The Search for the First Americans

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Published by University of Oklahoma Press

Davis, Robert V., Jr.
The Search for the First Americans: Science, Power, Politics.
Project MUSE. muse.jhu.edu/book/85071.

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CHAPTER 8

The Other Sciences: Genetics, Linguistics, and Physics

As (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.” 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. 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.

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.” 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.”

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.” 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 32,000 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.” 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.” 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.” ninth, 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.” tenth. 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. eleventh. 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.” twelfth 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. thirteenth. 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. fourteenth. 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. fifteenth. 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.”

Because American Indian haplogroups are not distributed equally across the New World population, geneticists can draw some conclusions from the variations in the distribution. 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. Based on genetic analysis, Theodore Schurr concluded that “the American progenitors left their homelands between 24,000 and 35,000 years ago.” 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. 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.” Conclusive answers are elusive, but new genetic evidence continues to be discovered that generally supports some version of a Beringia migration hypothesis.

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.”

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 grouping there are of modern native North Americans, much less the presumed number of migrations.”

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.

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.”

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. 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.

**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.” 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
Jefferson’s 1784 excavation of a mound that was determined to have been the product of American Indians, he concluded that linguistics dictated that American Indians and the people of northern Asia had a common origin, and that American Indian languages must be more ancient due to their greater diversity. However, Jefferson’s view was not universally shared. Benjamin Smith Barton (1766–1815)—a professor of medicine, natural history, and botany at the University of Pennsylvania—believed that the diversity of American Indian languages was such that they could only have separated from a common origin at a time that predated Bishop Ussher’s Earth-creation date of 4004 BCE.

By the nineteenth century, First American scientists were even more confident that linguistics could provide a powerful tool for tracing relationships between modern and ancient cultures. In 1874, John Wells Foster commented that “The study of languages affords a reliable guide in tracing the migrations of tribes, even where they have become intermingled with other tribes. In the social relations thus established, there would not result a total obliteration of the language of the one tribe, but certain words and forms of speech would be adopted and perpetuated.” When applied in the context of European languages, Foster believed that they “can be traced back to the Sanskrit as an approximate common source.” Ignatius Donnelly echoed Foster’s confidence in tracing modern Europe’s linguistic roots. “Philology is yet in its infancy, and the time is not far distant when the identity of the languages of all the Noachic races will be as clearly established and as universally acknowledged as is now the identity of the language of the Aryan family of nations.” Yet the nineteenth-century ground in which linguistics proved fertile for documenting European linguistic history was apparently barren in North America for the search for the First Americans. Foster concluded that “the language of the American Indian throws no light upon his origin,” and that linguistic efforts to trace the origin of American Indians were “utterly futile.” He could find no elements of the ancient Hebrew, Welsh, Hindu, Phoenician, Chinese, or Scandinavian languages that should be related to modern American Indian languages if those civilizations had supplied the ancestors of modern American Indians.

As the fields of anthropology and linguistics each developed into professional academic disciplines in the twentieth century, Edward Sapir (1884–1939) was among the first to combine the domains in his search for the First Americans. Because of the great diversity in American Indian languages, Sapir believed the explanation could be either that American Indians had been in North America for such an extremely long time that their languages had had sufficient time to
diverge, or more likely that the divergence resulted from a “series of movements of linguistically unrelated peoples.”

Understanding the application of linguistics in the search for the First American is important for what it reveals in how the science is practiced. It has frequently exposed the boundary lines between the scientific domains involved in the search. In 1987, Joseph H. Greenberg (1915–2001) published what was a then-seminal work titled *Language in the Americas*. In it, Greenberg concluded that the myriad languages of the indigenous North American people could be resolved into only three linguistic families, which he named Amerind, Na-Dene, and Eskimo-Aleut. It was generally accepted that these linguistic groupings were the result of three separate migrations from Asia, most likely via Beringia.

Greenberg’s thesis was presented in an increasingly interdisciplinary First American scientific environment that saw in the 1980s a series of papers on den-tochronology by Christy Turner analyzing the relationships of American Indian and Asian teeth that supported Greenberg’s three pulse migration thesis. For Turner, the issue has now become that his findings may have also been unduly influenced by Greenberg’s three-migratory-wave thesis. Moreover, Greenberg’s results have now been challenged as too simplistic. David Meltzer commented that “it is probably no more realistic to infer Pleistocene migration routes to North America by the number and distribution of modern language groups than it would be to infer Hernando de Soto’s route by looking at the number and distribution of Spanish dialects in the Southeast today—and at least we know that de Soto spoke Spanish.”

