20 The Dentition of American Indians: Evolutionary Results and Demographic Implications Following Colonization from Siberia

Christy G. Turner II · G. Richard Scott

Abstract

This chapter uses dental morphology to make inferences about how the New World was first colonized. The major emphasis is on the initial Macro-Indian migration based on dental traits observed in Paleo-Indian, Archaic, and more recent prehistoric crania. The major results are: (1) Arctic and Subarctic native dentitions differ enough from those of Macro-Indians to indicate separate migrations. (2) Clustered MMD values show three Macro-Indian branches of North Americans, South Americans, and mixed North and South. (3) There is no marked branching depth for these three dental divisions, which fits the hypothesis of a single rapid Paleo-Indian colonization event. (4) The minimally divergent North and South American dental divisions are most likely the microevolutionary result of dispersal-dependent population structure and lineage effects. (5) No genetic bottlenecking can be identified at Panama. (6) The small amount of New World internal dental divergence favors colonization of South America soon after the settlement of North America. (7) There are no obvious clines, frequency trends, or geographic groupings for individual dental traits. This suggests little or no selection and that after leaving Siberia, population size increased sufficiently to limit genetic drift. (8) There is no sign of any Old World or Oceanic dental pattern other than Northeast Asian Sinodonty. All things considered, including New World and Siberian linguistics, archeology, genetics, route considerations, and relevant natural history, dental analysis supports the Late Pleistocene Ice-free Corridor, Clovis or epi-Clovis settlement hypothesis, and the Greenberg Amerind or Macro-Indian language evolution model.

20.1 Introduction

This chapter reviews the dental morphological evidence for the pre-Columbian colonization of the New World. This evidence, in conjunction with genetic information, is used to challenge colonization scenarios based on measurements of prehistoric skulls. There are two main anthropological questions for which answers have been sought using the variation of New World dental morphology and comparative information from Old World and Pacific basin populations. First, how many colonizing migrations can be postulated on the basis of New World dental variation? To answer this question, analysts have tried to determine if there are any dental correspondences with modern or ancient New World culture areas (yes), environmental types (no; however, Jantz et al. 1992 found that anthropometric variation was correlated with geography), or linguistic families (yes) (Greenberg et al. 1986; Scott and Turner 1997). These findings suggest that New World dental variation is more closely linked to ethnicity (i.e., migration) than to environment (natural selection or physiological adaptation). Roughly put, dental variation is strongly caused by nature, whereas cranial variation has a significant nurture component (Kohn [1991 p 273] notes that "... environmental factors contribute a significant amount to the observed variability in craniofacial morphology and growth."). Because of linguistic and ethnic correspondences with dentition, Arctic and western Subarctic dental variation is most parsimoniously interpreted as due to two migrations of people dentally differentiated to a slight degree from an earlier migration (Clovis or epi-Clovis). All three inferred migrant groups possessed minor variants of the Sinodont dental pattern, and as such, are closely related and share a common Northeast Asian ancestor sometime in the relatively recent past. Presumably, each originated in different geogenetic regions of northeastern Asia (Turner 1985) after separating from the common ancestral stock that presumably lived further to the south, say central China. As will be shown, the earliest colonizers must have given rise to all modern North and South American populations except for Arctic and Subarctic groups. We refer to this first migrant group as Macro-Indian or Amerind, linguistic names (Ruhlen 2000), and Paleo-Indian or Clovis, synonyms used by archeologists (Haynes 1987). The term epi-Clovis has been recently proposed to denote the Late Pleistocene ancestral cultural condition in Beringia prior to the development of the fluted points that are the hallmark of the Clovis big-game hunters (Turner 2002). Another name used in Alaska to denote epi-Clovis is Nenana complex (Hoffecker et al. 1993). In addition to these just-cited articles, other major reviews of the archeological evidence for the peopling of the Americas can be found in Carlson (1991), Fiedel (2004), Haynes (2002a, which contains an immense bibliography, 2002b), Haynes (n.d.), Hoffecker and Elias

(2003), Madsen (2004), Meltzer (1993), Rogers et al. (1992), West (1996), Yesner (2001), Yesner and Pearson (2002), and many others. We emphasize the importance of archeology and archeologically derived teeth since both provide direct diachronic epigenetic evidence for human biocultural prehistory.

In the Old World, the Sinodont dental pattern occurs in modern and prehistoric Northeast Asians of China, Tibet, Mongolia, post-Jomon Japan, Korea, and eastern Siberia (Hanihara 1968; Zoubov and Haldeyeva 1979; Hanihara 1991; Scott and Turner 1997). In contrast, Late Pleistocene and recent peoples of mainland and island Southeast Asia (Thailand, Indonesia, Borneo, Philippines, Taiwan, Jomon Japan, etc.), as well as Polynesians, Micronesians, and early Sri Lankans, possess a dental pattern called Sundadonty, which is simpler and retains more of the character of a hypothesized earlier pattern (Proto-Sundadonty) than does the more specialized Sinodonty (Turner 1983, 1990a; Scott and Turner 1997). Modern and recent Europeans, as well as the earlier Cro-Magnons, possess a simplified dental pattern, which is similar to that found in modern India, north Africa, and western and central Asia (Irish 1993; Haeussler 1996; Hawkey 1998). The simplest of modern human dental patterns is found in Europe. It more closely resembles the dental pattern of modern Africans and Australians than Sinodonty.

The second question involves controversial archeological and craniometric evidence claims proposing that the New World was initially colonized by a pre-Clovis, Sundadont population that was less Mongoloid cranially than modern Indians. These claims presume an earlier entry into the New World than the classic Clovis-first model. Claims for pre-Clovis range widely, from 15,000 to more than 50,000 years BP. We also address this question.

To put the peopling of the New World into a broad framework of dental pattern evolution, we follow a phylogenetic reconstruction that seems to have the best general concordance with other lines of evidence derived from archeology, linguistics, genetics, and natural history. By dental pattern we mean a standardized set of independent discrete crown and root morphological traits whose occurrence (presence or absence) and expression (small, moderate, large, very large; shape variation, etc.) in one major geographic region, such as northeast Asia, differ considerably from what is found in other major natural regions, such as Europe. The authentication of these patterns has been based on repeated dental sampling of the geographic regions, which produces trait frequencies like those originally used to define the regional patterns. On dental grounds we exclude prehistoric Europeans and Africans as having anything directly to do with the peopling of the New World until the Christian era. Similarly, teeth indicate that peoples of Oceania and Southeast Asia played no role in the colonization of the New World. Long before Siberians reached Alaska, human populations had evolved their major modern dental patterns. Scott and Turner (1997) identify these as belonging to five groups: Africa south of the Sahara, western Eurasia (Europe, Middle East, north Africa, India), Sahul-Pacific (Australia, New Guinea, Melanesia), Sunda-Pacific (mainland and insular Southeast Asia, Polynesia, Micronesia), and Sino-American (northeast Asia and the Americas). Finally, we exclude as impossible all claims for an autochthonous creation of Native Americans, as based on some religious beliefs, as well as on very flawed reasoning (Tyler 1998).

To put the peopling of the New World into a broader human evolutionary context, we should first consider what we know about human evolution in Asia during the Upper Pleistocene. Sometime before 50,000 BP, there were anatomically modern humans living in Southeast Asia, although only the south China Liujiang skull may be this old or older (Pope 1992 p 275). However, the 50,000 BP date approximates the earliest archeological appearance of human-made stone artifacts in Australia (Roberts et al. 1994). All human skeletal remains found in Australia, some dating as far back in time as 30,000 BP, are anatomically modern. Australia could only have been colonized from Southeast Asia, and at a few locations along the route, only with the aid of some form of watercraft. We hypothesize that the early Southeast Asians and their Australian colonists possessed a dental pattern similar to what is found in modern Australians. Turner (1992c) has called this hypothetical pattern Proto-Sundadonty, which was estimated by averaging the dental trait frequencies obtained from archeologically and ethnographically derived skeletal samples collected in several localities throughout Australia. In their early terrestrial and oceanic dispersal eastward out of Southeast Asia, Proto-Sundadonts, in time, became ethnic Melanesians and Australians. Their dental pattern is much like that found in modern and recent Southeast Asians as well as modern sub-Saharan Africans suggesting Proto-Sundadonty and the African dental pattern were derived from an as yet unidentified common ancestral pattern. Before the end of the Pleistocene 10,000 years ago, Southeast Asian teeth had evolved into the slightly more specialized Sundadont pattern as part of the general drift toward dental complexity in eastern Eurasia, in contrast to the Late Pleistocene drift toward increased simplicity in western Eurasia. The areal extent of Sundadonty increased with the northward coastal expansion of these modern humans into Taiwan, and Jomon Japan, where Sundadonty remains to the present day in unadmixed Taiwan aborigines and the Ainu of northern Japan. In the more interior part of the East Asian mainland, probably in north China, Sundadonty evolved further into the even more complex and specialized Sinodont pattern. In time, nomadic groups possessing Sinodonty expanded into Mongolia, eastern Siberia, and eventually the New

World. In the later Holocene, Southeast Asians traveled the Pacific by large sailing watercraft to become island populations of Polynesians and Micronesians, retaining their Sundadont pattern. Thus, all around the Pacific basin there are three distinctive dental morphological patterns: Proto-Sundadonty (Sahulland: Australia and Melanesia), Sundadonty (Sundaland: mainland and island Southeast Asia; island East Asia), and Sinodonty (Sino-America). At least 50,000 years are involved in the evolution of this Asian-Pacific dental patterning. In terms of time involving only several thousands of years, these patterns are evolutionarily quite stable and remarkably consistent in ethnically related groups living in strongly dissimilar ecological settings. Such demonstrable stability is part of what makes dental morphology eminently useful for evaluating long-term diachronic and synchronic affinities, population origins, and microevolutionary processes.

20.2 New World Arctic and Subarctic dental variation

While all New World teeth conform with the Sinodont dental pattern, first defined on the basis of prehistoric Chinese teeth, those of Arctic and Subarctic Eskimos, Aleuts, and speakers of Na-Dene languages differ slightly from those of Macro-Indians (Scott and Turner 1997, n.d.). For example, pronounced upper incisor shoveling is less frequent in Eskimos and Aleuts than it is in Macro-Indians. It tends to be intermediate in Subarctic Indians. On the other hand, Eskimos and Aleuts have greater frequencies of three-rooted lower first molars than do Macro-Indians. Again, the western Subarctic tribes are intermediate. When the three New World groups—(1) American Arctic, (2) Northwest North America, and (3) North and South America—were graphed for mean trait frequencies and standard errors of 23 crown and root traits, 10 of the traits show the intermediate nature of Northwest North America viz. Eskimo-Aleuts and American Indians in general while 11 traits showed similar frequencies across the 3 groups (Scott and Turner 1997). The only two traits that failed to exhibit intermediary or similarity were incisor interruption grooves and odontomes, but the differences were not dramatic in either instance.

Multivariate and univariate analyses and comparisons show clearly that all New World groups are dentally more like Northeast Asians than like any other major geographic group in the world. Nevertheless, the teeth of New World Arctic and Subarctic peoples are generally more like those of Northeast Asians than are the Macro-Indian populations, which as archeological evidence suggests, means that the Macro-Indian colonization occurred before or separated from that of the modern Arctic and Subarctic populations. It has been inferred that the concordances between New World archeological groups and biological populations likely are: Big-game hunting Clovis fluted point makers = Paleo-Indian Sinodonts; smaller game-hunting Paleo-Arctic biface and microblade makers = Na-Dene/Greater Northwest Coast Sinodonts; Maritime Anangula blade makers = Aleut-Eskimo Sinodonts. What holds these concordances together is their individual geographic distributions for artifact types, dental divisions, and language families.

20.3 Macro-Indian dental variation

Comparative analyses of Native American dentitions by Haeussler and Turner (1992), Hanihara (1979), Perzigian (1984), Powell (1993), Scott (1973, 1991), Scott et al. (1983, 1988), Turner (1983, 1985, 1986, 1990a, 1992a, 1992b, 1993, 2002), as well as contemporary genetic studies by Callegari-Jacques et al. (1993), Cavalli-Sforza et al. (1988, 1994), Horai et al. (1991), Laughlin and Harper (1988), Stone and Stoneking (1993), Szathmary (1979, 1993), Torroni et al. (1992), others reviewed herein, and most osteological studies by Alekseev (1979), Kozintsev (1995), Steele and Powell (1992), and Brace et al. (2001), are in good agreement that the ancestors of Native Americans originated in northeast Asia. However, a few osteological studies are not in full accord with this general inference. Howells' (1989) worldwide craniometric analyses showed male Peruvians and Californians clustering with males from Europe, while his male Arikara Indians clustered with male New Zealand Moriori. Neves and Pucciarelli (1991) argued on multivariate grounds that early South American crania are morphometrically closer to Australians even though their principal components plots show the early South Americans equally similar to East Asians and Europeans. Inasmuch as archeology (West 1981, 1990; Dillehay and Meltzer 1991; Stanford and Day 1992; Meltzer 1993), linguistics (Greenberg et al. 1986; Greenberg 1990; Greenberg and Ruhlen 1992), and paleo- and neogeography (Hopkins 1982; Laukhin 1997), as well as dentition, genetics, and most osteology, strongly support a Northeast Asian origin for all Native Americans, the two cited craniometric studies are notable exceptions to the Northeast Asian-American anthropological and other correspondences as well as the Sino-American dental correspondences (Scott and Turner 1997). Nevertheless, in recent years there has been a concerted effort to bring back to life the notion of a pre-Clovis occupation of the Americas (Hall 2000).

