

Human Variation in the Americas

The Integration of Archaeology and Biological Anthropology

Edited by
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12. Human Settlement in the New World: Multidisciplinary Approaches, the “Beringian” Standstill, and the Shape of Things to Come

David G. Anderson

As we have seen from the papers in this volume, understanding the colonization and subsequent occupational history of the Americas is a daunting task. The events that unfolded and the reasons for them appear to be far more complex and diversified than the stories or models we as practitioners of individual disciplines have typically been producing. Fortunately, our understanding is growing all the time, and while our explanations are becoming ever more complex and qualified, they also appear to be closer and closer approximations to what was likely actually happening, at least in some times and some places and for some processes. What may seem on first inspection to be a confusing picture is actually a marked improvement on the state of our understanding compared to even a few years and certainly a few decades ago. We continue to explore the same questions raised by Fewkes, Hrdlička, and their colleagues about the origin of and variation among New World peoples (Fewkes et al. 1912; Auerbach, Chapter 1), but as the papers in this volume have demonstrated, the data, methods, and theoretical approaches we now bring to bear on these questions are immense, well-grounded, and sophisticated, and our understanding is improving daily.

Perhaps the most obvious common thread among the papers in this volume is their multidisciplinary nature, drawing on the findings of a number of disciplines, most notably physical anthropology and archaeology, but also commonly involving research by linguists, geneticists, paleoenvironmental scientists, and other special-

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ists. Because of this, the need for synthetic and synergistic theoretically informed analyses capable of interrelating evidence from numerous sources is arguably the greatest challenge facing us if we are to arrive at satisfying descriptions of and explanations for the colonization and postcolonization settlement history of the Americas. Specialized analyses by scholars working on their own or as part of collaborative ventures will remain critical and comprise the vast majority of research undertaken, but the results of this work will need to be considered, integrated, and evaluated from broader and multiple geographic, temporal, theoretical, and comparative analytical perspectives (see also commentary by Sassaman, Chapter 13).

Studying the peopling of the Americas, however, is also a classic example of a scientific research endeavor in which evidence from diverse subdisciplines—and even from various investigators within a subdiscipline—has sometimes yielded divergent or overtly contradictory results. Examples of this—such as the results of morphometric and genetic analyses suggesting that the location of New World source populations may have been in southeastern, eastern, or northeastern Asia or that one or more populations or migrations are implicated in the colonization (cf. Chapters 2, 11)—are readily apparent in the papers in this volume. When archaeology is added to the mix, it is evident that we don't currently know where classic late Pleistocene stone tool technologies like Clovis or Nenana originated (Goebel 2004), and homelands much farther afield than eastern Asia for colonizing populations have been advanced and heatedly debated, such as western Europe (cf. Meltzer 2009 and Strauss et al. 2005; Stanford and Bradley 2002 and Bradley and Stanford 2004). Linguistic arguments have been raised in favor of both comparatively recent and much more ancient dates for initial human entry into the Americas (cf. Greenberg et al. 1986; Nettle 1999; Nichols 1990, 2002, 2008), and while both the archaeological and genetic records are also somewhat ambiguous on this question, a later rather than an earlier initial entry, after circa 20,000 cal yr B.P. rather than upward of 25,000 or more years B.P. appears to be gaining ground (Goebel et al. 2008; Meltzer 2009; see Chapters 2, 11; cf. Madsen 2004a; Stanford et al. 2005).

What are we to make of results that are incompatible and hence in apparent disagreement, and how are we to proceed when they occur? The papers in this volume, including the introductory and concluding commentaries, offer examples of how multidisciplinary scientific research endeavors are undertaken and how their results can indeed be integrated into a better overall understanding of the past. Some of the major themes explored in this manner, as well as strengths and weaknesses of these approaches, are discussed in what follows. I conclude with some thoughts on sources of New World founding populations and, specifically, whether, where, and how the so-called Beringian Standstill may have occurred.

Tracing Population Movement in the Americas

Several papers in this volume illustrate how multiple lines of evidence can be combined in the reconstruction of the rates and routes of past population movements or migrations, often generating new insights in the process. Kemp and Schurr (Chapter 2) summarize how different kinds of genetic evidence are

employed, often in a complementary and mutually reinforcing manner in such studies, including nuclear, mitochondrial, and Y chromosomal DNA. Genetic data, several papers in this volume demonstrate, are being used to explore a wide array of big picture type questions, such as (1) how the settlement of the Americas may have proceeded, both initially and in subsequent, post-initial colonization population movements (Kemp and Schurr, Chapter 2); (2) how agriculture may have spread into the Southwest (Watson, Chapter 6); and (3) how the highland empires in western South America expanded into coastal regions (Shinoda et al., Chapter 9). Explicit correlates or genetic signatures for rapid versus slower patterns of movement as well as for greater or lesser affinity are employed in these efforts, illustrating the potential of genetic information to inform on much more than ancestral descendant relationships. If haplogroups and subhaplogroups occur widely, for example, it implies fairly rapid movement (at least faster than the mutation rate) as opposed to the occurrence of “nested sets of variation” produced by slower patterns of movement (Kemp and Schurr, Chapter 2). The same distributions can also be used to explore interaction between different groups, complementing archaeologically based analyses of spatiality in mating network, interaction, or political relationships, that is, how and why human populations position themselves as they do on landscapes (e.g., Kelly 1995; Wobst 1974, 1976).

The widespread occurrence of mtDNA subhaplogroups across the Americas, for example, suggests that population dispersal occurred very quickly, although the distinctive variation found within specific regions also implies that what some authors have called “tribalization” or the formation of more-or-less endogamous cultures or populations occurred quite early on (after Kemp and Schurr, Chapter 2; Malhi et al. 2002; Torroni et al. 1993; Watson, Chapter 6). Similar patterning is observed in the archaeological record (Figure 12-1), where restricted distributions of particular projectile point types are observed soon after 12,900 cal yr B.P., following the demise of the widespread Clovis culture, patterning interpreted as evidence for the emergence of subregional cultural traditions (Anderson 1990, 1995; Meltzer 2003, 2004, 2009). Watson (Chapter 6) suggests the emergence of distinctive cultures in the Americas is related to geographic isolation and the relative proximity of groups to each other.

In something of a contradiction, the widespread occurrence of mtDNA haplogroups and subhaplogroups also appears due, at least in part, to interaction among New World populations over fairly large areas, regardless of how isolated the archaeological assemblages might appear (Kemp and Schurr, Chapter 2; Chatters, Chapter 3). Determining the extent and directions over which interaction occurred, several papers in this volume demonstrate, is clearly an area where archaeology and physical anthropology can productively work together. Indeed, the other discussant for this volume, my friend and colleague Ken Sassaman, has argued that prehistoric population movement should be considered commonplace in prehistoric North America, the rule rather than the exception, and that traditional models positing that the cultures in a given area reflect descent and diversification from a local Pleistocene age founding population are likely to be wildly unlikely (Sassaman 2010; Sassaman, Chapter 13). I agree, as have scholars in many parts of North America, as migration, population replacement, and the

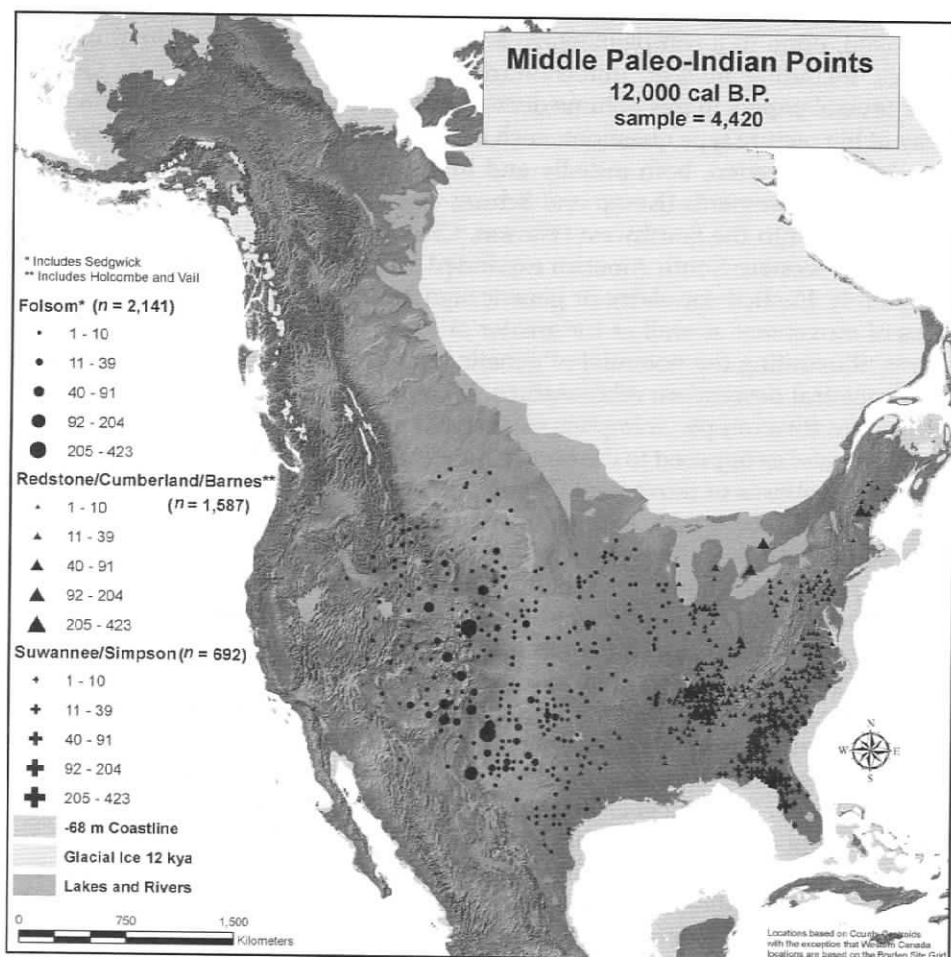


Figure 12-1. Subregional archaeological cultural traditions in the immediate post-Clovis period in North America, circa 12,850–12,000 cal yr B.P. (Image courtesy PIDBA [Paleoindian Database of the Americas, <http://pidba.utk.edu/>].)

