

## The Other Sciences: Genetics, Linguistics, and Physics

**A**S (SELF) IMPORTANT AS archaeology and anthropology are in the search for the First Americans, many of the advances of the last half century have come from the contributions of other scientific disciplines. This chapter examines these contributions as well as the inherent limitations of genetics, linguistics, and physics.

### Genetics

The search for the First Americans is, at its most fundamental level, a search for relationships. Even assuming that it was possible simply to find the physical remains of the very first human to set foot in the New World, and then to substantiate that the remains were indeed the primal First American, the most interesting scientific issues and popular public interests would still be unresolved. The critical discoveries would be those addressing human relationships, the ties of culture, the ancestral tree.

The science of archaeology is suited to the discovery and description of material artifacts. In some situations, it may be able to identify a similarity between tools used at different times and places. It is not, however, well situated as a science to make definitive determinations as to whether that similarity resulted from technology transfer between otherwise unrelated cultures, from independent development, or was nothing more than the discovery of two artifacts used by essentially the same culture at two different times and locations. Even when relevant information can be gleaned from these material artifacts, it is not the provenance of the artifacts that is ultimately of interest in the search for the First Americans, but rather what these items can suggest about their human creators and users.

What First American scientists and the popular American imagination ultimately seek are the cultural ties associated with the First Americans: where did they come from, how did they get here, and are their descendants still here? David Meltzer correctly stated that forming an estimated date for the arrival of

the First Americans “cannot be bracketed on a priori grounds, archaeological or otherwise.” Yet Meltzer also proclaimed that “the timing of the entry of people into the New World is a question that can be answered only by doing *archaeology* in the New World.”<sup>1</sup> Despite Meltzer’s contention, the science currently best situated to address these issues is genetics. Archaeology is much less able than genetics to calibrate the distance between human populations. Artifacts are proxies for drawing a relationship between cultures. Similarity in material artifacts is insufficient to confirm descendant ties between two populations. Moreover, artifactual dissimilarity is also not sufficient to dismiss biological ties. Genetics, while not perfectly descriptive, is able to offer a path to making judgments about direct relationships between the humans themselves, not between their cultural residue.

As discussed previously, bioanthropology can provide an estimate of human relationships based on the morphology, the structural traits, of human remains. However, given the scarcity of viable candidates for the remains of the First Americans, genetics provides scientists a mechanism for determining human relationships even when the remains are insufficient to provide morphological information. “More and more, we will see a lot of genetic information coming from fossil remains in which very little morphological information exists,” according to Svante Pääbo, a Swedish biologist who is director of the Department of Genetics at the Max Planck Institute for Evolutionary Anthropology in Leipzig, Germany.<sup>2</sup> He was speaking with regard to the results obtained from only a finger of what appears to be an archaic Denisovan human, a third *Homo sapiens* in addition to Neanderthals and modern humans, called X Woman, discovered in southern Siberia. A more recent set of Denisovan bones was found in Tibet, China. The initial conclusions were based on mitochondrial DNA, and tests have been run on nuclear DNA. In addition, human hair can also be used to sequence the ancient human genome according to Eske Willerslev at the University of Copenhagen. Based on an analysis of the hair, Willerslev concluded that a body found in 1986 buried in Greenland ice for four thousand years is related to people currently living in eastern Siberia, and he is now looking at the hair from ancient mummies in the Western Hemisphere.<sup>3</sup>

Archaeologists view themselves as being centered in the past, and, therefore, are to be accorded the status of arbiters of antiquity; they “only see what the Pleistocene left behind.”<sup>4</sup> To the extent that this is a valid characterization, it would appear to give archaeology a privileged ontological position vis-à-vis the other sciences in the First American debate. Only it would be able to make conclusive determinations. Yet, an epistemological domain, including archaeology,

can only perceive reality within the boundaries created by the methods and value systems extant in that field. Genetics offers a capability not available in archaeology to precisely fix human biological relationships and, therefore, from these biological ties to make projections concerning cultural affiliations. "Archaeologists have trouble enough deciding which stone tool assemblages belong together; we are even harder pressed to link archaeologically detectable patterns with those identified among modern languages or genes."<sup>5</sup>

The modern preoccupation with DNA is a daily occurrence. It is not only central to our biological identity, it is also a part of our political debate, our health care research, our judicial system, and a perceived path to a better future. DNA, however, is increasingly also a useful tool in attempting to clarify our past. Genetic evidence has documented a relationship between modern Asians, American Indians, and early Americans. By comparing ancient DNA (aDNA), when it is serendipitously available, with modern maternal mitochondrial DNA (mtDNA) or paternal non-recombinant Y-chromosomal DNA (NRY) material from current populations, geneticists can not only draw relationships between population groups but also project such relationships into the distant past.

