

Probing deeper into first American studies

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The initial peopling of the Americas has proved one of the most challenging episodes in reconstructing global prehistory, challenging because researchers struggle with the vagaries of early archaeological site preservation, and debates continue over the date and place of human entry, the rapidity and direction of dispersion, and the variety of cultural responses to climatic change during the terminal Pleistocene period. Despite many recent advances in our understanding of these issues, especially in the areas of genetics and new archaeological discoveries, the field continues facing limitations in the sampling and quality of data, the research problems defined, and the epistemologies and theories applied. Theoretical development of first American studies has been uneven, and its contribution to global issues of early human migration has been restricted. This essay discusses what is known and not known about the process of the first peopling of the Americas from the perspective of archaeology, genetics, and bioanthropology. Some approaches to fill voids in data, methods, and the broader conceptualization of the process also are considered.

Of the possible entry routes into the Americas, Beringia, a land bridge from Siberia to the interior and coastal areas of Alaska and northwest Canada (1, 2), is the most viable. Entry from the Atlantic side of the hemisphere is a competing proposal (3, 4). Yet, Beringia was certainly used when Asians first colonized North America south of the ice sheets, probably between $\approx 20,000$ and 15,000 years ago (20.0–15.0 KYA refers to calibrated radiocarbon ages), after the maximum advance of the last glaciation. As more archaeological data are collected, researchers may learn that multiple migrations and multiple routes were used at different times by different peoples from different places. Although entry into the Americas is earlier than previously thought, the date is late compared with other areas of the world. But what makes the American entry unique is that within just a few millennia, people spread rapidly throughout previously uninhabited landscapes, establishing diverse lifestyles and broad-spectrum diets, including the domestication of plants. When did people first reach the interior regions of the Americas, and how did they come to settle them? These and other questions are crucial because they are connected to the general process of first entry and adaptive radiation of people in any part of the world. Understanding this process involves more than just finding archaeological sites, but also developing new questions and fresh interpretative approaches. It is beyond the scope of this Perspective adequately to summarize the information relevant to all new findings. Recent reviews have done this (1, 5). Instead, comments focus on some recent work that bears on new developments and on problems and prospects.

Success in understanding the problem of the initial peopling of any part of the globe largely depends on finding the

archaeological, genetic, and skeletal signatures of individual migrations and their singular contributions to adaptive radiation. This is not an easy task. Early sites and human skeletal material are difficult to find and are generally not well preserved. Older sites have been around much longer and are thus more prone to disturbance and loss of data than younger sites. Flooding, erosion, reoccupation by humans and other forces in the past and present destroy or alter sites. These sites also are generally smaller, thus making them more difficult to find, and are characterized by a very narrow range of cultural artifacts and internal site features such as hearths and activity areas. Most preserved artifacts consist of stone tools and the bone remains of large, extinct fauna, although there may be carbonized plant material, chemical residues of decayed matter, and other debris. As a result, archaeologists are forced to focus most of their attention on technologically distinct and temporally sensitive stone tools, usually projectile points in the Americas, and on the integrity and chronology of the archaeological record set in a geological context. In short, much of our knowledge of early sites hinges on the dating of artifacts and on determining the validity of their contexts.

Places of origin, dates of entry, routes of dispersion, and types of early cultural lifestyles lie at the heart of the debate over the initial peopling of the Americas. Fresh thinking about these and other issues has occurred because of the recent demise of the Clovis-first paradigm to explain the initial peopling of the Americas (2, 6, 7, 8) and because of new and more flexible interdisciplinary research directions. But, as with any paradigm shift, differences of opinion exist within and between archaeology, genetics, and bioanthropology about the implications of old and new findings and future research directions. In fact, there

was considerable disagreement among colleagues and anonymous reviewers commenting on this Perspective regarding the current topics of greatest importance to the initial peopling of the Americas.

Culture and Climate Change

An understanding of the first Americans begins with a consideration of the climate conditions they faced. Paleoenvironmental data accumulated during the past 2 decades show that between ≈ 16.0 and 12.0 KYA, climatic changes occurred that influenced the distribution of people and the specific kinds of habitats and resources they exploited (9, 10). The climatic and environmental conditions of the late Pleistocene in most areas of the world were different from those in later periods, with no climatic analogues in modern ecosystems. Mosaics of plant and animal species also were different from those of today. Megafauna were becoming extinct, extensive ice sheets in high latitudes and altitudes receded, and before 12.0 KYA, sea levels rose ≈ 100 m, and littoral zones were submerged. Many forest and other vegetated environments were considerably different in their floristic compositions when compared with those in the same areas today. There also is strong evidence indicating some environments were wetter (Great Plains, Southwest, Great Basin) and others drier (Amazon basin) than today. Also revealed by these data are the human modification of landscapes, such as the burning of vegetation (11, 12), overexploitation of animal resources, and the

Author contributions: T.D.D. designed research, performed research, analyzed data, and wrote the paper.

