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A Family Study of Dermatoglyphic Traits in India: Resolution of Genetic and Uterine Environmental Effects for Palmar Pattern Ridge Counts

I.B. BORECKI, K.C. MALHOTRA, S. MATHEW, M. VIJAYAKUMAR, D.V. R. POOSHA, AND D.C. RAO
Division of Biostatistics, Departments of Preventive Medicine and Psychiatry (I.B.B., D.C.R.) and Department of Genetics (D.C.R.), Washington University School of Medicine, St. Louis, Missouri 63110; Anthropometry and Human Genetics Unit, Indian Statistical Institute, Calcutta, India (K.C.M., M.V.); Department of Human Genetics and Anthropology, Albert Ludwigs University, Freiburg, West Germany (S.M.); and Department of Human Genetics and Physical Anthropology, Andhra University, Waltair, India (D.V.R.P.)

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ABSTRACT The inheritance of palmar pattern ridge counts for individual palmar areas, combined distal areas, and all ten areas combined was investigated in families belonging to two strictly endogamous Brahmin castes of peninsular India. Ridge count phenotypes were obtained by the method proposed by Malhotra et al. (1981a), however, zero observations (indicating patterns not circumscribed by triradii) were excluded from analysis. Path analytic methods were applied in order to determine the relative influences of polygenes, intrauterine environment, and residual environment. The proportion of genetic variation was, in general, consistently greater in one population than the other, and significant intrauterine environmental effects were detected for the population with lower heritabilities. The results of this investigation suggest that a simple polygenic model may not be sufficient to explain the inheritance of ridge counts in the interdigital IV configurational area. Distal pattern ridge counts do not appear to be influenced by more or less uterine environmental effects than all areas considered together. The proportion of genetic variation for the total palmar pattern ridge count was 52% in both populations.

Dermatoglyphic traits are interesting and useful phenotypes for genetic studies. Dermal ridges first appear around 6–8 fetal weeks and are fully differentiated during the third and fourth fetal months (Cummins, 1929; Mulvihill and Smith, 1969). At this point, dermatoglyphics are morphologically fixed for the remainder of the gestational period, as well as in postnatal life. The configurations and their component ridges enlarge with the growth of the hand and foot, but all of their essential characteristics remain unchanged. The freedom from the effects of environmental influences is shared by few other morphological traits. This, along with the age-stable feature make these traits extremely suitable for genetic and developmental studies.

Although the genetics of finger pattern ridge counts have been extensively studied (see Cummins and Midlo, 1943), comparatively less work has been done with palmar dermatoglyphic traits. Quantitative genetic analysis has been applied to some palmar variables: interdigital ridge counts a-b, b-c, and c-d (Fang, 1950; Pons, 1964; Tiwari, 1965; Rogucka et al., 1971; Pateria, 1974; Sciulli and Rao, 1975; Poosha et al., 1982), main line index (Pons, 1954), maximal atd angle (Penrose, 1954), and A'd ridge counts (Glanville, 1965). The familial correlations obtained in most of these investigations were compatible with polygenic model, and the heritability

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TABLE 1. Descriptive statistics for variables analyzed in family series I and II

Variable name[1]	Family series I					Family series II				
	N	Mean	SD	γ_1	γ_2	N	Mean	SD	γ_1	γ_2
R I3 (max)	411	8.180	3.862	0.499	0.434	218	8.491	3.733	0.618	−0.380
R I3 (abs)	411	8.255	3.901	0.469	0.340	218	8.789	4.315	1.344	4.248
R I4 (max)	291	10.141	5.733	0.489	−0.589	173	10.555	5.130	0.564	0.553
R I4 (abs)	291	10.703	6.360	1.000	1.656	173	10.919	5.587	0.733	0.881
L H (max)	172	15.116	10.692	1.235	1.739	—	—	—	—	—
L H (abs)	172	17.370	13.599	1.616	3.377	—	—	—	—	—
L I4 (max)	424	8.462	5.286	1.129	2.758	215	9.633	4.786	1.311	4.941
L I4 (abs)	424	9.475	5.766	1.131	2.504	215	10.241	5.522	1.383	3.495
TPPRC (max)	617	30.366	20.878	1.474	2.758	380	32.216	21.974	1.161	1.350
TPPRC (abs)	617	33.877	24.048	1.648	3.895	380	34.095	24.206	1.296	1.923
DPPRC (max)	611	19.439	10.890	0.997	1.196	372	18.113	9.840	0.743	0.801
DPPRC (abs)	611	20.864	11.851	1.125	2.097	372	18.774	10.254	0.738	0.501

