

The Genetic Structure of a Tribal Population, the Yanomama Indians. VIII. Dermatoglyphic Differences among Villages

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As described in the first paper in this series [1], we are engaged in a multidisciplinary attempt to develop a comprehensive treatment of the genetic structure of the relatively unacculturated Yanomama Indians of southern Venezuela and the Roraima Territory of northern Brazil. Particular attention has been directed toward the collection of data on "groups" of biological characteristics of relatively high heritability. One objective of collecting such data has been to determine how well the magnitude of village differences with respect to one group of characteristics corresponds with those manifest when another group of characteristics is taken as reference point. Additional criteria of intratribal differentiation are supplied by ethnohistory and linguistic subdivisions within the tribe. The three groups of characteristics employed to date are a collection of some 20 genetic markers [2-4], 12 different anthropometric measurements [5], and dermatoglyphics. It is the latter which are the subject of this paper. In the present communication we shall describe the dermatoglyphic patterns of the Yanomama and compare them with those of the relatively few other Indian tribes of South America for whom adequate data are available. A subsequent paper will address itself to the congruence between the views of intratribal differentiation presented by the genetic markers, anthropometrics, dermatoglyphics, and geographic distribution.

MATERIALS AND METHODS

Sampling

Because of inadequate communication and a certain overenthusiastic attitude on the part of our subjects, satisfactory dermatoglyphics were difficult to obtain. Although

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some prints were collected in 12 different villages, for a total of 490 prints, only 246 prints could be scored for all 15 traits, and for only seven villages were data on 17 or more subjects with bilaterally satisfactory finger and palm prints available. Although a sample size of 17 is admittedly small, the aforementioned technical problems plus the fact that some Indian villages only contain 50-60 persons place severe limits on sample size. Since the subject of village microdifferentiation among the Yanomama is of especial interest, we will in this and the following papers, with all due caution, accept a sample as small as 17 as characterizing a village, recognizing (see below) the large sampling error that may be entailed. It should be mentioned that if as many as 10 loci are involved in the genetic control of the traits being scored, then, especially when multivariate means are involved, the actual number of genes sampled is of course very significantly more than twice the head count. The locations of these villages are shown in Ward [6]. The prints were obtained from the older children and adults of a village, many of whom are related to one another, some closely. The number of independent genomes is thus less than the head count. Lack of genealogical depth prevents a direct estimation of the mean coefficient of kinship between *randomly* selected couples (equivalent to coefficient of inbreeding in potential offspring), but on the basis of a computer simulation of four Indian villages, it is estimated to be not less than .0176 [7].

Technical Procedures

Finger and palmar prints were obtained utilizing the Faurot inkless method and then analyzed with reference to finger and palm pattern frequencies, abortive or absent C mainlines, total ridge count, a-b ridge count, mainline indices, and atd angles. Finger patterns were classified as arches, radial loops, ulnar loops, and whorls. The finger patterns were classified as described by Cummins and Midlo [8] and palmar patterns as suggested by Penrose and Loesch [9]. The latter classification system appears to provide an improved distinction between true patterns and other types of ridge arrangements and so to be preferable to the traditional methods described by Cummins and Midlo [8]. Furthermore, as noted by Loesch [10], the number of possible combinations of patterns present on a palm is substantially reduced, thus facilitating somewhat the study of the mode of inheritance of these features. Palmar traits which were absent (i.e., II and H_r) or exhibited very low frequencies (i.e., III, IV, and IV u) in all villages were not tabulated, nor were palmar triradii, because of their strong correlation with the various loop types. In the computation of the total ridge count, when two or more triradii from which a count could be made were present on a finger, the triradius yielding the larger count was utilized. The a-b count was defined as the sum of ridges lying between triradii a and b on both palms. The mean mainline index was calculated as suggested by Cummins and Midlo [8], and the mean atd angle computed using for each hand the most peripheral triradii a and d and the most distal triradius t.

In an effort to assess the magnitude of the "observer factor" in pattern classification and of measurement error for quantitative traits, two independently trained observers analyzed the same set of 20 prints for all categorical and quantitative characters considered in this study. Comparison of the results revealed that there was concordance in classifying finger patterns in 97% of the readings. The agreement in considering various palmar loop types present or absent was 100% for I, H, and II loops, 95% for III, and 90% for IV loops. Mainline A was assigned the same termination zone in 45% and mainline D in 75% of the readings. The high percentage of discrepancy in mainline A termination-zone assignment is mostly due to the fact that zones 2, 3, and 4 have somewhat ambiguously defined limits. It should be noted that in other interobserver variation tests [11], mainline A zone demarcation differences also constituted an important source of disagreement. There was a 100% concordance in considering mainline C either abortive or missing. The average discrepancy in counting ridges was 9.9 ridges per individual

for total ridge count and 1.7 ridges per individual for the a-b count of the palm. An average discrepancy of 0.60° per individual was detected for atd angle and 0.25 units for the mainline index, despite the low percentage of concordance for mainline A termination-zone assignment. The differences between the two observers in the quantitative traits were random rather than systematic.