The author declares no conflict of interest.

This article is a PNAS Direct Submission.

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transport of plant species into new environments.

Although climatic conditions are important, their impact on early human behavior and culture change may be overstated in some cases. Tsunamis, droughts, and other major short-term events must have had immediate effects on local resources and people. However, doubts exist about the degree to which long-term climate change impacted specific human generations (6, 13). No doubt, people gradually responded to prolonged droughts and permanent changes in temperatures, precipitation rates, and shifting resource zones, but these sorts of changes were probably unnoticeable to individual generations making decisions about technology, food supply, and mobility. And then some people may have been adept at adjusting to different climates and thus largely unaffected by changes because they were mobile and accustomed to adapting to new environments. Even if it were determined that past climate changes strongly influenced human behavior, it is difficult to securely document. The radiocarbon dating of geological events and archaeological occupations are too imprecise to fit a specific behavioral change, such as a shift from generalized foraging to specialized hunting to specific regional climatic conditions. Any matches are presently conjectural because the methods and hard data to determine whether natural or social conditions caused behavioral changes do not yet exist.

Also unresolved are the causes of extinction of certain large mammal species in the Americas. As in other parts of the world, it was likely a combination of various conditions, including human overkill, anthropogenic landscape change, and climate shifts (14, 15). In most regions, climatic change seems to have been the primary cause, although in open, arid areas where large game aggregated near scarce water resources, overkill possibly facilitated the demise of certain species. Without more regional data and more precise chronological dating, it is difficult to surmise the processes involved in the extinction of many species.

Archaeological Records

Compared with South America, North America has a more substantial archaeological record of the late Pleistocene. The record encompasses the gradual movement of people from Siberia to Alaska and significant technological, economic, and social transitions, including the development of new stone tool industries, although disagreement remains about the timing and process of

these events (1, 2, 9, 16). More data on Upper Paleolithic traditions in Siberia ≈ 32.0 KYA hint at a linkage between these traditions and eastern Beringia, as best evidenced at Swan Point in central Alaska, where microblade and burin industries date ≈ 14.0 KYA (1, 17). The best known industries are Ushki in Siberia and Nenana in Alaska and northwest Canada, dated between 13.8 and 13.0 KYA and are characterized by small blades and flakes made into bifacial and unifacial tools, and Sluiceway-Tuluq dated ≈ 13.2 KYA and associated with large lanceolate bifaces (16, 17). By 12.5 to 12.0 KYA, technologies are defined by blade, burin, bifacial (including projectile points), and unifacial tools indicative of increased regional diversity. Although these records suggest population movements and the transmission of new ideas and technologies corresponding to the tempos of glacial expansion and recession, no clear correlations exist between shifting technologies and climate changes. There also is no clear evidence of lanceolate bifacial and fluted points of the Clovis type in Alaska and northwest Canada.

Based on the discovery of classic fluted points at many sites throughout North America, the Clovis record came to be known as a “migratory culture,” and as the first culture in the Americas (16, 18). By linking Clovis points with early human migration, the Clovis-first model was born to explain the entire migration of people from Siberia to Tierra del Fuego. Yet, it has remained unclear for decades as to what “Clovis culture” was and what criteria were used to define it other than big-game kill localities, caches, a few campsites, and surface finds of fluted points. The Clovis model forced archaeologists to think about the past in a monolithic, essentialist way, and made them ignore contemporaneous adaptive and cultural variability across the Americas.

New advances have been made in understanding Clovis and subsequent technologies, including more knowledge that Clovis points were not just associated with big-game hunters but also with generalized foragers in some environments. The regularity of the Clovis technological spread, and the degree to which it was associated with population dispersion as opposed to diffusion of a new technology across existing populations, is not clear. Still, it is the stone technology of Clovis that is best known. Its social organization, domestic character, and subsistence patterns in different environments are not well understood, although progress is being made (19, 20).

Over the past several decades, archaeologists have found different varieties of projectile points dating to the late Pleistocene, some of which were different from Clovis points, and documented new site characteristics that do not always fit within the Clovis technology. With this comes the realization that some point types probably represent different technologies and thus different cultures, some of which dated before Clovis and others (nonfluted, stemmed points from the western United States) contemporaneous with it (20). Archaeologists also have realized that the duration of the technology, between ≈ 13.2 and 12.8 KYA, was not long enough to have migrated with people so quickly throughout North America (6, 7, 8, 20). The place of origin of the technology and whether it diffused across an existing population still is not known. However, it also is recognized that the Clovis-first model does not explain the first peopling of North America let alone South America (6, 13, 21).