[1]R = right; L = left; I = interdigital; H = hypothenar; Th = thenar; TPPRC = total palmar pattern ridge count; DPPRC = sum of palmar distal pattern counts for interdigital areas I2, I3, and I4.

estimates were lower than those obtained for finger ridge count variables.

Malhotra et al. (1981a, 1982) recently developed a technique to obtain ridge counts for the palmar configurational areas. These authors defined a new measure based on palmar pattern ridge counts analogous to total finger ridge counts. This measure, designated as total palmar pattern ridge count (TPPRC) is the sum of the single ridge counts on the ten palmar configurational areas of an individual.

The TPPRC trait was investigated in several studies (Malhotra et al. 1981b, 1982; and Malhotra and Rao, 1982). Among the conclusions from these studies were: 1) the distributions of ridge counts on individual palmar areas as well as the TPPRC are significantly non-normal, 2) counts on individual palmar areas are weakly correlated with the exception of interdigital III and IV which evidence a significant negative correlation. This result was subsequently confirmed by Malhotra et al. (1985a) in several Indian caste groups. 3) The heritability estimate for the size of the palmar patterns as measured by ridge counts (TPPRC) was 0.37 ± 0.06.

Palmar pattern ridge count differentiation among several populations from India and Iran was studied by Malhotra et al. (1985a, 1985b) and Kamali et al. (1985). These investigations showed a great deal of inter-population variability with respect to the size of the palmar patterns, and it was concluded that both the size and frequency of the patterns differ among populations at both the local and racial levels.

In view of these results, Malhotra (1981b) and Malhotra and Rao (1982) stressed the need to study the inheritance of ridge counts from individual configurational areas. Furthermore, the work of Loesch (1974) has provided evidence that environmental effects are apparently more pronounced on proximal palmar areas compared to distal areas. Therefore, it is also desirable to investigate the heritability of distal palmar counts, including interdigital areas II, III, and IV (DPPRC).

The purpose of the present study is to examine the multifactorial basis of palmar pattern ridge counts for individual palmar areas, combined distal areas, and all ten areas combined in families belonging to two strictly endogamous Brahmin castes of peninsular India.

THE FAMILY DATA

Dermatoglyphic prints were taken on related individuals from two different populations. Family Series I (FS-I) comprises 125 families with 625 persons. There are 375 children; 187 males and 188 females. The sampled families belong to a rigidly endogamous caste of Andhra Pradesh, called Velanadu Brahmins. Although they are found widely distributed in Andhra Pradesh, their main concentration is in the city of Waltair in the Visakhapatnam district. The sampled families were selected randomly from the city of Waltair and the prints were taken by S. Mathew.

Family Series II (FS-II) consists of 90 families with 414 persons. There are 235 children, 135 males and 100 females. These families belong to an endogamous Brahmin caste, the Havik Brahmins. They number over 60,000 and are found chiefly in the North and South Kanara districts of the western state of In-

dian Karnataka. The prints in this family series were collected by M. Vijayakumar.

In addition, a twin series consisting of 97 twin pairs (35 monozygotic : 21 male-male and 14 female-female; 61 dizygotic : 17 male-male, 23 female-female and 22 male-female) was sampled from in and around the city of Waltair in Andhra Pradesh. These data were collected by D.V.R Poosha. The twin sample does not belong to a particular endogamous group, and has been drawn from different castes, although a substantial number belong to the caste Velanadu Brahmins. The zygosity of the twins was determined on the basis of concordance with five genetic markers: ABO, MN, Rh (C, D, and E), ACP, and EsD.