Statistical Considerations

It has proved difficult to apply conventional statistical methods to the analysis of among-village dermatoglyphic variation. Not only (as we shall again demonstrate) are the patterns displayed by the various fingers intercorrelated, but the patterns of the fingers are correlated with some of the palmar traits, which are in turn partially intercorrelated. In theory, some of these problems can be met utilizing multivariate statistical techniques, such as Mahalanobis's generalized distance (D^2), which take the intercorrelation of traits into account, and we shall in a subsequent paper use D^2 as the best measure available. We note, however, that in this special case we are confronted with a mixture of qualitative and quantitative traits whose joint treatment imposes difficulties which cannot be circumvented by traditional techniques. Finally, there are the statistical complications presented by an Indian population such as this, deriving from the fact that the subjects in any one village are often biologically related and tend to present themselves in family units, and such a high proportion of the entire village is studied that the "sampling" approaches an enumerative procedure. The problems mentioned, coupled with the scantiness of comparable Amerindian dermatoglyphic data, motivated us to restrict the statistical analysis in this presentation to just one trait, total ridge count, considering the intratribal variability of the Yanomama, the intertribal variability of South American tribes (including the Yanomama), and a comparison of the magnitudes of the intra- and intertribal variation. In both of the intra- and intertribal comparisons we were not interested in the particular set of Indian villages or tribes so far studied, but rather in South American Indians in general, from which these villages and tribes can be considered a sample. Application of analysis-of-variance techniques to a linear model of "random effects" seemed therefore to be indicated. Sex is another source of total ridge-count variation. If this factor is incorporated into the analysis, we would be confronted by an unbalanced mixed layout: unbalanced, because village and tribal sample numbers are unequal, and mixed, because sex is undoubtedly a fixed factor. Unfortunately there is no simple solution for the problem of hypothesis testing in this case. Accordingly, we shall test sexes separately with respect to differences among tribal and village means.

By means of a modification of formulations described in Sokal and Rohlf [12], the intratribal variance estimate for the Yanomama was obtained as follows: Let Y_{ij} be the j th observation from the i th village. We shall use the random effect model given by

$$y_{ij} = \mu + a_i + e_{ij}, \quad i = 1, 2, \dots, r \text{ and } j = 1, 2, \dots, n_i,$$

where a_i is the deviation of the (true) i th village mean from the tribal mean μ , e_{ij} the deviation of the j th observation from the i th village mean, r the number of villages, and n_i the number of observations in the i th village. The quantities a_i and e_{ij} are assumed to be stochastically independent and to have zero means. We designate $\text{var}(a_i) = \sigma_v^2$ and $\text{var}(e_{ij}) = \sigma_e^2$. The value σ_v^2 represents the variance among villages and σ_e^2 the variance within villages.

We consider the two sums of squares

$$SS_v = \sum_{i=1}^r n_i (\bar{y}_i - \bar{y})^2; \quad SS_e = \sum_{i,j} (y_{ij} - \bar{y}_i)^2,$$

where

$$\bar{y}_i = \sum_j y_{ij}/n_i; \bar{y} = \sum_{i,j} y_{ij}/n; n = \sum_i n_i.$$

Their expectations will be

$$E(ss_v) = (n - n^{-1} \sum_i n_i^2) \sigma_v^2 + (r - 1) \sigma_e^2$$

$$E(ss_e) = (n - r) \sigma_e^2.$$

Thus we may use

$$\hat{\sigma}_v^2 = [ss_v - (r - 1)(n - r)^{-1} ss_e] / [n - n^{-1} \sum_i n_i^2]$$

as an unbiased estimator for σ_v^2 (and as usual $ss_e/(n - r)$ as an estimator for σ_e^2).

On the assumption of a normal distribution, the variances of ss_v and ss_e may be found from the lemma given in Scheffé [13]. Since ss_v and ss_e are independent estimates, the variance of the estimator is then obtained as $\text{var}(\hat{\sigma}_v^2) = [2(N_2 - 2N_3N_1^{-1} + N_1^{-2}N_2^2)\sigma_v^4 + 4(N_1 - N_1^{-1}N_2)\sigma_v^2\sigma_e^2 + 2(r - 1)(N_1 - 1)(N_1 - r)^{-1}\sigma_e^4] / (N_1 - N_1^{-1}N_2)^2$, where

$$N_m = \sum_{i=1}^r n_i^m; \quad m = 1, 2, 3.$$

In order to obtain an estimate σ_e^2 for the variability within tribes and an estimate σ_i^2 for the variability among tribes, with its variance $\text{var}(\sigma_i^2)$, the same procedure is followed after redefining y_{ij} as the j th observation from the i th tribe, a_i as the deviations of the tribal mean from a South American Indian mean, and e_{ij} as the deviation of the j th observation from the i th tribal mean, respectively.

RESULTS

Yanomama Dermatoglyphic Characteristics

Inspection of table 1, concerned with the relative frequency of finger patterns by village and sex, reveals considerable variation among Yanomama villages and to a lesser degree between sexes. The "miscellaneous" group should not enter into village comparisons because of its mixed origins, but will be utilized in the intertribal comparisons. Villages 03A and 03D show the highest and lowest frequency of whorls, respectively, the other villages showing intermediate values. The sex differences, although somewhat greater than usually observed, are in agreement with the trends in other major ethnic groups; males have in general more whorls and fewer arches. Palmar loop frequencies, shown in table 2, are even more variable. Particularly, I and Ir patterns are very common in village 03A but absent in villages 03KP, 03LMN, and 03RS. Interdigital IV patterns are common in all villages, exhibiting the highest relative frequencies in villages 03D and 03RS. The other palmar patterns and abortive or absent C mainline frequencies do not display consistent patterns of variation in both sexes.