abandonment and reoccupation of regions have again become acceptable phenomena for study (e.g., Anderson 1996, 1999; Anthony 1990; Cameron 1995; Lekson 1999, 2008; Pauketat 2007; Snow 1995, 2009; to cite a few of many such works). Too many archaeological analyses still never look beyond the site or locality, even though analyses of hunter-gatherer mobility and interaction indicate we should be thinking at much larger scales, encompassing large numbers of people over truly vast areas, and with population movement and replacement as likely as stasis and continuity (e.g., Kelly 1995:111–203; Wobst 1974, 1976). How regular and widespread gene flow was among culturally divergent populations would appear to be an ideal question to explore with genetic data in the Americas, as several papers demonstrate (e.g., Auerbach, Chapter 7; Shinoda et al., Chapter 9).

Other bioanthropological procedures used to explore important big-picture questions and employing archaeological, linguistic, or other lines of evidence include (1) the use of craniometric data to examine the possible spread of the Western Cordilleran cultural tradition into the Columbia Plateau during the Early Holocene (Chatters, Chapter 3); (2) the use of morphometric evidence to explore the emergence of distinct historical groups on the plains (Auerbach, Chapter 7); (3) the use of discrete dental traits to explore migration in the Southwest, in a test of one aspect of Lekson's (1999) "Chaco Meridian" argument that peoples from Chaco Canyon moved north to Aztec Ruins (Durand et al., Chapter 5); and (4) the use of genetic markers, discrete dental traits, molar wear angles, caries incidence, and other measures of skeletal biology and health to examine the spread of agriculture into the Southwest, and the changes that occurred in local populations following its adoption (Watson, Chapter 6). All of these studies made use of multiple lines of evidence, most commonly archaeological and physical anthropological data sets. When the results from individual analyses were not in agreement, decisions about which was more likely were typically based on the quality and preponderance of evidence (i.e., sample size, the number of different corroborating lines of evidence, how robust the analytical results were, and so on). Like Sassaman (Chapter 13), I accept that some kinds of evidence are more useful than others for resolving certain questions, but I remain sanguine, indeed unabashedly optimistic, about what we can learn using multiple approaches to the study of the past.

Physical anthropology, the chapters herein demonstrate, can sometimes provide direct evidence of population relationships that complement archaeological interpretations or clarify ambiguous or contentious archaeological results. The reaction of archaeologists in the Southwest to Lekson's (1999) arguments proposed in *The Chaco Meridian*, for example, has been decidedly mixed, with some scholars arguing that the meridional alignment of Chaco, Aztec, Paquimé, and other sites is due to chance and that no movements or relocations of peoples occurred between these centers. Lekson (1999, 2008:337–341), in contrast, thinks quite differently, arguing that the alignment of centers reflects direct interaction and population movements between these centers, albeit from one to another over time. In this regard, the bioanthropological evidence indicating that a direct movement of people apparently did occur between Chaco and Aztec Ruins (Durand et al., Chapter 5) shows that Lekson's argument has merit and that further aspects of it, such as the hypothesized movements of peoples to and from Aztec Ruin and Paquimé, or between other centers on the same meridian, are eminently testable.

Watson's (Chapter 6) examination of the spread of agriculture into the Southwest likewise serves as an excellent example of a well-integrated multidisciplinary approach that scholars in other regions should emulate. Archaeologists in many parts of the world have argued for generations about whether agriculture was adopted by indigenous groups, spread by the migration of peoples, or some combination thereof. A good way to begin to resolve the question, Watson notes, is to examine haplogroup frequencies and other bioanthropologically derived measures in pre-farming and initial farming populations and in any contemporary nonfarming neighboring groups (in addition, of course, to using other

lines of evidence). Such genetically based analyses should also prove useful to exploring language spread in various parts of the world. Diamond (1997, 2002), for example, has argued that demographic pressure led agriculturalists to expand, which is why the languages they spoke spread widely (see also Cavalli-Sforza 2003). Indeed, the distribution of dominant (in terms of numbers of speakers) languages or language families in the world reflects, in part, the spread of agricultural populations. Computer simulations can also prove useful in predicting and interpreting genetic data associated with possible population movements or differences to help take into account the effect of drift or low levels of gene flow (Cabana et al. 2008), among other things.

Of course, not all movement is unidirectional and long-distance. People move over the landscape all the time in the course of their normal subsistence pursuits and to exchange information, maintain mating networks, and familiarize themselves with resources in different parts of their normal ranges. Care must be taken to avoid confusing signatures of movement obtained from range mobility with outright migration or at least to recognize the possibility that hunter-gatherers can move over large areas and different habitats over the course of a year, a decade, or a lifetime (e.g., Binford 1983; Kelly 1995:111–160). Isotopic data can be used to determine homelands of origin, as in the famous case of the Amesbury archer found near Stonehenge, who originally appears to have come from central Europe (Fitzpatrick 2003; Richards 2007). Such analyses and interpretations, of course, can be complicated by many factors, including use of food sources that may themselves have come from long distances, such as anadromous fish (Cybulski, Chapter 4; see below).

Several of the studies in this volume, in fact, explore paleosubsistence practices and impacts using archaeological and bioanthropological data (e.g., Chatters, Chapter 3; Cybulski, Chapter 4; Watson, Chapter 6). Bioanthropological data, of course, has long been used to examine the impact of the adoption of agriculture on human populations. Conventional wisdom on this subject has it that only rarely have conditions improved for most people when this has occurred (e.g., Cohen and Armelagos 1984; Diamond 1987), although I personally think there is a lot to be said for the impact on human health of modern medicine, dentistry, or even clean water, some of the other things that resulted from agricultural food production and the generation of surpluses capable of supporting a wide range of specialists. The role foraging played in the transition—that is, how important wild resources continued to be—and how the adoption of agriculture influenced such things as gender and labor relations are considered less often but can be explored using a number of approaches, such as stable isotope analyses, molar wear angle, incidence of caries, robusticity, and other measures of relative health and diet (Watson, Chapter 6). That increased mechanical processing of agricultural foods can lead to changes in tooth wear angles and that wild plant foods with similar carbohydrate or isotopic signatures can mask the effects of the transition to agriculture are also things that researchers should routinely consider (Watson, Chapter 6). Finally, while one does not necessarily lead to the other, I find it interesting that relative skeletal health declined over the course of the Hohokam until the final collapse of this culture occurred

(Watson, Chapter 6). The success of complex organizational systems appears to some degree linked to the health of their constituent populations (e.g., Cohen and Armelagos 1984; Diamond 1987), a lesson we are not grasping very well in our own country at present.

Ecogeographic Variation in New World Populations

Several papers in this volume use morphometric analyses of skeletal or body proportions in conjunction with ecogeographic rules (Mayr 1956) to help determine the source populations of specific groups (Auerbach, Chapter 7) and New World populations in general (Jantz, Chapter 11; King, Chapter 10). That is, the settlement of the Americas would have likely resulted, over time, in clinal variation in body size, shape, or other characteristics (e.g., Auerbach 2007; Holliday 1997, 1999; Ruff 2002; Weinstein 2005:569), following classic ecogeographic rules like those of Bergmann (1847) and Allen (1877). Using the assumption that human morphology covaries with environment and length of settlement in that environment, several investigators have examined body shape and proportions to evaluate longevity of occupation in given regions and whether migration from elsewhere might have occurred (Auerbach 2007; Auerbach, Chapter 7; Jantz et al., Chapter 11; King, Chapter 10; Weinstein 2005). These kinds of analyses have generated useful insights about sources and rates of human movements in the Old World. Trinkaus (1981), for example, has demonstrated that the earliest Upper Paleolithic anatomically modern humans in western Europe exhibited morphological characteristics indicative of derivation from a warmer climate, probably Africa, and that over time these populations became increasingly cold adapted (see also Holliday 1997, 1999). Analyses of New World populations should, in a comparable fashion, provide clues about where their ancestral homeland(s) were located, provided they spent appreciable time there.

