Digital Dermatoglyphic Patterns of Eskimo and Amerindian Populations: Relationships between Geographic, Dermatoglyphic, Genetic, and Linguistic Distances

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Abstract Dermatoglyphic traits have been used to assess population affinities and structure. Here, we describe the digital patterns of four Eskimo populations from Alaska: two Yupik-speaking villages from St. Lawrence Island and two Inupik groups presently residing on mainland Alaska. For a broader evolutionary perspective, these four Eskimo populations are compared to other Inuit groups, to North American Indian populations, and to Siberian aggregates. The genetic structures of 18 New and Old World populations were explored using *R*-matrix plots and Wright's F_{ST} values. The relationships between dermatoglyphic, blood genetic, geographic, and linguistic distances were assessed by comparing matrices through Mantel correlations and through partial and multiple correlations. Statistically significant relationships between dermatoglyphics and genetics, genetics and geography, and geography and language were revealed. In addition, significant correlations between dermatoglyphics and geography, with linguistic variation constant, were noted for females but not for males. These results attest to the usefulness of dermatoglyphics in resolving various evolutionary questions concerning normal human variation.

The genetic differentiation of human populations has been explored through the use of several morphological, molecular, and biochemical markers. These include DNA restriction fragment length polymorphism (RFLP) markers, blood groups, red blood cell and serum proteins, and polygenic systems such as anthropometrics and dermatoglyphics. To better understand evolution and the genetic structure of subdivided human populations, some researchers have compared population affinities assessed by distance measures for polygenic versus monogenic traits. In addition, the interrelationship between genetic and phenetic traits and such factors as geography, ethnic history, language, and migration have been explored (Winkler and Sokal 1987; Stoneking et al. 1990; Relethford 1991). Der-

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matoglyphics has been used to infer population structure in a number of human populations (Crawford 1976; Lin et al. 1983, 1984; Blangero 1990).

Whether or not dermatoglyphic measures corroborate interpopulation affinities measured by other biological systems (e.g., genetics and anthropometrics) and geographic and linguistic distances (Meier 1980; Chai 1972; Neel et al. 1974; Rothhammer et al. 1979; Malhotra et al. 1980; Froehlich and Giles 1981) is still being debated. Apparently, the contradictory results stem from a combination of the dermatoglyphic variables selected and the method of analysis used.

In this study we examine dermatoglyphic variation among native North American groups on three different hierarchical levels: (1) variation among Eskimos [2 Yupik-speaking groups (Savoonga and Gambell villages of St. Lawrence Island) and 2 Inupik-speaking populations (King Island and Wales, Alaska)]; (2) comparison with 10 Amerindian and Eskimo populations [of the 10 populations, 5 are Eskimo groups (Savoonga, Gambell, Wales, King Island, Scoresbysund) and the others are North American Indian groups (Navajo, Apache, Seneca, Micmac, and Choctaws)]; and (3) analysis of relation statistics for a set of 18 populations (the 10 populations listed plus 4 Siberian Ngąnasan settlements, Baffin Island and Southampton Eskimos, and Commanche and Arapahoe Indians). We use digital pattern frequencies and the *R*-matrix method of Harpending and Jenkins (1973) to establish relationships among subdivided populations. The dermatoglyphic distances are compared with genetic, geographic, and linguistic distances.

Materials and Methods

Eighteen populations were analyzed at various levels. We selected these groups for several reasons. First, there are no other data on digital dermatoglyphic patterns for the populations of Savoonga, Gambell, Wales, and King Island; the fingerprints used in these analyses were collected during a field project in the summer of 1978. Second, we wanted to analyze the phylogenetic relationships among widely dispersed groups that transect various geographic areas and linguistic affiliations. Also, digital pattern frequency data were available for these New World and Siberian populations. Many of the published studies fail to include the frequencies of the patterns by finger; often, only pattern frequencies summed for all fingers are included in publications. And last, blood genetic data and dermatoglyphic individual finger pattern frequencies for the same populations are available for only 10 Eskimo and Amerindian populations.

We report the digital pattern frequencies for 350 persons (173 males and 177 females) obtained from four small Eskimo villages (Figure 1).

Figure 1. Bering Sea region between Alaska and Siberia and locations of the four study populations. [From Byard and Crawford (1991).]

Two of these communities, Savoonga and Gambell (located on St. Lawrence Island) are offshoots from the survivors of a genetic bottleneck that reduced the population from several thousand to 222 (Byard et al. 1983). With the introduction of reindeer in the 1920s, the survivors split into these two villages. The inhabitants of St. Lawrence Island speak a Siberian Yupik language and have close familial ties to the inhabitants of Chukotka on the Siberian side of the Bering Strait. Wales is a small village on mainland Alaska (Seward Peninsula) that is populated exclusively by Inupik-speaking Eskimos. The King Island population, originally located in the Bering Strait between Wales and St. Lawrence, has been transplanted en masse to Nome, Alaska.