THE PHENOTYPES

Bilateral rolled palm prints were obtained on each subject using the printer's ink method as in Cummins and Midlo (1943). Dermatoglyphic traits considered for analysis in the present investigation include palmar pattern ridge counts for each of ten individual configurational areas (hypothenar, thenar/interdigital I, II, III, IV, right and left palm), total palmar pattern ridge count (sum of the counts for each individual area), and distal palmar pattern ridge count (sum of ridge counts for interdigital areas II, III, and IV for both palms). The counts of true patterns in the palmar configurational areas were made according to the methods proposed by Malhotra et al. (1981a).

The ridged configurations in each individual area may be either patterned or unpatterned. The patterned areas are composed of sharply recurved ridges circumscribed by the triradial radiants, which determine the form of the pattern (like a loop or a whorl). Ridge counts are obtained by drawing a line from a triradius to the center of the pattern; the number of ridges intersecting the line are counted. It is possible to obtain multiple ridge counts for patterns having more than one triradius. Thus, two phenotypes have been traditionally considered: the maximum count (max) is defined as the largest of the multiple ridge counts obtained for a pattern, and the absolute count (abs) is defined as the sum of all the ridge counts for a pattern. In the case of a loop pattern resulting from a single triradius, the maximum count equals the absolute count. For the twelve phenotypes defined above, both the maximum and absolute measures were considered in the analysis.

Unpatterned areas are characterized by the absence of triradii, and the ridges simply course in some direction. These are considered open field patterns, and the lack of a triradius makes it impossible to obtain a ridge count by standard methods. Thus, unpatterned areas traditionally have been assigned a ridge count of zero. However, zero in this context cannot be considered as part of the quasi-continuous distribution of ridge counts; a similar argument recently has been advanced by Loesch (1983). Therefore, all zero observations were excluded from analysis, thereby treating these ridge counts as unmeasurable. As a result, the sample sizes for some variables became too small to obtain meaningful estimates of familial correlations, and only those variables with adequate sample sizes were retained for analysis.

Table 1 shows the descriptive statistics by family series for the variables used in this investigation. Owing to the exclusion of zeroes, the resulting distributions were truncated at one. The distributions of ridge counts generally were leptokurtic and positively skewed, especially in the case of absolute measures.

Pairwise correlations for these variables were computed for the FS-I data, shown in Table 2. The correlations were computed separately for the right and left sides, and then, assuming bilateral symmetry, the weighted average was taken using Fisher's z transformation. These average correlations are shown both retaining and excluding the zero observations for comparison. The sample sizes that are shown are the sum of the pairs of observations for the right and left sides.

Although several of the pairwise correlations became apparently more positive when zero observations were excluded, this trend was generally not significant when the standard errors of the estimates obtained in the reduced sample were considered. The notable difference was in the correlation between interdigital areas IV and III. Signficant negative correlations have been reported for ridge counts on these two areas (Malhotra et al. 1982, 1985a), as was found in the present study when using all of the observations. However, when the zeroes were excluded, the correlation became significantly positive.

QUANTITATIVE ANALYSIS

Path analysis

The methods of path analysis employed here reflect modifications of preexisting procedures. These were discussed in detail by Rao (1985) and Rao et al. (1984a). First, the nuclear family data was summarized in terms of estimates of familial correlations.

TABLE 2. Pairwise correlations between selected palmar pattern ridge counts based on family series I

VAR X	VAR Y	Including '0' r_{xy}	Including '0' N	Excluding '0' r_{xy}	Excluding '0' N
Maximum					
I3	H	−0.024	500	−0.073	81
I3	I2	0.082	500	0.129	43
I4	H	0.093	500	0.147	101
I4	Th	0.033	500	0.379	22
I4	I2	−0.049	500	0.231	31
I4	I3	−0.377	500	0.261	86
Absolute					
I3	H	−0.050	500	−0.213	44
I3	Th	−0.044	500	−0.283	23
I3	I2	0.092	500	0.151	43
I4	H	0.119	500	0.164	103
I4	Th	0.009	500	0.161	30
I4	I2	−0.027	500	0.206	31
I4	I3	−0.351	500	0.201	88

