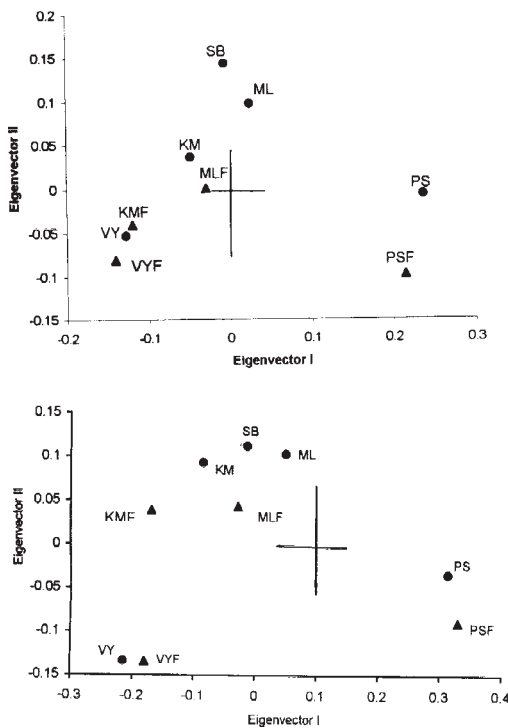
the estimates are highly significant (p< 0.01) in each of the three samples, males, females and male and female populations combined. This would suggest that the extent of differentiation depends on the type and number of variables used and it is necessary to use identical set of variables if the comparisons are to be valid.

The plots of first two scaled eigen vectors (scaled by the square root of their eigen values) from the principal coordinate analysis of the R-matrix based on all 22 variables and the 9 selected variables (Fig. 1) both suggest population configurations that are consistent with the known ethnohistorical relationships of the populations. For example, the geographically

Fig. 1. Relationships among the Telugu populations shown on the two scaled eigen vectors, derived through the principal coordinate analysis of the R-matrix, based on all 22 variables (above), and 9 selected variables (below). The two eigen vectors together explain about 73.4% (55.1 and 18.3%, by the I & II) of the total variation among the groups in case of the former, and 83.3% (66.9 & 16.5, respectively by the I & II) in case of the latter. See table 1 for definition of abbreviations. Filled circles represent males and triangles females.

contiguous/overlapping three rural groups are clustered compactly, far removed from both the urban upper caste *Vyshyas* inhabiting some 200 km away, and the migrant alien population *Pattusalis*. Similarly the latter two castes are placed quite apart from each other in the multivariate space. However, the known ethnohistorical relationships are much more vividly portrayed by the 9 most significant variables than when all the variables were included; in case of the latter, the separation of upper caste *Vyshyas* from the three rural castes of Sudra varna is not very clear. The sex-consistency in the pattern of population configuration is remarkable in the sense that each of the female populations is placed in close vicinity to its male counterpart in the multivariate space. This may increase the degree of confidence in the inference that the observed pattern of relationships being a biological reality.

Relative Patterns of Gene Flow

Table 3 provides group-wise averages of the observed and expected phenotypic variances and distance of the each group from the centroid (r_{ii}). Plots of observed mean phenotypic variance versus distance from the centroid and the theoretical regression lines, for 22 and 9 variables separately, are given in fig. 2. It is apparent from these plots that the migrant *Pattusali* presents itself as an outlier above the regression line indicating greater degree of heterozygosity, hence

Table 3: Dermatoglyphic distance to the centroid (r_{ii}), and observed, expected and residual mean phenotypic variance of the Telugu populations

| Population	R(ii)	Within-Group Phenogypic Variance		
		Obser-ved	Expe-cted	Residu-al
Mala, Males	0.0151	1.017	0.996	0.020
Mala, Females	0.0084	0.961	1.003	-0.042
Kamma, Males	0.0164	1.058	0.995	0.063
Kamma, Females	0.0379	1.010	0.973	0.037
Pattusali, Males	0.0603	1.290	0.951	0.339
Pattusali, Females	0.0580	1.211	0.953	0.258
Vyshya, Males	0.0291	0.682	0.982	-0.300
Vyshya, Females	0.0335	0.689	0.978	-0.289
Settybalija, Males	0.0253	0.899	0.986	-0.088
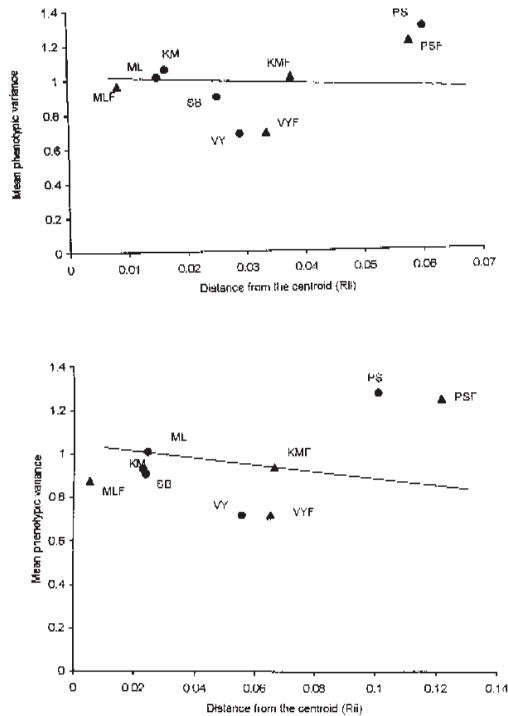
Fig. 2. Plots of observed mean phenotypic variance versus distance from the centroid of the studied Telugu populations and the theoretical regression line based on all 22 variables (above) and 9 selected variables (below). See Table 1 for defination of abveriation. Filled circles represent males and triangles females.

