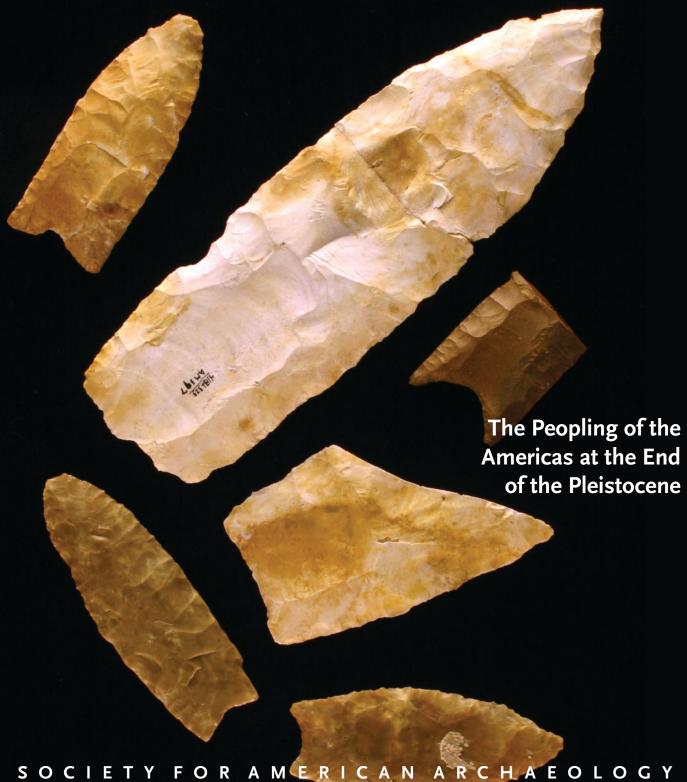
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On the cover: Clovis preforms and discarded Clovis projectile points from a 13,000- to 12,700-year-old lithic workshop buried in stratum 3 at Excavation Area 8 at the Gault site, Texas. This area was investigated by Texas A&M University. Photograph taken by Charlotte Pevny, Center for the Study of the First Americans. To learn more about this Clovis workshop, see Waters, Michael R., Charlotte Pevny, and David Carlson, 2011, Clovis Lithic Technology: Investigation of a Stratified Workshop at the Gault Site, Texas. Texas A&M University Press, College Station.





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EDITOR'S CORNER

Anna Marie Prentiss

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ne of the perks of editing the SAA Archaeological Record is the opportunity to develop article content. During my two terms as editor I have welcomed a wide range of submitted articles and special sections with discussions spanning global issues (climate change), human rights (LGBTQI issues, for example), new technologies (as in UAVs and video-technology), new theoretical models (e.g. anarchy theory), and diverse regional and topical areas (Patagonian to Viking archaeology). I have also maintained a long-standing goal of gender parity in authorship of our published articles. We were successful in our invited special section content but not quite as much in contributed articles where women's contributions remained at similar rates to that of American Antiquity. Clearly there is more work to do in that regard. Then, as the events of the recent annual meeting in Albuquerque so forcefully demonstrated, it is also clear that we must continue our efforts to better provide safe and welcoming environments for all of our members, whether at conferences, in the office, or in the field.

Peopling of the Americas is a central topic to many of us who work in this hemisphere and indeed it remains an essential issue for many scholars and publics around the globe. However, it is not a topic that has received very much attention in this periodical despite the extraordinary methodological, empirical, and ethical advances we have seen in recent years. So, for my final issue as editor, I asked Mike Waters, Ted Goebel, and Kelly Graf if they would organize and guest-edit a special section on this topic and I am very happy to provide the results of their efforts. Our special section, "The Peopling of the Americas at the End of the Pleistocene" features seven articles covering a diverse array of topics including genomic perspectives (Raff), community and indigenous partnerships in paleogenomic research (Malhi and Bader), Beringian archaeology (Goebel and Graf), routes into the Americas (Froese and colleagues), earliest occupations of North America (Waters), Pre-Clovis in South America (Politis and Prates), and the Clovis record (Jennings and Smallwood).

This issue includes important content beyond the special section. SAA President Joe Watkins offers his first "From the President" column. There is an important letter from the SAA Board of Directors concerning action on sexual harassment policy and safety concerns. Christyann Darwent authors our Volunteer Profile column. Katz and Kimmel contribute a timely discussion of safety in archaeology. Finally, we provide our annual reports stemming from the Annual Business and Awards Meeting. I thank the SAA staff, elected leadership, and membership for their support during my time as editor. I also thank the College and Humanities and Sciences and the Department of Anthropology at the University of Montana for supporting this venture. I thank Cheyenne Laue for being a great assistant and guest editor. Finally, it is my great pleasure to hand off the editorship of the SAA Archaeological Record to my esteemed colleague, Chris Rodning, of Tulane University. I have every confidence that the Record is in great hands for the coming years.

INTRODUCTION: THE PEOPLING OF THE AMERICAS AT THE END OF THE PLEISTOCENE

Michael Waters, Ted Goebel, and Kelly Graf

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ne of the most enduring debates in American archaeology centers on the late Pleistocene peopling of the Americas. For over 100 years, there has been much debate about fundamental questions: Who were the first Americans and where was their homeland? When did they arrive in eastern Beringia and what is the archaeological record of this region's earliest inhabitants? When did people travel south of the continental ice sheets that covered most of Canada? Which routes did the first Americans take to get south of the ice sheets blocking their path to the unglaciated portions of the New World? Once south of the ice, how did people explore and settle an unknown land with so many varied environments? These and other questions are important because genetic studies demonstrate that all modern Native people are descendants of the first humans to enter the Americas. The first Americans set the stage for all prehistory that followed.

These fundamental questions are discussed in the following set of seven essays. While these questions are far from being resolved, new archaeological, geological, and genetic studies over the last few decades are bringing us closer to the answers. The seven essays in this series provide an up-to-date overview of some of the important questions related to the peopling of the Americas. The first two papers discuss what we have learned from ancient and modern genomic research (Raff), and the importance of the Native American voice in this research (Malhi and Bader). Next, the archaeology and genomic data for Beringia are reviewed (Goebel and Graf). This is followed by an in-depth look at the corridors that were traversed as people moved from Beringia to the unglaciated areas south of the continental ice sheets (Froese, Young, Norris, and Margold). Two essays then review the early archaeological records of North America (Waters) and South America (Politis and Prates). The series concludes with a discussion of Clovis, the first widespread archaeological complex in North America (Jennings and Smallwood). These essays provide an up-todate summary of the state of our knowledge about the first Americans. We have come a long way, but there is much more work to be done.

GENOMIC PERSPECTIVES ON THE PEOPLING OF THE AMERICAS

Jennifer Raff

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ecent paleogenomics research on models for the entry and initial dispersals of humans in the Americas has focused on several questions: Which populations were ancestral to the First Peoples' of the Americas? What demographic events happened during this process? When did the inferred events occur?

The answers to these questions can serve as tests of longstanding archaeological hypotheses, such as the geographic origin of the ancestors of contemporary Indigenous peoples, the timing of the initial peopling, and even the route(s) taken during the initial peopling process. But, as we shall see, paleogenomics has also generated new hypotheses that need to be tested with archaeological ground-truthing.

Which Population(s) Were Ancestral to the First Peoples of the Americas?

Paleogenomics research in recent years has revealed that multiple populations contributed ancestry to the Indigenous peoples of the Americas. The genome of a 24,000-year-old child from the Upper Paleolithic Mal'ta site in south-central Siberia (Raghavan et al. 2014) showed that the population from this region, termed "ancient North Eurasians" (ANE), contributed between 14% and 38% of the ancestry seen in contemporary Indigenous peoples of the Americas. The remaining ancestry is related to present-day East Asian populations. However, these estimates should be interpreted cautiously; as Raghavan and colleagues note, they "assume unadmixed ancestral populations" (p 89). Paleogenomics has emphatically demonstrated that no population, ancient or contemporary, is "pure" or genetically homogeneous, and it is very likely that there was more genetic diversity present in these ancestral populations than our naming conventions imply. Indeed, a genomic investigation of ancient Siberian populations published on bioRxiv (Sikora et al. 2018), shows that ANE is a descendant of the "Ancient North Siberians" (ANS) that includes the population resident at the Yana RHS site (dating to ~31,600 calibrated years before present; all dates given here are calibrated), with additional ancestry

from early "Caucasus hunter-gatherer" (CHG), "Western hunter-gatherer" (WHG), and "Eastern hunter-gatherer" (EHG) populations. We can expect the East Asian ancestors of Native Americans themselves to have similarly complex genetic histories, although less is known about them at this time.

All genetic studies—whether based on uniparental markers or whole genomes—have emphatically ruled out a European source for pre-1492 ancestry of Native Americans as predicted under the Solutrean Hypothesis (Raff and Bolnick 2015; Rasmussen et al. 2014).

What Demographic Events Occurred during the Initial Peopling of the Americas?

Szathmary and colleagues (1978) suggested that all the peoples of the Americas were descended from a single ancestral population, and that the peopling of the Americas was a multi-stage process based on findings from classical genetic markers and cranial morphology. Comparative analyses of classical markers and mitochondrial and Y chromosome lineages revealed patterned variation consistent with expectations for a founder effect model (reduction in diversity compared to parent population, followed by radiation of new lineages). Analyses of mitochondrial genomes further identified a period of extended isolation (7,500-15,000 years) of the ancestral population, followed by one or more dispersals out of Beringia into North and South America, which has come to be known as the "Beringian Isolation," "Beringian Standstill," or "Beringian Pause" model (Tamm et al. 2007). Later analyses of whole mitochondrial genomes using a different mutation rate suggested a much shorter period of isolation, ranging from 2,400-9,000 years (Llamas et al. 2016).

Analysis of whole nuclear genomes has confirmed the Beringian Isolation model and revealed many additional details. Collectively, genomic analyses of contemporary and ancient peoples of the Americas (Moreno-Mayar 2018a, 2018b; Raghavan et al. 2014, 2015; Rasmussen et al. 2014; Rasmussen et al. 2015; Reich et al. 2012) show that the First Peoples are descended from an East Asian group that separated from its parental population

approximately 36,000 years ago. This group experienced gene flow with the parental population for an extended period of time (estimated to be around 11,000 years). At about the same time as this population ceased gene flow with its parent population, it experienced gene flow with the ANE population related to Mal'ta (at approximately 25,000 years ago). Following this event the population became isolated, during which time it evolved genetic variation unique to American populations. One explanation for the population fissions, gene flow, and isolation events is that they reflect population movements, perhaps in response to climatic events such as the Last Glacial Maximum (LGM).

The population isolated during the LGM (hereafter called "Ancestral First Peoples") split into at least three branches. One branch, known as the Ancient Beringians and represented by two genomes from the Upward Sun River and the Trail Creek Cave sites, diverged approximately 20,900 years ago, and continued living in Alaska after the end of the Last Glacial Maximum (Moreno-Mayar et al. 2018a). Another branch, currently referred to as "Unsampled Population A," diverged approximately 24,700 years ago. This group, which was first detected by its contribution to the genomes of the ancestors of the Mixe, has no currently known representatives in the archaeological record and is therefore poorly understood (Moreno-Mayar et al. 2018b). The third branch of Beringians moved south of the ice sheets. This branch split into three groups: one ancestral to Northern Native Americans (NNA), who include Algonquian, Na-Dené, Salishan, and Tsimshian speakers from Canada; one ancestral to Southern Native Americans (SNA), who include ancient and contemporary Central and South Americans, Anzick-1, Spirit Cave, and Lagoa Santa individuals; and one ancestral to an unnamed population represented by a 5,600-yearold individual from Big Bar Lake who appeared to have diverged prior to the NNA/SNA split (Moreno-Mayar 2018b; Posth et al. 2018; Rasmussen et al. 2014). It is likely that the Ancestral First Peoples also engaged in gene flow with a population ("Ancient Paleosiberians") in Siberia, as represented by the Kolymai genome (Sikora et al. 2018), presumably after northern Siberia was repopulated following the end of the LGM.

The two major genetic clades found in the Americas, NNA and SNA, are estimated to have diverged between approximately 17,500 and 14,600 years ago, just as routes for entry into the Americas were becoming open due to glacial retreat (Moreno-Mayar et al. 2018a). Gene flow between these two branches has been documented in the genomes of several descendant individuals, including Kennewick Man/The Ancient One (Moreno-Mayar et al. 2018b; Rasmussen et al. 2015; Scheib et al. 2018).

Details of the peopling of Central and South America have emerged in recent publications, revealing it to be a complex process marked by the migration of multiple genetically distinguishable groups at different times (Moreno-Mayar et al. 2018); Posth et al. 2018). One puzzling finding that has emerged from recent studies is a subtle genetic affinity between some South American Amazonian populations in the Amazon and Indigenous Australians, New Guineans, and Andaman Islanders (Raghavan et al. 2015; Skoglund et al. 2015). This affinity appears to be derived from a very ancient ancestor to both groups (called "Population Y" by the authors), rather than via a migration to the Americas by a group of Australasian ancestors (Skoglund et al. 2015). Some researchers have suggested that this signal is an artifact of sampling or analysis (Posth et al. 2018), but still others have confirmed it (Moreno-Mayar 2018b). Genomic characterization of more populations is needed to clarify this issue.

Implications for Archaeology

Although genetic data do not directly pinpoint the geographic location for the emergence of American-specific genetic diversity, the lack of gene flow between outside groups and the ancestral population is evidence in favor of this isolation having taken place within Beringia itself. It would have been difficult for a population to remain isolated within southern Siberia or coastal Northeast Asia, and the archaeological record indicates that central and northern Siberia were abandoned during this period, likely due to environmental conditions associated with the Last Glacial Maximum. Paleoclimatic reconstructions show that certain regions of Beringia experienced higher productivity and warmer average temperatures than central and northern Siberia, making them possible candidates for an LGM refugium (Hoffecker et al. 2016; Sikora et al. 2018). Additionally, the findings of Population Y, Unsampled Population A, and Ancient Beringians in addition to the ancestors of the Big Bar Lake population, NNA, and SNA clearly indicate that the Beringian ancestral population was not homogeneous. It may be that there was genetic structure within the initial population, as well as additional structure developed during its isolation. If the latter were true, this would imply some weak barriers to gene flow existed, either in the form of geographic dispersal over a large area, or perhaps subdivision in separate refugia. If this model is correct, there must be archaeological evidence of human occupation of Beringia during the LGM. Although much of central Beringia is now underwater and inaccessible, much of western Alaska remains under-surveyed. It is there that archaeological evidence of the Beringian Isolation could be sought.

Secondly, because descendants of both NNA and SNA branches are equally related to the Ancient Beringians, it is most likely that their divergence happened after migration into North America south of the retreating ice sheets, cutting off gene flow between them and the Ancient Beringians remaining in Alaska (Moreno-Mayar et al. 2018a). The genetic relationship between the Big Bar Lake individual and NNA/SNA fits a scenario for a

divergence of the ancestors of the Big Bar Lake population prior to this migration (Moreno-Mayar et al. 2018b). If this series of population splits left an archaeological signature, we might expect it to be found in Alaska and along potential dispersal routes.