Following Cummins and Midlo (1943) and Holt (1968), we classify pattern types into four categories: arches, ulnar loops, radial loops, and

Table 1. Population Samples Used in the Dermatoglyphic Analyses

Population	*Sex*[a]	*Sample Size*	*References*
Savoonga	M	81	Present study
	F	83	
Gambell	M	41	Present study
	F	39	
Wales	M	31	Present study
	F	28	
King Island	M	20	Present study
	F	27	
Scoresbysund	M	25	Ducros and Ducros (1972)
	F	25	
Baffin Island	M	234	Auer (1950)
	F	218	
Southampton Island	M	28	Popham (1953)
	F	34	
Navajo	M	48	Flickinger (1975)
	F	54	
Apache	M	44	Flickinger (1975)
	F	50	
Seneca	M	27	Doeblin et al. (1968)
	F	55	
Choctaw	M	53	Flickinger (1975)
	F	51	
Micmac	T	150	Chiasson (1960)
Arapahoe	T	50	Downey (1927)
Commanche	T	67	Cummins and Goldstein (1932)
Potapovo	M	26	Galaktionov et al. (1981)
	F	39	
Volochanka	M	78	Galaktionov et al. (1981)
	F	75	
Ust-Avam	M	61	Galaktionov et al. (1981)
	F	82	
Novaja	M	29	Galaktionov et al. (1981)
	F	28	

a. M = male; F = female; T = combined.

whorls. The frequencies of these categories are computed for each finger for each population. For these comparisons we selected populations from published data and used all the available dermatoglyphic publications that provided digital pattern information. The data sources and the sample sizes are reported in Table 1. Data were compiled from 18 North American Indian, Eskimo, and Siberian Nganasan populations. For comparisons between populations, sex differences were removed by averaging sex-specific digital type frequencies. However, sex-specific comparisons were made whenever the reported data were subdivided by sex.

Table 2. Population Samples Used to Compute Genetic Distances

Population	*Sample Size*	*Reference*
Savoonga	169	Crawford et al. (1981) Schanfield et al. (1990)
Gambell	80	Crawford et al. (1981) Schanfield et al. (1990)
Wales	67	Crawford et al. (1981) Schanfield et al. (1990)
King Island	54	Crawford et al. (1981) Schanfield et al. (1990)
Scoresbysund	246	Ducros (1979)
Navajo	237	Corcoran et al. (1962)
Apache	108	Gershowitz (1959)
Seneca	211	Doeblin and Mohn (1967)
Choctaw	69	Kasprisin et al. (1987)
Micmac	605	Chiasson (1963)

References for the blood genetic sources are summarized in Table 2. Information on both digital type frequencies and a reasonable array of blood marker frequencies was available for 10 populations. The genetic data analysis for the 4 Eskimo populations of St. Lawrence Island and mainland Alaska is based on 35 gene and haplotype frequencies. The systems included are ABO, Rh, MNS, Duffy (FY), P, Kidd (JK), Colton (CO), group-specific component (GC), haptoglobin (HP), acid phosphatase (ACP), esterase D (ESD), phosphoglucomutase (PGM), and immunoglobulins (GM and KM). The gene frequencies and population affinities for these four Eskimo groups have been described previously (Crawford et al. 1981; Schanfield et al. 1990).

Genetic data for the 10-population analysis include only 12 alleles and haplotypes from the ABO, Rh, and MN systems. The number of loci and alleles is reduced because of the need for common genetic information across the populations and the availability of populations with individual digital frequencies reported.

Analytical Methods

R-Matrix Analysis. *R* statistics for digital pattern frequencies were calculated to obtain a single expression of relationship between the Eskimo, Amerindian, and Siberian populations. Individual digital information provides 40 trait frequencies for each population. These traits are based on the scoring of 4 distinct digital types for each of the 10 fingers. Minimally, if we assume that the pattern on each finger is controlled by a locus with four alleles, then a matrix of digital pattern frequencies across populations can be subjected to *R*-matrix analysis in a manner similar to

that used for allelic frequencies. Such a matrix yields eigenvector patterns and Euclidean distances. Harpending and Jenkins (1973) described the method for constructing the variance-covariance matrix, which has become a standard procedure in population analyses. The mean of the diagonal elements (r_{ii}) provides an estimate of F_{ST}. The eigenvectors, scaled by their respective eigenvalues, are plotted to reveal population subdivision affinities. A Euclidean distance is derived from the R-matrix using the formula

$$d_{ij}^2 = r_{ii} + r_{jj} - 2r_{ij} \tag{1}$$

for each pair of populations i and j. In this study the dermatoglyphic and genetic distances were computed using the R-matrix method just described.

Matrices were constructed based on geographic and linguistic distances. The geographic distances were measured in miles as a straight-line distance (as the crow flies) between populations. The linguistic distances between populations were based on Greenberg's (1987) classification of Native American languages. Although we are aware of the criticism surrounding Greenberg's creation of a single Amerind language phylum, we use this classification to determine whether the observed dermatoglyphic diversity can contribute to answering the question of the peopling of the New World.

The hierarchical structure of the linguistic classification permits the conversion of the order of relationships into scores or distances. Thus linguistic distances are measured as follows. Tribes speaking different dialects of the same subgroup of languages are assigned a distance of 1. Tribes speaking languages that belong to different subgroups within a given group of languages are assigned a distance of 2. Distance 3 relates to tribes speaking different groups of languages that are in a given subbranch, and languages that fall into different subbranches of a given branch are separated by a distance of 4. If the languages belong to two different branches within a subfamily, they are separated by a distance of 5. Distance 6 relates to tribes speaking languages that fall into different subfamilies of a given family. If the languages being compared belong to two separate linguistic families, a distance of 7 is assigned.

Mantel Tests. To examine the interaction between dermatoglyphic, genetic, geographic, and linguistic distance matrices, we computed normalized product-moment correlations, partial correlations, and multiple correlations using the Mantel program (Relethford 1990).

