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Are the Biological Differences between North American Indians and Eskimos Truly Profound?¹

by Emőke J. E. Szathmary and Nancy S. Ossenberg

THE PREVAILING VIEW on the relationship between North American Indians and Eskimos is that the two groups are biologically distinct, although both are branches of the Mongoloid family tree. Eskimos are commonly held to be the latest migrants into the New World. As such, they are thought to be more similar to Bering Sea Mongoloids specifically (Levin 1963, Laughlin 1963, Oschinsky 1964) and to Asiatic Mongoloids generally (Laughlin 1966, Oswalt 1967, Stewart 1974) than to American Indians. That Eskimoan languages are grouped within a distinct language stock along with Aleut (Eskaleutian:

Swadesh and Marsh 1951) rather than within a North American Indian language stock is generally taken as support of the presumed biological distance between these populations. This perspective has had significant ramifications, particularly in the interpretation of the archaeological record with regard to Eskimo origin.

We propose to examine the assertion of great divergence between Eskimos and Indians by using both genetic-marker and cranial data. We begin with a brief consideration of some of the hypotheses of Eskimo origin. We then examine the genetic and morphological evidence in support of these hypotheses. Lastly we show that a different conceptual framework, based on our findings, can resolve the conflicting interpretations of the known cultural sequences in Alaska.

HYPOTHESES OF ESKIMO ORIGIN

Hypotheses of Eskimo origin have been numerous and varied since 1767, when David Cranz first suggested that Eskimos resembled the inhabitants of Tartary, between Mongolia and the Arctic Ocean. In the first half of the 20th century, two dominant but conflicting views claimed their adherents. One argued for inland North American roots for the Eskimos, while the other saw their beginnings in Siberia. The hypotheses arising from each of these views differed considerably in detail; we confine our discussion to the general outlines.

One set of hypotheses, most recently elaborated by Birket-Smith (1959) but first articulated by Rink (1887), Murdoch (1888), Boas (1888), and Steensby (1917), suggested that Proto-Eskimo populations originated in the interior of Alaska or, most likely, in central Canada between the Mackenzie River and Hudson Bay. From here Palaeo-Eskimos spread to the coast and moved along it to Alaska. Full adaptation to the maritime niche and influences from Siberia in the Bering Sea region gave rise to the whale-hunting Neo-Eskimos, who then spread along the Arctic coast from Alaska to Greenland. Only inland, in the barren lands of Canada's Northwest Territories, did Neo-Eskimos fail to gain a foothold. From this area, Eskimos pushed out to the coast in successive waves and superimposed themselves on the coastal Neo-Eskimo stratum, forming the culturally distinguishable group that Birket-Smith (1959) labelled the Eschato-Eskimo.

The conflicting view was that the origins of Eskimos and

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The present paper, submitted in final form 8 II 78, was sent for comment to 50 scholars. The responses are printed below and are followed by a reply by the authors.

their culture lay in Siberia, where initial adaptations were to an inland-hunting subsistence base (Jenness 1928, Collins 1937, Larsen and Rainey 1948). The orientation toward sea-mammal hunting was perfected in Alaska by the Palaeo-Eskimos, who evolved into Neo-Eskimos by absorbing both immigrants and cultural influences from Siberia. These Neo-Eskimos then spread along the coast to Greenland. Inland, in the Keewatin District of Canada, the Palaeo-Eskimos continued to hold sway, as exemplified by the caribou-hunting Eskimos of that region.

The earliest papers on Eskimo origin were based principally, but not exclusively, on ethnological data. Later papers reflected the addition of knowledge from Arctic archaeology and intensive studies on Eskimoan linguistics. The effort to coordinate the insights gleaned from these areas led to a shift in interpretation. The most favoured current view of Eskimo origin is an altered but lineal descendant of the Siberian theme. Eskimos and their linguistic relatives the Aleuts are considered to be the descendants of a series of adjacent populations that inhabited the Pacific shore from Umnak Island to Hokkaido during the last glaciation. Their maritime adaptations allowed further cultural elaboration and population expansion north and then east as Beringia sank and the Alaskan littoral came into existence (Laughlin 1963, 1975). Linguistic studies have shown connections between Eskaleutian and Chukotan, the northeastern Siberian language family that includes Chukchi, Koryak, and Kamchadal (Swadesh 1962), thereby corroborating the archaeologically based claims for a Bering Sea origin for the Eskimos.

The consequences of this view are the following theses: (1) Eskimos and Indians are the descendants of different populations that entered the New World at different times. (2) Eskimos and Indians entered the New World by different routes (coastal versus inland); thus contact between them was minimized and their biological distinctiveness maintained. (3) Culturally imposed barriers through time maintained the initial biological differences between Eskimos and Indians. (4) These cultural barriers are indicated by differences in language and technology. (5) The differences in technology are reflected in the archaeological record. Thus, although it is a dictum that physical type should not be inferred from the cultural record, archaeologists have seen ancestral Eskimos (i.e., biological Eskimos) as the makers of assemblages geared to a maritime hunting niche. Indians are presumed to be inland-, specifically forest-, oriented, and therefore Indian origin is ascribed to artifacts that either have a "forest flavour" or differ from known "Eskimo" traditions. While these distinctions may be warranted for recent horizons, the maintenance of the Indian-Eskimo dichotomy for traditions dated 10,000 B.P. is questionable. A pivotal issue as we see it is whether Eskimos and Indians are truly as distinct as has been claimed, or whether Eskimos and at least some Indians are the descendants of a common population substrate.

BIOLOGICAL EVIDENCE FOR INDIAN-ESKIMO RELATIONSHIP

At least two lines of evidence can be pursued to measure affinity. Blood-group and serum-protein gene-frequency data are available for a large number of populations; skeletal material is known for a smaller set. If both kinds of evidence are desired, contemporaneity of the groups is precluded. Assuming that the tribal or linguistic assignment of the skeletal series is reasonably correct (i.e., made on the basis of geographic provenience and/or cultural identification of grave goods associated with bones), there is no a priori reason to think that the bone populations represent lineal ancestors of the people from whom the genetic-marker data were obtained. There is a relationship, obviously, but not the one-to-one correspondence that

the tribal labels or regional identifiers would suggest. The two sets of data are, therefore, independent.

Table 1 lists the populations compared in this paper. We have made an effort to secure data from groups in the same geographic area, specifically, the Arctic, Subarctic, Northwest Coast, and Great Plains. Apache and Navajo are included because they are Northern in origin. Unfortunately, there is not a complete correspondence between the populations used for the genetic and for the skeletal analyses. For example, discrete-trait data for Greenland Eskimo and Chukchi skeletal collections are not yet available. Similarly, we lack gene-frequency data on some of the loci used in the analysis for Cheyenne, Dakota, Ingalki, and many of the specific Eskimo groups listed in the skeletal series. For this reason, we first examine each body of data separately and then compare our results.

THE GENETIC EVIDENCE

Gene-frequency data for eight different blood-group systems (ABO, Rh, MNSs, Diego, Duffy, Kell, Kidd, and P) and three serum-protein systems (albumin, serum α -globulin, and haptoglobin), comprising 35 alleles, were obtained for the populations listed in table 1. Since not all samples had been tested for precisely the same array of genes, it was necessary to group samples on a regional basis (e.g., "South Alaskan" Eskimo). The procedures used and blood-group gene frequencies for 14 of the populations are given in Szathmary (1977, 1978). Most of these populations consist of samples of 100 individuals or more, the Tlingit and Aleuts excepted. Blood-group gene frequencies and sample sizes for Chukchi, Asiatic Eskimos, Blackfoot, and Assiniboin, which were not included in the previous papers, are given in table 2. Serum-protein gene frequencies for all 18 populations are given in table 3.

Similarities between populations were determined with genetic-distance analysis, a procedure which uses all the genetic information available for any two populations to calculate a single statistic. The resultant measure indicates the magnitude of difference between the two populations. By inference, the smaller the statistic, the more similar are the groups compared. Distance analysis was carried out using Nei's (1972) standard distance statistic, which has been found to show high correlation (Chakraborty and Tateno 1976, Rothhammer, Chakraborty, and Llop 1977, Szathmary 1978) with distances obtained by the Cavalli-Sforza and Edwards (1967) method. The population distances with their standard errors are shown below the diagonal in table 4. None of the Mongoloid-Eskimo versus Mongoloid-Indian distances differed significantly from each other. Similarly, the Chukchi-Eskimo and Chukchi-Indian distances were not significantly different. There is, then, no statistical validity to the claim that Eskimos are closer to classic Mongoloids than are American Indians.

In a previous study (Szathmary 1978) comparing seven major population aggregates (Caucasoids, Negroids, Mongoloids, Siberians, Eskimos, Indians, and Ainu) on 25 blood-group genes, similar findings were obtained. Eskimos and Indians, the latter being representatives of Subarctic and Northwest Coast tribes drawn from three distinct language groups (Algonkian, Na-Dene, and Wakashan), were consistently closer to each other than to any other major population. It is worth emphasizing that total sample size in that study ranged from 1,000 to 5,000 (depending on the locus) for Eskimos and from 1,400 to 2,250 for Indians; hence the convergence is not likely to be a chance finding attributable to inadequate sample sizes. This study, which improves upon the former by examining more of the Indian and Eskimo genomes through the addition of three more genetic systems and more populations, provides further corroboration of Indian-Eskimo affinity.

A two-dimensional representation of the distances is shown in figure 1. Dendrogram construction was based on Nei's (1975)

modification of Sokal and Sneath's (1963) method. The resultant "tree" represents at minimum current genetic similarities between populations. It shows that Eskimos from Alaska to Greenland form a genetically recognizable unit that differs from the American Indian groups with which it is compared. The sole exception is the Blackfoot, who resemble the Eskimos in their genetic constitution. By far the greatest similarity of non-

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Siberian Eskimos is to North American Indians, specifically to Tlingit, Haida, Navajo, Northern Athapaskans, and Northern Algonkians. Other Indians, such as Assiniboin and Apache, are noticeably divergent, as are Asiatic Mongoloids, Aleuts, Chukchi, and Asiatic Eskimos.

TABLE 1
POPULATIONS REPRESENTED IN THIS STUDY

POPULATION	GENETIC DATA BY TRIBE OR REGION	SKELETAL DATA BY TRIBE OR REGION
Eskimos		
South Alaskan	Kodiak Island: Old Harbor, Karluk, Kaguyak Koniag isolates "X," "Y," "Z"	Kodiak Island Bristol Bay Nushagak River Kuskokwim River Hooper Bay Nunivak Island Pt. Barrow
North Alaskan	Pt. Barrow Wainwright Anaktuvuk Pass	
Central Arctic	Copper Aivilik Igloolik Okomiut Ft. Chimo Hudson Bay (east shore) Baffin Island Ungava Bay	Mackenzie Delta
Eastern Arctic	Augpilagtok Southwest Greenland hamlets Thule	
West Greenland	Angmagssalik Scoresbysund	
East Greenland	Commander Islands, U.S.S.R. Alaska	Kagamil Island, eastern Aleutians
Aleuts		
Indians		
<i>Na-Dene language phylum</i>		
Haida	Queen Charlotte Islands (Masset and Skidegate)	Haida
Tlingit	Sitka and Mt. Edgecombe, Alaska	Tlingit
Northern Athapaskans	Chilcotin Kutchin Slave Slave and Beaver Tuchone	Ingalk ^a Tanaina Kutchin, Hare, and Dogrib
Apache	Cibecue East and West White Mountain San Carlos Mescalero	Apache
Navajo	West Navajo Piñon, Ramah	Navajo
<i>Algonkian language family</i>		
Northern Algonkians	Cree Montagnais Naskapi Northern Ojibwa	
Blackfoot	Blackfoot Blood	Piegan, Blackfoot, and Blood
Cheyenne		Cheyenne
<i>Siouan language stock</i>		
Assiniboin	Assiniboin	Assiniboin
Dakota		Dakota
Asiatics		
Chukchi	Coast Chukchi	
Asiatic Eskimos	Naukan Chapline Sirenki	St. Lawrence Island ^b
Mongoloids	Japan, Korea	

^a This sample, from ten sites along the Yukon River and its tributary the Innoko, between Holy Cross and Refuge Creek/Holocachat, may include a few Koyukon Athapaskan skeletons.

^b St. Lawrence Island is part of Alaska, but in geographic, linguistic, archaeological, and historical terms the inhabitants are more closely related to Siberian than to Alaskan Eskimos (Oswalt 1967, Bandi 1969, Krauss 1973a).

In the examination of such a diagrammatic representation of genetic similarity, the obvious question is whether the pattern obtained is phylogenetic or can be explained by other micro-evolutionary events. Nei (1975) has stated that phylogenetic relationships will be portrayed if a large number of loci representing a random sample of the genome is used in the analysis. Under such conditions, the effects of genetic drift and natural selection, varying between loci, are "averaged out" (p. 199). Unfortunately, these conditions are almost never met in human population studies for a variety of reasons. Firstly, serum proteins and red-cell enzymes are not a random array of genetic traits, but only the ones that are electrophoretically detectable. Secondly, most of the published gene-frequency information is for blood groups only, and then generally for fewer than nine of the possible polymorphic systems. If selection has had an effect on the genetic markers, then the blood groups may be among the most affected, for several blood-group systems show great gene-frequency variability among populations (Cavalli-Sforza 1973).

It is all the more remarkable, therefore, that dendograms

based on a few blood-group systems (ABO, Rh, MNS, Duffy, Diego) show good correspondence to what would be expected on the basis of historical relationship (Cavalli-Sforza and Edwards 1964). Because the early analyses employed populations widely separated geographically, concordances (interpreted as indicating phylogeny) were not expected for more closely located and/or related groups. Recent studies of patterns of genetic similarity between groups known to be closely related (e.g., Ward and Neel 1970, Friedlaender et al. 1971, Spielman 1973, Spielman, Migliazza, and Neel 1974), however, have found good agreement between genetic dendograms and nonbiological criteria such as migration matrices and linguistic affiliation. The genetic markers used in these studies include blood groups, serum proteins, and occasionally red cell enzymes found at 7 to 11 loci. We deduce from these results that although 7 to 11 systems must constitute a small sample of the entire genome, they are an adequate sample of the known genome. Since they have indicated phylogenetic relationship adequately between recently diverging groups, they should be sufficient to do so for groups more distantly related and more dispersed. We emphasize, however, that the precision of the results depends mostly on the number of loci examined (Li and Nei 1975), and for this reason it is always desirable to examine more systems.

Our contention that the Indian-Eskimo dendograms show phylogenetic relationship would be strengthened if we could demonstrate, as all the foregoing studies have done, concordance between them and patterns based on nonbiological criteria. Of such criteria, linguistic affiliation can reflect phylogeny if it is assumed that native speakers of indigenous languages have learned them from their biological parents and that replacement of one language by another has not occurred. Studies on North American populations suggest that such comparisons are appro-

TABLE 2
BLOOD-GROUP GENE FREQUENCIES OF CHUKCHI,
ASIATIC ESKIMOS, ASSINIBOIN, AND BLACKFOOT

SYSTEM AND ALLELE	POPULATION			
	CHUKCHI	ASIATIC ESKIMOS	ASSINIBOIN	BLACKFOOT
ABO	(96)	(124)	(162)	(389)
<i>A</i>1967	.1620	.1611	.5526
<i>B</i>1223	.1480	.0000	.0103
<i>O</i>6810	.6899	.8389	.4371
Rh	(103)	(118)	(155)	(389)
<i>R</i> ¹4961	.3425	.4888	.5146
<i>R</i> ²2194	.3722	.3576	.3615
<i>R</i> ^z1252	.1532	.0144	.0227
<i>R</i> ⁰1592	.1321	.0202	.0000
<i>r</i>0000	.0000	.0942	.0908
<i>r'</i>0000	.0000	.0000	.0000
<i>r''</i>0000	.0000	.0248	.0104
MNSs	(78)	(95)	(145)	(339)
<i>MS</i>1906	.1083	.1979	.3202
<i>Ms</i>3286	.4391	.6883	.5308
<i>NS</i>1620	.0864	.0538	.0772
<i>Ns</i>3188	.3662	.0600	.0718
Duffy	(75)	(57)	(155)	(383)
<i>Fy</i> ^a2697	.1943	.6592	.7549
<i>Fy</i> ^b7303	.8057	.3408	.2451
P	(82)	(98)	(155)	(146)
<i>P</i> ¹2349	.1982	.6688	.4148
<i>P</i> ²7651	.8018	.3312	.5852
Kell	(79)	(86)	(162)	(148)
<i>K</i>0570	.0407	.0000	.0000
<i>k</i>9430	.9593	1.0000	1.0000
Diego	(66)	(54)	(104)	(148)
<i>Di</i> ^a *.....	.0955	.0973	.0000	.0239
<i>Di</i> ^b9045	.9027	1.0000	.9761
Kidd			(95)	(342)
<i>Jk</i> ^a †.....	.4775	.6056	.5803	.7190
<i>Jk</i> ^b5225	.3944	.4197	.2810

NOTE: All gene frequencies were recalculated from the literature using Reed and Schull's (1968) MAXLIK. Figures in parentheses are sample sizes.

SOURCES: Except as noted below, for Chukchi and Asiatic Eskimos, Rychkov and Sheremeteva (1972b); for Assiniboin, Chown and Lewis (1955); for Blackfoot, pooled data of Chown and Lewis (1953) and Rokala, Polesky, and Matson (1976).

* For this allele, data for Assiniboin are those of Pollitzer et al. (1967) for Siouan-speaking Catawba.

† For this allele, data for Chukchi are pooled data from non-Siberian Mongoloids (Szathmary 1977a), data for Asiatic Eskimos the frequency in all Eskimos (Szathmary 1977a), and data for Assiniboin those of Pollitzer et al. (1967) for Siouan-speaking Catawba.

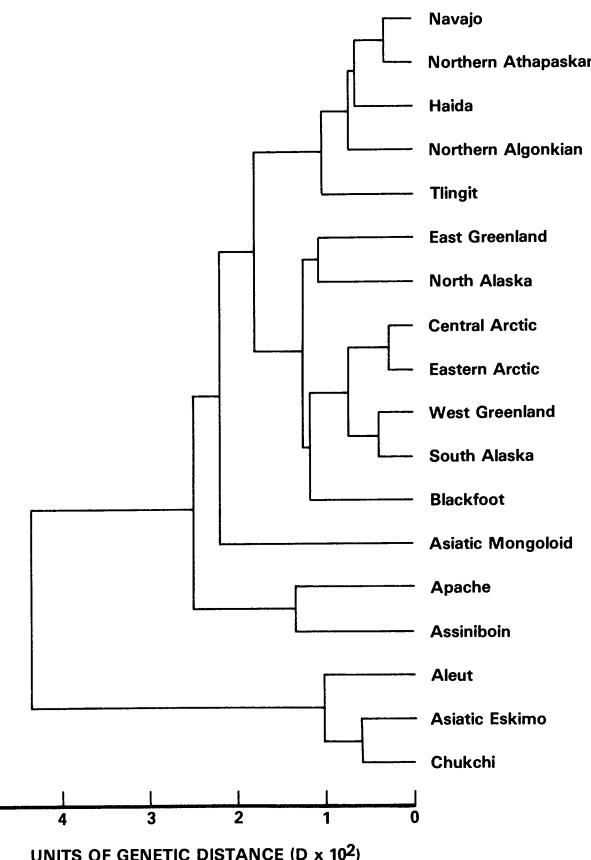


FIG. 1. Relationships among 18 populations, based on 35 alleles at 11 loci. Distances are read along the horizontal axis. Vertical positioning is immaterial.