20.3.1 A brief history of the pre-Clovis revival as it bears on dental variation

There has long been disagreement between Americanist scholars who line up with the late Aleš Hrdlička (1925) by arguing that the colonization of the New World was late compared to the amount of human evolution in the Old World, in contrast to scholars who believe there is evidence for much older human occupation in the New World. For example, Krieger (1964) (preprojectile occupation), Carter (1957) (very ancient occupation), Müller-Beck (1967) (Mousteroid element in Americas), and others posit very early migrations (>20,000 BP) of peoples from the Old to the New World. There have been any number of archeological claims for pre-Clovis occupation of the New World, but as Meltzer (1993) humorously noted, the claims usually have a "shelf life" of about five years. Among modern physical anthropologists, several revivalists of the pre-Clovis, and/or non-Mongoloid origins include Neves and Pucciarelli (1991, and several similar articles), Crawford (1992), Lahr and Haydenblit (1995), and Steele and Powell (1992).

Lahr and Haydenblit (1995) proposed that Sundadonty was present in a series of South American crania from Patagonia and Tierra del Fuego. In a lengthy review article, Lahr (1995) proposed that either Sinodonty evolved in parallel in Asia and the Americas, or there were two migrations ancestral to Native Americans, i.e., a Sundadont group followed by a Sinodont group. These proposals are inconsistent with our South American dental observations. No where has the senior author found any South American series or individual skull that could be considered as having the Sundadont pattern and this includes the Lagoa Santa remains housed in Brazil and those curated in Denmark, as well as Archaic samples from coastal Brazil, Chile, Ecuador, and Peru. We suggest that the observations of Lahr and Haydenblit on the degree of trait expression were impacted by dental attrition. Wear most likely caused the underscoring of crown traits that led them to incorrectly propose the presence of Sundadonty (Burnett et al. 1998; Turner et al. n.d.). Tooth wear might also have misled Powell and his associates in their observations on small Paleo-Indian samples.

When Steele and Powell (1997) evaluated the craniometric data of two ancient skulls from Nevada (Spirit Cave, Pyramid Lake) that dated ca. 9,500 BP, they found that the two skulls failed to cluster with any of the 22 comparative modern populations. Despite this result, they felt that the skulls were more closely aligned with south Asian, Pacific, and Australian populations than with North Asian and recent North American Indians. They concluded that "the studied Paleoindians arrived in the Americas prior to the establishment of the crania shape that is distinctive of recent Northern Asians and North American Indians, and that the colonization of the Americas was more complex than has previously been proposed" (Steele and Powell 1997 p 218).

Taken altogether, the form of the Paleo-Indian skull relative to most of the comparative samples is not only a reflection of geogenetic linkages but also sedentism and its related nutritional, growth, health, and activity benefits and stresses. Thus the Africans cluster together (geogenetic linkage) despite both nomadism and sedentism being represented. The same can be said for Europe, northeastern Asia, and the Oceanic set. Given that archeological remains of Paleo-Indians strongly suggest a nomadic hunting life way, then the cranial differences between Paleo-Indians and recent Native Americans should have been interpreted along economic lines as much as geogenetic. Only in the last sentence of their article do Steele and Powell (1992) remark on the possibility of "adaptational" factors contributing to the cranial differences between Paleo-Indians and recent Native Americans. All but one sentence in this article is clearly aimed at identifying possible "genomic" differences between Paleo-Indians and recent Indians.

It should be noted that Steele and Powell (1992 p 329) speak of Paleo-Indian crania as not being ". . . classically sinodont in craniofacial appearance. Instead, it differed by appearing as much like modern southern Asians [recall they use this term to refer to Chinese, who have traditionally been classified as Mongoloids] as it did recent North American Indians and northern Asians. In this respect our findings resemble the contentions of previous scholars that the earliest recovered samples were proto-Caucasoid or proto-Mongoloid."

As far as we know, there has never been any analysis carried out to show what sort of relationship there is between craniofacial morphology and Sinodonty or Sundadonty. Steele and Powell have assumed that vaults, faces, and teeth go together like a hand in a glove. In fact, Sinodonty is found in people whose craniofacial variation includes every shape in South and North America including very robust California Indians, heavy and long-skulled Southwest US Basketmakers, and very robust long-headed Archaic crania from Mexico, Brazil, and Chile, to very round-headed gracile Southwest Puebloans, Chinese, Japanese, Buriats, and a long list of other long- and round-headed Northeast Asians. As for early Native Americans having been proto-Caucasoids, a notion perhaps most strongly championed by Birdsell (1951), Harris and Turner (1974) showed that dental morphology was strongly in opposition to such typological thinking (Birdsell was a student of Hooton whose 1930 book *The Indians of Pecos Pueblo* was the ultimate in, but not the end of, typological thinking. The crania of Pecos Pueblo had such a wide variety of cranial forms that Hooton's typological classification of that within-group variation led Gladwin (1947) to publish his hilarious spoof on anthropology titled *Men Out of Asia*. Gladwin used Hooton's cranial classification to postulate multiple distinct migrations into the New World. The first to enter were coast-following plant-eating "Australoids." Next came meat-eating Clovis hunters, presumably of a Negroid strain. Algonquins entered third, Eskimos fourth, and Mongoloids, fifth). All this, of course, is a jumbled mix of typology, morphological dating, age-area concept, and primitive–modern scaling.

20.4 Genetics and the peopling of the New World

During the first half of the twentieth century, scholars who investigated issues relating to the settlement of the New World came primarily from archeology and skeletal biology. During the past 50 years, however, genetic data have played an increasingly important role in debates on Native American population history. Researchers have applied three different kinds of genetic data to the problem. Initially, focus was on nuclear genetic markers, from red blood cell antigens and serum proteins to red cell enzymes, immunoglobulins, and white blood cell antigens (cf. Mourant 1954; Mourant et al. 1976; Roychoudhury and Nei 1988; Cavalli-Sforza et al. 1994). In the 1980s, a new and different type of genetic marker was used, one derived from the single-stranded DNA of the mitochondria (mtDNA) which was transmitted, with but few exceptions, through maternal lineages (for reviews, see Cann 1988; Long 1993). Finally, in the 1990s, the Y chromosome was sequenced and a surprising variety of interesting polymorphisms emerged (cf. Hammer and Zegura 2002; Jobling et al. 2004). The literature in the field has expanded at an exponential rate during the past two decades. It is beyond the scope of this review to provide a detailed synthesis of genetic studies. Our goal is to highlight some of the results from the three different sorts of genetic data to determine the extent to which the analyses of synchronic genetic data corresponds with peopling models based on diachronic dental data.

20.4.1 Nuclear markers

Around 1950, the nascent field of human genetics started to weigh in on the issue of Native American origins. On that date, W.C. Boyd published his seminal work *Genetics and the Races of Man*. Therein, he utilized available data on three red cell antigen systems (ABO, Rh, MN) to set up a classification of modern human groups. He deemed Native Americans to be sufficiently distinct from other groups to warrant their own racial category. In this regard, he noted that Indians lacked the “r” allele of the Rh system and the A^2 and B alleles of the ABO system, although Eskimos did have a low frequency of B. Indians also showed a relatively high frequency of the M allele and a marked dichotomy in frequencies of the A and O alleles of the ABO system. Populations south of the US–Mexico border showed essentially 100% O alleles while some North American groups, in particular Algonquians, Athapaskans, and Eskimo-Aleuts, exhibited high frequencies of the A allele. While similarities to Asian populations were noted (lack of r and A^2), Boyd felt that the high frequency of the M allele and the very low frequency of B was sufficient to distinguish Asian and American “races.”

Laughlin (1951) used blood group data along with anthropometric and osteometric comparisons to assess the affinities of Aleut populations. He felt the presence of the B allele indicated Aleuts were closer to Eskimos than Indians. Moreover, he noted that the “B present in the Eskimos is an indication of their recent Asiatic heritage . . .” (Laughlin 1951 p 119). Throughout his career, Laughlin (1963, 1966) adhered to the notion that there were two major groups in the Americas—American Indians and Aleut-Eskimos. After comparing Native Americans to Siberians for data on the ABO and MN systems, Laughlin (1966 p 473) opined that the “essential affinity of the Eskimo-Aleut stock with Asiatic Mongoloids, rather than with American Indians, is well attested.”

With the development of starch gel electrophoresis in the early 1950s, there was a dramatic increase in the number of genetic surveys across the Americas and throughout the world and in the number of genetic systems that became standard markers for population profiles. By the 1970s, the original three RBC antigen standards were complemented by the addition of many more antigen systems and serum proteins (e.g., Diego, P, Duffy, Kell, Kidd, Haptoglobin, Transferrin, Albumin, etc.). By the time of their massive worldwide synthesis, Cavalli-Sforza et al. (1994) were able to tabulate data on 120 nuclear alleles.

Beginning in the 1970s, Szathmary (1979, 1981, 1993 and elsewhere) played an important role in making inferences on long-term population history based on the analysis of Native American gene frequency profiles. One of her early efforts, prepared with Nancy Ossenberg, had the eye-catching title “Are the Biological Differences Between Eskimos and North American Indians Truly Profound?” (Szathmary and Ossenberg 1978). This paper developed the position that Indians and Eskimos were not as distinct as many scholars had presumed (cf. Laughlin 1963, 1966), even suggesting that the two groups might have differentiated from a common stock after their arrival in the New World. Until this time, authors had disagreed on the number of possible migrations to the New World but the consensus was that the ancestors of Aleut-Eskimos constituted not only a separate migration but the last major migration across the Bering Strait. While the arguments and analysis in these works are interesting, Szathmary limited her comparisons between Aleut-Eskimos and northern Indians of the American Subarctic, to wit Athapaskans in the west and Algonquians in the east. We now know that these northern groups are much more similar to Eskimo-Aleuts than Indian groups from Mesoamerica, Central America, and South America (cf. Schanfield 1992; Cavalli-Sforza et al. 1994).

Authors who focus on GM allotypes have proposed different migration scenarios to account for variation in immunoglobulin genetic variants. Williams et al. (1985) observed that $\mathrm{Gm}^{1;21}$ was present in "Paleo-Indians," Na-Dene and Eskimo-Aleut samples with $\mathrm{Gm}^{1,2;21}$ absent in Eskimo-Aleuts, and $\mathrm{Gm}^{1;11,13}$ absent in Paleo-Indians. Na-Dene speakers had all three allotypes. This observation led the authors to conclude that Gm data supported the three-wave model of Greenberg et al. (1986) for peopling of the New World.

Also focusing on immunoglobulins, Schanfield (1992) pointed out that the work of both Szathmary (1993) and Williams et al. (1985) provided only a limited picture given their emphasis on North American native populations. When Schanfield synthesized Gm data from both North and South American populations, he found that South Americans differed consistently from non-Na-Dene North American Indians, Na-Dene speakers, and Eskimo-Aleuts. He feels his data suggest that "in the peopling of the New World, at least four separate migrant groups crossed Beringia at various times" (Schanfield 1992 p 381). He further suggests that the ancestors of South American Indians arrived before 17,000 BP while North American Indians arrived when the ice-free corridor opened up at the end of the Pleistocene. Both Eskimo-Aleuts and Na-Dene groups are thought to be later Holocene arrivals.

A grand synthesis of patterns of variation in nuclear genetic markers was accomplished by Cavalli-Sforza et al. (1994) in *The History and Geography of Human Genes*. This worldwide analysis of 120 markers in over 40 genetic systems devoted entire chapters to populations in each major geographic region, including a chapter on the Americas. To maximize the availability of genetic data across as many loci as possible, the authors combined data sets and came up with 23 New World groups, defined primarily on linguistic grounds. Importantly, the analysis included several Eskimo, Na-Dene, Siberian, North American, and South American groupings. After conducting a variety of distance analyses and two- and three-dimensional ordinations, Cavalli-Sforza et al. (1994 pp 340–341) concluded:

- The genetic patterns in the Americas fully confirm the three waves of migration suggested by dental and linguistic evidence: Amerinds, Na-Dene, and Eskimo. Their order in time is strongly suggested by their north-south geographical order. Further refinements may reveal that more than one entry contributed to the first wave, but the archeological information is contradictory and our understanding of the genetic pattern of Amerinds is incomplete, so that further investigations are required to settle this problem.

20.4.2 Mitochondrial DNA

When geneticists first discovered that mutationally induced variation in mitochondrial DNA (mtDNA) might help unravel human evolutionary history, there were severe sampling limitations. To harvest enough mtDNA for analysis, researchers had to collect human placentas, often a formidable task. The development of PCR (polymerase chain reaction) techniques in the early 1990s allowed researchers to obtain mtDNA samples from many kinds of tissue samples, including bone. This development revolutionized the study of mtDNA and research teams quickly pursued historical questions on every continent, among both living and earlier human populations.

Although mtDNA variation has been evaluated in groups throughout the world, the geographic region that has received an inordinate amount of attention is the New World. Because of sampling limitations, the early studies were regional in scope (Ward et al. 1991, 1993; Shields et al. 1992, 1993). With improved methods, expanding sample sizes, and cooperation among research teams, groups eventually addressed the bigger issues regarding the internal differentiation of New World populations and dispersal dates from ancestral Asian populations (Wallace and Torroni 1992; Torroni et al. 1993, 1994; Forster et al. 1996; Malhi et al. 2002; Eshleman et al. 2003).

