

HAPLOGROUP X2A: SEARCHING FOR THE ORIGINS OF CLOVIS IN THE
AMERICAS

HONORS THESIS

Presented to the Honors College of
Texas State University
in Partial Fulfillment
of the Requirements

for Graduation in the Honors College

by

Trixie Fenton

San Marcos, Texas
May 2017

HAPLOGROUP X2A: SEARCHING FOR THE ORIGINS OF CLOVIS IN THE
AMERICAS

by

Trixie Fenton

Thesis Supervisor:

Tom Williams, Ph.D.
Department of Anthropology

Approved:

Heather C. Galloway, Ph.D.
Dean, Honors College

ACKNOWLEDGMENTS

I sincerely want to thank my advisor, Dr. Tom Williams, for everything he has done for me these past two semesters. Thanks to his wonderful class, I was able to learn about a subject most people never get to learn. Without his class and guidance, I would not have been able to accomplish this thesis.

I would also like to thank Dr. Haas and Dr. Galloway. Due to the superb organization of the semester and helpfulness throughout, I was able to truly dive into my project without confusion. The Honors program overall has truly transformed me as a student. I have tried so many new things, including presenting at the Thesis Forum, because of the wonderful honors program at this school. I will always be grateful to the professors that are a part of the program.

Finally, I would like to thank my wonderful parents. They have always been the ones to push me in school, and they are the reason I have been able to experience the Honors College. Again, I really appreciate everyone that has helped me get this far.

ABSTRACT

The Clovis First theory suggests that big game hunters peopled the Americas about 12,800 years ago by way of a land bridge, Beringia, with a very distinct Clovis technology. For a while, almost every archaeologist believed this to be true, but some kept looking for different possibilities. This theory has since been refuted due to an increasing number of older sites. Since the Clovis theory has been proven incorrect, there has been a lot of controversy in the archeological world over how the Americas were first occupied. Different archaeologists have spoken up about new theories of how the Americas could have been peopled, but a majority of these theories have been unable to find a connection to Clovis. In order to support a theory, archaeologists must look at all sorts of evidence, such as artifacts, sites, or DNA. DNA is probably the most influential evidence because it gives direct information. Today, we can look at modern Native Americans' DNA to see who their lineage could be linked to. The most common descent found has been Siberian and Asian through haplogroups A, B, C, D, and X, but there is an anomaly that is haplogroup X2a. The haplogroup is found on the Eastern part of America and the Western part of Europe; this proposes that the Solutrean population could have gradually sailed across the Atlantic and populated the Americas. This paper will look at this phenomenon and how it connects to the Solutrean hypothesis by discussing the Solutrean and Clovis technologies, looking at some relevant sites, and analyzing the data of haplogroup X2a. The evidence presented produces the conclusion that the Solutrean hypothesis provides the most reasonable explanation for the origin of Clovis, yet this does not necessarily disprove other route theories. A clearer understanding of the peopling of the Americas will come from continuing research.

TABLE OF CONTENTS

ACKNOWLEDGEMENTS.....	iii
ABSTRACT.....	iv
CHAPTERS	
I. INTRODUCTION AND BACKGROUND.....	1
The Solutrean Hypothesis.....	1
DNA Concepts.....	4
II. SITE EVIDENCE.....	6
III. DNA EVIDENCE.....	8
IV. DISCUSSION AND CONCLUSION.....	13
REFERENCES.....	16

I. Introduction and Background

Since the 1930s, the Beringian land bridge hypothesis has been the most widely accepted migration route for the human entry into the Americas (Land Bridge Theory). This theory proposes that people came to the Americas via a land bridge that emerged between Siberia and Alaska during the LGM. The bridge "formed when Ice Age sea levels dropped during the buildup of the continental glacier" (Bradley et al 2004). The hypothesis also suggests that early people waited until the glaciers between "the Arctic and the rest of the Americas" diverged, creating an 'ice free corridor' for them to travel southward (Bradley et al. 2004: 460). Put simply, a small ancient group crossed this land mass and spread throughout the Americas. This small group were known as the Clovis culture and initially arrived in North America around 13,000 years ago (Smallwood et al 2014: 2). This view, that Clovis was the first culture to inhabit the Americas, was challenged in the 1950s. Archaeological excavations across the country demonstrated there were people at least 1,000-2,000 years before Clovis (Smallwood et al 2014). Recent studies have shown that the "ice free corridor" would not have been a viable route for migration until 12,600 years ago (Pedersen et al 2016). Thus, it cannot explain the arrival of the earliest population. While evidence for older populations predating Clovis continues to be found (Collins et al 2013), Clovis technology is still used as a benchmark for comparative purposes (Smallwood et al 2014: 3; Ardelean 2014).