TABLE 3
SERUM α -GLOBULIN, HAPTOGLOBIN, AND ALBUMIN GENE FREQUENCIES IN 18 POPULATIONS

POPULATION	SYSTEM AND ALLELE						
	SERUM α -GLOBULIN		HAPTOGLOBIN		ALBUMIN		
	Gc ¹	Gc ²	Hp ¹	Hp ²	Al ^A	Al ^{Na}	
Eskimos							
South Alaskan7027 (111)	.2973	.3028 (289)	.6972	1.000 (82)	0	0
North Alaskan6893 (103)	.3107	.3419 (291)	.6581	1.000 (268)	0	0
Central Arctic6524 (338)	.3373*	.3441 (356)	.6559	1.000 (356)	0	0
Eastern Arctic7014 (67)	.2985	.3496 (246)	.6504	.9933 (225)	.0067	0
West Greenland6921 (1,330)	.3079	.3400 (1,391)	.6600	1.000 (413)	0	0
East Greenland5718 (564)	.4282	.4837 (1,103)	.5163	1.000 (78)	0	0
Aleuts6803 (61)	.3197	.5313 (80)	.4687	1.000 (15)	0	0
Indians							
Haida6993 (409)	.3007	.5412 (413)	.4588	1.000 (365)	0	0
Tlingit8390	.1603†	.4375 (80)	.5625	1.000 (91)	0	0
Northern Athapaskans8964 (251)	.1036	.4078 (423)	.5922	.9460 (361)	.0540	0
Apache8390	.1603†	.5867 (98)	.4133	.9730 (641)	.0094	.0203
Navajo9776 (245)	.0224	.4430 (263)	.5570	.9574 (563)	.0373	.0053
Northern Algonkians8418 (411)	.1557‡	.4971 (1,365)	.5029	.9645 (1,927)	.0355	0
Assiniboin9150 (100)	.0850	.5400 (100)	.4600	.9942 (260)	.0058	0
Blackfoot8052 (95)	.1948	.4578 (95)	.5422	.9833 (180)	.0167	0
Asiatics							
Chukchi7241 (29)	.2759	.3095 (42)	.6905	.9772	.0228	0§
Asiatic Eskimos6053 (38)	.3947	.3583 (60)	.6417	.9989	.0011	0
Mongoloids7770 (583)	.2230	.2467 (1,074)	.7533	.9988 (4,029)	0	0#

NOTE: All gene frequencies were recalculated from the literature using Reed and Schull's (1968) MAXLIK. Figures in parentheses are sample sizes. Groupings and sources (except as indicated below) are as follows:

South Alaskan Eskimos—Yupik-speakers (Blumberg, Allison, and Garry 1959, Scott et al. 1966), St. Lawrence Island (Lampl and Blumberg 1977)

North Alaskan Eskimos—Inupik-speakers (Blumberg, Allison, and Garry 1959, Scott et al. 1966, Lampl and Blumberg 1977)

Central Arctic Eskimos—Igloolik (McAlpine et al. 1974, Cox, Simpson, and Janti n.d.)

Eastern Arctic Eskimos—Baffin Island (Mourant, Kopec, and Domaniewska-Sobczak 1976), Ft. Chimo (data of Auger in Simpson, Eriksson, and Lehmann 1976), Ungava Bay (Lampl and Blumberg 1977)

West Greenland Eskimos—Thule, unmixed, and West Greenland hamlets (Mourant, Kopec, and Domaniewska-Sobczak 1976), West Greenland (Lampl and Blumberg 1977)

East Greenland Eskimos—Angmagssalik and Scoresbysund (Mourant, Kopec, and Domaniewska-Sobczak 1976), East Greenland (Lampl and Blumberg 1977)

Aleuts—Alaska (Scott et al. 1966, Lampl and Blumberg 1977), Commander Islands (Rychkov and Sheremeteva 1972a)

Haida (Lovett 1967, Melartin 1967)

Tlingit—Sitka and Mt. Edgecombe, Alaska (Blumberg, Allison, and Garry 1959, Melartin 1967)

Northern Athapaskan—Slave and Beaver (Bowen, O'Callaghan, and Lee 1971), Kutchin (Blumberg, Allison, and Garry 1959)

Apache—students (data of Sutton in Blumberg, Allison, and Garry 1959), students (Johnston et al. 1969)

Navajo—Arizona (Mourant, Kopec, and Domaniewska-Sobczak 1976), families (Parker and Bearn 1961), students (Johnston et al. 1969)

Northern Algonkians—Montagnais and Naskapi (S. S. Agarwal, J. R. Martin, Liisa Prehn, and B. S. Blumberg, unpublished data, 1976), Northern Ojibwa (Szathmary et al. 1974), Saskatchewan Chippewa/Cree (Lampl and Blumberg 1977), Plains and Northern Cree (Bowen, O'Callaghan, and Lee 1971)

Blackfoot—Blood, Montana (Rokala, Polesky, and Matson 1976, Lampl and Blumberg 1977)

Assiniboin—Assiniboin (Bowen, O'Callaghan, and Lee 1971), Sioux (Lampl and Blumberg 1977)

Chukchi—Coast Chukchi (Rychkov and Sheremeteva 1972b)

Asiatic Eskimos—Naikan, Chaplino, and Sirenki (Rychkov and Sheremeteva 1972b)

Mongoloids—Japan (Omoto and Harada 1972, Ferrell et al. 1977)

* *Gc^{Igloolik}* also present with frequency .0103.

† Based on pooled data for all Indians; *Gc^{Chippewa}* also present with frequency .0007.

‡ *Gc^{Chippewa}* also present with frequency .0024.

§ Based on pooled data for all Eskimos and Subarctic Indians.

|| Based on pooled data for all Eskimos.

Two additional albumin variants present with a combined frequency of .0012.

TABLE 4
DISTANCE MEASURES BASED ON GENETIC AND SKELETAL DATA

	SOUTH ALASKAN ESKIMOS	NORTH ALASKAN ESKIMOS	CENTRAL ARCTIC ESKIMOS	EASTERN ARCTIC ESKIMOS	WEST GREENLAND ESKIMOS	EAST GREENLAND ESKIMOS	ALEUTS	HADA	TLINGIT	NORTHERN ATHAPASKANS	APACHE	NAVAJO	NORTHERN ALGONKIANS	ASSINTIBOIN	BLACKFOOT	CHUKCHI	ASIATIC ESKIMOS	MONGOLOIDS
	.041 (.004)	.036 (.016)	.020 (.010)	.021 (.009)	.008 (.005)	.038 (.011)	.069 (.051)	.034 (.015)	.059 (.024)	.036 (.016)	.041 (.019)	.030 (.014)	.027 (.011)	.040 (.011)	.039 (.015)	.033 (.017)	.034 (.023)	.023 (.013)
SOUTH ALASKAN ESKIMOS	.042 (.003)	.010 (.006)	.017 (.010)	.021 (.010)	.006 (.002)	.042 (.002)	.068 (.009)	.066 (.009)	.042 (.002)	.040 (.005)	.020 (.007)	.115 (.007)	.088 (.002)	.055 (.003)	.075 (.119)	.075 (.006)	.067 (.087)	.055 (.005)
NORTH ALASKAN ESKIMOS	.036 (.016)	.025 (.011)	.017 (.009)	.021 (.010)	.007 (.003)	.042 (.010)	.058 (.005)	.059 (.004)	.054 (.012)	.080 (.005)	.030 (.008)	.094 (.010)	.075 (.005)	.075 (.010)	.075 (.010)	.075 (.005)	.075 (.005)	.075 (.005)
CENTRAL ARCTIC ESKIMOS	.020 (.010)	.017 (.009)	.017 (.010)	.021 (.010)	.006 (.002)	.042 (.010)	.055 (.005)	.053 (.004)	.054 (.012)	.080 (.005)	.030 (.008)	.094 (.009)	.075 (.009)	.075 (.009)	.075 (.009)	.075 (.009)	.075 (.009)	.075 (.009)
EASTERN ARCTIC ESKIMOS	.021 (.009)	.021 (.012)	.021 (.011)	.021 (.010)	.006 (.002)	.042 (.010)	.058 (.006)	.059 (.006)	.054 (.012)	.080 (.005)	.030 (.008)	.094 (.009)	.075 (.009)	.075 (.009)	.075 (.009)	.075 (.009)	.075 (.009)	.075 (.009)
WEST GREENLAND ESKIMOS	.008 (.005)	.025 (.011)	.007 (.003)	.010 (.010)	.010 (.014)	.024 (.024)	.068 (.003)	.048 (.011)	.036 (.011)	.042 (.012)	.022 (.012)	.025 (.006)	.025 (.007)	.025 (.008)	.025 (.008)	.025 (.008)	.025 (.008)	.025 (.008)
EAST GREENLAND ESKIMOS	.038 (.012)	.021 (.012)	.017 (.012)	.014 (.012)	.006 (.010)	.024 (.010)	.068 (.003)	.048 (.011)	.036 (.011)	.042 (.010)	.022 (.010)	.025 (.006)	.025 (.007)	.025 (.008)	.025 (.008)	.025 (.008)	.025 (.008)	.025 (.008)
ALEUTS	.069 (.051)	.116 (.092)	.122 (.102)	.109 (.085)	.089 (.071)	.108 (.083)	.068 (.003)	.048 (.011)	.036 (.004)	.049 (.007)	.061 (.008)	.078 (.009)	.067 (.004)	.067 (.004)	.067 (.004)	.067 (.004)	.067 (.004)	.067 (.004)
HADA	.034 (.015)	.031 (.017)	.020 (.010)	.022 (.009)	.022 (.011)	.044 (.022)	.110 (.085)	.052 (.085)	.052 (.085)	.052 (.085)	.042 (.085)	.025 (.066)	.025 (.007)	.025 (.008)	.025 (.008)	.025 (.008)	.025 (.008)	.025 (.008)
TLINGIT	.059 (.024)	.025 (.014)	.031 (.012)	.028 (.011)	.040 (.016)	.052 (.024)	.163 (.126)	.015 (.066)	.015 (.066)	.062 (.011)	.035 (.014)	.024 (.015)	.024 (.015)	.024 (.015)	.024 (.015)	.024 (.015)	.024 (.015)	.024 (.015)
NORTHERN ATHAPASKANS	.036 (.016)	.026 (.013)	.025 (.011)	.021 (.010)	.021 (.013)	.051 (.024)	.118 (.085)	.011 (.085)	.008 (.085)	.008 (.085)	.052 (.003)	.017 (.007)	.044 (.008)	.047 (.009)	.047 (.009)	.047 (.009)	.047 (.009)	.047 (.009)
APACHE	.041 (.019)	.071 (.030)	.062 (.041)	.054 (.031)	.043 (.024)	.072 (.033)	.031 (.013)	.040 (.030)	.040 (.030)	.040 (.031)	.045 (.031)	.045 (.011)	.045 (.008)	.045 (.010)	.045 (.010)	.045 (.010)	.045 (.010)	.045 (.010)
NAVAJO	.030 (.014)	.038 (.015)	.030 (.014)	.028 (.011)	.024 (.012)	.060 (.026)	.095 (.064)	.016 (.010)	.022 (.009)	.006 (.003)	.030 (.019)	.036 (.019)	.036 (.013)	.039 (.013)	.039 (.013)	.039 (.013)	.039 (.013)	.039 (.013)
NORTHERN ALGONKIANS	.027 (.011)	.053 (.023)	.031 (.011)	.033 (.012)	.024 (.010)	.066 (.025)	.096 (.071)	.016 (.071)	.016 (.071)	.037 (.071)	.019 (.071)	.036 (.024)	.036 (.024)	.036 (.024)	.036 (.024)	.036 (.024)	.036 (.024)	.036 (.024)
ASSINTIBOIN	.040 (.017)	.072 (.039)	.039 (.015)	.045 (.022)	.028 (.012)	.076 (.041)	.101 (.056)	.027 (.013)	.059 (.036)	.037 (.023)	.027 (.016)	.021 (.013)	.021 (.012)	.021 (.012)	.021 (.012)	.021 (.012)	.021 (.012)	.021 (.012)
BLACKFOOT	.031 (.014)	.036 (.015)	.020 (.008)	.026 (.014)	.018 (.014)	.027 (.011)	.099 (.071)	.046 (.071)	.046 (.071)	.062 (.071)	.054 (.071)	.034 (.029)	.034 (.029)	.034 (.029)	.034 (.029)	.034 (.029)	.034 (.029)	.034 (.029)
CHUKCHI	.034 (.023)	.081 (.052)	.083 (.058)	.055 (.046)	.070 (.036)	.085 (.046)	.085 (.046)	.085 (.046)	.085 (.046)	.085 (.046)	.085 (.046)	.079 (.048)	.079 (.048)	.079 (.048)	.079 (.048)	.079 (.048)	.079 (.048)	.079 (.048)
ASIATIC ESKIMOS	.054 (.033)	.089 (.064)	.094 (.073)	.073 (.058)	.071 (.049)	.086 (.059)	.086 (.059)	.086 (.059)	.086 (.059)	.086 (.059)	.086 (.059)	.121 (.058)	.121 (.058)	.121 (.058)	.121 (.058)	.121 (.058)	.121 (.058)	.121 (.058)
MONGOLOIDS	.034 (.013)	.023 (.016)	.033 (.024)	.035 (.016)	.038 (.016)	.050 (.016)	.145 (.115)	.049 (.018)	.049 (.018)	.049 (.018)	.049 (.018)	.039 (.021)	.039 (.021)	.039 (.021)	.039 (.021)	.039 (.021)	.039 (.021)	.039 (.021)

Note: Below diagonal, genetic distances for 18 populations based on 11 systems, 35 alleles; figures in parentheses are standard errors. Above diagonal, morphological distances for the 12 populations for which both genetic and skeletal data are available, based on 24 discrete cranial traits; figures in parentheses are standard deviations.

priate here (Spuhler 1972), although elsewhere they may be unwarranted (e.g., Mexico: Roychoudhury 1975).

We were unable to use Spielman, Migliazza, and Neel's (1974) method of deriving a tree based on linguistic distances calculated from percentages of shared cognates (basic vocabulary items) because such lists were unavailable for the language families we were comparing. Consequently, we relied on visual observation of specific clusters and noted whether they conformed to aggregations expected on the basis of language-family relationship. Clearly, there are linguistically expected clusters, one properly called Eskimoan, the other Na-Dene. Each grouping, however, has one anomalous member and one unexpected exclusion. The unexpected position of the Algonkian-speaking Blackfoot has already been mentioned. Similarly, the Northern Algonkians would not be expected to group with the Na-Dene. The excluded populations are the Apache, who would be expected to group with the Na-Dene, and the cluster of Bering Sea groups (the Asiatic Eskimos, Aleuts, and Chukchi), who would be expected to group with their non-Siberian Eskimo relatives.

Some of these anomalies can be explained. The Aleut data, for example, derive mainly from a very small sample from the Commander Islands, which were settled in the early 19th century by a heterogeneous founding population that included Aleuts, Indians, and *Siberians*, as well as Europeans (Jochelson 1928, Krauss 1973a). Their position in the dendrogram is probably a consequence of their being a multihybrid group with considerable genetic input from indigenous Asiatic populations. The position of the Asiatic Eskimos is likely a consequence of ancient and continuous gene flow from the Chukchi, for Rychkov and Sheremetyeva's (1972b) demographic data attest to such admixture. This seems a reasonable interpretation because all other Eskimos from Alaska to Greenland exhibit recognizable genetic similarity.

The Apache-Assiniboin clustering would fit Neumann's (1952) reconstruction of North American history, which suggests that prehistoric populations ancestral to northern Plains tribes were significantly hybridized by assimilation of Na-Dene groups as the latter dispersed from Alaska. On the other hand, as this hypothesis would have Blackfoot as well as Assiniboin clustering with Na-Dene, and as the Apache-Assiniboin cluster is separate from the other North American populations, chance may be the best explanation for this particular association. Chance, in the guise of the founder effect, is probably also responsible for the unexpected position of the Blackfoot. Records show a population bottleneck occurring in 1879, at the time of the extinction of the buffalo herds: during that winter, some 600 Blackfoot starved to death (Graham-Cumming 1967); prior to that they had been decimated by smallpox.

What interpretations, then, can be made of the foregoing analyses? Firstly, contrary to the current hypothesis of Eskimo origin, neither Asiatic Mongoloids of the "classic" variety nor Bering Sea Mongoloids such as the Chukchi can be shown to be closer to Eskimos than are American Indians. Secondly, the greatest genetic similarity of the non-Siberian Eskimos as a group is to American Indians and, within this group, to speakers of languages of the Na-Dene phylum. Algonkian-speakers may be equally close, although eastern and southern Algonkians should also be compared before their affinity is considered conclusive.

THE SKELETAL EVIDENCE

Skeletal data representing the North American populations listed in table 1 were collected by Ossenberg.

A skeletal collection from an archaeological site is not a population sample; rather, it is in the nature of a total universe from one or more cemeteries and may include an indeterminate number of generations. This has important implications for skeletal studies, especially those which attempt to identify ancestor-descendant relationships in a limited regional and

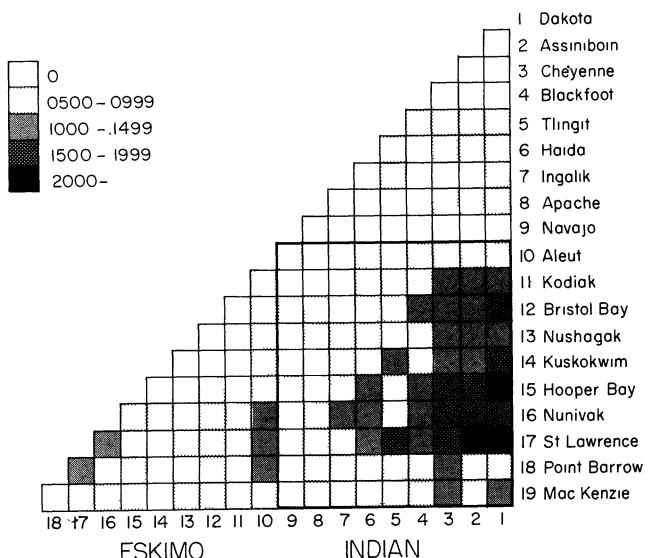


FIG. 2. Measures of divergence for Indian and Eskimo samples based on discrete traits of the skull. All MD values are statistically significant (i.e., more than twice their standard deviation) except the following: Assiniboin-Cheyenne, Tlingit-Navajo, Ingakl-Navajo, Bristol Bay-Nushagak, and Pt. Barrow-Mackenzie.

temporal context (Cadien et al. 1976). However, in our judgment it does not seriously affect the interpretations in this study, whose main objective is to examine affinities between two major groups, Indians and Eskimos, each being represented by several samples broadly representative of local populations in western North America.

Discrete morphological traits are those which are recorded in an individual skull as present or absent and in a cranial sample as percentage incidence. Historically, interest in this type of feature in man has been sporadic, although it dates back well before the present century. Renewed interest derives from research in genetics and zoology showing that skeletal variants in laboratory animals (analogous to those in man) are predominantly under genetic control (Grüneberg 1963) and are useful for investigating microevolutionary mechanisms at the infra-specific level (Berry 1963, 1969; Grewal and Dasgupta 1967; Grüneberg 1961; Hilborn 1974; Rees 1969). Concurrently, the past ten years have seen an accelerated output of anthropological studies aiming to trace the history and relationships of populations of *Homo sapiens* through the use of discrete cranial traits as these features assume increasing importance alongside the skull measurements more traditionally used for that purpose (Corruccini 1974, Ossenberg 1976).

