

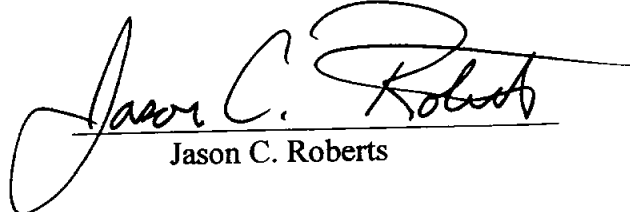
**IN THE UNITED STATES DISTRICT COURT  
FOR THE DISTRICT OF OREGON**

<b>ROBSON BONNICHSEN, et al.,</b>	)	
	)	
<b>Plaintiffs,</b>	)	
	)	
	)	
v.	)	
	)	
<b>UNITED STATES OF AMERICA, et al.,</b>	)	
	)	
<b>Defendants.</b>	)	

**Civil No. 96-1481-JE**

**CERTIFICATION**

The undersigned, as Park NAGPRA Consultant for the National Park Service, United States Department of Interior, under authority conferred upon me, hereby certifies that the documents annexed hereto constitute a full and accurate transcript of the entire record of proceedings for the Department of the Interior relating to this case.

  
Jason C. Roberts

Date: November 29, 2000

## WHO WERE THE FIRST AMERICANS?

Proceedings of the 58th Annual Biology Colloquium  
Oregon State University

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## **5. Peopling of the Americas: A Historical and Comparative Perspective**

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Analyses of early-Holocene human skeletal remains from North America have documented their closest morphological similarities to Asian, Australian, and more recent North American Indians. Within this morphological cluster, the early American remains differ from late-Holocene and recent North American Indians by more closely resembling southern Asian and Pacific Rim populations, while recent North American Indians more closely resemble recent north Asian samples. A historical review of related research examined in this paper documents that our conclusions, based upon the fossil record of the earliest Americans, are supported by more extensive dental and cranial comparisons of recent world populations with one another, as well as by the human fossil record from South America. We believe the modest morphological differences documented between early- and late-Holocene populations reflect ancestral/descendent relationships. The model we currently support is that the earliest Holocene Asian populations colonized the Americas prior to

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the establishment of the more distinctive morphological features of late-Holocene northern Asians. We do not feel that the current evidence supports proposing a specific population or area of origin within Asia as the founding population to first colonize the Americas.

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## Introduction

Human remains from the early Holocene of the Americas have rarely been recovered, and those remains recovered have generally been poorly preserved. Further, it has been difficult oftentimes to date the authentically early remains accurately and to identify those remains mistakenly considered ancient. Consequently, the early skeletal remains historically have not played a major role in our models for the peopling of the New World. However, with improved dating techniques and recent discoveries of additional early human remains, there has been renewed interest in the early biological evidence.

Recent craniometric examinations of the earliest well-dated North American remains have led us to conclude that the earliest known North American human remains: 1) are unequivocally of anatomically modern human descent; 2) bear their closest morphological similarities to Asian, Australian, and North American Indian populations; 3) differ from more recent North American Indians by resembling southern Asian and southern Pacific rim populations more closely than they do northern Asian populations; and 4) show a greater degree of regional variation than usually expected (Powell and Steele 1992; Steele 1989; Steele and Powell 1992, 1993, 1994, 1998). The distinctiveness of early-Holocene South American remains from more recent North and South American remains, and their greater similarity to southern Asian and southern Pacific rim populations has been noted as well (Neves and Pucciarelli 1989, 1991, 1998; Neves et al., 1993; Neves, Meyer, and Pucciarelli 1996; Neves, Munford, and Zanini 1996; Soto-Heim 1994).

This work, relying on the early-Holocene human skeletal remains to understand the population affinities of American Indians and the nature of the colonization of the Americas, has not been conducted in isolation, however. Other scholars utilizing dental and skeletal data to understand the affinities of human populations and the colonization of the Americas have based their assessments on detailed comparisons of late-Holocene or extant populations. Scholars following this research avenue include Howells (1969, 1973, 1989, 1995), Turner (1971, 1979, 1983a, 1983b, 1985a, 1985b, 1986a, 1986b, 1987, 1989), Turner and Byrd (1981), Brace and his colleagues (Brace and Hunt 1990; Brace and Nagai 1982; Brace and Tracer 1992; Brace et al. 1984; Brace et al. 1989; Li et al. 1991), and Lahr (1995). This review will document the relationship of these studies to the recent evaluations of early-Holocene North American human remains, and

indicate on which issues the various lines of evidence agree and on which they disagree.

## Foundation of the Model of the Colonization of the Americas

Our understanding of the ancestral/descendant relationships of the populations colonizing the Americas is based on two founding cornerstones. One of the cornerstones was laid in place principally by Aleš Hrdlička, the first physical anthropologist at the Smithsonian Institution. During the late nineteenth century and the early part of the twentieth century, many scholars believed that human antiquity in the New World was as great as it was in the Old World. Several human skeletal remains whose features were considered archaic, or were found in association with extinct fauna or ancient geological deposits, were proposed to support this belief. Most memorable of these were the Trenton, New Jersey, remains; the pelvis from Natchez, Mississippi; and the skull from Calaveras, California (Cotter 1991; Holmes 1899; Hrdlička 1907; Quimby 1956). Hrdlička, in extensive reviews of these remains, concluded that the proposed archaic features were misinterpreted and that in fact the remains were morphologically modern. He similarly dismissed their associations with ancient deposits and extinct fauna. Since he concluded that the remains were modern in appearance and of recent antiquity, he believed that the colonization of the Americas must have been a recent, post-Pleistocene event (Hrdlička 1902, 1907, 1918, 1923, 1937). It should be noted that the assessment of the modernity of the American prehistoric remains and their recent antiquity was measured by the standard of the archaic nature of the European Neanderthals of Pleistocene antiquity. Specifically, Europe had archaic-looking Neanderthal remains associated with an extinct fauna, while America had comparatively recent human remains and no extinct fauna (in his view). Therefore, as long as American fossil remains were associated with modern fauna only, they could only be anatomically modern in Hrdlička's view.

While Hrdlička's assessment of the relative modernity of human remains from the Americas compared with the archaic *Homo sapiens* of Europe has stood the tests of decades of later work, his view that the initial colonization of the Americas was a post-Pleistocene event has not. By 1927 the association of North American Indians and extinct fauna was established when a fluted projectile point was recovered from between the ribs of an extinct bison (Figgins 1927). Shortly thereafter, projectile points of prehistoric Indians were found in direct association with the remains of a mammoth (Figgins 1933). With these discoveries, the second foundation stone of our understanding of the colonization of the Americas had been laid. Humans had arrived in the Americas at least during the last moments of the Pleistocene, if not before.

Understanding the variation observed in the prehistoric American populations

and its possible significance for elucidating the colonization of the Americas has proven more controversial. A series of researchers (Dixon 1923; Hooton 1930; Hrdlička 1923, 1933; Neuman 1952, 1956; Stewart 1960, 1973, 1981) developed a model proposing that the first anatomically modern populations entering the New World differed from recent modern Asians by having relatively longer and narrower crania. After this founding population became established in the New World, they proposed, it was followed by a more recent northern Asian population whose descendants replaced the original colonizers in the more central and preferred regions of the New World. The descendants of these first colonizers were thought to have continued to exist as hunters and gatherers in more peripheral, isolated, and less productive regions.

With the discovery of late-Pleistocene human remains from the Upper Cave at Zhoukoudian, and Weidenreich's assessment (1938, 1939) that the old male cranium from these deposits "appears to represent not only a very primitive form of modern man, but at the same time also a type of primitive Mongolian," this specimen was incorporated into the model as the immediate forebear of America's first colonizers. Because of the Upper Cave male's cranial similarity to upper-Paleolithic remains of Europe, such as Cro-Magnon (Weidenreich 1938, 1939), some researchers felt this resemblance was evidence for the existence of an upper-Pleistocene Eurasian-wide population that had originated in the west and expanded eastward. Those supporting this hypothesis tended to label the population as proto-caucasoid. Weidenreich, however, had an alternative interpretation. He believed that the three individuals represented by crania from Upper Cave (skulls identified as 102 and 103 being female, and skull 101 being an old male), were all Asian in character. However, he felt each represented a different Asian population: the two female skulls representing northern and southern populations, and the male skull representing a population with a more generalized Asian conformation. It was the generalized features of the old male skull which suggested to Weidenreich that this skull could have represented the ancestral population to the other Asian populations; those supporting all or portions of Weidenreich's view tended to identify the generalized upper-Pleistocene population represented by the old male skull as protomongoloid.