Mitochondrial DNA variation is studied through a combination of restriction fragment length polymorphisms (RFLPs) and direct nucleotide sequencing of the relatively short hypervariable control region (HVR-I polymorphisms). Haplogroups are distinguished by a combination of RFLPs and HVR-I polymorphisms (Schurr 2004a).

Jobling et al. (2004 p 291) show the worldwide distribution of the major mtDNA clades, or haplogroups. Of the 27 major clades shown (lettered A to Z), New World populations exhibit the presence of only five haplogroups—A, B, C, D, and X. Numerous articles have been devoted to the issues of: (1) how these haplogroups vary within and among Native American populations; (2) whether or not they were brought by separate founding groups or differentiated after arrival in the New World; and (3) the time depth for the origin of each haplogroup.

Regarding mtDNA haplogroup variation, North, Central, and South American Indians (Amerinds), all exhibit haplogroups A, B, C, and D. Eskimo-Aleuts, by contrast, have essentially no B and very little C (Schurr 2004a). Athapaskans were initially thought to lack the B haplogroup (Lorenz and Smith 1994), but it now appears to be present but infrequent in Na-Dene-speaking groups. Haplogroup X is limited to northern North American Indians from the Northwest Coast and Subarctic culture areas (Brown et al. 1998).

While the pattern of mtDNA haplogroup variation is coming into focus, opinions on what this variation means have yet to reach a consensus. Some early studies favored the notion that the haplogroups indicated four separate migrations into the New World (Schurr et al. 1990; Horai et al. 1993; Lorenz and Smith 1996). Torroni et al. (1994) concluded there were three migrations: two Amerind migrations, with an early dispersal of A, C, and D and a later migration that involved the B haplogroup. Athapaskans, with an exceptionally high frequency of the A haplogroups, were thought to constitute a third migration. Starikovskaya et al. (1998) also believed there was an early migration that carried the A, C, and D haplogroups with a later migration bringing B. Although there are several proponents of multiple migrations, the majority of researchers contend that the mitochondrial DNA variation evident among all Native Americans is best explained by a single migration event with haplogroup differentiation occurring after arrival in the Americas (Merriwether 1995, 2002; Kolman et al. 1996; Merriwether et al. 1996; Bonatto and Salzano 1997; Malhi et al. 2002; Silva et al. 2002).

From the outset, geneticists have argued that mtDNA is useful for not only describing patterns of variation but also for estimating times of divergence on a branching tree. Using either coalescence or distance methods of estimation in conjunction with several assumed mutation rates, most researchers addressing the issue of the initial New World settlement have arrived at very old dates for this event (Schurr 2004b). Several authors contend the first wave of migrants arrived in the Americas more than 30,000 years ago (Bonatto and Salzano 1997; Starikovskaya et al. 1998). Other workers give dispersal estimates of between 20,000 and 30,000 BP (Torroni et al. 1994; Silva et al. 2002). Starikovskaya et al. (1998) dated early Amerinds at 34,000–26,000 BP with a later migration at 16,000–13,000 BP. Torroni el al. (1994) tried to come up with an estimate that either agreed with an early entry date (30,000+ BP) or a late entry date (ca. 13,000 BP) compatible with the Clovis-first model. Instead of coming down on one side or the other of this debate, their estimate fell in the middle with a range of 22,000–29,000 years ago.

Despite differing opinions on the numbers of migrations and times of dispersal, mtDNA geneticists are in fundamental agreement that Native American haplogroups are of Siberian origin. Torroni et al. (1994 p 1162) reflect the sentiments of many when they say “We accept that all significant human entry into the Americas was by way of Siberia during periods of glaciation, when a land bridge connected Siberia and the extreme northwest of the Americas." When haplogroup X was discovered in American Indians, this was initially thought to represent a possible migration from Europe, or at least some founding Amerinds had Caucasian ancestry (Brown et al. 1998). If so, why is there no haplogroup H in Native Americans, as this is far more common in Europeans (ca. 40%) than haplogroup X (ca. 2%) (Schurr 2004a). An alternative to a direct transAtlantic migration of X-bearing Europeans was developed by Reidla et al. (2003) who feel that haplogroup X represents a fifth rare mtDNA clade that came into the Americas across Eurasia, originating as far west as the Near East (Reidla et al. 2003). Finally, there are no haplogroups that link modern or ancient Americans to Southeast Asian or south Pacific populations, a population source for early Americans favored by some osteologists (Neves and Pucciarelli 1991; Steele and Powell 1992, 1997; Powell and Neves 1999).

20.4.3 Y chromosome

The latest rage in genetic studies that focuses on the settlement of the Americas comes from the analysis of recently discovered polymorphisms on the Y chromosome. The long neglected Y, whose strict paternal transmission nicely complements the maternal transmission of mitochondrial DNA, exhibits two major types of polymorphisms on the nonrecombining segment (NRY) of the chromosome. First, there are point mutations that result in single nucleotide polymorphisms (SNPs). The mutation rates for these polymorphisms are slower than for the second type of polymorphism—short tandem repeats (STRs). Taken together, researchers use SNPs and STRs to define a diverse array of haplogroups and haplotypes. As with mtDNA, Y chromosome polymorphisms have been used to estimate the number of migrations, the timing of dispersal of populations to the Americas, and the Old World sources for this peopling event.

Evolving and diverse nomenclatural systems applied to Y polymorphisms make the literature on this system difficult to decode for nonspecialists. To allay confusion, workers convened a consortium in 2001 to develop a common set of standardized terms for Y chromosome binary haplogroups (Y Chromosome Consortium 2002; Hammer and Zegura 2002). Based on this new system, it appears that most Native Americans exhibit haplogroup Q, an observation that led some workers to conclude that a single founding male lineage is sufficient to account for the ancestry of all Native Americans (Tarazona-Santos and Santos 2002; Jobling et al. 2004). Haplogroup Q is, however, defined on the basis of several distinct SNPs and STRs, which other workers have interpreted as indications of multiple migrations from Asia. Lell et al. (2002) suggest that the Q-M3 and P-M45a Y haplogroups dispersed eastward from central Siberia along with the C and D haplogroups of mtDNA. Moreover, these authors feel that the haplogroups P-M45b and RSP4Y came from south Siberia along with a subgroup of the A haplogroup of mtDNA (control-region sequence variant 16192T and the *Rsa*I polymorphism at np16392). Karafet et al. (1999) and Ruiz-Linares et al. (1999) also conclude there were at least two founding Y haplogroups in the Americas.

Regarding the timing of dispersal, most estimates for arrival in the New World favor the long chronology (cf. Schurr 2004b). For their two migrations, Lell et al. (2002) estimate the first wave arrived in the New World ca. 20,000–30,000 BP with the second wave arriving much later, ca. 7,000–9,500 years ago. In contrast to those who see great time depth for Y haplogroups in the Americas, Seielstad et al. (2003) attempted to set an upper limit for initial entry into the New World based on a mutation (M242) that occurred just before the arrival of populations in the New World. Using a mutation rate of 0.18% per generation, the authors estimated that M242 arose around 15,000 BP. These workers, who consider 18,000 an upper limit for New World settlement, thus favor an entry into the New World that followed, rather than preceded, the Last Glacial Maximum.

20.5 Macro-Indian dental variation

Now that we have briefly reviewed contrasting models for the peopling of the New World from skeletal biology and genetics, we present in more detail the case that can be made from tooth crown and root morphology. ❯ *Table 20.1* lists the archeologically derived Indian series used in this chapter. Altogether 3,584 individuals are represented in 17 North American groups and 11 South American groups. All the data in ❯ *Table 20.1* were collected by the senior author. A key set of 29 largely independent, normal, age- and sex-free crown and root traits were scored for occurrence and expression using the Arizona State University dental anthropology system (Turner et al. 1991). The overwhelming numbers of individuals are pre-Columbian. Hence, there is effectively no chance for European, African, or Oceanic admixture in this Panamerican assemblage, whose chronometric ages range from protohistoric to late Paleo-Indian. Although the exact modes of inheritance are still under investigation for these and other dental traits, it is believed that each has a substantial genetic component for occurrence and expression (Scott 1973; Harris 1977; Berry 1978; Scott and Turner 1988, 1997; Nichol 1990).

Table 20.1

Frequency variation in archeological New World dental samples[a]

Trait, tooth Break point	Shovel UI1 2-7/0-7		Uto-Aztec UP1 1/0-1		Enamel ext. UM1 1-3/0-3		One-root UP1 1/1-3	
Sample	%	No.	%	No.	%	No.	%	No.
North America								
Archaic Canada	86.9	38	0.0	34	12.9	84	78.7	80
Iroquois Canada	71.7	39	0.0	116	26.0	231	75.4	207
Maryland	93.7	48	0.0	54	35.8	106	81.9	94
Athapaskan	70.0	10	–	0	33.3	66	89.2	83
California	97.7	88	1.1	91	41.7	213	83.9	211
Grand Gulch, Utah	100.0	7	0.0	33	45.9	48	94.1	51
Chelly and Kayenta	97.6	42	1.7	59	61.4	96	97.4	76
Chevez Pass	71.4	7	4.2	24	55.1	29	83.9	31
New Mexico	87.5	120	0.8	128	45.9	170	91.5	141
Grasshopper	91.0	133	4.0	124	49.1	157	84.0	81
Pt. Pines early	87.5	24	2.6	38	58.8	51	85.0	40
Pt. Pines late	97.0	33	0.0	44	49.2	61	85.5	55
Arkansas	87.8	49	4.1	97	33.1	127	88.8	125
Alabama	97.3	146	1.9	159	34.0	203	77.8	108
Coahuila, Mex.	75.0	8	6.5	31	21.1	76	87.3	63
Cuicuilco and Tehuacan	94.7	38	1.7	59	33.3	66	91.2	57
Tlatelolco	100.0	39	0.0	85	50.8	122	91.0	122
No.		797/869		20/1176		743/1906		1386/1625
South America								
Panama	94.1	51	0.0	43	52.3	67	92.7	55
Ayalan, Ecuador	90.2	51	1.4	74	44.3	106	88.7	97
Cotocollao, Ec.	100.0	28	3.7	27	54.0	37	89.3	28
Chanduy, Ec.	88.2	17	0.0	12	40.0	20	94.7	19
Santa Elena, Ecuador	100.0	31	0.0	25	45.0	20	69.6	23
Paloma, Peru	86.5	52	0.0	29	46.2	78	88.1	101

Peru 1 and 2	90.0	50	0.0	118	48.4	310	86.7	450
Chile	92.2	64	0.0	65	71.7	127	96.9	128
Corondo, Brz.	95.0	20	0.0	34	36.0	61	90.5	42
Lagoa Sta, Brz.	91.4	35	1.8	56	33.3	78	83.6	73
Sambaqui, Brz.	91.1	68	0.0	74	55.5	146	84.7	111
No.		429/467		3/557		525/1050		992/1127
North America								
Mean	91.7		1.7		39.0		85.3	
Range	70.0–100.0		0.0–6.5		21.1–61.4		75.4–97.4	
South America								
Mean	91.9		0.5		50.0		88.0	
Range	86.5–100.0		0.0–3.7		33.3–71.7		69.6–96.9	
NA/SA χ^2 1 d.f.P	0.0160.9		3.892 0.05–0.02		$33.6 < 0.01$		4.2 0.05–.02	

Trait, tooth Break point	Cusp 6 LM1 1-5/0-5		4-cusped LM2 4/4-6		3-rooted LM1 3/1-3		Y Groove LM2 Y/Y+X	
Sample	%	No.	%	No.	%	No.	%	No.
North America								
Archaic Canada	65.2	69	8.3	84	10.5	124	5.3	76
Iroquois Canada	56.6	152	9.2	163	7.4	230	13.2	167
Maryland	41.8	91	8.8	102	6.0	150	11.5	96
Athapaskan	52.4	21	2.7	37	9.2	76	12.1	33
California	60.0	95	5.1	197	8.2	292	12.0	184
Grand Gulch, Utah	76.9	13	8.3	24	2.3	43	3.6	28
Chelly and Kayenta	57.1	49	10.8	74	7.2	97	3.7	82
Chevez Pass	61.5	13	25.0	20	3.8	26	18.2	22
New Mexico	39.4	94	8.0	138	4.2	167	8.6	152
Grasshopper	47.3	148	17.3	104	5.9	135	17.6	119
Pt. Pines early	45.9	37	16.0	50	4.8	63	3.6	56
Pt. Pines late	43.6	39	13.0	54	12.3	65	8.8	57
Arkansas	55.7	79	8.5	118	5.3	150	12.4	121

Table 20.1 (continued)

Trait, tooth Break point	Shovel UI1 2-7/0-7		Uto-Aztec UP1 1/0-1		Enamel ext. UM1 1-3/0-3		One-root UP1 1/1-3	
Alabama	67.7	127	3.4	178	5.1	178	7.6	170
Coahuila, Mex.	61.5	26	7.9	38	5.4	56	12.8	39
Cuicuilco and Tehuacan	51.9	52	2.8	72	10.1	89	7.4	81
Tlatelolco	65.2	132	5.3	151	5.2	173	16.9	154
No.		683/1237		130/1604		143/2114		177/1637
South America								
Panama	61.9	63	11.4	70	5.6	90	1.4	72
Ayalan, Ecuador	66.2	68	7.8	77	3.7	108	3.8	79
Cotocollao, Ec.	52.2	23	12.5	40	8.8	34	7.9	38
Chanduy, Ec.	35.7	14	15.8	19	3.6	28	5.3	19
Santa Elena, Ecuador	80.0	10	5.7	35	4.7	43	3.3	30
Paloma, Peru	43.1	51	1.5	66	2.8	107	7.6	66
Peru 1& 2	61.3	119	8.6	197	5.1	217	7.9	152
Chile	42.2	45	10.7	75	7.7	155	8.5	82
Corondo, Brz.	64.1	39	16.1	56	5.4	56	0.0	54
Lagoa Sta, Brz.	54.2	48	9.5	63	16.8	101	3.9	76
Sambaqui, Brz	60.9	69	6.2	113	3.1	161	19.5	128
No.		316/549		72/811		66/1100		61/796
North America								
Mean	55.2		8.1		6.8		10.8	
Range	41.8–76.9		2.7–25.0		2.3–12.3		3.6–18.2	
South America								
Mean	57.5		8.9		6.0		7.6	
Range	43.1–80.0		1.5–16.1		2.8–16.8		0.0–19.5	
NA/SA χ^2 1 d.f.P	0.85		0.42		0.697		6.02	
	0.5–0.3		0.7–0.5		0.5–0.3		0.02–0.01	

[a] Individual count, sexes pooled, all prehistoric except Athapaskan sample and some Iroquois. Sample provenience and break points are detailed in Turner (1985) and elsewhere. Scoring is done with ASU DAS (Turner et al. 1991).