Recognizing ecogeographical patterning can prove difficult, however, for a number of reasons. What environmental variables should be considered, and how have these changed over the last few tens of thousands of years, globally and in specific regions? How does culture (i.e., things like clothing, use of fire, and type of shelter) influence thermoregulatory response? How long does it take human populations to respond morphologically to climate conditions and to climate change? Are skeletal samples dating thousands of years after colonization likely to exhibit the same patterning as those of initial immigrants? Analyses to date based in part on comparison with changes in Old World populations suggest that some characteristics, such as intralimb proportions, take a long time to change significantly, from many thousands of years to upwards of ten or twenty thousand years (Auerbach 2007; Auerbach, Chapter 7; Holliday 1997; Jantz et al., Chapter 11; Ruff 2002; Trinkaus 1981). Franz Boas's (1910, 1912) classic research with immigrants, in contrast, showed that some things, such as human cranial morphology, can change rapidly in response to new conditions, particularly diet (see discussion below). Human body size may also be linked to extent of population duration within specific physiographic regions, such as mountain ranges or

low-lying plains, and to warmer and colder or wetter and dryer climates, particularly if studies from other species where such patterns have been observed can be applied to our own (James 1970; Trinkaus 1981:210).

However, the record from the New World on the subject of ecogeographic variation in human populations, as the papers in this volume indicate, is somewhat ambiguous and nowhere near as pronounced as observed in portions of the Old World (Auerbach 2007; Ruff 2002; Trinkaus 1981). This may be due to the much shorter time frame over which adaptation within our own species has played out in the New World as opposed to in the Old World, on the order of 20,000 as opposed to perhaps 150,000 or more years. Some patterns are evident, however. Auerbach (2007, Chapter 7) has argued that the New World colonizing population was “cold filtered” with wide bodies being one result. If so, this would suggest that the source populations for New World peoples spent appreciable time in a cold climate. Such an inference is plausible if their homeland was northeastern Asia and if the Beringian Incubation or Standstill (BIM/Standstill) described by Kemp and Schurr (Chapter 2; see discussion below) is correct, and the Standstill occurred in an area with a cold climate like Beringia during the last glacial period. King’s (Chapter 10) examination of postcranial variation in later Holocene North American populations was able to demonstrate fairly strong linkages between climate and morphology, indicating that New World/North American populations have also apparently undergone considerable adaptation to local climate conditions since colonization.

Jantz and his colleagues’ (Chapter 11) analysis of Boas’s modern body measurement data from native North American populations (Jantz 1995, 2003), in contrast, concluded that the sample provided little evidence for climate-linked patterning but instead reflected the colonization history of the continent. While regional clines in morphology were documented, these were mixed with regard to expectations based on ecogeographic rules, with the latitudinal occurrence of cormic indices¹ conforming to and mean shoulder breadth the opposite of expectations, with a further longitudinal component of trends from roughly northwest to southeast in these measurements (Jantz et al., Chapter 11; see also Auerbach and Ruff 2010). Ecogeographic factors, they argue, “have not had a significant impact on North American morphology, presumably because of limited time” and, more interestingly, that “limb proportions do not support long periods of cold adaptation in Native American ancestors” (Jantz et al., Chapter 11). Their analyses suggest instead that New World colonizing populations may have derived from more temperate climates or passed through a “warm filter” rather than developed over an extended period in a colder climate, as the BIM/Standstill and “cold filter” models suggest (although it should be noted that the BIM/Standstill model is actually neutral, save only in its name, as to where the colonizing populations actually “incubated”). The clinal distributions in morphological characteristics were used to suggest initial entry in the Pacific Northwest, followed by movement to the south and east (referencing Anderson and Gillam’s [2000] least-coast pathway analyses that suggest that dispersal in these directions is facilitated by physiographic features on the continental scale). The ultimate origins for New World populations were suggested to lie in mid- to lower-latitude Southeast

Asia, based on earlier craniometric studies (Jantz and Owsley 2001, 2005) and in part on recent analyses back plotting the ecological associations of Clovis sites to temperate portions of eastern Asia, suggesting early Paleo-Indian populations were better adapted to temperate than to arctic conditions (Gillam and Tabarev 2006; Gillam et al. 2007). If Jantz and colleagues' (Chapter 11) interpretations are correct, the "Beringian" part of the BIM/Standstill model may need to be renamed or at least acknowledge a different starting point for the populations that subsequently diversified (see discussion below).

Interestingly, Jantz and colleagues' (Chapter 11) analyses also examined modern Siberian body measurement data for comparative purposes and concluded that these populations exhibited more temperate body proportions, suggesting they hadn't been in Northeast Asia long enough to more fully adapt to the cold climate. This suggests that they, as well as the New World source populations presumed to have derived from them, likely came from somewhere else in the not-too-distant past, perhaps from farther south. Of course, the relationship of analyses based on measurements taken from living individuals as opposed to analyses of skeletal samples needs to be worked out (Auerbach and Ruff 2010). Ecogeographic patterning in the New World, it would appear, has been complicated by the comparatively short time since initial colonization and by subsequent population movements throughout prehistory (Auerbach 2007; Auerbach, Chapter 7; Jantz et al., Chapter 11). The research does highlight the critical importance of finding and examining early skeletal remains from both the New World and northeastern and eastern Asia.

Diet, Nutrition, and Warfare

Several case studies reported herein also show how other aspects of life—such as subsistence and warfare—are yielding new insights through the use of multiple analytical approaches, especially in times and places remote from ethnohistoric/ethnographic analogs (e.g., Chatters, Chapter 3; Cybulski, Chapter 4; Durand et al., Chapter 5; Watson, Chapter 6). Using analyses encompassing morphometrics, stable isotopes, and dental pathology, in conjunction with archaeological data, Cybulski (Chapter 4), for example, examines adaptations between different culture areas, the Northwest Coast and the Plateau, as well as within a culture area, the Plateau. Skeletal indications for watercraft use are more apparent in Northwest Coast populations, with greater use of plant foods relative to fish and animal protein inferred from higher caries rates among Plateau groups. In an important cautionary finding, anadromous sea fish consumption was shown to yield stable carbon isotope signatures suggesting appreciable consumption of marine resources by peoples located well inland; decreasing signatures for marine fish use with distance from the coast was also indicated (Cybulski, Chapter 4). Care must thus be taken to avoid inferring a coastal origin for peoples found in the interior if they consumed anadromous fish, as apparently initially happened with regard to the Kennewick remains; one way to do this, Cybulski shows, is to compare ancient skeletal samples with historically docu-

mented or modern samples of people from the same area whose dietary choices are well documented.

Multidisciplinary research can sometimes lead to surprising, indeed counterintuitive findings, as demonstrated by Schmidt and colleagues' (Chapter 8) examination of burial practices and remains in the later Archaic period American Midwest. Experimental studies showed there was a "right" way that was consistently employed to take body part trophies among local Archaic populations. These procedures, which were apparently different from butchering strategies employed with game animals, were in use for perhaps two thousand or more years, suggesting warfare was not intermittent or infrequent, but routinized, with specialized associated behaviors passed down from generation to generation. Our understanding of Archaic period warfare in the East has emphasized its presence, but evidence for its frequency has been more ambiguous (e.g., Dye 2009:61–67; Mensforth 2007:256ff; Milner 1999, 2004:46–47; Smith 1996). Schmidt and colleagues' (Chapter 8) analyses also showed that there were lengthy traditions as well as changes in the treatment of victims by aggressors and survivors alike over time. During the Archaic, at least in this part of the lower Midwest, trophy taking was fairly standardized, with most people, including victims, buried the same way. Victims of conflict in the Late Prehistoric era, in contrast, were subject to more diversified and seemingly more haphazard postmortem indignities and were sometimes placed in mass graves and given "less stylized treatment" than the burial treatment accorded individuals dying in times of peace. The treatment of victims over time, the example demonstrates, can be profitably evaluated and cannot be assumed to be consistent.

Craniometric Differences Between Earlier and Later New World Populations

A critical question touched on in several papers is why the earliest Americans were apparently morphologically quite different from later Holocene and modern Native American populations, particularly in craniofacial characteristics (see also Jantz and Owsley 2001, 2005). Small colonizing populations, founder effects, and genetic drift, as well as subsequent population movements all appear to have played a role (Auerbach, Chapters 1 and 7; Chatters, Chapter 3; Jantz et al., Chapter 11; King, Chapter 10). Chatters (Chapter 3), for example, argues that the hypothesized early Holocene Old Cordilleran expansion was one of many migrations from the north that resulted in the distinctive morphologies of later Holocene Native Americans and part of the movements that Sassaman (Chapter 13) argues had a major impact on cultural developments in the Eastern Woodlands, such as the rise of the Shell Mound Archaic.

The papers in this volume also highlight the fact that great care must be taken in interpreting craniofacial data. Human crania can be somewhat plastic in response to changes in diet and environment, as Boas (1912) first demonstrated. How "plastic" human crania are and the rates by which changes in morphology occur, in fact, remain a subject of some debate in physical anthropology (cf.

Gravlee et al. 2003; Powell 2005:232–236; Relethford 2004; Sparks and Jantz 2002, 2003; van Vark et al. 2003). While cranial plasticity clearly exists, however, no one today would argue that it completely erases the population structure and history information contained in cranial morphology. Softer diets and lower protein intake, brought about in part by increased consumption of small game and plant foods, may explain some of the differences between earlier and later New World populations (e.g., Chatters, Chapter 3; Sardi et al. 2006). Changes in craniofacial morphology were also likely accelerated when food-processing technologies like milling stones and ceramics came into widespread use and when domesticated plants appeared, reducing the need for more massive masticatory features. Likewise, the development of specialized stone tools reduced the need for the use of teeth as tools, producing a similar reduction (e.g., Brace 1962).