However, this two-population model for the peopling of the New World was not universally accepted. Other scholars (Hooton 1930; Neumann 1952, 1956), assuming that the human variation seen in New World populations was a reflection of ancestors from which they descended, proposed that several Old World populations colonized the New World. To refute these polyracial models, Laughlin and Washburn in 1949 devoted a symposium to present evidence of evolutionary changes that occurred within American Indian populations (Laughlin 1951). Birdsell, in his contribution to this volume, reconstructed the upper-Pleistocene populations of Asia and supported the view that only two Old World populations, both residents of Asia, colonized the Americas. Birdsell proposed that the first colonizers were eastern members of a Eurasian-wide population, principally located in the mid-latitudes of Asia (Figure 1). This founding Eurasian popula-

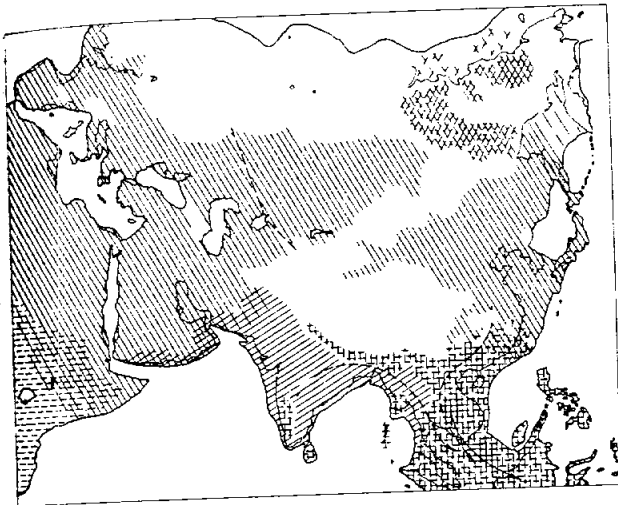


Figure 1. Joseph Birdsell's Eurasian-wide population (diagonal hatching) proposed to have occupied central Asia at the end of the Pleistocene. Blank areas represent Pleistocene glaciation. Birdsell proposed that the initial colonization of the Americas was from the eastern margin of this population; and a second, and later colonization of the Americas came from northern Asia (cross hatching). Figure modified from Birdsell (1951).

tion, identified by Birdsell as "Amurian," was characterized as possessing caucasoid features inherited from its European ancestors. The second colonization and later colonization of the Americas, he believed, was traceable to members of the northern Asian population.

## Research in the Last Half Century

In a large measure the Laughlin 1951 volume can be taken as a signpost signaling a conceptual and methodological change made by scholars of the second half century. While much of the work of the first half century was marred by racial and typological thinking, as effectively noted by Brace (1982) and Armelagos et al. (1982), most of the work conducted in the second half century is much more cognizant of the range of forces that create variation in human populations. Rather than presuming that virtually all differences seen between individuals and populations were a reflection of their Old World ancestry, biological anthropologists in the Americas began to recognize that a population's gene pool was influenced by gene flow from neighboring populations and by genetic drift, as well as by natural selection. Further, during the second half of the century scholars became much more aware of the influence of environments in shaping the individual phenotype.

As awareness grew of the difficulties encountered in unraveling the history of a gene pool, scholars sought ways to improve their comparisons of populations. Attempting to find traits more accurately reflecting an individual's genotype, researchers turned to observing discrete traits of the skeleton (Ossenberg 1969, 1974, 1976, 1977, 1986) and the dentition (Dahlberg 1951; Turner 1971, 1983a, 1983b, 1985a, 1987), and to observing blood types (e.g., Boyd 1950; Spuhler 1951). Those scholars conducting craniometric analyses avoided reliance on single measurements and

indices by turning to multivariate analyses, which permitted comparison of populations by many observations considered simultaneously, and permitted comparison based more upon shape than size.

Among the biologically oriented scholars of the second half-century, Turner (1971, 1983a, 1983b, 1985a, 1985b, 1986a, 1986b, 1987, 1989) was one of the first to compare large numbers of New and Old World populations, endeavoring to understand the biological nature of the colonizing populations. Turner chose to compare the populations on the basis of 28 discrete dental characters, believing these traits were under less selective pressure than craniometric features. He argued that the differences seen between populations based on these characters would more accurately reflect ancestral/descendant relationships, rather than adaptation by natural selection to local conditions. The expression of each trait, such as the shoveled shape of the lateral maxillary incisors, was recorded as present or absent, or was matched to a graded series of standards. The frequency of the character state of each trait was computed for the population, and the populations were compared by simultaneous consideration of the frequencies observed for each trait. The degree of similarity between any two populations was expressed as a number reflecting the sum of their shared similarities for the traits considered. All compared populations were then clustered in a dendrogram to display their relative similarities to one another (e.g., Figure 2).

On the basis of these analyses, Turner developed the following model to explain the origins of American Indian populations. Out of a founding population

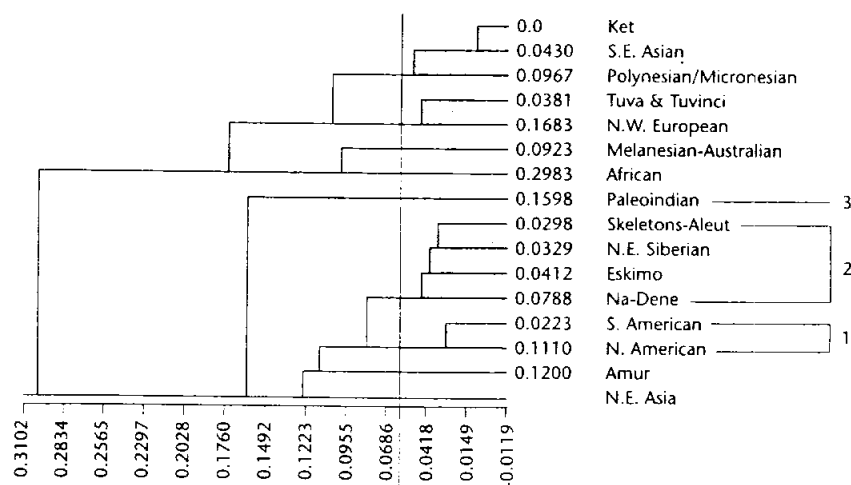


Figure 2. Christy Turner's (1985b: Figure 7) illustration of the relationships within and between Native American, Pacific, and Old World populations based on 28 dental trait mean measures of divergence clustered by unweighted pair group arithmetic averages method (Turner, 1985b:38). The figure has been modified by designating a line of differentiation at 0.0686 and emphasizing four clusters produced at 0.0686 level, and identifying three New World groups.



of early anatomically modern populations represented by skeletal remains from Tabon and Niah Cave, indigenous populations evolved on the Sunda shelf of southeast Asia. These populations, identified as Sundadonts, shared a generalized Asian dental pattern which was closely related to the ancestral dental pattern of the founding anatomically modern human population (Turner 1989:90). Turner estimated that the Sundadonts arose sometime between 30,000 and 17,000 years ago, basing this date on his assumption that they evolved after the colonization of Australia by more generalized anatomically modern humans. After their founding, some Sundadont populations migrated into northern Asia, evolving rather rapidly, he felt, into populations with a more specialized dental pattern selected for by the severe arctic conditions of northeastern Asia. These northern populations were identified as Sinodonts. The dental intensification seen in Sinodonts was created by traits which increased the mass of the tooth (1985b:33). The founding of the Sinodont populations in northern Asia, Turner felt, occurred about 20,000 years ago (1989:91).