The dermatoglyphic variability among villages revealed by the categorical traits is also reflected in the quantitative traits as shown in table 3. Villages in which the relative frequency of whorls is low also are in general characterized by lower mean total ridge counts, as expected. With a statistical test which assumes genetic

TABLE 1
RELATIVE FREQUENCIES OF FINGER PATTERNS BY SEX AND VILLAGE IN YANOMAMA INDIANS

VILLAGES	MALES					FEMALES				
	N	Arches	Radial Loops	Ulnar Loops	Whorls	N	Arches	Radial Loops	Ulnar Loops	Whorls
Village 03A	14	7.8	3.6	52.1	36.4	23	14.8	1.7	46.5	36.9
Village 03D	21	15.2	6.7	68.1	10.0	15	16.0	8.0	61.3	14.7
Village 03KP	25	4.4	6.8	64.8	24.0	17	10.6	3.5	69.4	16.5
Village 03LMN	16	6.2	9.4	50.0	34.4	15	19.3	3.3	58.0	19.3
Village 03RS	8	7.5	6.2	58.7	27.5	9	33.3	0.0	51.1	15.5
Village 03T	8	20.0	2.5	52.5	25.0	13	13.8	3.1	53.1	30.0
Village 11ABC	13	6.9	6.1	50.0	36.9	11	24.5	6.4	48.2	20.9
Miscellaneous*	14	11.4	7.1	61.4	20.0	24	19.2	4.2	56.2	20.4
Total	119	9.3	6.4	58.6	25.6	127	17.8	3.8	55.7	22.7

* Includes individuals from villages 03B, 03C, 03Q and 08U.

TABLE 2

RELATIVE FREQUENCIES OF PALMAR LOOPS BY SEX AND VILLAGE IN YANOMAMA INDIANS

MALES								
VILLAGES	N	I	Ir	H	\hat{H}	III	IV	Main Line C Absent
Village 03A	14	39.3	39.3	10.7	21.4	7.1	67.8	25.0
Village 03D	21	7.1	9.5	2.4	0.0	2.4	85.7	14.3
Village 03KP	25	0.0	0.0	2.0	28.0	20.0	56.0	24.0
Village 03LMN	16	0.0	0.0	3.1	15.6	9.4	75.0	21.9
Village 03RS	8	0.0	0.0	0.0	0.0	6.2	75.0	18.7
Village 03T	8	0.0	0.0	12.5	12.5	25.0	62.5	12.5
Village 11ABC	13	3.6	3.6	0.0	0.0	19.2	42.3	42.3
Miscellaneous*	14	21.4	28.6	7.1	10.7	32.1	67.8	10.7
Total	119	8.7	10.0	4.2	12.5	14.7	66.8	21.4
FEMALES								
VILLAGES	N	I	Ir	H	\hat{H}	III	IV	Main Line C Absent
Village 03A	23	34.8	30.4	4.3	4.3	28.3	43.5	34.8
Village 03D	15	30.0	23.3	6.7	6.7	13.3	76.7	10.0
Village 03KP	17	0.0	0.0	0.0	26.5	5.9	73.5	29.4
Village 03LMN	15	0.0	0.0	0.0	26.7	23.3	43.3	33.3
Village 03RS	9	0.0	0.0	0.0	5.5	11.1	77.8	11.1
Village 03T	13	7.7	7.7	0.0	0.0	26.9	57.7	23.1
Village 11ABC	11	4.5	9.1	0.0	9.1	22.7	54.5	22.7
Miscellaneous*	24	27.1	20.8	4.2	8.3	8.3	79.2	14.6
Total	127	16.1	13.8	2.4	11.0	17.3	63.0	23.2

* Includes individuals from villages 03B, 03C, 03Q and 08U.

independence of the individuals sampled, Yanomama village total ridge-count means were found to differ significantly for males but not females (table 4). Employing the random-effects model described earlier, the among-village variability was estimated for males as $\sigma^2_{vm} = 588.78$ and for females as $\sigma^2_{vf} = 115.60$. The variances of these estimates were calculated for males and females as $\text{var}(\sigma^2_{vm}) = 207,600$ and $\text{var}(\sigma^2_{vf}) = 32,220$, respectively. Village 03D shows the highest a-b ridge count and village 11ABC the highest atd angle and mainline-index means. Males have consistently higher mean total ridge counts and lower mean atd angles. Sex differences in total ridge count and atd angle mean are in agreement with the findings in other Amerindian tribes [11]. The a-b ridge count and mainline-index means do not show consistent sex differences.