The series of rapid population splits reflected in ancient South American genomes argues strongly for a peopling process "akin to leap-frogging across large portions of the diverse intervening landscape" (Moreno-Mayar et al. 2018b:18). This is consistent not only with the unimpeded movement of peoples into previously unoccupied lands, but also with the more rapid dispersal process via boat (rather than more slowly by foot across land). Indeed, evidence from eDNA taken from lake sediment cores in the center of the ice-free corridor region (Pedersen et al. 2016) shows that the interior route was not viable until about 12,600 years ago, supporting a coastal route as the most likely path of initial dispersal of pre-Clovis peoples. This too is a hypothesis that needs further testing with archaeological data.

The Future of Ancient DNA Research in the Americas

As I hope is clear from the above review, paleogenomics research has contributed immensely to the field in recent years. And yet, this contribution is not without critiques (some of them well-merited, some of them perhaps not). The concern I see voiced most frequently by the archaeological community is the occasional lack of a nuanced understanding of the work that has already been done in a research area prior to the undertaking of genetics research, and the lack of true partnership between geneticists and archaeologists (and other specialists) in developing projects and interpreting data. We geneticists would do well to pay attention to this critique—which obviously doesn't apply to all research groups—as the most accurate understanding of history derives from explanations that incorporate data from different sources. Meaningful interdisciplinary collaborations are essential for future research relating to questions about the initial peopling of the Americas.

In addition to DNA from humans, aDNA from nonhuman beings is increasingly being used to clarify details of early Pleistocene history. Environmental DNA and genomes from dogs, megafauna, pathogens, plants, and parasites can all provide insights into the environment and behavior of the first humans in the Americas, and I expect that this is one area of paleogenomics that will be extremely productive in future years.

Finally, it is important for all researchers in this area to be aware of ethical issues inherent in conducting genomic analyses of ancient and contemporary Indigenous peoples. The history of genetics research in the Americas is unfortunately marred by exploitation and insensitivity to the concerns and priorities of Native communities. I urge geneticists and archaeologists

both to center ethics and consultation in study design and implementation; guidelines for doing so have recently been published (Bardill et al. 2018). For a fuller discussion of this subject, I recommend reading the piece by Malhi and Bader (this issue).

Note:

I. I use this term in lieu of "First Americans" at the request of Indigenous colleagues to avoid projecting backwards in time the implication of membership in a colonizing nation-state.

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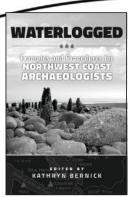
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HUMAN PALEOGENOMIC RESEARCH IN THE AMERICAS

A LOOK AT CURRENT DATA AND VISION FOR MORE INCLUSIVE PRACTICES NOW AND INTO THE FUTURE

Ripan S. Malhi and Alyssa C. Bader

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aleogenomic research is often touted as "revolutionizing the study of the past." Much of this excitement and optimism is due to advances in DNA sequencing technology and computational genomic analysis, such as the development of High-Throughput Sequencing (HTS) and the multitude of bioinformatic pipelines built to analyze the billions of DNA sequence reads that result from an HTS run. Initial ancient DNA studies of Indigenous ancestors in the Americas in the early 1990s focused primarily on analyzing parts of the mitochondrial genome, providing a window into the past based only on the direct maternal line. Human paleogenomic studies today have much more data because of the capacity to generate genome-wide data with information not only about the individual sampled but also about their ancestors expanding beyond the direct maternal line. This allows for a population-level analysis to occur with the sequencing of a single individual.

But as the field of paleogenomics continues to grow in exciting new directions, we face important considerations. First, the rapid expansion of DNA sequencing preparation methods means there are many different types of paleogenomic data accessible to researchers, but the various biases and limitations of these datasets have not been widely discussed. Second, the field is positioned at a critical point in its ethical development. While much of the early research in paleogenomics failed to incorporate meaningful elements of community engagement, or even consultation, paleogenomic researchers are increasingly working to use methods that are more inclusive. By using frameworks that center research on the linked Indigenous community instead of the academic lab, we will diversify the experiences and knowledge used in paleogenomic research, ensuring the results

are mutually beneficial to Indigenous peoples, researchers, and society as a whole.

Uses and Limitations of Human Paleogenomic Data in the Americas

Paleogenomic studies of Indigenous ancestors in the Americas have generated multiple types of DNA sequence data (Table 1). Comprehensive reviews of the technologies and analytical methods in human genomics used to generate these data have already been published, and we refer you to these articles in the References Cited. Specifically, the details of HTS and associated methods in paleogenomics are described in a recent issue of *The SAA Archaeological Record* by Hofman and Warinner (2019). In addition, Harris and DeGiorgio (2017) provide an overview of the conceptual principles of *f*- and *D*-statistics and other analytical methods that are currently being used in paleogenomic studies. Here, we categorize the existing DNA sequence data from the Americas into five sets and briefly discuss their uses and limitations.

I. There exist a small number of low-moderate coverage genomes from ancient individuals in the Americas (e.g., Moreno-Mayar et al. 2018; Rasmussen et al. 2014). Of the paleogenomic datasets that exist, these genomic data likely exhibit the least bias when inferring population history and genetic relationships among ancient and present-day individuals because nearly all of the information present in human genomes can be used to estimate genetic relatedness. Although this type of data is currently used to investigate questions on a continental scale, including the peopling of the Americas, low-moderate coverage

Table 1 Paleogenomic Datasets in the America	
	c

Data type	Nucleotides in human genome	Genomic region(s)
Low-moderate coverage genomes	1x–18x coverage	Full human genome
Genome-wide shotgun data	<ix coverage<="" th=""><th>Random coverage across human genome</th></ix>	Random coverage across human genome
Human Origins data	~1.2 million	Human regions previously identified as polymorphic in worldwide population panel
Whole-exome data	~40–60 million	Human protein-coding and adjacent regulatory regions
Metagenomic data (e.g., dental calculus/coprolites)	Usually <<.1x	Human-associated bacteria, pathogens, and consumed flora and fauna

genomes can also be useful when studying regional population history in the Americas—addressing hypotheses that may more strongly impact present-day Indigenous communities. Here, we note that all paleogenomic data likely exhibit unknown DNA damage patterns that manifest in a phenomenon called "ancient DNA attraction." That is, in some genomic analyses, geographically and/or temporally distant (presumably unrelated) individuals exhibit a closer genetic relationship than expected due to shared artifact structure, likely as a result of DNA damage. For continental-scale analyses, the extent of the bias caused by these unknowns is likely negligible, but may be more pronounced in regional-scale analyses.

- 2. A large proportion of human paleogenomic data in the Americas consists of genome-wide shotgun sequence data. This data consists of random DNA sequences across the human genome. Genome-wide shotgun sequence data have also been used to address continental-scale questions on evolutionary history when compared to whole genome data from ancient and present-day individuals (e.g., Scheib et al. 2018). This shotgun sequence data can show broad differences in ancestry between individuals from different geographic regions in the Americas. However, individuals with this type of data can rarely be directly compared because they will usually only have a small overlap of DNA sequence from homologous regions and this data is therefore much more limited when addressing regional-level questions.
- 3. The Human Origins dataset is derived from genomic capture methods. Practically, this means that the same genomic regions are sequenced and comparable in every sample, and so this data is useful for both continental-scale and regional-scale questions (e.g., Posth et al. 2018). The genomic regions captured and sequenced in Human Origins datasets are informative regions derived from sequencing genomes of present-day individuals

from a worldwide panel and should therefore exhibit less ascertainment bias. However, the worldwide panel included only one individual from South America and no individuals from North America, so it is likely that the Human Origins capture would exhibit bias among Indigenous peoples of North America as some genomic variants that exist in North American populations would not be represented in this dataset. As a result, populations in North America will artificially exhibit less variation when compared to populations in South America due to the genomic regions sequenced in this dataset. Also, researchers using this capture method in North America will have fewer variants to detect subtle admixture and other demographic events that occurred within North America in the past.

- 4. Whole-exome datasets in the Americas also use capture methods. In this case, the genomic regions being captured for sequencing are the protein-coding regions and adjacent regulatory regions of the human genome. Whole-exome data are much more limited in paleogenomic data in the Americas but have been used to address regional human population history. However, whole-exome data are ideally suited to assess environmental influences and natural selection acting on human genomes over time, because the genomic regions sequenced are directly translated to phenotypes (e.g., Lindo et al. 2016).
- 5. An emerging paleogenomic dataset in the Americas consists of meta-genomic data from sources like dental calculus and coprolites. This data usually consists of DNA sequences from human commensal bacteria, pathogens, and flora and fauna consumed by the ancient individual to address questions of diet and health in the past.

Knowledge of the uses and limitations of the many forms of paleogenomic data available from the Americas should facilitate better integration of archaeological and paleogenomic data for hypothesis testing.

Moving Toward More Inclusive Practices in Paleogenomic Research

Paleogenomic researchers studying Indigenous ancestors have the opportunity to revolutionize the study of the past not just by expanding the breadth of genomic tools available but also by strengthening the ethics of their research practice. Human paleogenomic studies in the Americas are beginning to undergo a shift in study design toward inclusion and community-based research methods. Most human ancient DNA studies in the Americas during the 1990s and the turn of the twentieth century were published with no consultation or engagement with local (to where the ancestral remains were found) Indigenous communities. Notable exceptions to this trend include ancient DNA analyses of Kwäday Dän Ts'inchį, or "Long Ago Person Found" (Monsalve et al. 2002), Shuká Káa (Kemp et al. 2008), and ancient individuals from the Great Basin and Aleutian Islands (O'Rourke et al. 2005). Over the last decade, a significant shift in research practices has occurred with some paleogenomics studies incorporating elements of community-based research practices.

This shift mirrors developments across several other related fields, including archaeology. Frameworks like Indigenous archaeology (Nicholas 2010; Watkins 2000) and community-based participatory research (Atalay 2012; Atalay et al. 2014) have worked to address similar challenges in the field of archaeology by decolonizing or Indigenizing archaeological methods and practices. These provide models for collaborative work with Indigenous communities where research intersects with Indigenous knowledge, upholds community values, redresses previous unequal research practices, and

broadens interpretations of the generated data (Nicholas 2010). Similar frameworks have been created in the field of health genomics as well, such as Hudson and colleagues' (2016) model incorporating a Maori knowledge base (Figure 1). In addition, the SING Consortium recently provided an ethical framework for health genomics research with Indigenous communities, where the community is central, instead of ancillary, to the research project (Figure 1; Claw et al. 2018). In summary, researchers do not need to start from scratch when developing inclusive methods to employ in paleogenomics research. Practitioners can incorporate and modify existing frameworks for Indigenous community engagement from other fields. Additionally, resources are already beginning to emerge within the field of paleogenomics, such as the ethical guiding questions for researchers developed by the SING Consortium (Bardill et al. 2018).

To better illustrate the potential for more inclusive and engaged paleogenomic research with Indigenous communities, we have created a "paleogenomic community engagement chart" based on three interrelated axes (Figure 2): I) Indigenous research team, 2) Community-centered approach, and 3) Local responsibility.

The *Indigenous research team* axis measures the proportion of the research team members who are Indigenous, including the Principal Investigator. Projects that include Indigenous team members, who potentially have shared histories and experiences with local community members linked to the ancestor(s) under study, may more effectively navigate the potential risks and needs of the communities. However, the ancient DNA field (and STEM fields in general) have a dearth of Indigenous practitioners and trainees

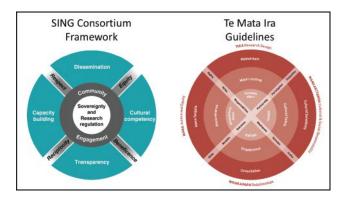


Figure 1. Ethical frameworks for health genomics research with Indigenous communities by Claw et al. (2018) left, and Hudson et al. (2016) right.

Paleogenomic community engagement chart

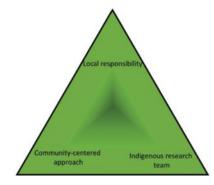


Figure 2. Paleogenomic community engagement chart.

in the educational pipeline to become paleogenomic researchers. To address this issue, the Summer internship for INdigenous peoples in Genomics (SING) program was founded in 2010 and is working to 1) increase the number of Indigenous leaders in genomic (including paleogenomics) fields, and 2) train Indigenous scientists to use genomics as a tool within an Indigenous framework and worldview. SING currently runs three week-long workshops annually in the US, Canada, and New Zealand. The program has graduated over 100 participants from Indigenous communities and has created a worldwide network of Indigenous scientists and scholars. The SING Consortium is under the umbrella of the SING program and consists of faculty and graduates of SING who publicly comment on and help create policy for genomic research with Indigenous communities. This program has been successful in creating a public voice for Indigenous scientists in genomics as well as mitigating isolation of Indigenous students in STEM fields. Both of these actions are helping to increase the number of Indigenous leaders in genomics and related fields.

The second axis, labeled Community-centered approach, measures the degree to which the study incorporates Indigenous knowledge, adheres to tribal research regulations and sovereignty, and involves linked community members in the research process. Studies that embrace a community-centered approach by incorporating community-held knowledge and values into the research process will create and test hypotheses that are of value to local Indigenous peoples as well as the broader scientific community. For example, Tsimshian society is based on matrilines, each of which have their own oral history, or adawx, to provide a record of historical events and key figures in the past. Adawx have an inherent chronology based on references to geological or historical events so that collectively, the adawx preserve a history of the Tsimshian from multiple perspectives (Martindale and Marsden 2003). Researchers who continue to use past colonial research practices and choose not to involve community members in the research process may miss details of local population history or demographic events that would strengthen their research questions or interpretation of results.

The third axis, labeled *Local responsibility*, measures how the study provides benefits to the linked community as well as to society more broadly. Paleogenomic studies that minimize risks to linked communities and provide tangible, more immediate benefits that meet the needs of the community exhibit local social responsibility and justice. For example, an ancestral cemetery on the coast at Point Barrow, Alaska, has been eroding and contributing to the loss of ancestral remains into the ocean. The Utqiagvik community partnered

with researchers at universities in the US to remove the remaining ancestors for reburial further inland, and the community encouraged skeletal and paleogenomic analyses of the ancestors before reburial to learn about ancient lifeways and local population history. Community high school students were hired to assist with the project and were taught scientific excavation and laboratory methods. Lastly, before the study is completed, there are plans for the research findings to be developed into accessible educational materials for community members (Bardill et al. 2018). These activities ensure that the paleogenomic research is not extractive, but part of a mutually beneficial collaboration between Indigenous communities and researchers.

Based on these three measures, studies that continue to use more colonial research paradigms by choosing not to engage with local communities or include Indigenous team members will reside on the edges of the chart. For example, studies where the only community engagement was to obtain permission to study the ancestral remains from a linked community would still fall on or near the edges of the chart. In contrast, paleogenomic studies that have multiple Indigenous team members, partner with communities throughout the research process for coproduction of knowledge, and have immediate tangible benefits for community members will be located more toward the center of the chart. The ideal community engagement methodology will vary based on the objectives, needs, and resources of the research partners. As a whole, human paleogenomic research studies in the Americas should continue the transition to more inclusive, community-centered practices, moving from the edges toward the center of the community engagement chart.