For each type of pattern ridge count studied, the following variables were defined for the members of a nuclear family with s children : P_F = phenotype of father, P_M = phenotype of mother, and P_i = phenotype of the i^{th} child (i = 1, ..., s). Assuming that (P_F, P_M, P_1, ..., P_s) follow a suitable multivariate normal distribution, the log-likelihood for the j^{th} of n families can be written, denoted by $\ell n\ L_j$. The overall log-likelihood for a random sample of n families is $\ell n\ L = \sum_{j=1}^{n} \ell n\ L_j$. Recent studies have shown that the method is robust against moderate departures from the assumption of multivariate normality, and neither hypothesis testing nor parameter estimation is seriously affected (Rao et al., 1984b). By assuming that all children are identically distributed, that a parent is equally correlated with any child, and that sib-pairs are equicorrelated, $\ell n\ L$ is a function of three means, three variances, and four correlations (spouse-spouse, father-child, mother-child, and sib-sib). The three variances and four correlations are estimated by maximizing the $\ell n\ L$ separately for each ridge count variable, fixing the means at sample values. At the end of estimation, an empirical variance-covariance matrix among the seven estimates is calculated, denoted by S. The 4 × 4 submatrix in S corresponding to the four correlation estimates was then inverted. This inverse, denoted by K, is the empirical information matrix among the four correlation estimates. This K matrix is used in the statistical method of analysis described later, and represents the information necessary to statistically correct for the bias introduced by the non-independent estimation of familial correlations.

MZ and DZ correlations were estimated from twin data in FS-I by analysis of variance. The number of twin pairs varies from phenotype to phenotype.

For path analysis of the correlation estimates obtained above, we considered a special case of a more general model (Rao et al., 1979), which is similar to the one used before for the analysis of ridge counts (Malhotra and Rao, 1982). The basic model postulates an additive genotype (G), and a uterine environment (U). Their effects are assumed to be additive. The two basic parameters are:

h = effect of genotype (square root of genetic heritability).
u = effect of uterine environment on phenotype.

While the polygenic component is the sole determinant of vertical transmission (parent-offspring), the uterine environment contributes u^2 to sibling and twin correlations.

For the first family study which included the twin series, an additional parameter is considered:

t_{TW} = a correlational path between the phenotypes of twins, perhaps induced by simultaneous sharing of the uterine environment, i.e., intrauterine effect.

In presenting the results of fitting the path models, only the significant components of

TABLE 3. Summary correlations for family series I with twins

Variable	Family data							Twin data			
	$\hat{r}_1$	$\hat{N}_1$	$\hat{r}_2$	$\hat{N}_2$	$\hat{r}_3$	$\hat{N}_3$	$\hat{r}_4$	$\hat{N}_4$	$\hat{r}_5$	N_{MZ}	$\hat{r}_6$	N_{DZ}
R I3 (max)	0.151	72	0.312	151	0.301	137	0.201	126	0.319	19	0.686	20
R I3 (abs)	0.145	72	0.297	148	0.309	136	0.203	121	0.319	19	0.441	20
R I4 (max)	0.239	38	0.339*	187	0.339*	187	0.215	106	0.818	15	0.490	12
R I4 (abs)	0.188	46	0.383	125	0.255	127	0.136	153	0.582	15	0.367	23
L H (max)	0.189	22	0.369	19	0.326	35	0.248	36	0.176	12	0.418	10
L H (abs)	0.054	10	0.293	41	0.229	41	0.174	58	0.144	12	0.423	10
L I4 (max)	−0.079	75	0.273	143	0.203	178	0.185	141	0.264	13	0.483	29
L I4 (abs)	0.098	61	0.227	171	0.086	220	0.058	178	0.489	13	0.444	28
TPPRC (max)	−0.074	125	0.240	258	0.259	262	0.217	361	0.654	34	0.545	57
TPPRC (abs)	−0.089	118	0.193	274	0.234	278	0.192	366	0.609	34	0.509	57
CPPRC (max)	0.076	119	0.330	249	0.328	238	0.280	290	0.724	34	0.586	53
DPPRC (abs)	0.070	118	0.299	263	0.230	255	0.250	313	0.705	34	0.612	53

*Pooled parent-child correlation.

the basic model were included (i.e., one or both of h and u). The significance of the twin intrauterine effect (t_{TW}) is tested as a null hypothesis. Thus, the most parsimonious models were sought.