There are now enough legitimate sites across the Americas to reveal a pre-Clovis human presence before ≈ 13.2 KYA. In Alaska and northwest Canada, a few pre-Clovis candidates exist (Bluefish Cave, Old Crow) but as yet are not proven sites (1, 16, 17, 20). Farther south are other possible sites containing modified bones of large mammals and/or stone tools: Schaefer and Hebior at ≈ 14.8 and 14.2 KYA, respectively, in Wisconsin, La Sena at ≈ 22.0 to 20.0 KYA in Nebraska, Lovewell at ≈ 19.0 KYA in Kansas, and Page-Ladson at ≈ 14.0 KYA in Florida. Other sites provide more solid evidence indicative of a pre-Clovis, for instance, Meadowcroft Shelter at ≈ 22.0 to 13.4 KYA in Pennsylvania, Cactus Hill at ≈ 20.0 to 18.0 KYA in Virginia, and possibly Topper at ≈ 13.5 KYA in South Carolina (1, 2). Complicating the recognition of these and other pre-Clovis sites is the repertoire of underappreciated, often nondiagnostic stone tools and other artifacts they harbor. The complexity of the archaeological and geological records at these sites raises significant methodological and interpretative issues of how to define and recognize early human cultures within the Americas, including those that may not be typical of the stone tool traditions initially transported from Siberia to the Americas. For instance, the stone tool industries at Cactus Hill and Page Ladson have no convincing antecedents in the Russian Steppe, Siberia, and Beringia, but some tools from these sites may share some manufacturing stages with industries of the Franco-Cantabrian Solutrean cul-

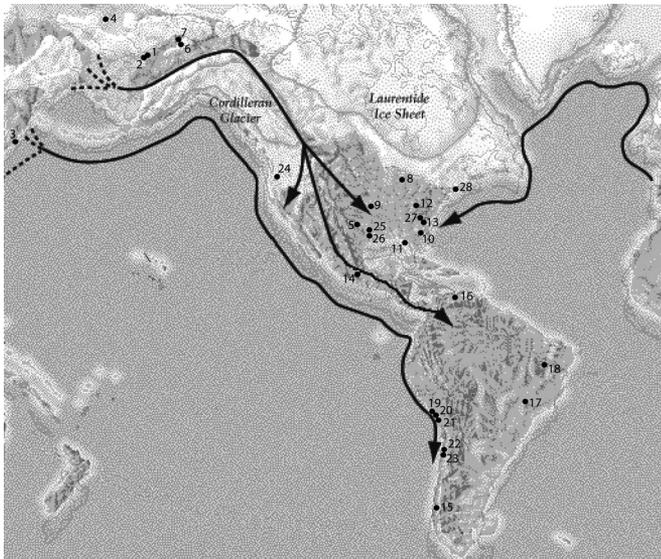


Fig. 1. Shows different possible migration routes into the Americas and sites discussed in text. 1, Swan Point; 2, Nenana; 3, Ushki; 4, Sluiceway-Tuluq; 5, Clovis; 6, Bluefish Caves; 7, Old Crow; 8, Schaefer/Hebior; 9, LaSena and Lovewell; 10, Page-Ladson; 11, Meadowcroft Rockshelter; 12, Cactus Hill; 13, Topper; 14, Tlapacoya; 15, Monte Verde; 16, Taima-Taima; 17, Santana do Riacho; 18, Lapa do Boquete; 19, Quebrada de Jaquay; 20, Quebrada de Tacahuay; 21, Quebrada de los Burros; 22, Huentelafquen; 23, Santa Juliana; 24, Paisley Caves; 25, Aubrey; 26, Gault; 27, Thunderbird; 28, Vail. Modified and reprinted with permission of *Archaeology Magazine*, Vol 53, Issue 6, www.archaeology.org (copyright, The Archaeological Institute of America, 2008).

ture in Europe that dates ≈ 21.0 to 18.0 KYA (3, 4).

Information on Central America, the land bridge between North and South America, is embarrassingly scarce and based primarily on the recovery of Clovis-like and other point types from surface sites. A few sites (e.g., Tlapacoya in Mexico) have been excavated and yielded stratigraphic data, but none have been adequately reported and convincingly tied to larger processes of migration in the Americas (Fig. 1). Although more systematic work currently is underway in Mexico, Panama, and other countries, more research in all of Central America is one of the greatest needs in American archaeology.