Archaeologists who are considering incorporating paleogenomic analyses into their research in the Americas should consider the uses and limitations of different types of DNA sequence data, and which ones might best address their research questions. Paleogenomic research can also impact present-day Indigenous communities. By using inclusive, community-centered practices, archaeologists can ensure that their studies are mutually beneficial to Indigenous peoples, researchers, and society as a whole.

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BERINGIAN ARCHAEOLOGY AND ANCIENT GENOMICS

A NEW SYNTHESIS

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enetic models based primarily on ancient DNA from archaeological specimens are now steering archaeological research in Beringia. They have incentivized archaeologists to search for archaeological evidence in new places, both geographically and geochronologically, and they are pushing us to reconsider long-held theoretical perspectives explaining technological variability in the Upper Paleolithic record.

Briefly, the current genomic model predicts that humans dispersed from two core areas in greater northeast Asia (central Siberia and eastern Asia) to Beringia, becoming isolated there by about 20,000 calendar years ago (cal BP). During the next ~5,000 years, a distinctive ancestral Native American population emerged, along with at least one other population that became uniquely Beringian. Around 15,000 cal BP, as western Canada's ice sheets were rapidly receding, the ancestral Native American population dispersed southward through one or two ice-free corridors, along the Pacific coast or east of the Cordillera.

The archaeological populations that contributed to the peopling of Beringia and America, therefore, are predicted to have been the Upper Paleolithic people of Siberia and eastern Asia, either mainland China and Korea or maritime Japan. Technologically, we know that these people primarily used two or three major lithic industries to produce the tools needed for survival: bifaces, blades, and, at least late in the Upper Paleolithic, microblades. In addition, Upper Paleolithic material culture included carefully formed osseous tools such as points, awls, and needles made of ivory, antler, and bone, as well as distinctive beads and pendants made of a variety of materials. These hunter-gatherers practiced a highly mobile lifestyle, although in places the remains of substantial dwellings suggest at least seasonal, likely winter, sedentism. Their

adaptation was fundamentally terrestrial and centered on large game, but subsistence also often included small fur-bearing mammals and waterfowl (even fish in some late Upper Paleolithic contexts). In the Japanese Archipelago, technologies included watercraft needed to colonize nearshore islands where important lithic resources like obsidian could be obtained. Generally, then, this well-documented assortment of northeast Asian Upper Paleolithic traditions, stretching from Lake Baikal in Siberia to Hokkaido Island in Japan, represents the immediate archaeological ancestors of the first Beringians and, ultimately, Native Americans.

Paleoecologically, without question the peopling of Beringia unfolded on the northern mammoth-steppe; however, our understanding of this important late-Pleistocene biome continues to evolve. Early portrayals of a northern Serengeti-like environment certainly were oversimplifications. A patchwork of different habitats existed during full-glacial times, from polar desert in upland areas to treeless tundra-steppe in low-elevation arctic and subarctic plains, in some places dominated by sedges and grasses, in others, herbs. Even isolated refugia of shrub tundra appear to have existed during full-glacial times, as Scott Elias and Barnaby Crocker have shown with fossil beetles, paleobotanical remains, and paleosols for the now-submerged central land bridge (Elias and Crocker 2008). Species-specific genomic histories and radiocarbon chronologies of the mammoth-steppe fauna indicate a dynamic and variable environment both geographically and temporally, with extinctions occurring asynchronously, under variable pressures. Wapiti (Cervus canadensis), for example, was once considered to have been absent from the mammoth-steppe during the full glacial; however, geneticist Ian Barnes and colleagues (Meiri et al. 2014) have shown that this browsing ungulate surprisingly persisted in low-population densities in



Figure 1. Late-glacial Beringia showing locations of archaeological sites mentioned in the text: 1) Yana sites; 2) Urez-22; 3) Nikita Lake; 4) Berelekh; 5) Ushki; 6) Serpentine Hot Springs; 7) Raven Bluff; 8) Lake E5; 9) Bluefish Caves; 10) Owl Ridge; 11) Teklanika West; 12) Nenana Valley sites, including Dry Creek, Walker Road, Moose Creek, and Panguingue Creek; 13) Eroadaway; 14) McDonald Creek; 15) Upward Sun River; 16) Swan Point, Broken Mammoth, Mead, Keystone Dune, and Holzman; 17) Linda's Point; 18) Little John; 19) Tangle Lakes sites.

isolated refugia in western Beringia through the last glacial maximum, and rapidly dispersed across the rest of Beringia to the Americas during the late glacial, paralleling the modeled dispersal of humans. Wapiti's spread to Alaska coincided with climate amelioration during earliest late-glacial warming.

A major expectation of the genomic model of human dispersal is that we should not expect a human population in Beringia that was immediately ancestral to Native Americans until after the last glacial maximum, which spanned 28,000–19,000 cal yr BP. If correct, then the amazingly preserved early Upper Paleolithic record at the 32,000-cal-BP Yana site (and others nearby that are potentially even earlier in age) in the high Arctic of Asian Beringia (Figure 1; Pitulko et al. 2017) is not directly tied to the peopling of the Americas. This is supported by newly reported ancient DNA recovered from human teeth at the site (Sikora et al. 2018). Genomically, the Yana people appear to represent a population of northern Siberians who contributed to the peopling of the Americas only indirectly, via a descendant Mal'ta or later Upper Paleolithic population who

existed around Lake Baikal in southern Siberia 24,000-14,000 cal BP. Nonetheless, the well-preserved Yana sites, with their osseous technologies (which include an amazing ivory bowl among other well-crafted decorative pieces), preserved features, and associated large-mammal remains, represent a sustained occupation of the arctic plain of western Beringia during a relatively warm interstadial, ~4,000 years before the onset of the last glacial maximum. So far we have no clear evidence of early Upper Paleolithic Alaskans, but a new study of sediment cores from Lake E5 on the North Slope suggests the presence of human fecal biomarkers in sediments dated to 31,000-22,000 cal BP (Vachula et al. 2019). These results are compelling but require verification (through archaeological survey and perhaps environmental DNA analysis) and a clear presentation of the taphonomy of such molecules, because they seem to be virtually absent from the Holocene component of the core, a time when we know humans existed in the area.

With the side-lining of Yana, we suddenly have no early footprint of the predicted Beringian population ~20,000–15,000



Figure 2. The Urez-22 Upper Paleolithic site. Photograph courtesy of Vladimir Pitulko.

cal BP, unless the early record from Bluefish Caves, Yukon (Canada), is validly archaeological and not just paleontological. Excavated by Jacques Cinq-Mars in the 1970s, for many years the fate of Bluefish as a full-glacial archaeological site hinged on acceptance of a 'core and flake' on mammoth bone (directly radiocarbon dated to 23,500 cal BP) as human-produced, but now it centers on possible cut marks on a horse and caribou bone, both directly dated to 24,000–22,000 cal BP (Bourgeon et al. 2017). These pieces, however, make up <0.01% of the faunal assemblage, and without clearly associated lithic artifacts the Bluefish record still fails to satisfy many northern archaeologists. Thus, we still lack unequivocal evidence of Upper Paleolithic Beringians at the genetically appointed time, ~20,000–15,000 cal BP.

After 15,000 cal BP, the record of Upper Paleolithic humans in Beringia mushrooms, on both sides of the land bridge. In western Beringia, Vladimir Pitulko's recent field surveys in the lower Yana-Indigirka lowlands, north of the Arctic Circle, have led to the discovery of Upper Paleolithic sites in addition to Yana. Most important is Urez-22, dating to the period of 14,800-14,100 cal BP and yielding lithic artifacts and bones of mammoth (Figure 2), as well as worked pieces of ivory, including a spear-point blank. The lithic industry includes clear microblade technology, an obvious sign of the late Upper Paleolithic Diuktai culture. Across the land bridge in Alaska the earliest unequivocal evidence of humans is still the Swan Point site, dating to ~14,100 cal yr BP. The record is similar to that from Urez-22, although more expressive, with Yubetsu-style wedge-shaped microblade cores having been reduced on site, as well as ivory materials having been worked into a variety of forms (Gómez Coutouly

2012; Hirasawa and Holmes 2017; Lanoë and Holmes 2016). Along with Urez-22, the Swan Point industry chronicles the dispersal of a Diuktai-like complex into Beringia, not surprising given the preponderance of such microblade technologies across interior northeast Asia in the millennia leading up to this time. More remarkable is the >15,000-year-gap that still separates these earliest late-glacial sites at 15,000-14,000 cal BP and Beringia's early archaeological record at Yana (32,000 cal BP). Equally confounding is the apparent 5,000-year lag between these first-known late Upper Paleolithic industries (<15,000 cal BP) and the genomically modeled timing of Asian dispersal to Beringia (i.e., 20,000 cal BP). Either we are still missing an important segment of Beringian prehistory, or the genomic models are inflating the timing of dispersal from Asia to Beringia.

After 14,000 cal BP, late Upper Paleolithic sites abound, but they have a decidedly Beringian character, what Roger Powers and John Hoffecker (1989) originally termed the Nenana complex. The first Nenana complex sites to be excavated and unequivocally dated to before 13,000 cal BP (the Allerød interstadial) were in the Nenana River valley of interior Alaska. Repeated stratigraphic contexts at Dry Creek, Walker Road, and Moose Creek produced a consistent lithic industry of small triangular or teardrop-shaped bifacial points (generally called Chindadn points), end scrapers, side scrapers, and marginally retouched blades and blade-like flakes, often associated with hearth features. Since these early excavations in the 1970s-1990s, additional Nenana complex-like industries from Allerød contexts have been found, and continued research has yielded much new information. Renewed excavations at the Dry Creek type-site, for example, have pushed the age of this earliest occupation of the Nenana valley to ~13,500 cal BP (Graf et al. 2015), and at the Owl Ridge site in neighboring Teklanika valley, another Nenana complex industry recently has been dated to 13,400-12,800 cal BP (Gore and Graf 2018). In the middle Tanana River valley, about 150 km to the east-northeast, David Yesner and Chuck Holmes in the 1990s established the presence of a Nenana-like industry at the Broken Mammoth site, with well-preserved remains of large mammals (e.g., bison) as well as waterfowl (e.g., swans), again dating in excess of 13,000 cal BP (Yesner 1995). Since those pioneering excavations at Broken Mammoth, additional industries potentially ascribable to the Nenana complex have been found at Linda's Point along the north shore of Healy Lake (Younie and Gillispie 2016) as well as at the nearby Keystone Dune, Mead, and Upward Sun River sites (e.g., Lanoë et al. 2018; Potter et al. 2013), all potentially predating 13,000 cal BP. The newest Nenana complex occupation to be excavated (and possibly the oldest yet found) is at McDonald Creek (Figure 3), located along the Tanana River about halfway between Dry Creek and Broken Mammoth. There we

have exposed a well-preserved ~13,800-cal-BP living floor with core-reduction and small retouch debitage, a triangular Chindadn point, and several biface fragments, associated with large-bodied mammals like steppe bison and elk, large birds such as swan or eagle, fur-bearers (possibly marten), and dog or wolf. Nenana complex industries appear to continue into the Younger Dryas, too, as late as 12,700 cal BP at sites like McDonald Creek (C2), Eroadaway in the upper Nenana River valley, and Little John in Yukon, Canada, and possibly even later at Swan Point (CZ3; see Goebel and Potter 2016). In none of these Nenana assemblages, from 13,800 to 12,700 cal BP, is a clear microblade industry present. Swan Point (CZ3) may contradict this pattern, but this is not surprising given its late age, after which microblades abound in the central Alaskan archaeological record.

The Nenana pattern is replicated in western Beringia, in both Kamchatka and the Yana-Indigirka lowlands. Kamchatka's Allerød record is dominated by the well-known early Ushki culture, with its well-preserved dwelling, hearth, and burial features, and its characteristic lithic industry with small bifacial points, albeit stemmed and not triangular or teardrop-shaped. A series of dates from two Ushki localities demonstrate this occupation occurred ~13,000 cal BP. Again, though, the most compelling new evidence from Asian Beringia has been found in the Yana-Indigirka lowlands, this time from the Nikita Lake site, located near Urez-22. Here Pitulko and colleagues (2017) recently unearthed butchered mammoth remains associated with teardrop-shaped bifacial points (which they unhesitatingly label Chindadn) as well as ivory debitage and spear-point preforms dating to 14,000-13,700 cal BP. Complementing this is Pitulko's renewed work at the Berelekh site along the lower Indigirka River, where he found a similar assemblage, again with teardrop-shaped Chindadn points and rough ivory artifacts, > 13,500 cal BP. Bifacial points with coarse stems have also been found at Nikita Lake and Berelekh, potentially linking them with Ushki. Importantly, neither the early Ushki nor the Nikita Lake/Berelekh assemblages contain microblades, a pattern reminiscent of the Allerød situation in Interior Alaska.

For us, this is one of the most satisfying aspects of recent Beringian research, that repeated excavations from one end of Beringia to the other have finally demonstrated the existence of a technological complex with a consistent set of bifacial and blade lithic tools and (when preserved) ivory tools, lacking microblade technology. Interpreting the meaning of this Nenana complex will take additional excavations, complete technological and subsistence analyses, and most obviously an ancient-human genome from a Nenana occupation. This is one reason why Brian Wygal and Kathryn Krasinski have



Figure 3. The exposed 13,800-cal-BP living floor preserved at McDonald Creek, Alaska. Photograph by Kelly Graf.

opened excavations at the Holzman site (near Mead), and why we continue working at McDonald Creek.

During the later Younger Dryas stadial and into the early Holocene, the archaeological record is primarily made up of wedge-shaped core and microblade industries, locally called the Denali complex in central Alaska and regionally the Paleoarctic tradition. For a long time, we considered Dry Creek's Component 2 to represent the earliest such industry in central Alaska, citing an early conventional radiocarbon age of ~12,500 cal BP from the 1970s excavation. Our recent excavations there, however, suggest it may date to only 11,000 cal BP or later. At nearby Moose Creek (C2) and Owl Ridge (C2), occupations ascribed to the Denali complex nonetheless consistently date as early as ~12,400 cal BP, while other Denali sites like Teklanika West (recently re-excavated by Sam Coffman), Tangle Lakes, and Panguingue Creek are likely centuries younger (Blong 2018; Goebel and Potter 2016). The new human genome from Xaasaa Na' (Upward Sun River) is associated with this later Denali complex, suggesting that genetically these people were 'Ancient Beringians,' a local lineage which had split from the Beringian lineage that eventually gave rise to Americans south of the ice sheets (Moreno-Mayar et al. 2018).

Another interesting development in the Younger Dryas archaeology of Alaska is the dating of fluted-point industries in the northern part of the state. With the recent excavations at Serpentine Hot Springs and Raven Bluff (Buvit et al. 2019; Smith and Goebel 2018), northern fluted points date to as early as 12,300 cal BP but no earlier, indicating they represent a post-Clovis phenomenon. Heather Smith's comprehensive geometric-morphometric/technological analysis of fluted points from Alaska, western Canada, and temperate North America strongly suggests an ancestral-descendant relationship between

Clovis and northern fluted points, with a sample of points in the interior, ice-free corridor representing an intermediate group (Smith and Goebel 2018). The parsimonious explanation of this evolutionary relationship is that Alaska's fluted points represent a back-migration from temperate North America during the Younger Dryas, coincident with the northward dispersal of plains bison into the corridor (Heintzman et al. 2016).