Given two distance matrices A and B, Mantel's (1967) test examines whether or not there is an association between the elements of the two matrices by using the statistic

$$Z_{AB} = \sum_{ij} A_{ij}B_{ij}, \tag{2}$$

where A_{ij} and B_{ij} are the elements of row i and column j of matrices A and B, which results in an unnormalized correlation coefficient. Following the methods of Dow and Cheverud (1985), Smouse et al. (1986), Dow, Cheverud, and Friedlaender (1987), and Dow et al. (1987), we normalized Z_{AB} into a product-moment correlation coefficient that ranges from -1 to $+1$. The significance of correlations is tested by comparing the observed correlations against a sampling distribution of Z based on a randomized B matrix B_R.

Mantel multiple tests, partial correlations, and multiple correlations were used to explore the relationships between various types of distance matrices (Dow and Cheverud 1985; Smouse et al. 1986; Dow et al. 1987; Dow, Cheverud, and Friedlaender 1987). Given matrices A (dependent distance matrix) and B and C (independent distance matrices), there are three possible partial correlation coefficients: $r_{AB(C)}$, $r_{AC(B)}$, and $r_{BC(A)}$. For example, the partial correlation $r_{AB(C)}$ measures the association between A and B distance matrices, keeping the distance matrix C constant. By using a least-squares regression method, we can regress the elements in the dependent matrix A on the corresponding elements of the C matrix to obtain the residual matrix R_1. The elements in the matrix B are regressed on the corresponding elements of C to obtain the residual matrix R_2. A product-moment correlation between the residual matrices R_1 and R_2 yields the partial correlation. The significance of the partial correlation is assessed by keeping one residual matrix as a target and randomly permutating the other.

The relative effects of the distance matrices B and C on the distance matrix A were ascertained through a multiple regression analysis. The product-moment correlation between the elements in the original dependent matrix (e.g., A) and the corresponding expected values in the prediction matrix ($\hat{A}$) results in a multiple correlation. Significance levels for this multiple correlation are derived from Mantel matrix permutation procedures in which matrix $\hat{A}$ is kept constant and matrix A is randomly permutated.

Results

Four-Population Analysis. Table 3 summarizes the frequencies of pattern types, subdivided by sex and finger, for four Eskimo villages. The sample sizes for these Eskimo populations appear to be relatively small; however, when the actual sizes of these settlements are taken into account, the samples constitute a solid proportion of the population. For example, although a sample of fingerprints was collected from only 59 individuals of Wales, Alaska, the total size of this village in 1978 was 125 people. Thus this sample constitutes 47% of the total population.

Table 3. Pattern Type Frequencies (%) among Four Eskimo Populations

		Arch		*Ulnar Loop*		*Radial Loop*		*Whorl*	
Population	*Digit*	*Left*	*Right*	*Left*	*Right*	*Left*	*Right*	*Left*	*Right*
Savoonga (M)	1	1.2	0.0	35.8	21.0	0.0	0.0	63.0	79.0
(n = 81)	2	2.5	6.2	56.8	38.3	3.7	16.1	37.0	39.5
	3	1.2	2.5	63.0	59.3	1.2	1.2	34.6	37.0
	4	1.2	0.0	34.6	30.4	0.0	0.0	64.2	69.6
	5	0.0	0.0	79.0	67.9	1.2	1.2	19.8	30.9
	Total	1.2	1.7	53.8	43.4	1.2	3.7	43.7	51.1
Savoonga (F)	1	1.2	0.0	43.9	43.4	1.2	0.0	53.7	56.6
(n = 83)	2	7.2	4.8	60.2	45.8	7.2	8.4	25.3	41.0
	3	2.4	2.4	69.9	79.5	1.2	1.2	26.5	16.9
	4	1.2	1.2	38.3	37.4	1.2	1.2	59.3	60.2
	5	3.7	2.4	76.8	72.3	0.0	0.0	19.5	25.3
	Total	3.2	2.2	57.9	55.7	2.2	2.2	36.7	40.0
Gambell (M)	1	0.0	0.0	43.9	26.8	0.0	0.0	56.1	73.2
(n = 41)	2	2.4	2.4	48.8	41.5	14.6	19.5	34.2	36.6
	3	0.0	0.0	70.7	63.4	2.4	4.9	26.8	31.7
	4	0.0	0.0	43.9	26.8	0.0	4.9	56.1	68.3
	5	0.0	0.0	85.4	75.6	0.0	0.0	14.6	24.4
	Total	0.5	0.5	58.5	46.8	3.4	5.9	37.6	46.8
Gambell (F)	1	2.6	0.0	43.6	41.0	0.0	0.0	53.9	59.0
(n = 39)	2	10.3	7.7	53.9	48.7	5.1	7.7	30.8	35.9
	3	2.6	2.6	76.9	84.6	2.6	0.0	18.0	12.8
	4	0.0	0.0	50.0	43.6	5.3	2.6	44.7	53.9

