Finger Prints as Criteria of Ethnic Relationship

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INTRODUCTION

DERMATOGLYPHICS provide a tool of unique value for human geneticists and physical anthropologists. The configurations are established long before birth and are not altered by age (except in size), and post-natal environmental circumstances. Permanent and accurate records may be obtained from an individual in a few minutes. Individual records require only a few sheets of paper, and hundreds of such records may be carried in a small traveling bag. Unlike blood samples, dermatoglyphics are not subject to spoilage and may be analyzed years after they are taken. Photographs can be deceptive, as it is often difficult to obtain comparable poses and lighting for a large number of individuals, whereas handprints are free from such disadvantages.

Dermatoglyphics are highly variable, not only from one individual to another, but also from one population to another. These variations are largely heritable, as demonstrated by the fact that monozygotic twins show as great or greater intra-pair than bilateral similarities. In general, the degree of similarity between individuals is correlated with the degree of family relationship. Doubtless multiple genes are responsible for variations in dermatoglyphics and this assumption has likely discouraged many investigators from considering them for research material. Actually such a situation offers several advantages over the employment of well known traits like the various blood groups and other simply inherited variations. A pair of handprints probably provides as much genetic information as do the tests for half a dozen different blood group series. True, we do not know the exact modes of inheritance or the total number of genes involved in dermatoglyphic variations, and perhaps we never shall. But the same may be said of the majority of variations of greatest concern, such as size, intelligence, longevity, disease resistance, and temperament.

Notable advances in livestock and plant breeding have been accomplished through the application of genetic principles, but largely by means of estimates of heritability of quantitative variations rather than through simply inherited one gene variations. Polygenic variations would seem to offer a distinct advantage over simple variations in the area of population genetics, in that they are less subject to the vagrancies of genetic drift. Certainly dermato-

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glyphics are of no importance from the standpoint of assortative mating, which cannot be said to be true of skeletal variations and pigmentation.

Dermatoglyphics are among our most inconspicious variations, and many of the classifications as to types of patterns and configurations are somewhat arbitrary. It requires practice for one to become proficient in analyzing them, yet the rewards would seem to more than justify the time and labor invested. I am not proposing that dermatoglyphics should supplant or are superior to other standard genetic and anthropometric criteria of group relationship. But they have long been neglected, and the time is long overdue when they should take their place alongside the blood groups, pigmentation, hair form, skeletal dimensions, somatotypes, dentition, and other criteria.

INHERITANCE

Data on finger prints far exceed those on other types of dermatoglyphics. Fingerprints vary in type of pattern, angle and size of patterns, and the number of ridges. We shall confine this paper to a discussion of pattern intensity, as expressed both by types of patterns and ridge counts. The two principle types of patterns include whorls and loops. Arches are patternless configurations. Ridge-counts in loops are determined by counting the number of ridges which transverse a straight line from the tri-radius to the pattern core. Whorls have two tri-radii (occasionally three), and ridge-counts include the total number of ridges between each tri-radius and the core. Arches have no ridge-counts.

Extensive investigations of twins and families indicate high heritability of pattern values. In families where both parents have high percentages of whorls, they also occur abundantly among the children, whereas arches are rare. In families where both parents possess high frequencies of arches, arches are frequent among their children and whorls are rare. More variable offspring occur in families where parents have high frequencies of loops, which might be expected, since loops are intermediate in pattern values, as contrasted with arches and whorls at the extremes (Elderton, 1920). Lack of dominance is strongly suggested. Monozygotic twins show greater homolateral than bilateral similarities in pattern types, whereas dizygotic twins manifest approximately two times as many dissimilarities in homolateral comparisons as do monozygotic twins (MacArthur, 1938).