We have used 24 discrete cranial traits in this study. Our distance measure is a modification of Smith's measure of divergence (MD) (Grewal 1962, Berry 1963). Previous analyses (Ossenberg 1969, 1976, 1977) provide descriptions of the individual features, methods for their scoring and statistical analysis, and evidence that this particular battery of traits yields valid taxonomical information. Table 5 lists separately the Indian and Eskimo frequency ranges of each trait and gives the percentage contribution of each to the mean Indian-Eskimo measure of divergence. The first three (supraorbital foramina, wormian bones, and mylohyoid bridge) account for 44% of the variation; the next five bring the cumulative percentage to 71; 12 traits of the 24 account for 86% of the mean measure of divergence.

The measures of divergence generated by all possible pairwise comparisons of 19 samples are displayed as a shaded matrix in figure 2, white denoting greatest similarity and black greatest dissimilarity. Most of the Indian-Indian and Eskimo-Eskimo

MDs (upper and lower triangular areas respectively) are white or near-white. Notably close and apparently forming clusters are four Plains samples (Dakota, Assiniboin, Cheyenne, Blackfoot), four Na-Dene samples (Haida, Ingalik, Apache, Navajo), and five Yupik-speaking Eskimo groups from southwestern Alaska (Kodiak, Bristol Bay, Nushagak, Kuskokwim, and Hooper Bay).

The Eskimo within-group distances are on the whole greater than the Indian, possibly owing to isolate divergence between Arctic communities. In contrast, increased contacts among Plains tribes during the protohistoric and historic periods presumably resulted in genetic mixture and convergence (Jantz 1973, Blakeslee 1975), while persistence of ancestral characteristics, rather than convergence, would account better for the close affinity among the geographically dispersed Na-Dene populations.

As expected, the Eskimo-Indian MDs (large square area) are represented by a larger proportion of dark shades. However, these are concentrated in the Eskimo-Plains area. Of the Plains tribes, Blackfoot are closest to Eskimos. The Eskimo-Na-Dene area shows a distribution of white, near-white, and grey remarkably similar to the Eskimo-Eskimo area, indicating considerable overlapping between the ranges of MDs for these comparisons. Kodiak, Nushagak, Nunivak, Pt. Barrow, and Mackenzie are each closer to Navajo than to seven of the nine Eskimo and Aleut samples; Kuskokwim and Hooper Bay are

closer to Apache than to six Eskimo and Aleut samples; Bristol Bay and St. Lawrence are closer to Ingalik than to four Eskimo and Aleut samples. Surprisingly, it is a Southwestern Athapaskan group, Navajo, rather than the Alaskan Athapaskan group, Ingalik, that is closest to Eskimo.

Measures of divergence place the Aleuts closer to five of the nine Indian than to any of the nine Eskimo samples. The affinity of Aleuts to Indians revealed by discrete-trait analysis can be attributed neither to sampling artifact nor to aberrant characteristics in a small isolate. Five other samples representing eastern (Fox), central (Andeanov), and western (Rat) island groups of the Aleutian chain and including Palaeo-Aleuts (2000 B.C.-A.D. 1000) from the Chaluka midden on Umnak Island are unanimous in their closer affinity to certain Indians than to Eskimos (Ossenberg 1969, 1971, and work in progress).

A dendrogram (McCammon and Wenninger 1970) based on measures of divergence for 19 population samples (fig. 3) reveals two distinct major clusters: Indian and Eskimo. With one notable exception (that Aleuts are with Indians), the dendrogram therefore conforms to the prevailing view of the distinctiveness of the two indigenous Northern American groups. Within the Indian cluster, the five Na-Dene groups plus Aleuts form a subcluster, with the closest relationship being Apache-Navajo. The four Plains tribes also form a subcluster. Similarly, within the Eskimo grouping there are two subclusters corresponding to the Yupik-Inupik linguistic subdivisions. The

TABLE 5
OCCURRENCE OF 24 DISCRETE CRANIAL TRAITS IN INDIANS AND ESKIMOS AND
CONTRIBUTION OF EACH TRAIT TO MEAN INDIAN-ESKIMO
MEASURE OF DIVERGENCE

TRAIT	PERCENTAGE OCCURRENCE		PERCENTAGE CONTRIBUTION TO MEAN OF 81 INDIAN-ESKIMO MDs
	Indian Range (9 samples)	Eskimo Range (9 samples)	
Supraorbital foramina.....	44-93	51-98	17.1
Wormian bones.....	19-71	50-87	14.5
Mylohyoid bridge.....	16-41	0-21	12.8
Marginal tympanic-plate foramen.....	9-47	7-22	7.3
Frontal grooves.....	25-58	12-37	5.7
Pharyngeal fossa.....	3-23	1-10	4.8
Tympanic dehiscence.....	27-50	8-47	4.5
Infraorbital suture.....	21-53	38-60	4.3
Clinoid bridge.....	12-33	6-14	3.8
Lateral pterygoid-plate foramen.....	3-19	0-11	3.8
Parietal process of temporal squama.....	2-19	0-7	3.7
Trochlear spur.....	0-16	0-11	3.6
Pterygobasal bridge.....	2-18	0-10	2.7
Intermediate condylar canal.....	30-55	23-37	2.3
Incomplete foramen spinosum.....	8-25	6-24	2.2
Paracondylar process.....	7-27	6-26	1.5
Trace os japonicum.....	12-25	17-35	1.3
Suppressed upper third molar.....	2-9	5-18	1.1
Divided hypoglossal canal.....	12-27	14-29	0.9
Squamoparietal synostosis.....	0-6	0-2	0.8
Absent postcondylar canal.....	7-21	12-23	0.6
Accessory mental foramen.....	4-20	0-14	0.4
Accessory optic canal.....	0-9	1-10	0.2
Pterygospinous bridge.....	5-15	3-9	0.1

NOTE: Frequencies of bilateral traits are based on total number of left plus right observations. Samples are as follows: Indians, Haida (144), Tlingit (17), Ingalik (72), Tanaina (7), Kutchin, Hare, and Dogrib (4), Apache (33), Navajo (27), Piegan, Blackfoot, and Blood (83), Cheyenne (29), Assiniboin (31), Dakota (146); Eskimos, Kodiak Island (100), Bristol Bay (35), Nushagak River (41), Kuskokwim River (69), Hooper Bay (28), Nunivak Island (102), Pt. Barrow (86), Mackenzie Delta (52), St. Lawrence Island (76). The data on Aleuts (111), Tanaina (7), and Kutchin, Hare, and Dogrib (4) listed in table 1 are omitted from this comparison.

SOURCES: Data recorded by Ossenberg in collections in the U.S. National Museum, Washington, D.C.; the American Museum of Natural History, New York; the Field Museum, Chicago; and the National Museum of Man, Ottawa. All but two of the samples are "recent," i.e., dating from approximately A.D. 1700-1900. Kodiak Island dates from about A.D. 1000-1500 (Clark 1966), Kagamil Island from about A.D. 1500-1700 (Turner 1967).

closest relationships, as expected on both linguistic and geographical grounds, are Pt. Barrow-Mackenzie (Inupik) and Nushagak-Bristol Bay (Yupik). Though Nunivak joins Inupik rather than Yupik, the linkage is loose. Here, as in figure 2, Nunivak and St. Lawrence appear to be the most divergent Eskimo groups, possibly reflecting the genetic effects of isolation on these island populations. Further, St. Lawrence is known to have closer ties—geographically, archaeologically, linguistically, and historically—with Siberian than with Alaskan Eskimos (Oswalt 1967, Bandi 1969, Krauss 1973a).

While a dendrogram is a useful graphic summary, delineating major groups and subgroups only hinted at in the matrix of distance measures, the clustering procedure necessarily sub-

merges details of relationships. Thus, apparently the Indian-Indian and Eskimo-Eskimo affinities are reciprocally strong enough to obscure Eskimo-Na-Dene overlapping apparent in the shaded matrix of figure 2. Nevertheless, overlapping of MD ranges is such that, for many comparisons, as noted in the examples above, Eskimos are actually closer to Na-Dene than to other Eskimos and Na-Dene are closer to Eskimos than to other Indians. It is this remarkable Eskimo-Na-Dene affinity on which we now focus as the skeletal evidence most relevant to the hypothesis herein explored.

COMPARISON OF GENETIC AND SKELETAL EVIDENCE

The independent assessment of the genetic and craniological data indicates that both sets of observations deviate from patterning that would be expected on other grounds. For example, discrete-trait analysis places the Aleuts with Indians rather than with Eskimos; genetic analysis places the Eskimos with Indians rather than with Asiatic Mongoloids. On the other hand, there are also similarities in overall topologies between the dendograms. To illustrate this more clearly, dendograms (figs. 4 and 5) were constructed by Nei's (1975) method for each set of data (table 4) for the 12 populations the two sets have in common (Aleuts, South Alaskan, North Alaskan, Central Arctic, and Asiatic Eskimos, Haida, Tlingit, Northern Athapaskans, Navajo, Apache, Assiniboin, and Blackfoot). In each tree the Asiatic Eskimos are most divergent from all groups, including the non-Siberian Eskimos. In each, the North American Eskimos form a distinct cluster (excepting the anomalous Blackfoot intrusion previously discussed) whose greatest similarity is not to Aleuts, but to Indians who are speakers of Na-Dene languages.

There are two ways in which different sets of biological distances and their derivatives (the dendograms) could be objectively compared. One would be to test the congruence of the dendograms by evaluating the two patterns obtained in terms of both overall "net length" and exact topological concordance (Spielman 1973). The minimum-net-length criterion is not applicable to our dendograms, since they were constructed by a different method than Spielman's. Furthermore, the solutions provided to meet both criteria are empirical,

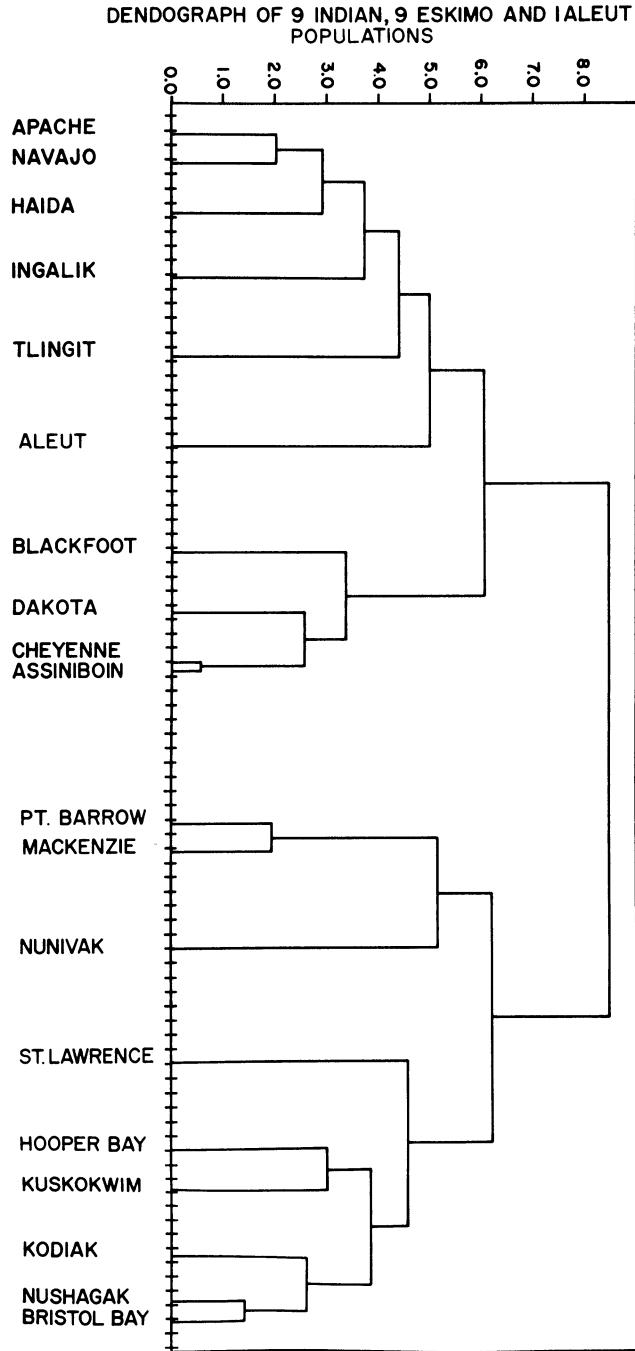


FIG. 3. Indian and Eskimo-Aleut affinities based on discrete traits of the skull. The numbers on the ordinate represent the distance values at which clusters are formed. The other axis gives between-group distances, i.e., distances between two adjacent groups.

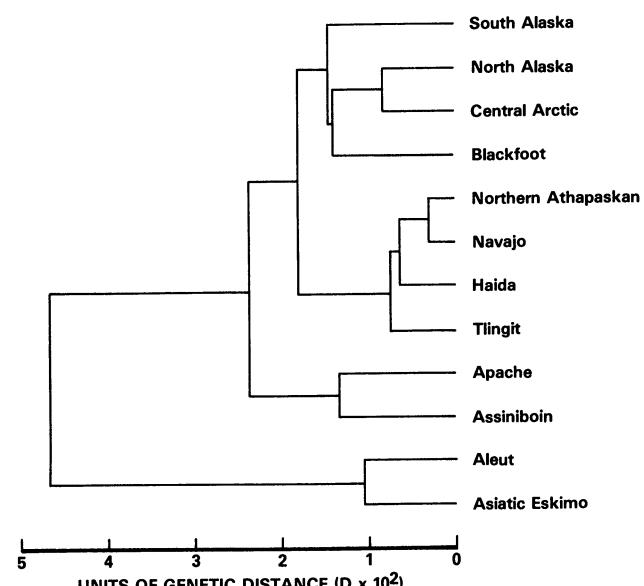


FIG. 4. Relationships among 12 populations based on genetic-marker data (11 systems, 35 alleles). Distances are read along the horizontal axis. Vertical positioning is immaterial.

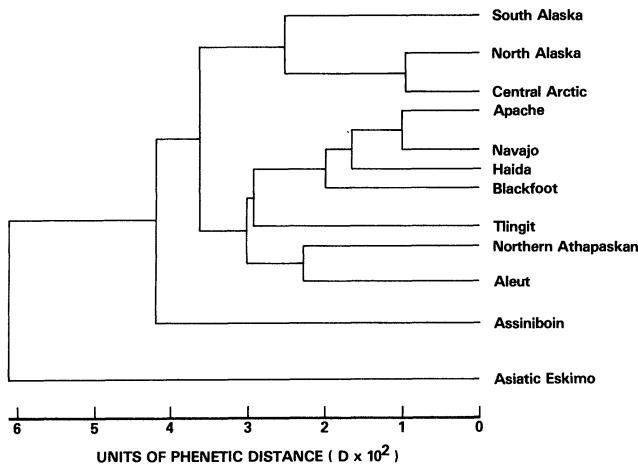


FIG. 5. Relationships among 12 populations based on discrete cranial traits. Distances are read along the horizontal axis. Vertical positioning is immaterial.

involving extensive computer simulation. We have therefore chosen a more direct approach, calculating the correlation between distances (Howells 1966). Because the distribution of distances is probably not normal, we have used rank-correlation methods (Ward and Neel 1970, Zegura 1975). Several authors, however, have pointed out the difficulty of determining the significance of the results with such an approach (Friedlaender et al. 1971, Spielman 1973). Because the multivariate distances within each set of observations are not independent, the degrees of freedom associated with the tests are inflated; hence the significance of the results cannot be readily judged. Neel, Rothhammer, and Lingoes (1974) have provided a solution for this problem based on the empirical demonstration of the distribution of the mean value of τ , Kendall's rank-correlation coefficient. We cannot do this because, with only two distance matrices to compare, we cannot calculate a mean τ value. Nevertheless, some comparisons with their results are in order.

With 12 populations, there are 66 distance pairs to examine; for these, $\tau = +.19$. By ordinary standards, the probability of obtaining such a value by chance is less than 10^{-2} . It is worth noting that Neel and his colleagues obtained $\tau = +.30$ from the comparison of only 21 distance pairs (anthropometric vs. genetic), a value they judged significant ($.05 > P > .02$).

Spearman's rank correlation was also calculated for our data, yielding $r = +.27$. Were 64 degrees of freedom associated with the test (given 66 distance pairs), this result would be judged highly significant ($.01 > P < .025$). In fact, such an r value would be significant at the 5% level even if as few as 55 degrees of freedom were associated with the test. We suspect, therefore, although we cannot prove, that there is significant concordance between the genetic and discrete-trait distances in this study.

We are unaware of other studies that have tested for correlation between discrete-trait and genetic distances, but genetic distances have been compared with anthropometric ones. These are more analogous to osteometric distances than are the discrete traits. If we assume that osteometric and attribute data yield similar patterns of relationship and that anthropometric = osteometric, then there is a body of data with which our findings may be compared.

Comparisons of osteometric and discrete-trait distances have been contradictory, some studies reporting a lack of correspondence in the patterns of relationship derived from the two sets of data (Howells 1976). A likely explanation of these findings is that the particular array of traits considered may not be the most appropriate or informative for the populations compared (Ossenberg 1976, 1977). When traits have been carefully selected, significant concordances between metric and

nonmetric cranial distances have been obtained (Ossenberg 1977). With respect to correspondence between genetic-marker and osteometric distances, in general, positive correlations have been found for the distances as well as the patterns of similarity (dendograms) derived from the data (Howells 1976). Our findings, therefore, are by no means exceptional. What is exceptional is the populations being compared. The inescapable conclusion is that two different sets of observations obtained from different temporal horizons agree in showing that non-Siberian Eskimos are more similar to specific Indian groups than to others and more similar to them than to their Asiatic relatives.

DISCUSSION

The viewpoint that Eskimos and Indians are the descendants of different populations is very strongly entrenched in physical anthropology (e.g., Brues 1977). Data furnished in support of these assertions have usually been of the single-trait variety. For example, Eskimos and Aleuts have blood-group gene *B*, while Indians do not; the former lack *Dia*, the latter possess it (Laughlin 1963). Morphological traits of the skull, such as presence of the mandibular torus in Eskimos and its near absence in Indians, have also been cited (Laughlin 1963), as have differing incidences of various pathologies (Stewart 1974), features of the dentition (Turner 1967), and metric dimensions of the skull (Levin 1964, Oschinsky 1964).

Periodically, however, studies that claim similarity of Eskimos to some Indians have been reported. These tend to fall into one of the following classes according to how the similarity is interpreted: (1) common origin, (2) gene flow, (3) late migration of Athapaskan-speakers, indicating that they differ from the Indian "type," and (4) combinations of these.

Of the first variety, the earliest is Shapiro's (1931), which reported anthropometric similarity between Chipewyans from Lake Athabasca and Eskimos from the Seward Peninsula, Smith Sound, and Coronation Gulf. These findings were subsequently confirmed and extended (Seltzer 1933), although others criticized the results on methodological grounds (Stewart 1939). More recent reanalysis (McGhee 1972) has shown that the difference between Chipewyans and Copper Eskimos, as measured by Penrose's coefficient of total population distance, is indeed small, but the similarity is almost entirely due to "size distance" rather than "shape distance." McGhee concludes that no phylogenetic relationship exists between these Indians and Eskimos and that their similarity in cranial size is probably a consequence of gene flow.

Craniometric similarity of Aleut populations to Indians has long been noted. Hrdlička (1945) postulated a phylogenetic relationship between these groups. Neumann (1952:29) hypothesized that the earliest "Deneid"-type people were similar to the Proto-Aleuts and that these were closer to the "common ancestor of the later Deneid and the Eskimo." In his model, the Deneids who became Aleuts borrowed an Eskimoan language from groups in the region of the Bering Sea. Others, dispersing from Alaska to the eastern edge of the Plains, were assimilated by populations ancestral to the historic Plains tribes, contributing Deneid physical traits to tribes such as the Arikara, Dakota, and Blackfoot and exchanging their own language for those of their hosts. Still other Deneids became the historic Athapaskan-speakers of the boreal forest and American Southwest.