Space limitations permit reviewing only a few of the 29 traits, so mainly those that distinguish Northeast Asian Sinodonty from Southeast Asian Sundadonty are presented (Turner 1983, 1987, 1990a). *Figures 20.1* and *20.2* illustrate five of these traits—incisor shoveling, double-shoveling, tuberculum dentale, and first and second lower molar root number.

Figure 20.1
Arrow 1 indicates right upper central incisor shoveling trait in a female skull from prehistoric Alabama site Lu25–425. Arrow 2 points to double-shoveling. Not discussed in this report, but one of the key traits used in the multivariate analysis, arrow 3 points to canine *tuberculum dentale* (CGT neg. no. 6-6-80:19)

Figure 20.2
Arrow 1 indicates left lower first molar with two roots in prehistoric Peruvian male from a cemetery in the Chicama Valley. Had there been a supernumerary third root, it would be out of view on the distolingual aspect. Not discussed in this report, but one of the key traits, arrow 2 points to a one-rooted lower second molar (CGT neg. no.7-3-80:7. Reprinted courtesy of Dental Anthropology Newsletter)

20.5.1 Findings

American Indian dental morphological variation, assessed against the background of archeological and linguistic information, led to the following inferences:

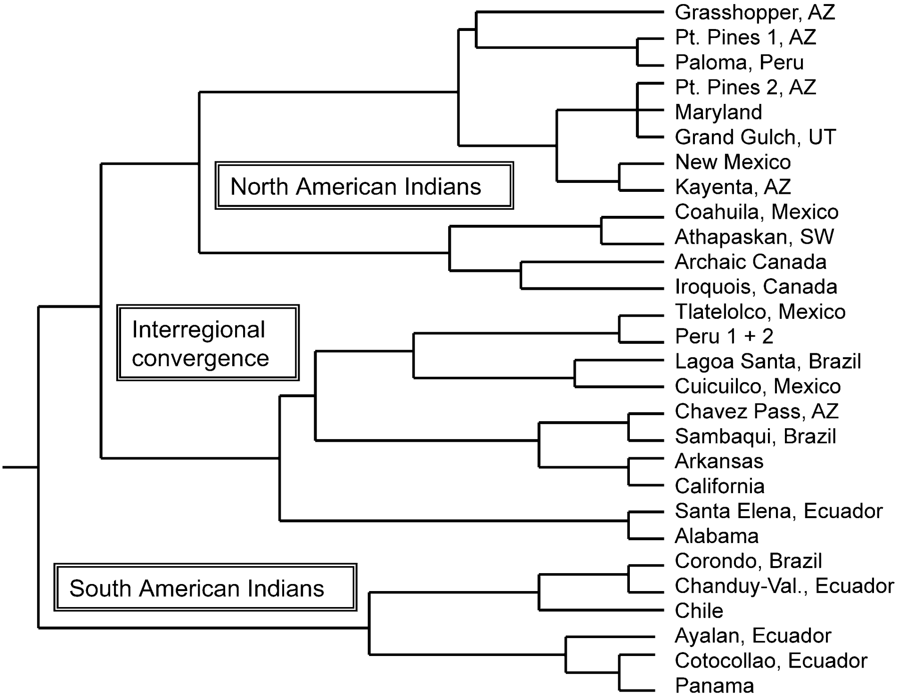
1. There are three dental clusters of Macro-Indians: North America, South America, and an interregionally convergent group.
2. Dental variation is relatively low among Macro-Indians.
3. The Macro-Indian dental divisions arose by local evolution.
4. South America was colonized soon after North America.
5. Individual dental trait frequencies show only random variation.
6. Only Northeast Asian Sinodonty is present in the New World.
7. Dental variation supports the Clovis/epi-Clovis prehistory and Greenberg language migration models.

1. *Three dental clusters*: ➲ *Figure 20.3* is a dendrogram computed with Ward's clustering method for the 106 possible pairwise Mean Measures of Divergence, a multivariate similarity/dissimilarity statistic developed by C.A.B. Smith (Berry and Berry 1967) with widely used adjustments for sample size and determination of statistical significance (references in Turner 1985). There are three primary dental groups: North America (at the top), South America (at the bottom), and a middle group that shows interregional convergence.

   The Paloma sample is surely a misclassification attributable to chance. Some interregional convergence is expected given that dental microevolution (in the sense of gene frequency changes) is probably best explained as caused largely because of random changes due to founder's effect, population structure, and local genetic drift. There is no archeological or other evidence to believe, for example, that the Ecuadorian Santa Elena series is similar to the Alabama sample because of ancestry closer than to each sample's respective regional relationships. Instead, the Santa Elena-Alabama similarity is most likely an example of the occasional convergences that should be expected if Macro-Indian dental evolution was mainly due to chance, not selection or gene flow. As will be discussed below, the relatively low amount of variation, despite the two main North and South American clusters, is not supportive of multiple Paleo-Indian migrations.
2. *Low dental variation*: Inspection of ➲ *Table 20.1* reveals a low amount of trait frequency variation between the 29 groups relative to that in, say, eastern Asia, or even New World Arctic people (Turner 1991). This limited New

Figure 20.3

Dendrogram of North and South American pre-Columbian dental relationships based on mean measures of divergence clustered with Ward's method, 29 dental traits. Computer reference: North and South America



World Indian dental divergence is probably what causes the rather limited treeness of the dendrogram in *Figure 20.3*. The limited treeness suggests either substantial gene flow throughout the Americas or a relatively recent colonization of the Americas with only minor *in situ* dental differentiation. Excellent treeness has been obtained throughout the New World (Arctic, Subarctic, non-Arctic) with these same dental traits and statistical methods (Turner 1987).

Table 20.1 shows that upper central incisor shoveling and lower first molar root number have very different overall frequencies in the New World. The former is a high frequency trait, the latter, a low frequency trait. Scott (1973) demonstrated that trait frequency was positively correlated with trait expression in the offspring of specific mating types, providing strong evidence for polygenic inheritance. As can be seen, shoveling is universally high (>70%) among the groups, whereas three-rooted lower first molars are uniformly at a low frequency, averaging about 6%. Both traits have little variation within and between North and South America. These two traits, like the other 27, show no sign of clinal variation from north to south, east to west, coastal to interior, or low to high elevation. Trait frequencies have no identifiable gross environmental correlates in the New or Old World that would suggest the effects of short term natural selection.

3. *Dental divisions arose by local evolution*: ❯ *Table 20.1* also lists the North and South American means and ranges for eight traits, seven of which distinguish Sinodonty from Sundadonty, plus a trait found almost exclusively in Native Americans—the Uto-Aztecan premolar. The tabulation shows that there are no statistically significant differences in some traits, and very little in all others except the enamel extension, between pre-Columbian North and South American Indians. None of these traits has a north–south mean difference greater than 6%(enamel extensions). There is no tendency to exhibit less "Mongolization" or Sinodonty in South America than in North America, that is, there is no evidence for Sundadonty. The differences between the means appear to be mainly random. What little difference there is between North and South America is better interpreted as due to post-colonization local evolution rather than to predifferentiated multiple migrations. Moreover, the archeology, craniology, and odontology the senior author has personally seen and read about in Russian sources for eastern Siberia, does not provide any cultural or biological basis for hypothesizing markedly differentiated source populations in Primorye, Chukotka, trans-Baikalia, or Yakutia. However, the fact that these Siberian geographic districts and their pre-Russian cultures are recognizable today and prehistorically, could mean that they were also distinctive even earlier in Late Pleistocene times as well, and would have served as incubator habitats for some amount of pre-Beringian biocultural and linguistic differentiation.
4. *No genetic bottlenecking at Panama*: Because there are few dental differences between North and South American Indians, again, relative to the smaller area of eastern Asia, it would appear that there was no meaningful Paleo-Indian genetic bottlenecking in Panama. The size of the Paleo-Indian population wave that advanced through the isthmus was large enough to contain a representative sample of the North American Indian dental gene pool. A trait-by-trait comparison of presumed North and South American Paleo-Indians (Turner 1992a) turns up no differences greater than the within-continent range of trait occurrence. However, as is well known from various studies of blood group and DNA markers (Spuhler 1979; Szathmary 1979; Shields et al. 1992), the initial Paleo-Indian gene pool probably did not contain as representative a sample of Chukotka genes, let alone the Pan-Northeast Asian gene pool. For example, allele B of the ABO system was seemingly not carried across the Bering land bridge by Paleo-Indian

colonists, and the three-rooted lower first molar gene(s) was carried by only a small proportion of the first Beringian migrants.

5. *South America colonized soon after North America*: In 1976, MacNeish suggested that North America was populated for some 100,000 years, while South America had been inhabited for only 25,000 years. Had this been the actual occupational history of the New World, and if continuous occupation and regular postcolonization dental microevolution are assumed (Turner 1986), then the North American samples should have exhibited in ➲ *Figure 20.3*, on the basis of time alone, about fourfold more internal dental divergence than do the samples from South America. That is, the secondary branching in North America should be much further to the left compared with South America. The dendrogram provides no support for unequal evolutionary time in North and South America, nor do the individual trait values in ➲ *Table 20.1*. Admittedly, variation in the rate of dental microevolution, connected as it surely must be to population structure, size, and demography, does not allow precise estimates of separation between branching populations, in this case North and South America. However, claims for 25,000–30,000 years of South American occupation are certainly pushing the envelope of credibility on the basis of both New World and Old World dental evolutionary considerations and most archeological evidence (Lynch 1991; Haynes 2002a; Fiedel 2004). In the Old World it is a question of antiquity of Sinodonty, which I suspect is around whatever age is finally agreed upon for the Upper Cave teeth, so far ranging between 11,000 and 30,000 years BP (Chen et al. 1992).
6. *Individual dental trait frequencies show only random variation.* Comparisons of the means for North and South American dental trait frequencies (➲ *Table 20.1*) show no identifiable trends that could be attributed to multiple migration, differential geographic selection, or some other type of localized natural selection directly affecting teeth. While these samples are not ideal for rigorously assessing the likelihood of selection pressure, the more obvious possible correlates are absent. Hence, the dental samples of the South American Pacific coastal populations of Chanduy-Valdivia, Santa Elena, Paloma, Peru, and Chile are not especially similar according to the analysis in ➲ *Figure 20.3*. These groups might be expected to be relatively similar due to some form of coastal environmental selection, but if this were so, then they should have also incorporated the coastal Sambaqui of Brazil.

   Samples from upland environments are not any better correlated than the coastal groups. Mountain-plateau-originating Grasshopper and Point of Pines 1 are linked to coastal Peru. Mountain-located Cotocollao clusters with coastal-lowland Panama. High rainfall and tropical coast Sambaqui folk are multivariately linked to low rainfall Arizona plateau Chavez Pass. The two long-lasting deep-winter Archaic Canada and Iroquois samples are joined, but their link with Coahuila from the cool winter high desert of northern Mexico does not suggest cold selection. Only city state organization versus noncity state seems to be a source of possible selection. Thus Tlatelolco, a late and large central Mexican Aztec metropolis, clusters with the similarly developed Peruvian samples. Their clustering together may be the result of oral and other disease selection associated with agricultural economies and highly processed cereal and tuber foods. However, if caries selection had been responsible, then city state-level Tlatelolco and Peru should have higher frequencies of simpler and potentially more caries-resistant teeth, such as 4-cusped lower second molars, less shoveling, and fewer first molar cusps 6, which is not the case for either sample. Still, disease selection needs further study with respect to dental morphology because caries are rare in hunters and gatherers but very common among agriculturalists.