	5	5.1	2.6	79.5	76.9	0.0	0.0	15.4	20.5
	Total	4.1	2.6	60.8	59.0	2.6	2.1	32.5	36.4
Wales (M)	1	0.0	0.0	48.4	35.5	0.0	0.0	51.6	64.5
(n = 31)	2	3.2	9.7	51.6	38.7	22.6	12.9	22.6	38.7
	3	3.2	0.0	80.7	90.3	3.2	0.0	12.9	9.7
	4	0.0	0.0	53.3	45.2	0.0	3.2	46.7	51.6
	5	0.0	0.0	74.2	76.7	0.0	0.0	25.8	23.3
	Total	1.3	2.0	61.7	57.1	5.2	3.3	31.8	37.7
Wales (F)	1	3.6	3.6	50.0	50.0	0.0	0.0	46.4	46.4
(n = 28)	2	7.1	0.0	35.7	60.7	10.7	10.7	46.4	28.6
	3	0.0	0.0	64.3	85.7	0.0	3.6	35.7	10.7
	4	3.6	0.0	39.3	37.0	3.6	0.0	53.6	63.0
	5	3.6	3.7	67.9	63.0	0.0	0.0	28.6	33.3
	Total	3.6	1.5	51.4	59.4	2.9	2.9	42.1	36.2
King Island (M)	1	0.0	0.0	23.8	15.0	0.0	0.0	76.2	85.0
(n = 20)	2	4.8	5.3	66.7	31.6	0.0	15.8	28.6	47.4
	3	0.0	0.0	66.7	65.0	0.0	0.0	33.3	35.0
	4	0.0	0.0	23.8	10.5	0.0	5.3	76.2	84.2
	5	0.0	0.0	57.9	45.0	0.0	0.0	42.1	55.0
	Total	1.0	1.1	47.6	33.7	0.0	4.1	51.5	61.2
King Island (F)	1	3.7	3.7	33.3	25.9	0.0	0.0	63.0	70.4
(n = 27)	2	3.7	0.0	55.6	63.0	11.1	3.7	29.6	33.3
	3	3.7	0.0	70.4	63.0	0.0	0.0	25.9	37.0
	4	0.0	0.0	23.1	22.2	0.0	3.7	76.9	74.0
	5	7.4	11.1	63.0	55.6	0.0	0.0	29.6	33.3
	Total	3.7	3.0	49.3	45.9	2.2	1.5	44.8	49.6

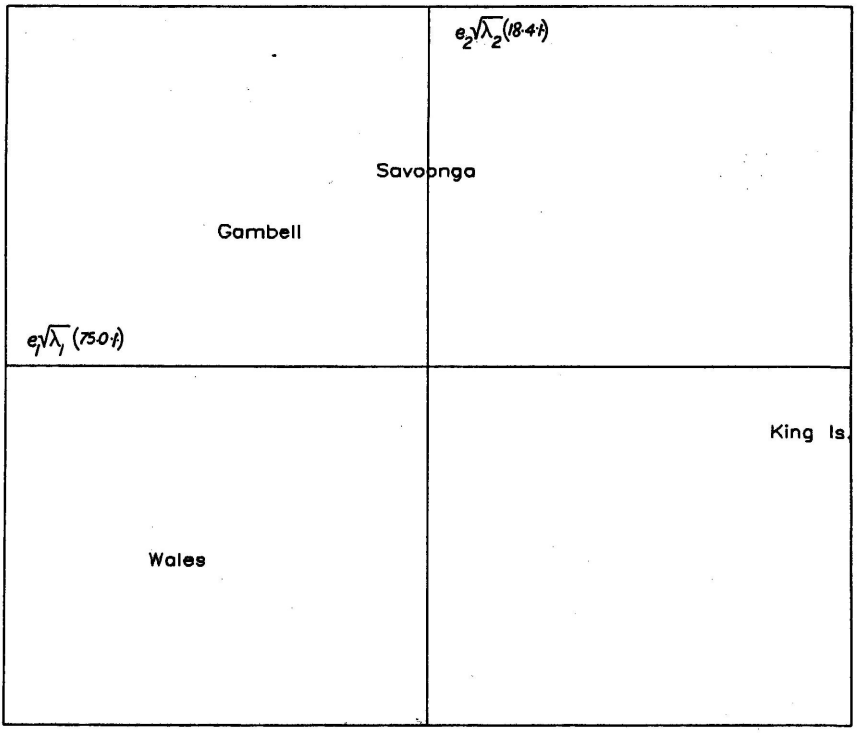

Figure 2. Least-squares reduction genetic map of four Eskimo populations based on dermatoglyphic traits (digital pattern frequencies).

Uniformly, loops and whorls are the most frequent patterns exhibited by the fingerprints of these Eskimos. The ulnar loop percentage for all 10 fingers varies from 62% in males from Wales to almost 48% in King Island males. There is considerable variation by sex and community when the pattern type frequencies are computed by individual finger. Arches and radial loops are the most infrequent pattern types, although right radial loops on the second digit of the right hand occur in 19.5% of Gambell males. Similarly, the left radial loop is found on the second finger of the left hand in 22.6% of the males from Wales. Based on these frequencies, it is evident that Gambell and Savoonga exhibit more similar pattern frequencies than those observed in Wales and King Island.

R-Matrix Analysis. Figure 2 is a plot of the first versus second scaled eigenvectors for the four Eskimo populations from which we collected original fingerprints; 93% of the variation is subsumed by these 2 eigenvectors. The first axis represents the dichotomy of whorls versus ul-