With the early archaeological record of the interior corridor currently suggesting a relatively recent back-migration to Alaska, many northern archaeologists are turning to the Pacific coastal corridor as a viable alternate route of human dispersal from Beringia to America. Although southwest and south-central Alaska have not yet yielded any Pleistocene-aged sites, in southeast Alaska Younger Dryas-aged sites have been known for some time, and the ancient genome of Shuká Káa, from On Your Knees Cave, suggests regional population structure had emerged by 10,300 cal BP (Lindo et al. 2017). Farther south in coastal British Columbia, Quentin Mackie, Daryl Fedje, and Duncan McLaren (2018) have convincingly shown that many late Pleistocene shorelines are now above the modern shoreline because of post-glacial crustal rebound after melting of the heavy Cordilleran Ice Sheet. Using a predictive model for locating paleo-coastal sites, they have quickly pushed the archaeological record along the Canadian coast back to as early as 13,000 cal BP. Risa Carlson and James Baichtal's (2015) similar work in southeastern Alaska has led to the discovery of sites on raised shorelines as early as 10,500 cal BP.

Obviously, this is an exciting time to be a Beringian archaeologist. The synthesis of archaeological and genomic evidence—human and nonhuman—is creating a dynamic marketplace of new ideas and new research efforts. As we move to the future, though, we need to expand dialogue with Native Alaskan and First Nations peoples of the Arctic and Subarctic, sharing the knowledge and experience. Already great strides have been made in this regard, the most evident involving the excavation, study, and repatriation of ancient human remains, most notably the recent genomic analysis of Shuká Káa, which was accomplished through sustained consultations between scientists, the US Forest Service, and two tribal organizations, the Klawock Cooperative Association and Craig Community Association of southeast Alaska. Similarly, the decision to conduct ancient-genomic analyses of the Xaasaa Na' remains from Upward Sun River was reached through dialogues involving the Tanana Chiefs Conference of central Alaska, University of Alaska archaeologists, geneticists, and the National Science Foundation (NSF). Importantly, however, these discussions had begun long before the discovery of the remains, early in the development of the excavation program. Such experiences only improve relationships between indigenous peoples,



Figure 4. Atlatl-throwing experience during Bering Sea Days on St. Paul Island, Alaska, led by Joshua Lynch, a PhD candidate in Anthropology, Texas A&M University. Photograph courtesy of Veronica Padula.

professional archaeologists, and government agencies, and they further enhance our understanding of the process of the peopling of the Americas.

Other important steps are being made every year by the newest generation of Beringian archaeologists, most notably through PhD dissertation support from the NSF. Angela Younie's excavations at Linda's Point, Healy Lake, is a case in point. Her dissertation project was co-sponsored by NSF and the Tanana Chiefs Conference, and through this collaboration, she actively engaged rural Native Alaskan schoolchildren in field and lab work, making them active partners in the research. Similarly, Joshua Lynch is sharing new knowledge of ancient projectile technology that he has gained through experimentation, using his NSF dissertation grant as a way to reach out to Native Alaskan schoolchildren in the remote Bering Sea region, introducing them to ancient Beringian subsistence practices (Figure 4). To these graduate students, the 'broader impacts' of their research are very important. Engaging indigenous communities in these ways undoubtedly enriches the research experience for all involved, and portends a healthy, more inclusive future for the study of Ice Age archaeology in Alaska.

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AVAILABILITY AND VIABILITY OF THE ICE-FREE CORRIDOR AND PACIFIC COAST ROUTES FOR THE PEOPLING OF THE AMERICAS

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otential routes between Beringia and continental North America have taken on special significance as a new generation of techniques have provided insight into the timing of human occupation of North America, including pre-Clovis sites (e.g., Waters et al. 2018), and the deep lineages preserved in modern and ancient genomes (e.g., Llamas et al. 2016). These approaches have pushed the limits of our understanding of potential routes, forced reassessment of the chronology of North American ice sheets, and, most recently, spurred new work to address these limitations (e.g., Darvill et al. 2018; Lesnek et al. 2018). Recently, several papers have provided assessments of the chronology, viability, and potential connectivity between Beringia and continental North America, as a means to understand peopling of the Americas (Braje et al. 2017; Darvill et al. 2018; Heintzman et al. 2016; Lesnek et al. 2018; Pedersen et al. 2016; Potter et al. 2018). These studies have largely highlighted a particular collection of dates or paleoecological data to make statements about the potential viability of either the Pacific Coastal Route (PCR) or the interior Ice-Free Corridor (IFC) during the critical interval from circa 16,000 to 13,000 cal yr BP. In this review, we assess these chronologies in terms of their constraints on ice sheet history, the reliability and internal consistency of these dates, and the viability of these environments as reflected in immediately post-glacial paleoenvironmental data.

Ice Sheet Chronologies: Caveat emptor

The most commonly cited reconstruction of the deglacial chronology for the Laurentide (LIS) and Cordilleran (CIS) ice sheets is that of Dyke and colleagues (2003). This chronology is based primarily on the large database of radiocarbon dates generated over the last ~50 years. In preparing the ice sheet summary, the authors place emphasis on the highest quality dates available, but given the history of investigations, they include many dates that were produced using methods that would not typically be used in modern studies. These include dates on materials such as mixed or bulk samples, including materials like aquatic macrofossils that may not have been in equilibrium with atmospheric CO2 at the time the organism was living, resulting in an erroneous date. As well, early dates were typically dated via radiometric methods, the only radiocarbon option available prior to the late 1970s. Radiometric (or conventional) radiocarbon dating is not in itself problematic, but the technique requires much larger sample sizes than modern Accelerator Mass Spectrometry (AMS) dating, and so it can be difficult to select discrete materials of sufficient size for reliable dating. In contrast, AMS radiocarbon dating allows isolation of particular organic remains such as individual plant macrofossils, or the opportunity to isolate discrete organic fractions, including in the case of bone, ultrafiltration of collagen, or even single amino acids, that can be advantageous in producing accurate radiocarbon dates (e.g., Waters et al. 2015). In the case of bone, ultrafiltration separates the high molecular weight proteins from shorter fragments that are the most common source of contaminants that may be incorporated in the bone following burial. These contaminants, which are most likely sourced from the environment and not the organism, are typically of younger age, and may preclude accurate dating (e.g., Froese 2014).

Radiocarbon-based chronologies can also have biases related to the relationship between the organic material and the dating of ice margin retreat. First, the period of ecesis, the time between the ice sheet leaving an area and colonization by a plant or animal, is generally unknown and may be significant. And secondly, the organic material is usually in a detrital context with some unknown period between the death of the organism and its inclusion in the sedimentary record. These biases and potential inaccuracies in the largely radiocarbon-based chronology for the LIS and CIS have led to alternative chronometers for dating ice sheet retreat, including luminescence (e.g., Munyikwa et al. 2017) and cosmogenic radionuclide dating (e.g., Menounos et al. 2017). There are, however, considerable differences between the uncertainties provided by radiocarbon dates (typically 1%-2% for modern calibrated dates at two standard deviations), and those from cosmogenic radionuclide and luminescence dates, where propagated uncertainties are typically ~8%-10% at one standard deviation. These uncertainties can be reduced through averaging of multiple ages associated with a particular landform or sedimentary unit. It should be noted that the multiple dating approaches used to constrain ice sheet chronology, including terrestrial cosmogenic radionuclide (e.g., ¹⁰Be, ³⁶Cl), calibrated radiocarbon, and luminescence dates, are broadly comparable and presented here as cal yr BP.

Routes into the Americas

Archaeological data indicate that early human populations were present in eastern Beringia by ~14,000–15,000 cal yr BP, with records potentially pre-dating that time (Potter et al. 2018). Sites south of the LIS and CIS indicate that people were present by at least 14,200 cal yr BP (Jenkins et al. 2012) and perhaps as early as ~15,000 cal yr BP (Waters et al. 2018). Two potential routes are generally considered either through the interior IFC route down the Mackenzie Valley or along the PCR (Figure 1). Typically the IFC route is shown as the over the top path into the northern Mackenzie Valley, available following the detachment of the LIS and CIS to the south along the mountain front (Figure 1). A variant of the IFC route is through the Yukon Plateaus of the northern Cordillera that may have been available with early deglaciation of the upland areas prior to the main valleys (e.g., Menounos et al. 2017; Figure 1).

Alternatively, if maritime adaptations were available, the PCR may have provided an abundance of natural resources (Braje et al. 2017; Fladmark et al. 1979). Understanding the PCR and the potential distribution of sites has been hampered by rapid sea level change, poorly constrained deglacial chronologies, and complex sea level histories along the coast, leading to the need to develop local sea level records repeatedly over short distances (e.g., Fedje et al. 2018; Josenhans et al. 1997; Shugar et al. 2014). The potential of these routes for the first people into the

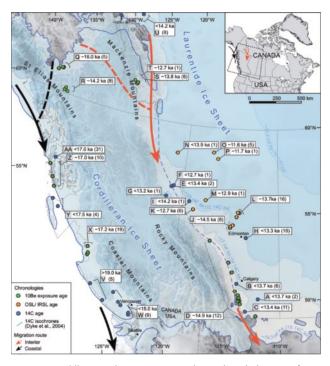


Figure 1. Cordilleran and western Laurentide Ice Sheet deglaciation from circa 19,000–11,400 cal yr BP (after Dyke et al. 2003). PCR and Interior IFC routes into continental North America from eastern Beringia (unglaciated Yukon and Alaska). The IFC includes the over-the-top route through the Mackenzie Valley and the alternative route through the Yukon Plateaus in northeastern British Columbia. Labels (A–Z, AA) show dates with groups (closely co-located sites) of dates with approximate age (OSL/IRSL, 10Be, 14C; Tables S1, S2, S3). Samples in close association have been grouped with outliers removed following original authors or as explained in text, and average ages indicated along with the number of samples (n) for each site. Individual dates, by indicated site, are plotted in Figures 2 and 4.

Americas is largely dependent on the geological constraints on the obstacle-forming ice sheets and sea level history, as well as on the extent to which these areas were biologically viable to early human populations.

Ice-Free Corridor Route

Three different scenarios have been proposed recently for the availability and viability of the IFC route. First, Pedersen and colleagues (2016), based on the analysis of two lake sediment cores, suggest that the LIS persisted much later than in other reconstructions, but also argue that sufficient biological resources were only available after ~12,600 cal yr BP. Alternatively, Potter and colleagues (2018) place emphasis on luminescence ages

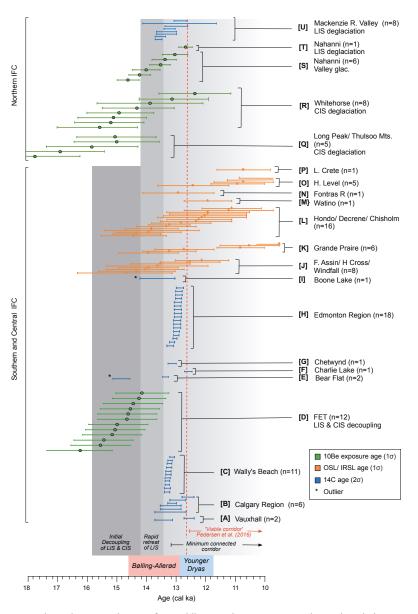


Figure 2. Synthesis of 10Be, OSL, and 14C dates (in cal yr BP) for Cordilleran and western Laurentide Ice Sheet deglaciation. Cosmogenic dates plotted at one standard deviation uncertainty with scaling, erosion rate, and production rate as indicated by authors. Luminescence dates plotted at one standard deviation uncertainty with propagation of error as indicated by authors. Radiocarbon dates calibrated and presented at two standard deviation uncertainty. Individual dates with references in Tables S1 and S3. [A] refers to locations on Figure 1.

from the region (Sites J–P, Figure 1), coupled with a date on a taiga vole (Site E, Figure 1), and to some extent regional cosmogenic dates, to argue that the IFC was potentially available as early as 15,000 cal yr BP. The third scenario, on the basis of bison phylogeography from ancient maternal lineages, indicates

that the earliest dispersal of Beringia bison (most closely related to Yukon and Alaska populations) took place by ~13,200 cal yr BP with the appearance of northern bison in northeastern British Columbia (Site G, Figure 2) and Edmonton (Site H, Figure 2; Heintzman et al. 2016). In order to evaluate these

hypotheses, we compiled the available chronologic information, not including dates on bulk sediments, terrestrial shells, or mixed assemblages known to be problematic in providing reliable chronologies, and present these graphically in Figure 2; individual 'higher quality' dates and their references are listed in Tables S1, S2, and S3 (please see https://www.saa.org/publications/the-saa-archaeological-record for supplementary materials).

The key means by which the coalescence and initial detachment of the LIS and CIS has been dated is the Foothills Erratics Train (Figure 3; Jackson et al. 1997; Margold et al. 2019). The Foothills Erratics Train is a linear concentration of large quartzite blocks derived from a rockfall onto the surface of a valley glacier, flowing from the Athabasca Valley, that carried the blocks to the eastern slopes of the Rocky Mountains where the glacier merged with the LIS (Figures 1, 3). These boulders, stretching over several hundred kilometres, were carried south along the Foothills, marking the zone of coalescence of the LIS and CIS. Jackson and colleagues (1997) used one of the early applications of cosmogenic dating (whole rock ³⁶Cl) to estimate the age of several erratics, with a central group of dates ranging between circa 19,900 and 10,800 cal yr BP. These dates were key to demonstrating the late Wisconsinan coalescence of the LIS and CIS and movement away from the primacy of the IFC for peopling of the New World (Ives et al. 2013). Recently, Margold and authors (2019) dated many of the same boulders using ${\rm ^{IO}}{\rm Be}$ concentrations from quartz to derive a more precise age (Table S3). Of the 16 boulders that were dated, 12 dates are tightly clustered between 16,300 and 14,200 cal yr BP, and provide a weighted mean age, including propagated uncertainty, of $14,900 \pm 900$ cal yr BP (Site D, Figures 1, 2). These dates indicate initial decoupling of the LIS and CIS took place at about 15,000 cal yr BP.

Munyikwa and authors (2017) place emphasis on luminescence ages from eolian sands to constrain deglaciation of the LIS in western Canada. The authors argue that, unlike radiocarbon-based approaches for ice sheet chronology, which require plants or animals to colonize the formerly glaciated terrain, luminescence dating of eolian deposits should more closely relate to the time of deglaciation. While this principle is strong, the large uncertainties associated with luminescence dating (typically 8%-10% at one standard deviation when uncertainty is propagated) make individual dates more difficult to interpret than radiocarbon dates. We plot the dates and their one standard deviation uncertainties, grouped by sites within 30 km, on Figure 2 (Sites I-P on Figure 1). We have removed outliers proposed by the original authors. By focusing on groups of dates, rather than individual dates, site means can be calculated where larger numbers of dates exist in close proximity. This



Figure 3. Quartzite block of the Foothills Erratics Train sampled for 10Be cosmogenic radionuclide dated to 15,500 \pm 1000 cal yr BP. Photo by Martin Margold.

approach gives mean site ages of circa 14,500 \pm 1125 (Site J: n = 8, Figure 2) and 13,700 \pm 1160 (Site L: n =16, Figure 2). Additional sites are consistent, though generally younger than these ages (Figure 2).