Linguists are confronted with the possibility that the results of their work may ultimately be irrelevant in the search for the First Americans. As was indicated in a Smithsonian Institution report, “No American Indian language is derived from an historically known Old World language.”

**Physics**

If archaeology or anthropology were to disappear, the discipline of physics would scarcely notice. If physics, however, were to disappear, First American science would largely revert to relying on the analytical tools of the nineteenth century for dating artifacts. In the search for the First Americans, one method of obtaining observational data is to document the environment of an artifact of interest; that is, for example, to situate the material within its known geological context. The best data, however, is obtained directly from the artifact. For the past sixty
years, the principal means of dating human and other life form remains has been what is popularly called carbon dating.

In 1947, the chemist Willard Libby established that the steadily predictable decomposition of the carbon 14 isotope into nitrogen 14 could be used to date ancient human remains. In 1960 Libby was awarded a Nobel Prize for his efforts.\textsuperscript{44} Carbon 12, 13, and 14 are taken in by plants through photosynthesis and then ingested by animals in relative proportion to that found in the environment and in their specific diet. Although carbon 12 and 13 are stable, carbon 14 decays. Upon death, carbon 14 is obviously neither absorbed during photosynthesis by plants nor ingested by animals. However, the carbon 14 that was already in the then-dead plant or animal continues to decay into nitrogen 14 at a rate such that after every 5,730 years, 50 percent of the remaining carbon 14 is gone. Based upon this known rate of decay, an estimate can be made as to length of time that has transpired since death. Archaeologists typically provide these dates in carbon dated years called “BP,” that is before present—with the present being standardized as 1950, when carbon dating began.

There are, however, limitations to using radiocarbon dating. The most advanced technique currently used by physicists is called accelerator mass spectrometry (AMS), which counts not only the carbon atoms that are decaying, but also counts all of the carbon 14 atoms present in order to make a very precise estimate of the decay ratio. Application of a technique as sophisticated as AMS is constrained in that it is expensive, so it cannot be used routinely. In addition, any “sample that is 35,000 years old will have only 2 percent of its original carbon-14 left. Even a tiny bit of a recent contaminant is enough to skew the radiocarbon date seriously.”\textsuperscript{45}

An additional difficulty in using carbon dating is that the amount of carbon 14 first in the atmosphere, then in plants, and subsequently in animals has varied over the millennia. By analyzing tree rings and the carbon trapped in ice caps, scientists have been able to provide a calibration for the radiocarbon dates that permits translation into an approximation of a chronological year. These dates can change by thousands of years, with the commonly accepted Clovis-first date being approximately 11,500 radiocarbon year BP (i.e., 1950) or thirteen thousand chronological years ago.

The difficulty is further compounded in that the ingestion of carbon is a function of a person’s diet. People who have a diet high in marine food sources have a lower rate of carbon ingestion than do those whose diet is primarily of terrestrial origin.\textsuperscript{46} In addition, over the past ten thousand years, human activity has pumped vast amounts of dead plant carbon into the atmosphere through the burning of wood and hydrocarbons.\textsuperscript{47}
The question then becomes: when is a year not a year? It is not a year when attempting to calibrate chronological years with those of the different disciplines used in the search for the First Americans. This complexity of the dating problem was aptly captured in an article by Ted Goebel, the first footnote of which was as follows: “All ages are presented as ka (thousands of calendar years ago). Dates relating to genetic events are in calendar years based on coalescent methods. Dates relating to archaeological events are derived by calibrating radiocarbon ages. Radiocarbon dates younger than 21,000 14C years ago were calibrated with Calib 5.0.1 (IntCal04 curve); older dates were calibrated by using CalPal Online (CalPal 2007 HULU curve).”

What Goebel’s methodological caveat means is that a chronological year does not equal a genetic year, which does not equal a radiocarbon year. Furthermore, even within a single discipline such as genetics, a mitochondrial DNA (mtDNA) year does not equal a non-recombinant Y-chromosomal DNA (NRY) year. As Goebel continued, “The differences in calculations are the result of several issues, including potential variation in mutation rates, variable and sometimes circular techniques of calibrating coalescent times to calendar years, time-dependency of mutation and/or substitution rates, and effects of genetic drift on the original founding population.”