The Solutrean Hypothesis

With the rejection of the Beringian land bridge hypothesis by the majority of researchers, archaeologists have proposed several new hypotheses on how the Americas

were populated. One of the most controversial of these is the Solutrean Hypothesis (Hall 2000). This hypothesis contends that during the Late Glacial Maximum (LGM), a small group of Solutreans travelled across the Atlantic sea ice to eastern North America, carrying with them technology of the Solutrean culture. The causes of this include the fact that during the LGM temperatures dropped "8–15°C below present-day values" (Brewster et al 2014). This formed an "extension of land-based ice sheets" over much of Northern Europe, while the Atlantic Ocean was covered with sea ice for the majority of the year (Brewster et al 2014; Bradley et al 2004). Although some would argue that the LGM climate was not as stable as proposed resulting in "irregular seasonal patterns of sea ice formation and fragmentation" (Phillips et al 2014). This change in the climate and environment forced animal populations to migrate southwards and toward the coasts and in turn human populations would have followed. The fauna during this time were moved to this extremely cold sub-Arctic sea environment, so it would be reasonable to form a hypothesis that the Solutrean culture, located mostly in the southwestern part of France and northern Spain, followed these fauna and started exploiting the mammals living on the ice-covered sea. If they were to have exploited these oceanic fauna, particularly the grey seal, those of the Solutrean culture would have been able to make it to the Americas by travelling across the Atlantic ice-edge corridor (Bradley et al 1998). This proposed Atlantic-Ice Crossing has been hypothesized to have been achieved between 22,000 and 17,000 BP (Oppenheimer et al 2014). Bradley and Stanford have argued that the purpose behind the Solutrean Hypothesis is to "propose an alternative hypothesis of early human entry into the Americas and to stimulate research" (Stanford et al 2013). Since there is no known explanation of how people populated the Americas, it is necessary to look at all

the possibilities because the origin of a country is valuable to those that live within it. It is important to note that the possible evidence to back these claims may have been "along the now deeply drowned shoreline where marine mammal-hunting peoples might be expected to be found" (Bradley et al 2006). If the Solutrean culture made it to eastern America by following the migration of the seals, researchers could start to explain the origin possibilities of the haplogroup X2a, which is a restricted to present day Native Americans (Reich et al 2012).

One of the major pieces of evidence presented by Stanford and Bradley is the similarities between the Clovis and Solutrean technologies and some cultural aspects. Clovis technology is found only in the Americas. An example of this is that Clovis points exhibit overshot flaking, which thins the projectile point. Overshot flakes remove "part of the edge opposite the platform" (Stanford et al 2012: 270) by striking a flake off that travels across the width of the point. The Solutrean population also uses this overshot method. This particular technique takes an immense amount of skill to master (Stanford et al 2012). As such, it seems to be less likely that these techniques would have developed independently (Stanford et al 2012: 149-150). Some archaeologists point out that there are other cultures that used overshot flaking (Straus et al 2006), but no other cultures besides the Solutrean and Clovis used this technique intentionally (Bradley et al 2006). When overshot flaking is found in other cultures it usually occurs from a mistake during manufacturing (Bradley et al 2006). Another important feature within Clovis technology is the presence of a fluted base; it is original because Clovis formed the flute basally as opposed to from the side (Bradley et al 2004). These two populations also share similar pre-core shaping. Clovis technology has more in common with Solutrean

technology than any other Asian technology (Bradley et al 2004). Due to this, Stanford and Bradley assert that the similarities could be much more than a coincidence. Although critics argue that there are a "large number of differences between Solutrean and the American assemblages" (Straus et al 2006). In contrast, Stanford and Bradley state that if Clovis was formed by a "very specific subset of the Solutrean" they could have developed different features from those Solutreans that did not cross the sea (Reich et al 2012).

Not only do the Solutrean and Clovis populations share similarities in technologies, but they also share some cultural aspects. One distinct feature of Clovis that is also found in the Solutrean was their occasional use of exotic materials. They would use material such as "bone, antler, and ivory tools" (Stanford et al 2012: 247). Clovis and Solutrean also exhibit caching behavior (Bradley et al. 2004). They are the only "two more-than-13,000-year-old archaeological cultures" to bury "extremely well made bifaces" (Stanford et al 2012). It has been discussed that both cultures' artifacts possibly had "non-utilitarian purposes" and that the manufacturing of them could have been for "symbolic and ritual meaning". While these similarities could be viewed as nothing more than that, the evidence could also be seen as showing a clear indication of the Clovis population descending from the Solutrean (Stanford et al 2012: 177).