Potter and colleagues (2018) emphasize the date on a taiga vole from northeastern British Columbia (Site E, Figure 2) to demonstrate the viability of the IFC route by circa 15,000 cal yr BP. That site produced several dates, ranging from nearly ~20,000 cal yr BP to late Holocene, most on mixed aliquots of charcoal, presumably including non-finite material, leading to unrealistically old ages for this glaciated area. Two voles at the site yielded dates of 15,150-14,565 cal yr BP and 14,225-13,030 cal yr BP (Table S1), while bounding charcoal ages are mid-Holocene (Hebda et al. 2008). Potter and colleagues (2018) focus on the earlier vole date to demonstrate the viability of the IFC by ~15,000 cal yr BP, but when considered within the scope of other ages in western Canada, the age is outside their distribution and clearly anomalous (Figure 2). This date pre-dates other regional chronologies, including the coalescence dates indicated by the Foothills Erratics Train (Site C, Figure 2), the average age of the luminescence dates, and all other vertebrate records we are aware of in deglacial settings in western Canada. These bone dates are on standard collagen, and the lack of ultrafiltration leaves open the strong potential for contamination. Given these caveats and its lack of replication, we treat this date as an outlier and remove it from discussion of the IFC (Figure 2).

Coastal Route

The PCR has taken on special significance because of the potential late opening of the IFC, the possibility of abundant resources along the coast, and the rapid passage that may

have been available for marine-adapted people (e.g., Braje et al. 2017; Fladmark et al. 1979;). Understanding of the geologic constraints on the PCR has been hindered by the complex record of sea level change along the coast, and the seeming differences in the history of advancing and retreating local and CIS glaciers through the late Pleistocene. Lesnek and colleagues (2018) used cosmogenic dating in the Alexander Archipelago along with earlier vertebrate dates to constrain deglaciation and the potential viability of the northern coast

(Figure 1). They demonstrate that the CIS extended onto the continental shelf until ~17,000 cal yr BP when ice retreated. The cosmogenic dates indicate that islands and other low-lying areas along the coast were increasingly ice free by about 16,000 cal yr BP (Site Z, Figure 1, Figure 4). This chronology is consistent with vertebrate records on Prince of Wales Island that show a hiatus in bone dates between ~19,800 and 17,200 cal yr BP with an increase in the frequency of dates and diversity of taxa after 15,000 cal yr BP (Figure 4). Similarly,

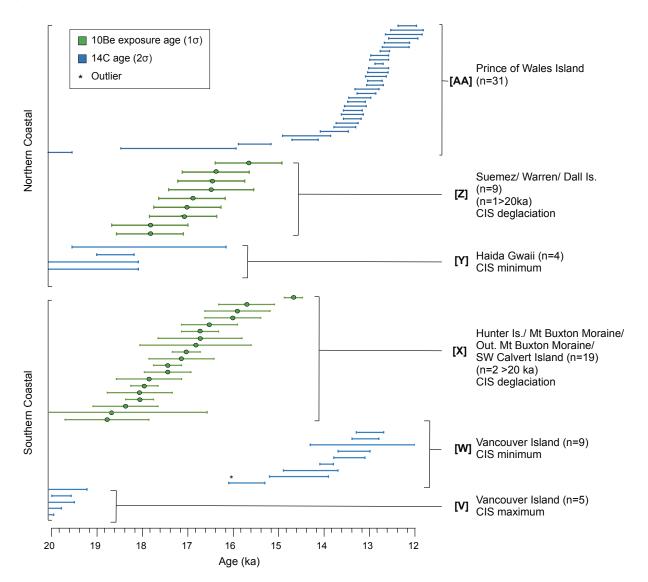


Figure 4. Synthesis of key late Pleistocene 10Be and 14C dates (in cal yr BP) on the Pacific Coast. Cosmogenic dates plotted at one standard deviation uncertainty with scaling, erosion rate, and production rate as indicated by authors. Radiocarbon dates calibrated and presented at two standard deviation uncertainty. Individual dates with references in Tables S2 and S3. [V] refers to locations on Figure 1.

sites on Haida Gwaii (Site Y, Figure 4) suggest the CIS reached the area after 22,000 cal yr BP and was retreating as early as 19,400 cal yr BP (Figure 4).

Along the central coast of British Columbia, cosmogenic dates on boulders indicate the CIS began retreating around 18,000 cal yr BP while still reaching its maximum in areas to the south at circa 17,000 cal yr BP (Darvill et al. 2018). Dates from sites further within the extent of the coastal CIS indicate ice was retreating and exposing lowland sites by ~16,000 cal yr BP (Site X, Figures 1, 4). This record is broadly similar to the radiocarbon-based chronology from Vancouver Island that indicates ice reached the area after ~19,000 cal yr BP and was retreating from the area after ~15,000 cal yr BP (Site W, Figures 1, 4).

Discussion and Conclusions

In terms of the interior IFC route, three hypotheses have been presented for its availability and viability. The first, the 'minimally-available and minimally-viable' IFC of Pedersen and colleagues (2016), argues that a significant bottleneck in the Peace River area maintained the LIS locally with a proglacial lake barrier extending to near Site F (Figure 1) until ~12,900 cal yr BP with the area only becoming biologically viable after 12,600 cal yr BP. LIS reconstructions and stratigraphic data place the LIS boundary in northeastern Alberta beyond sites O and P at that time in order to account for the northwest outlet of glacial Lake Agassiz and the Mackenzie Valley stratigraphy (e.g., Murton et al. 2010). This reconstruction of a lack of LIS barrier in central and northern Alberta at 12,900 cal yr BP is consistent with luminescence chronologies (sites J-L, Figure 2) and minimum radiocarbon dates from central Alberta (e.g., Site H). The argument with respect to the viability of the IFC prior to 12,600 cal yr BP is best addressed by the abundance of Quaternary vertebrate data and paleobotanical indicators that suggest a diverse grazing megafauna present in the central corridor region prior to 13,200 cal yr BP (sites G, H, I, Figure 2).

The second hypothesis, that of Potter and colleagues (2018) that the IFC was likely available by ~15,000 cal yr BP, places emphasis on questionable dates that have not been replicated, such as the taiga vole and the early ranges of date distributions of luminescence and cosmogenic dates (Figure 2). New dates on the Foothills Erratics Train, indicating coalescence until about 15,000 cal yr BP (Margold et al. 2019; Figure 2), provide further support to reject the early IFC availability, consistent with averaging closely spaced luminescence dates on sand dunes through central and northern Alberta (Figures 1, 2). Collectively the cosmogenic, luminescence, and minimum radiocarbon dates from the IFC present a consistent record

of LIS-CIS detachment beginning at ~15,000 cal yr BP with substantial retreat of the LIS only after circa 14,000 cal yr BP (e.g., sites A–C, H–L, Figures 1 and 2).

The intermediate IFC hypothesis of Heintzman and colleagues (2016) argues for a viable corridor connected to eastern Beringia by 13,200 cal yr BP at Site G (Figure 1) with the appearance of a Beringian bison. This provides a minimum age for IFC connectivity between Beringia and areas south of the LIS. However, it should be noted that this is a minimum age estimate and it is unlikely that the earliest bison was indeed sampled, leaving open the possibility for earlier IFC connectivity, although the extent of this bias is unknown.

Since the late 1990s, with the recognition of the rapid sea level change and potential for extensive areas to be potentially available along the coast (Josenhans et al. 1997), coupled with recognition that the LIS and CIS coalesced during the last glacial maximum (Jackson et al. 1997), attention has been drawn to the PCR. In recent years, with increasing numbers of deglacial dates spanning the southern through central coast, an emerging picture indicates initial retreat of the CIS along the outer margin beginning after ~18,000 cal yr BP with extensive lowland areas available by ~15,000 cal yr BP. It is more difficult to estimate the continuity of these landscapes than in the areas of the IFC because of the complex and variable relative sea level and ice margin histories (e.g., Shugar et al. 2014) necessitating careful, local reconstructions in the search for archaeological sites (e.g., Fedje et al. 2018).

The archaeological data south of the LIS and CIS indicate the presence of early human populations by at least 14,200 cal yr BP (Jenkins et al. 2012) and perhaps as early as 15,000 cal yr BP (Waters et al. 2018). Existing data for the IFC provide no compelling evidence for the availability or viability of this route until well after 14,000 cal yr BP and likely until nearer 13,200 cal yr BP. In contrast, the PCR provides suggestions for extensive lowland landscapes after ~15,000 cal yr BP and increasingly diverse and abundant vertebrate records by ~14,500 cal yr BP. If the first peoples did indeed traverse from Beringia to continental North America by ~15,000–14,500 cal yr BP, the existing evidence strongly favours the PCR.

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EARLY EXPLORATION AND SETTLEMENT OF NORTH AMERICA DURING THE LATE PLEISTOCENE

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xcavations at Folsom and Clovis, New Mexico, during the first half of the twentieth century revealed that people had entered the Americas at the end of the Pleistocene. During the second half of the century, more Clovis sites were investigated and Clovis became accepted as the first people to enter the Americas. This view changed, after much acrimony, with the reporting and acceptance of the 14,200-year-old Monte Verde site in southern Chile, excavated by Tom Dillehay (Meltzer 2009). Since Monte Verde, many new sites have been found and investigated and old sites reinvestigated with modern techniques and technologies in North America. Applying state-of-the-art Accelerated Mass Spectrometry (AMS) dating and pretreatment protocols revealed that Clovis dates to a narrow time window between 13,000 and 12,700 calendar years before present (cal yr BP), and that there are a number of sites older than 13,000 cal yr BP containing artifacts that occur in secure geological contexts that are accurately dated. These are scattered across North America (Figure 1) and date between ~15,500 and ~14,000 cal yr BP (Goebel et al. 2008; Madsen 2015; Pitblado 2011; Waters and Stafford 2014). These sites appear soon after the opening of the coastal corridor along the western edge of the Cordilleran Ice Sheet and provide the evidence of the first human presence south of the ice sheets.

Near the southern margin of the Laurentide Ice Sheet, at the Hebior site in southeastern Wisconsin, the disarticulated bones of a single woolly mammoth were excavated from pond clays by David Overstreet (2005). Cut and pry marks on the bones indicate that the animal was butchered by humans. Four lithic artifacts, including two bifaces, occurred in direct association with the mammoth bones. Three XAD-purified collagen ages on the mammoth bone are 14,850 \pm 150 cal yr BP. One kilometer south of the Hebior site, the disarticulated remains of a single woolly mammoth and stone artifacts were excavated from pond clays by Daniel Joyce at the Schaefer site



Figure 1. Map showing North America and key archaeological sites mentioned in the text. Artifacts from some of these sites are shown.

(Joyce 2014). The mammoth bones also show signs of butchering, including cut and pry marks. Two blade-like flakes made on local chert were associated with the mammoth. Thirteen radiocarbon dates on XAD-purified collagen from different elements of the mammoth and 16 radiocarbon ages on wood samples around the bone indicate that the site dates to 14,650 \pm 150 cal yr BP. In southern Alberta, Canada, seven butchered horses and one butchered camel were recovered from eolian sediments at the Wally's Beach site by Brian Kooyman and his colleagues. Only flake and core tools are associated with these carcasses. Twenty-seven XAD-purified collagen ages date these individual kill sites to ~13,300 cal yr BP (Waters et al. 2015).

In the American Southeast, the Page-Ladson site lies submerged under 9 m of water within a mid-channel sinkhole along a segment of the Aucilla River, 11.5 km inland from the Gulf of Mexico (Figures 2 and 3). The site was first investigated by S. David Webb and James Dunbar (Webb 2006) and most recently by Jessi Halligan and Michael Waters. At Page-Ladson, lithic artifacts, including a biface (Figure 1), made of local chert were associated with mastodon, camelid, and bison remains (Halligan et al. 2016). Six parallel, deeply incised grooves around the circumference of a mastodon tusk from the same deposits as the artifacts appear to have been made during the extraction of the tusk from the skull. The artifacts and modified tusk occur in an undisturbed geological context overlain by 4 m of sediments. Seventy-one radiocarbon dates were obtained to unequivocally show that the sediments were not disturbed and that these artifacts and the modified tusk date to ~14,550 cal yr BP. During the time people occupied the sinkhole, sea level was much lower than it is today and the site was ~175-250 km from the coast. The sinkhole would have been dry with a freshwater pond near the bottom that attracted animals and humans.

In the northwestern portion of the United States, Luther Cressman investigated Paisley Caves, Oregon, in 1938–1939 and reported the association of artifacts with extinct megafauna. Beginning in 2002, Dennis Jenkins returned to the caves and recorded a well-stratified sequence of deposits that he dated from the late Pleistocene through the Holocene by 190 radiocarbon ages (Jenkins et al. 2014). At the base of the sequence, five human coprolites are directly dated to ~14,200-14,100 cal yr BP. Mitochondrial DNA extracted from these coprolites belonged to Native American founding haplogroups A and B. Also within these deposits were stone tools and debitage. Farther north, at the Manis site, Washington, a single male mastodon was excavated from sediments at the base of a kettle pond by Carl "Gus" Gustafson (Waters et al. 2011). The bones of the right side of the mastodon were disarticulated and moved 0.6 m to 3 m from the rest of the skeleton and toward the bank of the pond. Some bones were spirally fractured, multiple flakes were removed from one long-bone fragment, and other bones showed cut marks. The only associated artifact was the tip of a projectile point made of mastodon bone that was embedded into the mastodon's fourteenth right rib. Four dates on XAD-purified collagen from the rib with the bone point and from the tusk ivory of the skeleton are ~13,800 cal yr BP.

In Central Texas, along Buttermilk Creek, are the Debra L. Friedkin and Gault sites. At the Friedkin site (Figure 4), in floodplain clays that are up to 1.4 m thick, is a record of human occupation going back to ~15,500 cal yr BP (Waters et



Figure 2. Excavations at the Page-Ladson site, Florida. Site lies between the pontoon boat and barges. Photo courtesy of the Center for the Study of the First Americans.



