

Pre-Clovis in the Americas: Characterizing Early Sites, Material Culture, and Origins

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ABSTRACT

The number of pre-Clovis sites and materials that have been documented provide far more than the mere validation that sites older than Clovis exist. Some seemingly similar pre-Clovis features, tools, materials, and technologies have been reported from many different regions. The task now is to determine what similarities or differences are reflected in these early materials, and what this can tell us about the people who made them. Additionally, a vast array of occupation environments has been described. The differing economies, and cultural preferences, that this indicates may be suggestive of distinct pre-Clovis entries.

This paper will focus upon these topics, but it will also include several additional issues. These include human groups and tool types that may have descended from a common but distant ancestor, as well as those specimens that appear to be unique. Questions about selected analysis methods, and index species thus far ignored, will also be introduced.

The purpose of the conference and this publication is to expand our familiarity with pre-Clovis. Simply put, to determine what defines pre-Clovis, other than age. To accomplish this, we will consider multiple sites with dates older than 11,050 RCYBP (radiocarbon years before present).¹ Sites, features, and cultural material predating that age threshold will be described in detail by other authors in this volume. Further, the vast array of environments that supported early populations will also be addressed, as the early human arrivals in the Americas are tied to these landscapes.

The sites reported at this conference span an extremely lengthy period of time. We now know that the Americas were occupied 20,000 years before Clovis aged cultures emerged. Well dated sites now extend beyond 31,000 years of age in both North and South America, and multiple sites dating from 30,000-17,000 are not uncommon.² While some areas are now submerged, others are well above sea level. Importantly, terrestrial coastline and submerged sites are consistently older than inland sites. This speaks directly to older theories that suggested inland migration routes for the initial peopling of the Americas, as the dating of early sites does not validate such inland models. Further, as

¹ Clovis dates are currently described as 11,500-10,900 ¹⁴C yr B.P., adjusted to 11,050-10,800 ¹⁴C yr B.P. (Waters and Stafford, 2007).

² Florida has a date of 31,550 +/- 240 BP (Stanford, 2012), nine sites have now been reported as dated from 27,900 +/- 230 BP to 17,820 +/- 170 along the East Coast, as far north as Chesapeake Bay (Lowery, 2012), and sites such as Meadowcroft in Pennsylvania are exceedingly well documented to 16,175 +/- 975 RCYBP, SI-2354 (Adovasio and Donahue 1990; Adovasio 2012).

demonstrated by geoarchaeological investigators, and geologists, ice free corridors are not part of the northern Pleistocene landscape (Clark, 2012; Bryson and DeWall, 2007).

Early habitation and use areas are tremendously varied. Numerous geophysical regions on both continents support early sites, and multiple ecosystems are utilized. Pre-Clovis cultural material occurs in rock shelters, on valley floors, and upon coastal plains in North America (Fig. 1).³ The variety of early site environments identified in South America is also becoming increasingly diverse (Araujo, 2012; Schneider, 2009). So many sites have now been identified, in nearly every environment, that the widespread occurrence of early populations is clearly indicated. A geographic preference, however, is not. This is an important fact, as it tells us a great deal about early entrants. The broad distribution also suggests multiple origins, rather than a single entry.



Figure 1. Map of some Pre-Clovis sites in the Americas, showing their broad distribution. Many different regions and different environments were utilized. Paisley Cave and the Stafek site in Oregon, and On Your Knees Cave in Alaska, are not shown, but the location of the original Clovis type site is depicted. Illustration courtesy of the Smithsonian Institution.

³ Documentation of these early sites is provided by the authors in this publication, plus others such as Dillehay (1997) and Stanford (2012).