The colonization of the Americas, Turner hypothesized, was then accomplished by three Sinodont populations, originating from three separate localities, each forging a different route across or along the Bering Land Bridge into the New World. More precisely, Turner has stated:

All three began in north China as a single expanding Sinodont population who in time dentally differentiated by drift and founder's effect into small bands of geographically isolated hunters and fisherfolk. Paleo-Indians exited Siberia by way of the Lena Basin, crossed Alaska in the interior of Beringia, and moved south as climatic changes caused formation of today's food-poor boreal forest. Ancestral Aleut-Eskimos exited Siberia by way of the Amur Basin, developed their coastal maritime culture on and near Hokkaido and Sakhalin, and entered Alaska along the southern coast of the Bering land bridge. The Diuktai people who lived between the Amur and Lena Basins crossed into Alaska just before the final flooding of the land bridge to become the dentally intermediate, forest-dwelling Na-Dene Indians of modern Alaska. (1986b:44).

Turner has further concluded that the distinctiveness of the three populations within the Americas can be traced directly back to their separate points of origin in northern Asia, and does not reflect evolutionary changes which occurred as adaptations to conditions in the Americas. For this reason, American populations are considered Sinodonts as well.

Specifically assessing the dental pattern observed in a Chilean sample which he and Junios Bird (1981) identified as Paleo-Indian, Turner concluded that early Chileans were more similar to North American Indians and northern Asians than Europeans. Describing the dental pattern of the Paleoindians in more detail, Turner (1985b:36) stated:

Paleo-Indian teeth exhibit Sinodonty as follows: marked frequencies of the 3-rooted lower first molar, shoveling, parastyle, 1-rooted upper first premolar and double-shoveling. Also conforming to later Sinodonty are the absence of 4-cusped lower second molars and the lack of examples of third molar reduction or congenital absence. If not due to small sample sizes, some degree of Sundadonty may be reflected in the frequency of the & groove pattern, 3-rooted upper second molar, enamel extension, Carabelli's trait and

incisor winging. But altogether, palaeo-Indian teeth are much more Sinodont than Sundadont and far removed from the Northwest European pattern.

Figure 2 is a dendrogram from Turner's paper (1985b: Figure 7) illustrating the structural relationships of Paleoindians, American Sinodonts, and Northeast Asian Sinodonts compared with other populations of the world. In examining the similarities reflected in this dendrogram, Turner has emphasized the similarity of his Paleoindians to the American and northern Asian Sinodonts. This relationship is reflected in the dendrogram by the Paleoindian sample linking to the Northeast Asia sample before all the Sinodonts link to the combined cluster of the rest of the world populations. Turner has specifically noted the dissimilarity of his Paleoindians to the Sundadonts, which in this dendrogram link to other world populations before they, in combination, link with the Sinodonts.

We would like to emphasize a different facet of the relationships of Turner's Paleoindians to the rest of the Sinodonts, depicted in the dendrogram. Of all the American samples examined, the Paleoindian sample differs the most, all the American Indian, Na-Dene, and Aleut-Eskimo samples in this dendrogram being more similar to one another than they are to the Paleoindians. This difference is reflected in the dendrogram by the way that all American and Aleut-Eskimo samples link to one another before they, combined, link with Turner's Paleoindians. The degree of resemblance is so modest between Turner's Paleoindians and other Native American and/or Sinodont populations that, based upon this figure, Turner's Paleoindians cluster with the other Sinodonts near the same level (between 0.1488 and 0.1760) as the southern Asian and Pacific Island groups cluster with the European populations. Although not addressing this point specifically, Turner (1985b:36) did allude to the distinctiveness of his Paleoindians in the quote above (Turner 1985b:36) when he indicated that if the sample of Paleoindians is not skewed by the small sample size, then it may reflect a degree of sundadonty presumably greater than that seen in other Sinodonts.

Powell (1993), testing the robustness of Turner's three-population (tripartite) model of the origin of native Americans, corroborated the distinctiveness of the Paleoindian dental pattern. Turner's analyses of similarity relied on mean measures of distance (MMD) and dendrograms generated by the unpaired group method using arithmetic averages (UPGMA). This method of establishing similarities between populations presumes that all dental traits have the same rate of evolution in all populations. Powell reasoned that if Turner's branching sequences were not an artifact of the method of analysis, but reflected phylogenetic relationships, then comparative analyses which do not assume a homogeneous rate of evolution should produce similar dendrograms. Powell based his analysis on a reduced set of 11 populations for which there were published data (Turner 1985b:67-74). Replicating Turner's UPGMA analysis on the reduced set produced nearly identical results with those of Turner (1985b:38). Again, Turner's Paleoindians were the most distinctive sample of the American Sinodonts; and Paleoindians proved as distinctive when the samples were compared in a Wagner distance tree and a maximum parsimony consensus tree. The Wagner distance tree reproduced here (Figure 3) reflects

the distinctiveness of the three major American clusters of native populations and also illustrates that the Paleoindian sample is the most distinctive of the American samples. While Powell's 1993 analysis does not correct for a possible sampling error in the Paleoindian sample, it is clear that the Paleoindian's distinctiveness is not an artifact of the comparative analyses used.

W. W. Howells (1969, 1973, 1989, 1995) conducted the first comprehensive multivariate analysis of a selection of worldwide populations based on craniometric

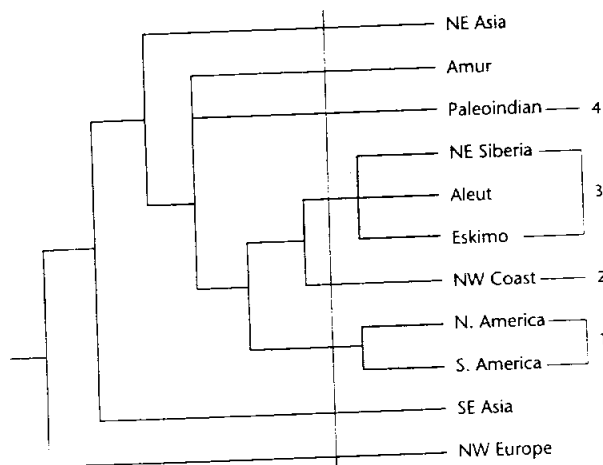
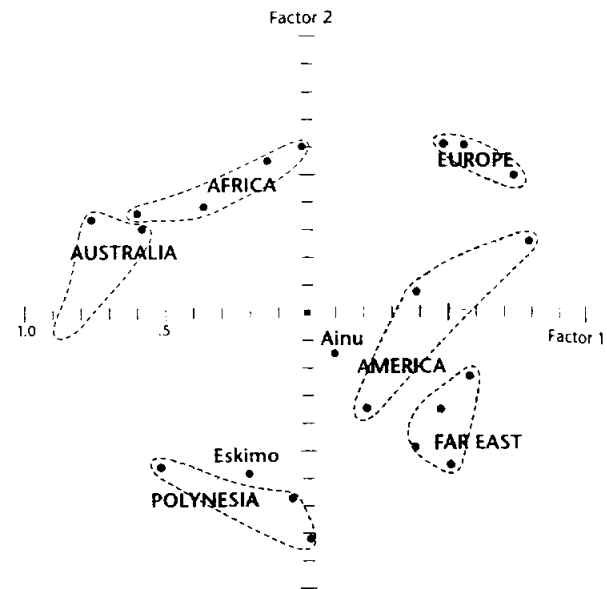


Figure 3. Joseph Powell's dendrogram (1993:811, Fig 2) based on Turner's data but using different analytical techniques. The figure has been modified to emphasize the distinctiveness of Turner's Paleoindian sample from all other Sino-dont samples. Note that at the marked level of comparison, four Native American groups can be recognized: 1) a North and South American sample, 2) a Northwest Coast sample, 3) an Eskimo-Aleut sample, and 4) Turner's Paleoindian sample.

data. Specifically, Howells compared 28 samples from different localities on the basis of 57 measurements of the cranial vault and facial skeleton (for descriptions of samples and measurements, see Howells 1969, 1973, 1989). The samples were all from populations of anatomically modern humans, and were implicitly considered to represent populations of the late Holocene. Several points were made by Howells's landmark analysis which are pertinent for interpreting the distinctiveness of early-Holocene remains from the Americas. Figure 4, which depicts one of Howells's two-dimensional Q-mode analysis plots of the 28 male samples, illustrates that populations from the same geographical region generally cluster together, a reflection of their craniometric similarities. Of the clusters of geographical samples, the American Indian cluster is the most dispersed, indicating the extent of craniometric heterogeneity between American populations. The American cluster, along with the broadly overlapping Far East cluster, also forms the central portion of a morphological gradient that extends from the Europeans at one extreme to the Polynesians at the other. Within this gradient, two of the American Indian samples are closest in proximity to the Far East cluster, while the third American sample is structurally more similar to Europeans. In this respect, special note should also be made of the close approximation of the Ainu sample to the American cluster, a

Figure 4. W. W. Howell's Figure 5b (1989: 48) plot of factors 1 and 2 of a Q-mode analysis of 18 male groups representing the major geographical regions of the world. Unlabeled groups from a common geographical area are encircled; labeled groups were added by back-scoring. Figure has been modified to emphasize Asian and European geographical clusters, and by deletion of back-scored groups not relevant to present analysis.



similarity that is reflected in analyses conducted by other researchers as well (e.g. Brace and Hunt 1990; Brace and Tracer 1992).