Figure 3. Excavations underwater at the Page-Ladson site, Florida. Photo courtesy of the Center for the Study of the First Americans.

al. 2018). At the site, 120 diagnostic projectile points define a Late Prehistoric horizon, overlying Late Archaic and Early Archaic components, which in turn overlay a layer with Late Paleoindian artifacts. Below this is a discrete layer with Folsom and Clovis diagnostic artifacts. A 15 cm thick layer is below this, with over 300 stone tools and 100,000 pieces of debitage that define the Buttermilk Creek Complex. Seventy-one Optically Stimulated Luminescence (OSL) ages, primarily from four columns through the floodplain sediments, date the sediments and the contained artifacts. OSL ages from the Early Archaic, Late Paleoindian, Folsom, and Clovis horizons correspond well with the known age of these archaeological time periods. Nineteen OSL ages from the zone with Buttermilk Creek

Complex artifacts range from ~15,500 to ~13,500 cal yr BP. The artifacts in this layer include blades, bladelets, scrapers, bifaces, bifacial discoidal cores, snap-fracture tools, retouched flakes, expedient tools, and ground hematite. In addition, 11 complete and fragmentary lanceolate stemmed projectile points (Figures 1 and 5) were found in the ~15,500-13,500 cal yr BP sediments, and I triangular lanceolate projectile point with a concave base and basal thinning occurs in the layers dated between ~14,000 and ~13,500 cal yr BP. At the Gault site, 250 m upstream of the Friedkin site, Michael Collins has headed investigations of the Clovis and "Older than Clovis" layers at the site. In the "Older than Clovis" layers, Collins and his colleagues report 5 stemmed and 2 lanceolate base projectile points that are dated to ~16,000 cal yr BP and occur below a dated Clovis horizon (Williams et al. 2018). One of the stemmed points from the Gault site is similar to the stemmed point from the Friedkin site. The remaining points have two distinct base morphologies (Figure 1), which may have resulted during the resharpening process. The concave lanceolate base points are smaller, but similar to the specimen from the Friedkin site. These points occur with biface and blade-andcore lithic technologies. Points similar to those from central Texas were excavated from lacustrine deposits associated with mammoth skeletons at the Santa Isabel Iztapan I and II sites in Mexico that are bracketed by ~14,500 and ~10,800 cal yr BP tephra (Figure 1; Arroyo de Anda and Maldonado-Koerdell 1953; Waters et al. 2018). A stemmed projectile point, along with other artifacts, was associated with the bones of a single mammoth buried in undisturbed lacustrine sediments at Santa Isabel Iztapan I. Four hundred meters away, at Santa Isabel Iztapan II, two stemmed points were associated with butchered mammoth bones in the same lacustrine sediments.

These early sites are not without critics (Haynes 2015). At the Hebior and Schaefer sites, the taphonomic evidence for butchering has been challenged. In addition, it has been suggested that the artifacts are intrusive from overlying layers even though no vounger artifacts occur above these sites, and they were found in dense clay deposits. At Paisley Caves, the human origin of the coprolites has been challenged. The proposed bone projectile point tip embedded into the rib of a mastodon from the Manis site has been suggested to be the result of an elk goring the mastodon, an internal self-inflicted bone injury sustained while this animal fought with another mastodon, or even an injection by a backhoe during excavation. At the Friedkin and Gault sites, it has been suggested that the thousands of artifacts found in the layers below Clovis are intrusive due to trampling and natural processes. The investigators of each of these sites have addressed these concerns by conducting additional studies and providing more data. Interestingly, the evidence from the Page-Ladson site is



Figure 4. Excavations at the Debra L. Friedkin site, Texas, in 2015. Photo courtesy of the Center for the Study of the First Americans.



Figure 5. Stemmed point dating ~15,000 cal yr BP in situ at the Debra L. Friedkin site, Texas, in 2015. Photo courtesy of the Center for the Study of the First Americans.

so secure that no challenges have been raised about the integrity of the site since its publication in 2016, except to suggest that it may represent a site of a failed migration.

What makes these sites—Hebior, Schaefer, Paisley Caves, Manis, Wally's Beach, Page-Ladson, Debra L. Friedkin, and Gault—important is that the artifacts at each site were found in a secure geological context, and that this context and the associated artifacts could be dated using reliable and accurate dating methods. These data demonstrate that humans were present in North America by ~15,500 cal yr BP and widely dispersed in the period 15,000 to 14,000 cal yr BP, with Clovis

and the Western Stemmed Tradition emerging from the biface, blade, and osseous technologies carried by the earliest pioneering groups.

You might ask, what about Meadowcroft Rockshelter, Pennsylvania? At Meadowcroft Rockshelter (Figure 1), James Adovasio (1993) excavated hearths and ~700 artifacts from Stratum IIa including blades, unifacial and bifacial knives, gravers, edge-modified flakes, debitage, and a lanceolate projectile point (Haynes 2015; Madsen 2015; Waters and Stafford 2014). Charcoal from two hearths brackets the lanceolate point between 11,300 \pm 700 14C yr BP (12,200–14,100 cal yr BP) and 12,800 ± 870 14C yr BP (13,900-16,300 cal yr BP). Because of the large standard errors associated with these ages, the calibrated ages could be correlated with either the early Paleoindian period or pre-date Clovis. The five other radiocarbon samples from hearths in Stratum IIa also have wide standard errors resulting in calibrated ages ranging from 14,300 to 20,700 cal yr BP. Another issue with the radiocarbon ages from Stratum IIa is that they appear to be contaminated by older particulate and soluble organics as demonstrated by two charcoal-humate date pairs from two Stratum IIa hearths. In both cases, the soluble organics produced ages that were 7,000 and 12,000 radiocarbon years older than the insoluble charcoal. Only new dates and additional chronological studies at the site will resolve the chronological issues at Meadowcroft Rockshelter (Goebel et al. 2008; Haynes 2015; Madsen 2015; Waters and Stafford 2014).

A number of sites are proposed that pre-date 16,000 cal yr BP, before either corridor was open, which means that humans would have entered the Americas prior to the Last Glacial Maximum (LGM). In North America at the Calico Hills and Texas Street sites, California, core tools dating >100,000 cal yr BP have been reported from alluvial fan deposits. At the Topper site, South Carolina, Late Prehistoric through Clovis artifacts are found in colluvium overlying a terrace of the Savannah River. Albert Goodyear (2005) reports that a core and microlithic industry occurs at the base of the ~15,000-year-old colluvium and in the >50,000-year-old terrace alluvium. At the Burnham site, Oklahoma, chert debitage and bison bones occur in alluvium dated to ~36,000-35,000 cal yr BP. Similarly, at the Coats-Hines-Litchey site, Tennessee, lithic debitage is association with mastodon and other extinct fauna in alluvial deposits dated to ~35,000-27,000 cal yr BP. While the geology and dates from these sites are secure, the reported artifacts are geofacts-objects made by natural processes that appear to look like artifacts (Haynes 2015; Madsen 2015; Meltzer 2009; Waters and Stafford 2014).

From unconsolidated eolian dune sand at the Cactus Hill site, Virginia (Figure 1), lithic artifacts, including small prismatic blade cores, blades, and two basally thinned heavily resharpened subtriangular bifacial points were recovered 5–15 cm below a Clovis horizon by Joseph and Lynn McAvoy (McAvoy and McAvoy 2015). Charcoal from two reported hearths range from ~18,400 to ~17,100 cal yr BP. Concerns at this site center around possible movement of artifacts in the sandy unconsolidated dune sediments due to post-depositional processes (Goebel et al. 2008; Haynes 2015; Madsen 2015; Waters and Stafford 2014), which is why the evidence from the site remains equivocal.

The Miles Point site is located along the edge of the Chesapeake Bay on the western side of the Delmarva Peninsula (Figure I). Here, Darrin Lowery reports that a polyhedral blade core, blade flakes, bifacial lanceolate projectile point, bipolar core, hammerstones, and anvil were recovered in situ within the Tilghman paleosol that developed on the Miles Point Loess, which in turn is overlain by the Paw Paw Loess (Lowery et al. 2010). Nine additional artifacts were found in the surf zone and thought to have been eroded from the site. Three radiocarbon ages on carbonized plant material range from ~31,300 to 25,700 cal yr BP. Two OSL ages yielded similar results. At a new site on Parson's Island, Darrin Lowery reports that artifacts occur in loess deposits of a similar age. However, until excavations at these sites are conducted, the processes of site formation and chronology will remain uncertain.

Several localities with mammoth, mastodon, bison, or sloth remains are suggested to be archaeological sites (Goebel et al. 2008; Haynes 2015; Madsen 2015; Waters and Stafford 2014). Stone tools are absent from these localities and the evidence of human activity is based entirely on bone breakage patterns, interpretation of surface marks on bones, and the spatial arrangement of the bones (Goebel et al. 2008; Haynes 2015; Madsen 2015). Steve Holen proposes that proboscidean bone breakage patterns and the position of different skeletal elements are the result of human activity at the ~130,000-yearold Cerutti Mastodon site, California (Holen et al. 2017); the ~22,400-year-old La Sena site, Nebraska; and the ~23,500-yearold Lovewell site, Colorado (Holen and Holen 2014). At the Lindsey site, Montana, a nearly complete skeleton of a mammoth was excavated from late-Pleistocene loess by Les Davis. On four different bone elements, 15 butchery marks made by stone tools were identified and inferred to have been made while stripping meat and disarticulating the carcass. These bones are also broken and show chop marks. No stone tools were found at the site; however, directly associated with the mammoth remains are 8 sandstone blocks, which are suggested to have been used to break open and splinter the bones. Three XAD-purified collagen ages on the bone are 14,200 ± 100 cal yr BP (Waters and Stafford 2014). Other examples of

proposed human-modified bone includes the 13,200 \pm 100 cal yr BP Burning Tree Mastodon, Ohio, and the 13,850 \pm 50 cal yr BP bison remains from Ayer Pond, Washington. The evidence from these sites is equivocal, because stone tools are absent from these sites and alternative taphonomic processes can break bone, creating spiral fractures and percussion marks, and create surface marks that mimic cut marks (Haynes 2015; Madsen 2015). Some of these localities may indeed be archaeological sites, but this evidence will remain equivocal until researchers can define a reliable and consistent way to identify human interaction with carcasses where stone tools are absent.

In short, the archaeological evidence of a human presence in North America during and before the LGM is equivocal. The evidence from most of these sites is problematic, with uncertainties related to a site's geologic context, geochronology, or the absence of definitive human-made artifacts.

Genetic information from contemporary Native Americans and prehistoric human skeletons provides a fresh and different perspective on the origin and population history of the first Americans. Genetic studies provide estimates on the timing of the entry of the first Americans and the homeland of these first people. Studies of modern and ancient genomes show that people were south of the ice sheets sometime between ~17,500 and 14,600 cal yr BP (Moreno-Mayar 2018). Analysis of mitochondrial genomes places the arrival of humans into unglaciated America at ~16,000 cal yr BP (Llamas et al. 2016), and Y-chromosome estimates place this between ~19,500 and 15,200 cal yr BP (Pinotti et al. 2019). These estimates are consistent with archaeological evidence suggesting that people entered the Americas by ~15,500 cal yr BP. Genetic estimates on the entry of humans into North America are inconsistent with the hypothesis that Clovis represents the first people to enter and explore the Americas. The genetic estimates also do not support a pre-LGM occupation of the Americas, again agreeing with the archaeological data. If a pre-LGM occupation occurred, these people left no genetic legacy. The biological evidence shows that there was a single migration into the Americas and genetic continuity between the first inhabitants of North America and all the Native Americans that followed. This tells us that the biface, blade, and osseous technologies carried by the earliest pioneering populations that explored the Americas eventually gave rise to later Clovis and Western Stemmed Tradition technologies.

Our understanding of the late Pleistocene peopling of the Americas has undergone rapid change in the last few decades. New archaeological discoveries and the reinvestigation of old sites using modern technologies have shed new light on the first Americans, and genetic studies have illuminated their population ancestry. Both are converging to tell a new and consistent story of the first Americas, with people first arriving by ~15,500 years ago, spreading across the Americas, and leaving both an archaeological and genetic signal we are just beginning to understand. We will continue to advance our understanding of the earliest people to enter North America by undertaking more genetic studies and excavating more archaeological sites, with special attention paid to site geology, site formation, and geochronology.

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THE PRE-CLOVIS PEOPLING OF SOUTH AMERICA

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he peopling of America is perhaps one of the longest and most controversial debates in world archaeology, one in which South America has played a central role. There have been several competing models for the first peopling of the Americas, but with the exception of the controversial hypothesis of an Atlantic-Solutrean migration, there is major agreement among archaeologists and ancient geneticists that the first colonizers entered America from Northeastern Asia via Beringia and its shorelines. South America is fundamental to this basic agreement and is considered the final step in the colonization of the Americas.

In the last two decades, the acceptance of Monte Verde II as a site dating ~14,500 cal BP in southern Chile (Dillehay 1997) has broken the "Clovis barrier" (~13,000 cal BP), but deepened the debate: If the first Americans were from Asia via Beringia, why is the oldest site on the continent the most southern? As sites in North and South America were dated at a similar age, these data suggested that America was peopled before Clovis and that the colonizing process was very rapid. However, previous and recent claims for a pre-Late Glacial Maximum (LGM, dated between ~25,000 and 18,500 cal BP) age would indicate an alternative view that humans were in America long before ~14,500 cal BP, and therefore several sites during or before this period are the result of a much slower adaptation process to different environments. The tension between these two opposite views is the essence of the debate and perpetuates the arguments.

South American data are crucial to this discussion, although with the exception of Monte Verde II, it is not always fully considered in the continental models. The geographic coverage of research in South America is markedly uneven. Some regions, such as the Central Andes, Patagonia, and Pampas, are relatively well studied, while in others, such as Amazonia and Chaco, the density of early sites remains very low due to

low archaeological visibility/preservation and less scientific effort. Therefore, any discussion on the mode of expansion, the preferred environments, the speed of the colonization, and the routes of entry must accept these biases as well as the fact that geographic coverage and data are highly variable.

We must consider the basal timeline of the peopling of South America, a period agreed upon in general terms by the great majority of New World archaeologists. This line is around 14,000-14,500 cal BP and is defined by three sites with similar ages: Monte Verde II, Huaca Prieta, and Arroyo Seco 2 (Figure 1). There are also other sites, dated around 13,000 cal BP, across South America that are the same age as Clovis (for example, Quebrada Santa Julia in Chile; Cerro Tres Tetas, Piedra Museo, and Cueva Casa del Minero in Argentina; Lapa do Boquete and Caverna da Pedra Pintada in Brazil, etc.). Several "classic" sites such as Taima-Taima (13,000 \pm 200 BP; 15,453 cal BP) in Venezuela, El Abra 2 (12,400 ± 160 BP; 15,511 cal BP) in Colombia, and Tibitó (11,740 + 110 BP; 13,530 cal BP) in Colombia, provided dates between 13,000 and 15,500 cal BP, but they did not meet contemporary dating accuracy criteria. Nothing is inherently wrong with these sites or with the dates (although the measurement errors are large), but they should be redated to ensure their chronology in contemporary standards, and a re-excavation will be crucial to do geoarchaeological and taphonomic studies. In their present status they cannot be used as proof of pre-Clovis occupations in South America. Also, the human footprints and track from Pehuen Co cannot be considered yet, because despite being intimately associated with the tracks of Pleistocene fauna, they have not been adequately dated (see discussion in Bayón et al. 2011).

