

Quantitative Dermatoglyphic Variation among Five Reddi Populations of Southern Andhra Pradesh

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ABSTRACT Bilateral finger and palm prints of 1000 Reddi males, 200 each of five endogamous groups namely Pokanati (PNR), Pedakanti (PKR), Panta (PTR), Akuthota(ATR) and Palle (PLR), were studied for eight quantitative dermatoglyphic traits. The finger pattern intensity index (FPII) ranging from 12.74 (PNR) to 13.79 (PTR) shows higher values for right hands of all populations. With regard to mean ridge counts (RCs and SRCs) no clear trend is observed. The mean TFRC (132.81) and AFRCs (177.59) are higher in the PTR and PKR respectively. Transversality of ridges on right palms was found to be more as indicated by their uniformly and significantly higher main line index (MLI) values. The bilateral differences for a-b ridge count are insignificant. The five Reddi groups do not show considerable variation in the mean atd angle, the bilaterality being significant with the exception of ATR. F-Values for all traits were calculated to understand the between and within population variations. The distance calculated according to Mahalanobis D^2 between PLR and PKR was found to be more (0.1148) compared to the rest of the pairs of populations. The minimal cluster is formed between PTR and ATR showing lesser within cluster variability.

INTRODUCTION

The quantitative method is a relatively new approach developed to study dermal ridges. This method enables the application of significance tests as also the elimination of arbitrariness of certain qualitative classifications. The widely studied quantitative dermatoglyphic characters include finger pattern intensity index (FPII), total finger ridge count (TFRC) and absolute finger ridge count (AFRC) on fingers, and main-line index (MLI), a-b ridge count and atd angle on palms. Holt (1968) opines that of all the quantitative characters TFRC, is strongly determined by heredity excepting only 5% of its total variability caused by environmental effects. However, Jantz and Hawkinson (1979) believe that in order to discern meaningful population patterning individual digit ridge counts provide additional information. Owing to its strong correlation with TFRC, the pattern intensity index may have an important genetic component also but its inheritance studies are scanty (Salzano and Benevides, 1971). The absolute finger ridge count (AFRC) also has been utilized to a greater extent in biological comparison of populations (Mukherjee, 1967, Chakraborty and Malhotra, 1981 among others). Palmar quantitative characters such as main line index (MLI), a-b ridge count and atd angle are studied for understanding the mode of inheritance and for delineating the bisexual and inter and intra

population variations (Mahapatra and Behera, 1970, Pateria, 1974, Naffah, 1974, Prokopec and Sedivy, 1976, Murillo et al., 1977, and Harvey and Suter, 1983).

Against this background the present study among five Reddi populations has been attempted to assess the extent of dermatoglyphic variability through quantitative finger and palmar traits and to compare with the one expressed by qualitative dermatoglyphic characters (Chandrasekhar Reddy et al., 1990).

The Reddis with numerous endogamous groups among them although belong to the fourth or last of the Hindu Varna system, in the present day socio-economic and political set-up, occupy the place next to Brahmins. The five Reddi populations of study. Pokanati (PNT), Pedakanti (PKR), Panta (PTR), Akuthota (ATR) and Palle (PLR), are found widely distributed in Southern Andhra Pradesh. Their socio-cultural pursuits are nearly similar to other caste groups of the region as also those from other parts of Southren India. The sub-caste endogamy to a great extent is prevalent in rural areas. Monogamy is the accepted pattern. About 30 to 50% of marriages are found to be related ones, the inbreeding coefficients ranging from 0.366 to 0.0485.

MATERIAL AND METHODS

The data was collected from thirty randomly selected villages in Chittoor district forming the

Southernmost region of Andhra Pradesh. It includes bilateral finger and palm prints taken on a plain paper using ink, from 1000 males, 200 each representing the five Reddi sub-castes in the age range of 10-50 years. Finger prints were studied for pattern intensity index (FPII), sum of higher ridge counts (RC) and sum of both ridge counts (SRC) for individual digits and for both the hands separately, total finger ridge count (TFRC) and absolute finger ridge count (AFRC) and palm prints for main line index, a-b ridge count and maximal 'atd' angle following Holt (1968), Plato (1970) and Mavalwala (1978).