Even within our relatively small sample of early New World crania, however, appreciable variability is evident (González-José et al. 2008; Jantz and Owsley 2001, 2005). How much this reflects sampling variability, and perhaps the emergence of isolated populations in minimal interaction with one another, is unknown. Many of these specimens, including some of the best known like Kennewick or Spirit Cave, actually date up to several millennia after widespread archaeological evidence for settlement circa 13,000 cal yr B.P. (González-José et al. 2008; Meltzer 2009:175–181). Even given a small and fairly uniform founding population (itself something that is not too likely given the genetic variation evident in descendant populations), perhaps such morphological variability should not be too surprising, since it had thousands of years to develop. To effectively resolve questions about the affinities and morphological and genetic characteristics of the earliest Americans, including their relationship with later Americans, the analyses herein demonstrate that we need many more human skeletal remains, ideally with accompanying well-preserved genetic material, from the late Pleistocene of the Americas and Northeast Asia.

Implications of the Beringian Incubation/Standstill Model

Genetic evidence appears to be narrowing toward a robust and well-grounded consensus about when and from where the Americas were colonized: It took place sometime after 20,000 cal yr B.P., from a single source population located somewhere in eastern or northeastern Asia (e.g., Kemp and Schurr, Chapter 2; Tamm et al. 2007). The evidence from genetics, however, is at odds with current interpretations based on archaeological research, which has shown that multiple stone-tool industries were present in Northeast Asia, Alaska, and North America in the late Pleistocene and, hence, presumably reproductively more or less distinctive human populations as well (e.g., Goebel 1999, 2004; Goebel and Slobodin 1999; Goebel et al. 2008; Hamilton and Goebel 1999). Morphological analyses, in turn, particularly craniometric analyses have, as discussed above, somewhat controversially suggested that the earliest human populations in North America, so-called Paleoamericans were distinct from later Holocene and recent American

Indians (e.g., Jantz and Owsley 2001, 2005; Jantz et al., Chapter 11). Consideration of the Beringian incubation model, or BIM/Standstill, offers the opportunity to reconcile some of these and other apparent contradictions, as well as indicates how genetic and morphometric data can guide archaeological research.

What is the modern genetic consensus on the colonization of the Americas, and how does the BIM/Standstill hypothesis fit into it? Analyses of mtDNA mutation rates, as summarized by Kemp and Schurr (Chapter 2), indicate that New World populations apparently split from a single Old World source population comparatively recently, probably after circa 25,000 cal yr B.P., and whose modern descendants are located in the Lake Baikal/Altai mountain area of eastern Asia. Entry into the Americas occurred sometime afterward, probably between around 20,000 to 15,000 cal yr B.P. The difference between time of divergence and time of entry, on the order of 5,000–10,000 or more years, is because the populations that ultimately settled the New World were apparently genetically isolated from their Old World source population for a long period of time, sufficient for distinctive haplotype/lineage mutations to occur. This period of isolation has been called the Beringian Incubation or Beringian Standstill model, here shortened to BIM/Standstill (Kemp and Schurr, Chapter 2; Tamm et al. 2007). That isolation of the proto-Native American population *must have occurred* is apparently not in question among geneticists at present. A contrasting scenario, the “Direct Colonization Model,” no longer considered viable, held that New World populations moved into Beringia and beyond into the Americas with minimal genetic, and hence temporal, separation from their Asian source populations (Kemp and Schurr, Chapter 2).

What is remarkable about the BIM/Standstill model is how quickly it was replicated and essentially confirmed, with four major studies appearing within a few months of one another, encompassing mtDNA, Y chromosomal DNA, and autosomal marker studies (Achilli et al. 2008; Fagundes et al. 2008a, 2008b; Kemp and Schurr, Chapter 2; Kitchen et al. 2008; Tamm et al. 2007). This consensus among geneticists, of course, conflicts with arguments from linguistics, skeletal biology, and archaeology favoring multiple migration events, as well as linguistic and archaeological evidence and arguments, albeit some quite controversial, for a much greater antiquity for the peopling of the Americas. When evidence from differing disciplines or at least scholars is in significant disagreement, as it is with the peopling of the Americas, then we must either find a way to reconcile these differences or admit that something is not right and re-examine our fundamental assumptions (i.e., mtDNA mutation rates, language diversification rates, and archaeological evidence). Archaeological remains from earlier failed migrations (*sensu* Meltzer 1989) may, of course, still be found from peoples who entered the New World much earlier yet left no surviving genetic signatures. Unlike artifacts, though, people had to survive to pass on their language, suggesting that linguistic models used to advocate a very early entry, on the order of 30,000–40,000 years B.P. (e.g., Nichols 1990, 2002, 2008), need some rethinking. Specifically, if the genetic evidence holds up, and no archaeological evidence is found for occupations earlier than circa 15–20 k cal yr B.P., then New World languages must have diversified at a much faster rate than assumed in some models (e.g., Nettle 1999).

There are details to consider when using genetic evidence, of course. Are the mtDNA mutation rates well established and constant, or might they have been different or varied in the past? How long have the presumed source populations whose descendants are currently living in the Lake Baikal source area actually resided there?² Were they there since the Last Glacial Maximum (LGM) or earlier, or did they arrive from somewhere else in more recent times (i.e., from farther south in temperate Asia, perhaps pushed there in recent millennia by expanding agricultural populations)? Wherever the source populations were located, how and why did a subset of these people come to be isolated from the parent group for several thousand years? Why is there so little evidence for reverse migration, a backflow of people and mtDNA and Y chromosomal lineages into Asia early on, especially when it is clear that both cultural and genetic exchanges occurred later, including by modern Eskimos (Forsyth 1992; Karafet et al. 1997:307–309)? That is, why was the initial movement of people that resulted in the widespread settlement in the New World apparently only in one direction? Or are we simply not recognizing or missing the evidence that it was not? While the presence of fluted points in Alaska has been taken by some to be possible evidence for a “back-migration” of people, most likely Clovis and immediate post-Clovis hunter-gatherers living farther south, these technologies and hence presumably the people who made them did not get beyond the Seward Peninsula nor into Northeast Asia (Goebel and Slobodin 1999; Hamilton and Goebel 1999).³

At present there is no strong archaeological evidence for people living in or near Beringia, at least not in extreme Northeast Asia for many thousands of years prior to circa 14,000 or 15,000 cal yr B.P. (e.g., Goebel 2004; Goebel and Slobodin 1999), even though the genetic evidence indicates that a standstill or incubation interval did indeed occur.⁴ Assuming no flaws in the BIM/Standstill model develop (cf. Meltzer 2009:367, who remains properly cautious until more time has passed), *the challenge facing archaeologists is thus to determine where, when, how, and why the “standstill” or “incubation” took place.* Furthermore, if New World source populations were isolated prior to circa 15,000 cal yr B.P., it means the standstill also took place prior to the opening of the ice-free corridor in Canada, which was not traversable from circa 34,000 until sometime after circa 15,000 cal yr B.P., although movement along the intermontane valleys of the western Cordillera may have been possible somewhat longer, to perhaps 24,000 cal yr B.P. or slightly later, when this region too was closed by expanding ice sheets (Dyke 2004; Madsen 2004b:12; Mandryk et al. 2001). Glacial conditions thus all but ensure that human settlement of the Americas south of the North American ice sheets, if it initially occurred between circa 24,000 and 15,000 cal yr B.P., was almost certainly via a Pacific coastal route, which in turn means sophisticated watercraft had to have been used. This latter inference, fortunately, is not at all problematic, since extended maritime voyaging by our species dates well back into the last glaciation, and support for coastal entry using this technology has been mounting (Dixon 1999; Erlandson 2002; Fedje et al. 2004:120–123; Fladmark 1979; Madsen 2004b).

But where would be a favorable place for incubation or standstill to occur, and where would the use of boats have been likely? Several possibilities come to mind, including late glacial era Japan, the Russian Far East, and southern Ber-

ingian coastal regions and archipelagoes.⁵ Human use of the first two regions, apparently with a well-developed maritime adaptation, dates well back into the last glaciation, upward of 15,000 cal yr B.P., and they have indeed been suggested as possible source areas of New World populations (Dixon 1999; Fedje et al. 2004:135; Goebel 1999, 2004; Goebel and Slobodin 1999; Ikawa-Smith 2004; Madsen 2004b:6). The problem with areas to the south in the Russian Far East and Japan is that it is difficult to conceive how a long period of isolation from other human populations could have occurred, something essential for the BIM/Standstill to be viable. Coastal and indeed much of the now-submerged portions of Beringia, in contrast, offered a vast and potentially resource-rich area that may well have been sufficiently distant and difficult to access, providing the necessary isolation. Central Beringia certainly had to be negotiated to reach the Americas, either by land in the interior or by boat along the coast, barring movement exclusively along the Aleutian island chain. While the latter is a possibility, there were formidable water gaps between some of the islands in the Aleutians, even at the LGM, such as from western Kamchatka in the Gulf of Kamchatka/Ozernoi Gulf area and Ostrov Beringa and Ostrov Medneyy / the Medneyy Seamount (>75 km), and particularly between there and the seamount defined by the modern islands of Attu, Agattu, Alaid, Niski, and Shemya (>400 km), although beyond this part of the late Pleistocene Aleutians, islands—most appreciably larger and with more area available for colonization than at present—would have been fairly closely spaced all the way to the Alaska Peninsula and the continental mainland.