The best known and fully published pre-Clovis site is Monte Verde II in southern Chile (Dillehay 1997). The site dates to ~14,500 cal BP, although a recent ¹⁴C data analysis suggests that the human occupation of the site is between 14,485 cal BP and 14,160 cal BP (Politis and Prates 2018). The site is interpreted



Figure 1. Map with the sites mentioned in the text.

as a contemporaneous cultural event: a semipermanent camp resulting from a year-round occupation. Expediency tools made from local cobbles characterize the lithic technology; subsistence was oriented toward a broad spectrum of resources, with plants being dominant. The second site is Huaca Prieta, a famous mound along the Chicama Valley in northern Peru, which has a pre-mound phase with intermittent occupation between ~14,500 and 7500 cal BP (Dillehay 2017; Figure 2). More recently, new dates have been published that extend occupation of the site to ~14,800 cal BP (Dillehay et al. 2017). Stone tools were made primarily from locally available cobbles of rhyolite, basalt, andesite, and quartzite; subsistence was based on marine resources (e.g., sharks, sea lions, marine birds, and bony fish) despite the sea at ~15,000 cal BP being 100 m below today's elevation, and the coastline being 20-30 km from the site (Dillehay et al. 2017). Finally, the Arroyo Seco 2 site in the Argentine Pampas shows evidence of two occupation events that are interpreted as temporary processing camps for megafauna—the former at ~14,000 cal BP when a giant ground sloth (Megatherium americanum) and American horse (Equus

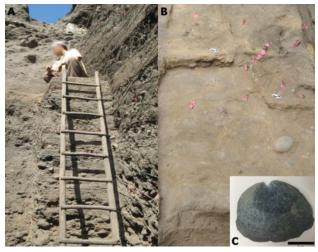


Figure 2. A) Upper portion of 29m deep pit (Unit 15) in the Huaca Prieta mound; B) Late Pleistocene use-surface at the 29m level. Note the burned areas and stone tools, radocarbon dated at ~14,5000 cal BP; C) basalt flake embedded in use-surface. Close-up of flake shows impact scar and bulb of percussion. Photo and caption courtesy of Tom Dillehay.



Figure 3. A) Aerial view of the Arroyo Seco 2 site showing the area excavated 1979-2018; b) Lithic artefacts, made on quartzite (upper row) and basalt seashore cobbles (lower row), associated with megafaunal remains.

neogeus) were butchered, and the latter, dated at ~13,000 cal BP, when two genera of American horses (*Equus* and *Amerhippus*) were processed (Politis et al. 2016; Figure 3). In both components, lithic tools were unifacial and made from nonlocal raw materials (e.g., quartzite, whose closest outcrop is >100 km from the site) as well as chalcedony, chert, and rounded marine cobbles. No projectile points have been found.

Monte Verde II, Huaca Prieta, and Arroyo Seco 2 indicate that people were contemporaneously occupying and exploiting very different environments, and were using different

technologies, economies, and settlement patterns. This could suggest a previous longer presence of humans in South America and a reason for the different, distinctive adaptive patterns. However, the archaeological record (and the human DNA studies) does not fully support this hypothesis, an argument that is summarized below.

The proposed pre- or contemporaneous-LGM sites in South America are divisible into two groups. The first comprises several sites in northeastern Brazil, in the Piauí state, where French-Brazilian research teams (Niède Guidon, Eric Boëda, Christelle Lahaye, and others) have proposed ages from 15,000 to ~100,000 BP based on thermoluminescence and radiocarbon dating; however, recent papers lower the time to at least 60,000 BP (Parenti 2014). The most famous site is Boqueirão da Pedra Furada, where a Pleistocene human occupation, divided into four phases, has been proposed based on hearths and a lithic industry based exclusively on simple artifacts using local quartz and quartzite (Parenti 2001, 2014; Figure 4). The main criticism about Pedra Furada is that the purported artifacts are made from the same lithic material that is the dominant rock type in the conglomerate forming the cave's roof. Critics also questioned the lack of technological variation over tens of thousands of years and strongly suggested that gravity and falling quartz and quartzite cobbles caused the flaking, not humans. The monograph published by Parenti (2001; see also Parenti 2014) responds to these criticisms; however, some doubts still persist.

New excavations have been performed in the area by Eric Boëda and his team in several interesting sites-Toca do Tira Peia, Sitio do Meio, and Vale do Pedra-all of which date as pre-or contemporaneous-LGM (up to 35,000 cal BP; Boëda et al. 2013, 2016). Each site has specific problems needing clarification in order to evaluate the findings and interpretations (see critique in Borrero 2016; Schmidt Dias and Bueno 2014). For example, the Toca do Tira Peia publication (Lahaye et al. 2013) focuses on Optically Stimulated Luminescence (OSL) dates which, according to the authors, date the human occupation as >22,000 BP. However, little information has been published on the lithics, geology, and taphonomy of these sites, which are crucial to evaluating the context. In a second publication, there are some descriptions (asystematic) of the lithics and geology, although their relationships are confusing (see Boëda et al. 2013:453-454).

Certainly, these sites are promising and would change our view about the peopling of the Americas, opening new opportunities to study the LGM period. It is necessary to recognize the effort to identify new sites, excavate them carefully, and construct chronologies using different dating methods, but specific



Figure 4. View of the Toca do Boqueirão do Pedra Furada after the site was almost completely excavated. Photo taken by Gustavo Politis during the site visit organized by Niede Guidon in December 1993 at the Reunião Internacional Sobre o Povoamento das Américas in São Raimundo Nonato, Brazil.

analyses need to be performed before Boëda and his team's interpretations are accepted. We suggest the following agenda.

First, information should be fully published. Systematic description of lithics and features are needed. Because most artifacts are made from naturally outcropping rock at these sites, it is crucial to identify the provenience of the nonlocal raw materials (especially from those interpreted as manuports). Second, taphonomy and site formation processes should be included in the research design more systematically; raw data and results should also be available. For example, it is crucial to know the proportion between the natural cobbles and the artifact in each layer to quantify the lithic background noise. The association between the lithics and the dated samples or sediments must be confirmed and documented. Third, a new rock-breakage agent in Serra da Capivara should be considered: the Sapajus libidinosus (bearded or black-striped capuchin monkey; Fiedel 2017). As recent papers from primatologists (e.g., Proffitt et al. 2016) have shown, these monkeys recurrently produce sharp-edged flakes and cores with quite similar features and morphologies to human artifacts. New studies need to develop a methodology to clearly discriminate these "artifacts" (biofacts or faunal lithics) from the true, human-manufactured tools. Obviously, capuchin monkeys could not produce all the artifacts found in all levels of these sites, but they might be responsible for some. Ignoring this disconcerting origin for lithics that might not be of human origin will hinder interpreting the prehistory of the area.

A second group of sites in South America has a different degree of resolution and integrity: for example, Pubenza

in Colombia, Pilauco in Chile, and Santa Elina in Brazil. Evaluating these sites requires more published details on basic contextual data (for an exception, see Vialou 2005) and more systematic analyses, specifically on taphonomy and site formation processes. Some of these sites deserve brief discussion: Arroyo del Vizcaíno (Fariña et al. 2014), Chinchihuapi I and II, and Monte Verde I (Dillehay et al. 2015).

The Arroyo del Vizcaíno site in Uruguay has yielded more than 1,000 bones, most from the giant sloth Lestodon armatus, in the streambed of Arroyo Vizcaíno. Dates on the site are between ~32,200 and 31,200 cal BP (Fariña et al. 2014). Briefly, the main problems include the following: First, the site is in a streambed where the stream becomes deeper, forming a natural pond on a substrate of a cretaceous silicified rock. This is a typical location for a bone trap. Second, the very few lithic artifacts are not convincing, and even if they were artifacts, their presence in a bone assemblage in a streambed makes any association questionable. Third, the main argument for the human origin of the bone assemblage is the presence of some bones having marks, interpreted as the result of human tool use (Fariña et al. 2014); however, discriminating between trampling and cut marks (in a bone assemblage full of marks of different origin) is extremely difficult because these modifications overlap morphologically. Equifinality cannot be ruled out. Finally, excavation outside the streambed (a place where any association will be difficult to support) is urgently needed in order to evaluate the context and the interpretation.

In a recent paper, Dillehay and others (2015) published new research at the Chinchihuapi I and II and Monte Verde I sites, all in the Monte Verde area (southern Chile). The recent excavation of 30 test pits, 10 block areas, and 54 sedimentary cores yielded 39 lithics, 12 burned features, and 8 taxonomically unidentifiable animal bones. Based on these data, the authors proposed the occurrence of "short term anthropogenic activities that were most likely associated with hunting and gathering, heating food in small hearths, and producing and discarding expedient tools" (Dillehay et al. 2015:21). Dillehay and others dated these findings between ~18,500 and 14,500 cal BP. One limitation of the evidence is the scarcity of archaeological materials at these sites. This problem is magnified by the large extent of the excavated surface, and the wide temporal range of the artifacts. As Dillehay and collaborators have indicated, several studies were still in process and some results were therefore preliminary. Based on the limitations above, we consider that the evidence from Chinchihuapi I and II and Monte Verde I is promising but, at the moment, it is too weak, too chronologically broad, and too spatially sparse to support human presence in southern Chile immediately after the LGM.



Figure 5. A) Panoramic view of the Cerro de los Onas showing the entrance of the Tres Arroyos 1 cave site in Tierra del Fuego (Chile); B) Detail of the excavation of the 12,700 cal BP layer. Bifacial tool associated with a Hippidion saldiasi rib. Photo courtesy of Mauricio Massone.

Final Thoughts

It is clear that humans were in South America when Clovis people expanded in North America and that these populations were there at least 1,500 years before Clovis. No projectile points (except the few broken points in Monte Verde II) were found in any pre-Clovis South American sites, and megamammals constitute a significant occurrence only in Arroyo Seco 2. The first evidence of *continuous* human occupation in South America is found between ~14,500 and 14,000 cal BP. At ~13,000 cal BP, in coincidence with Clovis in North America, there is a significant increase in sites, and these are scattered in the main regions of South America. This rise could be associated with the expansion of Fishtail projectile point technology, and with other less popular types of projectile points such as Paijan or El Jobo, and would be related to a second pulse of peopling and/or the advantages brought by the incorporation of new hunting technologies.

In South America, humans were present in the southern tip of Patagonia at ~12,700 cal BP in Fell's Cave and in Tres Arroyos I in Tierra del Fuego, suggesting the final step for the expansion phase of *Homo sapiens* on the continent. Despite active research and dating programs over the last 40 years, and favorable conditions of visibility and preservation for early sites in Patagonia, the ~12,700 cal BP baseline remains firm, suggesting an actual temporal threshold.

Several issues should be resolved in order to test the validity of a pre-LGM human occupation of the continent. First, if the

pre- and contemporaneous-LGM sites were confirmed, the human occupation of South America would reflect a discontinuous signal in both regional and temporal scales. Second, because the most accepted ancient DNA models state that New World humans have Asiatic origins (after a period of isolation in Beringia known as the Beringia standstill during the LGM) and that all known human remains found until now are linked to this population, a pre-LGM occupation would imply a regional extinction of earlier humans throughout South America. There is no evidence of such a process, and it seems unlikely. Third, a pre-LGM peopling would also lead to the consideration of a human occupation of South America prior to or at the same time as the earliest confirmed presence of Homo sapiens in Western Beringia, the Yana RHS site (dated to ~30,000 BP). At the present stage of archaeological and genetic knowledge, this hypothesis also seems very unlikely. Finally, because the oldest human remains in South America are dated to ~ 12,300 cal BP, we have to ask this pivotal question: Where are the human bones of the people inhabiting South America before and during the LGM? So far, none have been found.

*Additional suggested readings pertaining to this article may be found at https://www.saa.org/publications/the-saa-archaeological-record.

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THE CLOVIS RECORD

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lovis is still the best-documented early occupation of North America. Since the initial discovery of the type site Blackwater Draw near Clovis, New Mexico, Clovis points have been recovered from sites, and thousands more as isolated finds, throughout much of North America south of the Wisconsin ice sheets and as far south as Mexico. Clovis hunter-gatherers left behind their culturally diagnostic Clovis projectile point, a lanceolate point with a flute that initiates at the base and terminates about halfway up the biface.

The earliest decades of Clovis research were dedicated to defining the culture based on shared traits. Assemblages from buried sites yielded radiocarbon dates placing Clovis at the end of the Pleistocene, as well as stone assemblages of fluted points and large bifaces, and faunal remains from kill sites suggestive of a subsistence strategy focused on hunting Pleistocene megafauna. More recent research has helped refine the timing of Clovis, identify regional stylistic and adaptive variations in technology, and recognize diversity in settlement and subsistence practices. With this, we now have a more complete picture of the chronology, technology, and adaptations of Clovis populations living throughout North America.

Clovis Chronology and Environment

The discovery of new sites with buried components and the increased precision of radiocarbon dating techniques, allowing for redating of previously discovered sites, has led to significant refinement in Clovis chronology. Clovis dates to a 400-year-span from 13,050–12,650 cal BP. This range was proposed by Waters and Stafford (2007), who redated sites, assessed previously reported dates from early sites, and identified 11 sites they consider to have well-dated Clovis occupations (Figure 1). Their criteria include precision error of 75 years or less, the presence of Clovis diagnostic artifacts, and unambiguous association between the dated material and the Clovis occupation of the site. Since their 2007 study, most new dates from other Clovis sites also fall within this chronological span. Yet, there are a few sites that provide hints of an earlier Clovis record. One new site, El Fin del Mundo, Mexico, has

produced a date of 13,390 cal BP (Sanchez et al. 2014). This date is ~350 years older than the oldest of the sites considered by Waters and Stafford (2007). Friedkin, Texas, and Aubrey, Texas, are sites with lithic assemblages that include features typical of Clovis technology and have also produced ages potentially older than 13,050 BP. However, both sites have dating shortcomings. At Friedkin, the Clovis and pre-Clovis assemblages are dated with the optically stimulated luminescence (OSL) technique, which has the limitation of larger error ranges. Dates from Aubrey suffer from questions related to the association between the dated material and the Clovis artifacts (Waters and Stafford 2007). While recognizing these limitations, it is interesting to note that Aubrey, Friedkin, and El Fin del Mundo all occur well south of Beringia, the glacial ice sheets, and the ice-free corridor. When combined with the absence of Clovis points in Beringia and the far northeast (Smith and Goebel 2018), these three Clovis sites provide intriguing evidence that Clovis fluted point technology dates oldest and may have originated in southern North America.

While the start and end of Clovis continues to be refined, it is clear that Clovis populations lived in North America in the late Pleistocene and experienced major environmental changes. Perhaps most significantly, the end of the Ice Age brought with it the extinction of 37 genera of North American mammals (Grayson and Meltzer 2015). Last appearance dates of several species, including ground sloth, giant bear, sabertooth, and gomphothere, coincide with the time of Clovis. Other species such as Pleistocene horse, Yesterday's camel (also known as Western camel or American camel), American mastodon, and mammoth all were alive beyond the time of Clovis and were clearly hunted by humans. Thus, Clovis people witnessed and had to cope with the regional/local, if not continental, loss of four large-game food resources as these animal populations dwindled toward extinction. In addition to extinctions, Clovis groups also experienced the onset of the Younger Dryas, a global cooling event that lasted from 12,850-11,650 BP. Once thought to represent a severe, rapid event uniformly affecting landscapes like river systems and biotic communities

across the continent, it is now clear that the Younger Dryas had time-transgressive effects that varied in severity regionally and locally (Meltzer and Holliday 2010). Like the extinctions, the impacts of the Younger Dryas would have been felt differently and at different times by Clovis hunter-gatherers across the continent. Further, it has been proposed that a cosmic impact may have detrimentally affected environments and Clovis populations throughout the continent. The idea that an extraterrestrial object burst in the atmosphere above North America or impacted the ice sheets and initiated the Younger Dryas has received much attention since its initial proposal. Some researchers continue to find increased concentrations of possible impact-related markers in Younger-Dryas-aged sediments. The most commonly discussed include platinum group elements, magnetic spherules, and nanodiamonds. Other researchers have either failed to replicate increased concentrations of these markers in Younger-Dryas-aged sediments, found equal or greater concentrations in earlier or later sediments, or proposed alternate explanations (such as ordinary cosmic rain becoming concentrated by natural geomorphic processes). Thus, the debate continues, and we are left with three possibilities. Either 1) a comet burst over or impacted North America, spewing fire across the continent, igniting the Younger Dryas, and causing extinctions leading to a Clovis population crash; 2) cosmic and/or geomorphic processes resulted in increased sedimentary concentrations of some extraterrestrial materials that can be used as a geochronological marker for the Younger Dryas onset; or 3) there is no continental pattern, and concentrations and absences need to be explained within local contexts.