external gene flow into it, and the *Vyshyas* having placed below suggest relatively greater isolation. The three agricultural groups, both males and females, are all placed either on or very close to the regression line. There is a remarkably high degree of consistency in the way the male and female samples of a particular population project themselves on the regression plot, suggesting high probability of the observed pattern being a biological reality. Each of the female samples are placed in close vicinity of its male counterpart on the regression plot. Here again the plot based on 9 selected variables brings out the picture relatively more emphatically.

DISCUSSION

The results of R-matrix analysis of the finger dermatoglyphic variables endorse, by and large,

the known ethnohistorical information on the groups. For example, the three rural castes constituting the sudra varna with contiguous/ overlapping distributions show much closer affinities among them vis-à-vis the geographically somewhat distant and ethnically distinct upper caste *Vyshyas* on the one side and the alien migrant *Pattusalis* on the other. The latter two also show wide divergence between them. It is also significant that the male and female populations of each of the groups are placed compactly together in the multivariate space, reflecting probably the biological validity of the observed relationships between groups. It is apparent that most of the heterogeneity observed among these Telugu populations is among the three major categories- *Vyshyas, Sudras* and the migrant alien *Pattusalis*. Differentiation among the three rural groups (*Kamma, Settybalija and Mala*) within the broad category "Sudra" is relatively small. These findings may be taken as strongly supporting the suggestion that dermatoglyphs are advantageous polygenic markers and help in tracing ethnic and/or prehistoric relationships among the human populations (Rife 1954). For example, Mavalwala and Hunt (1964) among Pacific islanders, Froelich and Giles (1981 a,b) and Lin et al. (1983) among the indigenous New Guinea populations, Krishnan and Reddy (1994) and Reddy et al. (1999) among the Indian populations, Jantz and Hawkinson (1979) and Jantz et al. (1982) among the African populations, and Leguebe and Vrydagh (1981) among the world-wide populations found dermatoglyphics to portray expected ethnohistorical relationships as well as broad geographic patterns, rather convincingly.

This pattern of sex-consistency is also reflected in the regression plots of the observed mean phenotypic variance versus the distance from the centroid, where the male and female samples of a population present identical patterns of gene flow or isolation. Only the migrant *Pattusalis*, both males and females, are placed as outliers, above the regression line, suggesting greater degree of heterozygosity, hence more external gene flow, and *Vyshyas* being below the line suggest greater degree of isolation. The three rural groups fall on or near the line suggesting average gene flow. The *Vyshyas,* being an upper

caste and having been restricted to business maintain high degree of group identity and genetic isolation, hence, no wonder, least heterozygous.

On the other hand, some earlier studies suggested that migrants experience greater external gene flow compared to the residents (Crawford 1975; Crawford et al. 1976; Reddy and Chopra 1999). The greater heterozygosity of the migrant *Pattusalis* can have the following two plausible explanations. It may be that the migrants were not kin groups, but a random assortment of people migrated due to certain pull and push factors. Given this, and that they had come from such far way place in Gujarat, it is conceivable that the subsequent marriages must have had occurred among the distant and unrelated migrant families, resulting in a relatively greater heterozygosity. In fact, quite a strong but indirect empirical evidence for such a possibility has come through the historical analysis of the data on marriage patterns among the marine fishermen, who are relatively recent migrants to the Puri coast in Orissa (Reddy and Chopra 1999; Reddy 2001). On the other hand, if one assumes that the migrants were originally small in numbers, the distances to their parental places are so large that they would have been forced to seek mates locally, albeit from the lowly ranking castes, probably because of the crisis in finding marriageable partners from their own group, thus enhancing genetic heterogeneity of the population. The above two possibilities either individually or jointly might have been responsible for the above average heterozygosity of the *Pattusalis*.

From the analysis of the foregoing results, it appears that the R-matrix analysis and especially the Relethford and Blangero (1990) extension of the model to the quantitative traits is useful in unravelling the local population structure, and for getting insights into the possible roles of migration and drift in the evolution of local populations.

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