An easier and potentially environmentally far richer passage to the New World was available, however, a comparatively short distance to the north. The continental-scale Beringian landmass was exposed and accessible, and along its southern margins were a remarkable series of archipelagoes (Figures 12-2 through 12-7) that persisted for some ten thousand years following the LGM, with new islands and island chains appearing and disappearing as sea levels rose (Brigham-Grette et al. 2004:59; Erlandson et al. 2007, 2008:2234; Manley 2002). The existence of these archipelagoes was dramatically illustrated in a video by Manley (2002), showing the flooding of Beringia from circa 21,000 cal yr B.P. to the present in 1,000-year intervals, based on bathymetric data available at the time. The potential of southern Beringia for human settlement was evaluated in a subsequent paper by Brigham-Grette and her colleagues (2004:36–40, 57–61), who presented a figure created from Manley's video that included highlighted outlines of several of the larger islands present at six moments in time during the late Pleistocene and after, when sea levels were -120, -88, -77, -64, -54, and 0 meters below the modern stand (Brigham-Grette et al. 2004:38). Manley's video was developed from the 2001 version of the ETOPO2 database with elevation and bathymetric data from a two minute latitude-longitude grid (i.e., with cells ca. 3.7 km on a side) and approximately 1 meter vertical precision (U.S. Department of Commerce 2006; this is the most recent version of the database available online).

It is now possible to evaluate changes in topography, including the extent of the Beringian / Aleutian archipelagoes at higher resolution, employing the newly available ETOPO1 database employing elevation and bathymetric data from a 1-minute grid, with cells approximately 1.85 km on a side (Amante and Eakins

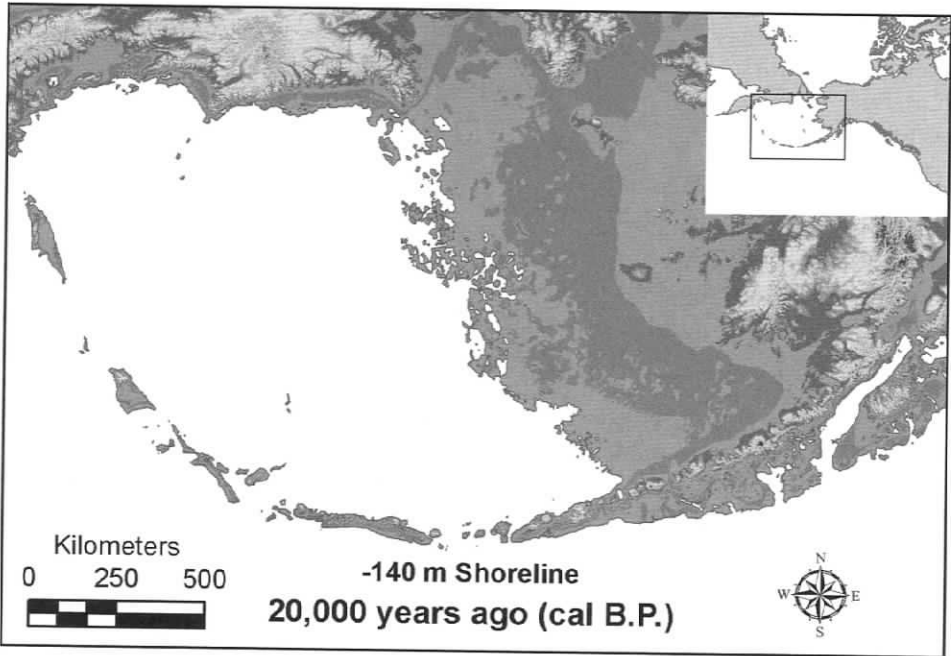


Figure 12-2. The island archipelago of southern Beringia and the Aleutians at circa 20,000 cal yr B.P.⁶

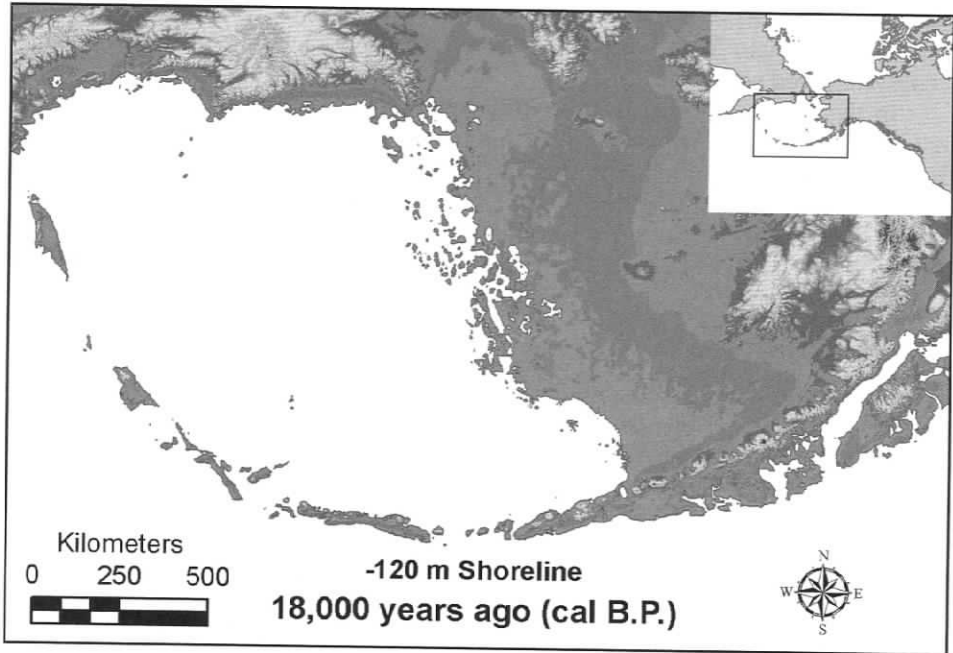


Figure 12-3. The island archipelago of southern Beringia and the Aleutians at circa 18,000 cal yr B.P.⁶

2009). Using Manley's (2002) depth values for global sea-level change for the Late Pleistocene, which correspond to reconstructions derived from multiple locations (Lambeck et al. 2002), it proved possible to use the ETOPO1 data to produce a series of maps (Figures 12-2 through 12-7) showing shorelines and land areas at circa 2,000 year intervals, from the LGM at circa 20,000 cal yr B.P. to the early Holocene at circa 10,000 cal yr B.P. (Anderson et al. 2010). Whether sea levels were at the exact elevations indicated on these maps at the specific moments indicated is debatable. As discussed by Brigham-Grette and colleagues (2004:36–40), well-dated sea-level curves need to be worked out for different parts of Beringia to control for isostatic and tectonic factors. Fortunately, corrected sea-level values for specific areas and times, once determined, can be fairly easily substituted into these maps. Regardless of precisely when sea levels were at the stands illustrated, there is no question that they were at these stands at some point in the Late Pleistocene, as sea levels rose from a low of perhaps -140 m at the LGM (Lambeck et al. 2002:358). What is apparent from inspection of these maps is that a remarkable number of islands were present along the southern margins of Beringia throughout the Late Pleistocene. These islands were closely spaced, furthermore, allowing for movement between them without likely losing sight of land. Movement could have proceeded to the southeast to the Alaska Peninsula, with people either looping around the peninsula and then heading back to the east and south along the Pacific Northwest coast or moving to the west out into the Aleutians. Both routes were likely taken once people reached the Alaska Peninsula. A route through the archipelagoes of southern Beringia and out into the Aleutians from the east likely would have been far less dangerous than crossing the Aleutian chain from west to east from Kamchatka, even during periods of greatly reduced sea level.

In the absence of much direct physical evidence, considerable uncertainty exists as to how productive those portions of the now-submerged Beringian landmass and coastal zones actually may have been to human populations. Up to several months of open water, free of sea-ice cover and a rich habitat for marine life, however, has been inferred to have been present on the southern Beringian coast during much of the last late glacial era, including during the LGM (Brigham-Grette 2004:59-61; Clague et al. 2004:82; Sancetta et al. 1985). As Erlandson and colleagues (2008:2234) note:

Once portrayed as a harsh and relatively unproductive area for human habitation (e.g., Hopkins et al., 1982), recent research suggests that the south coast of Beringia may have been "geomorphically complex during the late glacial, with hundreds of islands located just off a coast riddled with bays and inlets" (Brigham-Grette et al., 2004, p. 59). During the summer months, such convoluted coastlines—when combined with the low gradient of the Beringian platform—may have offered broad expanses of productive intertidal and near-shore habitats for early maritime peoples to hunt, forage, and gather in. Even covered with sea ice much of the year, the south coast of Beringia would have provided rich habitat for seals, walrus, and a variety of other marine organisms. Erlandson et al. (2007) have argued that much of Beringia's south coast may have supported productive kelp forests after the end of the LGM.