It is worth noting that Neumann (1952:25) classified the Eskimos separately, as the "Inuid" cranial type, recognizably different from American Indians. To this, however, he added a caveat, namely, that "the uniqueness of the Eskimo may have been overstressed."

Brennan and Howells (n.d.), using multivariate statistical methods on a large number of Old and New World crania (measured by Hrdlička), find good agreement with Neumann's theories of group relationship, although they do not read

phylogeny from their clustered hierarchy. In particular, they find that the majority of non-Siberian Eskimos form a unit that is closest to Chukchi and Siberian Eskimos, while the Aleuts, Koniag Eskimos, some other Eskimos, tribally undefined Northwest Coast Indians, Tlingit, Apache, and Navajo form a unit that clusters with other Indians. Because such an aggregation is "erratic," they deduce that the "grouping should in part be the result of intermixture in the area" (p. 28).

Indeed, gene flow is the recurrent theme furnished to explain unexpected convergence of Indians and Eskimos-Aleuts. For example, the "Eskimo morphological modification" in an Alaskan Athapaskan (Ingalik) series (Oschinsky 1964:25), the placement of the same series within the Eskimo population cluster (Brennan and Howells 1976:31), and the clustering of Haida and Bella Coola with Yukon Eskimo (Finnegan 1974) have been attributed to admixture. When populations share a common geographic boundary, gene flow is possible. It is dubious as an explanation, however, for the clustering of geographically distant groups. In Brennan and Howell's study, for example, if the aggregation of Aleuts, Koniag Eskimos, and Na-Dene-speakers is due to gene flow, then that admixture is ancient, for it would have had to occur not just prior to the dispersal of the Athapaskans, but prior to the differentiation within Na-Dene.

Alternative explanations of similarity between Indians and Eskimos-Aleuts have been provided. Turner (1971) has found that of the many North American Indian groups he examined for presence of three-rooted mandibular first molars, only Navajo have a high frequency.² Among other indigenous North American populations, only Eskimos and Aleuts have still higher frequencies. On this basis, plus geographic distance of the populations from the Bering platform, he postulates that there were at least three waves of migration into the New World and that, as Hirsch (1954) suggested, Na-Dene-speakers preceded the Eskimos. The implication of this schema as we see it is that the next-to-last arrivals must have shared more genes (at least for three-rooted mandibular first molars) with the latest migrants (Eskimos) than did the first group of Siberian emigrés.

Our purpose in recounting past studies is to illustrate that others have found convergence between Eskimos-Aleuts and some Indian populations, almost always speakers of Na-Dene languages. Since these similarities do not fit the accepted hypothesis of the relationship between Indians and Eskimos, various mechanisms have been presented to explain their occurrence. The important question at this point is whether the patterns of similarity between Eskimos and speakers of Na-Dene languages seen in our data indicate phylogenetic relationship or can be more readily explained by other factors.

Recent gene flow is necessarily suspect, since there is archaeological (Holmes 1975), ethnohistorical (Osgood 1940, Oswalt 1967), physical anthropological (Hrdlička 1930), and even linguistic (Krauss 1973b) evidence of its occurrence. Many of our samples were obtained from populations that live on the Indian-Eskimo boundary today. If there was extensive gene flow between some Eskimos and some Indians, then groups on the population boundary would converge. It is worth noting, therefore, that we found no aggregation of North Alaskan Eskimos and Northern Athapaskans, no aggregation of Haida or Tlingit and South Alaskan Eskimos.

Since our samples consist of pooled data, we should add that

Szathmary's unpublished observations on blood-group gene frequencies of tribal groups show that, of the Northern Athapaskans, the Kutchin (pooled data from Arctic Village, Ft. Yukon, and Old Crow) and Tlingit cluster with the North Alaskan Eskimos. The Kutchin and Eskimos are geographically adjacent, while the Tlingit are in southwestern Alaska. On the other hand, the Slave and Tuchone are more similar to other Athapaskans as well as to other Eskimos, although the former inhabit the southeastern part of the Yukon Territory and do not share a geographic boundary with Eskimos. We admit, then, that pooling data as we have for both Eskimos and Indians obscures the details of respective intrapopulation heterogeneity. At the same time, however, pooling reveals overall patterns, and these patterns conform in general to expectations based on linguistic criteria. Neither recent gene flow nor adaptive (genetic or plastic) response to particular ecozones can account for these patterns, since these mechanisms would have led to the breakup of the linguistic clusters.

The last point that we wish to stress is that our sets of observations are not only independent, but obtained from different temporal horizons. At minimum the skeletal series reflects data from contact times; the genetic data are modern. By comparing temporally different samples we may be comparing populations at two different stages of microevolution, and therefore concordance in the pattern of relationships is not necessarily expected. Nevertheless, the two sets of data agree in showing close affinity between Eskimos and Na-Dene-speaking Indians. In our view the correspondence between two such inherently different sets of data means that the relationship we have found is not merely a peculiarity of a limited temporal, regional, or demographic context.

No one would dispute that the clustering of North American Eskimos in the dendograms (figs. 1, 3, 4) indicates biological relationship, not just similarity. By the same token, the unlikely aggregation of Navajo (and Apache) with Haida, Tlingit, and Northern Athapaskans must have a biological base. In this instance, linguistic relationship between the groups (Sapir 1915, Krauss 1973b) gives credence to the claim that the genetic and morphological similarity is phylogenetic. Continuing this logic a step further, the clustering of Eskimos and Na-Dene-speakers must indicate either that they are offshoots of the same ancestral population or that extensive and ancient gene flow produced convergence between them prior to their dispersal.

HISTORICAL INTERPRETATION

About 4,000 to 6,000 years ago, the occurrence of a climatic maximum saw the spread of boreal forest throughout the interior of Alaska (Holmes 1975, Dumond 1969a). This period coincided with the spread of a new tool type—the side- or corner-notched point—north along the Mackenzie River Valley in Canada, west along the Brooks Range in Alaska, and then south into the forested regions adjacent to the Bering Sea coast (Anderson 1968, Cook 1975) as far as the Naknek Drainage of the Alaskan peninsula (Dumond 1969b). The new points have been found in the Tuktu complex at Anaktuvuk Pass (Campbell 1961) and in Palisades II at Cape Krusenstern (Giddings 1971) and Onion Portage (Anderson 1968) (fig. 6). Some (e.g., Anderson 1968) have compared them to Indian artifacts from the Eastern Woodlands, others (Dumond 1969a, Workman 1974) to artifacts from the Plains. Given the coincidence of forest, new tool type, and access to Alaska from the south and east, there seems to be consensus that these artifacts indicate Indian occupation of the localities in which they are found.

² Other reports of high frequency of three-rooted mandibular first molars comparable to that reported by Turner for Navajo include 24% of 25 Haida skulls from Moresby Island (Ossenberg, unpublished data), 25% in Kwakiutl (J. S. Cybulski, personal communication, 1976), and an estimated 25% in 250 Assiniboin, Cree, and Blackfoot children in Alberta (Somogyi-Csizmazia and Simons 1971). It is noteworthy that these are Northern groups and include Na-Dene-speakers (Haida) as well as groups having some hypothesized relationship with them (Neumann 1952).

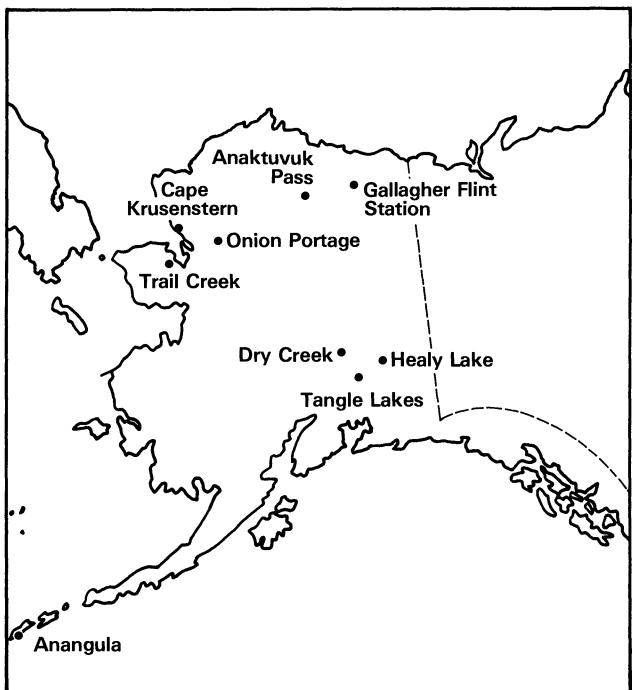


FIG. 6. Archaeological sites in interior Alaska.

There is considerable debate, however, about the affinities of other complexes in Alaska which pre-date or are contemporaneous with the period that saw the final inundation of the Bering land bridge (10,000 b.p.: Hopkins 1967). Generalized unifacial core and blade industries have been recovered from the Gallagher Flint Station on the North Slope (10,500 b.p.), from Onion Portage on the Kobuk River (Kobuk complex: 9,500–8,000 b.p.), and at Trail Creek on the Seward Peninsula (10,000–8,000 b.p.) (Dixon 1975). The youngest of such sites is on Anangula Island in the Aleutian chain, where a unifacial core and blade industry dated 8,500–7,000 b.p. has been excavated (Laughlin 1975). Markedly different assemblages defined by characteristic microblades, wedge-shaped cores, burins, and bifacially flaked tools have been found at many sites in the interior of Alaska, notably Healy Lake, Tangle Lakes, and Dry Creek in the Tanana River watershed, in the time range 11,000–8,000 b.p. or earlier (Chindadn and Denali complexes: Cook 1975, West 1975, Holmes 1975). A bifacial assemblage (Akmak) has also been found at Onion Portage (Anderson 1968, 1970) stratigraphically below the unifacial Kobuk complex.

Several different hypotheses have been put forth as to the affinities of the people that inhabited these localities. The strongest contention is for Aleut or Proto-Aleut occupation of Anangula, where continuity exists in the archaeological record from the Anangula blade site (8,500–7,000 b.p.) through the Anangula village site (6,400–4,500 b.p.) to the Chaluka midden deposits (4,000–500 b.p.) on nearby Umnak Island (Laughlin 1975, Laughlin and Aigner 1966).

Proto-Eskimo origin has been claimed for both Kobuk and Akmak complexes at Onion Portage (Anderson 1968, 1970), which are judged to be like neither the Chindadn and Denali complexes nor Anangula (Anderson 1970). Focusing on the unifacial-versus-bifacial dichotomy, Dixon (1975) links the Kobuk complex with other unifacial industries of that temporal horizon (Trail Creek, Gallagher Flint Station, Anangula), considering them to be the cultural remains of ancestral Eskimos and Aleuts; by inference, tool kits with bifacial implements (Akmak, Chindadn, and Denali complexes) are Indian.

Indeed, Indian origin has been suggested for all Denali or Denali-like (Dry Creek, Healy Lake) complexes. Borden (1970)

and Dumond (1969a), focusing on the microblades in these assemblages, ascribe them to Na-Dene. Cook (1975), seeing continuities in the archaeological record of interior Alaska, suggests a link between them and speakers of Athapaskan. Others disagree. For example, Bandi (1969) lumps Denali with other microblade complexes in an "American Epi-Gravettian" tradition which he ascribes to Eskimos.

It appears, then, that the variability and overlap of traits among early microblade assemblages (Anderson 1970, Bandi 1969, Dixon 1975, Workman 1974, Cook 1975, West 1975) permit several conflicting interpretations. Certainly there is no consensus in the assignment of mainland Alaskan assemblages in the time range 11,000–8,000 b.p. to speakers of either Eskaleut or Na-Dene. An interpretation that would account for this archaeological "confusion" as well as for our genetic and skeletal findings is that at this time level these two groups were neither biologically nor culturally distinct. Rather, a single heterogeneous population was present, showing regional variability in both biological and cultural traits.

The obstacle that stands in the way of this hypothesis is that Eskaleut and Na-Dene are different language stocks. Anthropologists have tended to assume that this distinction implies considerable biogenetic and cultural cleavage between the groups. This, however, is not necessarily true, and there is some evidence that these language stocks may indeed be connected.

Krauss (1973a, b) notes that in Morris Swadesh's worldwide schema of language relationships, both Eskaleut and Na-Dene belong to the Finno-Dene network. Within Finno-Dene, the closest connections of Eskaleut are with Kutenai (24 cognate pairs), Wakashan (26 cognate pairs), and Chukotan (22 cognate pairs) (Krauss 1973a:852). Of these postulated connections, only the Chukotan has been examined in detail, and it has been shown to be correct (Swadesh 1962, Krauss 1973a). Na-Dene's closest postulated relationships are with Wakashan, Kutenai, and Japanese (Krauss 1973b:964). Thus, according to Swadesh, Eskaleut and Na-Dene are not only both related to the same North American language families (Wakashan and Kutenai), but themselves distantly related. We are aware that the majority of linguists, Krauss included, consider these assertions unproven. Nevertheless, they are at least as strong as the much-touted relationship of Na-Dene to Sino-Tibetan (Shafer 1952). Given that Swadesh has been found correct with respect to Eskaleut and Chukotan, it remains to be seen whether he was correct concerning Eskaleut and Na-Dene as well. Insofar as linguistic connections may imply biological connections, generic relationship between Eskaleut and Na-Dene peoples is not excluded.

An alternative hypothesis which could account for convergence of Eskimoan and Na-Denean clusters in the dendograms is ancient and extensive gene flow between populations that differed somewhat genetically, linguistically, and perhaps technologically. Dixon (1975) has argued that at least two distinct cultural traditions were present in Beringia and interior Alaska in late Wisconsin times. Some of his assertions are impossible to prove, since the relevant sites are unknown and are under water (Black 1966). Nevertheless, given the climate of that period, the groups would have exploited similar ecological niches (hunting on open tundra) until the submergence of Beringia. Adaptation to a maritime niche could have occurred as the land sank, the process being in full swing at Anangula as early as 8,000 years ago (Dixon 1975).

It is worth emphasizing that if there was admixture of the magnitude required to produce the relationships depicted in the dendograms, most of it would have had to occur prior to the differentiation within each cluster. This does not preclude later local contact between adjacent populations, however. Indeed, the closer affinity of six Aleut samples (including Palaeo-Aleut from Chaluka, 4,000–1,000 b.p.) to the Na-Dene than to the Eskimo suggests virtually total population replacement in the Aleutians (Ossenberg, work in progress).

We have now offered two interpretations of our finding of biological affinity between Eskimos and Na-Dene-speakers. The first is that the two clusters diverged perhaps 10,000 years ago from a common North American population, a "founding" group probably composed of small bands which exhibited genetic heterogeneity comparable to that in modern hunters and gatherers. The second is that the founding group was composed of two populations that were linguistically distinct and at least minimally different biologically. Within each group, population structure was similar to that of the founding group under the first interpretation. Thus, local bands exchanged genes with each other; moreover, they also did so with local bands of the other population.

In our view, these hypotheses are equally plausible explanations for the affinity of Eskimo and Na-Dene clusters in our dendograms. In any case, we have no rigorous means of choosing between them. We see no *a priori* reason to doubt the occurrence of gene flow between adjacent bands, whatever their origin, particularly in the period 10,000–8,000 B.P., when most Alaskans (Anangula excepted) inhabited open tundra. Even minimal admixture would have retarded genetic differentiation among such groups. Therefore, meaningful biological divergence of these populations would not have occurred until lifeways diverged to such a degree that gene flow became a rare event.

We suggest that Eskimo–Na-Dene divergence was initiated by significant changes in the ecozone following the onset of the Hypsithermal about 8,000 years ago. The disappearance of the tundra and encroachment of the boreal forest in interior Alaska coincide with an apparent cultural hiatus at Onion Portage (8,000–6,000 B.P.) and in the Tanana Valley (8,000–4,000 B.P.) (Holmes 1975). Coincidental also are hypothetical migrations of the Na-Dene southward in adaptation to the boreal forest (Dumond 1969a). Other groups may have dispersed to the coastal regions to become ancestral Eskimos. Thus, occupation of different ecological zones would have been the precipitating factor; culturally or geographically imposed barriers to gene flow would have augmented the differentiation process.

Archaeologists suggest that a biologically distinct population (Indians of the Northern Archaic Tradition) was responsible for the cultural remains in the forested regions of Alaska 5,000 to 6,000 years ago. Some 1,000 years after that, artifacts unequivocally attributed to Eskimos appeared in North Alaska (Denbigh Flint Complex: Dumond 1965), while Aleuts were clearly present on the eastern Aleutians (Chaluka: Laughlin 1963). By those times, then, the three groups were culturally distinct. In all likelihood they were also biologically distinct—and this distinctiveness has served to obscure their common origin.

Comments

by MARIE S. CLABEAUX

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It is always refreshing to encounter a study which puts into practice what the discipline preaches. Those of us engaged in teaching introductory courses in anthropology will at some point find ourselves sermonizing on the "four-field" approach. Yet, how often do we actually apply this approach to limited, clearly defined anthropological questions? While this strategy has been used to some extent in sorting out historical relationships, the authors of this paper have brought together very disparate sets of data, including types not previously compared (genetic and discrete-trait). Because they have analyzed the problem from all possible aspects, I feel a bit let down that their conclusions are not more definitive. Of course, they cannot be,

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given the constraints imposed not only by the available data, but also by the very nature of historical reconstruction.

There is some disagreement about the genetics of discrete cranial traits. That the authors find (or strongly suspect) concordance between discrete-trait and genetic distances further strengthens the argument for the use of these traits in the study of biogenetic affinities between and among populations. It is tempting to criticize them for comparing apples with oranges in their handling of genetic-marker data. However, the data base is simply insufficient, and it is better to work with what is at hand than to wait for the perfect, complete set of data—which will never be forthcoming in any event. (A similar criticism could be made with regard to the osteological data, especially the problem the authors cite concerning the nature of a skeletal population, and with regard to the comparison of two such sets of incomplete data.) Synthesizing studies such as this one point to the necessity for clarity and completeness in the gathering and reporting of raw data.

Do the authors have a specific model in mind for their second interpretation—a founding group composed of two linguistically distinct and minimally biologically different populations? Their first interpretation is simpler and more "logical" from a cultural perspective and appears to follow from their arguments with more consistency.

If the viewpoint that Eskimos and Indians are the descendants of different populations is strongly entrenched in physical anthropology, it is probably because we have not completely discarded from our mental tool kits the glass eyeballs and ceramic skin-color charts of our intellectual predecessors. Eskimos, after all, look different from Indians. In a discipline as observationally based as anthropology, the evidence of appearance is difficult to discount. Intellectual stereotypes are heuristically restrictive and probably more prevalent than we would care to admit. The present study demonstrates the utility of reexamining a given from a new perspective. One may hope that it will engender more comparisons of genetic and discrete-trait data.

by DELLA COLLINS COOK

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From Blumenbach forward, physical anthropologists have concerned themselves with the correspondence between biological and cultural differences among human populations. The equivalence of biological, linguistic, and archeological information about past relationships among human groups has provided a common focus for what are otherwise rather loosely linked subdisciplines. Szathmary and Ossenberg make a useful contribution to this literature; however, a closer examination of the scale of their study in the context provided by similar studies is in order before their results can be assessed.