While dry land sites such as Meadowcroft and Monte Verde have long been documented and tightly dated, more underwater resources are being recognized. Cultural areas now include numerous saturated environments, including oceans, estuaries, rivers, and even high elevation lakes.⁴

Site features include some interesting challenges. This is due in part to their diversity, but also because of the many different types of environments in which they are observed. Features can occur as isolates, or with a distribution that covers a limited area or group of sites. Alternatively, some features may occur only within 300 miles of the current shoreline, but on several coasts.⁵ The interpretation, too, can be difficult, as some features do not occur at more recent sites. This lack of a more current proxy suggests changing life ways, and eliminates the possibility of looking to the historic or proto-historic record for explanation.

It is potentially significant that, like some site features, early cultural materials often evidence stylistic or technological attributes not observed in more recent materials. This change in technologies and tool types encourages the consideration of changing populations over time. As many early forms do not occur at more recent sites, despite the continued presence of many of the same food resources, a change in human populations is indicated.⁶

One of the exceptions to changing types over time is the Western Stemmed point. This type demonstrates that styles and technologies can extend over time, and in a large area. Thus, when other types from other areas do not persist, a replacement of populations may well be indicated.

Despite the challenge of identifying parent populations, the discussions need to happen if founding groups are to be recognized. One important issue is whether habitation and subsistence patterns, as well as artifacts, can reflect population origins.

⁴ Submerged sites are documented from 6,400øin elevation, down to sea level (Hemmings, 2012; Vastag, 2012; Stenger, 1997).

⁵ An early feature that is without explanation is a paper thin circular stain that is reported only in South Carolina and in Oregon (Lyttle, 2005; Goodyear, 2005; Stenger, 2012, 2005). Both site areas are terrestrial, and appear to be pre-Clovis.

⁶ While extinction of some megafaunal species occurred, many large terrestrial mammals continued forward into modern times. Further, at least some early human groups were not reliant upon megafauna, but instead focused upon many alternative food sources. This is well defined at the Gault Site (Speth et al, 2010).

The results of continued efforts to compare and contrast material culture would suggest that this is true. The styles and technologies of some woven and twined materials, and some lithics, compare well between Old and New World traditions (Adovasio, 2012; Stanford, 2012; Bradley, 2012).

The large, bipointed lithic biface styles of Europe have now been documented along segments of the east coast of North America (Fig. 2). Based upon the dating of organics associated with some of these lithics, the large temporal separation between the paleoamerican and Solutrean sites has been eliminated (Stanford and Bradley, 2012). The analysis of woven and twined cultural materials is similarly linking populations and technologies between the Old World and the New World (Adovasio, 2012).