Traitwise bilateral variations for the above traits using Student's t-test, and F-values were calculated to estimate the intra-population differences among the five Reddi populations. The six traits studied were subjected to Mahalanobis' D^2 (1938), combining the values observed for left and right hands, to obtain an overall dermatoglyphic distance measure.

RESULTS AND DISCUSSION

Pattern Intensity Index (FPII): The mean FPIIs ranges from 7.03 ± 0.12 for right hands of PTR to 6.26 ± 0.13 for left hands of PNR (Table 1). For combined figures also the PTR and PNR show the highest (13.79) and lowest (12.74) mean values respectively. The deviations in the mean FPIIs are in accordance with the higher and lower proportions of whorls in the populations concerned. Among all populations, the right hands tend to show higher mean FPII values than left ones. Similar trend was noticed by Plato et al. (1975), and Narahari (1982). However, the t-values for bilateral differences are insignificant.

Sum of Higher Ridge Counts (RC): Digitwise ridge counts (RC) show a uniform trend of highest mean count for digit I followed by digit IV and

the lowest for digit II. Such trend was reported among five caste groups and Parsees by Malhotra et al (1980), where as in tribal populations the IV digit was found to have highest count. The mean ridge count (RC A) Values (Table 1) range from 57.28 ± 1.33 on the left hand among PLR to 66.53 ± 1.25 on the right hand among PTR. Excepting the PKR among all the populations the mean RC A for right hands is more than left ones. However, the t-values for the differences of bilaterality fall short of significance among all populations.

Sum of Both Ridge Counts (SRC): The digitwise trends of variation observed for summed ridge counts (SRC) are almost in accordance with those observed for RCs. In general the IV digit with higher frequency of whorls is found to show higher mean SRCs. The digit V of either hand among all populations is represented by the lowest mean SRCs. As shown in Table 1 the highest mean average summed ridge count (SRC A) – the total of individual SRCs on five digits (89.19 ± 2.49) is found for the right hand among PTR and the lowest (76.44 ± 2.39) for the left hand among PLR. In all sample series save for PKR, the mean average SRCs are higher for right than left ones. But significant bilateral difference was found only in PNR. The overall distributions of RCs and SRCs on either hand are in tune with the distribution of papillary patterns.

The mean TFRC and AFRC values among the five populations are presented in Table 1.

Total Finger Ridge Count (TFRC) and Absolute Finger Ridge Count (AFRC): The highest mean TFRC value is reported among PTR (132.81 ± 2.44) and the lowest among PLR (116.07 ± 2.51). The PKR show the highest mean AFRC (177.59 ± 4.78), while the lowest is noticed among PLR (154.55 ± 3.78). Though the frequency of whorls was observed to be higher among PLR

Table 1: Means and standard errors of quantitative finger dermatoglyphic characters

		FPII		RC A		SRC A		TFRC		AFRC	
		Mean	S.E.	Mean	S.E.	Mean	S.E.	Mean	S.E.	Mean	S.E.
PNR	L	6.26	0.13	63.18	1.49	81.39	2.63	128.48	2.93	165.51	4.34
	R	6.48	0.13	64.30	1.55	84.13	2.71				
PKR	L	6.71	0.14	66.43	1.51	88.91	2.84	132.47	2.97	177.59	4.78
	R	6.71	0.14	66.05	1.56	88.68	2.94				
PTR	L	6.76	0.12	66.28	1.30	87.22	2.49	132.81	2.55	177.40	3.99
	R	7.03	0.12	66.53	1.25	89.18	2.49				
ATR	L	6.33	0.12	64.31	1.40	81.87	2.56	128.62	2.79	166.07	4.31
	R	6.64	0.13	64.32	1.45	84.21	2.75				
PLR	L	6.57	0.13	57.28	1.33	76.44	2.40	116.07	2.51	154.55	3.79
	R	6.71	0.13	58.79	1.31	78.11	2.39				

compared to PNR and ATR, both the mean TFRC and AFRC values are lower indicating smaller pattern size. Except PLR, the other four Reddi populations show higher mean TFRC values than the average (131.48) reported for South Indian populations (Bhasin and Walter, 2001).