Ridge-count comparisons in the two types of twins also indicate high heritability of pattern values. Geipel (1939) compared the intra-pair differences in ridge-counts in 469 pairs of monozygotic twins with those of 405 pairs of same-sexed dizygotics, and 107 pairs of opposite-sexed dizygotics. The monozygotics showed a mean intra-pair difference of 11.1 ± 0.4 in total ridge-count; whereas the like-sexed dizygotics showed a difference of 39.3 ± 1.4; and unlike-sexed dizygotics a mean difference of 42.3 ± 4.8. Newman (1937) found intra-pair correlations of +0.46 in 50 pairs of dizygotic twins and of +0.95 in 50 pairs of monozygotic twins, and estimated the heritability of differences in the dizygotic twins to be approximately 90 per cent. These findings present convincing evidence that heredity is the major factor in bringing about individual and group variations in type of pattern and ridge-counts.

As might be expected, ridge-count values show positive correlations with percentages of whorls. The former provides a quantitative criterion, the latter a qualitative criterion of pattern intensity. Accurate ridge-counts require complete and legible prints of all digits, requirements which all too frequently are not fulfilled. Comparatively few data have been compiled pertaining to average total a ridge counts in various ethnic groups. Table 1 shows samples from 9 populations. Note that Egyptians, Northern Sudanese,

TABLE 1. RIDGE COUNT VALUES

POPULATION	NUMBER	MEAN
Northern Sudanese, males	84	193.57 ± 9.61
Egyptian Moslems, males	54	201.61 ± 13.69
Egyptian Copts, males	40	195.37 ± 12.85
American Jews, males	63	185.30 ± 7.93
American Jews, females	50	182.40 ± 11.17
Egyptian females	22	165.86 ± 13.30
Nilotic Negroes, males	79	137.58 ± 7.51
American Protestants, males	50	159.30 ± 7.06
American Protestants, females	50	137.10 ± 8.79

and American Jews show similar values, and that males show higher values than females. Nilotic Negroes and American Protestants, the latter principally of British and northwestern European origin, show considerably lower frequencies than do the peoples of Middle Eastern origin. These trends parallel those observed in the incidence of pattern types, as shown in figure 3.

The most extensive work on the inheritance of ridge-counts was done by Bonnevie. She postulated three independent pairs of alleles, each lacking dominance, as being responsible for the genetic variations. One pair determines the thickness of the epidermis, which in turn regulates the number of ridges. Thickness of epidermis is negatively correlated with ridge count. The genotype is determined by the maximum number of ridges on any of the ten fingers. Bonnevie included only one count in whorls, the one having the highest value. Maximum values of 22 or more indicate genotype *vv*; of from 16 to 21 genotype *Vv*; and those of 15 or less genotype *VV*. Cushioning is postulated as being responsible for wide differences between various fingers of an individual. One pair of alleles (*U* and *u*) determines cushioning for the ulnar side (ring and little fingers) and another pair (*R* and *r*) determines it for the radial side (thumb, index, and middle fingers). A difference of more than 10 ridges between the maximum count on a hand and one of the ulnar fingers indicates genotype *UU*; of 5–10 ridges genotype *Uu*, of 4 or less genotype *uu*. Corresponding differences between any digit on the radial side and the maximum on the hand are suggestive of genotypes *RR*, *Rr*, and *rr* respectively.

Bonnevie's interpretation agrees closely with family data. It does not agree so well, however, with data from various ethnic groups. This is brought to light by gene frequency analyses. Correctness of a hypothesis to the effect that a single pair of alleles lacking dominance is responsible for observed variations may be easily tested. If the population is in equilibrium the sum of the square roots of the frequencies of the two homozygous phenotypes should not deviate significantly from unity. This test may be employed to

TABLE 2. CALCULATED FREQUENCIES OF GENES *V*, *v*, *R*, *r*, *U*, AND *u* IN FIVE DIFFERENT POPULATIONS. ONLY MALES ARE INCLUDED