7. Only Sinodonty is present in the New World.

   a. Shoveling: *Figure 20.4* illustrates upper central incisor shoveling. *Tables 20.1* and *20.2* show crown and root trait frequencies within

Figure 20.4
Circum-Pacific and European frequencies of upper central incisor shoveling

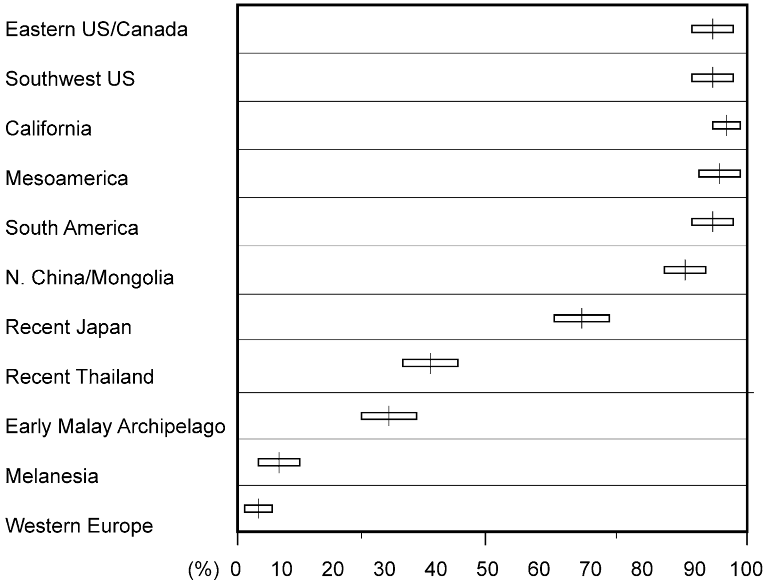


Table 20.2

World dental frequency variation for the eight distinguishing Sinodont and Sundadont morphological traits[a]

Trait tooth Break point	Shovel UI1 2-7/0-7	Double-shovel UI1 2-6/0-6	1-root UP1 1/1-3	Enamel extension UM1 1-3/0-3
Arctic[b]	78	75	95	46
Eastern USA and Canada	91	78	80	31
SW USA	91	65	89	51
California	98	90	84	42
Mesoamerica	94	93	89	39
So. America	92	90	87	49
No. China-Mongolia	84	30	77	51
Recent Japan	66	20	75	55
Recent Thailand	37	9	66	39
Early Malay Archipelago	30	28	68	18
Melanesia	9	5	57	4
Australia	20	1	58	9
West Europe	2	4	58	2

Trait tooth Break point	Peg-Reduced-C.A. UM3 prc/norm+prc	Deflecting wrinkle LM1 1-3/0-3	3-root LM1 3/1-3	1-root LM2 1/1-3
Arctic[b]	20	30	30	31
Eastern USA and Canada	18	45	6	32
SW USA	21	35	6	29
California	17	45	6	32
Mesoamerica	19	28	6	29
So. America	25	38	6	37
No. China-Mongolia	53	29	34	42
Recent Japan	42	35	24	33
Recent Thailand	18	19	11	31
Early Malay Archipelago	0	11	6	33
Melanesia	13	18	3	5
Australia	5	23	5	6
West Europe	12	7	1	27

[a] Individual count, sexes pooled, historic and prehistoric native groups, sample provenience, and break points detailed in Turner (1985) and elsewhere.

[b] Unpublished new grouping contains Aleut, Eskimo, Greenland Eskimo, Alaska Peninsula, Bering Sea, Kachemak, and Kodiak (computer file name: Arctic94).

U denotes upper; L, lower; CA, congenital absence.

the Americas, eastern Asia, Melanesia, Australia, and western Europe. Shoveling is very common throughout the Americas and in Northeast Asia. There is no significant difference in the shoveling frequencies of North America (91.7%) and South America (91.9%). It is less common in Southeast Asia, Australia, much less so in Melanesia, and very rare in western Europe. This trait alone shows that Paleo-Indians more likely originated in the north China-Mongolia gene pool than in those of the other areas. That gene pool, in turn, had to have had its morphogenetic origin in the Sundadont dental pattern of Southeast Asia and South China—the closest dental pattern in the world to Sinodonty. Clearly, Paleo-Indians did not originate in Europe, Oceania, or Southeast Asia according to the distribution of the incisor shoveling genes. The African dental pattern is too different from that of Sinodonty to be considered relevant to Native American origins considerations (Turner 1992b).

The frequency of shoveling in the earliest North and South American crania is high (ca. 90.1%) (Turner 1992a p 18), nearly identical to that of recent populations (➲ *Table 20.1*). This apparent similarity is not what would be expected for the stated implication that the Kennewick skeleton was not a Sinodont (Powell and Rose 1999), as well as the claim that early South American skeletons were also not Sinodonts (Lahr 1995 p 163).

b. Enamel extensions: ➲ *Figure 20.5* shows the frequencies for the enamel extension polymorphism, a quasi-continuous trait found on the buccal surface of the upper first permanent molar. While shoveling might conceivably have some minor adaptive value (Mizoguchi 1985), it is difficult to imagine how selection could favor the tiny extension of enamel on the subgingival root surface. In fact, these smooth enamel extensions could have a slightly negative value because they do not provide a porous surface for periodontal tissue attachment, hence, favoring the formation of peridontal disease pockets in the adjacent alveolar bone. Enamel extension variation provides essentially the same frequency picture as shoveling; namely, extensions are common in Indians and Northeast Asian Sinodonts, slightly less so in Southeast Asian Sundadonts and very uncommon in Melanesians, Australians, and Europeans.

c. One-rooted upper first premolar: ➲ *Figure 20.6* shows the frequencies for the upper first (P3 in paleontological notation) premolar root number polymorphism, which can have one to three roots. As with the shoveling and enamel extensions, one-rooted upper first premolars are common in Northeast Asian Sinodonts and all pre-Columbian Indians, less common

Figure 20.5
Circum-Pacific and European frequencies of upper first molar enamel extension

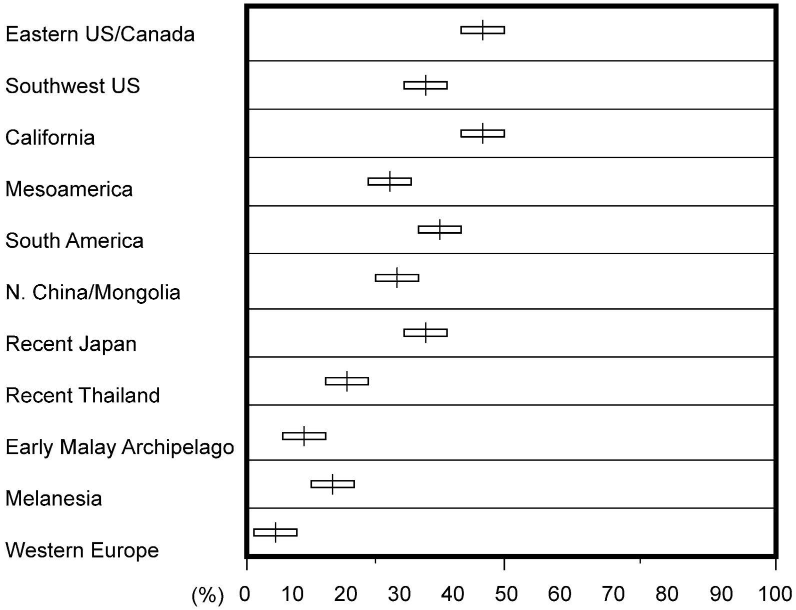
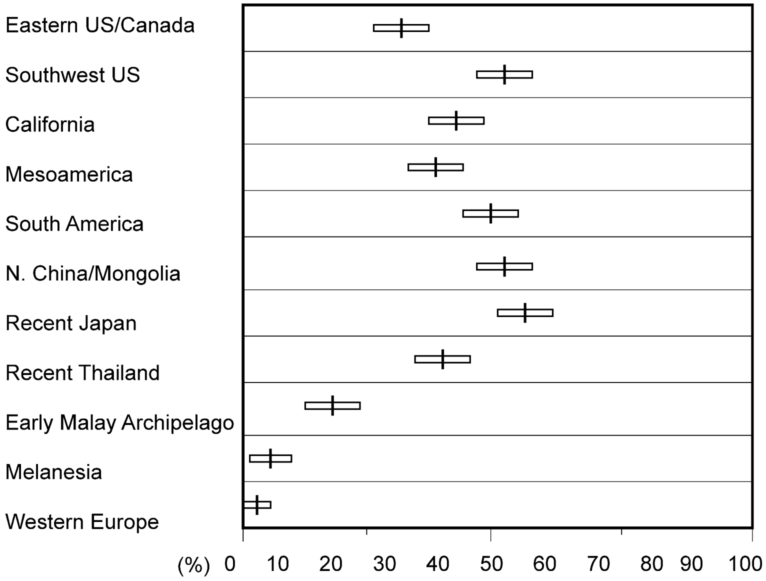


Figure 20.6
Circum-Pacific and European frequencies of one-rooted upper first premolars (P3)



in Southeast Asian Sundadonts, and slightly less common in Melanesians, Australians, and western Europeans. While there is less continental Old World and South Pacific islander occurrence of one-rooted upper first premolars, there is nothing in the data to suggest that American Indian ancestry was anything other than from Northeast Asian Sinodonts.

d. Deflecting wrinkle: *Figure 20.7* shows the frequencies of another tiny secondary trait, the first permanent molar deflecting wrinkle. This polymorphism is the degree of distalward deflection from none to pronounced of the medial ridge of cusp 2 (mesiolingual cusp). This feature has almost no potential for adaptation as it is usually worn off the first molar by the beginning of reproductive age. The deflecting wrinkle is common in pre-Columbian American Indians and Northeast Asian Sinodonts. It is less frequent in Sundadonts and western Europeans. Melanesians and Australians are highly variable for the deflecting wrinkle, and the present Oceanic samples have a substantial frequency, fitting the geographic expectation of an old Southeast Asian origin for the ancestors of Pacific Islanders.

Figure 20.7
Circum-Pacific and European frequencies of lower first molar deflecting wrinkle

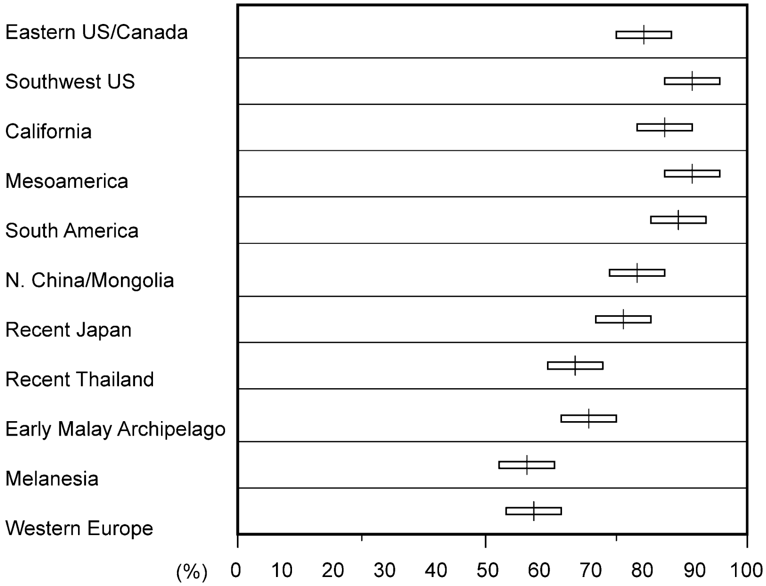
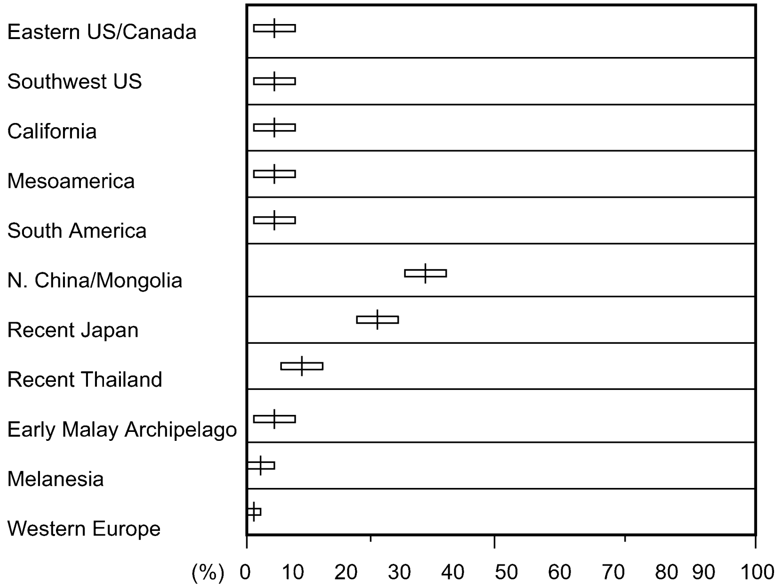


Figure 20.8
Circum-Pacific and European frequencies of three-rooted lower first molars



e. Three-rooted lower first molar: *Figure 20.8* shows the frequencies for the three-rooted lower first permanent molar, another root polymorphism with one to three possible roots. Lower molar and upper premolar root number are statistically unrelated morphogenetic features. By far, worldwide, the two-rooted condition is most common for the lower first molar root number. The oldest known example of a three-rooted lower first molar in anatomically modern humans is the 22,000-year-old mandible fragment from the Tabon Caves site on Palawan Island in the western Philippines, excavated by Fox (1970). The fragment has three root sockets at the first molar location. Three-rooted lower first molars are a Sinodont characteristic, but, like the missing B allele in living American Indians, Paleo-Indian colonists almost failed to carry to the New World the gene(s) responsible for this accessory root on the lower first molars.

