

Where did the people who first populated the Americas come from, and how did they get here?

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ABSTRACT:

This paper explores the possible origins and routes of the first people in the Americas. For decades, the dominating hypothesis was that Beringia, a land bridge between Asia and North America, was exposed during the last Ice Age. People from East Asia traveled across the land bridge about 13,000 years ago to follow their food sources, and then migrated east and settled in parts of North and Central America around 11,000 years ago (referred to culturally and technologically as Clovis evidence of settling). New skeletal remains were recently discovered on the eastern coasts of North and Central America that could possibly refute the hypothesis of the Beringia crossing. The morphological features of the remains did not match those of East Asians, nor did they match modern Native Americans. Additionally, the remains were carbon dated and found to be 13,000 years old, around the same time that East Asians were migrating across Beringia in the classic hypothesis. Some scientists think this may be an indication that not all Paleoamericans are of East Asian origin, and that the Beringia migration event was not the first or the only time humans came to the Americas. They suggest that the expansion of humans would be too fast to be possible. Alternatively, the migration across the continent could have been much faster than originally thought, and the differences in morphological features between the eastern coast skeletons, modern Native Americans and today's East Asians can be attributed to evolutionary differences once the groups who came across Beringia began to split and migrate east. Based upon the evidence presented in this paper, it seems most likely that Beringia was the mode of peopling the Americas, and the migration occurred at least 13,000 years ago.

INTRODUCTION:

For decades, scientists believed that the land bridge of Beringia was the only pathway for peopling the Americas (Laughlin and Harper, 1979; Dixon, 1993; Flannery, 2001); (Figure 1). The land bridge would have existed during the end of the last Ice Age, connecting what is now Siberia with Alaska. Thus, it was widely believed that the earliest people in the Americas were of Asian origins. They travelled across Beringia either to follow food or to find a hospitable landscape for their families or groups of people (Laughlin and Harper, 1979). These people eventually spread throughout the rest of North and South America, leaving a technological trail of unique nature (known as Clovis). The hypothesis dates the migration across the land bridge at 13,000 years ago, and groups would have settled in Central America around 11,000 years ago (Flannery, 2001). If this hypothesis were true, modern Native Americans would be East Asian in lineage.

Recent studies of early Americans have begun to challenge this hypothesis of Beringia being the first passage that was used to populate the Americas (Lovgren, 2003; Fiedel, 2000; Chatters et. al., 2013). The discovery of a skeleton off of the Yucatan Peninsula that predates any other human remains found has led to a re-evaluation of the Beringia timeline (Lovgren, 2003). Isotope dating revealed that the skeleton to be over 13,000 years old, dating the skeleton around the same time as the Beringia crossing (Lovgren, 2003). More remains were found more recently on the western coast of North America that were also dated around 13,000 years of age (Waters and Stafford, 2007). This would suggest either a rapid expansion or a pre-Clovis migration event into the Americas. It is troubling for scientists to find this evidence because they are unable to hypothesize an alternate mechanism of migration.

Many studies of Paleoamerican remains have compared DNA and structural features to modern Native Americans and to modern East Asians to determine relatedness and point of

origin for the earliest Americans (Fagundes et. al, 2008; Chatters et. al., 2014). The results of such DNA testing are largely inconclusive; no clear pattern, timeline, or method of population and migration is evident in these studies. Some geneticists note that the differences in DNA and skeletal features between east coast Paleoamericans, East Asians, and modern Native American could be evolutionary that these people did, in fact, originate from East Asia and cross on the land bridge (Chatters et. al, 2014).

The competing evidence yields three possible hypotheses as to how and when the first people arrived in the Americas. The first hypothesis, and the most well-known, is that modern-day Native Americans are of East Asian origin, and that the first Americans populated the continents 12000 years ago after crossing the Beringia land bridge. This hypothesis has more recently lost credibility as a result of new and competing evidence possibly negating it. The second hypothesis is that there were two entirely separate migrations to the continents, one using the Beringia land bridge and the other migrating from Southern Asia and/or Australia. Unfortunately, a mechanism for the latter group travelling across the oceans to get to the Americas is not suggested. The third, and the most likely hypothesis, is a single migration event across Beringia 13,000+ years ago.

HYPOTHESIS: BERINGIA MIGRATIONS 13,000 YEARS AGO AND SETTLEMENT 11,000 YEARS AGO:

The most widely popular hypothesis regarding the population of the Americas was that people travelled from Asia to North via a land bridge (Beringia) caused by low sea levels due to cold temperatures during the last Ice Age (Figure 1). Decades of studies were conducted in

Alaska regarding the migration route because it was thought to be the "best" location in North America to find evidence of the earliest American life (Dixon, 1993). It is possible that the East Asians who migrated to the Americas were following their food sources, as the land bridge was a livable environment for animals (Laughlin and Harper, 1979).

About 11,000 years ago, these groups began settling down, as is evident in archeological sites in Central America (Flannery, 2001; Hoffecker et. al., 1993; Waters and Stafford, 2007; Dewar, 2002). Scientists have a plethora of evidence of Clovis technology throughout North America, including flake-and-blade technology and projectiles that are double-sided (Hoffecker et. al., 1993). Some sites also include animal bones, an indication of organized hunting for a settlement (Waters and Stafford, 2007). Hoffecker et. al. (1993) hypothesize that the distribution of these sites suggest an extremely rapid migration and expansion of the East Asians after crossing Beringia.