NO.	NORTHERN SUDANESE (85)	EGYPTIANS (53)	NILOTES (75)	AMERICAN JEWS (64)	AMERICAN PROTESTANTS (50)
V	.433	.412	.529	.279	.378
v	.563	.713	.346	.661	.648
$V+v$	0.996 ± 0.054	1.125 ± 0.068	0.875 ± 0.058	.941 ± 0.087	1.026 ± 0.070
R	.717	.752	.660	.707	.824
r	.447	.412	.475	.301	.141
$R+r$	1.164 ± 0.054	1.164 ± 0.068	1.135 ± 0.058	1.008 ± 0.087	0.965 ± 0.070
U	.447	.713	.489	.625	.678
u	.553	.474	.565	.414	.489
$U+u$	1.000 ± 0.054	1.187 ± 0.068	1.054 ± 0.058	1.049 ± 0.087	1.167 ± 0.70

particularly good advantage where it is possible to test several populations, differing from each other in frequencies of the traits under consideration. The M and N blood types provide an excellent sample of a trait of this sort. The calculated gene frequencies obtained by this method may also be compared with the actual frequencies. Populations from all over the world have been tested and the calculated frequencies almost always total approximately unity, and agree closely with the actual.

Inspection of table 2 reveals significant deviations from unity in 6 of the 15 gene frequency calculations among the 5 populations. Moreover, comparisons of the frequencies do not always indicate differences in the various populations which are outstanding, both in total ridge counts and in pattern frequencies (See table 3). These observations cast some doubt on the correctness of Bonnevie's hypothesis.

It is of interest to note that with one exception all deviations of significance in table 2 are greater than one. This suggests that Bonnevie may have allowed too small a phenotypic range for the heterozygotes. It should also be re-

TABLE 3. PATTERN INDICES OF VARIOUS POPULATIONS

POPULATION	NUMBER	INDICES ♂	♀	♂ + ♀	INVESTIGATOR
Congo Pygmies	101	8.60			Abel
Pygmies	347	9.90			Geipel
	369		9.3		Geipel
	153	10.37			Dankmeijer
	54		10.70		Dankmeijer
Dutch	278		11.36		Dankmeijer
	2,222	11.85			Dankmeijer
Negroes, West Africa	105		11.94		Dankmeijer
	238	12.02			Dankmeijer
Negroes, Spanish Guinea	53		11.40		Pons
	221	12.31			Pons
Spaniards	100		11.89		Pons
	100	12.32			Pons
Russian	11,000		11.89		Semenovsky
	11,000	12.59			Semenovsky
Norwegians	24,518			11.83	Bonnevie
American Catholics (N.W. Eur. & British descent)	122	11.90			Rife
	91		12.04		Rife
American Protestants (British descent)	258		11.91		Rife
	230	12.14			Rife
English	5,000			12.05	Scotland Yard
	2,000	12.03			Waite
Sudan Negroes					
Dinka	132	12.30			Rife
Shilluk	106	12.33			Rife
Bari	72	12.75			Rife
Nuer	110	11.58			Rife
Germans, East Prussia	346		12.18		Duis
	416	12.47			Duis
American Protestants (European descent)	150		12.10		Rife
	154	13.23			Rife
German, Saxony	99,400	12.75			Heindl
Portugese	1,00		12.61		Valadares
	1,000	12.99			Valadares
Ainu	319		12.12		Koya
	213	13.14			Koya
Javanese	1,000		12.94		Dankmeijer
	1,000	13.32			Dankmeijer
Negroes, Sierra Leone	58			13.53	Cummins
Italians	1,579	13.14			Falco
Gypsies, Rumania	187			13.56	Abel
Chilean Indians	246			12.80	Henckel
American Jews	347		13.26		Rife
	144	13.80			Rife
Jews, New Orleans	100		13.95		Cummins & Midlo