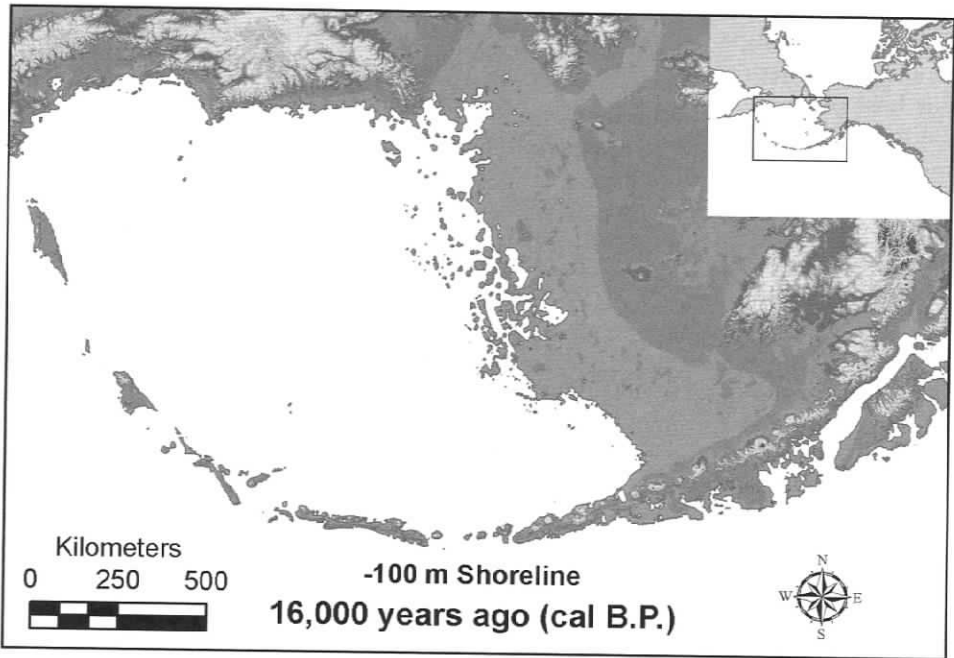


Figure 12-4. The island archipelago of southern Beringia and the Aleutians at circa 16,000 cal yr B.P.⁶

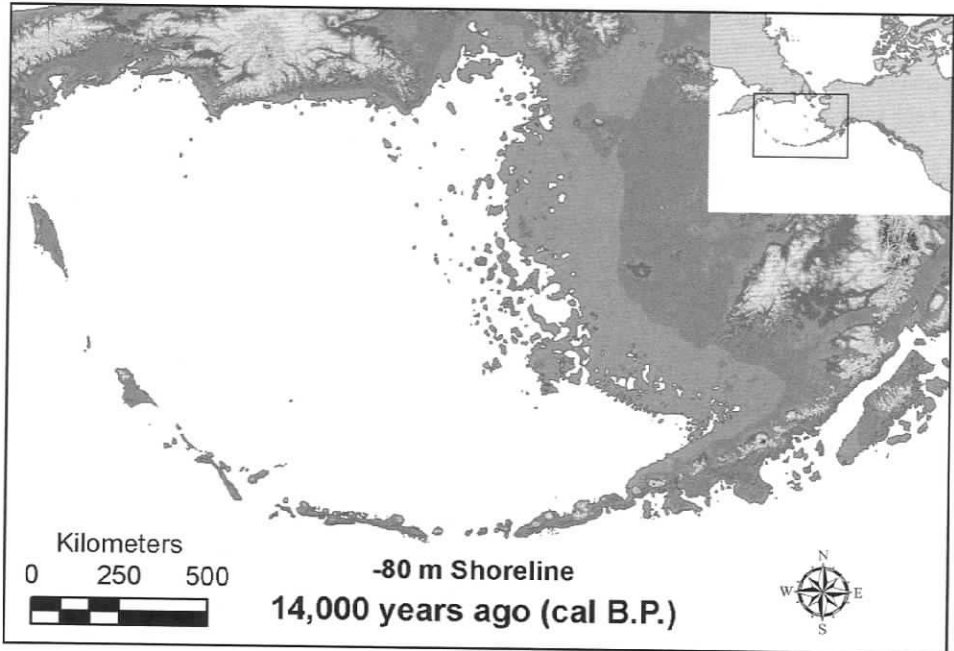


Figure 12-5. The island archipelago of southern Beringia and the Aleutians at circa 14,000 cal yr B.P.⁶

If southern Beringia's coasts and offshore islands were habitable, given the existence of precursor maritime populations in Japan and quite likely in the Russian Far East prior to 20,000 cal yr B.P., the island archipelagoes that existed on the southern coast of Beringia in the millennia prior to the flooding of the land bridge might well have been settled early on and could have served as an ideal habitat for human populations to exist, "incubate" and, indeed, thrive. The area, minimally, would have offered a navigable route into the Americas with numerous islands and bays along the way, obviating the need to make much if any use of the terrestrial resources of the Beringian continental landmass to the north and east.

Living in the potentially rich and diversified environments of the Beringian archipelago would have facilitated coastal migration and maritime adaptations, since watercraft would have been essential for survival in such a setting. As sea levels rose following the LGM, the location and extent of the islands in the archipelago and the shoreline of the larger Beringian landmass itself shifted dramatically over time (Figures 12-2 through 12-7), with new islands appearing as old ones were submerging (Brigham-Grette et al. 2004; Manley 2002). Living in such a habitat would have predisposed coastal migration, especially as sea levels rose and people were forced to move to other islands within the Beringian archipelago, and would have made feasible further movement to the south and west into the Aleutians and, ultimately, to the east and southeast along the northwest Pacific Coast.⁷ Given the numerous closely spaced islands revealed by the bathymetric data, furthermore, early populations could have island hopped much of the way from northern Kamchatka to the eastern Aleutians and only rarely been out of sight of land or another island. Movement very far inland on the Beringian landmass proper may not have been necessary or even attempted, if the numerous coastal bays and offshore islands proved to be sufficiently attractive habitats to sustain a maritime fisher-forager way of life.

Unfortunately, likely locations along the southern Beringian coast and coastal archipelagoes where hypothetical early Amerind precursor populations could have incubated are now submerged beneath some of the most treacherous waters on the planet. Archaeological verification of human settlement in this area, while feasible, would be challenging (e.g., Fedje et al. 2004; Josenhans et al. 1997). Deep-water surveys for LGM and later Pleistocene archaeological sites and shorelines have been considered or are under way in several locations, such as the eastern Gulf of Mexico, off Baja California, along the Pacific Northwest coast, and on the Atlantic continental shelf of eastern North America, but even in these locations the logistical challenges are daunting (e.g., Adovasio and Hemmings 2008; Faught 2004; Josenhans et al. 1997; Stright 1986).⁸

Alternate or indeed several incubator locations may exist, of course, such as somewhere in eastern Asia, in Alaska-western Beringia, in the Pacific Northwest, or even perhaps south of the North American ice sheets.⁹ LGM climate conditions appear to have been instrumental in creating the conditions necessary for population isolation and incubation. Subarctic eastern Siberia from around 55° to 65° N latitude was apparently colonized only after circa 30,000 cal yr B.P., and perhaps as late as circa 26,000 cal yr B.P. (Goebel 2004:319) and was largely depopulated after circa 22,000 cal yr B.P., during the LGM, "except perhaps in

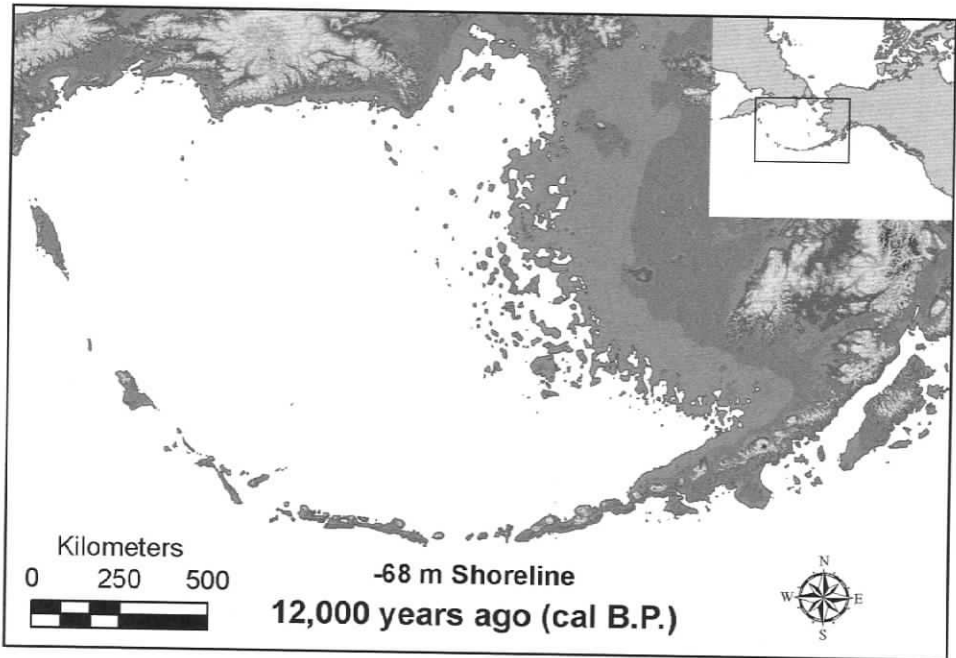


Figure 12-6. The island archipelago of southern Beringia and the Aleutians at circa 12,000 cal yr B.P.⁶