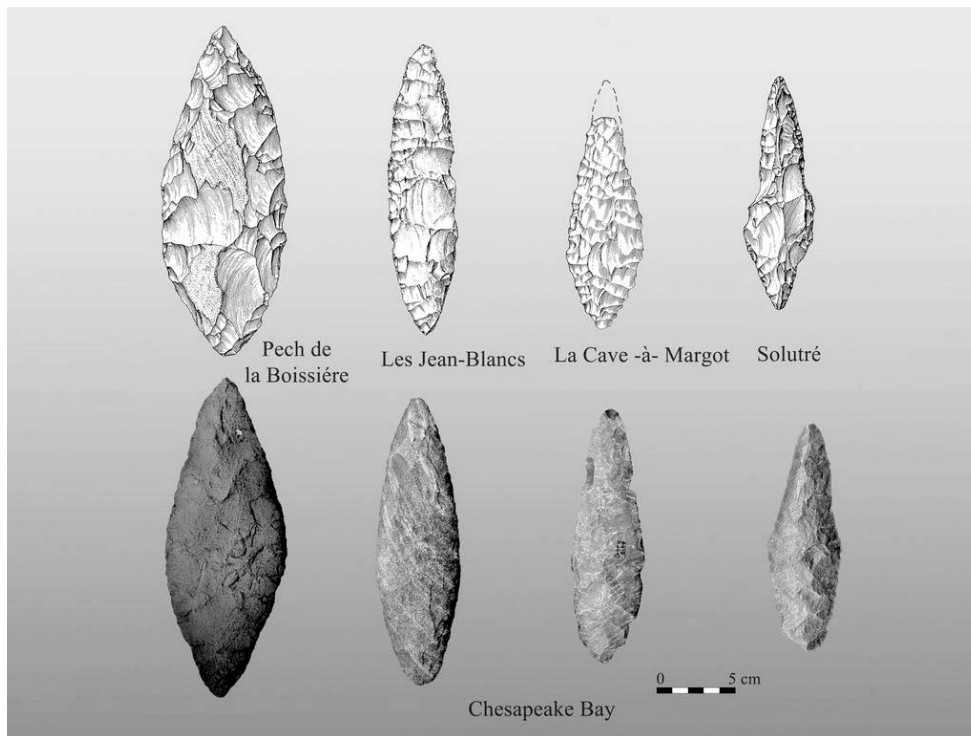


Figure 2. The large, bipointed lithic biface styles of Europe have now been documented along segments of the east coast of North America. The Solutrean style is no longer recognized exclusively in Europe. This figure courtesy of Chip Clark, and Dennis Stanford, Smithsonian Institution.

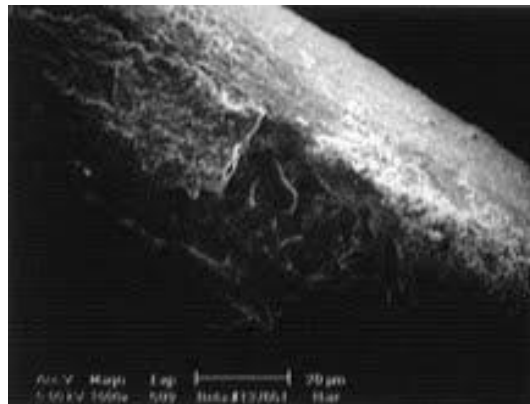
Underlying this line of inquiry regarding founding populations is the question of whether most culture bound behaviors translate well into new environments. Thus, do any of the early sites represent a new population that quickly failed? Can that account for the scarcity of some artifact types, and the seemingly unique features that are

documented? Would this explain the older skeletal material, and specifically cranial elements, that do not compare well with more recent population attributes?

The study of founding populations includes the analysis of mtDNA, when it is viable, as well as morphological studies. Yet the validity of the data is problematic. Importantly, morphological phylogeny is often at odds with molecular phylogeny. In other words, when studying ancient individuals, the results of cranial studies often contradict mtDNA findings (Chatters, 2012). Conflicting analytical results occur in other populations, as well. The anatomical and DNA studies of widely disparate species, from bears to lizards, yield the very same types of contradictory findings (Hailer et al, 2012; Losos et al, 2012).⁷

Added to the complexity of classifying early people in the New World is the lack of biological relationships with past populations. Some early New World human mtDNA reflects populations that have not been genetically mapped elsewhere (Baker 2,000). These ancient individuals appear to be an indirect ad-mixture of several different populations, but without a direct relationship to any known groups (Chatters, 2012).

A human hair from a pre-Clovis site in Oregon is an example of previously unmapped human DNA. The hair is morphologically human (Fig. 3). Genetically, it is *Homo sapiens sapiens*. Yet, while this specimen is from a fully modern human, it is unlike the mtDNA from any modern population group whose DNA has been mapped (Fig. 4). Just as we observe in the cranial studies of early Americans, the ancient people are distinct from contemporary populations.



⁷ As stated in the Losos article, “State-of-the-art molecular and morphological phylogenies differ fundamentally.”

Figure 3. Photomicrograph of the first Pleistocene human hair documented within Mill Creek drainage in Woodburn, Oregon. Authentication provided by Intermountain Forensics Laboratory, and image courtesy of Beta Analytic Radiocarbon Laboratory.