TABLE 3. CONTINUED

POPULATION	NUMBER	INDICES ♂	INDICES ♀	INDICES ♂ + ♀	INVESTIGATOR
	100	13.75			Cummins & Midlo
Jews Germany	1,037	13.87			Kirchmair
Hindu, India	27	13.41			Schlaginhaufen
Hindu, Calcutta	50	14.03			Bisivas
Arabs, Mitwali	138			13.95	Cummins & Shanklin
Egyptians, unselected	1,000	13.70			Rife
	300		13.14		Rife
Egyptians, Coptic, Assint	113	14.03			Rife
Egyptians, Coptic, Cairo	61	14.65			Rife
Egyptians, Moslems, Assint	20	14.60			Rife
Egyptians, Moslems, Cairo	77	14.30			Rife
Northern Sudanese	100	14.22			Rife
Lebanese	1,061	14.30			Shanklin & Cummins
Syrians	1,004	14.55			Leriche
Armenians	179	14.12			Abel
Indians (Mexico & Central America)	633			13.50	Cummins, Cummins Leche & Steggerda
North American Indians (Navaho, Pueblo Arapahoe, Comanche)	400			14.57	Cummins; Downey, Cummins & Goldstein
Ramah Navaho	270			15.39	Spuhler & Bean
Koreans	700			14.46	Kubo
Chinese	300			14.79	Shuno & Mikami
Japanese	12,940			14.90	Kanazawa
Eskimo, Greenland	68			17.40	Abel
Australian Aborigines	89		17.21		Cummins & Setzler
	84	17.73			Cummins & Setzler

membered that each of the populations tested here was of one sex, another possible source of discrepancy, in view of the fact that males possess higher ridge counts than females. She was doubtless correct in assuming that at least one pair of alleles (*Vv*) has a common effect on all digits, and that dominance is lacking.

Most observations seem to indicate that interpopulation trends show similarities in all digits and on both hands. Patterns and ridge counts do not occur at random on the ten digits or on right and left sides. But these interdigital and bilateral variations show essentially similar trends in different populations. Whorls occur more frequently on right fingers, arches on left fingers. Whorls also occur with greatest frequencies on ring fingers and thumbs, arches on index and middle fingers. Moreover, the incidence of arches bears an inverse relationship to the incidence of whorls, although the range of variation is considerably greater in the latter. These trends are well illustrated in figures 1 and 2. While the five populations show great difference in percentages of patterns, the interdigital and bimanual trends are essentially the same. The greatest interpopulation variation is with respect to the relative percentages of whorls on thumbs and ring fingers. Poll (1938) investigated this phenomenon and pointed out that in some ethnic groups (Negroes, American Indians) the corresponding fingers of right and left hands show greater similarities than do any two fingers of the same hand. This is known as the all pair rule. Caucasians and Mongolians manifest comparable degrees of similarity in the occurrence of whorls on thumbs and ring fingers. The two right and two left digits may show fewer differences than right and left thumbs