In the next paper in this series [14] we shall compare Mahalanobis's inter-village dermatoglyphic distances with intervillage distances based on genetic markers and on anthropometric measurements. In comparing these distance matrices it is important to have some appreciation of the developmental indetermi-

TABLE 3
VILLAGE MEANS AND STANDARD DEVIATIONS BY SEX OF QUANTITATIVE DERMATOGLYPHIC TRAITS

VILLAGES	MALE					FEMALE				
	N	Total Ridge Count	a-b Ridge Count	atd Angle	Main Line Index	N	Total Ridge Count	a-b Ridge Count	atd Angle	Main Line Index
Village 03A	14	121.43 ± 51.39	74.07 ± 8.21	89.64 ± 16.17	6.64 ± 1.98	23	110.96 ± 48.07	78.69 ± 7.36	98.91 ± 15.69	6.93 ± 1.80
Village 03D	21	77.38 ± 31.14	85.05 ± 10.84	89.28 ± 13.35	6.19 ± 1.78	15	74.87 ± 34.35	83.73 ± 11.04	93.67 ± 9.37	5.63 ± 1.97
Village 03KP	25	125.36 ± 49.48	78.16 ± 9.40	88.84 ± 12.62	7.60 ± 1.73	17	100.12 ± 51.33	76.23 ± 9.21	88.65 ± 6.01	7.35 ± 1.58
Village 03LMW	16	157.87 ± 55.82	82.62 ± 7.00	85.25 ± 7.87	7.09 ± 1.25	15	107.02 ± 58.75	78.67 ± 8.82	91.13 ± 11.21	7.73 ± 1.76
Village 03RS	8	130.37 ± 63.69	82.50 ± 10.82	85.62 ± 9.33	6.62 ± 0.99	9	68.11 ± 67.08	82.78 ± 9.79	84.22 ± 9.52	6.55 ± 1.83
Village 03T	8	102.37 ± 66.34	83.87 ± 9.26	83.87 ± 11.88	7.25 ± 1.22	13	112.54 ± 56.40	82.62 ± 9.89	92.85 ± 9.56	6.35 ± 1.72
Village 11ABC	13	130.54 ± 46.37	74.92 ± 12.60	93.46 ± 8.84	7.96 ± 1.23	11	82.09 ± 57.50	71.54 ± 8.29	98.18 ± 11.44	8.09 ± 2.22
Miscellaneous*	14	114.78 ± 49.47	76.71 ± 13.03	95.78 ± 15.16	7.39 ± 1.65	24	88.17 ± 45.58	78.25 ± 7.18	93.25 ± 9.15	5.73 ± 1.68
Total	119	118.91 ± 53.91	79.65 ± 10.69	89.30 ± 12.58	7.10 ± 1.65	127	95.12 ± 52.02	79.46 ± 8.88	93.20 ± 11.34	6.72 ± 1.94

* Includes individuals from villages 03B, 03C, 03Q and 08U.

TABLE 4
ANALYSIS-OF-VARIANCE LAYOUT FOR TESTING DIFFERENCES BETWEEN (a) YANOMAMA VILLAGES AND (b) SOUTH AMERICAN INDIANS TOTAL RIDGE-COUNT MEANS

SOURCE OF VARIATION	MALES				FEMALES			
	SS	df	MS	F	SS	df	MS	F
a) Among villages	66,597.07	6	11,099.51	4.45*	26,633.65	6	4,438.94	1.61
Within villages	244,226.69	98	2,492.11	...	265,064.87	96	2,761.08	...
Total	310,823.76	104	291,698.52	102
b) Among tribes	148,639.52	8	18,579.94	6.58*	331,611.44	8	41,451.43	13.56*
Within tribes	1,855,732.77	657	2,824.55	...	1,926,369.33	630	3,057.73	...
Total	2,004,372.29	665	2,257,980.77	638

* $P < .001$.

nacy of the traits. In the case of the dermatoglyphics, a measure of this indeterminacy is provided by the degree of departure from a perfect correlation between the right and left hands. Product-moment correlation coefficients between the number of triradii on different fingers and ridge counts on different fingers have been calculated and are given in table 5 (lower and upper triangular matrices, respectively). In table 6 we present the correlation coefficients between presence or absence on right and left palms of the various loop types, C mainlines, and the right-left correlations of the four quantitative traits studied (i.e., total ridge count, a-b ridge count, atd angle, and mainline index). In addition, familial correlation

TABLE 5

CORRELATION COEFFICIENTS FOR PAIRED FINGERS BETWEEN NUMBER OF TRIRADII (LOWER TRIANGULAR MATRIX) AND RIDGE COUNT (UPPER TRIANGULAR MATRIX)

	LV	LIV	LIII	LII	LI	RV	RIV	RIII	RII	RI
LV69	.59	.57	.52	.84	.66	.56	.54	.51
LIV	.4665	.65	.53	.70	.81	.64	.63	.54
LIII	.42	.4860	.48	.54	.62	.74	.66	.45
LII	.31	.45	.4550	.60	.64	.61	.74	.48
LI	.39	.33	.32	.3354	.53	.50	.48	.75
RV	.66	.42	.37	.32	.3969	.58	.55	.53
RIV	.36	.60	.53	.45	.29	.3862	.63	.52
RIII	.40	.45	.55	.39	.32	.39	.4364	.46
RII	.42	.54	.53	.63	.39	.36	.48	.5048
RI	.36	.33	.35	.37	.63	.34	.35	.35	.38	...

NOTE.—For triradii, $N = 208$; for ridge count, $N = 329$.