C. L. Brace and colleagues (Brace and Hunt 1990; Brace and Tracer 1992; Brace et al. 1989; Li et al. 1991) have undertaken the most detailed series of craniometric analyses designed specifically to illuminate the origins and dispersal of population of the Pacific rim. Initially 18 measurements concentrated around nasal and mid facial regions were used because these regions most effectively discriminated sample from the islands of Japan, the initial area of research interest (Brace et al. 1989). Later, the battery of measurements was expanded to 21 measurements and six indices when it was realized that the more variables that were considered, the more accurate the analyses reflected phylogenetic relationships (Brace and Tracer 1992). Ultimately, samples from 28 localities were analyzed. For the analysis, measurements and indices were converted into sex-specific Z-scores, and these in turn were converted to mean C-scores. Then a mid value between the male and female C-scores was used to generate Euclidean coefficients of dissimilarity. Dendrogram were constructed using a mean unweighted pair grouping method (more detailed descriptions of samples, measurements, and methods are provided in Brace et al. 1989 and Brace and Hunt 1990).

Figure 5 illustrates one of their earlier dendrograms (Li et al. 1991). Based on 2-measurements which emphasized differences in nasal shape, the dendrogram indicates strong similarities of American Indians with European samples, and strong similarities between African and Australo-Melanesian populations. In retrospect the authors felt that the nasal region was probably under strong selective pressures, the northern populations of eastern and western Eurasia being subjected to selec-

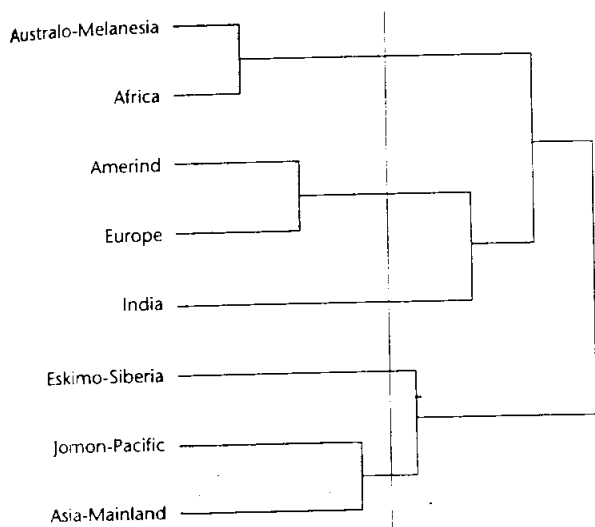


Figure 5. Dendrogram of Lit et al. (1991:273 Fig 1) depicting the relationships of samples from the major geographical regions of the world. Dendrogram is based upon 24 craniofacial measurements converted into C scores and analyzed with a Euclidean Distance program. Figure modified here by defining a line of comparison, and emphasizing the clusters recognized at that level.

tion for elongated and elevated noses, while the tropical populations were being subjected to selection for broad nasal apertures with low bridges. Consequently, the close associations of these geographically disparate populations could reflect parallel evolution rather than ancestral/descendant relationships. Figure 6 illustrates a more recent dendrogram presented in Brace and Tracer (1993:459), which is based on the more complete battery of measurements which includes measurements of the braincase. Here the diagram reflects the strong similarities of the Jomon-Pacific combined sample (includes Ainu, Burma, Guam, Hawaii, Maori, Marquesas Islanders, and Micronesians) to American Indians (divided into a north to east group and a west to south group). Other Native American relationships to note in the dendrogram are the close ties of the Athabascan sample to Northeast Asians and

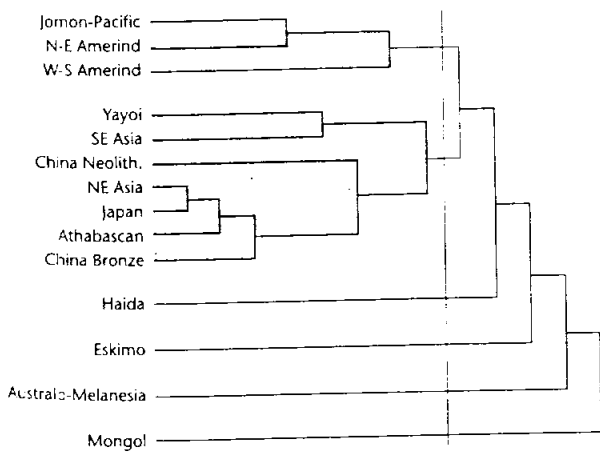


Figure 6. Brace and Tracer's dendrogram showing the relationships of samples from Asia, Oceania, and the Americas (1992:459 Fig 26.7), with the following number of samples: Jomon Pacific, 7; N. E. Amerind, 6; W-S Amerind, 4; Australo-Melanesian, 10. The figure has been modified by identifying a line of comparison, and emphasizing the two clusters recognized at this level.

Japan, and the disparity of Haida and Eskimo samples. The outlying position of the Mongol sample is also noteworthy.

Brace and his colleagues (particularly Brace and Hunt 1990, and Brace and Tracer 1992) have proposed the following model of the origins and dispersions of the populations of the Pacific rim. During the late Pleistocene, a population spread from the Andaman Islands through Borneo, the Philippines, and the Melanesian islands including New Guinea and Australia. A second population, best represented by the late-Pleistocene/early-Holocene Jomon of Japan in these analyses, colonized the Micronesian and Polynesian islands in relatively recent times. The ties of the Jomon population to the eastern rim of Asia are reflected in the craniofacial similarities of the Jomon to the late-Pleistocene specimens from central mainland China (Zhoukoudian and Liujiang) and Okinawa (Minatogawa). Living descendants of the Jomon are the Ainu of the northern islands of Japan. A third Asian population evolved in the northeast, possibly associated with the rise of agriculture (Brace and Tracer 1992:463), and probably derived genetically from more central and southern Asians as represented by the Jomon in their samples.

Considering the colonization of the Americas, Brace and Tracer (1992) concluded that the close structural similarities of most American Indian populations to the Jomon-Pacific sample reflected their ancestral/descendant relationships with them as well, rather than with the Northeast Asians. Of the two major clusters of American Indians recognized by Brace and Tracer, the closer similarity of the North-East American Indians to the late-Pleistocene/early-Holocene Jomon sample suggested to Brace and Tracer that these populations represented the earlier entrants into the New World. Considering the outlying Athabascan sample in the dendrogram, the authors felt that their closer structural similarities to Northeast Asian populations indicated they were descendants of later colonizers, with greater genetic ties to the Northeast Asians. The distinctiveness of the Haida and the Eskimo were also noted, but specific Asian antecedents were not inferred.

Marta Lahr (1995) provided another analysis addressing human biological issues of the peopling of the Americas. Her examination of samples from Tierra del Fuego and Patagonia revealed that these samples from southernmost South America were some of the most robust of anatomically modern humans, and compared most closely in terms of robustness with Australian and Eskimo samples. These similarities shared by the three samples, Lahr concluded, reflected adaptations to biomechanical stresses. When the Tierra del Fuegian and Patagonian samples were compared craniometrically with other world samples they compared most closely with the Asian and American Indian samples in general. Considering just the Asian samples, they resembled the southern Asians more than the northern Asians. Comparing the Tierra del Fuegians and Patagonians with other world populations, Lahr stated the following.