According to Tom Dillehay, genetics has "become a powerful tool in suggesting the origins of the first Americans."<sup>6</sup> However, not all experts agree on the conclusions that genetics-based data might produce. On the one hand, leading scholars at Texas A&M University and at the University of Kansas believed that "current genetic evidence implies dispersal from a single Siberian population toward the Bering Land Bridge no earlier than about 30,000 years ago (and possibly after 22,000 years ago), then migration from Beringia to the Americas sometime after 16,500 years ago. The archaeological records of Siberia and Beringia generally, but not conclusively, support these findings, as do archaeological sites in North and South America dating to as early as 15,000 years ago."<sup>7</sup> On the other hand, Dillehay suggests that "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."<sup>8</sup> As can be seen from these two examples, reputable scientists can, and do, make divergent conclusions based on the same genetic data base.

The disbelief that all human "races" with their variations could be traced to a single source was a part of the nineteenth-century debate surrounding the nascent fields of evolution and bioanthropology. Charles Lyell was concerned with reconciling the perceived differences in intellect between the "Negro and European" against theories of "a unity of origin" of the races that had subsequently

“diverged from the common stock.”<sup>9</sup> John Wells Foster concluded that “there will be found continuous and uninterrupted causes which shall explain all the diversities in the different branches of the human family, without the necessity of resorting to independent creations.”<sup>10</sup> It was the genetics of the twentieth century that began to provide meaningful answers to these nineteenth-century questions of human origin and divergence.

What exactly is the basis of the genetics that First American scientists use in their search? There are two primary tests for using human DNA to determine an ancestral relationship. The first is mitochondrial DNA (mtDNA), which is non-nuclear and traces a single-nucleotide polymorphism (SNP) and its associated mutations that are passed down maternally. The other is based on the Y-chromosome (Y-DNA), also called non-recombining Y (NRY), and provides documentation on Y-based SNP and its mutations that are passed down paternally.<sup>11</sup> The rate of mutation can be estimated and, therefore, provides a sort of genetic clock that can be used to estimate the convergence toward a common ancestor. Based on the central tendencies of commonality across these mutations, geneticists have created populations called haplogroups.

Having two separate genetics clocks, however, is a problem of its own sort. Since the rate of mutation of mtDNA is faster than that of Y-DNA, it sometimes is considered to provide a more accurate calibration, much like measuring time in days instead of years. However, because there are more haplogroups identified in NRY, it provides a finer discrimination tool and is considered “the most informative haplotyping system.”<sup>12</sup> But the differing mutation rates for mtDNA and Y-DNA can result in different estimates. As a result, it is difficult to assign one-to-one correspondences between the two haplogroup structures, which might permit accurate calibrations between the two systems.<sup>13</sup> Moreover, the two approaches give different answers for genetic relationships. For example, one NRY analysis in South America would lead us to believe that there is such genetic consistency that virtually the entire indigenous population can be represented within one haplogroup. However, the results of an mtDNA analysis are substantively different from that of NRY and indicates that there are four different haplogroups that have provided substantive ancestral DNA.<sup>14</sup> Both answers cannot be correct, and it is possible that neither is entirely accurate.

According to James Chatters, the mtDNA of modern American Indians typically falls into five distinct haplogroups. Three of those haplogroups—A, C, and D—are also found today in Siberia. A fourth—haplogroup B—is typical in modern southeast Asians. Finally, haplogroup X—typically Eurasian—is also found in modern American Indians.<sup>15</sup> It should be remembered that these

associations are not between *First* Americans and *ancient* non-New World inhabitants, but rather between *modern* American Indians and *modern* Old World inhabitants. The difficulty comes in projecting these relationships back through time. According to Meltzer, the ultimate reward is “to firmly link the most ancient and most modern Native Americans, determine the number of migrations, from whence and where they came, or even the route(s) traveled.”<sup>16</sup>

Because American Indian haplogroups are not distributed equally across the New World population, geneticists can draw some conclusions from the variations in the distribution.<sup>17</sup> “The pattern is suggestive of a sequence of migrations, a first one with D and C, a second one dominated by B, and a third consisting only of type A individuals. When haplogroup X came cannot be surmised from the geographic patterns, although there is some indication it may have first arrived on the northwest coast of North America.”<sup>18</sup> Based on genetic analysis, Theodore Schurr concluded that “the American progenitors left their homelands between 24,000 and 35,000 years ago.”<sup>19</sup> This is some ten to twenty thousand years earlier than either the Clovis or Monte Verde cultures that have been documented by First American scientists. The roughly one dozen ancient human remains in North America from which mtDNA has been analyzed have produced only haplogroups B, C, and D. “Haplogroup A, the most common haplogroup among living native North Americans, has not yet been found in remains older than 6000 B.C.,” which supports contentions that modern American Indians are descendants from a later migration from Siberia and not the First Americans.<sup>20</sup> The subtlety of this analysis, both genetically and politically, is further compounded by aDNA studied by Frederika Kaestle at an ancient archaeological site in Windover, Florida. Kaestle concluded that the remains are “not A, not B, not C, not D, and not X. We’ve been able to prove what they’re not, but we don’t know what they are.”<sup>21</sup> Conclusive answers are elusive, but new genetic evidence continues to be discovered that generally supports some version of a Beringia migration hypothesis.<sup>22</sup>