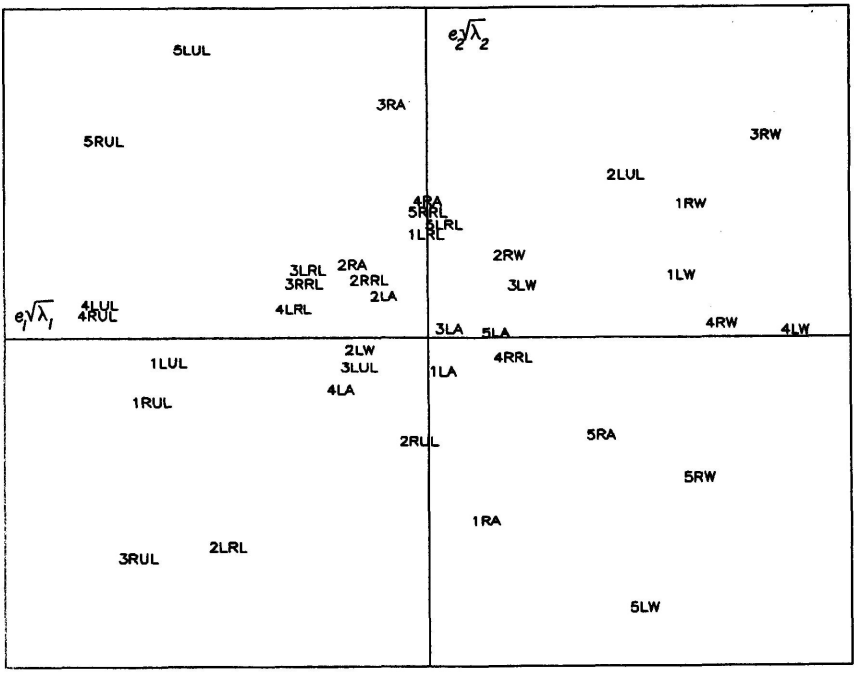

Figure 3. Distribution of digital patterns along the first and second scaled eigenvectors for four Eskimo populations. The number denotes the digit, the first letter defines the hand (R = right, L = left), and the remaining letters indicate the trait (UL = ulnar loop, RL = radial loop, W = whorl, A = arch).

nar loops. A combination of traits accounts for the dispersal along the second axis. As expected, Savoonga and Gambell are most similar because they resulted from the fission of a single group of survivors in the 1920s. Although King Island and Wales belong to the same language subgroup, Inupik, they show little similarity based on these dermatoglyphic traits.

Figure 3, a plot of the distribution of digital pattern types dispersed along the two eigenvectors, indicates that the two St. Lawrence Island populations are distinguished from the other groups by the right and left ulnar loops of the fifth digit. In addition, the arches on the third finger of the right hand contribute to the dispersion of the Yupik populations in this *A* matrix plot. Wales is distinguished by the frequencies of the right ulnar loops and left radial loops on the third and second fingers, respectively. King Island is separated from Wales by the right and left whorls of the fifth digit and by the left whorl of the fourth finger. This plot assists in the interpretation of the relationship map (Figure 2).

Table 4. Comparison of Dermatoglyphic and Genetic Distance Matrixes

Sex	*Correlation*	*p (Significance Level)*
Male	0.414	0.087
Female	0.854	0.000
Combined	0.553	0.087

A comparison of F_{ST} values, Wright's measure of genetic differentiation of subdivided populations, based on dermatoglyphics and blood genetics for the four Eskimo populations reveals less differentiation for dermatoglyphic traits.

Genetic and Dermatoglyphic Analyses. Based on the four-population analysis, subdivided by sex, we compared the dermatoglyphic and genetic distance matrices. The results are given in Table 4. The congruence between genetics and female dermatoglyphics is exceptionally high, as revealed by a statistically significant correlation coefficient of 0.854 ($p = 0.000$), whereas the male and the combined sample exhibit moderate correlations, although the significance levels fail to reach the conventional threshold.

Ten-Population Analysis. Figure 4 exhibits the dispersal of 10 North American native populations along the first 2 eigenvectors from an *R*-matrix analysis. These 2 scaled eigenvectors account for 76.7% of the total variation, with the first axis explaining 53.6% and the second axis explaining 23.1%. The first eigenvector separates the Eskimo and the NaDene populations from the three northern so-called Amerind-speaking groups. The second eigenvector separates the Yupik-speaking populations. Surprisingly, Wales (an Inupik-speaking village) clusters with the two Yupik villages from St. Lawrence Island.

Figure 5 is a plot of the traits that underlie the population separation along the first and second eigenstructures. The first axis contrasts the differences between whorls and a combination of ulnar loops and arches, and the second vector represents ulnar loops and a combination of other types, such as arches. Wales, Gambell, and Savoonga differ from the other populations primarily because of their ulnar loop frequencies on the second and third digits. King Island and Scoresbysund Eskimos are distinct from all the other populations because of their whorl frequencies on the first, fourth, and fifth digits. The Choctaw Amerindian population can be distinguished by the unique frequencies of arches on the second and third digits. The Navajo, Apache, and Seneca samples are closest

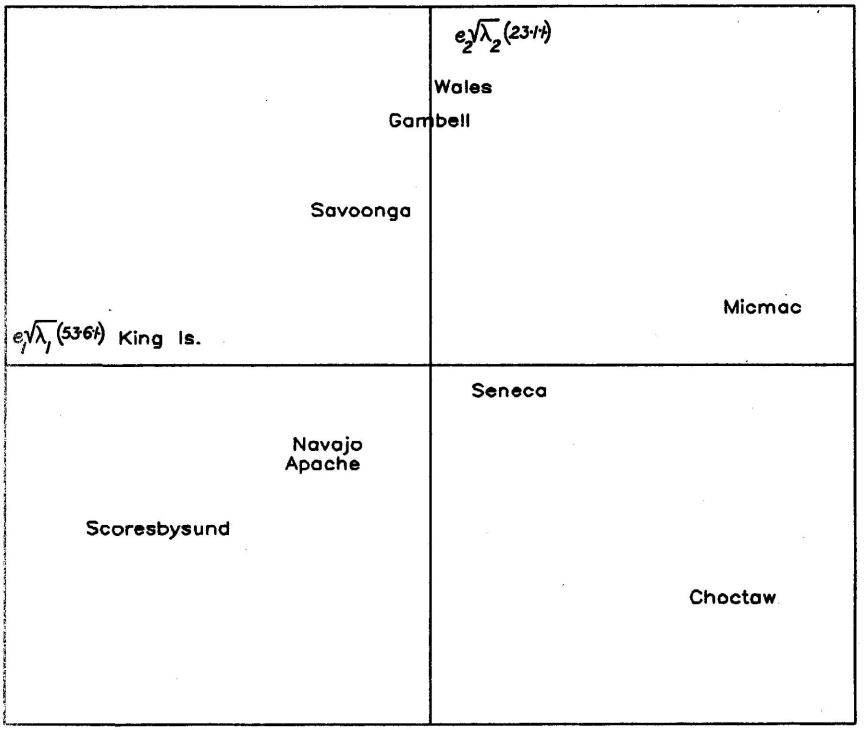

Figure 4. Genetic map of 10 native North American populations (5 Eskimo and 5 North American Indian groups) based on digital pattern types.

to the centroid of distribution and can be characterized on the bases of whorls and arches.