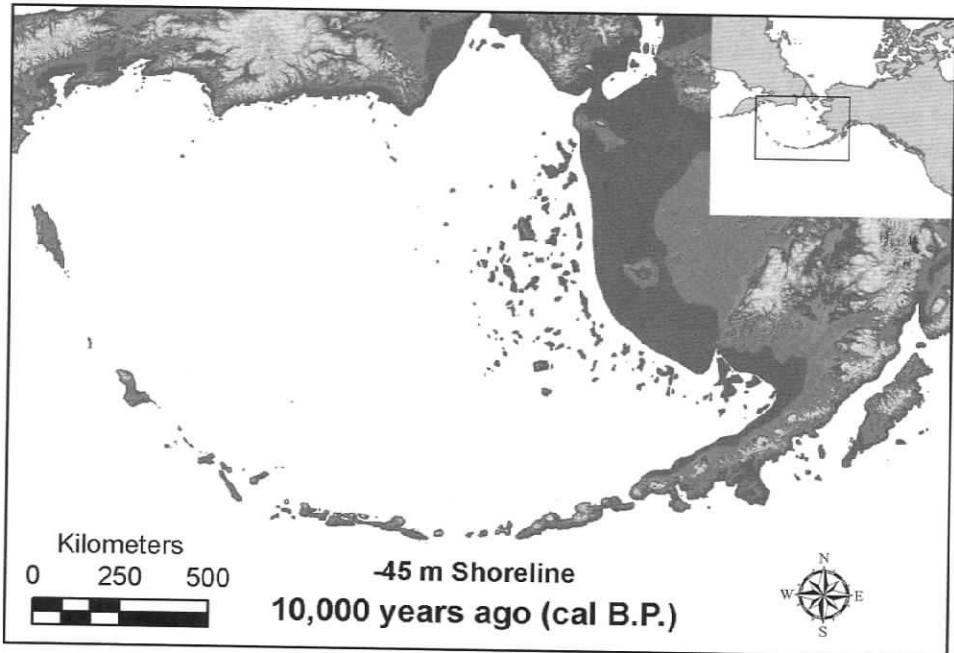


Figure 12-7. The island archipelago of southern Beringia and the Aleutians at circa 10,000 cal yr B.P.⁶

small refuges like the southern Yenisei or Transbaikal region" (Goebel 1999:222). The extreme cold not only likely resulted in Northeast Asian populations retreating south and eastward (Goebel 1999, 2004; Goebel and Slobodin 1999; Madsen 2004b:11) but would have also lowered sea levels (opening up new coastal habitats) as well as creating cold and ice-sheet barriers to movement. Whether human populations occupied coastal regions or the hypothesized interior refugia of Northeast Asia (and perhaps Alaska) during the millennia on either side of the LGM is unknown, but these are areas that, if settled, could have provided the time required of the BIM/Standstill model. The recolonization of northwestern Siberia after the LGM occurred fairly quickly, within a few thousand years, with human populations inferred to have reached Beringia by circa 14,000 cal yr B.P. (Goebel 1999:224; 2004:344; Goebel et al. 2003). Whether human populations reached or at least passed through Beringia earlier than this remains controversial, but movement along southern Beringia would appear likely given archaeological sites near the west coast of the Americas at this time, at Monte Verde, Chile, (Dillehay 1997, 2000) and possibly at Paisley Caves, Oregon, (cf. Gilbert et al. 2008; Goldberg et al. 2009; Poinar et al. 2009).

If the now-submerged coastal habitats in eastern Asia and southern Beringia were not where population isolation occurred, what would be the likely characteristics of other possible locations? First, they would have to be at some distance or separated by some barrier (i.e., ice sheets, mountains, ocean crossings) from the source populations, since the closer the incubating populations were, the greater the likelihood of gene flow back and forth, something that does not appear to have occurred (and why incubation in the Russian Far East or Japan appears improbable). Second, incubating groups likely stayed in environments they were familiar with, which if located in coastal settings may have precluded much likelihood of gene flow with their source populations if these were in the interior. But what about completely different possibilities? Could human populations have reached eastern Beringia or areas to the south prior to the LGM or been pushed there during the LGM as climate deteriorated? That is, could population refugia have been established earlier than currently thought in Alaska or in the Pacific Northwest, perhaps during the LGM or slightly earlier? Or could people have even made it south of the ice sheets prior to the LGM, as some archaeologists have controversially suggested (e.g., see summaries in Meltzer 2009; Stanford et al. 2005)? Admittedly, there is no convincing archaeological evidence in support of such inferences (Fedje et al. 2004; Goebel 2004; Goebel et al. 2008; Hamilton and Goebel 1999; Madsen 2004b), nor is it very likely that human populations could have existed for as long as 10,000 years in Alaska, in the Pacific Northwest, or south of the ice sheets without leaving a significant archaeological signature, given likely human population growth rates (Anderson and Gillam 2000; Bettinger and Young 2004; Fedje et al. 2004:132-135; Goebel 2004:354; Madsen 2004a:392-395). Resolving whether such scenarios are plausible will require far more research, and it is clear that archaeology—both on land in Northeast Asia and Alaska, as well as underwater along the submerged coasts and archipelagoes of eastern Asia, southern Beringia, and northwestern North America—will be essential to substantiating the argument for the BIM/Standstill model currently based on genetics.

The BIM/Standstill model, fortunately, does help reconcile some major problems and contradictions in existing arguments. For one, it provides more time for the linguistic diversity observed in the Americas to have developed. If Nichols (1990, 2002, 2008) is correct about the time it takes languages to diversify, than genes may not have been the only thing incubating: Languages might have been as well. The standstill also allows time for the so-called high-latitude cold or “germ filter” to develop, that is, to allow populations to shed at least some of their Old World disease burdens, albeit with tragic consequences millennia later once contact between the hemispheres was reestablished (Dillehay 1991; Stewart 1973:19–20). It also helps explain why archaeologists have so much trouble identifying New World progenitor technologies in eastern Asia and why such diversity in stone-tool industries exists across Beringia from circa 14,000 to 12,000 cal yr B.P., as is evident at the Denali, Nenana, and Dyuktai complexes and in the assemblages at Uski-1 and Ushki-5 in Kamchatka (Goebel 2004:353–356; Goebel and Slobodin 1999; Goebel et al. 2003). Extended isolation from the presumed eastern Asian source populations likely had an influence on other aspects of culture as well. Jomon pottery, for example, was being made in the Japanese archipelago and the Russian Far East at the same time that Clovis was radiating in North America (Kuzmin 2006; Lutaenko et al. 2007:362–364; Odai Yamamoto I Site Excavation Team 1999), but no evidence for ceramics has been found on New World Paleo-Indian sites. Finally the BIM/Standstill model gives ecogeographically linked human body characteristics more time to incubate, such as those presumably related to cold adaptation (e.g., Auerbach 2007; King, Chapter 10). Given what it helps explain, if the BIM/Standstill model had not been posited by geneticists, archaeologists might well have had to invent it themselves.

Conclusions: The Shape of Things to Come

Beyond valuable insights into particular research questions, the papers in this volume offer important lessons for researchers contemplating working with a wide array of data types. As Kemp and Schurr (Chapter 2) noted in their review of the history of mtDNA research, for example, a conscious attempt to simplify analyses led to a reduction in interpretive ability. Eliminating high-resolution sequencing precluded resolving variation within haplogroups, which was later shown to be critically important. Haplogroup X found in North American populations was initially assumed by some researchers to represent ancient European contacts with the Americas (e.g., Bradley and Stanford 2004; Stanford and Bradley 2002:265) yet, upon detailed analysis, was shown to be different from that found in western Europe (Derenko et al. 2001; Kemp and Schurr, Chapter 2). A similar situation was noted in skeletal studies (Durand et al., Chapter 5), where the analysis or consideration of more rather than fewer discrete dental traits was found to yield more satisfying analytical results. Data can always be removed from consideration, but it is better to have collected it in the first place whenever possible. The genetics example also shows that we don't always know what kinds of information might be important down the line. For

the future, doing more research and data collection would appear to be far better than doing less.

Another important lesson from this volume is that bioanthropological analyses can tell us incredibly valuable things about the past and answer major questions of broad interest to scholars and the general public alike, but only if we have the samples to work with. The amount of well-preserved Late Pleistocene human DNA and skeletal material available for examination from the Americas and from eastern Asia is small, which is unfortunate given how much can be learned from these remains. We need to become better at finding early human remains and at working with descendant populations to ensure access to those that are found. With regard to the first point, two examples from the southeastern United States indicate human remains might not always be where we expect to find them and that we need to cast our searches wider. The Late Paleo-Indian Dalton culture Sloan site in Arkansas, dating to circa 12,000 cal yr B.P., was a cemetery located on a sand dune well away from known occupation sites (Morse 1997). While the associated artifacts—hypertrophic Dalton points and other tools—are fairly well known in the central Mississippi Valley, no other burial areas like Sloan have been found, probably because neither archaeologists nor collectors spend much time looking in places where they don't expect to find things.¹⁰ The second unusual location in the Southeast where human remains were found was at the Windover site in Florida, a “subaqueous cemetery” with burials placed and in some cases staked down in a pond (Doran 2002). Fortunately, Windover is not unique, as several other similar submerged burial sites have been found in Florida, most dating from circa 10,000 to 7000 cal yr B.P. Of course, cultural practices in the past and present, such as the widespread use of cremation or scaffold burial, or the locations where archaeological research tends to occur can also skew sample availability. Well-preserved remains may just not exist from certain cultures, nor do archaeologists routinely look in some parts of the landscape, most notably in swampy terrain or water-saturated soils.