The chronological year has the merit of being easily understood and universally observed, and having been constant within a few seconds since well before human existence. It is also the standard against which these various “scientific” years attempt to calibrate themselves. Yet the disparities can be quite large. Geneticists have their problems with establishing chronologies. Geologists have their own set of issues. Carbon dating is a function of the mix of dietary intake and atmospheric gases, which have varied substantially over the period that covers the peopling of the Americas. This all produces a temporal incongruity where fifteen thousand radiocarbon years ago (i.e., before 1950) equates to over eighteen thousand chronological years ago (i.e., before today). At least that is the discrepancy that scientists currently believe is correct based on analysis of tree rings and ice core samples.

As advances occur in the ability of physics to provide other mechanisms for dating nature, more complications appear to arise. For example, by determining a point at which radioactive thorium 230 and radioactive uranium 234 reach an equilibrium point in their decay, it is possible to use a different physical clock to calibrate the carbon dating technique. Unfortunately, uranium-thorium dates raise questions as to the believed calibration between radiocarbon and chronological dates. First American scientists were confronted with one
of their members arguing that they faced the prospect that “the actual time of Clovis expansion may have been about 11,500 B.C., not 9,500 as indicated by radiocarbon.” The point is not whether that proposal prevailed, but rather that what is believed known may be proved wrong. Such is the very nature of science in general.

Other dating-associated problems arise. As discussed above, it is known that radiocarbon years can vary depending on annual variations in the natural creation of the carbon 14 isotope that is taken in by plants and animals. Consequently, it was necessary to find a reliable mechanism to calibrate radiocarbon years with chronological years. A method of choice has been provided by the science of dendrochronology—the counting of annual tree rings, a practice known at least as far back as Leonardo da Vinci—which has provided a calibration back to the start of the Holocene approximately ten thousand years ago. One of the first reported instances of the use of tree rings in support of the search for the First Americans was in 1788 by Manasseh Cutler to date American Indian mounds in Ohio.

As valuable as tree ring counting may be for some purposes, its use as a dating mechanism is generally conceded to extend only through the past approximately ten thousand years. Regardless of who they were or when they came, it is clear to First American scientists that the migrations to the New World happened before that time. Consequently, the calibrations between radiocarbon and chronological years become increasingly more suspect the farther back scientists venture into the critical period of interest in the search for the First Americans.

Another method for calibrating radiocarbon dating results with chronological years is the counting of layers of ice cores, typically in Greenland. However, it too has its share of controversies. One debate is centered on the extent to which the Earth’s climate is relatively stable, the uniformitarian hypothesis, and that annual layers of ice are relatively thin. Others counter that the climate is not stable, and the layers can be quite thick. The irony of using ice cores to calibrate radiocarbon dating is that ice cores themselves have to be calibrated and scientists use such measures as deep sea cores and volcanic acidity spikes in the ice cores.

Physics has contributed other techniques. Some are useful to the period of interest in the First American search. One is thermoluminescence dating, developed in the 1960s, which measures the amount of light released in crystalline materials when heated in a laboratory. The amount of light released is proportional to the time elapsed since the material was formed. Thermoluminescence is useful for dating these minerals between several thousand and a few hundred thousand years ago. It has been used effectively to document the forty-thousand-year-old
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The presence of humans in Australia. The decay of potassium $^{40}$ in minerals into argon $^{40}$ can only provide estimates beginning several hundred thousand years ago, since it takes over a billion years for even half of a sample of potassium $^{40}$ to decay into argon $^{40}$.

Despite the several weaknesses cited above to using radiocarbon dating in the search for the First Americans, a cottage industry has arisen offering dating to those who can afford the tariff. Sponsored by the Society for American Archaeology, commercial vendors set up booths offering services at the annual SAA academic convention with price lists for radiocarbon dating based on either AMS or liquid scintillation counting, and, of course, to be performed under the supervision of a staff of PhDs.

The tools of physics have become critical in the evidentiary debates surrounding the search for the First Americans. Yet, as Edwin N. Wilmsen originally wrote as early 1965, “radiocarbon dating is no miraculous tool; sound stratigraphy, observation, and correlation with geological and paleontological evidence become even more necessary as more precision in dating becomes possible.”