In this 10-population analysis the correlation between dermatoglyphic and genetic distances are moderate but highly significant. Among populations subdivided by sex males have a correlation of 0.47 (p = 0.005) and females have a correlation of 0.48 (p = 0.002). For the combined sample the correlation is 0.436 (p = 0.002). These results indicate that there is congruence between genetics and the genetic information contained in the digital pattern frequencies.

A comparison of F_{ST} values for dermatoglyphics and genetics among the 10 populations suggests that polygenic dermal traits may be less differentiated than Mendelian blood markers. Although the F_{ST} value based on genetics is 0.056, it is 0.035 for dermatoglyphics. However, such comparisons must be viewed with caution; Williams-Blangero and Blangero (1989) have argued that the phenotypic-based F_{ST} values are minimum estimates.

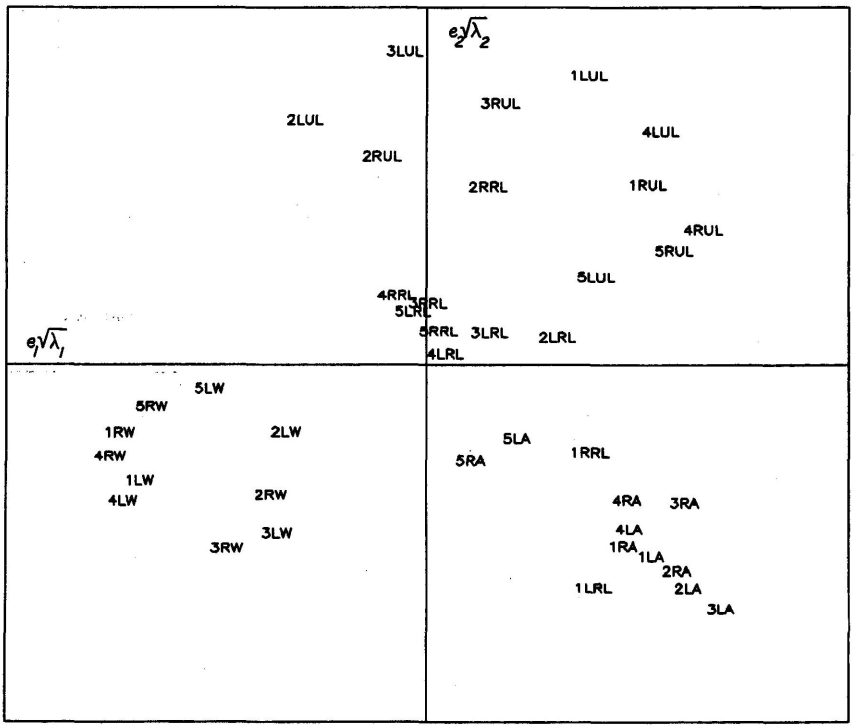

Figure 5. Distribution of digital pattern types along the first and second scaled eigenvectors for 10 Native American populations.

Eighteen-Population Analysis

R-Matrix Analysis. Figure 6 is a genetic map for 18 populations (4 Siberian, 7 Eskimo, and 7 North American groups) that reside on both sides of the Bering Strait in the New and Old Worlds. This sample of populations provides a wider geographic context for the Eskimo groups described here and permits a comparison of New and Old World groups. The first two eigenvectors account for 75.1% of the observed dermatoglyphic variation, with the first axis explaining 56.8% and the second axis explaining 18.3%. The first axis separates the four aboriginal populations of northern Siberia from the other groups. The proximity of Scoresbysund to the Siberian cluster supports earlier suggestions that the Eskimos from the eastern coast of Greenland have experienced less admixture and are more proximal genetically to the northern Asian populations (Ducros and Ducros 1972; Galaktionov et al. 1981). The second axis separates the northern Amerind groups, with the exception of the Arapahoe, who cluster with the Eskimos. The distribution of traits that