Statistical analysis

Fitting path models to the sample correlations from nuclear family data followed a method of analysis, presented in Rao et al. (1984a), called Method 2. Let four sample correlations be denoted by r_1 = spouse correlation; r_2 = father-child correlation; r_3 = mother-child correlation; r_4 = sib-sib correlation.

Assuming the joint distribution of the four sample correlations to be approximately multivariate normal, the log-likelihood may be approximated by:

$$\ell n\, L = -\tfrac{1}{2}\chi^2 + \text{constant}$$

$$\chi^2 = \sum_{j=1}^{4}\sum_{i=1}^{4} (r_i - \rho_i)\; K_{ij}\,(r_j - \rho_j)$$

where the ρ's are predicted correlations derived as functions of the path coefficients, and K_{ij} are elements of the K matrix obtained earlier. Goodness-of-fit of a model was measured by the residual χ^2 with 4-w df, where w is the number of parameters estimated. Likelihood ratio tests of specific null hypotheses were carried out by subtracting the residual χ^2 under the general model from that under the null hypothesis. Degrees of freedom are obtained by a similar subtraction. The fundamental assumption underlying this method of analysis, that of multivariate normality of the four sample correlations, appears reasonable in moderate sample sizes, but its appropriateness in small samples is not certain (Fang and Krishnaiah, 1982). All these methods are implemented in PATHMIX2, a FORTRAN program on a HARRIS computer. The program may be obtained from the authors.

The χ^2 is slightly modified for FS-I to include the twin correlations:

$$\chi^2 = \sum_{j=1}^{4}\sum_{i=1}^{4} (r_i - \rho_i)\, K_{ij}\,(r_j - \rho_j) + N_5\,(z_5 - \bar{z}_5)^2 + N_6\,(z_6 - \bar{z}_6)^2$$

where the z_i is Fisher's z transformation of a sample twin correlation with sample size N_i and $\bar{z}_i$ is the z-transformation of the corresponding predicted correlation:

$$z_i = \tfrac{1}{2}\,\ell n\,\frac{1 + r_i}{1 - r_i} \text{ and } \bar{z}_i = \tfrac{1}{2}\,\ell n\,\frac{1 + \rho_i}{1 - \rho_i}$$

where i = 5 for MZ and i = 6 for DZ. In this case, the df for the residual χ^2 is taken as 6-w.

RESULTS

Maximum likelihood estimates of the sample correlations for both family series are shown in Tables 3 and 4. The estimated sample sizes are also shown, which correspond to the effective number of independent pairs of observations. Spouse correlations ranged from −0.31 to 0.24. These correlations were in general not significantly non-zero owing to the relatively small number of spouse pairs for each variable. Father-child and mother-child correlations differed for some variables, but were generally of the same magnitude. Only for R I4 (max) in FS-I was there significant heterogeneity (χ^2_1 = 4.72) where the

TABLE 4. Summary correlations for family series II

Variable	r_1	N_1	r_2	N_2	r_3	N_3	r_4	N_4
R I3 (max)	−0.287	18	0.272	47	0.043	46	0.318	62
R I3 (abs)	−0.310	31	0.190	40	0.006	54	0.275	64
R I4 (max)	0.027	29	−0.224	43	0.134	64	0.034	87
R I4 (abs)	0.134	20	0.016	26	0.081	52	−0.020	77
L H (max)	—	—	—	—	—	—	—	—
L H (abs)	—	—	—	—	—	—	—	—
L I4 (max)	−0.007	22	−0.140	77	0.205	67	0.316	56
L I4 (abs)	−0.053	37	−0.105	99	0.174	75	0.173	71
TPPRC (max)	−0.168	73	0.105	101	0.233	108	0.370	120
TPPRC (abs)	−0.242	72	0.084	101	0.172	110	0.379	107
DPPRC (max)	0.215	72	0.146	116	0.258	105	0.363	130
DPPRC (abs)	0.142	70	0.110	123	0.212	104	0.333	133