The late Pleistocene archaeology of South America is different because no single culture dominated the continent the way Clovis did for a relatively short period in North America. Instead, regional cultural diversification by at least 13.0 KYA is a major feature of the archaeological record of South America (5, 6, 13, 21–25). Less understood in South America is the extent to which spatial and temporal patterning in stone and other technologies is discernible. The earliest technologies consist of different types of stone tools, including a wide variety of short-lived and contemporaneous bifacial point styles (Monte Verde, Fishtail, Paiján, El Jobo) and expedient unifacial tools. Better-dated sequences show a succession of often

radically different artifact industries, especially in the Andes, eastern Brazil, and Patagonia. Several factors likely account for early diversity in the southern hemisphere, including geographic barriers to human movement (Andes and Amazon River), climatic change, shifts in resource zones, and social conditions.

The only possible link between North and South America has been the presence of fluting on Clovis and possibly Fishtail points, respectively, yet this association is unconvincing to some specialists (6, 13, 22–24). Although Fishtail points have been dated between ≈ 13.1 and 12.6 KYA in southern Patagonia, they are no older than ≈ 11.9 KYA in other areas, leading some specialists to suggest that they were invented in Patagonia and diffused northward (25). Several sites predate the ≈ 13.2 KYA Clovis barrier, including Monte Verde at ≈ 14.5 KYA in Chile, possibly Taima-Taima at ≈ 13.0 KYA in Venezuela, Santana do Riacho and Lapa do Boquete at ≈ 14.0 and 14.1 KYA, respectively, in Brazil, and a few others. Other sites hint at very early occupations but their deeper cultural layers have not been well dated (6).

Big-game hunting was only one of many different economic practices and never achieved the wider spread practice it did in some open environments of North America, although the hunting of wild guanaco predominated in the Pampa and Patagonia grasslands. Sev-

eral areas in South America witnessed the development of broader-based foraging diets by at least ≈ 13.0 KYA, including parts of the northern and central Andes and the eastern tropical lowlands. Less mobile foragers were engaging in processes of economic intensification, as suggested by specialized maritime adaptations between ≈ 13.0 and 12.0 KYA along the central Pacific coast at Quebrada de Jaguay, Quebrada de Tacahuay, and Quebrada de los Burros in Peru and Huentelafquen and Santa Juliana in Chile and by plant domestication in a few localities approximately ≈ 10.8 KYA (26). It also is becoming clearer that the use of plant foods and grinding stone and food storage technologies at some localities, such as northwest Peru and the eastern tropical lowlands, set the stage for the development of horticulture and sedentary settlements between as early as ≈ 10.5 and 8.0 KYA (27). How do we explain the early movements toward greater forager complexity and less mobile lifestyles in some environments of South America? The availability of wetter and more vegetated environments in some regions is one factor. Another may be sustained territoriality and population aggregation in these environments. Also important is increased cooperation among groups (6).

Genetic Signatures

The reconstruction of human biological relationships and population movements employing mtDNA and NRY data has significantly changed the study of the peopling of the Americas. Not only has genetics become a powerful tool in suggesting the origins of the first Americans but, like archaeology and bioanthropology, it has recorded diversity in ancient populations. Much like these disciplines too, the diversity of thought and knowledge in genetic studies is partly shaped by the different approaches taken by researchers and by the different sources of data and methodologies used, in addition to the varying genetic records of different regions. Reconstructing human phylogenies from genetic data entails inferring points of divergence and estimating rates of change along branches. These can vary considerably depending on the models and mathematics used to build the phylogenetic trees, sampling biases, and the methods used to calibrate the molecular clocks.

Genetic analyses, based on modern mtDNA and Y-chromosome (NRY) data, indicate that most present-day Native American populations have a single, Asian source and possess 5 different haplogroups (A–D and X), all of which are considered founding lineages (28–35). The distribution of these haplo-

groups are seemingly consistent with either a single major migration from Asia to the New World (28, 29, 34, 36–38) or multiple migrations from one genetically homogenous source population somewhere in northeast to east Asia (33, 39, 40). Ancient DNA markers from human skeletons also show North American haplotypes of Asia origin (30, 31) as well as a non-Native American haplotype (M: 35). Recent analyses have confirmed the presence of several sub-haplogroups (e.g., A2, B2, C1, D1) and their derivatives, suggesting geographically isolated autochthonous mutations in Beringia or a neighboring region (41, 42) before their spread deeper into the Americas. Also reported is the recovery of mtDNA from 14 human coprolites dated around ≈ 14.1 KYA from Paisley Cave in Oregon (43). These samples belong to the 2 most common haplogroups (A, B) among modern Native Americans, suggesting affinity with ancient people from east Asia. (This finding further indicates that an early human presence can be established by materials other than artifacts and human skeletons.)