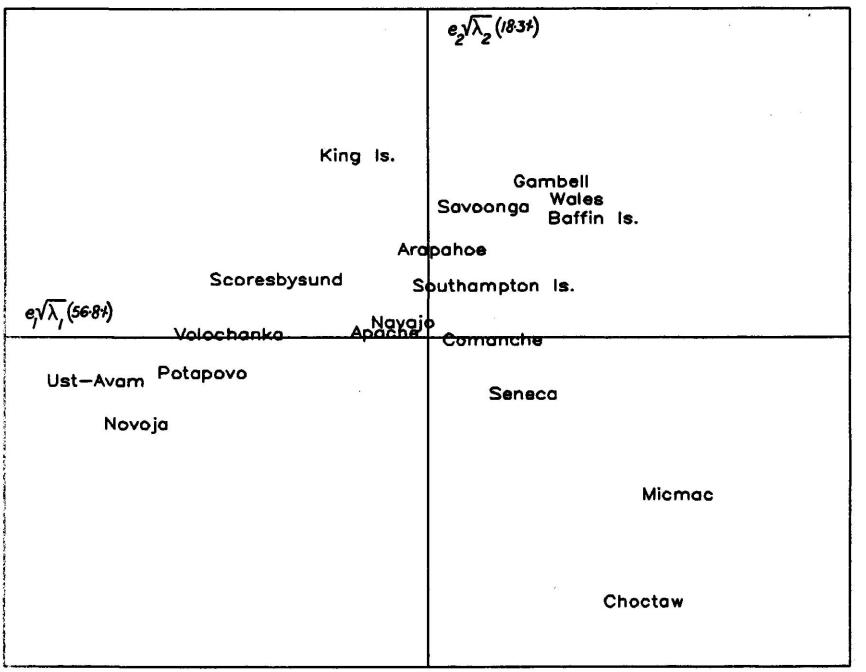

Figure 6. Genetic map of 18 populations from both sides of the Bering Strait (4 Siberian, 7 Eskimo, and 7 North Amerindian groups) based on digital pattern frequencies.

separate these populations are depicted in Figure 7. As in the earlier analysis, the first axis exhibits a dichotomy between whorls and ulnar loops and the second eigenvector contrasts the arches from the loops. The Nganasan of Siberia are distinguished from the New World populations primarily by the frequencies of whorls on all five digits. What clusters Scoresbysund with the Siberian populations is the similarity in the frequencies of whorls, particularly on the first digit. Distinctive frequencies of arches and radial loops separate the Amerindian groups from the other populations.

The F_{ST} value derived from this 18-population analysis is 0.045, the highest degree of dermatoglyphic differentiation noted in this study. These results are not surprising because the analysis is based on groups that reside on both sides of the Bering Strait and that are highly diverse biologically. However, the high F_{ST} level observed confirms the association demonstrated by Jorde (1980) and Crawford and Enciso (1982) that the F_{ST} value is correlated linearly with the number of population subdivisions.

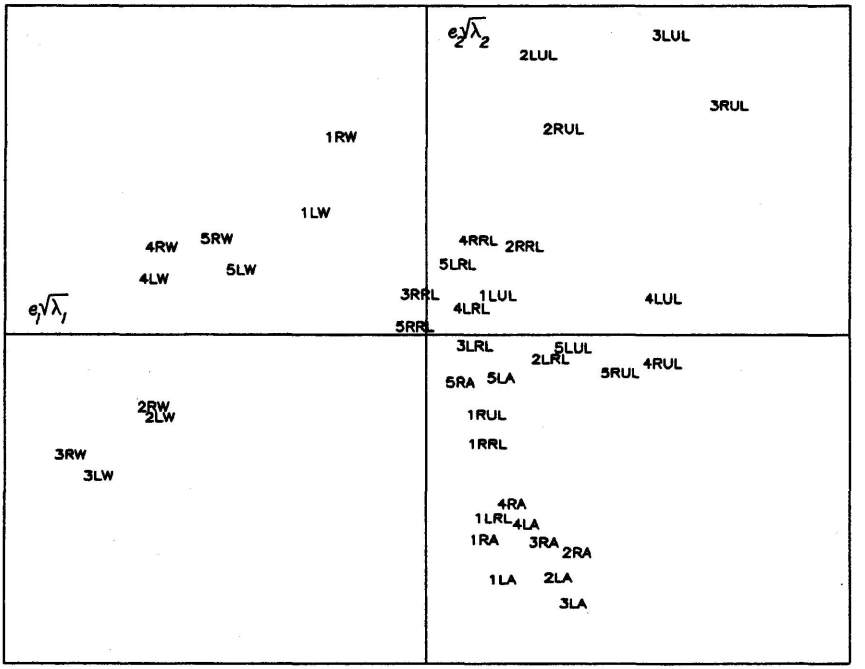

Figure 7. Distribution of digital pattern types along the first and second scaled eigenvectors for 18 populations.

Concordance between Distances. Table 5 summarizes the results of the pairwise Mantel tests. At the population level the product-moment correlations between any given two distance matrices are all significant, indicating the existence of relationships between dermatoglyphics, genetics, geography, and language. This observation contrasts markedly with earlier reports by Neel et al. (1974) and Rothhammer et al. (1979). However, when the sexes are analyzed separately, the association between male dermatoglyphics and geography ($r = 0.215$, $p = 0.153$) and between dermatoglyphics and language (male: $r = 0.217$, $p = 0.168$; female, $r = 0.187$, $p = 0.199$) becomes weak, showing no statistical significance. There are moderate to high correlations, statistically significant, for all other pairwise comparisons.

Partial correlations were made on the genetic, dermatoglyphic, geographic, and language matrices (Table 6). When language is kept constant, only females show a moderate association between dermatoglyphics and geography ($r = 0.423$), which is highly significant ($p = 0.008$). Although the other partial correlations reported in Table 6 are mostly insignificant, correlations between genetics and geography have signif-

Table 5. Pearson's Product-Moment Correlations for Dermatoglyphics (DERM), Blood Genetics (GENE), Geographic (GEOG), and Linguistic (LANG) Distance Matrix Comparisons among Native American Populations

Test of	*Male*[a]		*Female*[a]		*Combined*[b]	
Relationship	*Correlation*	*p*	*Correlation*	*p*	*Correlation*	*p*
DERM*GENE	0.470	0.005	0.479	0.002	0.436	0.002
DERM*GEOG	0.215	0.153	0.441	0.003	0.318	0.017
DERM*LANG	0.217	0.168	0.187	0.199	0.301	0.029
GENE*GEOG	0.375	0.006	0.375	0.006	0.380	0.006
GENE*LANG	0.310	0.027	0.310	0.027	0.331	0.003
GEOG*LANG	0.631	0.004	0.631	0.004	0.638	0.001

a. Relates to nine populations in which the data were subdivided by sex.

b. Relates to 10 populations in which the data were combined by sex. The nine populations from note (a) are included.

icance levels slightly above convention. Thus partial correlations between dermatoglyphics and language and between geography and dermatoglyphics fail to provide any additional information.