DNA Concepts

Before discussing the archaeological and genetic evidence, it is important to outline some basic information concerning DNA. DNA stands for deoxyribonucleic acid; the major function of this is to store genetic information (Hoefnagels 2015: 36). The child

inherits this genetic information from their parents. The DNA being discussed in this paper is mitochondrial DNA (mtDNA) (Brown et al 1998). mtDNA is found in the mitochondria within cells (Genetics Home Reference 2017). mtDNA is inherited along the maternal line. For example, if researchers look at a person's genetic history, the nuclear DNA would have come from many men and women while the mtDNA would have been passed down the maternal line (Groleau 2002). Because of this, it is much easier to look at the long-term ancestry of a population through mtDNA. Another necessary aspect to consider are mutations; they take time to accumulate. This means that if there are many mutations found on one person's DNA and not that many found on another's, the person with more would have been from an older population (Hoefnagels 2015: 274).

One important line of evidence to consider is DNA. A haplogroup is "a genetic population or group of people who share a common ancestor" ("International Society of Genetic Information"). Restriction Fragment Length Polymorphism (RFLP), is a way to detect the differences within DNA fragments which helps determine a distinction between particular groups (Reilda et al 2003). Through extensive RFLP analysis it was discovered that there were probably four main founding mtDNA haplogroups of the Americas. These haplogroups are labeled as: A, B, C, D (Reilda et al 2003; Brown et al. 1998). These haplogroups account for 97% of the modern Native American population (Brown et al. 1998). Haplogroups A, B, C, and D are all found in the "ancient Siberian mitochondrial gene pool" along with some forms of group X (Forstere et al. 1996). Although the modern Native Americans are closely related to this Siberian population, there is a haplogroup that cannot be accounted for in this region of the globe. That group

is called X2a, and it is found in Native American populations near the Great Lakes region and in European populations around Western Eurasia (Brown et al 1998; Oppenheimer et al 2014). However, this particular group is nearly absent in Eastern Eurasia. A question arises from this information; where did this mtDNA X2a haplogroup come from, and how did it get into the Americas?

Site Evidence

If Native Americans located in the northeast of America share haplogroup X2a with Western Eurasians, what are the possible routes for its arrival in the New World. There are three sites in particular that help support a Solutrean group coming to the Americas and passing on their unique stone manufacturing to Clovis (Stanford et al 2012).

The following few sites are on the east coast and could be some of the first sites where the Solutreans began their transfer of information to Clovis. The first site that Stanford and Bradley address when discussing this particular route is Meadowcroft Rockshelter. Although these site's dates have been criticized (Adovasio et al 1990), the oldest date that can be matched with human occupancy is between 13,955 and 14,555 years ago (Adovasio et al 1990). The next site to consider would be Cactus Hill. This site has been dated to around 15,000-18,000 14CBP. Finally, the Page-Ludson site has been dated to around 14,345 14CBP. These dates are all extremely important in supporting the possible route from Western Europe (Stanford et al 2012). The reason is that these dates bridge the gap that some critics argue refute the whole Solutrean hypothesis. According to Jelinek, the Solutrean population could not be related to Clovis because there is a

6,000 year difference (Bradley et al. 2004). The Solutrean population is estimated to have lasted between 22,000 and 16,500 BP (Bradley et al 2004), while Clovis in the Americas dates between 13,200 and 12,900 BP (Bradley et al 2004). These sites help bridge the gap in the missing years argument. Not only do these sites help close the gap, but they also show possibilities of there being a transitional period from the Solutrean culture to Clovis. At these sites, there were pre-Clovis artifacts found. This could possibly mean that the unique technologies of the Solutrean went through a transitional period before becoming Clovis technology (Bradley et al 2004). Critics of this hypothesis argue that the evidence demonstrates similarities but that this does not mean the two are related and until there is more concrete proof the argument stated above will remain unconvincing (Straus et al 2006).

Finally, The *Cinmar* boat discovered a "bifacially flaked, bi-pointed stone blade" off the east coast. It has been recorded that a fisherman pulled up this bi-point along with parts of a mastodon, which was later tested to be around 22,760 +/- 90 RCYBP, Radio Carbon Years Before Present. Those who study the Solutrean Hypothesis find this discovery to be further support, but others think there are holes in this argument. While the point found may be similar to distinct points of the Solutrean culture, some researchers have argued that the bone is dated to be 2000 years earlier than the establishment of the Solutrean culture in Europe (Eren et al 2015). Although this evidence could help support the hypothesis, further research is necessary to confirm its true age.