TABLE 5. Best fit solutions to the path model

	Family series I with twins				Family series II			
Variable	χ^2	df	$h^2 \pm$ SE	$c_{TW} \pm$ SE	χ^2	df	$h^2 \pm$ SE	$u^2 \pm$ SE
R I3 (max)	7.37	5	0.53 ± .09	0	2.98	3	0.49 ± .14	0
R I3 (abs)	4.01	5	0.51 ± .09	0	4.81	3	0.38 ± .14	0
R I4 (max)	4.80	4*	0.61 ± .10	0	6.15	4	0	0
R I4 (abs)	12.12	5	0.49 ± .09	0	0.73	4	0	0
L H (max)	2.77	5	0.46 ± .16	0	—	—	—	—
L H (abs)	1.85	5	0.40 ± .14	0	—	—	—	—
L I4 (max)	3.86	5	0.49 ± .08	0	0.07	2	0	0.32 ± .12
L I4 (abs)	7.87	5	0.28 ± .08	0	4.70	3	0	0
TPPRC (max)	2.40	4	0.52 ± .07	0.23 ± .11	6.02	3	0.52 ± .10	0
TPPRC (abs)	2.19	4	0.45 ± .07	0.24 ± .11	4.91	2	0.35 ± .11	0.21 ± .10
DPPRC (max)	5.68	5	0.66 ± .06	0	5.01	2	0.31 ± .13	0.19 ± .09
DPPRC (abs)	2.22	4	0.55 ± .07	0.27 ± .12	2.37	2	0.27 ± .13	0.19 ± .09

*Pooled parent-child correlation.

father-child correlation exceeded that of the mother-child. These were pooled into a parent-child correlation to avoid inflating the residual χ^2, since a biological explanation for this observation was not apparent.

Twin correlations with respective sample sizes are also shown (Table 3), with DZ correlations exceeding MZ correlations in some cases. This was likely to be an artifact since the standard errors of these estimates were quite large, indicating that the estimates were subject to substantial sampling variation.

Table 5 shows the fitted path models. The proportion of variability attributable to polygenes was moderate, ranging from 0.28 to 0.66. Uterine environmental effect (u) was not significant for any variable in FS-I, in contrast to FS-II. Additional intrauterine effect for twins was detected for the total phenotypes, i.e., total palmar and total distal ridge counts.

The variable R I4 (abs) showed a significantly poor fit of the path model for the FS-I data. Inspection of the correlations indicated that the reason for this was a significantly lower sib-sib correlation than parent-child. Under a polygenic model, the sibling correlation is expected to be at least as great as the parent-child correlation. Whatever other factors may be operating, there was evidence for polygenic family resemblance.

Estimates of the heritability for FS-II were in some cases strikingly different from FS-I. In FS-II, there was no evidence of polygenic heritability for R I4 (max and abs) and L I4 (max and abs), and estimates of h^2 were significantly lower for the DPPRC (max and abs). Uterine environmental effects were evident for the total phenotypes, except for the TRRPC (max) where u was only significant at the 7% level.

DISCUSSION

As ridge counts represent "pure" biological traits that are virtually unaltered by complex forms of postnatal environmental influences, they represent relatively simple traits for genetic analysis by current statistical methods. A method of scoring ridge count

phenotypes in palmar configurational areas has been recently developed which allows quantitation of the size of true patterns. The proposed method provides a rational approach for counting ridges in true patterns, but not for open field patterns without triradii. The standard practice is to assign a ridge count of zero for those configurational areas that are not circumscribed by triradii. This poses a serious statistical problem as well as a confounding of the phenotype. There are actually two phenotypes to be considered: the presence or absence of a pattern, and the number of ridges. Clearly, open field patterns are defined by ridges even though there is no standard accepted method of counting them. For these reasons, the zero values were excluded from the present analysis as unmeasurable. There may well be a factor determining the presence or absence of a pattern, but the results presented here refer to the multifactorial basis of palmar pattern ridge count variables circumscribed by triradii.