20.5.2 Dentition supports Ice-free Corridor, epi-Clovis/Clovis first, and Macro-Indian models

Unlike the other dental traits discussed here, three-rooted lower first molar frequency is less than that of Northeast Asian Sinodonts, and this trait is generally uncommon although uniformly present at about 5% in pre-Columbian Indians. These characteristics imply two events. First, the initial number of Siberians to reach eastern Beringia was apparently small and not strongly representative for all genetic characters. Second, the trait's Panamerican uniformity suggests (1) that after crossing the ecologically patchy Bering land bridge, group size increased significantly because similar dental gene samples were carried southward to all other parts of the New World; and (2) all American Indians discussed here are descended from the founding Siberian epi-Clovis migrants whose archeological record for colonizing Alaska and Chukotka begins about 12,000 BP (Goebel et al. 2003). The demographic events of rapid population growth and widespread territorial expansion, leading to genetic stabilization in North and South America, could have occurred first in interior Alaska or later after subsequent generations reached and passed through the inhospitable and limiting corridor between the Cordilleran and Laurentide ice sheets of Canada. Unfortunately, there is nothing that we can identify in the dental data that helps us better understand where and how the rapid expansion began, regardless of how one defines migration (i.e., wavelike, pulsed, clonal spread, chaotic drift, niche-based, continuous leakage, leap-frogging, etc.), or which migration route one chooses ("ice-free corridor," Pacific coast, ice-crossings and polar desert trek to Atlantic coast, or some combination of these). However, given the rarity of Paleo-Indian sites in Alaska, the recent Fairbanks and Brooks Range finds notwithstanding (West 1981, 1996; Powers et al. 1990; Hoffecker et al. 1993; Kunz and Reanier 1994; Yesner 2001; Yesner and Pearson 2002, others), we lean toward the demographic growth, related faunal extinctions (Martin 1990), and genetic drift stabilization as having explosively started at the southern exit of the western Canadian ice sheet corridor. We prefer the corridor entry over the coastal route because of the severe boating difficulty of getting past the Late Pleistocene glacial ice mass on and around the Alaska Peninsula (Elias 2002; Turner 2002; Hoffecker and Elias 2003). In contrast to the rarity of Clovis or Clovis-like fluted points along the entire Pacific coast of North America, Carlson (1991) identified at least 40 archeological sites in the ice-free corridor area of British Columbia and Alberta that had various types of fluted points.

Elsewhere the senior author (Turner 1992a) inventoried a number of dental observations from crania that were "candidates" for Paleo-Indian chronometric status. None of these incomplete individuals deviated from the Sinodont pattern. Since then, he has examined the teeth of four other crania that are dated as Paleo-Indian or Early Archaic. These include Sulphur Springs woman, excavated in southern Arizona by Waters (1986), Horn Rock Shelter double burial near Waco, Texas, and the Wilson-Leonard female, also from Texas (Young et al. 1987; Steele 1989; Steele and Powell 1992). These four also conform to the Sinodont dental pattern as best as can be determined given the considerable amount of tooth wear they and other hunter–gatherers worldwide exhibit.

Finally, some archeologists (reviewed in Dixon 1999; for opposition see Carlson 1991; Haynes 2002b) and geneticists (discussed previously) have argued for a Pacific coastal entry route to North and South America from Siberia despite the absence of archeological evidence for, and Alaska Peninsula glacial evidence against, such a route (Workman 2001; Turner 2003). Moreover, Macro-Indian language family distributions in the Americas, Penutian, for example (Ruhlen 2000), do not suggest Pacific coastal entry. As for dental morphology, the Pacific coast samples presented in *Table 20.1* show no sign of meaningful differences with interior samples as would be expected, had there been an earlier more Sundadont-like migration or a fourth American variant of Sinodonty.

20.6 Concluding discussion

In assaying the different types of biological data brought to bear on the peopling of the Americas, there are disagreements on the numbers of migrations and their timing, but there are many points of agreement as well. The homogeneity among American Indians indicated by dental morphology is paralleled by mtDNA and Y chromosome haplogroup data. The dentition shows a dichotomy between North American and South American Indians and this is also evident in genetic markers. Several studies critique the three migration model of Greenberg et al. (1986), but these often fail to include data on Eskimo-Aleut populations. If researchers argue that mtDNA and Y chromosome data support a position that Eskimo-Aleuts differentiated from American Indians after the arrival of a common ancestor in the New World, there are serious problems with their data sets (or the interpretation thereof). On the basis of teeth, nuclear markers, and even craniometry, Eskimo-Aleuts are consistently more closely aligned with recent Asian populations than are American Indians.

The placement of other northern groups, especially Na-Dene speakers, is a bit less certain than the Eskimo-Aleut case. Based on similarities in mtDNA, Shields et al. (1993) concluded that Eskimo-Aleuts and Athapaskans were very closely related, diverging from one another in the American Arctic as recently as 7,000 years ago. This same general position has long been advocated by Szathmary (1979, 1981, 1993; Szathmary and Ossenberg 1978) based on the variation in blood group and serum protein polymorphisms. Cavalli-Sforza et al. (1994) found Na-Dene groups fell between Eskimo-Aleuts and Amerinds in general. This intermediary position is also indicated by dental morphological variation (Turner 1985; Scott 1991; Scott and Turner 1997). When ancillary fields are taken into account, especially linguistics and archeology, it is hard to reconcile common origins for Eskimo-Aleuts and Na-Dene speakers in the Holocene. Even rare genetic markers speak against this purported tie—Albumin Algonkin (formerly Albumin Naskapi) is found in polymorphic frequencies in Athapaskans and Algonquians but not in Eskimos (Lampl and Blumberg 1979). Eskimos have the B allele and Subarctic Indians do not (Harper 1980). The Y chromosome haplogroup C-M130 has also been found exclusively in Athapaskan and Algonquian populations (Schurr 2004a).

The level of genetic diversity in the Americas has led some authors to conclude that the New World was peopled long before the Last Glacial Maximum, with many estimates exceeding 30,000 years BP. To a considerable extent, this flies in the face of what is known about the archeology of Siberia and Beringia, let alone Australia whose aborigines' biology, tools, and language have evolved so much that few resemblances remain with their Southeast Asian homeland. The New World founding population had to have been in place in northeast Asia before any groups could start budding off to colonize the Beringian landscape. In a recent synthesis of mtDNA and Y chromosome analyses, Schurr (2004a) proposes three major peopling events from Asia to the Americas: (1) the initial founding population in the Americas came from south-central Siberia and arrived in the New World between 20,000 and 14,000 cal year BP; given the presence of ice-sheets across the breadth of Canada, the route of this migration is presumed to be coastal; (2) a second migration, following an interior route, contributed to many of the populations of North and Central America; and (3) Beringian populations, including the ancestors of Aleuts, Eskimos, and Na-Dene speakers, came into New World following the Last Glacial Maximum.

Although Schurr's reconstruction parallels in a number of ways our dental findings, we still contend that the degree of dental differentiation in the New World favors a late entry model, a position more in line with current archeological knowledge (Haynes 2002a; Fiedel 2004) and some genetic studies (cf. Seielstad et al. 2003). In principle, we have no objection to an earlier date for the peopling of the New World. At present, however, we do not feel a case has been made for this position, especially in light of archeological success in Australia in finding very early sites by a much smaller number of archeologists and geologists (Jelinek 1992). If a coastal migration did take place, more evidence for this event is required. For example, of all the pre-Clovis archeological sites listed by Schurr (2004a) to support early entry, none are along the Pacific coast. Scholars will continue to find "pre-Clovis" sites and develop molecular clocks and models of linguistic differentiation that indicate early human entry into the Americas, but the final arbiter of dispersal will come from archeological sites that have excellent stratigraphy and no dating issues.

The dental characteristics of pre-Columbian American Indians easily fit with the hypotheses of a rapidly expanding, Clovis- or epi-Clovis first colonization event, long advocated by Martin (1990) and Haynes (1991, n.d.), and the Macro-Indian language evolution model developed by Greenberg (1990). Because all prehistoric and unadmixed living Native Americans, including Na-Dene Greater Northwest Coast and Aleut-Eskimo, only briefly discussed here, have the Sinodont dental pattern, it would seem that when a date for the emergence of full-blown Sinodonty in Asia is established with some certainty, then that will have to be the earliest possible date for the subsequent colonization of the Americas, assuming that early and late similarity actually means genetic continuity. Inasmuch as the Upper Cave crania seem to have a Sinodont dental pattern, then whatever date is finally settled on for that assemblage will provide a reasonable time estimate for the potential colonization of the Americas.

We focus on Upper Cave since there are only a few sites in Siberia with Late Pleistocene human remains. One, near Lake Baikal, called Mal'ta, seems to have European- rather than Asian-like teeth (Turner 1990b). Two sites west of Lake Baikal have physical anthropological signs of Mongoloid or Sinodonty. These are the Late Pleistocene Yenisei River sites in and near Krasnoyarsk. In the city is Afontova Gora, the river bank section from which came a fragment of a subadult frontal bone that the late Russian physical anthropologist Alekseev (1998) believed to have been Mongoloid because of the size and form of the adhering nasal bones. Upstream ca. 35 km (21 mi) is Listvenka, from which came a mandible of a child whose unerupted first molar is slightly more Asian than European in overall appearance. Hence, broadly speaking, the pre-Arctic ancestral homeland of Paleo-Indians must have been in north China, Mongolia, and southern Siberia. It is easy to envision the newly evolved Sinodonts quickly expanding into northeastern Siberia, after they succeeded in domesticating the dog for hunting and hauling, perhaps drifting north out of China via the Vitim River system. Since there were no known resident Siberians above the Arctic Circle, the ancestral Paleo-Indian northward drift would have been rapid, and without human resistance in Beringia, and equally so southward from eastern Beringia. Because the dental differences between the north China-Mongolia group and all unadmixed Indians is so small compared with the much larger difference between Northeast and Southeast Asians, we can only conclude that the relatively small amount of intra-trait dental variation within the New World reflects the simple evolutionary fact that Sinodonts have been in the Americas for a relatively short period of time, less time than it took for Sinodonty to evolve out of Sundadonty. Moreover, the colonists and their dogs were so reproductively successful that the usual genetic drift cause of short-term dental trait frequency change was reduced or negated by the large population size that quickly grew south of the east Beringian Arctic steppe. This evolutionary scenario, despite years of bioarcheological research, does not differ much from that first proposed on craniological grounds by Hrdlička (1925). While some readers may find such lack of theoretical and empirical change as unthinkable in the rapidly changing world of science, others, ourselves included, recognize it as a tribute to Hrdlička's empirical orientation, and one of the more probable scenarios in the complex world history of Late Pleistocene human microevolution and dispersal. For the present, Macro-Indian dental variation is not supportive of a Pacific coastal entry route to North and South America, leaving the late entry Ice-free Corridor model as dentally most parsimonious.

Acknowledgments

The dental data were collected with aid provided by the National Science Foundation, National Geographic Society, Arizona State University, IREX, US National Academy of Sciences, and the (former) USSR Academy of Sciences, including the Siberian Branch. Many of the data were collected with the help of Jacqueline A. Turner and Korri Dee Turner, with computer data processing by Linda S. Watson and Rhea Jacanin. Many individuals and institutions are represented, and each has been acknowledged in other publications. *Figures 20.1* and *20.2* were photographed with permission of the Departments of Anthropology, respectively, of the US National Museum of Natural History (Douglas Ubelaker) and the University of Alabama (Kenneth Turner).

References

Akazawa T, Aoki K, Kimura T (eds) The evolution and dispersal of modern humans in Asia. Hokusen-Sha Pub. Co., Tokyo, pp 415–438

Alekseev VP (1979) Anthropometry of Siberian peoples. In: Laughlin WS, Harper AB (eds) The first Americans: origins, affinities and adaptations. Gustav Fischer, New York, pp 57–90

Alekseev VP (1998) The physical specificities of Paleolithic hominids in Siberia. In: Derev'anko AP, Shimkin DB, Powers WR (eds) (Laricheva IP, trans) The Paleolithic of Siberia: new discoveries and interpretations. University of Illinois Press, Urbana, pp 329–335

Berry AC (1978) Anthropological and family studies on minor variants of the dental crown. In: Butler PM, Joysey KA (eds) Development, function and evolution of teeth. Academic Press, New York, pp 81–98

Berry AC, Berry RJ (1967) Epigenetic variation in the human cranium. J Anat 101: 361–379

Birdsell JB (1951) The problem of the early peopling of the Americas as viewed from Asia. In: Laughlin WS (ed) The physical anthropology of the American Indian. Viking Fund, New York, pp 1–69

Bonatto SL, Salzano FM (1997) Diversity and age of the four major mtDNA haplogroups, and their implications for the peopling of the New World. Am J Hum Genet 61: 1413–1423

Boyd WC (1950) Genetics and the races of man. Little, Brown and Company, Boston

Brace CL, Nelson AR, Seguchi N, Oe H, Sering L, Qifneg P, Yongyi L (2001) Old World sources of the first New World human inhabitants: a comparative craniofacial view. Proc Natl Acad Sci 98: 10017–10022

Brown MD, Hosseini SH, Torroni A, Bandelt H-J, Allen JC, Schurr TG, Scozzari R, Cruciani F, Wallace DC (1998) mtDNA haplogroup X: an ancient link between Europe/western Asia and North America. Am J Hum Genet 63: 1852–1861

Burnett SE, Irish JD, Fong MR (1998) How much is too much? Examining the effect of dental wear on studies of dental morphology. Am J Phys Anthropol Suppl 26: 115–116

Callegari-Jacques SM, Salzano FM, Constans J, Maurieres P (1993) Gm haplotype distribution in Amerindians: relationship with geography and language. Am J Phys Anthropol 90: 427–444