The results . . . clearly show that the Fuegian-Patagonian population appears within a larger Mongoloid cluster as Pacific rim, close to Polynesian crania. They do not appear close to other South American populations or current Northeast Asians. These results support the hypothesis that these crania present a generalized Mongoloid morphology which differentiates them from other recent Amerindian remains. (Lahr 1995:1822)

Reminiscent of Brace and his colleagues, Lahr envisioned that a morphologically generalized Asian population, rather than a more morphologically derived and specialized population like those presently in Northeast Asia, was the founding population for the first colonizers of the Americas.

## **Recent Research on the Early-Holocene Remains from the Americas**

A common methodological thread in the research just reviewed is that when American Indian populations were evaluated, they were treated as populations representative of a single point in time, a methodological construct similar to the concept of the "ethnographic present." American Indian populations were compared with other world populations, also considered as representing a single point in time. This methodological construct was, in essence, forced upon the scholars because they chose to examine only those crania which were complete enough to permit a large battery of measurements to be made. Samples which contained crania complete enough for such an analysis were typically from the most recent portion of the Holocene, because time had not yet worked its destructive ways upon the remains.

The exception to this methodological pattern of analysis was when comparisons were made with Asian upper-Pleistocene or early-Holocene samples such as Niah Cave, Tabon, Minatogawa, Upper Cave remains from Zhoukoudian, and the Jomon samples. These earlier samples were added to the comparison as models of the Asian populations from which the first American colonizers were derived.

While identification of features shared by descendant Asian and American Indian populations can provide some information about the ancestors of the American Indians, and an examination of the late-Pleistocene/early-Holocene Asian samples can provide further evidence about the populations whence American Indians came, an examination of the earliest available remains from the Americas provides the third line of evidence, and a most important line of evidence, for understanding the biological ancestry of American populations.

The high cost for the immediacy of this line of evidence, however, is that the skeletal remains are far fewer in number and typically far less complete. When we began (Powell 1993; Powell and Steele 1992; Steele 1989; Steele and Powell 1992, 1993, 1994; Young 1987) looking at the early-Holocene skeletal remains from North America we felt that fewer than 25 individuals could be considered as much as 8500 years old or somewhat older. Of these, only four (two females and two males) had complete enough crania to permit comparisons of more than one or two traits (Steele and Powell 1992:307; 1993:140; 1994:142-145). Because of the limited nature of our line of evidence, we were cautious in the conclusions we drew and the inferences we made.

At the most general level of assessment, we affirmed that the remains from the early Holocene which we examined were all the immediate descendants of ana-

tomically modern humans and exhibited no features reminiscent of earlier archaic *Homo sapiens*. Cranial features that traditionally have been considered diagnostic of archaic *Homo sapiens* and that we did not find in our early-Holocene samples are: 1) massive and protruding brow ridges, particularly in their lateral aspect; 2) low rising frontal and marked postorbital constriction, suggesting minimal development of the frontal lobe of the brain; 3) thick cranial elements, a prominent and protruding occipital, and small mastoids; and 4) a massive face reminiscent of the European Neanderthal. When we did find evidence of a robust feature, such as noted for the brow ridges for the Horn Shelter male, it was apparent that the feature was within the range of anatomically modern humans, and the robust character was incorporated into the craniofacial pattern of an anatomically modern human (see Steele and Powell 1992:309). While in most respects such validation of the anatomical modern nature of North American early-Holocene samples we examined seems self-evident, it is worth reiterating now that 1) there is a probability of the presence of humans in northern Asia possibly as early as 200,000 years ago (Waters, et al, 1997); 2) there are sites predating Clovis in South America (Dillehay 1986, 1989, 1997; Dillehay and Meltzer 1991; Dillehay et al. 1992; Meltzer et al. 1997); 3) there is the occasional paper interpreting robust features seen in anatomically modern human crania as features indicative of Archaic *Homo sapiens* (e.g., Givens 1968a, 1968b); and 4) there is a misinterpretation of what we reported in our 1992 paper (Lahr 1995:170).

We also examined the early-Holocene Paleoindian sample in 1992 to verify the presence of the relatively narrower shape of the braincase that had been attributed to early American Indian samples by scholars of previous decades. We found the Paleoindians, both male and female samples, did not differ significantly from the majority of the samples with which they were compared. For example, of the 36 male samples compared with the Paleoindian sample, 13 differed in cranial length and five differed in width (Steele and Powell 1992: Tables 3 and 4). Of the 33 female comparisons we made, five differed significantly in length and four in width. Similar results were seen in facial dimensions (Steele and Powell 1992: Tables 3 and 4). Surprisingly, most of the significant differences were between the early-Holocene Paleoindian sample and late-Holocene North American Indian populations, rather than with other geographical regions (Steele and Powell 1992:313). Bivariate plots of the cranial lengths and widths, and the facial lengths and widths, further documented the general similarities of the male and female early-Holocene Paleoindian samples to more recent samples. These bivariate plots also documented that when the Paleoindian samples differed, they differed by having relatively narrower and longer braincases and relatively narrower and shorter faces. The North American samples of Archaic later times tended to also exhibit similar relationships to the more recent American Indian samples.

To gain a more comprehensive understanding of the craniofacial features of the early-Holocene Paleoindians, and also get a better understanding of the ancestral/descendent relationships of these Paleoindians to more recent American populations, we compared our samples using multivariate analytical techniques; specifi-



cally, Principal Components and Discriminant Function Analyses. The Principal Components method of analysis was chosen because no a priori assignment of any of the samples was made. In the Discriminant Function analysis, however, individual samples with which the Paleoindian, Upper Cave, Minatogawa, and Jomon samples were compared were assigned to the major geographical regions. The four fossil samples were not assigned to a geographical region. Consequently, the Discriminant Function analysis reflects the relationships of the fossil samples to geographical groups more so than the individual samples within each geographical group. Male and female samples were analyzed independently of one another as a simple test of comparability. The Paleoindian samples were compared with 33 recent samples which had originally been analyzed by Howells (1973, 1989, 1995), later prehistoric North American samples, and three Eurasian late-Pleistocene and early-Holocene fossil samples: the Jomon sample from Japan, the Minatogawa specimens from Okinawa, and the Upper Cave male from mainland China. The North American Paleoindian male sample consisted of the Brown's Valley and Sauk Valley, Minnesota, specimens, and the female sample consisted of the Pelican Rapids, Minnesota, specimen and the Gordon Creek, Colorado, specimen. During the time of analysis (1992-1994) these were considered the oldest and most complete specimens available. Eight measurements (cranial length and width, facial height and breadth, nasal height and breadth, and orbit height and breadth) were used in the multivariate analyses, the limited number being dictated by the incomplete condition of the crania.

Figure 7 illustrates the Principal Components analysis based on size-corrected data for male and female samples. The male samples fall to the periphery of the North American sample distribution, between the North American and Australian/southern Pacific rim samples, and away from the northern Asian samples. The female samples exhibit a similar distribution, with the Paleoindian sample falling between the North American and Australian/southern Pacific rim samples, and away from the northern Asian samples. These samples show similar relationships to one another in the Canonical Analysis as well (see Steele and Powell 1994: Figures 8-9).