TABLE 6

RIGHT-LEFT CORRELATION COEFFICIENTS FOR 11 DERMATOGLYPHIC TRAITS IN THE YANOMAMA, WITH FAMILIAL CORRELATIONS AND HERITABILITY ESTIMATES FROM CAUCASIAN POPULATIONS

TRAIT	YANOMAMA RIGHT-LEFT CORRELATION	OTHER STUDIES			References
		Parent-Child Correlation	Sib-Sib Correlation	h^2	
I	.46	.14	.16	0.36	[10]
Ir	.52				
H	.32	.19	.17	0.30	[10]
Ĥ	.65	.27	.33	0.78	[10]
III	.24	.27	.25	0.46	[10]
IV	.48	.13	.18	0.46	[10]
Total ridge count	.94	.48	.50	1.04*	[15]
a-b ridge count	.69	.24	.26	0.56*	[15]
atd angle	.81	.29	.37	0.90*	[16]
Main line index	.67	.52	.48	0.88*	[17]
Main line C absent	.40

* These h^2 values were computed according to the expression $h^2 = 4r_{ps} - 2r_{pc}$ [18] from the parent-child and sib-sib correlations given by the authors.

and heritability estimates for these traits as calculated by different authors are given. Inspection of these coefficients reveals that for individual fingers (table 5), the correlation between homologous fingers for number of triradii averages .61 and for ridge count, .78, with smaller correlations between nonhomologous fingers, the correlations tending to decrease as distance between the fingers increases. These findings are in general agreement with those of Holt [15] in Englishmen, of Mavalwala [19] in Indian Parsis, and of Loesch [10] in Poles.

Since the genetic constitution of all fingers is presumably the same, it is apparent that unknown factors play a large role in the determination of individual finger patterns. However, for total ridge count the correlation between the two hands is .94 (table 6). Similar high correlations have been observed by others [15]. Relatively high right-left correlations were also observed for a-b ridge count, atd angle, mainline index, and \hat{H} palmar loops. Table 6 reveals that the characters with high right-left correlation coefficients in this study are in general those which in other studies have yielded the highest heritability estimates. Somewhat arbitrarily, on the basis of these correlations and the heritability indices, we have elected to use the following traits in the construction of the dermatoglyphic distances to be derived in a later paper: ulnar loops, whorls, \hat{H} loops, total ridge count, a-b ridge count, atd angle, mainline index, absence of C mainline, and a combination of palmar loops (i.e., I, Ir, III, and H).

Dermatoglyphic Variation among South American Indian Tribes

There are some 25 studies of the dermatoglyphics of South American Indians in the literature. These studies unfortunately suffer from various weaknesses which diminish their usefulness for definitive comparisons: for example, small sample size, inadequate tabulation of the results, and incomplete analysis of the data. Thus, for only six tribes are there palmar pattern frequencies, and for only four tribes are palmar quantitative traits available. A comparison at this time is perforce restricted to digital patterns and total ridge count. We selected for comparison those samples meeting the following criteria: (1) sample size greater than 20 and (2) both sexes analyzed and tabulated separately. This reduces the number of tribes available for comparisons of finger patterns and total ridge count to 11. The findings in these samples are given in table 7.

Comparison of tables 1 and 7 demonstrates that the Yanomama have conspicuously high arch and low whorl frequencies. It is noteworthy that the samples drawn from Indian populations belonging to the Gê-Pano-Carib linguistic family [29] (Caingang, Trio, Xavante, and Xikrin [Cayapo]) exhibit higher whorl frequencies than most of the samples from the tribes belonging to the Andean equatorial family (Aymará, Cashinahua, Jivaro, Mapuche, and Pwenche), and these groups, in turn, exhibit more whorls than the Yanomama. The relatively low total ridge-count means presented by the Yanomama when compared with other series reflect their low number of whorls. The analysis-of-variance of intertribal differences for male and female total ridge-count means for the Yanomama and the various South American Indian tribes listed in table 7 was of course restricted