While the sites above have been used to support the hypothesis, there are a number of early sites that challenge the Solutrean Hypothesis.

Sites that challenge the Solutrean Hypothesis have DNA evidence, but that does not necessarily mean that the sites completely refute the route. The first site to look at is the Anzick site on the west coast in Montana (Rasmussen et al 2014). At this site, a child's skull was discovered near Clovis antlers. The skull was dated at about 14C 12,707-12,556 BP while the Clovis antlers were dated at 14C 13,039-12,763 BP (Oppenheimer et al 2014). The other site is located in Oregon at Paisley Caves which is also located on the west coast. Here, coprolites were discovered along with non-Clovis materials. Radiocarbon dating on the coprolites dated them to around 14,500 BP, which is older than Clovis (Bradley et al 2004). Finally, the Washington site, again on the west coast, that produced the skeleton known as Kennewick Man must be noted. The remains were dated to 8,690-8,400 cal yr BP (Raff et al 2015). It is important to note that these are the only sites presented that have direct DNA evidence, but only one of the sites has a connection to the Clovis technology. The DNA discovered will be discussed further in the following section.

DNA Evidence

Haplogroup X first emerged around 30 kya spreading widely (Reilda et al 2003; Fernandes et al 2012; Sarac et al 2014) and originated in the Near East (Sarac et al 2014; Fernandes et al 2012). Haplogroup X2 expanded during or after the LGM (Sarac et al 2014). Although, if it expanded after the LGM the connection with the Solutrean population is lost because the proposed migration occurs during the LGM. This group is spread geographically wider than Haplogroup X1, but it shows up in lower frequencies (Sarac et al 2014). X2 is found in Northern Africa and Western Eurasia, while it is rarely recorded in Eastern Europe, Central Asia, Siberia, and India (The Arabian, Raff et al

2015; Reilda et al 2003). There are two places that seem to exhibit higher frequencies of X2: the Orkney Islands near Scotland and Drunze, Syria (Raff et al 2015; Sarac et al 2014). The Orkney Islands are clearly located in Western Eurasia, while Drunze is on the west side of Syria. X2a's presence in Scotland may be related to the migration of X2a in Northern Europe, but modern genetic populations aren't the same as ancient genetic populations. A major mutation that is found in an overwhelming majority of European X haplotype is 225A (Derenko et al 2001; Fernandes et al 2012). This mutation is an important part of haplogroup X and will be discussed briefly later. The presence of X2, which is the "mother" X2a, in more Western areas than Eastern raises questions. If an Eastern group founded haplogroup X2a, wouldn't the maternal group show up more? Although this is puzzling, the near absence of X2a in the east does not necessarily confirm the Solutrean hypothesis. There is an exception to the absence of X2 in the East. A southwestern Siberian population called Altaian exhibit this haplogroup thus giving argument to those that refute the Solutrean Hypothesis (Reilda et al 2003; Raff et al 2015).

Derenko et al. (2001) conducted a study on Asian populations where they searched for haplogroup X. They screened 790 individuals from 10 aboriginal Siberian populations. What they found was a 3.5% frequency of X in the Altaian people. During the study, the researchers found through RFLP that the Altaian haplogroup X did not exhibit the major marker for the group, 225A (Derenko et al 2001). Another study found that 3 out of 14 Native Americans tested had mutation 225A (Derenko et al 2001; Fagundes et al 2008). The absence of this mutation in the Alatian population presents an argument that their population and, more broadly, the Eastern Asian population in general

could not be related to the Native American haplogroup X2a, but this argument would not be too convincing since this variant is only present in some Native Americans. Instead, this data suggests that there is missing information. Since some of the Native Americans did have the mutation 225A, a conclusion could be made that "intermediate lineages have been lost" (Derenko et al 2001; Fagundes et al 2008). While some may argue that there is simply a gap in the genetic data that would otherwise clearly present a linear descent from Western Europeans to Eastern Asians to the Native Americans, others would state that "the few Siberian X lineages that have been identified are not plausible ancestors" to the Native American haplogroup X2a (Fernandes et al 2012). The Altaian population's haplogroup X appeared <6,700 years ago (Reilda et al 2003). This age is so much younger than X2a that it is difficult to suggest an ancestral connection between the two. X2 appearing in the Southern Siberian Altai people is "more likely explained by recent gene flow from Europe or from West Asia" (Raff et al 2015; Reilda et al 2003).