Szathmary and Ossenberg are successful in demonstrating closer resemblances within Eskimo and Indian groups than between, despite several inconsistencies in both their serological and cranial data. These inconsistencies are certainly not unusual in studies that attempt continental-scale assessments of population affinities. For example, Brennan and Howells (n.d.) define five clusters using craniometric data: Plains Indians and Asiatics, including Iroquois, pre-Aleuts, and one California series (18 groups), Athabaskan Indians and Aleuts, including Koniag Eskimo (10 groups), Gulf States (3 groups), General United States, including five California Indian groups (13 groups), and Eskimo and Related, including Chukchi, Siberian Eskimo, and one Alaska Indian sample (27 groups). To summarize these results as supporting a close relationship between Na-Dene-speakers, or American Indians in general, and Eskimos

is inappropriate. The first and fifth clusters are clearly consistent with traditional explanations for the peopling of the New World and for the differences seen by most scholars between Indians and Eskimos. While Szathmary and Ossenberg single out the second cluster as supporting their argument, Brennan and Howells argue convincingly for gene flow, citing both linguistic and historical data in confirmation. They point out that their analysis supports the traditional, multiple-migration model for the peopling of the New World as elaborated by Neumann.

Szathmary and Ossenberg present data on a relatively small number of groups that are widely distributed in space and time and definable as populations on very different levels, for example, Cibeque Apache versus Japan, Korea (table 1). Since distance and cluster statistics are based on the comparison of within- and between-group variance, the use of samples ranging from small communities to regional and national aggregates is cavalier at best. The effect of the nature of the samples on the results should be assessed, and some effort should be expended in finding Asiatic Mongoloid samples that are more appropriately matched in scale to the North American data. It is unclear why the study was limited to the groups chosen here when other, more appropriate samples are available (Brennan and Howells n.d., Spuhler 1972, and South American sources).

Scale is important in the interpretation of these results in another way. Small-scale studies of the congruence of linguistic and biological attributes have generally been quite successful. For example, Spielman (1973; Spielman, Migliazza, and Neel 1974) compared serological, anthropometric, and linguistic data on Yanomama villages and found good agreement among the resulting dendograms, and both Ossenberg (1977) and Zegura (1975) have reported good congruence between linguistic and cranial data on Eskimo populations. In contrast, Spuhler's (1972) extensive analysis of serological, linguistic, and geographic data on North American aboriginal groups fails to demonstrate a significant correlation between biological distance and glottochronological distance. Instead, Spuhler finds that geographic distance and, by extension, gene flow are highly correlated with biological distance. Studies on the correspondence between biological and cultural trees are analogous to the biological-clock problem and as such are based on, among others, two assumptions: that nonphylogenetic sources of resemblance such as gene flow and diffusion are unimportant and that the chance reappearance of similarities in two diverging lines is rare (Spuhler 1972, Byles 1976). As time depth increases in the absence of efficient isolating mechanisms, these assumptions must become less and less tenable. Given the geographic distances, great time depth, and relatively small numbers of groups used in the Szathmary and Ossenberg study, it is not surprising that the results are not entirely consistent with the traditional picture of Eskimo-Indian relationships. The problem at hand, however, is not whether the traditional model fits all available data perfectly, but whether it provides a better explanation than do alternative models. A research strategy like that used by Spuhler, in which more than one model explaining population relationships is applied to the data and the fit of these models is compared using an explicit statistical evaluation, provides a satisfactory solution to the problem. Szathmary and Ossenberg use neither simulation techniques nor correlation to test the correspondence of their dendograms to the various historical models they present. Their results would be better presented if these models were stated in a testable form, for example, as trees, and fit to the biological data in an explicit fashion. Post-hoc explanations appealing to gene flow, to incomplete summaries of the archeological record, and to ecological oversimplifications (for example, Haida and Maritime Archaic are maritime Indians, Barren Grounds and Brooks Range are inland Eskimo) are no substitute, and the time involved in the necessary computations is no excuse.

by MICHAEL H. CRAWFORD

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In science, the constant challenging of old dogma is a sign of intellectual health and vitality. Uncritical and premature acceptance of explanatory hypotheses as fact can retard the progress of investigation. All too often, research becomes stagnant when established theories remain unchallenged and are passed on from one intellectual generation to another as "truths." Szathmary and Ossenberg raise some significant questions concerning one of the established truths, namely, that "Eskimos and Indians are descendants of different populations that entered the New World at different times, following different routes." Implicit in this "truth" is that the Eskimos are latecomers into the New World, which was peopled earlier by the Amerindians. While the questions posed by the authors may not be answerable at this time, it is hoped that their synthesis will stimulate additional research.

On the basis of multivariate statistical analyses of blood-marker frequencies and discrete cranial traits, an affinity is noted between the Eskimo and the Indian Na-Dene-speakers. The affinity is interpreted in two possible ways; (1) the two groups had a common founding or ancestral group some 10,000 years ago, or (2) the founding group had two components that were linguistically and biologically distinct.

In studies of gene flow and racial admixture, gamma globulin (*Gm*) haplotypes are particularly informative as to ethnic origin (Schanfield 1976). Unfortunately, such data were not available to Szathmary and Ossenberg in evaluating the affinities of the Na-Dene-speaking Indian and Eskimo groups. The *Gm* distribution patterns of Alaskan, Siberian, and Indian groups suggest that the New World Eskimo haplotypes are unique. Unhybridized New World Eskimos totally lack *Gm^{a;s}* but exhibit *Gm^{a;s}* and *Gm^{a;bst}* at moderate frequencies. Siberian indigenous populations have a high incidence of *Gm^{a;s}* with lower frequencies of *Gm^{a;s}* and *Gm^{a;bst}* (Schanfield and Crawford, unpublished data). The absence of *Gm^{a;s}* in New World Eskimos better supports the second of the two interpretations proposed by Szathmary and Ossenberg, namely, that the founding group had two components which were biologically distinct—the parental Amerindian group possessing the *Gm^{a;s}* haplotype while the founding Eskimo group lacked it. It is possible that the founding Eskimo population was small and did not represent the Siberian indigenous gene pool.

As information on more genetic markers becomes available, the likelihood of these alternative explanatory hypotheses may have to be amended. In addition, other explanations may become more plausible with the addition of genetic and morphological information from Siberia.

by DON E. DUMOND

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Although most initial reservations against the authors' use of specifically archaeological data are in the long run too insignificant to mention, I do wish to raise two points by way of supplement rather than criticism.

1. The citation (Laughlin 1963, 1975) of work said to set out the "most favoured current view" of Eskimo and Aleut origins fails entirely to do justice to the recent recognition and attempted treatment of a most complex set of related problems by a number of investigators (e.g., Clark 1974, 1975; Dumond 1970, 1974, 1977, 1978; Dumond, Conton, and Shields 1975; Dumond, Henn, and Stuckenrath 1976; Irving 1970; McCartney 1971; McGhee 1976, 1978; Turner and Turner 1974). These problems involve relationships not alone between Eskimos and Aleuts, but also between the somewhat anomalous "Pacific Eskimos" and their northern brethren.

2. Even though pioneering, from the point of view of this archaeologist the effort published here does not go far enough in reassessing relationships between Eskimo-Aleuts, on the one hand, and Indians, on the other. Specifically, recent developments in the archaeology of the Northwest Coast and its near interior hinterland have led to the recognition of early cultural complexes that can be reasonably compared with assemblages from the Arctic. In the north these include microblade-core collections from southeastern Alaska and northernmost British Columbia (Ackerman 1974, Smith 1971). Farther south they number assemblages from interior British Columbia that on the basis of continuity with later materials have been tentatively attributed to ancestral Salish (Sanger 1969, 1970) and collections from the coast that may well have been properties of peoples ancestral to more recent ethnic groups of that vicinity. Indeed, in the Strait of Georgia region, makers of certain relatively early assemblages were nearly ten years ago suggested to be related to depositors of contemporaneous collections from the Pacific Eskimo region, and more recent research intensifies that impression (material summarized in Borden 1975). On the basis of all of this, it is possible to hypothesize that a sphere of indirect, but continual, interaction long existed from the vicinity of Kodiak Island in the north to British Columbia in the south (related arguments summarized in Dumond 1978)—this despite the fact that so much of the intervening area is little known archaeologically. This leads in turn to the question of whether not only Eskimo-Aleuts and Na-Dene, but Wakashan and Salish as well—all of them speaking languages with no obvious relatives farther south in America—constituted a block of immigrants to the New World, all derived from a single population, or related set of populations, that had existed in unglaciated Alaska during terminal Pleistocene times.

These quibbles aside, the work summarized in this paper must receive a joyous welcome by prehistorians interested in the American Arctic: its apparently definitive questioning of the long-held, Hrdlicka-derived dogma of a basic physical cleavage between Eskimos and Aleuts, on the one hand, and American Indians, on the other, must serve to free speculation and hypothesis in crucial directions that are sure to bring new and important insights into native American history.

by ROBERTA L. HALL

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The most important contribution this paper makes is to establish that there is no easy way to use biological data to interpret prehistory and, conversely, that it is not valid to use archeological remains to infer the physical attributes of members of an extinct culture. The entire paper is concerned with the first point; the authors make the second point by challenging traditional images of culture bearers of premodern Indian sites as morphological Indians.

Basically it is a well-argued paper presenting an important thesis. However, some problems remain.

An obvious problem concerns the position of the Aleut sample in respect to North American Eskimo populations, North American Indian populations, and Asiatic peoples. Scrutiny of the five figures indicates (see my table 1) that the Aleuts are closer to North American Indians than to Eskimos, and all figures except one (fig. 5) indicate that the Aleuts are closer to Asiatic Eskimos than to North American Eskimos. These two results appear contradictory, although the particular historical relationships discussed by the authors may resolve them. In addition, scrutiny of the five tables does not indicate that the tribes whose individual languages are considered in the Na-Dene family are consistently closer to Eskimos than to other Indians.

These two observations suggest that in spite of attempts to disentangle their analysis from culturally based classifications, the authors may have given too much credence to the higher-level categories in linguistic taxonomy and may still consider them to represent prehistoric biological units. (It also may be argued that too much credence is given to high-order "major race" units, specifically "Mongoloid.")

I am suggesting that it is more meaningful to make biological comparisons between local populations on a unit-by-unit basis. For instance, it may be interesting to compare trait frequencies of Koreans and North American Eskimos—or Navajo and Aleuts—but it is not useful to consider the Korean and Japanese groups as "base Mongoloid" or Navajo as "base Na-Dene."

Of what value in a study like this are the "higher-order" categories? Though it may be useful to think of Navajo people as, to some extent, related to other populations categorized within Na-Dene, the Navajo's history as a population interacting with other Southwestern peoples cannot be neglected. Another case in point: the Blackfoot do not fall in the Na-Dene category that the authors feel is closely related to "base Eskimo," but by my reading of the genetic distances given in table 4 the Blackfoot appear no farther from Eskimo populations than are populations such as Haida and Navajo (Na-Dene groups). Similarly, Navajo and Apache are no closer together than the Navajo are to several of the Eskimo samples. This result suggests that local-unit uniqueness is a reality often obscured by the use of "higher-order" categories; one exception is that the various North American Eskimo samples do appear to share many traits and to diverge, as a group, from all other units.

To conclude: this study indicates that "Eskimo" is an operationally valid unit even though it represents a geographically dispersed group. Beyond that, it suggests that Eskimos have at least some biological roots in North America. Most importantly, it suggests that the search for "ultimate origins" of any mobile, adaptable, flexible, opportunistic, biological population of *H. sapiens* is bound to result in no indisputable conclusions. Per-

TABLE 1
SUMMARY OF GENERALIZED DATA FROM FIGURES 1-5

	1	2	3	4	5
Are Aleuts more similar to Asiatic Eskimos than to North American Eskimos?	yes	not applicable	not applicable	yes	no
Are Aleuts more similar to North American Indians than to Eskimos?.....	not determinable	yes	yes	not determinable	yes
Are North American Eskimos more similar to Indians than to Asiatics?....	yes	not applicable	not applicable	yes	yes
Are Na-Dene-speakers more similar to Eskimos than to other Indians?....	some—not all	not determinable	no	no	no

haps heretofore we have asked the wrong questions, as we sought the origin or the affinity of any one human population. By contrast, the authors' question—"Are the biological differences between North American Indians and Eskimos truly profound?"—is an appropriate one that they have addressed creditably.

by ALBERT B. HARPER

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The essence of Szathmary and Ossenberg's investigation is to include Athabaskans as a member of the species. So be it. But are Athabaskans really biologically more similar to Bering Sea Mongoloids (Aleuts, Koniags, Yupik, and Inupiaq Eskimos) than to other North American Indians? If this should be the case, then are the implications of a close genetic or biological association between Bering Sea Mongoloids and Athabaskans truly profound?

The punch line of this paper is that the two interpretations of the Eskimo-Athabaskan affinities are functionally equivalent to the respective population histories of each group and therefore cannot be distinguished. What is important about this finding is not that Bering Sea Mongoloids and North American Indian populations once shared a common genome—obviously they did—but how long these groups have been subjected to different selection regimes and population structures. The inference is that the time may be much shorter than the 10–15,000 years asserted by Laughlin (1963). A divergence of only 8–10,000 years would place a severe constraint upon the school that argues for the early (20,000 years) arrival of humans in the New World.

There are some points that one may wish to cavil with. For example, J. Winslow in 1722 was the first to describe a human skull complete with a missing third molar (Pedersen 1949). It is not entirely chance that this was an Eskimo skull from Dog Island, Greenland. Similarly, there are several studies on nonmetric variants in Greenlandic Eskimo skulls (Laughlin and Jørgensen 1956, Sellevoid 1977, Fröhlich 1978) that provide excellent data on divergence within a closed population system.

Other points detract significantly from the validity of the study. First, the Nei distance measures are not consistent with the interpretations placed upon them. Can we really believe that the Eskimos of Western Greenland are equally divergent from Eastern Greenlanders (.024) and from Navajo (.024)? Could the Apache really be lost Chukchi wandering in the desert? Of course not! Szathmary explains, quoting Nei (1975), that "phylogenetic relationships will be portrayed if a large number of loci representing a random sample of the genome is used in the analysis. Under such conditions, the effects of genetic drift and natural selection, varying between loci, are 'averaged out.'" This does not appear to be the case with these data.

The problem is that genetic data for many polymorphic loci are unavailable for many Arctic and American populations. The need for extensive investigation was a constant theme in the Burg Wartenstein conference "Origins and Affinities of the First Americans" (Laughlin 1977). In the absence of such data, we still find that "Eskimos form a genetically recognizable group" and that the incursion into the Eskimo distance space comes from the Athabaskans and Algonquins, which act as mimicking groups. Spuhler (1978) has also noted this boundary problem.

The same situation occurs in the skeletal series, even though key traits of the dentition, mandibular torus, and others are omitted. Eskimos are clearly grouped with other Eskimos, and the Indian series are most similar to other Indian series (fig. 3). That Aleuts do not group with their nearest neighbors is not unexpected. Table 4 establishes Hrdlička's belief that the indigenous American populations were best viewed as a hand with two thumbs representing Aleuts and Eskimos.

The Aleuts are nearly equally removed from all other populations except for the spurious incursion of Apache. This is more in line with the view that Aleut-Eskimo divergence occurred prior to the establishment of Anangula (8,700 b.p.). The data may also be interpreted to indicate that Aleuts have evolved independently since that time. The great time depth, cultural continuity, and population persistence in the Aleutian Islands are most likely an Aleut achievement and not the result of replacement of Paleo-Aleuts by Koniags, Athabaskans, or, in this case, Apache (Beman and Harper 1975, Harper 1975).

It is difficult to believe that a large, well-adapted, high-density population such as the Aleut (Harper 1978) could be swamped by invading Athabaskans. If any close resemblance between the Aleut and Athabaskan Indians truly exists, it is more likely that the Aleut were the seminal population. Carrying this one step farther, it is difficult to present a cogent argument that the Eskimos originated in areas such as Central Canada, characterized by small population size, low population density (Burch 1972), and short life expectancy (Harper 1978). Southern Beringia, in contrast, was an environment capable of supporting a greater diversity of life, hence more capable of supporting large, diverse seminal populations that independently evolved into Aleuts and Eskimos.

by MARSHALL G. HURLICH

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Szathmary and Ossenberg are to be complimented for an innovative application of taxonomic procedures to an anthropological dispute of long standing. I find their argument well-structured, convincing, and demonstrating a nice use of interdisciplinary data. My comments, therefore, are limited to methodological matters which a study such as this must address. There are at least five points to consider: (1) determining which genetic and/or morphological traits to use to unravel phylogeny; (2) deciding which variables best describe a particular population for purposes of phylogenetic assessment; (3) testing for the intercorrelation between variables; (4) dealing with the problem of using (skeletal) traits which are continuous and thus potentially introducing relationships which reflect environmental effects rather than phylogeny; and (5) determining the nature of the populations compared in terms of their genetic closure and intrapopulational versus interpopulational variability. The first and second of these issues are dealt with by using all available genetic data and a large number of cranial traits in the hope that variability in the rates of change (mosaic effects) will be randomized. There is no way yet available to deal with the third problem except to use traits with a high degree of heritability in order to minimize the likelihood of phylogeny's reflecting convergence. If this is done, it solves the fourth problem, but it remains to be fully demonstrated that the cranial traits listed in table 5 are all equally heritable in humans despite their appearance as highly heritable in laboratory rats (Grüneberg 1961, 1963) and wild mice (Berry 1963). As Ossenberg (1976) has written, work is needed to refine scoring, weighting, and heritability estimates of discrete cranial traits and to determine the influences of pooled-sex samples. For example, Zegura (1975), Corruccini (1974), and Finnegan (1972) all report sexual dimorphisms for cranial observations while Ossenberg (1976) does not. How this issue affects conclusions about North American populational phylogeny awaits further skeletal studies. However, data "noise" due to higher variances from male-female cranial differences should distort or obscure phylogenetic assessments, yet, remarkably, there is fairly high congruence in this study between genetic and skeletal data. The fifth problem is probably of little importance in this study, since the populations included are well separated by space and time. The major difficulty is, as Ossenberg

indicates, in determining if a cemetery population is equivalent to a group of living villagers for purposes of phylogeny. Further, a major weakness in data now available is the almost complete lack of skeletal materials from the Northwest dating at or before the climatic maximum of 4–6,000 b.p., when one would expect (hope for?) convergence of populational variances in discrete-cranial-trait data on the basis of the hypothesis presented here.

These comments are not meant to detract from Szathmary and Ossenberg's argument, which remains an elegant test of theory, but to indicate additional points of profitable inquiry.

by PAUL L. JAMISON

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"No scientific falsehood is more difficult to expunge than textbook dogma endlessly repeated in tabular epitome without the original data" (Gould 1978:504). Szathmary and Ossenberg have taken on the task of revising a piece of textbook dogma in what I think will be one of the most thought-provoking studies on population differentiation to appear in recent years. There are two comments that I would like to make, one relating to the research design and the other to the interpretation of the data. The difficulties inherent in conducting a study such as this one are numerous, as the authors are well aware. Therefore I see no reason to dwell on circumstances such as the independence of the skeletal and genetic samples, the variable time depth, the necessity of lumping data from a number of populations, thus creating regional groups, in order to provide gene frequencies for all loci, and the question of extrapolating from data on contact and recent populations to reflect population differences of 5–10,000 years ago.

Ossenberg (1976:707) provides a statement of what is necessary in the design of a study such as the present one. She suggests that one should "choose samples comparable in regional scope and diversity, [and] include a large number of samples so that conclusions can be based on a *consensus* rather than on the evidence of one sample per group. . ." The authors recognize that they did not adhere to the first requirement, but they fail to point out that the second could not be met. Until more data are available on Asiatic Mongoloids and Eskimos, single samples will have to suffice, but the present results could be anomalous for that reason.