TABLE 7
RELATIVE FREQUENCIES OF FINGER PATTERNS AND TOTAL RIDGE COUNTS IN VARIOUS SOUTH AMERICAN INDIANS

TRIBES	MALES					FEMALES					REFERENCES	
	N	Arches	Loops	Whorls	Total Ridge Count	N	Arches	Loops	Whorls	Total Ridge Count		
1. Aymará:												
Chapiquiña	59	3.0	54.1	42.9	122.7 ± 46.05	57	7.7	56.8	35.4	111.3 ± 69.51	*	
Belen	20	5.5	55.5	39.0	125.9 ± 56.61	31	4.2	61.9	33.9	113.4 ± 47.48	*	
Socoroma	29	1.0	65.9	33.1	125.7 ± 42.75	41	7.1	64.6	28.3	103.0 ± 57.06	*	
2. Caingang:												
Rio Das Cobras ...	37	0.5	35.1	64.3	171.0 ± 41.48	26	0.4	38.1	61.5	176.5 ± 35.54	[20]	
Ivai	27	1.5	25.3	73.1		20	3.3	27.8	68.8		[11]	
3. Cashinahua	54	7.5	74.5	18.0	107.8 ± 41.10	60	12.0	77.4	10.7	70.9 ± 35.40	[21]	
4. Guaraní:												
Rio Das Cobras ...	21	2.9	68.1	29.0	112.7 ± 44.62	24	2.1	67.5	30.4	116.6 ± 48.70	[20]	
5. Jívarof	183	6.1	50.6	43.3	136.8 ± 55.63	144	8.1	53.6	38.2	136.5 ± 58.32	[11, 22]	
6. Mapuche†	88	5.7	56.2	38.1	137.1 ± 63.57	40	9.2	62.3	28.5	108.6 ± 53.14	[23]	
7. Pewenche:												
Pedregoso	77	10.5	63.7	25.9	111.6 ± 60.63	79	16.6	57.5	25.9	95.6 ± 67.73	[24]	
8. Suruis	20	2.0	42.0	56.0	144.3	19	6.8	47.9	45.3	115.6	[25]	
9. Trio	33	4.5	50.9	44.6	138.9 ± 43.00	44	5.9	59.1	35.0	117.0 ± 51.90	[11]	
10. Xavante:												
São Domingos	37	3.0	50.5	46.5	149.0	39	2.8	48.5	48.7	159.0	[26]	
Simões Lopes	91	1.5	39.4	59.1		71	2.6	38.2	59.2		[27]	
11. Xikrinis	37	4.9	49.3	45.8	130.1	26	1.2	36.3	62.6	152.0	[28]	

* Y. Lacassie, personal communication.

† The numbers on which total ridge-count means are based are 129 and 110 for males and females, respectively.

‡ Although Mapuche and Pewenche can be considered Araucanians, we have chosen to present them as different tribes because they have maintained separate mating systems for a considerable period of time.

to those for which means and standard deviations were available (eight tribes). The differences were found to be highly significant (table 4). Since the individual ridge counts for other Indian tribes were not available to us and we had to compute the sum of squares for the analysis-of-variance on the basis of published means and standard deviations, these results should be interpreted cautiously. It should also be noted that the majority of the tribes are represented in the analysis by only one sample. Exceptions are the Aymará (three samples) and the Yanomama (seven samples plus the miscellaneous group). The intertribal variability for males was estimated as $\hat{\sigma}^2_{im} = 219.98$, whereas for females $\hat{\sigma}^2_{if} = 562.66$. Thus, in contrast to the intratribal findings for the Yanomama, between-tribes females are conspicuously more variable than males. Variances of these estimates were computed as $\text{var}(\hat{\sigma}^2_{im}) = 19,800$ for males and $\text{var}(\hat{\sigma}^2_{if}) = 115,200$ for females.

The absence or low frequency of thenar (I and Ir) patterns in four Yanomama villages (table 2) is remarkable, since high frequencies of these patterns were thought to be an Amerindian characteristic. However, frequencies of other palmar-pattern features follow the trends reported for Amerindians, that is to say, low hypothenar, low II, and high III pattern frequencies. The Yanomama a-b ridge-count means are within the South American Indian range [11]. Palmar mainlines are longitudinally aligned (as in most Amerindian series), and mean atd angles show neither unusually high nor low values when compared with the scanty information available [11].

DISCUSSION

Four major points emerging from the analysis of Yanomama dermatoglyphic data deserve explicit statements.

1. As mentioned earlier, total ridge-count variability estimates differ for males and females. The former exhibit greater intratribal and the latter greater intertribal variation. In this connection, we have analyzed the difference between male and female variances for total ridge count in samples from 11 different and widely dispersed population groups, on the basis of the data of table 8. The estimates with variances are for males, $\sigma^2_{pm} = 145.02$ and $\text{var}(\sigma^2_{pm}) = 6,586$, and for females, $\sigma^2_{pf} = 166.39$ and $\text{var}(\sigma^2_{pf}) = 8,831$. Among-population variability estimates for both sexes were shown to be significantly different from zero. The greater degree of variability among females is more consistent with the among-tribes than the among-villages findings of this paper. In seeking an explanation for the higher among-village variability of the males, we have only one suggestion. Marriage among the Yanomama is strongly patrilocal, so that in theory the women of a village should have a more diverse origin than the men and thus exhibit less variation among villages.

2. A considerable variation of single-gene traits has been encountered among Yanomama villages [2-4]. The mean intervillage genetic distance based on allele frequencies at six loci was found to be approximately 85% of the mean intertribal distance for 12 South American Indian tribes [33]. It is of interest to inquire whether a similar situation exists with respect to dermatoglyphic quantitative

TABLE 8

TOTAL RIDGE-COUNT MEANS FOR SEVERAL POPULATIONS REPRESENTING MAJOR ETHNIC GROUPS

GROUP	MALES			FEMALES			REFERENCES
	<i>N</i>	\bar{x}	SD	<i>N</i>	\bar{x}	SD	
American Indians	666	127.6	53.15	639	109.3	55.30	Present study
British (United Kingdom)	825	145.2	50.49	825	127.0	52.33	[15]
Chileans	107	137.4	48.66	69	121.7	41.95	[30]
French	351	132.4	45.28	360	121.4	46.48	[15]
Japanese (Brazil)	379	151.4	44.70	465	142.4	43.80	[11]
Jews (U.S.)	63	185.3	62.94	50	182.4	78.98	[31]
Mexicans (Mexico City)	250	149.8	49.60	250	139.2	51.70	[11]
Negroes (Cuba)	500	123.2	45.16	500	122.1	47.03	[11]
Parsis	200	139.8	45.39	200	135.9	41.27	[32]
Portuguese	100	140.5	42.00	100	126.3	46.00	[15]
Swedish	204	139.7	49.47	188	120.7	52.81	[15]