Main Line Index (MLI): The MLI, the measure used to estimate the obliquity of ridges, ranges from 7.96±0.12 among PKR to 8.62±0.13 among PLR on left palms and on right palms from 8.50 ±0.13 among PKR to 9.22±0.12 among PLR (Table 2). The values are uniformly higher for right palms than left ones among all populations, indicating more transversality of ridges on the right palms. Similar trend was observed by Mahapatra and Behera (1970), Naffah (1974) and others. The standard errors of the means with relatively shorter ranges are less variable. The bilateral differences in all populations are highly significant.

a-b Ridge Count: The mean values of a-b ridge counts as shown in Table 2 are found to be high for both the palms of PNR (L=38.90±0.41; R=38.5±0.42) whereas the PLR (L=35.58±0.39; R=35.48±0.39) show the lowest values. In all the populations but PTR there occur uniformly higher means on left than on right palms but their t-value for bilateral differences fall short of significance.

'atd' Angle: For the maximal atd angle, the highest and lowest mean values are found among PNR and ATR, respectively for either left (44.52±0.61, 41.17±0.39) or right (43.03±0.54, 41.28±0.48) palms. Among all study samples, the left palms show higher mean values compared to right ones with their bilateral differences being significant excepting ATR.

To estimate trait wise intra- population and inter- population variation among the five Reddi populations, the analysis of variance (ANOVA)

Table 2: Means and standard errors of palmar quantitative dermatoglyphic characters

		MLI		a-b Ridge count		atd angle	
		Mean	S.E.	Mean	S.E.	Mean	S.E.
PNR	L	8.04	0.14	38.90	0.41	44.52	0.61
	R	8.74	0.12	38.51	0.42	43.03	0.54
PKR	L	7.96	0.12	36.82	0.33	44.01	0.56
	R	8.50	0.13	36.81	0.35	43.02	0.56
PTR	L	8.34	0.13	36.59	0.35	44.40	0.50
	R	8.68	0.13	36.82	0.36	43.02	0.43
ATR	L	8.37	0.13	38.00	0.39	41.17	0.39
	R	8.81	0.13	37.44	0.45	41.28	0.48
PLR	L	8.62	0.13	35.88	0.39	43.77	0.47
	R	9.22	0.12	35.48	0.39	42.74	0.48

has been calculated for both RCs and SRCs on individual digits and hands separately and for the three palmar quantitative characters (Table 3). Highly significant F-values are observed for both RCs and SRCs, including RC A and SRC A owing to much less within group variance than that of between groups. Hertha De Villiers observed (1980) no such high variance in a comparative study of 17 South African Bantu male populations. In our series higher F-Values are noted in general for left digits. In the matter of the three palmar quantitative characters also the Reddi populations are highly heterogeneous as suggested by highly significant F-ratios; F-value is however insignificant for maximal atd angle of Right palms. Our series are further found to be heterogeneous in the distribution of both Galton's and Henry's finger pattern types (Chandrasekhar Reddy et al. 1990).

The squared quantitative dermatoglyphic distance D² (lower) and D (upper) values for populations are shown in Table 4. The distance between PLR and PKR as that for qualitative dermatoglyphic traits is the highest (0.1148) compared to other pairs of populations. The minimal distance (0.0323) is observed between ATR and PTR. Though three distinctive clusters are observed for quantitative traits also (Fig.1), the major feature appears to be the dichotomy of PKR, PTR and ATR with the two populations of PLR and PNR, which in turn form a cluster. The