Cann RL (1988) DNA and human origins. Annual Rev Anthropol 17: 127–143

Carlson RL (1991) Clovis from the perspective of the ice-free corridor. In: Bonnichsen R, Turnmire KL (eds) Clovis: origins and adaptations. Center for the Study of the First Americans. Oregon State University, Corvallis, pp 81–90

Carter GF (1957) Pleistocene man at San Diego. Johns Hopkins Press, Baltimore

Cavalli-Sforza LL, Piazza A, Menozzi P, Mountain J (1988) Reconstruction of human evolution: bringing together genetic, archaeological, and linguistic data. Proc Natl Acad Sci USA 85: 6002–6006

Cavalli-Sforza LL, Menozzi P, Piazza A (1994) The history and geography of human genes. Princeton University Press, Princeton

Chen T, Hedges REM, Zhenxin Y (1992) The second batch of accelerator radiocarbon dates for Upper Cave site of Zhoukoudian. Acta Anthropologica Sinica 11: 112–116

Crawford MH (1992) When two worlds collide. Hum Biol 64: 271–279

Dillehay TD, Meltzer DJ (1991) The first Americans: search and research. CRC Press, Boca Raton, Florida

Dixon EJ (1999) Bones, boats, and bison. University of New Mexico Press, Albuquerque

Elias SA (2002) Setting the stage: environmental conditions in Beringia as people entered the New World. In: Jablonski NG (ed) The first Americans: the Pleistocene colonization of the New World. Memoirs of the California Academy of Sciences 27, San Francisco, pp 255–271

Eshleman JA, Malhi RS, Smith DG (2003) Mitochondrial DNA studies of native Americans: conceptions and misconceptions of the population prehistory of the Americas. Evol Anthropol 12: 7–18

Fiedel SJ (2004) The Kennewick follies: “new” theories about the peopling of the Americas. J Anthropol Res 60: 75–110

Forster P, Harding R, Torroni A, Bandelt H-J (1996) Origin and evolution of Native American mtDNA variation: a reappraisal. Am J Hum Genet 59: 935–945

Fox RB (1970) The Tabon caves: archaeological explorations and excavations on Palawan Island, Philippines. National Museum Monograph 1, Manila

Gladwin HS (1947) Men out of Asia. McGraw-Hill, New York

Goebel T, Waters MR, Dikova M (2003) The archaeology of Ushki Lake, Kamchatka, and the Pleistocene peopling of the Americas. Science 301: 501–505

Greenberg JH (1990) The American Indian language controversy. Rev Archaeol 11: 5–14

Greenberg JH, Ruhlen M (1992) Linguistic origins of Native Americans. Sci Am 267: 94–99

Greenberg JH, Turner II, CG Zegura SL (1986) The settlement of the Americas: a comparison of the linguistic, dental, and genetic evidence. Curr Anthropol 27: 477–497

Haeussler AMF (1996) Dental anthropology of Russia, Ukraine, Caucasus, Central Asia: the evaluation of five hypotheses for Paleo-Indian origins. Ph.D. dissertation, Department of Anthropology, Arizona State University, Tempe

Haeussler AM, Turner CG II (1992) The dentition of Soviet central Asians and the quest for New World ancestors. In: Lukacs JR (guest ed) J Hum Ecol (Special Issue) (Culture, Ecology and Dental Anthropology) 2: 273–297

Hall DA (2000) Charting a new era. Mammoth Trumpet 15: 1–7

Hammer MF, Zegura SL (2002) The human Y chromosome haplogroup tree: nomenclature and phylogeny of its major divisions. Annual Rev Anthropol 31: 303–321

Hanihara K (1968) Mongoloid dental complex in the permanent dentition. Proceedings of the VIIIth International Congress of Anthropological and Ethnological Sciences, Vol. 1. Science Council of Japan, Tokyo, pp 298–300

Hanihara K (1979) Dental traits in Ainu, Australian Aborigines, and New World populations. In: Laughlin WS, Harper AB (eds) The first Americans: origins, affinities, and adaptations. Gustav Fischer, New York, pp 125–134

Hanihara T (1991) The origin and microevolution of Ainu as viewed from dentition: the basic populations in East Asia, VIII. J Anthropol Soc Nippon 99: 345–361

Harper AB (1980) Origins and divergence of Aleuts, Eskimos and American Indians. Annual Hum Biol 7: 547–554

Harris EF (1977) Anthropological and genetic aspects of the dental morphology of Solomon islanders, Melanesia. Ph.D. dissertation, Department of Anthropology, Arizona State University, Tempe

Harris EF, Turner CG II (1974) Sjo-68 dental morphology and its bearing on the “dihybrid” theory of American Indian origins. Contributions of the University of California Archaeological Research Facility No. 22, pp 1–46

Hawkey DE (1998) Out of Asia: dental evidence for microevolution and affinities of early populations from India/Sri Lanka. Ph.D. dissertation, Department of Anthropology, Arizona State University, Tempe

Haynes Jr CV (1987) Clovis origins update. Kiva 52: 83–93

Haynes Jr CV (1991) More on Meadowcroft radiocarbon chronology. Rev Archaeol 12: 8–14

Haynes CV Jr (n.d.) Clovis progenitors: from Swan Point, Alaska to Anzick site, Montana in less than a decade? Manuscript in author’s possession

Haynes G (2002a) The early settlement of North America: the Clovis era. University of Cambridge Press, Cambridge

Haynes G (2002b) Reviews of bones, boats, and bison: archaeology and the first colonization of Western North America, by EJ Dixon; and The settlement of the Americas: a new prehistory, by TD Dillehay. North Am Archaeol 23: 72–78

Hoffecker JF, Elias SA (2003) Environment and archeology in Beringia. Evol Anthropol 12: 34–49

Hoffecker JF, Powers WR, Goebel T (1993) The colonization of Beringia and the peopling of the New World. Science 259: 46–53

Hooton EA (1930) The Indians of Pecos Pueblo. Yale University Press, New Haven

Hopkins DM (1982) Aspects of the paleogeography of Beringia during the Late Pleistocene. In: Hopkins DM, Matthews Jr, JV Schweger CE, Young SB (eds) Paleoecology of Beringia. Academic Press, New York, pp 3–28

Horai S, Kondo R, Murayama K, Hayashi S, Koike H, Nakai N (1991) Phylogenetic affiliation of ancient and contemporary humans inferred from mitochondrial DNA. Philos Trans R Soc Lond B 333: 409–417

Horai S, Kondo R, Nakasawa-Hattori Y, Hayashi S, Sonoda S, Tajima K (1993) Peopling of the Americas, founded by four major lineages of mitochondrial DNA. Mol Biol Evol 10: 23–47

Howells WW (1989) Skull shapes and the map: craniometric analyses in the dispersion of modern Homo. Papers of the Peabody Museum, Harvard University No. 79, Cambridge

Hrdlička A (1925) The origin and antiquity of the American Indian. Smithsonian Report for 1923, Publication No. 2778. Smithsonian Press, Washington, pp 481–494

Irish JD (1993) Biological affinities of late Pleistocene through modern African aboriginal populations: the dental evidence. Ph.D. dissertation, Department of Anthropology, Arizona State University, Tempe

Jantz RL, Hunt DR, Falsetti AB, Key PJ (1992) Variation among North Amerindians: analysis of Boas's anthropometric data. Hum Biol 64: 435–461

Jelinek AJ (1992) Perspectives from the Old World on the habitation of the New. Am Antiquity 57: 345–347

Jobling MA, Hurles ME, Tyler-Smith C (2004) Human evolutionary genetics: origins, peoples & disease. Garland Science, New York

Karafet TM, Zegura SL, Posukh O, Osipova L, Bergen A, Long J, Goldman D, Klitz W, Harihara S, de Knijff P, Wiebe V, Griffiths RC, Templeton AR, Hammer MF (1999) Ancestral Asian source(s) of New World Y-chromosome founder haplotypes. Am J Hum Genet 64: 817–831

Kohn LAP (1991) The role of genetics in craniofacial morphology and growth. Annual Rev Anthropol 20: 261–278

Kolman CJ, Sambuughin N, Bermingham E (1996) Mitochondrial DNA analysis of Mongolian populations and implications for the origin of New World founders. Genetics 142: 1321–1334

Kozintsev AG (1995) Where did the American Indians come from? Am J Phys Anthropol (Suppl) 20: 126

Krieger AD (1964) Early man in the New World. In: Jennings JD, Norbeck E (eds) Prehistoric man in the New World. University of Chicago Press, Chicago, pp 23–91

Kunz ML, Reanier RE (1994) Paleoindians in Beringia: evidence from Arctic Alaska. Science 263: 660–662

Lahr MM (1995) Patterns of modern human diversification: implications for Amerindian origins. Yrbk Phys Anthropol 38: 163–198

Lahr MM, Haydenblit R (1995) Traces of ancestral morphology in Tierra del Fuego and Patagonia. Am J Phys Anthropol Suppl 20: 128

Lampl M, Blumberg BS (1979) Blood polymorphisms and the origins of New World populations. In: Laughlin WS, Harper AB (eds) The first Americans: origins, affinities and adaptations. Gustav Fischer, New York, pp 107–123

Laughlin WS (1951) The Alaska gateway viewed from the Aleutian Islands. In: Laughlin WS (ed) The physical anthropology of the American Indian. The Viking Fund, Inc., New York, pp 98–126

Laughlin WS (1963) Eskimos and Aleuts: their origins and evolution. Science 142: 633–645

Laughlin WS (1966) Genetical and anthropological characteristics of Arctic populations. In: Baker PT, Weiner JS (eds) The biology of human adaptability. Clarendon Press, Oxford, pp 469–495

Laughlin WS, Harper AB (1988) Peopling of the continents: Australia and America. In: Mascie-Taylor CG, Lasker GW (eds) Biological aspects of human migration. Cambridge University Press, Cambridge, pp 14–40

Laukhin SA (1997) The late Pleistocene glaciation in the northern Chukchi Peninsula. Quat Int 41/42: 33–41

Lell JT, Sukernik RI, Starikovskaya YB, Su B, Jin L, Schurr TG, Underhill PA, Wallace DC (2002) The dual origin and Siberian affinities of Native American Y chromosomes. Am J Hum Genet 70: 192–206

Long JC (1993) Human molecular phylogenetics. Annual Rev Anthropol 22: 251–272

Lorenz JG, Smith DG (1994) Distribution of the 9-bp mitochondrial DNA region V deletion among North American Indians. Hum Biol 66: 777–788

Lorenz JG, Smith DG (1996) Distribution of four founding mtDNA haplogroups among Native North Americans. Am J Phys Anthropol 101: 307–323

Lorenz JG, Smith DG (1997) Distribution of sequence variation in the mtDNA control region of Native North Americans. Hum Biol 69: 749–776

Lynch TF (1991) Lack of evidence for glacial-age settlement of South America: reply to Dillehay and Collins and to Gruhn and Bryan. J Hum Evol 21: 261–273

MacNeish RS (1976) Early man in the New World. Am Sci 64: 316–322

Madsen DB (ed) (2004) Entering America: Northeast Asia and Beringia before the last glacial maximum. University of Utah Press, Salt Lake City

Malhi RS, Eschelman JA, Greenberg JA, Weiss DA, Schultz BA, Schultz Shook BA, Kaestle FA, Lorenz JG, Kemp BM, Johnson JR, Smith

DG (2002) The structure of diversity within New World mitochondrial DNA haplogroups: implications for the prehistory of North America. dAm J Hum Genet 70: 905–919

Martin PS (1990) 40,000 years of extinctions on the "planet of doom." Palaeogeogr Palaeoclimatol Palaeoecol 82: 187–201

Meltzer DJ (1993) Pleistocene peopling of the Americas. Evol Anthropol 1: 157–169

Merriwether DA (1995) Distribution of the four-founding lineage haplotypes in Native Americans suggests a single wave of migration for the New World. Am J Phys Anthropol 98: 411–430

Merriwether DA (2002) A mitochondrial perspective on the peopling of the New World. In: Jablonski NG (ed) The Pleistocene colonization of the New World. Memoirs of the California Academy of Science 27, San Francisco, pp 295–310

Merriwether DA, Hall W, Vahlne A, Ferrell RE (1996) mtDNA variation indicates Mongolia may have been the source for the founding population of the New World. Am J Hum Genet 59: 204–212

Mizoguchi Y (1985) Shovelling: a statistical analysis of its morphology. University of Tokyo Press, Tokyo

Mourant AE (1954) The distribution of the human blood groups. Blackwell Scientific, Oxford

Mourant AE, Kopec AC, Domaniewska-Sobczak K (1976) The distribution of the human blood groups and other polymorphisms. Oxford University Press, London

Müller-Beck H (1967) On migrations of hunters across the Bering land bridge. In: Hopkins DH (ed) The Bering land bridge. Stanford University Press, Stanford, pp 373–408

Neves WA, Pucciarelli HM (1991) Morphological affinities of the first Americans: an exploratory analysis based on early South American human remains. J Hum Evol 21: 261–273

Nichol CR (1990) Dental genetics and biological relationships of the Pima Indians of Arizona. Ph.D. dissertation, Department of Anthropology, Arizona State University, Tempe

Perzigian AJ (1984) Human odontometric variation: an evolutionary and taxonomic assessment. Anthropol 22: 193–198

Pope GG (1992) Craniofacial evidence for the origin of modern humans in China. Yrbk Phys Anthropol 35: 243–298

Powell JF (1993) Dental evidence for the peopling of the New World: some methodological considerations. Hum Biol 65: 799–819

Powell JF, Neves WA (1999) Craniofacial morphology of the first Americans: pattern and process in the peopling of the New World. Yrbk Phys Anthropol 42: 153–188