characteristics, utilizing total ridge count as an indicator. We note that estimates of intertribal total ridge-count variation for both sexes and of intratribal variability for males are substantially larger than similar estimates for widely dispersed populations. Because of the inadequate nature of many of the samples of tribes, we hesitate to accept this finding as established. However, even with these reservations differences are marked enough to suggest that quantitative traits, such as total ridge count, are also highly variable within the Yanomama as well as among South American Indian tribes.

3. The extent of the intervillage variation of total ridge count and also the high variability revealed by inspection for most of the remaining dermatoglyphic traits are not likely to be unique to the Yanomama. A considerable intervillage variability has also been encountered among Aymará-speaking Indians of northern Chile (Y. Lacassie, personal communication). These findings clearly indicate that, as in the case of blood polymorphisms, wherever practicable several villages should be sampled in order to characterize a tribe.

4. The Yanomama are unusual among South American Indian tribes with respect to the absence of the Diego and acid phosphatase polymorphisms (except where they appear to have been introduced by recent admixture with other tribes [2, 4, 34]) as well as in their small stature [5]. Their material culture is less complicated than that of the surrounding tribes [35-37]; their language is not readily identified with any of the principal linguistic stocks of South America [38]. To this list of biological and cultural peculiarities we now add some remarkable dermatoglyphic features, such as the low frequency of whorls, high frequency of arches, and low frequency of thenar/first interdigital (I and Ir) palmar patterns. These additional findings strengthen our earlier suggestion [39] that the tribe represents the descendants of a relatively small founding population and has enjoyed a relatively high degree of genetic isolation for a considerable period of time.

SUMMARY

Dermatoglyphic data on 15 characteristics (digital arches, digital radial loops, digital ulnar loops, digital whorls, I loops, Ir loops, H loops, \bar{H} loops, III loops, IV loops, mainline C absence, total ridge count, a-b ridge count, atd angle, and mainline index) are presented for 246 Yanomama Indians of southern Venezuela and northern Brazil. The detailed analysis is restricted to the villages for which 17 or more sets of prints were available. A considerable amount of intervillage variability was encountered for most characters considered in the analysis. Developmental indeterminacy in these traits was measured by the degree of correspondence between right and left hands; the correlations varied from .24 to .94. Intratribal (Yanomama) and intertribal (South American Indian) total ridge-count variability estimates were obtained for males and females. The former exhibit greater intratribal and the latter greater intertribal variation. Among the most salient dermatoglyphic features of the Yanomama, when compared with other South American Indian series, are a low frequency of whorls, high frequency of arches, and low frequency of thenar/first interdigital (I and Ir) palmar patterns.

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REFERENCES

1. NEEL JV: The genetic structure of a tribal population, the Yanomama Indians. I. Introduction. *Ann Hum Genet* 35:255-259, 1972
2. GERSHOWITZ H, LAYRISSE M, LAYRISSE Z, NEEL J, CHAGNON N, AYRES M: The genetic structure of a tribal population, the Yanomama Indians. II. Eleven blood-group systems and the ABH-Le secretor traits. *Ann Hum Genet* 35:261-269, 1972
3. WEITKAMP LR, ARENDS T, GALLANGO ML, NEEL JV, SCHULTZ JS, SHREFFLER DC: The genetic structure of a tribal population, the Yanomama Indians. III. Seven serum protein systems. *Ann Hum Genet* 35:271-279, 1972
4. WEITKAMP LR, NEEL JV: The genetic structure of a tribal population, the Yanomama Indians. IV. Eleven erythrocyte enzymes and summary of protein variants. *Ann Hum Genet* 35:433-444, 1972
5. SPIELMAN RS, DAROCHA FJ, WEITKAMP LR, WARD RH, NEEL JV, CHAGNON NA: The genetic structure of a tribal population, the Yanomama Indians. VII. Anthropometric differences among Yanomama villages. *Amer J Phys Anthropol* 37:345-356, 1972
6. WARD RH: The genetic structure of a tribal population, the Yanomama Indians. V. Comparison of a series of genetic networks. *Ann Hum Genet* 36:21-43, 1972
7. NEEL JV, WARD RH: The genetic structure of a tribal population, the Yanomama Indians. VI. Analysis by F-statistics (including a comparison with the Makiritare and Xavante). *Genetics*. In press, 1973
8. CUMMINS H, MIDLO C: *Finger Prints, Palms and Sole*. New York, Dover, 1961
9. PENROSE LS, LOESCH D: Topological classification of palmar dermatoglyphics. *J Ment Defic Res* 14:111-128, 1970
10. LOESCH D: Genetics of dermatoglyphic patterns on palms. *Ann Hum Genet* 34:277-293, 1971
11. COOPE E, ROBERTS DF: Dermatoglyphic studies of populations in Latin America, in *The Ongoing Evolution of Latin American Populations*, edited by SALZANO FM, Springfield, Ill., Thomas, 1971, pp 405-453