The distance matrix presented in Szathmary and Ossenberg's table 4 provides opportunity to suggest some different aspects of interpretation than those the authors emphasize. They point out that neither the Mongoloid-Eskimo versus Mongoloid-Indian genetic distances nor the Chukchi-Eskimo versus Chukchi-Indian genetic distances are significantly different. No significance level is given, nor is the test statistic described, but in 1976 Ossenberg used the Mann-Whitney *U* test (Siegel 1956) for this purpose. Since Eskimos and Indians are the crux of this paper, I compared distances between each of the Asiatic representatives and the six Eskimo groups versus the five Indian groups having Na-Dene languages. My table 1 presents mean distances for both the genetic and the discrete cranial traits along with the probability that the distributions are from the same population of values as tested by the Mann-Whitney *U* statistic. Viewed in this way, the tendency for non-Siberian Eskimos to be closer to Asiatic groups than to Indians is rather consistent. In addition, the distributions of distances between the Asiatic Mongoloids and Eskimos versus Indians are significantly different according to the *U* statistic. However, the criticism of using single samples for the Asiatic groups is just as appropriate here as it is for Szathmary and Ossenberg's analysis.

A second question concerning the interpretation of these distances relates to a hypothesis that Ossenberg tested in 1976, namely, "that within-race distances . . . are smaller than be-

TABLE 1
MEAN DISTANCES BETWEEN ASIATIC GROUPS AND ESKIMOS
VS. NA-DENE SPEAKERS IN SZATHMARY
AND OSSENBERG'S DATA

GROUP AND KIND OF TRAIT	MEAN DISTANCES		SIGNIFICANCE OF <i>U</i> STATISTIC
	Eskimos	Na-Dene- speakers	
Genetic			
Asiatic Mongoloids.....	.0355	.0560	.015
Asiatic Eskimos.....	.0778	.0824	n.s.
Chukchi.....	.0680	.0758	n.s.
Cranial			
Asiatic Eskimos.....	.0870	.1056	n.s.

tween-race" ones (p. 702). If the distances in the authors' table 4 are examined in this regard, the non-Siberian Eskimo distances plus the Na-Dene-speaking Indian distances can be contrasted with the Eskimo-Indian distances. For genetic distances $U = 615$ ($z = 4.05, p < .0003$), while for the discrete-cranial-trait distances $U = 38.5$ ($p < .05$). Thus for both types of data the within-population distances are significantly smaller than the between-population distances.

Szathmary and Ossenberg at times express surprise at the systematic nature of their results in spite of the problems with their data. I share their surprise, but mine is based on the degree to which their results conform to expectations based on past research. Figures 1, 3, and 4 appear to me to display a common feature: a cluster of Eskimo groups linked at some higher level to a cluster of (primarily) Na-Dene-speaking Indians. Or am I simply operating in what Gould (1978:504) calls "the middle ground of unappreciated bias . . . in the interest of a 'truth' passionately held but inadequately supported"? Regardless, I expect that a good deal of research will be stimulated by this interesting article.

by B. JØRGENSEN

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Szathmary and Ossenberg's paper will be of great interest to all scientists working with aboriginal Americans, especially those concentrating on Arctic peoples.

For many years the theory of successive waves of populations invading America via the Bering Sea land bridge has prevailed. The time has now come to test this theory once more against the older one, first formulated by Rink, of the interior American origin of the Eskimos. The present paper offers interesting new evidence in support of this older theory.

The much closer relationship between North American Indians and Eskimos than between either of these groups and Asiatic Eskimos and Siberian peoples is convincingly demonstrated by the authors. Eskimos and Indians show low intra-population variation and larger differences between them; it is still necessary to consider them two different populations. Evidence of their contemporary or successive immigration to the Western Hemisphere does not appear from this investigation. The fact that North American Eskimos and Indians differ from contemporary Asiatic Eskimos and other Siberian peoples does not disprove that they may have originated in Asia or have had common ancestors in Asia 10,000 years ago.

The data for the Asiatic peoples, and the dating of the skeletal series, are only superficially touched upon. At least some of the blood-group series from southwestern Alaska must be very small and originate from populations with a great influx of Caucasian genes. The "pooling" of other series (e.g., Green-

landic) is daring. The skeletal materials appear to have been collected in a somewhat random way. The Eskimo series are small, and comparisons are made over very long distances instead of proceeding through more laborious analyses of close relationships.

Szathmary and Ossenberg's work definitely throws valuable and interesting new light on the question of the origin of the American Eskimos and deserves attention. Some details of the definition and use of the materials, however, need closer scrutiny.

by KENNETH A. KOREY

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The authors' reexamination of Eskimo-Amerind relatedness reopens persuasively the question of Eskimo origins. Infra-specific phylogeny cannot be reconstructed entirely from biological evidence, as the authors are aware, and their findings have important implications for future linguistic and archeological inquiry. I leave others to consider the accord of the phylogenetic hypotheses with the linguistic and prehistoric evidence already available, restricting my own comments to the biological relationships indicated for these populations.

The typological similarities of dendograms constructed from two effectively independent data sets are reassuring (figs. 4 and 5), but close inspection of the distance matrices in table 4 suggests that much of this congruence results from similar clusterings for New World populations of Na-Dene- and Eskimoan-speakers. If the distances involving the five populations of Na-Dene-speakers are aggregated as averages weighted inversely by the variances of the constituent distances, and if the distances involving the three New World groups of Eskimoan-speakers are correspondingly consolidated, then the comparison of 66 distance pairs between 12 groups reduces to that of 15 distance pairs between 6 groups whose relationships are of principal importance to the thesis. For the latter comparison of genetic and skeletal distances, Spearman's rank-correlation coefficient is without significance at the 5% level with even 15 degrees of freedom (i.e., $r_s = .07$). A number of factors may be implicated. Although the theoretical distributions of the two distance statistics employed are imperfectly correlated, this should have limited influence upon the nonparametric measure of association. More probably, the diminished correspondence between data sets results from increased representation in the paired comparison of Aleuts and Blackfoot, since distances involving these groups are the most discrepant between data sets (for reasons which the authors consider). Alternatively, distances based upon nonmetric skeletal traits may become increasingly unreliable as the relatedness of the groups compared declines (see, for example, Ossenberg 1976). The analysis of these traits, whose etiologies are as yet unknown, is still in its infancy, and, at least as expressed by unadjusted trait frequencies, their taxonomic value remains moot. Circumparietal wormian bones, to cite a single case, are generally known to be asymmetrically regressive with age, so that computing their frequency as the proportion of sides affected (instead of the proportion of crania affected) emphasizes this bias. Their appearance, furthermore, has been found to vary between populations by sutural site, raising the possibility of multiple etiologies. While further methodological refinements here are certainly desirable, I suspect that the relatedness of these populations is sufficiently close that the problem of widely different trait etiologies is not of great concern. Whatever the disparities between the distance pairs, the central proposition—that the affinities of Na-Dene-speakers and North American Eskimos are not remote—is unambiguously borne out by both sets of data.

Finally, it would seem worthwhile to repeat these analyses when more samples and more loci have been surveyed. Genetic differences between Alaskan Eskimos and Indians in the excretory rate of β -amino-isobutyric acid (Allison, Blumberg, and Gartler 1959) and in the ability to taste phenylthiocarbamide (Allison and Blumberg 1959) have already been demonstrated, and inclusion of such loci might alter the results reported here. While it is unnecessary to emphasize the potential importance of the Siberian skeletal series (e.g., Uellen, Tigara, and Ipiutak) to this study, various Thule series, from Keewatin to Angmagssalik, are readily accessible and should be included in any future work. In the interim, the findings presented here form a valuable contribution to deciphering the prehistory of these peoples, and the authors must be commended for their achievement.

by MAKOTO KOWTA

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At least two separable issues are addressed by Szathmary and Ossenberg. The first of these is whether or not Eskimos and northern Indians show a significant level of genetic and cranial similarity. The authors provide ample evidence that they do, to the point that their suggestion of possible descent from a common earlier population seems not unreasonable. The second issue is to what extent the similarity reveals the origins of the Eskimos. The authors' view, drawing heavily (though not exclusively) on their interpretation of the physical anthropological data, is that the Eskimos emerged both culturally and biologically in the New World. This view is contrasted with one to which they ascribe the following theses (among others): "(1) Eskimos and Indians are the descendants of different populations that entered the New World at different times" and "(2) Eskimos and Indians entered the New World by different routes (coastal versus inland); thus contact between them was minimized and their biological distinctiveness maintained."

Given this model of successive migrations by biologically distinct populations as the alternative view, it is easy to see how Szathmary and Ossenberg's physical anthropological analyses might have led them to their conclusions about Eskimo cultural origins. The issue is complicated, however, by a third possibility—namely, that Eskimos and Indians entered the New World at different times and possibly by different routes but were drawn from the same Old World founding group, one composed of small groups exhibiting genetic heterogeneity. If this had been the case, it could very well account for the observed similarities (and differences) between Eskimos and Indians and would also seriously weaken the authors' arguments for a New World origin for the Eskimos.

Szathmary and Ossenberg have helped to place the facile observation of Eskimo-Indian distinctiveness in proper perspective with regard to Eskimo origins. Their study should serve to pinpoint additional facets of the problem requiring further investigation.

by ROBERT McGHEE

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I am encouraged to see physical anthropologists applying their knowledge to the elucidation of questions of interest to prehistorians. The genetic relationships of Eskimo populations to one another and to Aleuts, Old World Mongoloids, and Amerindians are useful information for anyone attempting to sort out the problems of Eskimo prehistory. The conclusions are welcome to those of us who suspect that ancestral Eskimos reached North America during the early Holocene, perhaps as

the last of a series of population expansions which brought at least some ancestral Amerindians to northwestern North America during the closing phases of the Wisconsin glaciation. Yet when the two techniques presented reach unexpected and often contradictory conclusions on the degrees of similarity between individual Indian and Eskimo populations, and when the general conclusions are at odds with traditional concepts, we might be advised to question the techniques rather than the traditional views.

Two sets of questions may be asked. The first arises perhaps from a prejudice impressed on me as a student by the late Lawrence Oschinsky: that the characteristics which make gene-frequency and discrete-trait analysis very useful for micro-evolutionary studies (relatively simple and known mode of inheritance) make them less useful for the study of deep historical relationships. Oschinsky (1962) claimed that the relative lability of monogenetically controlled traits, their little understood susceptibility to selective forces, and the resulting possibility of parallelism detracted severely from their usefulness in tracing relationships between populations which have been isolated for several hundred generations. On the other hand, traits which are apparently under more complex polygenic control could be expected to be more stable in a population over time and more useful in assessing problems of the deep past. On the basis of such traits, Oschinsky (1964) claimed to have defined an "Arctic Mongoloid" population including Eskimos, Aleuts, and northeastern Asiatics and excluding Amerindians. These results are more consistent with the linguistic evidence, and with our traditional views of prehistory, than are the results of the present study.

The second question involves the statistical treatment of distance measurements. The cluster analyses on which most of the concluding statements are based are attractive to prehistorians because the resulting dendograms can be easily transposed into, or mistaken for, "family trees." Yet when we are dealing with a set of numbers as similar as those dealt with here, the shape of a dendrogram is dependent on arbitrary decisions regarding the mode of linkage used and the levels at which links are to be made. Another technique of comparing numbers, a simple calculation of mean distances between sets of populations listed in table 4, yields a somewhat different picture. For example, it is stated with reference to gene frequencies that "the greatest genetic similarity of the non-Siberian Eskimos as a group is to American Indians and, within this group, to speakers of languages of the Na-Dene phylum." Yet the mean genetic distance between non-Siberian Eskimos and Indians (.038) is slightly greater than the distance between Eskimos and Old World Mongoloids (.034), although the difference is not significant (Kolmogorov-Smirnov $D = .27$); the distance between Indians and Old World Mongoloids is significantly higher at .064 ($D = 9.52$, $p = .02$). The mean distance between non-Siberian Eskimos and Na-Dene-speakers is .038, identical to that between Eskimos and non-Na-Dene-speaking Indians. This would appear to place Eskimos somewhere between Old World Mongoloids and Amerindians as a single group, which fits traditional patterns of interpretation. These results are of course no more valid than are the results of the cluster analysis used by the authors, but merely indicate that we cannot expect an unambiguous approximation of reality to emerge from the manipulation of the numbers presented in table 4.

Despite the ambiguity of the results reported, I consider this to be a useful article. The scheme of prehistory presented by the authors, although making rather naive use of the small amount of archaeological evidence available, is as convincing as any previously proposed. I hope that other physical anthropologists, linguists, and culture historians are stimulated to undertake similar studies bearing on the relationships of Eskimos to Indians and to Siberian populations.

Szathmary and Ossenberg: INDIAN-ESKIMO BIOLOGICAL DIFFERENCES

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This article must be viewed as a tour de force. The results obtained account for a number of anomalies present in the available data. Especially impressive is the congruence of the two sources of information, given previous disagreements in this area. More than anything, however, I welcome the reopening of these questions in a manner removed from preconceptions and axioms.

I would still like to raise some points that require clarification, discussion, or, simply, recognition. Further work will be needed before a new synthesis is complete.

1. The congruence of data of differing types has often been less clear than is seen here (e.g., Corruccini 1974, Gaherty 1971, Pietruszewsky 1977, Zegura 1975). Means to solve this problem are often ad hoc. The types of data compared here provide an innovative step. However, the battery of traits used in the phenetic section has a validity based partly upon the congruence of results from another study (Zegura 1975; see Ossenberg 1977). Choice is thus partly based upon the previous performance of the traits in congruence studies rather than upon intrinsic biological factors. Can it then be fully asserted that the phenetic-trait analysis provides independent confirmation of the genetic analysis? Other questions regarding the statistical behavior of nonmetric traits, such as their normal distribution or lack of it, might have been given further discussion (see Sjøvold 1977).

2. There are some anomalies in the data base presented. The generalized Mongoloid sample is closer to all other genetic samples than is the Chukchi, as close as some Eskimo samples are to each other. The Haida sample is closer to the Assiniboin than to the Tlingit, the Assiniboin closer to the South Alaskan Eskimo than is any population to the East Greenland Eskimo. Some testing of the strength of the derived clusters appears to be in order. Group overlap may be obscured by the use of dendograms, a discrepancy built into the methodology of some multivariate methods, especially when applied to populations below the level of the species (see Thorpe 1976).

3. Rethinking of elements in Arctic and Subarctic prehistory is obviously in order. The authors may themselves be in danger of accepting axiomatic positions in their own comments. Both McGhee (1976) and I (1978) have recently queried the Eskimo affinities of the Arctic Small-Tool tradition (ASTt) and, more particularly, the affinities of Dorset-age skeletal remains from the Canadian Arctic (Oschinsky 1960, 1964). The evidence linking the northern ASTt and southern Alaska areas is weak. The unity of an Eskaleutian linguistic stock appears to predate the earliest known ASTt material. There is possible archaeological continuity in southern Alaska going back to the earliest sites (Anangula, Ground Hog Bay). There is thus strong evidence for positing a development of the Eskaleut stock and its subsequent dichotomy within southern Alaska.

On the other hand, there is evidence for typological connections between the ASTt and the Siberian "Neolithic" (e.g., Bel'Kachi). There is no clear connection of northern and southern Alaska in an early ASTt context. ASTt populations appear to be undoubtedly Arctic Mongoloids (Oschinsky 1964). Association with linguistically defined Eskimos may be misleading. Dorset skeletal material is separable from that of North American Indians, but the studies undertaken were not designed to separate them from Siberian populations. Both McGhee and I have suggested that the first northern group that can be biologically and linguistically identified as Eskimo is the Norton tradition (possibly including Choris). In Canada the earliest true Eskimos would be the Thule. Further work is clearly required to solve such questions. The affinities of

atypical populations such as Ipiutak should be included in any such assessment.

4. Against the above queries stands the homogeneity of results in this article. The similarity of Eskimos and Athapaskans has been noted before. This article suggests that these similarities are real. The results of Oschinsky (1962, 1964) are clarified. My own recognition of similarities in the facial morphology of Eskimos and Northwest Coast Indians seems more reasonable (Meiklejohn 1968). Some of Neumann's (1952) results should be reexamined. This article provides a basis for considerable further work.

by TURHON A. MURAD

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I have always valued attempts such as this by Szathmary and Ossenberg to shed new light upon the complex problems of human variation and biological distance. The problem the authors have chosen to investigate is complex if for no other reason than that much contradictory information has been published about the biological relationship between North American Indians and Eskimos. While the present article aids by placing the problem in historical perspective and summarizing the work of others, I believe it provides a less than profound answer to the question of biological differences between North American Indians and Eskimos. In particular, I am concerned with why more serious consideration was not given to the possibility that the differences between North American Indians and Eskimos could be explained by events which may have taken place in the Old World.

The authors point out that from the genetic data in table 4 it can be seen that "none of the Mongoloid-Eskimo versus Mongoloid-Indian distances differed significantly from each other" and that, "similarly, the Chukchi-Eskimo and Chukchi-Indian distances were not significantly different." They go on to conclude that "there is . . . no statistical validity to the claim that the Eskimos are closer to classic Mongoloids than are American Indians." The question is whether the alternative—that Eskimos show greater genetic affinity to North American Indians than to classic Mongoloids—can be demonstrated to have any greater statistical validity.

From the genetic data in table 4 it can be determined that the Asiatic sample is the most heterogeneous (the average distance among Asiatics is .125). Eskimos, on the other hand, appear to be the most homogeneous of the three groups, the average distance among them being .019. The average biological distance among North American Indians is .047, intermediate to those among Asiatics and among Eskimos. Why can't these results be used to suggest that the Eskimos represent a homogeneous subgroup derived from a larger heterogeneous Asiatic population which has only more recently arrived in the New World? It could be suggested that the North American Indian sample appears intermediate because it represents various migrations over a longer period of time, allowing greater divergence.

If this alternative can be suggested for the genetic data, which are more nearly complete, what of various interpretations of the skeletal data? While the authors cannot be faulted for the lack of available material, it is, as they suggest, unfortunate that "there is not a complete correspondence between the populations used for the genetic and for the skeletal analyses."

I enjoyed the authors' review but am only more convinced that the classic benediction to research, calling for further work, is appropriate here.

by CLEBER BIDEGAIN PEREIRA

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25 v 78*

Sucessivas pesquisas têm evidenciado que os Eskimos e índios Norte Americanos são biologicamente distintos. No entanto,

em nosso ponto de vista, estas diferenças não são suficientemente profundas para afastar a sua origem comum, separada a não mais de 10.000 anos atrás. Isto é comprovado pelas similitudes biológicas identificadas entre Eskimos e algumas tribos de índios Norte Americanos. (Shapiro's e trabalhos subsequentes). Eu acredito como Neumann (1952:29): «the uniqueness of the Eskimo may have been overstressed».

Como tese geral, aceito a origem mongólica dos índios Americanos, na tradicional rota do Mar de Bering. Também os índios Sul Americanos, com os quais temos trabalhado em pesquisas dentárias (Pereira and Mooney 1972, Pereira and Harris 1975, Jacobson and Pereira 1977), têm os dentes em «forma de pá» e outras características mongólicas. Talvez algum ponto de dúvida surgisse na rota migratória dos ameríndios Sul Pacificos.

[A series of studies has demonstrated that Eskimos and North American Indians are biologically distinct. In my opinion, however, the differences are not so profound as to deny a common origin no more than 10,000 years ago. This is confirmed by the biological similarities between Eskimos and some North American Indian tribes (Shapiro's and subsequent work). I agree with Neumann (1952:29): "the uniqueness of the Eskimo may have been overstressed."