Estimation of path coefficients in a model incorporating both polygenes and intrauterine effects gave evidence that palmar ridge count phenotypes are moderately heritable for the most part. In general, the proportion of heritable variation was smaller in FS-II for all variables studied; the same population evidenced more instances of significant intrauterine environmental effects.

The notable exception was found for interdigital area IV on both the right and left palms in FS-II. The estimated proportion of genetic variability for these phenotypes was zero, in contrast to substantial heritability estimates in FS-I. It is difficult to conceive that polygenic variability exists in one population, but not in the other. This may occur in extreme cases of phenotypic assortative mating, and it is possible that mates directly assort on the basis of other traits that are associated with dermatoglyphic traits, but this seems an unlikely explanation. The familial correlations estimated from the FS-II data indicate that at least for the left interdigital IV area, mother-child and sib correlations were substantial while fathers' ridge counts were negatively correlated with those of their offspring. It is interesting to note that in all of the parent-child correlations for the interdigital IV area in FS-I, the father-child exceeded the mother-child correlation, the difference being significant in one instance. In addition, the parent-child correlation exceeded the sibling correlation for R I4 (abs) in FS-I. The reconciliation of these observations with a simple biological hypothesis is not obvious. The results suggest that there may be other mechanisms or interactions operating in the developmental sequence for the interdigitial IV palmar area.

It is not possible to determine from these analyses whether there are separate elements of genetic control for individual configurational areas versus a series of genes directing the development of ridges on the palm as a whole. However, with the possible exception of the interdigital IV area discussed above, there was no evidence of significant intrapopulation differences in the degree of genetic control among the variables studied. For both the TPPRC and the DPPRC, significant intrauterine environmental effects were found, although in FS-I, such effects were only pronounced for the simultaneous sharing of the uterine environment as occurs for twins. There was no evidence to support the notion that distal areas are under relatively greater degrees of genetic control than the palm as a whole (Loesch, 1974), at least as far as ridge count phenotypes are concerned.

Parent-child correlations exceeding sib correlations was observed for several variables. This observation is incompatible with the expected correlations under a polygenic mode of inheritance, and this became apparent in the misfit of R I4 (abs) in FS-I. This phenomenon has been reported before (Bener, 1981), although neither that author nor we can offer any explanation. This may well be a consistent effect deserving further investigation.

Albeit that dermatoglyphic traits are amenable to genetic analysis in principle, one of the problems in this area appears to be the definition of ridge count phenotypes for open field patterns not circumscribed by triradii. Then genetic analyses will neither have to be conditional on the presence of triradii, nor biased by the arbitrary practice of assigning a ridge count of zero for open field patterns.

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LITERATURE CITED

Bener A (1981) Can parent-child correlation exceed sib-sib correlation? Results from dermatoglyphic data. Dermatoglyph. 9:8–11.

Cummins, H (1929) The topographic history of the volar pads (Walking pads; Tastballen) in the human embryo. Contrib. to Embryol. Carnegie Institute of Washington *20*:103–126.

Cummins, H, and Midlo, C (1943) Finger Prints, Palms and Soles. Research Publishing Co., Inc., 1976 Ed. South Berlin, Mass.

Fang, TC (1950) The inheritance of a-b ridge-count on the human palms, with a note on its relation to mongolism. Ph.D. thesis, University of London.

Fang, C, and Krishnaiah, PR (1982) Asymptotic joint distributions of functions of the elements of sample covariance matrix. In G Kallianpur, PR Krishnaiah, JK Ghosh (eds): Statistics and Probability: Essays in Honor of C.R. Rao. New York: North Holland Publishing Company.

Glanville, EV (1965) Heredity and Line A of palmar dermatoglyphics. Am. J. Hum. Genet. *17*:420–424.

Kamali, MS, Malhotra, KC, and Chakraborty, R (1985) Palmar pattern ridge count differentiation in 12 Iranian populations (Manuscript).