Present in the DNA of living populations are 2 NRY haplogroups (C, Q), which also are considered paternal founding lineages. Q and its derivatives have been detected in nearly all Native Americans and reveal affinity to a source in Siberia (29, 32, 33). The widespread presence of subhaplogroup Q3, which likely arose through and autochthonous mutation in the New World, probably reflects some kind of founder effect and a common origin for all Native Americans. Recent findings also suggest that all modern Native Americans share a relatively high frequency of the 9AR allele at D9S1120 (44). Its spread throughout the Americas at the end of the Pleistocene explains its broad distribution among modern Native American populations. This pattern suggests that all indigenous groups derive from a common ancestral population, which would explain the widespread dispersal of this allele throughout the Americas at the end of the Pleistocene. But even with the discovery of specific ancient genetic marker like the 9AR allele, it is difficult to deduce the population origin and nature of early demographic processes. Another study suggests that a single ancient population of Siberians entered the Bering Strait and Alaska and spread along the Pacific coast to Central and South America (45). This study examined 678 autosomal markers and found that one of them is linked to every Native America group.

Collectively, the genetic data suggest that all major lineages found in living Native Americans are represented in modern-day populations in northeastern Asia and that there were 1 to 4 separate migrations from somewhere in this region to the Americas. The most accepted interpretation is a single migration between ≈ 20.0 and 12.0 KYA either along the Pacific coast or along an interior route (28, 34, 36, 42) and possibly a later one passing through the northerly inland route between the Laurentide and Cordillera ice sheets ≈ 14.5 KYA. Other studies point to multiple migrations along the coast and into the interior (40). It is tempting to link these movements to demographic pulses from the effects of the onset of climatic amelioration in Asia between ≈ 18.0 and 16.0 KYA and/or to new human behavioral strategies resulting from exchange systems and new technologies. However, there presently is no hard archaeological evidence to support these possibilities. For now, the molecular clocks for human entry into the Americas range widely, from ≈ 30.0 to 15.0 KYA, depending on genetic variation and estimating rates of change. Of course, this clock depends on radiocarbon-dated archaeological chronologies (2).

In South America, the genetic signatures are less clear than in North America, currently making it more difficult to estimate ages and number of entry migrations. Current evidence suggests that South America is related to North America, but less than North America is connected to Siberia (37, 41–46). This pattern is expected given the great distance between the north and south, the possibility of different demographic, biological, and environmental processes altering the record through time and space, and the greater opportunity for interaction between Beringian and North American groups since the initial expansion of people into the Americas. Studies also suggest that Andean populations are genetically different from those in the eastern tropical lowlands, which could be the result of 2 different initial migrations, different population levels, and/or gene flows within and between regional populations, the latter being affected primarily by population densities and geography (45, 46). Geneticists also have suggested that less population structure and more genetic diversity occurred in western than in eastern South America, even though both were probably derived from the same founder population. These trends may be correct. However, there are sampling problems in these studies, and more data are needed from more regions to confirm these patterns. Geneti-

cists have not yet fully entered into the debate on the date of entry into the southern hemisphere, thus no correlation can be made with archaeological dating.

The archaeological record of South America generally corresponds with the patterns produced by genetic studies, indicating that the east and west sides of the continent have different chronologies, different archaeological records, and different human histories. As noted earlier, the geographical barriers of the Andes and the Amazon basin probably contributed to these differences, as well as regional population dynamics and settlement patterns.

Although genetic studies have been a welcome addition to the study of early human movements by providing insights that are unattainable in archaeology, they are not without limits, especially as they relate to results in other disciplines and to sampling biases. To reconcile the findings of genetics and other disciplines, researchers must agree on the units of measurement for the populations under study. That is, how are study populations defined, as demographic units, as genetic groups, and as haplogroups, and for what purposes? Further, living local populations generally have been the unit of scrutiny for geneticists, although more genetic studies of ancient skeletons is now underway. But in the past, what was a local population and how can it be measured genetically and archaeologically? Is it a breeding group, a residential group, a mortuary and cemetery group, an archaeological site-level group? Most genetic studies lump available ancient human skeletal material into a single sample supposedly representing a local or regional biological population where several archaeological sites have been sampled. However, there often is little spatial or temporal uniformity in the material selected for analysis. This is not necessarily the fault of geneticists. They select what is available to them in local site collections. Thus, they sample by availability and by lumping. However, this lumping may add considerable variation to the sample and present problems in defining and interpreting the units of study.