As a general thesis, I accept a Mongolian origin for the North American Indians along the traditional Bering Sea migratory route. South American Indians, among whom I have done dental research (Pereira and Mooney 1972, Pereira and Harris 1975, Jacobson and Pereira 1977), also show "shovel-shaped" teeth and other Mongolian traits. This may raise some doubt as to the migratory route of South Pacific Amerindians.]

by SUSAN PFEIFFER

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Szathmary and Ossenberg have made an admirable effort to synthesize a broad range of information. Competent discussion of relevant genetic, skeletal, archeological, and linguistic evidence is no mean feat, and such an attempt underlines the continuing importance of "general" anthropology. Those skeletal biologists who have turned their research attention to discrete traits will certainly be gratified by the concordance of Ossenberg's work with Szathmary's. Nevertheless, a rather oversimplified view may have been given of the confounding factors in an analysis of such traits. In the present study, the reader must assume that the researcher gave sufficient attention to age and sex dependencies. I would have appreciated statistical justification for the pooling of left and right frequencies of bilateral traits and for the inclusion of variables recognized to have a substantial environmental component, like wormian bones. An analysis of continuous skeletal traits (measurements) and their division into size and shape components, as in McGhee's work, would have been a valuable addition to this already impressive research.

The most stimulating aspect of Szathmary and Ossenberg's work lies not in the statistical methodology, however, but in their interpretation of their results. It draws attention to a ubiquitous problem: we tend to push significant hypothesized events back to a prehistoric stage about which we know so little that we cannot test our hypotheses. I am referring here to the placement of an Eskimo-Na-Dene divergence in pre-Archaic times, when population density was presumably very low and the conditions affecting gene flow are virtually unknown. It is encouraging to see that evidence for recent gene flow appears to be missing from the dendograms. This helps to substantiate the idea that the Eskimo-Na-Dene connection is an ancient one. Nevertheless, I remain uneasy about attributing major biological patterns to the behaviour of prehistoric inhabitants of Alaska about whom we know so little. My own work with Archaic populations of the Great Lakes region has impressed

me with the high degree of temporal and spatial variability that can accompany low population density. Further, continuity of skeletal size and shape from Archaic to more recent times has not been adequately demonstrated for any geographical region. How, then, can we expect such continuity for blood-group systems? One would like to be able to attach a statistical probability to the formation of a relatively stable, homogeneous ancestral population prior to 8000 b.c. and its survival, in more than remnant form, to the present day. It does appear from the data and discussion presented that one should perhaps think twice before attaching the label of "Indian" to very early skeletal remains from a boreal region.

by FRANCISCO M. SALZANO

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Szathmary and Ossenberg have assembled a large amount of data from many different sources, analyzed them with modern methods, and placed the results in proper context. This is a valuable contribution to our understanding of the relationships between North American Indians and Eskimos. I have only one reservation about their approach: admixture with non-Indians is completely ignored. This is particularly surprising if we consider that in a recent paper (Szathmary and Reed 1978) one of the authors acknowledged the possibility of as much as 30% of Caucasian admixture in one of the tribes included here. Differing amounts of foreign genes in modern or past Indian or Eskimo populations may significantly blur past relationships or suggest false concordances. The fact that the blood-group tests were made at different times with reagents from multiple sources and using different methods should also have been stressed as a cautionary note.

by DAVID S. WEAVER

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Szathmary and Ossenberg have provided a powerful and interesting examination of the question of the relationship between the Eskimos and North American Indians. It does seem likely that a closer relationship than is usually inferred is the case. Several points seem worthy of comment, however.

First, a minor point: It is not clear to me why "gene flow or adaptive response" should lead to the breakup of linguistic clusters. It would seem, especially when the populations involved are small, that significant genetic exchange need not force linguistic changes. Especially early, single individuals exchanged by groups could have substantial genetic effects while having little linguistic impact.

Why shouldn't gene flow between initially small groups be sufficient reason for the observed similarities in blood-group and skeletal nonmetric data? At best, the adaptive significance of the traits used by Szathmary and Ossenberg is speculative. Flow between populations of initially small size can provide surprising homogeneity. That homogeneity, once established for traits of no clear adaptive significance, might well persist as populations increased. Drift effects within the divergent populations could be compensated for by rather minimal later gene flow. Admittedly, common origin is a more attractive hypothesis, but we must remain alert to the other available hypotheses.

If the traits used in the study are of adaptive significance, there is a more serious difficulty, of course. Distance measures, it is widely acknowledged, do not adequately distinguish between lack of divergence and convergence. Adaptive convergence would appear to be phylogenetic similarity.

Also, the assumption that, since phylogeny can be shown in recently divergent groups by use of a certain number of loci, the same number of loci will be sufficient to evaluate phylogeny in more distantly related groups is questionable. If the perturbing

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effects of drift, flow, and selection are to be minimized, it would seem that more loci should be used the more distant the proposed relationships between groups. The use of cranial nonmetrics does add a number of loci to the evaluation, of course. As the authors point out, the problems of linking skeletal samples to modern inhabitants are substantial, however. In addition, the number of loci, and even the degree of genetic control of the traits, for cranial nonmetrics is uncertain, at best. One is clearly limited to available data, but conclusions are weakened by the character of those data.

Finally, if Neumann's (1952) suggestions are correct and the proto-Aleuts were in fact Amerindians, the classification, using discrete-trait analysis, of Aleuts with Amerindians and not with Eskimos would make perfect sense. This situation might also address some of the confusion present in the archaeological interpretations of the area. The concept that "artifacts equal people" has been ceremoniously buried more than once (see Willey and Sabloff 1973) but is still an occasionally pervasive influence in interpretation. Since people can and do borrow and adopt cultural behavior without regard to physical form, Neumann's suggestion provides considerable indirect support for at least a portion of the present authors' hypothesis.

All in all, Szathmary and Ossenberg's hypothesis of common origin of the Eskimos, Aleuts, and Amerindians is more satisfying than a hypothesis of recurrent waves of new physiological (and linguistic) types washing across northern North America. Perhaps some drift simulations, based on an assumption of common origin, followed by simulated small-scale gene flow at various points during the expansion into North America, would provide provocative support for their hypothesis.

by STEPHEN L. ZEGURA

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Investigators interested in the historical relationships of North American Indians, Eskimos, and Asiatic Mongoloids owe a debt of gratitude to Szathmary and Ossenberg for their fine attempt at a synthesis of the serological and discrete cranial data which provide a heuristic framework for discussing the biological affinities of these populations. The limitations inherent in the data base have unfortunately made rigorous tests of taxonomic congruence impossible; however, the data have led to potentially productive scenarios offered as explanations for the surprisingly close biological affinities between North American Eskimos and the Na-Dene.

The dendrogram representation of the genetic distances contains few unexpected clusterings (with the exceptions of the Blackfoot and Apache positions). Overall, the dendrogram based on discrete cranial distances coincides with currently accepted relationships even more closely, thereby emphasizing the value of discrete cranial traits for biological-distance analyses. In fact, only the Aleuts exhibit a curious clustering on the basis of these data. On the other hand, the assumption that osteometric and attribute data yield "similar" patterns of relationship (which is made by the authors for comparative purposes) is open to question, given the many empirical data sets for which this has turned out to be false. The authors should be more explicit concerning their usage of the term "similar." In general, pattern similarity usually does obtain; however, detailed population placements often vary, as do higher-order clustering patterns upon occasion. Taxonomic congruence can be quite low, and sometimes a statistically significant level of correlation is not achieved.

The cranial data presented lead to statistically significant biological distances in many more comparisons than do the genetic data. Is this a function of environmental interaction, the differing biological bases of the traits, historical patterning,

the effects of evolutionary forces, or the statistical techniques used to manipulate the data? It also seems that the traditional thesis that "culturally imposed barriers through time maintained the initial biological differences between Eskimos and Indians" is unsupported by these data in that the temporally later gene-frequency data show convergences not reflected in the earlier cranial data base. As the authors point out, recent gene flow and adaptation to particular ecozones are not always satisfactory explanations. It is unfortunate that the two explanations put forth for the Eskimo-Indian affinities are at present untestable (here, indeed, is a fertile field for future research).

As with any paper, there are a few minor points that might not meet with universal acceptance. "Migration matrices" represent biocultural phenomena and not "nonbiological criteria." Discrete morphological data should be recorded as "prevalences" and not "percentage incidence." While it is true that the multivariate distances for a set of data are not independent and that the degrees of freedom are inflated, this does not mean that "the significance of the results cannot be readily judged." Application of the Bonferroni inequality to the simultaneous test situation can restore the appropriate *alpha* levels. The dendrogram aggregation of Navaho and Apache with the Northern Athapaskans does not seem "unlikely" and, indeed, could be expected both linguistically and ethnohistorically. Not all anthropologists would agree that the Denbigh Flint Complex is "unequivocally attributed to Eskimos." Finally, although the paper has demonstrated that North American Eskimos and some North American Indians are "closely related," the problem of the phylogenetic relationships among Aleuts, Asiatic Mongoloids, and the aforementioned American Indians and Eskimos is far from resolved.

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The literature on microevolution and population differentiation in anthropology demonstrates the same type of analytical problem throughout. This is no fault of the researchers but relates to a lack of proper statistical tools. By proper tools, I mean ones that can accommodate the data that exist for living and extinct human populations.

As in most other studies on the differences between human populations, Szathmary and Ossenberg are obliged to spend most of their analytical labors in reconciling their choice of statistical tools with the characteristics of their data. Many problems they are compelled to solve, e.g., testing and comparison of the dendrographs or pooling of samples in the osteological population, would not have arisen if their statistical procedures had not been designed for use with data from large universes that could be repetitively sampled. Ossenberg is acutely aware of this, as her statement about the uniqueness of skeletal populations shows.

A strength in any scientific study is independent verification from two data sources. This study possesses that potential in the separate data sets used, but independent verification is weakened by the lack of correspondence between the universe composed by the osteological material and that composed by the blood-group material. It would be strengthened by demonstration of direct lineal similarity between the two data sets, but this is not possible.

Occasionally attempts are made by those knowledgeable in statistics and anthropology to create procedures that are applicable to human microevolutionary data. Two such efforts (Rothhammer et al. 1977, Spielman 1973) are cited, but, as can be seen, they do not fit the data presented here. We badly need more work in the field to aid in the solving of problems such as those approached in this work. Given the state of the art, it would seem that the analysis of population differences presented is as clear as can be expected.

Reply

by E. J. E. SZATHMARY and N. S. OSSENBERG

Hamilton, Ont., Canada. 20 VII 78

Whether all this means simply extensive past mixture, or whether, as would seem, the Alaska Indians as a whole are nearer physically to the Eskimo than are the tribes in the States, remains to be determined. Among the Athapaskan Mescalero Apache, who have reached as far south as New Mexico, a somewhat Eskimoid tinge to the face, especially in young women, was by no means very unusual 25 years ago when I studied this tribe. . . . [Hrdlička 1930:82]

Our intent in this paper was to demonstrate that the biological differences between Eskimos and specific North American Indian populations were not as great as some have claimed. This perspective grew out of work each of us had done independently, using genetic-marker and cranial data respectively. It appeared logical to us to combine our efforts to deal with a viewpoint that had assumed the proportions of dogma and was confounding interpretations of the archaeological record.

We shall concentrate here on the questions that commentators have raised most frequently or that we consider most important. These include consideration of (1) statistical methods, (2) research design, (3) interpretation of results, (4) appropriateness of genetic markers and/or discrete cranial traits for answering questions of population affinity, and (5) miscellanea.

1. *Statistical methods.* We chose Nei's (1972, 1973) *D* over other measures of genetic distance (e.g., Cavalli-Sforza and Edwards's [1967] *E* or Balakrishnan and Sanghvi's [1968] *B*) because (1) *D* is strongly correlated with *E* (Chakraborty and Tateno 1976, Szathmary 1978) and *E* with *B* (Sanghvi and Balakrishnan 1972) when closely related populations such as human "races" (Nei 1975) are considered; (2) unlike that of *E* and *B*, the precision of *D* can be determined; and (3) unlike *E* and *B*, *D* affords a straightforward genetic interpretation, at least for electrophoretically detectable loci.

The calculation of *D* depends upon the probability that two alleles at the same locus in two different populations are identical. That is, if A and B are different populations, the normalized probability that two alleles, one from each group, are identical at locus *l* is $I_l = \Sigma a_i b_i / \sqrt{(\Sigma a_i^2)(\Sigma b_i^2)}$, where a_i and b_i are the frequencies of the *i*th allele in populations A and B, respectively. The value of *I* is 0 when no alleles are held in common between the groups and is 1 when the alleles in A and B occur in identical frequencies. When several loci are considered, the mean genetic identity is $I = J_{AB} / \sqrt{(J_A J_B)}$, where J_{AB} , J_A , and J_B are the arithmetic means over all loci of $\Sigma a_i b_i$, Σa_i^2 , and Σb_i^2 , respectively. The probability of having different alleles over all loci is given by $D_A = 1 - J_A$, $D_B = 1 - J_B$, and $D_{AB} = 1 - J_{AB}$, respectively. The mean genetic distance is given by $D = -\log_2 I$ (Nei 1972, 1973, 1975). Thus *D* depends only upon the frequencies of the alleles examined in a set of populations and not, as Cook asserts, upon within- and between-group variances.

Similarly, our clustering procedures are not dependent upon within- and between-group variances. Both the McCammon and Wenninger approach (fig. 3) and the Nei approach (figs. 1, 4, 5) are based on the unweighted pairwise group mean average method described by Sokal and Sneath (1963). In these procedures, the first groups to be clustered are the two with the smallest distance. These groups are then combined and treated as a single group. New estimates of distance between the combined group and other groups are computed and the clustering procedure repeated. This continues until all groups are clustered into a single family. Cook may be referring to Ward's (1963) error-sum-of-squares method, which is distinct from the method just described.

Cook and Hall question the effect on our comparisons of disparities in the scope of the samples (i.e., the fact that a few represent a single community, while others may be large regional aggregates). In only three instances—Aleut, Assiniboin, and Tlingit blood groups—were gene frequencies largely ob-

tained from single samples. The serum-protein data for even these populations either are pooled data from several sources (see table 3) or were obtained from different samples (e.g., Assiniboin and Tlingit) than the blood groups. The Chukchi data were obtained from two different villages (Nuniamo and Sirenki), while the Asiatic Eskimo frequencies were pooled for three different villages (Naukan, Chaplino, Sirenki). This latter fact should perhaps have been made clearer.

While there is a great disparity between 79 Tlingit and 817 Asiatic Mongoloids (ABO data) in absolute numbers, we would be unable to sample an equivalent number of Tlingit in Canada, since the entire Tlingit population in 1967 was 482 (Department of Indian Affairs and Northern Development 1967). The issue, of course, is not comparable size, but representativeness, of samples. As a rule, researchers do not give the size of the population from which samples are drawn; hence we have no means by which to determine whether our samples are proportional in size to the populations they represent. Lest this be taken as cause for concern about the precision of the genetic distances, we point out that Nei and Roychoudhury (1974) and Li and Nei (1975) show that the variance of D is much more dependent on the number of loci examined than on sample sizes, even when as few as 20 individuals are examined. It is for this reason that we employed data from 11 genetic systems—the maximum that we could obtain for the groups in which we were interested. That the samples in some instances are based on as few as 60 individuals (e.g., Commander Aleuts) or as many as 532 (e.g., Asiatic Mongoloids for the Rh locus) does not bias the precision of D .

With respect to the influence of disparities in the scope of samples on the skeletal measures of divergence, we note the following: Although we excluded nonmetric cranial traits that are known to be affected by the environment, we cannot be certain that the variability in trait expression of the remainder is entirely produced by genetic variance. In general, owing to drift, including founder effect, as well as local inbreeding and possibly unknown environmental effects, single small communities may not provide a good representation of the genome of the regional population or tribe and will tend to show greater divergence from other groups than would a pooled sample drawn from several communities. For example, six samples were pooled to form the South Alaskan Eskimo aggregate. Of these, two (Hooper Bay and Kodiak) represent single villages. Though each of the other four represents several villages, each is fairly localized and could be affected by drift and isolate inbreeding. Pooling the six may have the effect of "cancelling out" effects of microevolutionary divergence between them. The measure of divergence between our pooled sample and Blackfoot is $.088 \pm .002$. Had we represented South Alaskans by a single village, Hooper Bay, the measure of divergence with Blackfoot would have been $.146 \pm .008$. Had we selected the Kuskokwim River group, it would have been $.090 \pm .004$. Although these measure-of-divergence scores may not be significantly different (we have not tested), the position of South Alaskans in the dendograms would change depending on the value employed. Certainly if Hooper Bay, for example, were our *only* South Alaskan sample, our conclusions would be different than they would be if our only sample happened to be Kuskokwim River. For this reason it is wise to be cautious about conclusions based on single samples. We have emphasized that we are not drawing conclusions on the basis of a single sample each of Na-Dene, Eskimo, Plains, and Asiatic populations; therefore we do not think that there is any serious bias in our results.

Cook, McGhee, Meiklejohn, and Zegura caution against too much reliance upon patterns of similarity obtained from dendograms, because different methods of tree construction may lead to different patterns. We agree. The reliability of any pattern increases when topological concordance is obtained between trees based on the same data but using different clustering methods or between trees based on biological and

nonbiological data respectively. For this reason it is worth stating that the tree-building method employed by Cavalli-Sforza and Edwards (1967), which differs considerably from Nei's (1975), nevertheless yielded very similar patterns of affinity in an earlier study (Szathmary 1978); Eskimos and speakers of Na-Dene were closer to each other than to any other population. Similarly, other studies have shown closeness of Eskimos and North American Indians. Cavalli-Sforza and Edwards (1964) found Eskimos of Victoria Island to cluster with Arizona Indians rather than with any of the 13 other South American, Asiatic Mongoloid, Southeast Asian, European, and African groups they examined. Although they did not specify the tribal origins of their Arizona sample, they did state that five blood-group loci (18 alleles) were employed. The only appropriate studies of Arizona Indians published before 1964 were by Brown et al. (1958) and Corcoran, Rabin, and Allen (1962). The former included ABO, Rh, and MNS data for Apache, Navajo, Pima, Mohave, Hopi, and Maricopa, Rh data for all but Mohave, MNS data for Navajo, Pima, Hopi, and Maricopa, and Duffy data for Pima. The latter gave information for a large sample of Navajo on all the loci (ABO, Rh, MNS, Diego, and Duffy) employed by Cavalli-Sforza and Edwards. There is, therefore, a sizeable Athapaskan component in the Arizona sample. Whatever the case, Cavalli-Sforza and Edwards also found Indians and Eskimos to be closer to each other than to any other population. Thompson (1975), using the same data but employing her maximum-likelihood method for dendrogram construction, also found Arizona Indians and Victoria Island Eskimos to cluster together.

With respect to agreement between dendograms based on biological and cultural data respectively, we can only reiterate what we have already said. Given the geographic distances between our populations and the absence of detailed information, such as could be used to construct a migration matrix, indicating contact between them, linguistic evidence was the only evidence that could be used to test relationships. We cannot be faulted for the nonexistence of lists of cognate pairs in Eskimo and relevant Subarctic Indian languages which could be used to construct a linguistic dendrogram. Our approach was the next best—to show that some linguists, such as Swadesh (as Dumond points out), have postulated connections between Eskaleut and some American Indian languages. We remain impressed by the obvious goodness-of-fit of clusters based on biological data to "higher-order" categories (see Hall) such as language families. In our view, it would be asking too much to expect detailed correspondence of biology and language within these groups, though some of our critics (e.g., Harper) would demand nothing less.

We agree with Korey that nonparametric tests of correlation are appropriate for the data at our disposal. As we stated, we do think that the results we obtained are significant, as indeed they are if the usual degrees of freedom apply (i.e., 64 d.f. for 66 comparisons). On the other hand, we felt compelled to discuss the reservations some authors have had about the results of tests using similar data. Whatever the statistical resolution, our results are independently important. We couldn't agree more with Fleischman that improvement in statistical techniques that could be applied to problems of this kind is highly desirable.