Clovis Technology

Lanceolate, concave-based, fluted Clovis points are the most well-recognized and diagnostic artifacts of the Clovis culture. The flute is a distinguishing characteristic of the point's design. By directly striking the base of an unfinished biface with a hammerstone or billet, Clovis flintknappers removed a flake that extends no more than halfway up to the tip, leaving an endthinning or flute scar (Bradley et al. 2010). The features of this flake removal help to distinguish Clovis from later Paleoindian types like Folsom and Cumberland points, which have flutes that run the entire length of the point, and other points, which have no flutes. Clovis points regularly exhibit impact damage on the tip indicating they were thrust or thrown, and microscopic usewear traces suggest Clovis points also served as knives (Smallwood 2015). While the flute is a defining characteristic of the point, archaeologists have not settled on a single explanation for the purpose of fluting in Clovis. Possibilities include that the flute was a form of stylistic expression, may have been associated with ritualistic



Figure 1. Map showing locations of dated Clovis sites (1-14; after Waters and Stafford 2007), other Clovis sites mentioned in text (15-20), and examples of Clovis points recovered from select sites: 1. Lange-Ferguson, SD; 2. Sloth Hole, FL; 3. Anzick, MT (image permission courtesy of H. Smith); 4. Dent, CO (image permission courtesy of M. Eren); 5. Paleo Crossing, OH; 6. Domebo, OK; 7. Lehner, AZ; 8. Shawnee-Minisink, PA (image by A. Smallwood); 9. Murray Springs, AZ (image by A. Smallwood); 10. Colby, WY; 11. Jake Bluff, OK; 12. Topper, SC; 13. Sheriden Cave, OH; 14. La Prele, WY; 15. El Fin del Mundo, Mexico; 16. Friedkin, TX; 17. Aubrey, TX; 18. Gault, TX; 19. Blackwater Draw, NM (image by A. Smallwood); 20. Carson-Conn-Short, TN (image by A. Smallwood); 21. Hogeye, TX (image permission courtesy of M. Waters and T. Jennings).

behavior, or could have helped secure the point in the haft, or that the flute design had shock-absorbing properties that improved point resilience (see Thomas et al. 2017). Though all Clovis points are lanceolate-shaped with incurvate bases, the depth of concavity of the base and the excurvature of the blade varies from region to region (Figure 1). Recent advances with geometric morphometrics have helped document this variation. These studies generally find regional and subregional differences in point shape across North America that were not the result of resharpening and raw material characteristics. Instead, the variation is likely the result of Clovis populations throughout the continent locally adapting to subregions and uniquely altering aspects of their technology (Anderson et al. 2015; Buchanan et al. 2014; Smith and Goebel 2018).

Clovis flintknappers crafted their points using bifacial reduction, and the debris from this reduction process and remnant flake scars on bifaces have helped Paleoindian archaeologists describe their reduction techniques. Clovis bifaces were thinned and shaped using overface flaking and endthinning, and these flaking strategies were used throughout the

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reduction process. The creation of overshot flakes—removals that travel across the biface and remove a portion of the biface edge—has long been identified as a feature of Clovis biface and debitage assemblages (Bradley et al. 2010; Figure 2). However, recent research has highlighted the risk of biface width loss associated with these removals and proposed that overface flaking, the removal of flakes that travel past the midline but terminate prior to the opposite bifacial edge (Smallwood 2012), may have been the primary goal. Overshots may be frequently produced diagnostic mistakes of this strategy. Endthinning, the removal of blade-like flakes parallel to the long-axis, was used to longitudinally thin bifaces. To create the characteristic Clovis point flute, some point bases were shaped around earlier-stage endthin removals; for others, the removal of an endthinning flake to create a flute scar was one of the last steps of production. Like variation in point morphologies, the application of these thinning strategies by Clovis knappers varied regionally (Smallwood 2012). These reduction techniques were also used to craft bifacial cores, large disc-shaped bifaces with edges prepared for the removal of wide, thin flakes. Bifacial cores were important parts of the mobile toolkit because they could serve as tools and cores; bifacial cores had sharp, durable edges, and thinning flakes struck from bifaces were often retouched and used as flake tools (Kelly and Todd 1988). However, recent experiments have shown that bifacial cores were not the most efficient core reduction technology in terms of the amount of usable flakes produced. With smaller initial core sizes, the reduction process becomes increasingly inefficient. Bifacial reduction creates an abundance of flakes that are too small to be effectively used as tools and significantly fewer usable flakes than amorphous cores, cores reduced from multiple edges or many directions (Jennings et al. 2010). Still, bifacial cores are commonly found in Clovis assemblages (Bradley et al. 2010; Waters et al. 2011), suggesting Clovis hunter-gatherers may have favored other advantages of bifacial cores and been less concerned with minimizing stone transport costs and efficiently conserving stone.

Clovis technology is also characterized by the production of blades—flakes that are twice as long as they are wide (Bradley et al. 2010; Waters et al. 2011; Figure 3). Clovis blades were struck from conical and wedge-shaped cores; both were specifically prepared core technologies designed for the removal of elongated, parallel-sided blades that had trapezoidal cross sections and were often curved from the proximal to distal ends. Conical blade cores were prepared for the removal of multiple blades from a single platform surface around the entire circumference of the core, converging at the distal end to create a cone shape. Wedge-shaped cores were prepared for the removal of blades from the acute edge of two intersecting core surfaces. Blades were removed from the intersecting

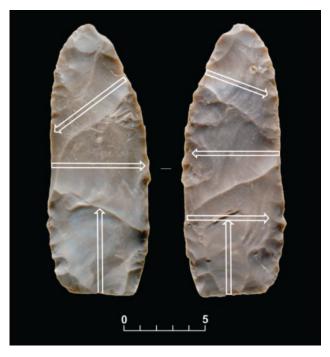


Figure 2. Clovis biface from the Hogeye site, TX, with arrows indicating the direction of overshot/overface and endthinning flake scar removals. Image permission courtesy of M. Waters and T. Jennings.

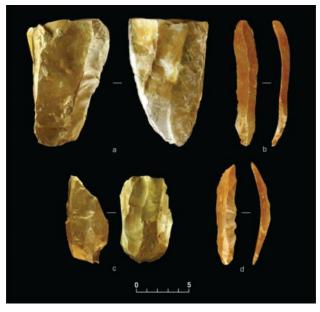


Figure 3. Clovis blade cores and blades from the Gault site, TX (images permission courtesy of M. Waters): (a) conical blade core; (b) blade; (c) wedge-shaped blade core; (d) blade.

edge in one or multiple directions, creating a wedge shape. Clovis blade edges were modified to create a variety of tools, including endscrapers, gravers, and serrated blades, and unmodified blades also show evidence of use. Like bifacial cores, experimental studies show that blade cores were not efficient in terms of transport weight costs; large blade cores produce many usable blanks, but with smaller initial core size, the production efficiency of usable tool blanks decreases. Based on assemblages from sites in the Southern Plains and Southeast, Clovis people produced blades at sites immediately next to raw material sources where stone was abundant.

Clovis assemblages also include a variety of other formal tools (Eren and Buchanan 2016; Figure 4). Toolkits vary from site to site, as a product of site use, and researchers have noted that some tool types are more commonly found in some regions than others. For example, high densities of endscrapers occur at sites in the Great Lakes and Northeast. These tear-drop or triangular-shaped flake tools have steep bits and abraded lateral edges, suggesting they were hafted and possibly used to scrape materials like hides. Denticulated scrapers, with teeth-like projections along the edges possibly used for processing plant materials, occur in collections from the Southeast. Adzes, once thought to have originated with later Paleoindians, have now been found at Clovis sites in the Southern Plains, Southeast, and Great Lakes, providing evidence that Clovis hunter-gatherers also created robust tools for woodworking. Though more rare than stone tools due to preservation issues, points and foreshafts crafted from bone and ivory are found at Clovis sites across the continent, and ivory points and foreshafts are particularly common in collections from Florida (Bradley et al. 2010). Bone points were split, beveled, and tapered on the one end, and foreshafts were beveled and cross-hachured on both ends. Ivory was carved and polished into points and foreshafts, like bone, and some specimens were incised at the base.

Clovis Adaptations

Clovis hunter-gatherers have long been recognized as some of the most highly mobile in North America, in some cases carrying stone hundreds of kilometers across the landscape (Kelly and Todd 1988). Once thought to be a consistent, continent-wide pattern, it is now clear that regional variation also existed in how Clovis populations organized their settlement and subsistence strategies.

In the Southern Plains and periphery, the Clovis record is characterized by large and medium-sized camp sites, megafauna kill sites, and caches. Camp sites tend to be concentrated along the periphery close to stone sources while kill and cache sites are located out in the Plains proper. Caches are places



Figure 4. Clovis tools from various Clovis sites: (a) endscraper from Gault, TX (image permission courtesy of M. Waters); (b) denticulate from Topper, SC (image by A. Smallwood); (c) sidescraper from Blackwater Draw, NM (image by A. Smallwood); (d) serrated blade from Gault, TX (image permission courtesy of M. Waters); (e) bone artifact from Blackwater Draw, NM (image by A. Smallwood).

where Clovis people intentionally placed small collections of stone together in an isolated location on the landscape. Clovis settlement in the region appears to have been organized, at least seasonally, with a logistical mobility strategy to target megafauna refugia and cache stone as insurance supplies in favored hunting grounds. Small groups would venture into the Plains on hunting trips, cache stone for future excursions, and return to southern base camps. At other times of the year, Clovis bands may have moved residential camps to target other seasonal resources. Raw material and site distribution studies show that Clovis populations intensively occupied the region and created a tightly knit "small-world" social network created and maintained by the logistical movements from peripheral camps into the Plains (Buchanan et al. 2019).

The Great Lakes is unique because it represents the only region where Clovis people were clearly colonizers of recently deglaciated landscapes (Ellis 2011)—neighboring Northeastern fluted point populations, whose points are morphologically distinct from classic Clovis points and whose sites postdate Clovis by hundreds of years, also appear to have later colonized unglaciated lands. In the Great Lakes, the presence of caches, large camp sites, and long-distance stone transport provides evidence for similar logistical mobility organization to that of

the Southern Plains. However, rather than primarily targeting megafauna refugia, Clovis populations may have instead been seasonally targeting caribou herds in logistical hunts.

In the Southeast, some important regional differences are evident. Like elsewhere, Clovis populations established relatively large camps at sites in Kentucky, Tennessee, South Carolina, and Virginia. Described as staging areas (Anderson et al. 2015), large camps are located in resource-rich locations near major rivers and high-quality stone outcrops. Southeastern Clovis knappers also relied on the relatively transport-inefficient strategies of biface and blade reduction. However, caches are absent in the region. Thus, logistically targeting large-game herds, and caching stone to support logistical hunts, may have been less common. Instead, staging areas could represent seasonally occupied, subregional macroband centers utilized by relatively more residentially mobile bands (Miller 2016). In other words, perhaps mobile bands periodically came together at larger staging areas for social rather than purely subsistence needs. The Southeast has also produced the greatest density of Clovis points, which suggests the region may have been occupied by the highest populations or for the longest duration. Elsewhere in the Southeast, the lower Gulf Coastal Plain of Louisiana and Mississippi has produced very few Clovis points and no large sites, suggesting that this stone-poor landscape was minimally occupied by Clovis populations.

The Southwest is one region that stands out for its untapped research potential. While Clovis sites, particularly megafauna kill sites, have been repeatedly documented in the US side of the region, collaborative efforts to explore the record in Mexico are showing that Clovis populations ranged much further south (Sanchez et al. 2014). No doubt this ongoing work will continue revealing the extent to which Clovis behaviors in the Southwest are similar to or different from other regions.

Three extensively studied regions have provided evidence for the geographic frontier of Clovis—the Northern Plains, Northwest, and Great Basin. The Clovis record in these regions includes points in relatively low densities, some caches, including ritual caches associated with burials, and few, small camp sites. The Clovis network in the Northern Plains region is also much more dispersed and disconnected than in the Southern Plains (Buchanan et al. 2019). Thus, it appears that small groups of Clovis bands explored the Northern Plains, Northwest, Great Basin, and surrounding Rocky Mountains but never settled these areas to the extent or intensity seen in the neighboring Southern Plains and Great Lakes.

Finally, debate continues over the relative importance of megafauna in the Clovis diet and the extent to which Clovis hunters "overkilled" or contributed to the extinction of some species (Grayson and Meltzer 2015; Surovell et al. 2016). As noted, the environmental changes accompanying the end of the Pleistocene regionally and locally varied in significance and timing (Meltzer and Holliday 2010). Some species appear to have gone extinct prior to human colonization while other extinctions, including animals clearly hunted by Clovis groups, directly overlap with the earliest human occupation of the continent. There is, however, broad agreement that Clovis populations relied on megafauna, with particularly abundant evidence for mammoth hunting, as an important component of their diet and that they also consumed smaller animals as well as gathered plant resources.

Enduring Questions

For all that we have learned about Clovis in recent decades, key questions remain unanswered. Two of these have been at the heart of Clovis research since the earliest discoveries at Blackwater Draw and other sites 90 years ago. When and where did the suite of characteristics we now call "Clovis" originate? How did Clovis spread throughout much of North America?

Chronology data and comparisons to pre-Clovis are providing hints that Clovis point and bifacial reduction technologies may have originated in southern North America. It is also likely that not all elements of what we now consider distinctive Clovis technologies evolved simultaneously. The process might have varied spatially and temporally. For example, Clovis blade techniques may have developed independently from (and earlier than?) point and biface reduction techniques.

Tracking and explaining the spread of Clovis has been equally challenging. Mapping the spread chronologically has been unsuccessful because core Clovis settlement regions such as the Southeast have produced so few dated sites. It is also not clear whether the spread resulted from migration, diffusion, or some combination. Paleoindian archaeologists are interested in the social contexts surrounding how Clovis bands across the continent retained shared technologies while also modifying design templates and production recipes to create regional variants and local traditions. With the continued work of dedicated researchers and a little bit of archaeological luck, it hopefully will not take another 90 years to answer these and other enduring Clovis questions.

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