Because of the small number of individuals representing the Paleoamerican samples used, in our initial analysis in 1992 and 1994 we were justifiably cautious in our interpretation of these results. In our 1992 paper, for instance, we proposed that the population from which our sample was drawn was not classically northern Asian and North American in facial appearance. Rather, they differed by having narrower braincases and narrower and shorter faces, features which were similar to samples from Australia and the southern Pacific rim. We further stated that we were avoiding referring to the Paleoindians as protocaucasoid or protomongoloid because we felt those terms too value-laden. Finally, we raised the issue of the cause of these distinctive features of the Paleoindians, querying whether they reflected differences in the gene pool between the earlier and more recent North American samples; or whether this comparison reflected some adaptational difference, an adaptation accomplished either by natural selection or by the plasticity of human growth and development (Steele and Powell 1992:329). Similarly cautious inter-

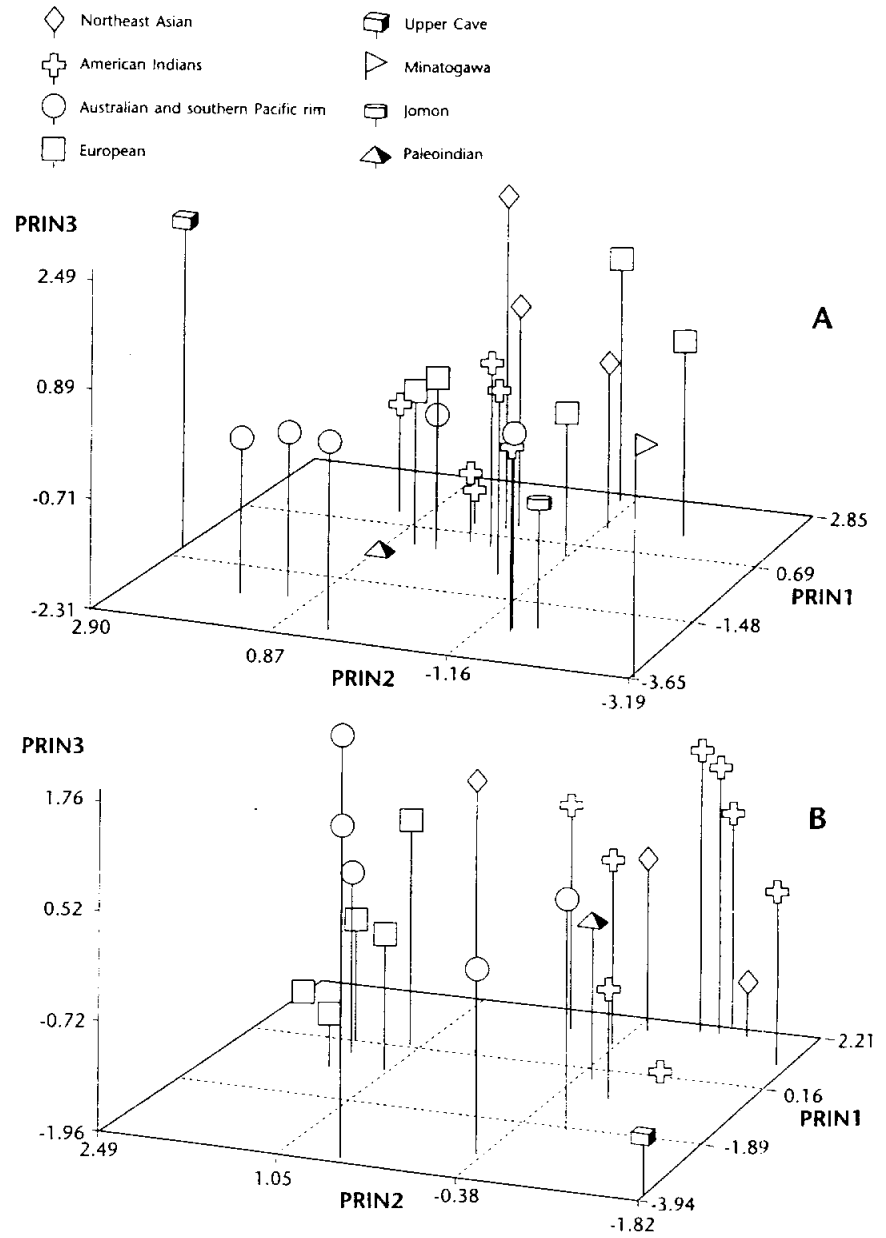


Figure 7. Steele and Powell's depiction (1994:154, Figs 6 & 7) of a Principal Component Analysis of size-corrected data of male samples (A) and female samples (B) from Europe, Asia, Australia, and four fossil samples (Upper Cave, China, Menatogawa, Jomon, and the Paleoamerican samples. Analysis based on size-corrected PC data.

pretations of the causes for these differences were stated in subsequent papers (Steele and Powell 1993:141; 1994:158).

Walter Neves and colleagues (Neves and Pucciarelli 1989, 1991; Neves, Meyer, and Pucciarelli 1996; Neves, Munford, and Zanini 1996; Neves et al. 1997, 1998), conducting multivariate analyses of the oldest well-documented crania from South America, also have documented the distinctiveness of these early-Holocene American samples from late-Holocene and recent American samples, thus independently corroborating our North American evidence. Further, their work has documented the similarity of the early South American samples to Australian and southern Pacific Island populations. These scholars inferred from these metrical relationships that the first Americans, Australians, and peoples of the southern Pacific rim shared a common ancestor in central Asia, and that these early American remains may represent a fourth migration, earlier than was proposed by Greenberg et al. (1986) in their well-known three-migration model of the peopling of the Americas.

Most recently, confirmation of the distinctive cranial features of the early-Holocene samples from North America has been provided by two male skeletons (Spirit Cave and Wizards Beach), recovered in Nevada and recently dated as approximately 9,200 years old. (Kirner et al. 1998). Spirit Cave is a mummy with a virtually complete cranium. The Wizards Beach cranium is also very well preserved, so that these two specimens could be compared with the reference samples on the basis of more measurements than available for the Minnesota crania in our previous studies. As before, we used a Principal Components analysis to evaluate the structural similarity of the early-Holocene specimens to 25 samples from Eurasia, Australia, the Pacific Islands, and the Americas. For one analysis (Figure 8) we chose to pool the two Nevada specimens as if they were from one population, and treat the original American sample as a separate Paleoindian sample. In this analysis the comparison was limited to the eight measurements that were available for the Minnesota specimens. In the second study (Figure 9) the Minnesota males were not included in the analysis, and the Nevada males were treated as if they represented separate populations. This approach permitted the analysis to be based on more measurements or different measurements. Tables 1 and 2 identify the measurements used in the analysis (column 1) and their eigenvector scores for each component (Columns 2-4). The eigenvalues and cumulative values for the Principal Components are provided in the last two rows of each table.

Figure 8, based upon the first three Principal Components, reflects 56.2 percent of the variance observed in the analyses. No other combination of three components reflected as high a commutative value. In this diagram the two Paleoindian samples are peripheral to the more recent North American Indians and northern Asians and lie closer than they do to the southern Asians, Pacific Islanders, and Australians (particularly along Principal Component 1). This follows the same distribution pattern as documented in our earlier studies. For the first Principal Component, those samples with positive scores tend to have relatively broader and longer faces, while those with negative scores tend to have longer braincases and narrower facial dimensions. For Principal Component 2, longer crania and more projecting

**Table 1.** Principal Components Analysis of the Minnesota and Nevada male Paleoamerican samples. Eigenvectors and Eigenvalues for the first three Principal Components using Q-mode corrected data for shape only are provided.

measurement	P. C. 1	P. C. 2	P. C. 3
QGOL glabello-occipital length	-.183951	0.375858	-.097444
QXCB maximum cranial breadth	0.216027	-.190767	0.309282
QBNL basion-nasion length	-.133323	0.421688	-.359120
QNPH nasion-prosthion height	0.450606	0.066901	-.162544
QBPL basion-prosthion length	-.350624	0.301039	-.241825
QOBH orbital height	0.362459	0.176817	0.087903
QOBB orbital breadth	-0.66676	0.416150	0.421604
QEKB biorbital breadth	-.283160	0.078928	0.493355
QDKB interorbital breadth	-.233467	-.471596	-.068906
QNLH nasal height	0.466592	0.040721	-.192192
QNLB nasal breadth	-.279451	-.300364	-.130073
QMAB external palate breadth	-.047129	-.098972	0.137019
QZYB bizygomatic breadth	0.084882	0.121112	0.418005
Eigenvalue	3.13446	2.21130	1.95314
% variance	24.11	41.18	56.20

**Table 2.** Principal Components Analysis of the Nevada male Paleoamerican samples analyzed separately. Eigenvectors and Eigenvalues for the first three Principal Components using Q-mode corrected data for shape only are provided.

measurement	P. C. 1	P. C. 2	P. C. 3
QGOL glabello-occipital length	0.121449	-.044504	0.412334
QXCB maximum cranial breadth	-.171481	0.209020	-.280261
QBNL basion-nasion length	0.024946	-.217277	0.518225
QFMB bifrontal breadth	0.382085	0.346762	-.073116
QNPH nasion-prosthion height	-.433894	0.041970	0.057213
QBPL basion-prosthion length	0.248533	-.237258	0.404557
QOBH orbital height	-.311780	0.252377	0.093870
QOBB orbital breadth	0.144989	0.478813	0.277066
QEKB biorbital breadth	0.379898	0.375936	-.057523
QDKB interorbital breadth	0.210505	-.266354	-.411433
QNLH nasal height	-.436906	0.010195	0.041262
QNLB nasal breadth	0.202454	-.322756	-.199771
Eigenvalue	3.46082	2.27928	2.22412
% variance	24.72	41.00	56.89

faces were positive numbers, while broader faces were negative numbers. Although the dispersion is less along Principal Component 2, the Australian, Paleoindian, American Indian, and northern Asian samples again create a general gradient with the Australian being at one extreme, the northern Asians at the other, and the Paleoindians in a more central position, aligning more closely with the southern Asians and Australians than do the recent American Indians and northern Asians.