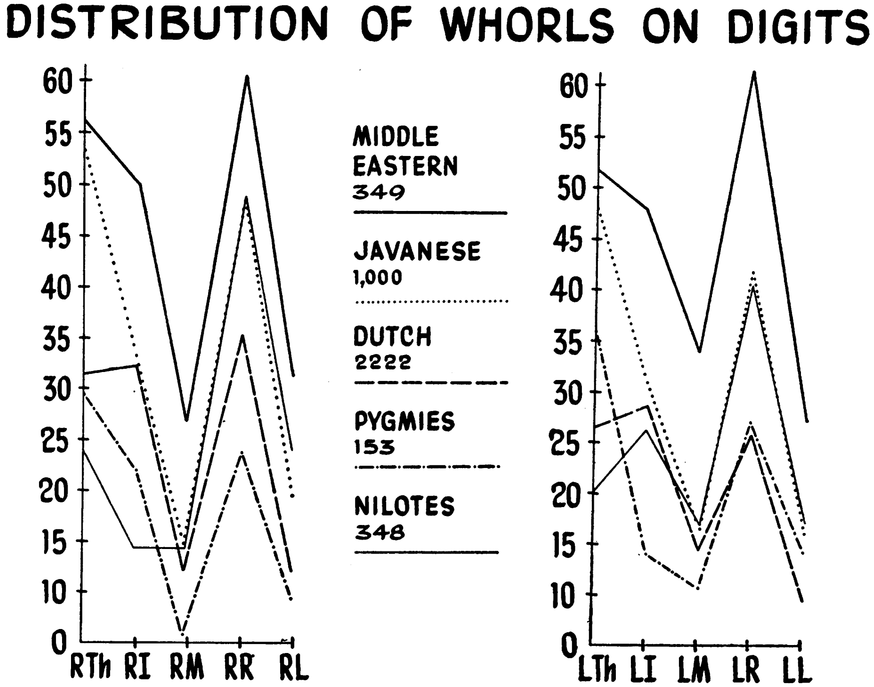

FIG. 1. Percentages of whorls are shown, beginning with the right thumb, followed by index, middle, ring, and little fingers. Data on the Pygmies, Dutch, and Javanese were collected by Dankmeijer (1938). Data on the Middle Easterners include Egyptians, Northern Sudanese, and American Jews; Nilotes include data from Dinka, Shilluk, and Nuer tribes (tables 1 and 3).

and right and left ring fingers. Other fingers still manifest greater bimanual than intra-digital similarity. This is known as the pair group rule.

In figure 1, Middle Easterners, Dutch and Javanese conform to the pair group rule (Dankmeyer, 1938), while Pygmies and Nilotes belong in the all-pair category (Rife, 1953). Nilotes possess more than twice as many whorls on ring fingers as on thumbs, whereas Pygmies have the highest frequencies on thumbs. Javanese and Nilotes show rather striking similarities in percentages of whorls on ulnar fingers, but marked differences on the radial digits. This trend is also apparent in the occurrence of arches.

Dissimilar ulnar and radial trends present the basis for Bonnevie's assumption that a gene (U) partially inhibits patterns on the ulnar digits and that another gene (R) has a similar inhibiting effect on the radial digits.

Pons (1952) compiled observed gene frequencies (V, v, R, r, U, u) for various populations. Unfortunately, these frequencies do not provide the reader with a very clear picture of the distributions of pattern types and ridge counts in the various populations. Bonnevie may have been correct in postulating three pairs of alleles as being responsible for variations in ridge counts. But the phenotypic criteria do not appear to be very accurate. Her analyses demonstrate the difficulties in making accurate gene frequency estimates for traits whose expression not only depends upon multiple genes, but may also be

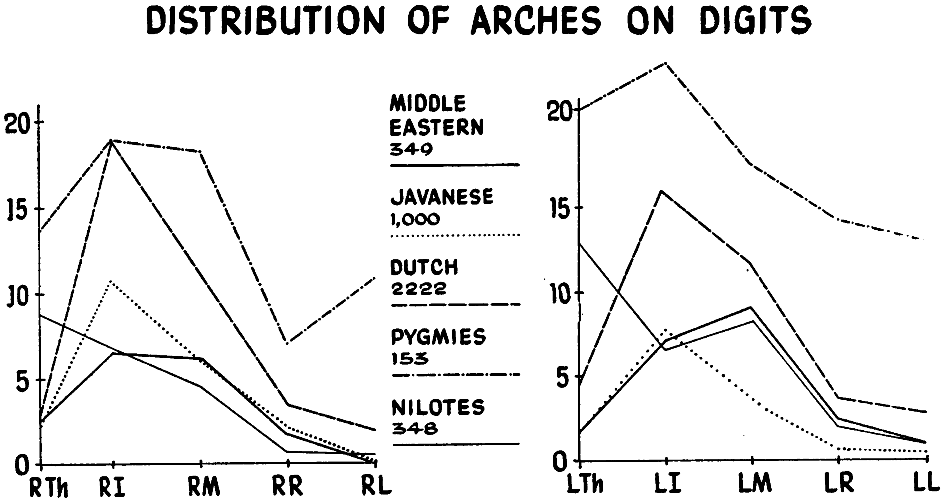

FIG. 2. Data on the percentages of arches among the same populations recorded in figure 1.

modified by non-genetic factors. Fortunately, no dominance seems to be involved, rendering it possible to obtain a more accurate concept of genotypes than if the reverse were true.