Powell JF, Rose JC (1999) Report on the osteological assessment of the "Kennewick Man" skeleton (CENWW.97.Kennewick). Internet Parknet

Powers WR, Goebel TE, Bigelow NH (1990) Late Pleistocene occupation at Walker Road: new data on the central Alaskan Nenana Complex. Curr Res Pleistocene 7: 40–43

Reidla M, Kivisild T, Metspalu E, Kaldma K, Tambets K, Tolk H-V, Parik J, Loogväli E-L, Derenko M, Malyarchuk B, Bermisheva M, Zhadanov S, Pennarun E, Gubina M, Golubenko M, Damba L, Fedorova S, Gusar V, Grechanina E, Mikerezi I, Moisan J-P, Chaventré A, Khusnutdinova E, Osipova L, Stepanov V, Voevoda M, Achilli A, Rengo C, Rickards O, De Stefano GF, Papiha S, Beckman L, Janicijevic B, Rudan P, Anagnou N, Michalodimitrakis E, Koziel S, Usanga E, Geberhiwot T, Herrnstadt C, Howell N, Torroni A, Villems R (2003) Origin and diffusion of mtDNA haplogroup X. Am J Hum Genet 73: 1178–1190

Roberts RG, Jones R, Smith MA (1994) Beyond the radiocarbon barrier in Australia. Antiquity 68: 611–616

Rogers RA, Rogers LA, Martin LD (1992) How the door opened: the peopling of the New World. Hum Biol 64: 281–302

Roychoudhury AK, Nei M (1988) Human polymorphic genes: world distribution. Oxford University Press, New York

Ruhlen M (2000) Some unanswered linguistic questions. In: Renfrew C (ed) America past, America present: genes and languages in the Americas and beyond. McDonald Institute for Archaeological Research, Cambridge, pp 163–175

Ruiz-Linares A, Ortiz Barrientos D, Figueroa M, Mesa N, Munera JG, Bedoya G, Velez ID, Garcia LF, Perez-Lezuan A, Bertranpetit J, Feldman MW, Goldstein DB (1999) Microsatellites provide evidence for Y chromosome diversity among the founders of the New World. Proc Natl Acad Sci USA 96: 6312–6317

Schanfield MS (1992) Immunoglobulin allotypes (GM and KM) indicate multiple founding populations of Native Americans: evidence of at least four migrations to the New World. Hum Biol 64: 381–402

Schurr TG (2004a) The peopling of the New World: perspectives from molecular anthropology. Annual Rev Anthropol 33: 551–583

Schurr TG (2004b) Molecular genetic diversity in Siberians and Native Americans suggests an early colonization of the New World. In: Madsen DB (ed) Entering America: Northeast Asia and Beringia before the last glacial maximum. University of Utah Press, Salt Lake City, pp 187–238

Schurr TG, Ballinger W, Gan YY, Hodge JA, Merriwether DA, Lawrence DN, Knowler WC, Weiss KM, Wallace DC (1990) Amerindian mitochondrial DNAs have rare Asian mutations at high frequencies, suggesting they derived from four primary maternal lineages. Am J Hum Genet 46: 613–623

Scott GR (1973) Dental morphology: a genetic study of American White families and variation in living Southwest Indians. Ph.D. dissertation, Department of Anthropology, Arizona State University, Tempe

Scott GR (1991). Continuity or replacement at the Uyak site, Kodiak Island, Alaska: a physical anthropological analysis of population relationships. University of Oregon Anthropological Papers 44, pp 1–56

Scott GR, Turner II CG (1988) Dental anthropology. Annual Rev Anthropol 17: 99–126

Scott GR, Turner II CG (1997) The anthropology of modern human teeth: dental morphology and its variation in recent human populations. Cambridge University Press, Cambridge

Scott GR, Turner CG II (n.d., in press) Dentition. In: Ubelaker D (ed) Handbook of North American Indians. Vol 3: Environment, origins, and population. Physical anthropology. Smithsonian Institution Press, Washington DC

Scott GR, Yap Potter RH, Noss JF, Dahlberg AA, Dahlberg T (1983) The dental morphology of Pima Indians. Am J Phys Anthropol 61: 13–31

Scott GR, Street SR, Dahlberg AA (1988) The dental variation of Yuman speaking groups in an American Southwest context. In: Russell DF, Santoro JP, Sigogneau-Russell D (eds) Teeth Revisited, Mémoires du Muséum National D'Histoire Naturelle C53. Brill Academic Publisher, pp 305–319

Seielstad M, Yuldasheva NS, Underhill P, Oefner P, Shen P, Wells RS (2003) A novel Y-chromosome variant puts an upper limit on the timing of first entry into the Americas. Am J Hum Genet 73: 700–705

Shields GF, Hecker K, Voevoda MI, Reed JK (1992) Absence of the Asian-specific region V mitochondrial marker in native Beringians. Am J Hum Genet 50: 758–765

Shields GF, Schmiechen AM, Frazier BL, Redd A, Voevoda MI, Reed JK, Ward RH (1993) MtDNA sequences suggest a recent evolutionary divergence for Beringian and northern North American populations. Am J Hum Genet 53: 549–562

Silva Jr, WA Bonatto SL, Holanda AJ, Ribeiro-dos-Santos AK, Paixão BM, Goldman GH, Abe-Sandes K, Rodriguez-Delfin L, Barbosa M, Pacó-Larson ML, Petzl-Erler ML, Valente V, Santos SEB, Zago MA (2002) Mitochondrial genome diversity of Native Americans supports a single early entry of founder populations into America. Am J Hum Genet 71: 187–192

Spuhler JN (1979) Genetic distances, trees, and maps of North American Indians. In: Laughlin WS, Harper AB (eds) The first Americans: origins, affinities, and adaptations. Gustav Fischer, New York, pp 135–183

Stanford DJ, Day JS (eds) Ice age hunters of the Rockies. University Press of Colorado, Niwot

Starikovskaya YB, Sukernik RI, Schurr TG, Kogelnik AM, Wallace DC (1998) MtDNA diversity in Chukchi and Siberian Eskimos: implications for the genetic history of ancient Beringia and the peopling of the New World. Am J Hum Genet 63: 1473–1491

Steele DG (1989) Recently recovered Paleoindian skeletal remains from Texas and the Southwest. Am J Phys Anthropol 78: 307

Steele DG, Powell JF (1992) Peopling of the Americas: paleobiological evidence. Hum Biol 64: 303–336

Steele DG, Powell JF (1997) Biological affinities of the oldest recovered North Americans: the Spirit Cave and Pyramid Lakes data. Am J Phys Anthropol Suppl 24: 218

Stone AC, Stoneking M (1993) Ancient DNA from a pre-Columbian Amerindian population. Am J Phys Anthropol 92: 463–471

Szathmary EJE (1979) Blood groups of Siberians, Eskimos, and Subarctic and Northwest Coast Indians: the problem of origins and genetic relationships. In: Laughlin WS, Harper AB (eds) The first Americans: origins, affinities, and adaptations. Gustav Fischer, New York, pp 185–209

Szathmary EJE (1981) Genetic markers in Siberian and northern North American populations. Yrbk Phys Anthropol 24: 37–73

Szathmary EJE (1993) Genetics of aboriginal North Americans. Evol Anthropol 1: 202–220

Szathmary EJE, Ossenberg NS (1978) Are the biological differences between North American Indians and Eskimos truly profound? Curr Anthropol 19: 673–701

Tarazona-Santos E, Santos FR (2002) The peopling of the Americas: a second major migration? Am J Hum Genet 70: 1377–1380

Torroni A, Schurr GG, Yang C-C, Szathmary EJE, Williams RC, Weiss KM, Wallace DC (1992) Native American mitochondrial DNA analysis indicates that the Amerind and the Nadene populations were founded by two independent migrations. Genetics 130: 153–162

Torroni A, Schurr TG, Cabell MF, Brown MD, Neel JV, Larsen M, Smith DG, Vullo CM, Wallace DC (1993) Asian affinities and continental radiation of the four founding Native American mtDNAs. Am J Hum Genet 53: 563–590

Torroni A, Neel JV, Barrantes R, Schurr TG, Wallace DC (1994) Mitochondrial DNA "clock" for the Amerinds and its implications for timing their entry into North America. Proc Natl Acad Sci USA 91: 1158–1162

Turner CG II (1983) Sinodonty and Sundadonty: a dental anthropological view of Mongoloid microevolution, origin, and dispersal into the Pacific Basin, Siberia, and the Americas. In: Vasilievsky RS (ed) Late Pleistocene and early Holocene cultural connections of Asia and America. U.S.S.R. Academy of Sciences, Siberian Branch, Novosibirsk, pp 72–76 [in Russian]

Turner CG II (1985) The dental search for Native American origins. In: Kirk R, Szathmary E (eds) Out of Asia: peopling the Americas and the Pacific. Journal of Pacific History, Australian National University, Canberra, pp 31–78

Turner CG II (1986) Dentochronological separation estimates for Pacific rim populations. Science 232: 1140–1142

Turner CG II (1987) Late Pleistocene and Holocene population history of East Asia based on dental variation. Am J Phys Anthropol 73: 305–321

Turner CG II (1990a) The major features of Sundadonty and Sinodonty, including suggestions about East Asian microevolution, population history, and late Pleistocene relationships with Australian Aboriginals. Am J Phys Anthropol 82: 295–317

Turner CG II (1990b) Upper Paleolithic Mal'ta child (Siberia). News from the Siberian Branch of the U. S.S.R. Academy of Sciences 2: 70–71 [in Russian]

Turner CG II (1991) The dentition of Arctic peoples. Garland Publishing, New York

Turner CG II (1992a) New World origins: new research from the Americas and the Soviet Union. In: Stanford DJ, Day JS (eds) Ice age hunters of the Rockies. University Press of Colorado, Niwot, pp 7–50

Turner CG II (1992c) The dental bridge between Australia and Asia: following Macintosh into the East Asian hearth of humanity. Perspect Hum Biol 2/Archaeol Oceania 27: 143–152

Turner CG II (1993) Southwest Indians: prehistory through dentition. Natl Geogr Res Exploration 9: 32–53

Turner CG II (2002) Teeth, needles, dogs, and Siberia: bioarchaeological evidence for the colonization of the New World. In: Jablonski NG (ed) The first Americans: the Pleistocene colonization of the New World. Memoirs of the California Academy of Sciences No. 27, San Francisco, pp 123–158

Turner CG II (2003) Three ounces of sea shells and one fish bone do not a coastal migration make. Am Antiquity 68: 391–395

Turner CG II Nichol CR, Scott GR (1991) Scoring procedures for key morphological traits of the permanent dentition: the Arizona State University dental anthropology system. In: Kelley MA, Larsen CS (eds) Advances in dental anthropology. Wiley-Liss, New York, pp 13–31

Turner CG II, Bennett BH, Burnett SE (n.d.) The effect of wear on scoring of dental crown trait occurrence and expression (in preparation)

Tyler DE (1998) Homo americanus: an original American species. Discovery Books, Ontario, Oregon

Wallace DC, Garrison K, Knowler W (1985) Dramatic founder effects in Amerindian mitochondrial DNAs. Am J Phys Anthropol 68: 149–155

Wallace DC, Torroni A (1992) American Indian prehistory as written in the mitochondrial DNA: a review. Hum Biol 64: 403–416

Ward RH, Frazier BL, Dew-Jager K, Paabo S (1991) Extensive mitochondrial diversity within a single Amerindian tribe. Proc Natl Acad Sci USA 88: 8720–8724

Ward RH, Redd A, Valencia D, Frazier B, Paabo S (1993) Genetic and linguistic differentiation in the Americas. Proc Natl Acad Sci USA 90: 10663–10667

Waters MR (1986) Sulphur Springs woman: an early human skeleton from southeastern Arizona. Am Antiquity 51: 361–365

West FH (1981) The archaeology of Beringia. Columbia University Press, New York

West FH (1990) Archaeology in the press: science misserved? Rev Archaeol 11: 25–32

West FH (ed) (1996) American beginnings: the prehistory and palaeoecology of Beringia. University of Chicago Press, Chicago

Williams RC, Steinberg AG, Gershowitz H, Bennett PH, Knowler WC, Pettitt DJ, Butler W, Baird R, Dowda-Rea L, Burch TA, Morse HG, Smith CG (1985) GM allotypes in Native Americans: evidence for three distinct migrations across the Bering land bridge. Am J Phys Anthropol 66: 1–19

Workman WB (2001) Reflections on the utility of the coastal migration hypothesis in understanding the peopling of the New World. Paper presented at the Alaska Anthropological Association, Fairbanks, March

Y Chromosome Consortium (2002) A nomenclature system for the tree of human Y-chromosomal binary haplogroups. Genome Res 12: 339–348

Yesner DR (2001) Human dispersal into interior Alaska: antecedent conditions, mode of colonization, and adaptations. Quat Sci Rev 20: 315–327

Yesner DR, Pearson G (2002) Microblades and migrations: ethnic and economic models in the peopling of the Americas. In: Elston G, Kuhn SL (eds) Thinking small: global perspectives on microlithization. Archeological papers of the American Anthropological Association No. 12, pp 133–161

Young D, Patrick S, Steele DG (1987). An analysis of the Paleoindian double burial from Horn Shelter No. 2, in central Texas. Plains Anthropol 32: 275–298

Zoubov AA, Haldeyeva NI (1979) Ethnic odontology of the U.S.S.R. Nauka, Moscow (in Russian)