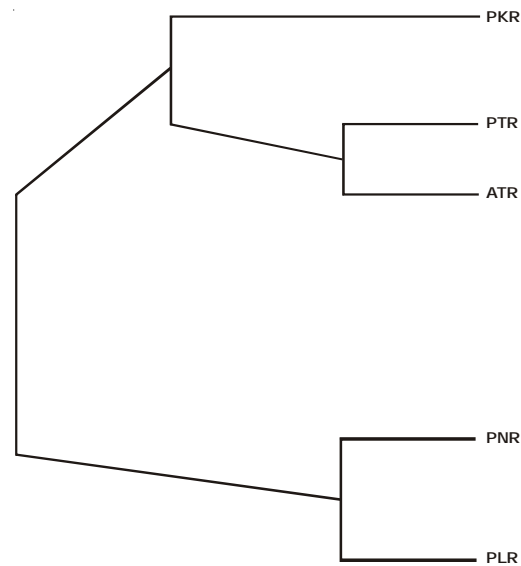


Fig. 1. Clusters by bindry split (Fusion)

Table 3: Analysis of variance (ANOVA) results for different dermatoglyphic traits

<i>Character</i> <i>1</i>	<i>Source</i> <i>2</i>	<i>D.F.</i> <i>3</i>	<i>SS</i> <i>4</i>	<i>M.S</i> <i>5</i>	<i>F</i> <i>6</i>	
RC I	L	Between Groups	4	578.6200	144.6550	
		Within Groups	995	26315.3550	26.4476	5.47***
	R	Between Groups	4	913.0700	228.2675	
		Within Groups	995	30579.9050	30.7336	7.43***
RC II	L	Between Groups	4	459.5300	114.2750	
		Within Groups	995	31591.2450	31.7500	3.62**
	R	Between Groups	4	469.1000	111.2750	
		Within Groups	995	32482.8750	32.6461	3.59**
RC III	L	Between Groups	4	479.1740	119.7935	
		Within Groups	995	26427.1850	26.5600	4.51**
	R	Between Groups	4	260.8700	65.2175	
		Within Groups	995	24321.9050	24.4441	2.67**
RC IV	L	Between Groups	4	634.8500	158.7125	
		Within Groups	995	23196.7500	23.3133	6.81***
	R	Between Groups	4	350.1740	87.5385	
		Within Groups	995	23836.9050	23.9567	3.65**
RC V	L	Between Groups	4	609.1140	152.2785	
		Within Groups	995	17401.3500	17.4888	8.71***
	R	Between Groups	4	353.2360	88.3090	
		Within Groups	995	17256.9400	17.3437	5.09**
RC A	L	Between Groups	4	11145.1660	2786.2915	
		Within Groups	995	3934346.7850	396.3284	7.03***
	R	Between Groups	4	7588.5840	1897.1460	
		Within Groups	995	406369.3800	408.4114	4.65**
SRC I	L	Between Groups	4	1138.6460	284.6615	
		Within Groups	995	96310.7850	96.7448	2.94*
	R	Between Groups	4	1051.8060	362.9515	
		Within Groups	995	107888.8300	108.4310	3.35**
SRC II	L	Between Groups	4	1112.1760	278.0440	
		Within Groups	995	97565.0200	98.0553	2.84*
	R	Between Groups	4	1527.2660	381.8165	
		Within Groups	995	107071.6300	101.5795	3.76**
SRC III	L	Between Groups	4	1253.1160	313.2790	
		Within Groups	995	89547.0400	89.9970	3.48**
	R	Between Groups	4	999.0460	249.7615	
		Within Groups	995	79734.7450	80.1354	3.12*
SRC IV	L	Between Groups	4	1566.9960	391.7490	
		Within Groups	995	94722.2350	95.1982	4.12**
	R	Between Groups	4	1013.3460	253.3365	
		Within Groups	995	101680.8450	102.1918	2.48*
SRC V	L	Between Groups	4	621.6840	155.4210	
		Within Groups	995	39748.0730	39.9478	3.89**
	R	Between Groups	4	486.7040	121.6760	
		Within Groups	995	40659.2150	40.8635	2.98*
SRCA	L	Between Groups	4	19919.8660	4979.9615	
		Within Groups	995	1332486.5650	1339.1825	3.72**
	R	Between Groups	4	15948.6740	3987.1685	
		Within Groups	995	1407310.4450	1414.3824	2.82*
MLI	L	Between Groups	4	57.7340	14.4335	
		Within Groups	995	3302.8700	3.3192	4.35**
	R	Between Groups	4	57.1260	14.2815	
		Within Groups	995	3243.9300	3.2602	4.38**
a-b	L	Between Groups	4	1331.8100	332.9525	
		Within Groups	995	27544.5650	21.6830	15.36***
	R	Between Groups	4	1046.7140	261.6785	
		Within Groups	995	31034.0050	31.1900	8.39***
atd	L	Between Groups	4	1515.3360	378.8340	
		Within Groups	995	51915.3050	52.1762	7.26***
	R	Between Groups	4	460.6900	115.1725	
		Within Groups	995	49790.0850	50.0403	2.30