GEOGRAPHIC AND ETHNIC DISTRIBUTIONS OF PATTERN INDICES

Data on percentages of whorls, loops, and arches are more abundant than on total ridge counts and gene frequencies. Various indices have been devised for expressing the pattern values as obtained from the percentages of whorls, loops, and arches. Table 3 shows the pattern indices of several populations, and figure 3 illustrates the distribution of pattern values throughout the world. The pattern index is that Cummins, (Cummins and Midlo, 1943) and is obtained by adding twice the number of whorls to the number of loops. An individual having 10 arches has an index of 0, while an individual having 10 whorls has an index of 20.

Inspection of table 3 shows a range of mean pattern values of from 8.+ to 17.+. Most of the populations range between 11 and 15. Australian aborigines have the highest indices of all, African pygmies the lowest of all. It is of interest to note that Australians not only have over 70% whorls, but less than 1% arches; whereas Pygmies have around 20% of both whorls and arches. Bushmen have frequencies corresponding to those pygmies. Thus the two extremes in pattern values are represented by two of the most primitive ethnic groups. Eskimoes also have very high indices. Mongoloid peoples and North American Indians have indices averaging from 14 to 15, followed by Middle Eastern peoples. Some of the indices of Middle Easterners in table 3 exceed 14.25, the value assigned on the map. But these high values are for

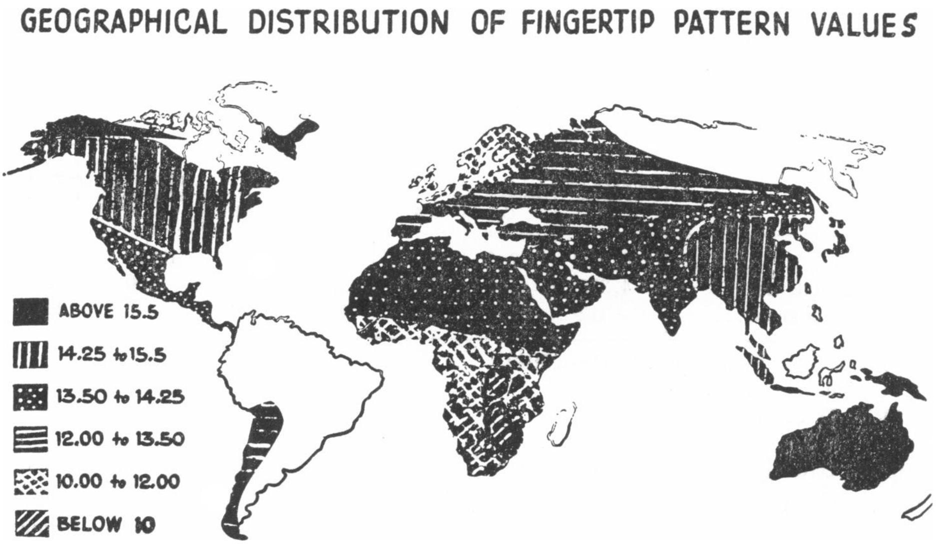

FIG. 3

male populations, who usually have higher pattern frequencies than females. The average is below 14.25. Note that Syrians, Lebanese, Arabs, Egyptians and Jews (both American and German) have essentially similar pattern values. In eastern and southwestern Europe the indices are significantly lower, 12 to 13.50. In Northern Europe and the British Isles values are below 12. The geographical distribution of indices in Europe and Asia is similar to that of blood group antigen B, both increasing from west to east in Europe and Asia, and from north to south in Europe.