Most genetic modeling of the initial peopling of the Americas is based on mtDNA and more recently Y chromosomes of modern groups, not ancient populations. But are the results of studies of ancient genetic material the same as those of modern material? Genetic studies also have regularly assumed that early Holocene human skeletons, such as Kennewick Man in Washington, Spirit Cave Man in Nevada, and Buhl Woman in Idaho, represent late Pleisto-

cene populations, despite the fact that several millennia of demographic processes separate the 2 population samples. To what extent do these later skeletal remains represent the first Americans, given that they are descendants removed by at least 350 generations during which time many processes could have altered the genetic record? This is not to say that Holocene skeletons do not reflect early American genetic and morphological traits. We see other issues represented by them, including the continuous and transformational processes of demographic exchange among different groups over extended time and space, and how these processes have added or reduced variation in the sampled populations. An appropriate model of early American origins should not only question the apparent phylogenetic linkage and extended time period between late Pleistocene and early Holocene samples, but also the possibility of their separation due to various factors, including genetic drift, gene flow, geographic isolation, and so forth. The end result may be that confidence in being able to distinguish between what is real from what is hypothetical in the genetic representation of Pleistocene skeletons can be diluted by the intrusion of later populations typed as first Americans. Finding more human skeletal and genetic material dated to the late Pleistocene is another major need in first American archaeology.

First American Skeletons

The extreme paucity of human burials known from the late Pleistocene in the Americas, in contrast to their more visible presence in Australia and other parts of the world, is intriguing. The reason for this paucity remains undetermined, other than sampling biases where archaeologists search for sites, cremation of human remains, or burial patterns in bogs, crevices, and other topographic settings outside of campsites and localities where archaeologists usually search (6).

In recent years, researchers have turned from ancient tooth forms to comparative multivariate analyses of cranial morphology of ancient skeletons from various regions of the globe to study the first Americans. Initially, these studies observed variation in skull form and suggested that early Americans had ancestral links with ancient populations known from Asia and that the variation can be accommodated in a single biological population, the Mongoloids (47), a conclusion also made by early genetic studies. However, crania analyses also show an increasingly wide range of characteristics, leading some researchers to believe that 2 early populations had different times of entry

into the Americas and diverse biological and genetic origins (47–51), not only including northeast Asia but south Asia and possibly Europe, Africa, and Australia-Melanesia. The earlier form is the Paleoamerican, which is believed to show more similarity to that of the first modern humans still present today in living Africans and Australo-Melanesians (47, 50, 52); the later form is Mongoloid. Rather than representing different source populations, these 2 types may instead be extreme forms along a morphological continuum of variation (49). This dual pattern contrasts with the genetic evidence that suggests homogeneity in terms of haplogroups from east Asia (28, 33, 44). Some researchers believe that cranial affinities exist between early South Americans and ancient and living Africans and Australo-Melanesians (50, 52) and that this suggests the entry of different biological populations into the southern hemisphere. Different populations are also suggested for North America, but with less clear affinities to non-Asian populations (48, 51, 54). Also observed in the South American crania is a discontinuity in morphology between early and middle Holocene periods (50, 52), a pattern also observed in North America (48, 53, 54).

The possibility of 2 distinct and chronologically separate populations entering the Americas is perhaps most pronounced in the early to middle Holocene skeletons of South America, where narrow and long, prognathic faces occur in the west and short and wide, orthognathic faces are in the east (50, 52). These regional differences agree with the current genetic evidence from South America, which also indicates differences between the east and west sides. It is not known whether genetic drift, the division of a single founder population after people first entered the continent, the founder effects in 2 different colonizing groups splitting east and west, or selection explain this pattern.

What does variation in the early skull forms mean? Some researchers believe it is indicative of climatic adaptations more than genetic signals (55). Others point to gene drift and adaptations to local evolution after the first people arrived and then spread out over the Americas (49). Whatever the reason may be, the combined data reveal significant variation in early crania morphology, probably suggesting separate migrations into the Americas from different source areas and/or the first immigrants were already heterogeneous at the time of entry.