Through high-resolution RFLP analysis, it was discovered that some of the Native Americans and about 4% of Europeans had an mtDNA that did not fall into the haplogroup A, B, C, or D. The group that was found in common with these two populations was X2. Brown et al. (1998) formulated a study of 36 people in order to further study this information. The researchers used RFLP and CR sequence analysis to study the haplogroup X. While looking at the 22 Native Americans and 14 Europeans, they found that the mtDNA between the two populations were related, but the relation was very old. It was found that about "25% of the Ojibwa, 15% of the Sioux, 11-13% of the Nuu-Chah-Nulth, 7% of the Navajo, and 5% of Yakima" tribes had the haplogroup X2a. The study concluded that the only credible explanation for the date found is that

West Eurasians came to the Americas by following the Atlantic because of the lack of evidence in Asian cultures. The reason for this is that the Native Americans that were used in the study were all in the north-east region of America. If there is a connection between Western Eurasia and the north-east of America, and the population diverged a long time ago it is reasonable to conclude that the way this particular haplogroup got to America was by the method proposed by the Solutrean hypothesis. The authors of the paper suggest that the haplogroup X2 might have been a minor founding population to the Americas along with the major four A, B, C, or D (Brown et al. 1998).

It is worth noting that there are three proposed criteria that a founding lineage must meet in order for it to be considered a major founding lineage. The first criterion is the American sequence should be connected to an Asian ancestor. With this being said, there is no way that the haplogroup X2 could be a major founding lineage since it is connected to European populations because it is not found in Asia. Second, a founding sequence must “occupy central branching nodes in phylogeny” (Forester et al. 1996). Finally, a major founding sequence must be widespread, and the derived sequences would have a limited distribution. The haplogroup X2 is not widespread, but that does not mean it cannot be a minor founding haplotype. It is stated that these criteria do not apply to possible minor founders (Forester et al. 1996).

As discussed in the site evidence section, the Anzick site supports a route theory other than one involving the crossing of the Atlantic. The DNA evidence found supports a gene flow, which is the movement of genetic material between populations, from Asia into North America (Eren et al 2015; Understanding Evolution Team 2017). The flow was from a Siberian population found at Mal'ta into Native American ancestors

(Rasmussen et al 2014). This evidence supports a migration route from Asia, along the Pacific coast and into North America. Though the DNA did not point towards a European population, it does not contradict an Atlantic route possibility. When researchers tested Anzick-1's DNA, many looked at the boy as a link to Clovis, but this is debatable. Since they were both discovered at the same site in Montana, it was assumed that they had to be related, but the dating contradicts this argument. The dates discussed earlier present a large gap in time. Some have argued that the bone rods could have been an artifact passed down in the family, but there is not enough information to support or refute this idea. The minimum difference between the two remains found is 56 years while the largest is 483 years (Oppenheimer et al 2014). While some argue that this refutes the Solutrean hypothesis, the data found only supports a later arrival from Asia.

Even though this study does not refute the Solutrean Hypothesis, there are other DNA studies that clearly support an out of Siberia hypothesis like the Beringia land bridge. DNA evidence from Paisley Caves in Oregon supports a route from Siberia. Archaeological excavations at this site found human coprolites. After testing the coprolites, haplogroups A2 and B2 were found. These particular mtDNA groups are found in Siberian and Asian populations today which support the Asian decent hypothesis. This information supports a route from Siberia, but this site is not relevant to any hypotheses surrounding Clovis because the cave did not yield any Clovis technologies. From the information that has been discovered at this site, one could not disprove the Solutrean hypothesis. Instead, it suggests that there is more than one route that the first people of the Americas took (Bradley et al. 2004).

Another thing to consider when discussing genetics is the possibility of admixture. There is a complication in studying Native American genetic history due to the possibility of "admixture with European and African immigrants since 1492" (Reich et al 2012). Although this is a viable concern, pre-European remains such as Kennewick Man provide evidence of X2a being in the Americas before the "result of post-1492 admixture" (Raff et al 2015). However, the presence of X2a in the Kennewick Man does not necessarily suggest a "trans-Atlantic gene flow" (Raff et al 2015). Kennewick Man is currently the "most basal lineage of X2a yet identified", and the remains "give no indication of recent European ancestry and moves the location of the deepest branch of X2a to the West Coast" (Raff et al 2015). The problem with this is that X2a formed around 14,200- 17,000 cal yr BP, which leaves a rather large gap for movement across the country (Raff et al 2015). The Solutrean culture could have come and landed on the East Coast, then a small group might have traveled to the west while reproducing with other possible populations at the time thus creating a difference within the DNA. This would of course need to be tested and studied more. It seems to some that there is "no compelling reason to think that X2a is more likely to have come from Europe than Siberia" (Raff et al 2015).