* Significant at 5% level of Probability
 ** Significant at 1% level of Probability
 *** Significant at 0.1% level of Probability

minimal cluster is formed by PTR and ATR showing lesser within cluster variability. However, such a cluster for qualitative traits is formed by PNR and ATR. The PKR which is distantly placed for qualitative traits is clustered herewith PTR and ATR, but is separated at the second level of clustering.

Table 4: Per character D² (Lower) and D (Upper) values

	PNR	PKR	PTR	ATR	PLR
PNR		0.2696	0.2458	0.1954	0.2260
PKR	0.0727		0.1951	0.2243	0.3388
PTR	0.0604	0.0381		0.1797	0.2854
ATR	0.0382	0.0504	0.0323		0.2589
PLR	0.0511	0.1148	0.0815	0.0670	

In the 3-dimensional representation (Fig.2) based on principal coordinate analysis (Table 5), population dispersion on the I coordinate accounts for 54.04% followed by the dispersions of II (19.12%) and III (16.29%) coordinates. This analysis shows similar interrelationships between the populations as revealed by the cluster analysis. The figure indicates the movement of

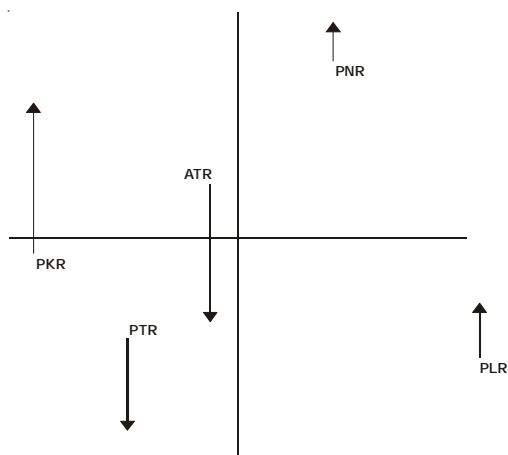


Fig. 2. Principal coordinate analysis

Table 5: Principal coordinates

Population	I	II	III	IV
PNR	0.0710	0.1127	0.0206	-0.0452
PKR	-0.1491	-0.0077	0.0893	0.0257
PTR	-0.0799	-0.0633	-0.0579	-0.0666
ATR	-0.0194	0.0346	-0.0837	0.0689
PLR	0.1775	-0.0763	0.0316	0.0172
Variability Explained	0.0665	0.0238	0.0198	0.0122
%	54.04	19.62	16.29	10.05

Total Variability = 0.1213

PTR and ATR in one direction while that of the other three populations in a different direction.

The differences in the clustering patterns arrived at for qualitative and quantitative traits may be due to the variation in their heritable nature. The clustering patterns for both sets of characters also differ markedly with those of morphological (Chandrasekhar Reddy et al., 1986) and anthropometric characters (Rami Reddy et al., 1986). The clustering pattern of qualitative dermatoglyphic traits however closely simulates that for morphological traits. The data on dermatoglyphic traits is found to have low agreement with the other sets of traits as revealed by majority of the earlier works (Chai, 1972, Neel et al., 1974; Jantz and Hawkinson, 1980). The population patterning arrived at by the present study through qualitative or quantitative dermatoglyphic traits does not demonstrate a clear picture of ethnic and / or geographical closeness among the five Reddi populations. More or less similar conclusion has been reached earlier by Friedlaender (1975).

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