Some Issues and Incentives

How do the different findings from different disciplines fit together in produc-

ing a more coherent understanding of the first peopling of the Americas? Should they? Perhaps they should not because each tends to have its own theoretical, methodological, and empirical approaches to addressing questions. But, they study the same phenomenon and thus should ultimately reach an accord on some issues. Although the 3 disciplines present competing, and at times mutually exclusive, models of the peopling process, there is some general agreement. For instance, researchers agree that there is more archaeological, genetic, and morphological diversity than previously recognized and that people entered the Americas before Clovis times. Yet, data and interpretative differences also occur. For instance, the genetic and cranial evidence disagree over the number of initial biological populations entering, with the former favoring 1 and the latter advocating 2. Some convergence is expected in this case as more data are collected, because the same evolutionary forces are acting on genes and cranial forms (56). Differences in the nature and size of the databases studied by each discipline, whether they are stone tools, human crania, or genetic molecules, matter significantly because discoveries and results pertain to the scale and sampling biases of those data. The challenge reaching a consensus grows exponentially more difficult when each discipline attempts to offer valid models of the initial peopling of the entire Americas. The challenges to interdisciplinary research thus are most clearly seen in the controversies that exist at the boundaries between differing temporal and spatial scales, as evidenced in estimates by archaeologists and geneticists in dating the first entry of people and in configuring different routes of entry and dispersion. Perhaps plotting gene frequencies as continuous gradients on GIS maps overlaid and layered with archaeological, genetic, skeletal, linguistic, and paleoecological maps will provide new ways to perceive data and to ask new questions and make new inferences. Computer simulation models also can attempt to model the demographic processes that led to the distribution of genes and archaeological traits, but the social and cultural patterns producing them will be difficult to ascertain. But, methodologies in and across disciplines also must be critiqued, sampling problems addressed, analogies modified, and distinctions and similarities clarified.

Another issue relates to our poor understanding of social organization and domestic structures. How people lived and how they organized themselves to face different challenges during the peo-

pling process are important for understanding the motives for remaining in certain environments and migrating to others. We currently do not have the hard evidence to evaluate these topics. Human burials, rock art, and formally organized domestic space in sites offer opportunities to study these topics but all 3 are minimally represented in first American archaeology. One reason for poor knowledge of domestic site structure is the paucity of large-scale excavation of open-air sites where space was likely less limited by rock walls or fallen boulders, which is the case in caves and rockshelters. Although a few sites offer glimpses into site structures (Monte Verde in Chile, Aubrey and Gault in Texas, Thunderbird in Virginia, Vail in Maine, Quebrada Jaguay in Peru), several important localities are rockshelters and caves, especially in South America, that contain evidence of multiple visits, which intrude into and often destroy previous occupation deposits. Open-air sites, on the other hand, are often specialized activity areas, especially kill, butchery, or processing places. Large-scale excavation of single occupation and minimally reoccupied open-air sites, which are less likely to have been disturbed by reoccupations and more likely to contain various kinds of activities, is one solution. Another record that has received little attention is rock art, which has not been integrated with excavated data, except in Brazil, Argentina, and parts of the American southwest. Rock art provides the opportunity to study gender, technological and dietary choices, and symbolism, but then the problem is dating it.

This brings us to the nature and extent of human migration, diffusion, and social interaction networks, and their influence on regional material records. Keeping in mind the recurrent population contractions and extinctions and the geographic barriers to movement that geography and climatic change must, at times, have produced throughout the Americas, then it is likely that there were disruptions in the movement of people and in the transmission of new ideas, technologies, and genes. As populations aggregated in some areas, people presumably found it easier to locate mating partners within more restricted areas, with consequences for information and gene flow rates within and between regional populations. Material culture and sites also likely were used differently as more regular contact was established between groups. For instance, more people staying for longer periods of time in a site implies more extended domestic space and probably more planning of the internal layout of

a site, as well as the accumulation and discard of more material in the archaeological record.

Archaeologists often assume that, if they can identify cultural patterns in the material records of sites, they can make better sense of migration, diffusion, and interaction processes. Missing in first American studies, however, are clear ontological and theoretical frameworks for interpreting and explaining the patterns at the local, regional, and hemispherical levels of analysis. This absence can produce interpretative tensions and differences within and between disciplines.

The Hemispherical Onion and Conceptualizing the Initial Peopling Process

Currently, the interpretation of interdisciplinary data on the first Americans boils down to the application of and tension between 2 distinct ontological approaches: essentialism and materialism [or population thinking (57)]. Essentialism is the idea that artifacts and human behaviors are packaged and discoverable and thus can be represented by discrete types, such as projectile points, haplogroups, and distinct cranial forms. Materialism differently insists that things are constantly changing, that variation is important, and that the function and meaning of artifacts and behaviors cannot be placed into neatly ordered types. Essentialism dominates first American studies. It results in artifact, genetic, and skeletal typologies tied to expected norms that poorly identify and explain cultural, demographic, and social patterns. Variation and change from a materialism perspective attempts to explain behavioral change but has not yet received much attention in first American studies. A solution to this problem is the application of material behavior, behavioral ecology, and evolutionary archaeological approaches to build a more applicable epistemological framework.