12. SOKAL RR, ROHLF FJ: *Biometry*. San Francisco, Freeman, 1969
13. SCHEFFÉ H: *The Analysis of Variance*. New York, Wiley, 1959
14. NEEL JV, ROTHHAMMER F: The genetic structure of a tribal population, the Yanomama Indians. JX. Agreement between village distance matrices based on different sets of characteristics. *Amer J Hum Genet*. Submitted, 1972
15. HOLT SB: *The Genetics of Dermal Ridges*. Springfield, Ill., Thomas, 1968
16. PENROSE LS: The distal triradius on the hands of parents and sibs of mongol imbeciles. *Ann Hum Genet* 19:10-27, 1954
17. PONS J: Quantitative genetics of palmar dermatoglyphics. *Amer J Hum Genet* 11: 252-256, 1959
18. PENROSE LS: Notes on the interpretation of intrafamilial correlation coefficients. *Ann Hum Genet* 34: 291-293, 1971
19. MAVALWALA JD: Correlations between ridge-counts on all digits of the Parsis of India. *Ann Hum Genet* 26:137-138, 1962
20. ROBERTS DF, CHAVEZ J, SALZANO FM, DA ROCHA FJ: Dermatoglyphics of Caingang and Guarani Indians. *Man* 6:61-78, 1971
21. JANTZ RL, JOHNSTON FE, WALKER GF, KENSINGER KM: Finger dermatoglyphics of the Peruvian Cashinahua. *Amer J Phys Anthropol* 30:355-360, 1969
22. SUNDERLAND E, RYMAN R: PTC thresholds, blood factors, color vision and finger prints of Jivaro Indians in eastern Ecuador. *Amer J Phys Anthropol* 28:339-344, 1968
23. ROTHHAMMER F, DIXON M: Microevolution in human Chilean populations. IV. Dermatoglyphics in Araucanian Indians. *Z Morph Anthropol* 61:217-223, 1969
24. ROTHHAMMER F, COVARRUBIAS E, DIXON M: Dermatoglyphics in Pewenche Indians. *Hum Biol* 41:151-160, 1969
25. VIEIRA-FILHO JPB: Os dermatóglifos palmares dos índios Suruis e suas afinidades com diversos grupos étnicos. *Ciênc Cult* 22:327-341, 1970
26. NEEL JV, SALZANO FM, JUNQUEIRA PC, KEITER F, MAYBURY-LEWIS D: Studies on the Xavante Indians of the Brazilian Mato Grosso. *Amer J Hum Genet* 16:52-140, 1964
27. NISWANDER JD, KEITER F, NEEL JV: Further studies on the Xavante Indians. II. Some anthropometric, dermatoglyphic, and nonquantitative morphological traits of the Xavantes of Simões Lopes. *Amer J Hum Genet* 19:490-501, 1967
28. VIEIRA-FILHO JPB: Os dermatóglifos palmares situando os índios brasileiros Xikrins no contexto mundial. *Ciênc Cult* 22:182-198, 1970
29. STEWARD JH, FARON LC: *Native Peoples of South America*. New York, McGraw-Hill, 1959
30. ROTHHAMMER F, PEREIRA G, CAMOUSSEIGHT A, BENADO M: Dermatoglyphics in schizophrenic patients. *Hum Hered* 21:198-202, 1971
31. RIFE DC: Finger prints as criteria of ethnic relationship. *Amer J Hum Genet* 5:389-399, 1953
32. MAVALWALA JD: Quantitative analysis of finger ridge-counts in the Parsi community in India. *Ann Hum Genet* 26:305-313, 1963
33. NEEL JV, WARD RH: Village and tribal genetic distances among American Indians and the possible implications for human evolution. *Proc Nat Acad Sci USA* 65:323-330, 1970
34. LAYRISSE M, LAYRISSE Z, WILBERT J: Blood group antigen tests of the Waica Indians of Venezuela. *Southwest J Anthropol* 18:78-93, 1962
35. BECHER D: *Die Surára und Pakidái: Zwei Yanonámi-Stämme in Nordwest-brasilien*. Mitteilungen aus dem Museum für Völkerkunde, vol 26, Hamburg, 1960
36. ZERRIES O: *Waika: Die kulturgeschichtliche Stellung der Waika-Indianer des oberen Orinoco im Rahmen Völkerkunde Südamerikas*. Band I. *Ergebnisse der Frobenius-Expedition 1954/1955 nach Südostvenezuela*. Munich, 1964

37. CHAGNON NA: *Yanomamö: The Fierce People*. New York, Holt, Rinehart & Winston, 1968
38. MIGLIAZZA E: Yanomama grammar and intelligibility. Ph.D. thesis, Univ. Indiana, 1972
39. NEEL J, ARENDS T, BREWER C, CHAGNON N, GERSHOWITZ H, LAYRISSE M, LAYRISSE Z, MACCLUER J, MIGLIAZZA E, OLIVER W, SALZANO F, SPIELMAN F, WARD R, WEITKAMP L: Studies on the Yanomama Indians, in *Proceedings 4th International Congress of Human Genetics*, Paris 1971, Amsterdam, Excerpta Medica. In press, 1973