Loesch D (1974) Genetical studies of sole and palmar dermatoglyphics. Ann. Hum. Genet. *37*:405–419.

Loesch D (1983) Quantitative Dermatoglyphics: Classification, Genetics and Pathology. Oxford: Oxford University Press.

Malhotra, KC, Chakraborty, R, and Karmakar, B (1985a) Palmar pattern ridge count variation among the 20 Dhangar casts of Maharahtra. (Manuscript).

Malhotra, KC, Karmakar, B, and Chopora,VP (1985b) Palmar pattern ridge count differentiation in 19 populations from Western India. In MG Abdushelishvilli and KC Malhotra (eds): Biology of Man in Western India. Moscow: Academy of Sciences of USSR, (in press).

Malhotra, KC, Karmakar, B, and Vijayakumar, M (1981b) Genetics of palmar pattern ridge counts. Technical Report No. Anthrop. *1/81*. Calcutta: Indian Statistical Institute.

Malhotra, KC, Karmakar, B, and Vijayakumar, M (1982) Progress in the genetics of palmar ridge counts in man. In CS Bartsocas (ed): Progress in Dermatoglyphic Research. Alan R. Liss, Inc., N.Y. pp. 111–128.

Malhotra, KC, and Rao, DC (1982) Path analysis of total palmar pattern ridge counts. Am. J. Phys. Anthrop. *58*:187–189.

Malhotra, KC, Vijayakumar, M, and Karmakar, B (1981a) Methodology for counting ridges of true patterns in human plantar configurational areas. Technical Report No. Anthrop. *12/81*. Calcutta: Indian Statistical Institute.

Mulvihill, JJ, and Smith, DW (1969) The genesis of dermatoglyphics. J. Pediatr. *75*:579–589.

Pateria, HN (1974) Genetic basis of a-b, b-c and c-d ridge-counts on human palms. Am. J. Phys. Anthrop. *40*:171–172.

Penrose, LS (1954) The distal triradius t on the hands of parents and sibs of mongol imbeciles. Ann. Hum. Genet. *19*:10–27.

Pons, J (1954) Herencia de las lineas principales de la palma. Contribución a la genética de los caracteres dermopapilares. Barcelona: Trab. Inst. "Bernardino de Sahgún" de Antropologia y Etnologia del CSIC *14*:35–50.

Pons, J (1964) Genetics of the a-b ridge-count on the human palm. Ann. Hum. Genet. Lond. *27*:273–277.

Poosha, DVR, Satyanarayana, M, Mathew, S, and Rao, CS (1982) Genetics of palmar total interdigital ridge counts. South Asian Anthrop. *3*:13–15.

Rao, DC (1985) Application of path analysis in human genetics. In PR Krishnaiah (ed): Multivariate Analysis-VI. New York: North-Holland Publishing Co.

Rao, DC, McGue, M, Wette, R and Glueck, CJ (1984a) Path analysis in genetic epidemiology. In A Chakravarti (ed): Human Population Genetics: The Pittsburgh Symposium. Stroudsburg, PA: Hutchinson Ross Publishing Company.

Rao, DC, Morton, NE, and Cloninger, CR (1979) Path analysis under generalized assortative mating. I. Theory. Genetical Research *33*:175–188.

Rao, DC, Province, MA, Wette, R, and Glueck, CJ (1984b) The Role of Path Analysis in Coronary Heart Disease Research. In DC Rao, RC Elston, et al. (eds): Genetic Epidemiology of Coronary Heart Disease: Past, Present, and Future. New York: Alan R. Liss, Inc.

Rogucka, EZ, Szczotkowa, Z, and Szczotka, H (1971) The differentiation and inheritance of the number of dermal ridges in palmar interdigital spaces. Mat. Prace Anthrop. *81*:159–174.

Sciulli, PW, and Rao, DC (1975) Path analysis of palmar ridge counts. Am. J. Phys. Anthrop. *43*:291–294.

Tiwari, SC (1965) Genetical analysis of the a-b ridge counts. The Anthropologist *12*:25–28.