Discussion and Conclusion

After looking over the evidence, one could draw two conclusions. One would be that Clovis came with the groups that populated America from Siberia. While the other could be that there was more than one route taken to get into the Americas, and those that populated from Western Eurasia brought Clovis with them. After looking at all the DNA evidence, it is apparent that there is a definite lineage from the Siberian population, but

the small fraction of people that are part of the haplogroup X2 must be considered. When looking at the DNA evidence for this portion of the modern Native American haplogroups, one finds that the haplogroup X2a quite possibly could have descended from Western Eurasia which poses the question how did they get there. If the Solutrean population came to America, the shortest route would have been to use the Atlantic Ocean to get here. All while living off marine animals to which they would have adapted to. Not only does the DNA evidence need to be considered, but the sites and technologies as well. The sites presented either support or refute this claim, but the older sites on the East Coast seem to present questions. Why would there be older sites on the East than on the West? Are there undiscovered sites? Is there more than one route possible? The technologies are also extremely important because no Asian technology, thus far, has proven to be an ancestor of Clovis, and the Solutrean technology seems the most reasonable. Until there is clear evidence from either side of the argument, all hypotheses should be extensively tested.

The biggest issue that this information faces is that there still is not enough evidence to definitively say that there was a viable route taken to populate the Americas from Western Europe. This topic is important regardless because until someone finds either Clovis or Solutrean burials, anything can help. In conclusion, there is evidence to suggest the reason there is a small amount of Native Americans with haplogroup X2a is that a group of the Solutrean population came on boats from Western Europe and helped start the population of the Americas. It could also be said that the Solutrean population transitioned into Clovis. Although the Solutrean hypothesis could have occurred, any other route hypothesis is feasible as well. The most important thing to take from these

data are that research needs to be done with an open mind. Criticism is healthy in order to spark conversation but rejecting an idea completely could lead to these questions never being answered. The only way to discover how the Americas were really peopled is through further research.

REFERENCES

Adovasio, James M., J. Donahue, and R. Stuckenrath.

1990 The Meadowcroft Rockshelter Radiocarbon Chronology 1975-1990."

American Antiquity 55, no. 2: 348-54. Accessed December 1, 2016.

<http://www.jstor.org.libproxy.txstate.edu/stable/pdf/281652.pdf>.

Ardelean, C.F.

2014 The early prehistory of the Americas and the human peopling of the Western Hemisphere. An overview of archaeological data, hypotheses and models. In: S. Marinescu-Bîlcu (ed.). *Studii de Preistorie 11*. Bucharest, Romania: Asociația Română de Arheologie, pp. 33–95.

Bradley, Bruce, and Dennis Stanford.

2004 "The North Atlantic Ice-Edge Corridor: A Possible Palaeolithic Route to the New World." *World Archaeology* 36, no. 4: 459-78. Accessed December 1, 2016.

<http://eds.a.ebscohost.com.libproxy.txstate.edu/eds/pdfviewer/pdfviewer?sid=b6e0b96b-3586-4b8f-a623-974a1ecd1ccc%40sessionmgr4010&vid=4&hid=4205>.

Bradley, Bruce, and Dennis Stanford.

2006 "The Solutrean-Clovis connection: reply to Straus, Meltzer and Goebel."

World Archaeology 38, no. 4: 704-14. Accessed April 12, 2017. Taylor & Francis Online.

Brewster, Ciarán, Christopher Meiklejohn, Noreen Von Cramon-Taubadel, and Ron Pinhasi.

2014 "Cranio-metric analysis of European Upper Palaeolithic and Mesolithic samples supports discontinuity at the Late Glacial Maximum." *Nature Communications*. Accessed April 11, 2017.
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5010115/>.

Brown, Michael D., Seyed H. Hoesseini, Antonio Torroni, Hans-Jurgen Bandelt, John C. Allen, Theodore G. Schurr, Rosaria Scozzari, Fulvio Cruciani, and Douglas C. Wallace.
1998 "MtDNA haplogroup X: An ancient link between Europe/western Asia and north America?" *American Journal of Human Genetics*, 1852-861. Accessed December 1, 2016. doi:10.1086/302155.

Collins, M.B., Stanford, D.J., Lowery, D.L. & Bradley, B.A.

2013 North America before Clovis: Variance in Temporal/Spatial Cultural Patterns, 27,000-13,000 cal yr BP. In: K. E. Graf, C. V Ketron, & M. R. Waters (eds.). *Paleoamerican Odyssey*. College Station, Texas: Center for the Study of the First Americans, pp. 521–539.