There also is a tension between 2 different approaches to the interpretation of human adaptive radiation in the Americas: reductionism and emergence. The reductionist view sees the whole interdisciplinary record of initial peopling as an onion, with successive layers to be peeled back from the hemisphere-long migration of people to the regional and local scales until the historical patterning of the process is revealed (1, 7, 18, 58). This approach assumes that the same migratory forces, whether represented by single or multiple pulses, and human behaviors from Siberia to Tierra del Fuego are ordered in a rational and intelligible way and that all archaeologi-

cal, genetic, and bioanthropological data should be mutually legible. This was the approach taken by the Clovis-first model, which believed that all of the Americas were connected by the same migration process and tidy set of typological traits (e.g., fluted Clovis points, big-game hunting, rapid movement), which is essentialism. Emergent thinking, on the other hand, believes that each scale is describable by self-contained cultural and behavioral patterns (6, 13, 21, 22). That is, some researchers place sites within only local and regional settings for the time they were occupied without connecting them to broader processes. Thus, the reconstruction of patterns is a matter of temporal and spatial scale that varies from site to site. But there has to be an overarching behavioral mechanism to connect all of the patchy local sites, because presumably people reached Tierra del Fuego from North America. But what is the connectivity and how is it identified archaeologically, genetically, and bioanthropologically? So far, hemispherical to local approaches have not answered this question, and this is where we are today. The question must be answered at all scales and by all disciplines.

Along these lines, researchers need to anticipate the first peopling process empirically and theoretically, observe its material, skeletal, and molecular correlates, and its variation and linkage at different scales, and relate them to similar issues on a global scale, meaning cross-cultural comparison to the study of early migration behavior in Old World archaeology, as well. Variability in the peopling process can be studied by a wide range of paradigms, including biological, ecological, and anthropological paradigms. Flexibility between local, hemispherical, and global questions, between context and artifact, between essentialism and materialism, between reductionism and emergence, and between different datasets to create inclusive analyses and more theoretical understanding of the process in an interdisciplinary manner is one goal. Another is to integrate the sheer complexity of multiple databases beyond the traditional focal points of sites, artifacts, genes, and skeletons and integrate them into a descriptive and analytical whole. To do so requires both an interdisciplinary scientific and theoretical framework.

With few exceptions, the proxy records used to study these and other issues currently lack the fine-grained chronological, ecological, cultural, and social data needed more fully to assess and theorize them. The limited theoretical contribution of first American research to wider problems of early

human migration was noted earlier. Despite this limitation, several unique and important contributions have developed, including recognition that anatomically modern humans colonized previously unoccupied landscapes in the Americas (6, 8), that within a few millennia of human entry people began to domesticate plants (27) and take the initial steps toward increased social complexity and that many first Americans were generalized foragers more than big-game hunters. The first people entering previously uninhabited territories evidently dealt with environmental variability and uncertainty and faced all sorts of challenges by developing new technologies and new organizational skills. If anatomically modern *Homo sapiens* moved as rapidly as some scholars think through the Americas, this movement must have

involved more enhanced social and cognitive learning as a means of responding rapidly and collectively to immediate challenges (59). Differing contexts of social learning combined with varying transitions of technological innovations, including the initial steps toward plant domestication, could have given some groups an advantage in adapting to changing conditions. Significant changes also must have taken place in the integration of new tools in strategies of landscape use, as well as in methods of tool-making that imply greater planning and the need for learning than conceived previously. But technological innovation alone seems insufficient to explain these adaptations. A greater understanding of the social and cognitive developments accompanying changes is needed. Such developments would have

contributed greatly to the maintenance of increasingly complex social networks, broad-spectrum economies, and the transmission of practical information about the physical world. Much remains to be unpacked and conceptualized by researchers before we more fully understand these and other issues about the timing, geographic extent, and causes of the first peopling of the Americas. These are exciting and productive times in the study of this subject. As more interdisciplinary studies are carried out in the future, we will continue to find that the story of the peopling of the Americas is far more complex than we ever imagined.

ACKNOWLEDGMENTS. I thank L. Borrero, P. M. Castillo, M. B. Collins, D. J. Meltzer, P. J. Netherly, D. Piperno, T. Schurr, D. Stanford, and 2 anonymous reviewers. Paige Silcox prepared Fig. 1. Any errors and omissions are the responsibility of the author.

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