2. Research design. Cook has taken us to task for not stating historical models in testable form, and both Jamison (explicitly) and Jørgensen (implicitly) refer to our research design. It was not our intent to test explicitly any particular model of Eskimo or Indian origin, for one of us has done that elsewhere. Szathmary (1978) has compared the majority of the populations in this paper plus Nootka, Ainu, and Siberian for eight blood-group systems (24 alleles), using distances E and D . The models tested in that paper are (1) the "Eskimo wedge" hypothesis, (2) the "modern" hypothesis (great separation between Eskimos

and Indians, the former being closer to Mongoloids, the latter to Siberians), and (3) the "Dorset" hypothesis. The findings do not support any of these models. Rather, the most conclusive finding is that some North American Indians—namely, speakers of Na-Dene—and Eskimos are closely related. Independently, we had both observed that the existing models of Indian-Eskimo affinity did not fit the results of our previous studies. Our concern in this paper was to examine whether distances obtained from different sets of biological data representing different temporal horizons agreed with each other and to offer historical interpretations of our findings as a stimulus to further research. Use of computer simulation techniques to test various models of population affinity under different mechanisms of evolutionary change is, in our view, a separate problem, one which did not concern us here.

Jørgensen, Kowta, Murad, and Pereira refer to the hypothesis that the New World was populated by successive waves of migrants from Siberia. While their comments are not identical or equivalent, we can address this issue in general. Our results neither prove nor disprove the successive-migration theory for the peopling of the Americas, for the study was not designed to answer it.

Cook asks why we restricted ourselves to the populations we employed when "more appropriate samples" are available. Certainly, we would have preferred to include skeletal samples more comparable to the populations for which genetic-marker data are available, recognizing especially the crucial importance of Asiatic and Siberian evidence for a thorough test of our hypothesis. The deficiencies in the skeletal samples partly reflect the fact that until summer 1976, when we discovered that our independent lines of inquiry were revealing similar patterns, we had no notion of collaborating in this study. Ossenberg's work had been restricted to western North American populations. We saw that data for these samples could, nevertheless, provide worthwhile insights into the broader issue of Eskimo affinities. It is worth emphasizing that existing models of Eskimo origins and affinities are concerned with Arctic, Subarctic, and Northwest Coast populations. Examination of those models requires examination of populations in those localities. As detailed above, earlier findings (Szathmary 1978; Ossenberg, unpublished data) did not support the models, but showed, rather, affinity of Eskimo and speakers of Na-Dene. This study was undertaken with this in mind, hence the restriction of data (excepting Navajo and Apache) to groups north of the Canadian border.

Lastly, it should be said that acquiring information for 11 genetic systems or 24 discrete cranial traits for a large array of populations is difficult. Even Spuhler (1972) had to restrict his analysis to six genetic loci for his 21 North American groups, and "dummy values" (p. 75) had to be substituted for some frequencies because appropriate tests for that system had not been done. Highly informative genetic systems, such as the Gm system mentioned by Crawford, must often be excluded because no information is available either at the tribal or at the regional level. Sometimes key populations in a region (e.g., in this study, Nootka of the Northwest Coast) have to be omitted simply because no serum-protein or red-cell-enzyme data have been collected for it. Similar difficulties obtain for skeletal material. While the Greenlandic series Harper lists are undoubtedly large, skeletal data for Subarctic Algonkian-speakers and Athapaskan-speakers are either unavailable or vanishingly small (witness that four crania represent three tribal groups of Northern Athapaskans, table 1). We would not, therefore, agree that "more appropriate" samples are readily available. We have done what we could with the data we acquired and are grateful to those who appreciate that data collection alone is an arduous task.

3. Interpretation of the results. Jamison, Korey, McGhee, and Murad have taken the trouble to calculate various statistics with our data. It is disappointing that Korey's careful analysis

does not show significant agreement between the pooled data sets. However, as he points out, the independent evidence from genetic and cranial traits, respectively, is still sufficiently strong to support our assertion of Na-Dene-Eskimo affinity.

Jamison and McGhee question the clusterings in the dendograms by selecting specific sets of distances for examination. Since the dendograms in figures 1, 4, and 5 were constructed by an unweighted pairwise group method, it is appropriate to use *unweighted* distances in a nonparametric test only if all the data that went into the building of the dendrogram are considered. The reason is that the position of any population in the tree is dependent on its distance relations with all other populations. One cannot challenge clusterings in the dendograms by using only part of the data that went into their construction.

If information about the affinities of specific groups is desired exclusive of the dendograms, then the error estimate associated with each distance has to be taken into account. For this reason, we have repeated Jamison's calculations, first weighting each distance by the inverse of the variance. Because the variance measures the precision of each distance estimate, weighting by the "invariance" (Neel and Schull 1966:180) adjusts each distance measure by the amount of information available for that measure. In all instances (Asiatic Mongoloid-non-Siberian Eskimo versus Asiatic Mongoloid-Na-Dene; Asiatic Eskimo-non-Siberian Eskimo versus Asiatic Eskimo-Na-Dene; Chukchi-non-Siberian Eskimo versus Chukchi-Na-Dene), for both cranial and genetic distances, the Mann-Whitney statistic is *not* significant. The null hypothesis in all these tests, that there is no difference between the distances for the sets compared, cannot be rejected. The significance level we use in these and all our tests, unless otherwise stated, is .05.

McGhee's calculations have also been repeated, again taking the error estimate associated with each distance into account. None of the Kolmogorov-Smirnov *D* scores is significant.

Both McGhee and Jamison calculate mean distances for specific distance aggregates. It is worth mentioning that if distances are treated as ranked data, on an ordered scale (as is done both in the Mann-Whitney test and, initially, in the Kolmogorov-Smirnov test), means should not be calculated at all (Thomas 1976:307). If means are computed, distances should first be tested to see if the calculation of mean values is appropriate. If so, then the significance of the difference between means can be computed.

The mean of the genetic distances d_i of a specific set of data can be obtained as a weighted average from $\bar{d} = \Sigma W_i d_i / \Sigma W_i$, where the weight $W_i = 1/\sigma_i^2$. The heterogeneity between d_i values obtained from k population pairs can be approximately computed from $\chi^2_{(k-1)} = \Sigma [(d_i - \bar{d})^2 / \sigma_i^2]$.

McGhee lists a series of "mean distances." We have attempted to recalculate only three of them and added one of our own. The results are shown in table 6. To test whether these means are different, *t*-tests can be done if our interest is only in pairwise comparisons. Nonsignificant results were obtained for all (1) non-Siberian Eskimo-Mongoloid \bar{d} compared with Mongoloid-Na-Dene \bar{d} ($t_9 = 1.89$); (2) Mongoloid-nón-Siberian Eskimo \bar{d} compared with non-Siberian Eskimo-all Indian \bar{d} ($t_{34} = .370$);

TABLE 6
MEAN DISTANCES BETWEEN SOME
POPULATIONS LISTED IN TABLE 4

POPULATION DISTANCE	χ^2	d.f.	$\bar{d} \pm$ s.e.	McGHEE'S "MEAN"
Non-Siberian Eskimo-Indian.....	25.34	47	.029 ± .002	.038
Non-Siberian Eskimo-Mongoloid	1.37	5	.032 ± .006	.034
Non-Siberian Eskimo-Na-Dene.....	20.27	29	.030 ± .003	.038
Mongoloid-Na-Dene...	4.87	4	.044 ± .008	not done

(3) Mongoloid-non-Siberian Eskimo \bar{d} compared with non-Siberian Eskimo-Na-Dene \bar{d} ($t_{52} = .336$); (4) Na-Dene-non-Siberian Eskimo \bar{d} compared with non-Siberian Eskimo-all Indian \bar{d} ($t_{76} = .045$).

We conclude that the following populations cannot be shown to differ significantly in their genetic distances: (1) Mongoloids and either non-Siberian Eskimos or Na-Dene-speakers; (2) non-Siberian Eskimos and either Mongoloids or all Indians; (3) non-Siberian Eskimos and either Mongoloids or speakers of Na-Dene; (4) non-Siberian Eskimos and either Na-Dene-speakers or all Indians. McGhee's assertion of a statistical middle position for Eskimos is, therefore, unfounded.

Some may be surprised at such an outcome, but similar results have been reported previously for human populations (e.g., Nei and Roychoudhury 1974, Szathmary 1978). It was precisely because of such observations that we emphasized our dendograms. These depict differences between populations that only rarely reach the level of statistical significance.

One of the factors responsible for such findings is (as Weaver points out) probably gene flow between subpopulations that have diverged from the same ancestral group. Chakraborty and Nei (1974) have shown that genetic differentiation in such groups becomes appreciable only when the migration rate between them is very small, on the order of 10^{-4} or 10^{-3} . A more important consideration is that, given the sensitivity of the variance of D to the number of loci included in the analysis and the limited data available, significant differences between genetic distances will not commonly be obtained. This is a powerful argument for the need to gather more data, a need on which all of us who participated in the Burg Wartenstein conference (to which Harper refers) agreed.

Murad's question concerning greater Eskimo affinity to North American Indians than to classic Mongoloids is answered above. The significance tests on individual distances reported in our paper are based on the observation that the tail of the inverse J-shaped distribution curve (Nei and Roychoudhury 1974) is approximately normal, provided that a large number of loci is used in the calculations. Reliability of the results increases with the number of loci employed. Murad's question has prompted us to reexamine the results reported. In the 48 tests between Mongoloid-Eskimo distances and Mongoloid-Indian distances, Northern Algonkians and Apache were significantly farther from Mongoloids than were all Eskimos. However, 2/48 significant results are well within the proportion (.05) of significant results that could be expected to occur by chance. We erroneously reported that none of the Chukchi-Eskimo versus Chukchi-Indian distances were significant. In fact, the Chukchi-Apache distance was significantly larger than the Chukchi-North Alaskan, -Central Arctic, -Eastern Arctic, and -East Greenland distances. Harper is correct: the Apache are not lost Chukchi wandering in the desert after all!

4. *Appropriateness of genetic markers and/or nonmetric traits for answering questions of population affinity.* As most of the theoretical foundation for the use of nonmetric skeletal traits rests on genetic research in laboratory animals, Hurlich quite properly expresses concern over the assumption that such traits are inherited in humans. The strongest support to date for this assumption is Lane's (1978) demonstration that variance in kinship, estimated for the Allegany Seneca in a pedigree including approximately 6,000 individuals and accurate to six generations, explains a significant proportion of the variance of nonmetric cranial traits in a cemetery sampling obtained from that population. Our own study, as Clabeaux observes, offers indirect support for the heritability of discrete cranial traits, simply because of the concordance of our two distance data sets, one of which is based on traits whose heritability is beyond dispute.

Hurlich, Korey, and Pfeiffer draw attention to the problem of age, sex, and environmental influence on discrete cranial traits. Pooled-sex data were used because it has been demon-

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strated that distance measures based on the particular trait battery employed in this study are not greatly distorted by a component due to sex (Ossenberg 1976). The rationale for inclusion of subadult data for certain features has also been discussed (Ossenberg 1969, 1976). No doubt there is some bias in the distance measures accruing from age and sex, but in our judgment the distance measures are not distorted as much as they would be by splitting small samples into male and female subsamples to be subjected, in turn, to further manipulations attempting to control for age regression.

In selecting this battery of 24 traits, features known or suspected to be influenced primarily by dietary, pathogenic, functional, or mechanical factors were excluded. For example, mandibular torus, recommended by Harper, was excluded because of its apparent plastic response to change in diet and habits (Mayhall 1970). Wormian bones, included in the battery, have been shown to be influenced by artificial cranial deformation, but, with the exception of the Kodiak skulls, which exhibit slight occipital flattening, all the other series used in this study are undeformed.

Certainly environmental factors influence cranial morphology. According to the theory of threshold variants (Falconer 1960), the manifestation of a discrete trait in the individual represents the outcome of interaction between environmental and genetic factors. In utilizing the features for historical-phylogenetic investigations, however, we assume that the genetic component of trait variability predominates. That we are justified in this assumption is suggested both by Lane's (1978) work and by our results, i.e., the concordance between relationships based on nonmetric traits and those expected on the basis of other criteria (Ossenberg 1976, 1977). In this study, while the dispersal of Na-Dene-speaking people in habitats as diverse as the desert Southwest (Navajo, Apache), north Pacific coast (Haida, Tlingit), and boreal forest (Ingalik) undoubtedly is reflected in their different patterns of trait frequencies, nevertheless the influence of environmental variability is apparently not strong enough to obscure the evidence of this particular trait battery for the historical affinity of these groups; i.e., the five Na-Dene samples cluster together.

Pfeiffer and Korey query our pooling of right and left observations of bilateral traits. Though this is a controversial problem, the current view is that scoring in sides is preferable to scoring in individuals but that a factor should be applied to correct for inflated sample size and redundancy of information due to bilateral symmetry (Sjøvold 1977, Green, Suchey, and Gokhale 1978). In our study, however, such a factor was not applied. We suspect that additional analyses are required for solution of this complex problem.

Harper would have liked us to include dental traits, Pfeiffer cranial measurements. These are undoubtedly useful, but their absence does not invalidate the evidence gleaned from nonmetric cranial traits. Our conviction in this regard is not mere opinion, but born of reasoned judgment. The traits we employed have been shown to discriminate between and within Eskimos and Indians, as judged by concordance of phenetic distances and language categories (Ossenberg 1976, 1977).

McGhee and Pfeiffer question the usefulness of genetic markers in assessing population affinities. The advantages of using genetic markers are as follows: (1) The mode of inheritance of the traits is simple and known, unlike that of metric characters. (2) Genetic markers are unaffected by the environment, while metric characters are notoriously malleable. For example, a secular trend is manifest in stature in North America and Europe in the past century; considerable shape distortion in the mandible has been shown to follow intentional muscular damage (Avis 1961); cranial deformation, intentional and otherwise (e.g., through swaddling or the use of cradleboards), is a well-known environmental effect. (3) Laboratory determini-

nation of phenotypes from blood and sera can be done by anyone following standardized procedures. In consequence, there is little risk of bias in employing genetic-marker data, while in the case of metric traits interobserver, and often intraobserver, error is considerable.

Genetic-distance measures have both theoretical and statistical foundations. D , for example, is based on the theory that divergence between populations is a slow process that depends largely on the accumulation of new mutations in two groups since their separation from a common ancestral population. It is for this reason that D can be viewed as the average proportion of codon differences between populations that have accumulated since initial divergence (Nei 1973, 1975). The Cavalli-Sforza and Edwards (1967) approach assumes that population divergence is caused principally by genetic drift and selective drift (i.e., selection operating differently in different places and times). In spite of varying theoretical positions, for closely related groups such as human populations these measures (and others) have been shown to be highly correlated. Evolutionary population genetics is a discipline in itself. McGhee and others who have the honesty to admit that their bias against the usefulness of genetic markers in answering questions of anthropological importance stems from outmoded information should be encouraged to overcome that bias through reasoned inquiry. We recommend some recent updates: Cavalli-Sforza and Bodmer (1971), Nei (1975), and Dobzhansky et al. (1978).

5. *Miscellanea.* We share Hall's reservation concerning the validity of considering Koreans or Japanese as "base Mongoloids." As we have pointed out, D is a measure of the proportion of codons that have accumulated between two groups since their initial divergence. The theory does not allow either group to be considered "ancestral" to the other, nor have we done so. It is unfortunate that Hall chooses to emphasize the contradictory positions attained by the Aleuts in our dendograms. We have discussed this disagreement at length. The genetic characteristics of the Commander Aleuts are the least reliable of all the groups we have considered because of the large number of Siberian genes that have entered their gene pool. Blood-group frequencies of North American Aleuts are unknown for seven of the eight systems we included (MN data are available, but not MNSs), though serum-protein information exists and was included in our analysis. Until better information is available for additional groups of both Siberians and Aleuts, it seems wiser to place more reliance on cranial traits in this case than on the genetic markers.

Cook, Salzano, and Weaver refer, from different perspectives, to the problem of admixture. Perhaps the best illustration in our genetic dendograms of clusterings probably caused by recent gene flow is the group of Asiatic Eskimos, Chukchi, and Aleuts. The Asiatic Eskimos are known to have a high degree of recent Chukchi admixture; the Aleuts have had gene flow from various Siberian groups. Weaver might consider the contrast this group provides to the geographically dispersed non-Siberian Eskimos, who are nevertheless a recognizable genetic unit with its closest affinity to a cluster of Na-Dene-speakers.

Salzano is incorrect in his assertion that our Northern Algonkian sample includes gene frequencies of a group whose ancestry is approximately 30% European. The Ojibwa data described in table 1 come not from Wikwemikong (Szathmary and Reed 1978), excluded here because it is not a Subarctic group, but from Pikangikum, a community with less than 3% European admixture.

No corrections were made for European admixture in our data for the following reasons: (1) A previous attempt at correction (Szathmary 1978) found that the mean amount of gene flow could not be calculated for some Indian and Eskimo populations because significant interlocus heterogeneity was observed in the admixture estimates, precluding calculation of the value by which correction was to be done. (2) Genetic characteristics

of Siberians are not well enough known to give information on alleles that could be considered to be of European origin. For example, C^w of the Rh system has been considered by some to be a "European marker" (e.g., Simpson, Eriksson, and Lehmann 1976), yet the world's highest frequencies of this allele have been reported from Siberia (Rychkov et al. 1969). For the sake of consistency, therefore, no correction of gene frequencies was done for any group.

Further justification is provided by the fact that Spuhler (1972) found that within-linguistic-group distances in North America were smaller than between-group distances. That is, the pattern of aboriginal biological relationships still reflects the pattern expected on cultural grounds. This suggests that non-Indian admixture has not distorted biological relationships in North America to any great degree. It is worth stating that Spuhler claimed his groups each had less than 5% non-Indian admixture. The facts are that his judgment of that depended on the presence or absence of low-frequency alleles (A^2 , B , K , Lu^a , or M^i , J^s , V , V^w , and Wr) that are infrequent in non-Indian populations themselves. A reexamination of his data indicates that 8 of his 20 Indian groups have more than 5% admixture.

We cannot exclude the possibility that European admixture affects the clustering of populations to some degree. The clustering of South Alaskan Eskimo and West Greenland Eskimo is probably an example, since both these groups have larger measured amounts of European admixture than other Eskimos and have been exposed to Europeans longer (Szathmary 1978). It is worth noting that this admixture appears to distort the dendrogram only in detail, not in overall topology; although admixed with Europeans, the South Alaskans and West Greenlanders still cluster with other Eskimos and not with Indians, some of whom presumably may also have had large amounts of European admixture.

Summary. We much appreciate the additional archaeological information provided by Dumond and Meiklejohn. We restricted ourselves to interior Alaska (excepting Anangula) because it seemed to us that that was where the "action" was in the period 8,000–10,000 years ago. It is equally possible, however, that this decision was, as McGhee observes, archaeologically naive.

We are very grateful to our commentators for their detailed and thoughtful responses. While positive comments are always gratifying, negative ones also have their place. We do not expect our work to be the last word on the subject and anticipate that additional information may well provide a different framework for interpreting Eskimo-Na-Dene history. Our results, however, obtain from analysis of currently available data, and these show a different configuration of Eskimo and Na-Dene-speaking populations than is commonly expected.

We began by quoting Hrdlička, who repeated his observations of Indian "Eskimoidness" and Eskimo "Indianness" in Alaska no less than seven times in his report (Hrdlička 1930:82, 134, 151, 156, 161, 250, 361). We think it appropriate to let him also have the last word (1930:361):

In general the farther west we proceed the less exceptional on the whole the Eskimo becomes and the more he approximates the Indian, particularly the Indian of Alaska and the northwest coast. As this cannot, in the light of present evidence, be attributed alone to mixture, it is plain that if it were possible to proceed a few steps farther in this direction the differences between the Eskimo and the Indian would fade out so that a distinction between the two would become difficult if not impossible.

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