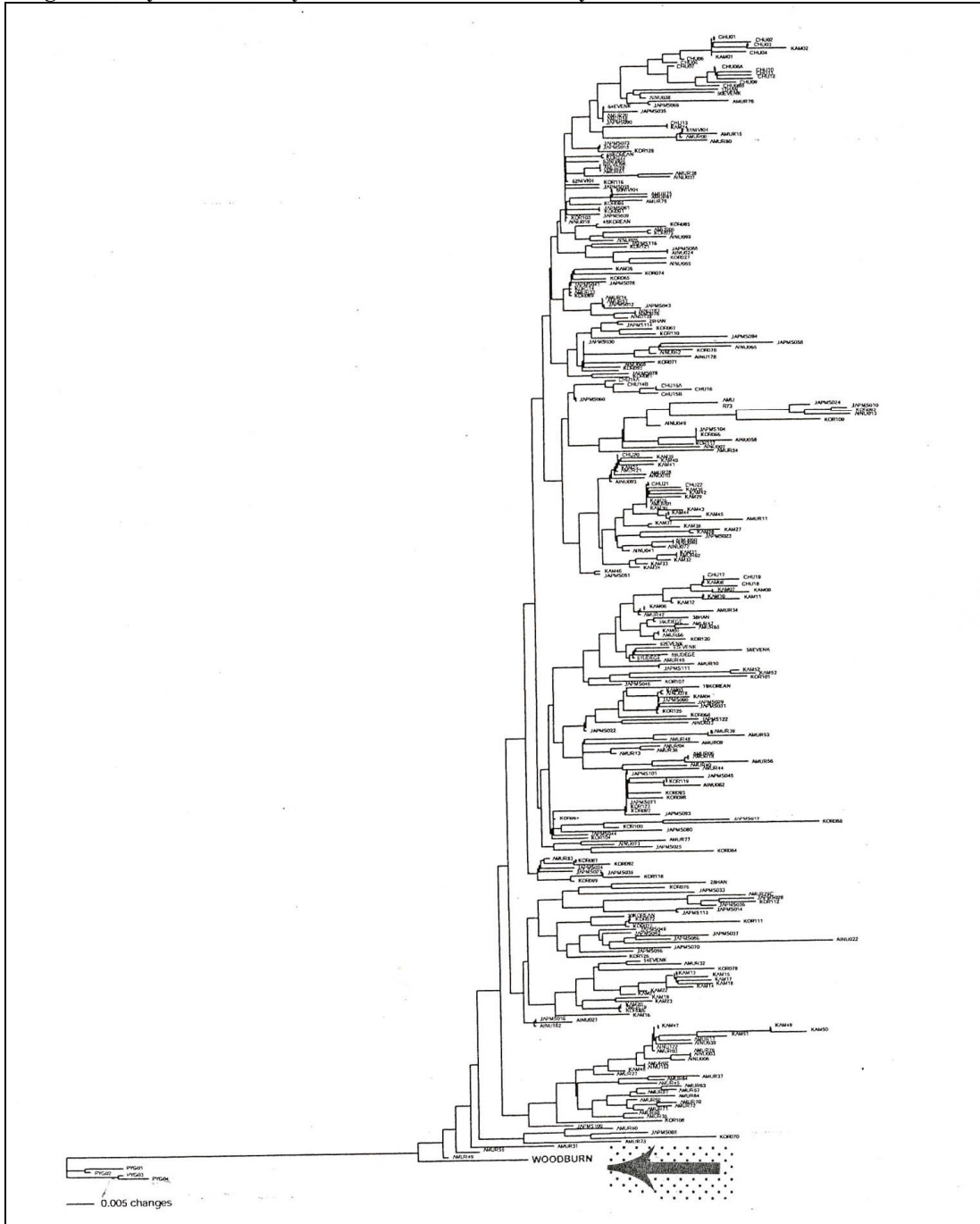


Figure 4. When the mtDNA from an ancient hair in western Oregon was analyzed, it proved to be unrelated to any previously identified population (Baker, 2000). The mtDNA from that hair is identified by an arrow at the base of this graphic, and labeled as Woodburn.