Because geography and language are highly correlated ($r = 0.638$, $p = 0.001$), the interrelated effects of geography and language on dermatoglyphics and genetics were examined (Table 7). The multiple correlations associated with dermatoglyphics are highly significant in females ($r = 0.456$, $p = 0.002$) and in the combined sample ($r = 0.342$, $p = 0.006$), although male dermatoglyphics show no significance for the same association. However, the proportions of variance explained in the female and the combined sample dermatoglyphics by the interrelated effects of language and geography are only 20.8% and 11.7%, respectively.

The multiple regression analysis of genetic distances on both geographic and dermatoglyphic distances yielded highly significant results

Table 6. Partial Correlation between Two Matrices While Controlling for the Third Matrix

	Male[a]		*Female*[a]		*Combined*[b]	
Test of Relationship	*Correlation*	*p*	*Correlation*	*p*	*Correlation*	*p*
DERM*GEOG (LANG)	0.103	0.284	0.423	0.008	0.172	0.110
DERM*LANG (GEOG)	0.108	0.302	−0.130	0.735	0.134	0.231
GENE*GEOG (LANG)	0.244	0.081	0.244	0.081	0.233	0.067
GENE*LANG (GEOG)	0.102	0.282	0.102	0.282	0.122	0.196

a. Nine populations.

b. Ten populations.

Table 7. Multiple Correlation Coefficients of One Distance Matrix on Two Other Matrices

	Males		*Females*		*Combined*	
Test of Relationship	*Multiple Correlation*	*p*	*Multiple Correlation*	*p*	*Multiple Correlation*	*p*
DERM*GEOG, LANG	0.240	0.123	0.456	0.002	0.342	0.006
GENE*GEOG, LANG	0.387	0.009	0.387	0.009	0.397	0.002

(combined sample = 0.397, $p = 0.002$). Although some studies have observed higher correlations between language and phenetics or genetics [e.g., Dow et al. (1987) and Sokal (1988)], this study confirms the existence of an intimate association between geography and dermatoglyphics (Froehlich and Giles 1981; Lin et al. 1983, 1984; Enciso 1983).

Discussion

Pairwise and multiple correlation analyses suggest that a relationship exists between geography and dermatoglyphics (in female and combined samples) and between dermatoglyphics and language in the combined sample. Partial correlation analysis failed to document such a pattern. Multiple correlation analysis associated with dermatoglyphics is highly significant (in both the female and combined samples). This suggests that the geographically patterned population expansion (or migration) and localized random genetic processes within language clusters are the probable factors responsible for the observed dermatoglyphic variation in native North American populations. However, much of the unexplained variation may be due to relative degrees of gene flow, unique historical events, and possibly the interactions between genetics and environment that influence the phenotypic expression of individual digital patterns.

The elevated correlation between geographic and dermatoglyphic distances in female samples compared to male samples has been noted in several other investigations. For example, Enciso (1983) found a much better fit between dermatoglyphics and geography for Tlaxcaltecan females (0.968 versus 0.648). This comparison was based on MATFIT and included few populations. Similarly, Lin et al. (1984) observed the same trend in black Carib populations with a correlation between the matrices for females of 0.64 versus 0.38 for males. These differences in the relationships have been interpreted to indicate that males are more mobile, and the poorer fit of genetics and geography reflect differential rates of migration between the sexes. This interpretation makes sense for the black Carib populations, where the males migrate for economic reasons while

the females maintain matrilocal households. However, the Tlaxcaltecan communities are patrilocal, with females establishing residence in the males' household. This apparent contradiction may be the result of a higher rate of male migration for wage labor into adjoining communities and towns. Differential patterns between males and females have also been explained by invoking arguments of maternal and paternal effect (Bener 1982; Erk and Bener 1980). Unfortunately, no embryological or genetic mechanism has been proposed to explain this phenomenon.

In this study we have analyzed samples subdivided by sex or samples of combined sex (by mathematically removing the effects of sex). This analysis of combined-sex samples is possible because the underlying patterns of polygenic traits, such as dermatoglyphics, are Mendelian in nature and both the male and female subsamples of a population are part of a single gene pool. Such analyses not only enchance the statistical power but also eliminate the need to provide (often contrived) sex-related (genetic) explanations of intergroup differentiation.

The high correlations between digital pattern frequencies and blood genetics indicate that these phenotypes are particularly useful in assessing population genetic affinities. These dermal phenotypes provide 40 trait frequencies per population instead of the few comparative data obtained when only total ridge counts or palmar characteristics are considered. Ridge counts per finger produce some unique distributions and statistical noise because of the arbitrary assignment of zero ridges for those fingers containing arches [see Crawford (1977)].

This study demonstrates that dermatoglyphics is a highly informative polygenic system that can be used to study evolutionary processes and population structure. Various multivariate methods, such as principal components, multiple regression, and partial correlation analyses, are valuable analytical tools that are much more informative than descriptive statistics, which are all too often used to characterize complex evolutionary processes.

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