Figure 9 illustrates the distribution of the samples when they are compared on

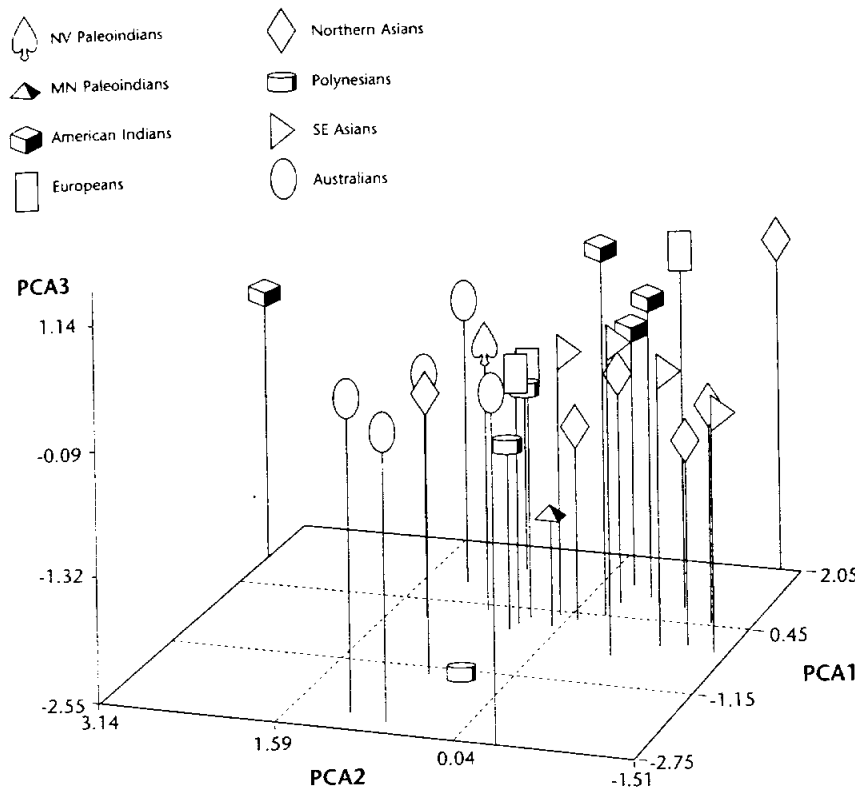


Figure 8. Principal Component Analysis of two Paleoamerican male samples (Spirit Cave and Wizard's Beach sample, and pooled Paleoamerican sample excluding the Nevada remains) with male samples representing more recent human populations from Australia, Eurasia, the Pacific Islands, and the Americas. Distribution is based on first three components. Data was size-corrected. List of comparative samples is provided in Steele and Powell (1994:144, Table 2).

the basis of 14 measurements, and the Nevada Paleoindian samples are considered as representing separate populations. Most noticeable in this analysis is the more peripheral position of the Nevada specimens to virtually all of the other samples. In effect, it suggests that they were distinct from more recent populations, and that no recent population resembled them. Powell (1995), based on his odontometric research, has noted this phenomenon in mid-Holocene populations.

It is also noteworthy that the two Nevada specimens are quite separated from one another, suggesting either that there was a large degree of difference between populations at that time, or that there was a high degree of heterogeneity within a single population. Though they are distinctive from recent American Indian samples, it is also clear that the recent samples most closely resembling these two specimens are Polynesians and Australians, both populations distinguished by their relatively

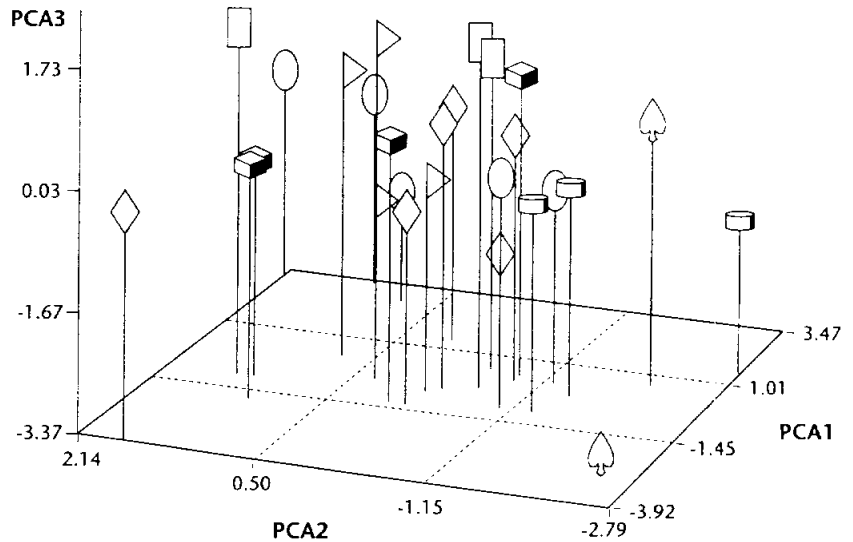
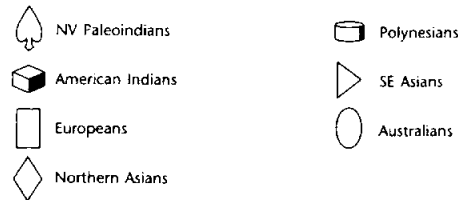


Figure 9. Principal Component Analysis of the two Nevada Paleoamerican specimens considered separately. Distribution is based on first three components, and the data were size-corrected.

narrow faces, longer crania, and more projecting faces. Jantz and Owsley (1997), reporting the most complete analysis to date on the Spirit Cave mummy of Nevada, concluded:

Our analysis of the Spirit Cave Mummy agrees with features attributed to early Americans in a number of respects, including long narrow cranium, low face combined with high orbits, and narrow orbits. The Spirit Cave Mummy bears a number of similarities to European populations, as Steele and Powell (1992) observed in their sample. The South Asian similarity observed by Steele and Powell (1992) is weaker in the Spirit Cave individual, although the similarity to Ainu, which shares morphometric features with Polynesia (Brace and Hunt 1990), might be viewed in this way. (Jantz and Owsley 1997:82).

## Discussion

In this review of the skeletal and dental evidence for the peopling of the Americas, we have emphasized that there is a large body of evidence, accumulated by a large

number of scholars over time, that has supported the view that the earliest populations colonizing the Americas, while members of anatomically modern *Homo sapiens*, differed from more recent American Indian populations. This concept of the distinctiveness of early populations from more recent American populations also has a long history, being expressed in the professional literature as early as the 1920s (e.g., Dixon 1923). However, by mid-century the view that early populations in the Americas could be distinguished from recent American and northern Asian populations began to be seriously challenged.

The challenge came along several conceptual fronts. One line of evidence arguing against the existence of a distinctive early American population or populations in the New World was the high degree of homogeneity inferred for recent Native Americans. The evidence for Native American homogeneity was based principally upon examination of soft tissue features such as hair morphology and color, eye and skin color, and blood type characteristic in living populations (Boyd 1950; Stewart 1960, 1973). The perceived high degree of homogeneity, as well as the view that the peopling of the Americas was a very recent event, argued against the possibility of the early colonizers differing from recent northern Asian and American populations.