When researching the origin of the first Americans, the question of biological affinity is crucial. The artifacts and how they were used allows for an association with specific cultures, but to positively identify a population, biological attributes need to be evident (Jantz and Owsley, 2001; Jantz and Owsley, 2005). Thus, the current lack of corroboration between cranial studies and mtDNA suggest that a new approach to analyzing the DNA from early people may be useful. The most informative method of study, to date, is the examination of nuclear DNA.⁸ Due to cost, however, Y-chromosomal studies in combination with mtDNA are expected to lend plausible answers (Oppenheimer, 2012). This approach, of looking at more than mtDNA, may resolve the contradictory issues that sometimes exist between DNA and cranial studies.

Biological relationships between past and present population groups also need to be reconsidered. Reports of the findings from mtDNA studies often state direct relationships between groups, when descent from a common ancestor may be far more accurate. Two populations may actually have no direct relationship to each other.

The analysis of North American specimens is particularly troublesome, as the interpretation that is most often used is, at best, misleading. For example, early American remains are now often associated through mtDNA to areas such as Siberia and Beringia. Two profound questions accompany such an association. The first is whether the Siberian or Beringian populations are directly related to the American remains from below Canada. Or, do the groups from these very different geographic regions have an ancestor in common, but no direct ties to each other?

The second issue is even more problematic. Some scientists seem able to identify > 8,000 year old mtDNA from Siberian that associates with early American mtDNA (Gilbert et al, 2008). However, other notable scientists find no such association of early remains. These researchers reveal a total absence of similar material, between North America and Siberia, older than a few thousand years (Oppenheimer, 2012; Stanford and Bradley, 2012). This issue, in itself, suggests that mtDNA analysis is actually still in its early developmental stages, and very prone to interpretive error.

⁸ Nuclear DNA demonstrated very different results from mtDNA in bear populations, suggesting that mtDNA results may be extremely misleading, or even fully incorrect (Hailer et al, 2012).

The often incorrect description of mtDNA findings is shared with the public, and with special interest groups. As some public policies are formed based upon these results, it is important that the results are accurately conveyed. The lack of consensus among molecular biologists makes this impossible.

The many types of sites described in this publication, and the data obtained from them, should allow for many new aspects of site investigation. This may include the recognition of unanticipated DNA, and the detection of ancient bacteria and viruses. Additionally, in future work, pathogenic DNA sequences need to be considered. What pathogens have we missed, that could be pivotal in the survival of a Pleistocene species? Importantly for field personnel and site interpretation is the topic of continued viability of pathogens. Which pathogens may have survived millennia? The Mimi and Mega viruses are two examples of quite ancient pathogens that have only been identified in the past 24 months (Van Etten, 2011; Randerson, 2003). The previous lack of recognition was due only to the size of these viruses. As they far exceeded known viral sizes, no one expected them to exist. While this is reminiscent of "Clovis First" thinking, and not looking for evidence of older cultures, it is also a warning that we may be overlooking significant data. Other indicators of ancient origins do exist.

Due to the sensitivity of many pathogens, they may prove useful as index species, and hint at New World population origins. Studies of the hookworm parasite have shown its intolerance for environments that are too cold. Thus, the discovery of dead hookworms in pre-Columbian remains from colder environments strongly suggests population movement (Meggers, 2006; Jett, 2004, 2007).

All of these issues, from DNA and parasites to the study of site distribution, need to be addressed if we are to successfully synthesize the existing body of knowledge on pre-Clovis in the Americas. These data, now substantial in volume, will finally allow researchers to define paleoamerican populations.

The accurate histories of both North and South America are dependent upon conferences and publications such as this one. It is through the efforts of the Smithsonian Institution in hosting the Pre-Clovis in the Americas conference that the communication of these very important, new ideas can be communicated between scientists and the interested public.

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