Sharp differences between the pattern indices of peoples living in adjacent areas are found in Africa. Arabs, Egyptians, and other Caucasian peoples inhabiting North Africa are characterized by indices averaging around 14, whereas their neighbors to the south have indices averaging close to 12. This is especially noticeable in the Sudan, where the Nilotes in the south have indices of approximately 12, whereas the northern Sudan of mixed Arab-Negro origin possess indices of over 14. West African Negroes show variable frequencies from one group to another, some well over 12, other considerably below. These fluctuations are too great to be shown on the map, figure 3.

Among American Indians, those in Chile manifest the lowest, and North Americans the highest values. Farther to the north, Eskimoes have even higher indices.

DISCUSSION

Like other criteria of ethnic relationship, pattern indices alone do not give an accurate estimate. The indices of African Negroes are similar to those of west Europeans and British, and those of Semitic peoples do not differ greatly from those of Mongolians. Among Caucasians marked differences are apparent between northwestern Europeans and Semitic peoples. This observation

TABLE 4. ABO BLOOD GROUP DISTRIBUTIONS AND FINGER PATTERN INDICES AMONG EGYPTIANS AND NORTHERN AND SOUTHERN SUDANESE

	NUMBER OF PERSONS	BLOOD GROUPS (%)				NUMBER OF PERSONS	PATTERN INDICES
		O	A	B	AB		
Egyptians	10,045[1]	32.6	35.4	24.3	7.4	1,271	14.25
Northern Sudanese	4,370[2]	45.4	27.8	22.2	4.5	100	14.22
Southern Sudanese	312[3]	52.5	25.6	18.2	4.1	420	12.17

[1] Abdoosh, Y. B. and Salah El-Dewi. 1949.
[2] Corkill, N. L. 1949.
[3] Rife, D. C. 1953.

applies equally well to other criteria. The A, B, O blood groups show marked similarities in their frequencies among Chinese, Negroes and Arabs. Egyptians differ quite significantly from both Arabs and Negroes. It is only when several independent criteria, such as pattern indices, different blood group series, skeletal dimensions, hair form, etc., are employed that one can obtain an accurate estimate of ethnic interrelationships. The problem here is essentially the same as in twin diagnosis or disputed paternity. Similarity between two populations with respect to any single criterion does not necessarily imply they are closely related, whereas a highly significant difference does suggest no close relationship. But marked similarity in many independent criteria certainly indicates close ethnic relationship.

Comparisons of patterns indices and ABO blood group frequencies among Egyptians, northern and southern Sudanese, as shown in table 4, provide an example of the value of independent criteria in evaluating group relationship. Note that northern and southern Sudanese show somewhat similar blood group frequencies whereas they show a great difference in pattern indices. Egyptians show highly different blood group frequencies from those found in both northern and southern Sudanese, yet the pattern indices of northern

Sudanese and Egyptians are strikingly similar. Blood group data alone might lead one to conclude that northern and southern Sudanese are closely related whereas Egyptians are not closely related to either groups of Sudanese. Finger print data alone suggests close relationship of northern Sudanese and Egyptians, but no close relationship between southern Sudanese and either of the other populations. But when both traits are considered it becomes apparent that no very close relationships exist between any of the three populations.

SUMMARY

Dermatoglyphics provide a tool of unique value for human population genetics. More data are available on finger prints than on other types of dermatoglyphics. Pattern indices of finger prints range from approximately 17 among Australian aborigines to below 10 among African pygmies. Mongoloid peoples possess higher pattern frequencies than Caucasians and Negroes. Among Caucasians, Semitic peoples possess the highest pattern indices, northwestern Europeans and English the lowest indices. African Negroes manifest pattern indices similar to western Europeans. American Indians range from 12 in Chileans to over 14 among North Americans.

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