Finding ancient human remains is only part of the challenge; we must also be able to excavate and analyze them, which means we must work with and be considerate of the concerns of locally resident and presumed descendant populations (e.g., Fine-Dare 2002; Thomas 2000).¹¹ The papers in this volume provide excellent examples of what can be learned from the responsible study of human remains and can provide guidance in making the case for their examination when found. In the United States, collection and analysis protocols for presumed Native American human remains are shaped by the wording, implementation regulations, and legal decisions associated with the Native American Graves Protection and Repatriation Act (NAGPRA), as well as by state and local laws and regulations. If we are ever to understand the settlement of the Americas, cooperation with descendant populations must always guide our actions, and they must be the first peoples we inform when such remains are found. But we must also, as a last resort and when all else has failed, be willing to raise legal challenges when appropriate (cf. Kintigh 2004; Schneider 2004; Schneider and Bonnicksen 2005; Watkins 2004). In my opinion, human remains of Pleistocene age found in the Americas clearly meet such a threshold, that is,

where both full consultation as well as thorough analysis should occur. Given the likelihood that Pleistocene age human remains uncovered in the Americas may have no living descendants or descendants near where the remains were found, genetic and other bioanthropologically informed analyses would appear to be the logical and appropriate first step. While analyses directed to recovering DNA or isotopic data require destructive analysis, the samples involved are small compared with the information gained, to the point of becoming truly microscopic in some cases. Furthermore, many analyses, such as of skeletal morphology or discrete dental traits, are entirely nondestructive, an important consideration in the event that DNA and other analyses are precluded (Durand et al., Chapter 5).

Above all, the papers in this volume have shown that bioanthropological analyses can provide effective evidence where traditional archaeological signatures of relationship (i.e., basketry, pottery, architecture, specific stone-tool forms) are rare, lacking, ambiguous, or contentious, as in the case of population movements associated with the hypothesized "Chaco Meridian" (Durand et al., Chapter 5; Lekson 1999, 2008). The best analyses, we have seen, focus on important questions, bring together information and analyses from a range of sources, and produce results that help advance the theoretical foundations and interpretations of the subject matter under investigation. Of course, as Auerbach (Chapter 7) also notes, the "correlation of biological variation with cultural identity, let alone history, is problematic" and our inferences and models still all too often suffer from an oversimplification that does not accurately reflect the complexity of past behavior. We are outgrowing these limitations, however, as we come to view different kinds of evidence as complementary sources of information and insight. While the integration of different disciplinary theoretical perspectives, data sets, and analyses is far from perfect (see commentaries by Auerbach, Chapter 1, and Sassaman, Chapter 13), the papers in this volume demonstrate how consideration of skeletal biology, genetics, and archaeology can synergistically arrive at more complex and compelling models of the colonization and postcolonization history of the Americas. Let us all continue to work together to make it so.

Acknowledgments

I wish to thank Benjamin M. Auerbach for asking me to participate in the commentary on the papers in this volume. While I would have liked to attend the SIU Visiting Scholar Conference this volume is based on, that weekend I was attending "Early Paleoindian Colonization of the North American Midcontinent," a workshop at the University of Illinois Urbana-Champaign. Thanks also to my fellow discussant, Kenneth E. Sassaman, for his thoughts on these subjects, as well as to Ben Auerbach, Ted Goebel, Richard Jantz, and two anonymous reviewers for their comments on the draft manuscript. The maps of topographic change in the Beringian area in the late Pleistocene employing the ETOPO1 database were produced by informatics/GIS guru Stephen R. Yerka of the Archaeo-

logical Research Laboratory at the University of Tennessee. His help is deeply appreciated. Mary Lou Wilshaw-Watts did an excellent job editing the manuscript, and I appreciate the time and effort she put into improving my prose. Any errors or omissions are, of course, the responsibility of the author.

Notes

1. The cormic index, or sitting height to total height (SH/H), is a measure of trunk to leg length. The ratio is expected to be larger in cold-adapted and smaller in warm-adapted populations, following expectations for ecogeographic rules (see Jantz et al., Chapter 11).

2. Multidisciplinary research by the Baikal Archaeology Project, directed to documenting the Mid-Holocene record of hunter-gatherers of the Lake Baikal region, should help answer this question (e.g., Schurr et al. 2008; Weber et al. 2008).

3. While large bifaces are fairly common in northeastern Siberia, fluted points have not been found to date. The only example of such an artifact, a biface from the Uptar site in Siberia, has a “flute” that appears caused by impact damage, from the tip to the base, representing an accidental rather than an intentional production (King and Slobodin 1996; Meltzer 2009:189).

4. The Yana RHS site (ca. 28–25 rc yr B.P.) on the Yana River in Siberia near the Laptev Sea/Arctic Ocean—at 71° N latitude located well above the Arctic Circle and east of the Verkhoyansk Mountains in Siberia—is a possible exception (Meltzer 2009:189–190; Pitulko et al. 2004). Although located well to the west of extreme northeastern Asia, its presence demonstrates that people were able to live north of the Arctic Circle prior to the Last Glacial Maximum. The genetic differentiation postulated by the BIM/Standstill could have occurred among such northern populations, assuming they were indeed isolated from other groups, as might have happened during the LGM, and assuming they remained in the north instead of retreating southward. Where in the north they may have stayed is currently unknown, although herein I suggest the Beringian archipelago may be one possibility. Another, of course, would be Alaska, while a third possibility could be elsewhere in eastern Asia. A final possibility could be in the Americas themselves, south of the ice sheets, assuming a rapid movement from eastern Asia; there is little evidence to support this at present.

5. The inspiration for this idea comes from many sources that I have tried to acknowledge, but it is perhaps most explicitly stated in a paper by Fedje and his colleagues: “[W]e suggest that areas that were near-shore coastal archipelagoes during and immediately after the Last Glacial Maximum (LGM) might be key for early maritime-adapted peoples and therefore worthy of the most intensive investigation” (Fedje et al. 2004:135).

6. The island archipelagoes of southern Beringia and the Aleutians at various periods in the late Pleistocene and initial Holocene (based on sea-level data in Manley [2002] and Lambeck and colleagues [2002], bathymetric data from <http://ngdc.noaa.gov/mgg/global/global.html> [Amante and Eakins 2009], and a

mapping approach adapted from Manley [2002] and Brigham-Grette and associates [2004:38]).

7. Some human populations, of course, may have moved into the interior from these coastal habitats, colonizing central and northern Beringia, including interior Alaska. Such movement into the interior may have been prompted by fluctuating or rising sea levels, although if watercraft were present it may have been viewed as a last resort for these coastally adapted peoples.

8. As global sea levels rise in the decades and centuries to come, our profession should get better and better at examining underwater archaeological resources, assuming archaeology remains a priority in a civilization likely to be severely challenged by the flooding of so much densely occupied or farmed terrain (Anderson et al. 2007:15–18).

9. In his comments on this paper, Ted Goebel noted that central Alaska still remains the only area where late-glacial pre-Clovis sites have been found in eastern Beringia, like Swan Point and Broken Mammoth. He further suggested that, based on evidence for a surprisingly early opening of the Alaska Range passes into southern Alaska (Dyke 2004; England et al. 2006)—especially the pass connecting the upper Tanana and Copper River valleys—that the opening of an ice-free corridor along the Copper River drainage could have occurred prior to the opening of the western Canadian interior corridor. This would have given people a way out of the Alaskan interior to the coast at a very early date. That is, it is possible that the BIM/Standstill may have occurred in interior central Alaska, with people reaching the northern northwest coastal archipelagoes in the Gulf of Alaska region well before Clovis times, perhaps meeting groups moving into the area from the western Beringian and Aleutian archipelagoes or perhaps, if the first to reach the area, adopting their own maritime technology and moving onward on their own. Of course, and as Goebel also noted, a lot of archaeological and geological research will be needed to evaluate these arguments. Given the increasing numbers of apparent pre-Clovis sites in the Americas, it is even possible that a more southerly incubator may ultimately be considered feasible, rather than or in addition to one in central Alaska.

10. Unfortunately, “collectors” finding early cemetery sites like Sloan may be unlikely to report them, given the market value of the associated artifacts. Indeed, another unfortunate criterion influencing whether burials are likely to be preserved is whether they possess associated funerary objects of value to looters and traffickers in antiquities.

11. Determining who the descendants of a given sample or population are remains a major challenge that can often only be resolved with any degree of certainty by using physical anthropological evidence, such as discrete dental traits or genetic evidence. The 10,300 cal yr B.P. human remains found at On Your Knees Cave on Prince of Wales Island, Alaska, for example, were shown to represent a distinct and previously unknown haplotype of haplogroup D, whose closest genetic match in the Americas were the Cayapa of Ecuador (Kemp et al. 2007:616–617). The On Your Knees Cave analysis, coupled with the discovery of two circa 5,000-year-old individuals at the China Lake site in British Columbia possessing mtDNA haplogroup M, not found in modern New World populations

(Malhi et al. 2008), indicates that early settlers in the Americas were more genetically heterogeneous than once thought and that some of this early variation has been lost through the extinction of local groups at some time in the past. Some early populations in the New World, quite simply, may not have modern descendants, while others may have moved great distances from where their ancestors' remains occur.

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