Although the genetic analysis supporting the search for the First Americans has largely centered on humans, there are other life forms that have coevolved with humans over the millennia and can be considered markers for a human presence. As an example, the HTLV (Human T-Lymphotropic Virus) retrovirus has been used in an attempt to identify prehistoric migrations. If the results of that study are to be believed, “Japanese sailors were the first people to reach the Americas, millennia before Siberians wandered across the Bering Strait.”<sup>23</sup>

Regardless of whether the genetic analysis has been performed on the DNA of humans or on other life forms, genetic science has inserted itself in significant

ways into the search for the First Americans. It has identified ties between modern American Indians and current groups in Asia. It has also provided evidence of multiple migrations into the New World. What it has not done is identify either the First Americans or locate their Old World progenitors. As Meltzer has commented, "Genetic studies thus far cannot confirm conclusively how many major groupings there are of modern native North Americans, much less the presumed number of migrations."<sup>24</sup> The difficulty in reconciling the results of genetics, bioanthropology, archaeology, and geology is that genetics suggests an earlier arrival date into the New World for the First Americans when compared with archaeological results based on material artifacts. Comparison of Asia-New World migration chronologies suggested by different theories of human migration from Siberia to the Western Hemisphere indicates a potentially earlier presence in the Americas than material archaeological findings have discovered to date.<sup>25</sup>

In the search for the First Americans, genetics suffers much of the same fate as bioanthropology: it is impossible to isolate the practice of genetic science from the social context of politics, race, and cultural identity. As an example, scientists at Arizona State University took blood samples from several hundred Havasupai Indians who live in the western end of the Grand Canyon. The Indians had given permission for the general study of medical disorders, and apparently many thought that the blood samples were to be used only for a study of diabetes. "When they learned years later that the DNA samples had been used to investigate things they found objectionable, they felt betrayed. Researchers had . . . traced the tribe's ancestral origins to Asia, contradicting traditional stories holding that the Havasupai had originated in the Grand Canyon."<sup>26</sup>

There are two principal issues involved in the Havasupai controversy. First is the potential ethical issue of performing genetic research without the informed consent of the human subjects. This concern is not confined to the search for the First Americans. The second, and much more subtle, issue is what amounts to a confrontation between genetics as a science and the substantive challenge that it can present to the cultural beliefs of American Indian tribes. The Native American Graves Protection and Repatriation Act (NAGPRA) gives American Indian tribes legal control of human remains, regardless of their age, found on their or federal lands when a cultural or geographical affiliation can be demonstrated between those remains and a particular American Indian group. In recent years, genetics has increasingly been offered as a means for determining such affiliation when other evidence is ambiguous. As demonstrated in the Havasupai example, not only can genetics provide strong evidence as to a biological affiliation, it can also directly challenge the existential myths of an American Indian culture.

In 2000, the secretary of the interior—who was given statutory authority by NAGPRA to make cultural affiliation determinations—ordered that DNA tests be conducted on some human remains. This proved to be a controversial directive for both the American Indians and the First American scientists involved. The American Indians objected because DNA testing was an affront to their religion and a belief that cultural identity was based on more than simple genetics. Interestingly, some of the scientists also objected, arguing that culture is learned and therefore has no relationship to biology.<sup>27</sup> As Vine Deloria Jr. has pointed out, one of the most controversial problems today between First American scientists and American Indian groups is the application of genetics as a proof of tribal affiliation.<sup>28</sup>

## Linguistics

First American linguists are largely trapped in the evidentiary present. In the absence of any evidence of written languages for both the First Americans and even pre-Columbian modern American Indians, linguistic theories can only be validated through comparing known languages of the past few hundred years. If linguistic tools are of value when applied against the written and spoken records in Europe and Asia, they are of considerably less value in the context of the human history of the Americas where there are few written records, and none associated with the First Americans. Moreover, in attempting to generate a linguistic tree for American Indians, some scholars contend that modern American Indians are not direct descendants of Paleoamericans; consequently, a linguistic tree that cannot examine a missing branch is of little value. Finally, there is no independent reality against which linguists can recalibrate either their hypotheses of Paleoamerican linguistic relationships or the clock on the rate of linguistic evolution. “One cannot recover fossil languages, at least not until the development of writing.”<sup>29</sup> Accurately estimating a linguistic tie between two cultures that is chronologically inaccurate by, say, two thousand years can be the difference between a simply interesting result that ties together two neighboring cultures in Siberia, as opposed to a theory-invalidating result that ties together a culture in Siberia with one in North America. Nevertheless, there has been an active linguistics effort that searches for clues in the languages of modern Native Americans that could lead to an ancestral linguistic convergence that might be associated with the First Americans.

Early in American history there was a sense that linguistic evidence might have a bearing on the source of the First Americans. As a part of Thomas