Derenko, Miroslava V., Tomasz Grzybowski, Boris A. Malyarchuk, Jakub Czarney, Danuta Miscicka-Sliwka, and Ilia A. Zakharov.

2001 "The presence of mitochondrial haplogroup X in Altaians from South Siberia." *American Journal of Human Genetics*, 237-41. Accessed April 3, 2017.

<http://www.sciencedirect.com.libproxy.txstate.edu/science/article/pii/S0002929707614657>.

Eren, Metin I., Matthew T. Boulanger, and Michael J. O'Brien.

2015 "The Cinmar discovery and the proposed pre-Late Glacial Maximum occupation of North America." *Journal of Archaeological Science: Reports*, 708-13. Accessed February 5, 2017.

<http://www.sciencedirect.com/science/article/pii/S2352409X15000280>.

Fagundes, Nelso J.R., Ricardo Kanitz, Roberta Eckert, Ana C.S. Valls, Mauricio R.

Bogo, Francisco M. Salzano, David Glenn Smith, Wilson A. Silva, Jr., and Marco A.

Zago.

2008 "Mitochondrial Population Genomics Supports a Single Pre-Clovis Origin with a Coastal Route for the Peopling of the Americas." *AJHG* 82, no. 3. Accessed February 22, 2017.

<http://www.sciencedirect.com.libproxy.txstate.edu/science/article/pii/S0002929708001390>.

Forster, Peter, Rosalind Harding, Antonio Torroni, and Hans-Jurgen Bandelt.

1996 "Origin and Evolution of Native American mtDNA Variation: A Reappraisal.", 935-45. Accessed April 11, 2017.

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1914796/pdf/ajhg00023-0194.pdf>.

Fernandes, V., F. Alshamali, M. Alves, MD Costa, JB Pereira, NM Silva, L. Cherni, N. Harich, V. Cerny, P. Soares, MB Richards, and L. Pereira.

2012 "The Arabian Cradle: Mitochondrial Relicts of the First Steps along the Southern Route out of Africa." *The American Society of Human Genetics*. Accessed March 15, 2017. <https://www.ncbi.nlm.nih.gov/pubmed/22284828>.

Understanding Evolution team

2017 Evolution 101: "Gene Flow." Understanding Evolution your one-stop source for information on evolution. Accessed February 13, 2017. http://evolution.berkeley.edu/evolibrary/article/evo_21.

Groleau, Rick.

2002 "Tracing Ancestry with MtDNA." PBS. January. Accessed April 02, 2017. <http://www.pbs.org/wgbh/nova/neanderthals/mtdna.html>.

Hoefnagels, Marielle.

2015 *Biology: concepts and investigations*. New York, NY: McGraw-Hill Education.

"International Society of Genetic Genealogy Wiki ISOGG Wiki." Haplogroup - ISOGG Wiki. March 26, 2017. Accessed April 02, 2017. <http://isogg.org/wiki/Haplogroup>.

"Land Bridge Theory." Migration Theories. Accessed December 1, 2016.

<https://ows.edb.utexas.edu/site/hight-kreitman/land-bridge-theory>.

O'Brien, Michael J., Matthew T. Boulanger, Mark Collard, Briggs Buchanan, Lia Tarle, Lawrence G. Straus, and Metin I. Eren.

2014 "On thin ice: problems with Stanford and Bradley's proposed Solutrean

colonisation of North America." *Antiquity* 88, no. 340: 606-13. Accessed April 5, 2017.

<http://search.proquest.com.libproxy.txstate.edu/docview/1545873943?accountid=5683>.

Oppenheimer, Stephen, Bruce Bradley, and Dennis Stanford.

2014 "Solutrean hypothesis: genetics, the mammoth in the room." *World*

Archaeology, 752-74. Accessed December 1, 2016.

doi:10.1080/00438243.2014.966273.

Pedersen, M.W., Ruter, A., Schweger, C., Friebe, H., Staff, R.A., Kjeldsen, K.K., Mendoza, M.L.Z., Beaudoin, A.B., Zutter, C., Larsen, N.K., Potter, B.A., Nielsen, R., Rainville, R.A., Orlando, L., Meltzer, D.J., Kjær, K.H. & Willerslev, E.

2016 Postglacial viability and colonization in North America's ice-free corridor.

Nature.

Phillips, Kelly M.

2014 "Solutrean Seal Hunters? Modeling Transatlantic Migration Parameters

Fundamental to the Solutrean Hypothesis for the Peopling of North America."

Journal of Anthropological Research 70. Accessed February 12, 2017.