A correlated argument against the possibility of documenting early American population differences was based upon the concept that the amount of variation present within each local American population was nearly equal to the sum of the variation seen in all groups. If populations were recently differentiated from one another, and they shared similar gene pools because they had not been in the New World long enough for natural selection to have molded populations to local conditions, or for gene flow or genetic drift to have structured the populations, then it follows that within-group and between-group variations approximate one another. If within-group and between-group variations are close, then very specific traits or very modest metrical differences separating the populations would have to exist; and the early samples used to evaluate the possibility of the distinctiveness of early American populations would have to be large enough to find such rare traits or such modest mean dimensional differences.

At the same time, questions were also being raised about the biological mechanisms that were creating the shape, size, and character of the human body. Biological species were found to possess far more structural variability within a population than previously recognized; and the plasticity of the human body to adapt, during the maturation of the individual, to a wide range of environmental constraints was becoming better understood. Adaptation of the individual to local environmental conditions in particular raised issues concerning comparisons of two populations on the basis of size and shape of the skeleton. Did any metrical differences detected reflect developmental adaptation; or did they represent changes brought about through natural selection; or did they accurately reflect the genome of their ancestor?

In spite of the seeming immensity of the difficulties facing scholars interested in understanding how humanity colonized the continents of the world, there has

been a steadily increasing understanding of the roles the genome and the environment play in developing the individual and the population. Additionally, the employment of computer analyses, allowing scholars to compare large samples with one another more effectively on the bases of many traits, to reduce the influence of differences in size, and to emphasize shape in the comparisons, has facilitated studies of the colonization of the Americas. As critical as the refinement of the techniques of analysis has been to improving our understanding, equally important has been the recognition that multivariate analyses of the cranium and the dentition can be as accurate in reflecting genomic relationships as the analysis of blood and serum proteins. Work by the geneticists Spielman and Smouse (1976) has documented this accuracy on the basis of data on living populations of the Yanomama. Howells (1973, 1989, 1995) has documented the strong similarities in cranial shape of human populations occupying common geographical regions and presumably sharing a high number of genes. And Lahr (1995) has documented that in spite of similarly strong natural selective pressures the Fuegians of the southern tip of South America and the Eskimo of the northern tip of North America faced, the two populations have each maintained their unique underlying craniofacial features.

With renewed interest in the origins and the biological nature of the people who colonized the last major land masses of the earth, recent researchers have followed two independent lines of evidence. One approach has emphasized the craniometric comparison of relatively recent samples, geologically speaking; and the most recent and comprehensive of the comparisons have been of samples representing peoples of the Pacific rim. Basically, these studies (e.g., Brace and Hunt 1990; Brace and Tracer 1992; Li et al. 1991) have concluded that the earliest colonists in the Americas probably lacked the craniofacial features common in northern Asian populations today. The model that has been proposed most frequently is that many of the features were similar to those seen in some European populations and in populations from southern Asia. After the founding of these earliest populations in the Americas, presumably from a central or southern Asian founding population, subsequent colonizers have been genetically tied to more recent northern Asians. Consequently, the recent Native Americans look more like northern Asians of today than their earlier ancestors did.

This model has been based primarily on the assumption that the craniofacial similarities recognized reflect the genome. While it has been recognized that natural selection acting on different populations may create features which are similar because of a common adaptation rather than a recently shared ancestor (Li et al. 1991:274), the general assumption has been that if samples resemble one another, these resemblances reflect to some degree their ancestral/descendent relationships (Brace and Hunt 1990:345; Li et al. 1991).

Using the same basic model of analysis, a comparison of well-represented samples, which are generally by default geologically recent samples as well, and assuming that similarity between samples reflects relative recency of descent, Christy Turner (e.g., 1983a, 1985b, 1987) reached a different conclusion based



upon the examination of dental attributes. He concluded that American Indians look dentally like recent northern Asian populations, and that the closeness of the similarity warrants classifying them within a common group identified as the Sinodonts. He further concluded that the northern Asian Sinodonts crossed into the Americas so recently that there has not been enough time for them to differentiate significantly from one another. The main differences seen between American samples, he presumes, are a reflection of their coming from different founding populations in northern Asia. Noting that the dental evidence differed from the cranial evidence, Turner argued that the dentition was more conservative in reflecting natural selective pressures and the effects of developmental adaptation; consequently, the dentition more accurately reflected ancestral/descendent relationships than did craniofacial dimensions.

Our work and the work of scholars in South America (e.g., Neves and Pucciarelli 1989, 1991) have taken the second basic approach in studying the colonization of the Americas, that of examining the oldest available human remains from the Americas. This approach adds a temporal dimension to the analysis. The oldest known remains, even though based on meager samples, have consistently differed from more recent American and northern Asian skeletal samples. The North American male and female samples examined separately by us (Steele and Powell 1992, 1994) both appeared different from later American and northern Asian populations, and both differed from them by resembling southern Pacific rim populations more closely. Neves and colleagues (Neves and Pucciarelli 1989, 1991) reached similar results based on South American remains. Recently dated early-Holocene remains of two Nevada males provided yet another opportunity to verify these conclusions independently, and generally they did. Most recently, work by Neves et al. (1998) on the Lapa Vermelha IV individual from the Lagoa Santa region of central Brazil, dated to 11,000 to 12,000 years ago, has substantiated these findings as well. With this substantiation of our original observations made on such limited remains, we now feel confident that some, if not all, early-Holocene samples will be distinctive from later-Holocene populations.

This conclusion still leaves the hardest issue to address. Do these differences reflect ancestral/descendent relationships with specific Old World populations; or do they reflect adaptational differences, brought about by common natural selective mechanisms, or by some specific developmental adaptation which we do not as yet recognize or understand? Certainly, craniometric research has shown that structural similarities can reflect the genome as well as adaptation to a common natural selection force. However, the spatial distance, and the disparity of the environments from which were drawn the American samples documenting the distinctiveness of the early-Holocene populations from more recent American populations, suggest that natural selection acting on the American populations once they arrived is not the cause of the differences. Lahr's careful analysis (Lahr 1995) comparing Fuegian and Eskimo samples clearly documents that while some cranial features were brought about through similar natural selective pressures, there is an underlying cranial form that clearly distinguishes the two samples and reflects their ances-

try rather than the effects of adaptation to common natural selective pressures. Similarly, to envision that phenotypic developmental adaptations resulted in the similar craniofacial shapes distinctive of more recent American Indian populations over such a broad space is equally implausible. Therefore, we feel the evidence most strongly supports the hypothesis that the differences seen reflect differences in the gene pools between the distinctive early-Holocene samples and the more recent American Indian and northern Asian populations with which they were compared.

Accepting that the evidence best supports the view that the differences reflect ancestral/descendent relationships, we feel the following model, which has been articulated at least in part by a wide variety of scholars who have studied the evidence, can be proposed for the peopling of the Americas. The founding population of anatomically modern humans that first colonized the New World entered via the Bering land bridge prior to the establishment of populations in northern Asia which bore the facial features characteristic of northern Asians of today. This view has also been proposed by Birdsell (1951), Brace and Tracer (1992), Lahr (1995), Neves and Pucciarelli (1989, 1991, 1996), and Neves et al. (1998). We do not feel the evidence at this time warrants proposing a more specific area of origin for the ancestors of the earliest documented American remains, other than that they were an Asian population or populations which filtered through or along the margins of the Bering land bridge. The apparent heterogeneity seen among the early-Holocene samples suggested by the multivariate analyses indicates that by 9,000 years ago natural selection, gene flow, and genetic drift had created differences between the regional populations. This view is substantiated by the extensive dental variation Powell (1995) has documented in mid-Holocene North American populations. Both the distinctiveness of the early Holocene populations and their heterogeneity fit comfortably with the earlier period of occupation of the Americas that the Monte Verde site substantiates. We feel the strong similarities documented between more recent northern Asian populations and those of more recent American Indians indicates a marked degree of gene flow, brought about by subsequent colonizations of the Americas by more recent northern Asians. This view has also been proposed by Brace and Tracer (1992). Finally, we believe that Turner's robust analysis of the American dentition has predominantly documented the more recent colonization event; but possible evidence for earlier, more distinctive populations may be reflected in his analyses as well, as we have indicated in this review.

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