<http://www.journals.uchicago.edu.libproxy.txstate.edu/doi/pdfplus/10.3998/jar.0>

521004.0070.404.

Raff, Jennifer A., and Deborah A. Bolnick.

2015 "Does Mitochondrial Haplogroup X Indicate Ancient Trans-Atlantic Migration

to the Americas? A Critical Re-Evaluation." *PaleoAmerica* 1, no. 4: 297-304.

Accessed March 30, 2017.

<http://www.tandfonline.com.libproxy.txstate.edu/doi/abs/10.1179/2055556315Z>

.00000000040.

Rasmussen, Morten, Sarah L. Anzick, Michael R. Waters, Pontus Skoglund, Michael DeGiorgio, Thomas W. Stafford, Jr., Simon Rasmussen, Ida Moltke, Anders Alberchtsen, Shane M. Doyle, G. David Poznik, Valborg Gudmundsdottir, Rachita Yadav, Anna-Sapfo Malaspinas, Samuel Stockton White, V, Morten E. Allentoft, Omar E. Cornejo, Kristiina Tambets, Anders Eriksson, Peter D. Heintzman, Monika Karmin, Thorfinn Sand Korneliussen, David J. Meltzer, Tracey L. Pierre, and Jesper Stenderup.

2014 "The genome of a Late Pleistocene human from a Clovis burial site in western

Montana." *Nature Letter*, 225-29. Accessed January 15, 2017.

<http://www.nature.com/nature/journal/v506/n7487/full/nature13025.html>.

Reich, David, Nick Patterson, Desmond Campbell, Arti Tandon, Stephane Mazieres, Nicolas Ray, Maria V. Parra, Winston Rojas, Constanza Duque, Natalia Mesa, Luis F. Garcia, Omar Triana, Silvia Blair, Amanda Maestre, Juan C. Dib, Claudio M. Bravi, Graciela Bailliet, Daniel Corach, Tabita Hunemeier, and Maria Caitra Bortolini.

2012 "Reconstructing Native American population history." *Nature* 488, no. 1711: 370-74. Accessed January 17, 2017.

<http://eds.b.ebscohost.com.libproxy.txstate.edu/eds/detail/detail?vid=1&sid=3e091315-64df-4482-9b5e-d99e7bc76b72%40sessionmgr101&hid=104&bdata=JnNpdGU9ZWRzLWxpdmUmc2NvcGU9c2l0ZQ%3d%3d#AN=78913291&db=fsr>

Reidla, Maere, Toomas Kivisild, Ene Metspalu, Katrin Kaldma, Helle-Viivi Tolk, Juri Parik, and Eva-Liis Loogvali.

2003 "Origin and Diffusion of mtDNA Haplogroup X." Accessed February 10, 2017. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1180497/>.

Sarac, J., T. Saric, N. Jeran, L. Kovacevic, S. Cvjetan, AP Lewis, E. Metspalu, M. Reidla, N. Novokmet, M. Vidovic, B. Nevajada, A. Glasnovic, D. Marjanovic, S. Missoni, R. Villems, and P. Rudan.

2014 "Maternal genetic heritage of Southeastern Europe reveals a new Croatian isolate and a novel, local sub-branching in the x2 haplogroup.", 178-94. Accessed April 1, 2017. <https://www.ncbi.nlm.nih.gov/pubmed/24621318>.

Smallwood, Ashley M., and Thomas A. Jennings.

2014 *Clovis: on the edge of a new understanding*. College Station: Texas A & M

University Press. December 2014. Accessed April 13, 2017.

<http://site.ebrary.com.libproxy.txstate.edu/lib/txstate/detail.action?docID=11017>

142.

Stanford, Dennis J., Bruce Bradley, and Michael B. Collins.

2012 *Across Atlantic Ice: the origin of America's Clovis Culture*. Berkeley, CA:

Berkeley: University of California Press, 2012.

Stanford, Dennis, and Bruce Bradley.

2013 "Reply to O'Brien et al.". Accessed April 5, 2017.

<http://search.proquest.com.libproxy.txstate.edu/docview/1545873943?accountid=5683>.

Straus, Lawrence Guy, David J. Meltzer, and Ted Goebel.

2006 "Ice Age Atlantis? Exploring the Solutrean-Clovis 'connection'." *World*

Archaeology 37, no. 4: 507-32. Accessed March 30, 2017.

<http://www.tandfonline.com/doi/abs/10.1080/00438240500395797>.

Genetics Home Reference

2017 "What is DNA? - Genetics Home Reference." U.S. National Library of Medicine. Accessed April 02, 2017. <https://ghr.nlm.nih.gov/primer/basics/dna>.