HYPOTHESIS: TWO MIGRATIONS:

Artifact Evidence:

Based on their dates of Clovis artifacts, Waters and Stafford (2007) suggest the possibility of two entirely separate migration routes, one predating the Clovis migration. This would mean that the Beringia passage was responsible for bringing East Asian people to the Americas, but there also would have been an entirely separate migration route from Africa to the Americas, or even from Southern Asia or Australia to the Americas (see Figure 2). Clovis artifacts from early sites across North and South America were dated by Waters and Stafford (2007). They found that all artifacts dated within a 200-year period of one another, around 11,000 years ago. The sudden and widespread appearance could be a result of a previously

existing but culturally unspecific human population in North America (Waters and Stafford, 2007). The contact between this population and the migrating populations would allow for Clovis technology to be shared and developed in the stationary, unspecified population as well as continue to move and expand with the migrating populations. Because pre-Clovis groups left few traces as a likely result of little cultural cohesion, it is possible that the adoption of Clovis technology helped them to maintain their permanent establishments (Flannery, 2001).

Skeletal/Morphological Evidence:

Chatters et. al. (2014) has noted that the Yucatan Skeletons cannot classify morphometrically with modern Native Americans or East Asians. Their facial features specifically did not appear to be Mongoloid in origin, as the modern Native Americans (Lovgren, 2003). Gonzalez-Jose et. al. (2003) note that more recent skeletons in Baja California, Mexico share features of Southern Asians and Australians. Given the cranial similarities, it is entirely possible that another migration event came from South Asia (Fiedel, 2000). Interpreting this information has led to the hypothesis that Southern Asians migrated to Australia and then to the Americas (Pucciarelli, 1991). The issue with the “two migrations” hypothesis is that no mechanism has been suggested for transportation to the Americas and within the continent. Gonzalez Gonzalez et. al. (2008) suggest possible routes of migration, but are unable to hypothesize how these routes would be travelled (Figure 2). Without a mechanism, the hypothesis remains incomplete.

HYPOTHESIS: A SINGLE MIGRATION: 13,000+ YEARS AGO AND RAPID

SETTLEMENT:

Using DNA Technology and Morphological Evidence:

Due to lack of explanation of a mechanism of migration, many studies in many disciplines have deviated from the idea of two separate migrations, favoring a single, earlier migration. Many geneticists have looked at the DNA of modern Native Americans and East Asians and compared them to the ancient DNA found in Paleoamerican skeletons found across North and South America. Modern Native Americans have developed five haplogroups, four of which are frequent in northeastern Asia (Fagundes et. al., 2008). This directly points to strong Asian ancestry, and is in agreement with the old Beringia theory. The remaining haplogroup was accounted for by a transitional period when the population diverged from their Asian ancestors, meaning that it is most likely a “Clovis” haplogroup (Fagundes et. al, 2008). This likely would have begun before expansion through North America (although after crossing from East Asia), but continued after the group had spread out across the continents (Fagundes et. al, 2008). Chatters et. al. (2014) suggest that the differences in Paleoamericans, East Asians, and modern Native Americans occurred as a result of mutation and progression after being separated.

The DNA mutation evidence supports the Beringia hypothesis, with only minor adjustments in the timeline of events. The differences between Paleoamericans, East Asians, and Native Americans was then an in situ adjustment that happened within the modern Native Americans (Chatters et. al., 2014). Fagundes et al. (2008) speculated that the East Asians who populated the Americas already possessed the haplogroups after colonizing northeast Asia before the Ice Age began.

DISCUSSION:

In 2014, DNA testing and analysis on the first skeleton associated with Clovis was released (Willerslev, 2014). The “Clovis boy” had a strong DNA resemblance to modern Native

Americans, and support a single-source population as the ancestors of Native Americans (Rasmussen et. al., 2014). Willerslev (2014) acknowledges that the results do not give any conclusive evidence to whether the Clovis population was the first people into the Americas. Rasmussen et. al. (2014) states that more analyses are needed to determine if there is DNA evidence of another population present.

However, it is clear that Clovis was established 11,000-12,000 years ago, and that this particular population has shown likeness to East Asian and modern Native American populations. The discovery could fit into either hypothesis of a single or numerous migration events. It is possible that there were two migration events and the two populations were separated, either culturally or physically, for an extended period of time. Due to the high number of Native Americans who share DNA similarities with the Clovis boy (about 80% of Native Americans in the test (Wellerslev, 2014), it doesn't seem likely that there would be another population present, but the Yucatan Peninsula remains present different findings. The remains on the Yucatan coast were thought to have shared characteristics with South Asians and Australians. Skeletal remains in Baja California, Mexico were also found to have similar features

The hypothesis that the Americas were settled 11,000 years ago is one that has been disproven by dating artifacts throughout the continents. While it is possible that there were still migratory groups in the area, there were also populations already settled in the Americas, as evidenced by carbon dating of skeletons around the continent. The studies supporting this hypothesis (Dixon, 1993; Laughlin and Harper, 1979; Hoffecker et. al., 1993) were biased due to the location of their studies and used evidence from a very narrow area to draw conclusions. Their studies assume that the Clovis evidence that they are reviewing is the oldest evidence to be found, but there has since been older evidence discovered.

While it does appear that there is strong evidence for two migration events, it seems more likely that one migration event occurred, by way of Beringia, 13,000 years ago and the population spread rapidly throughout the continents. The skeletons found in Baja California, Mexico and near the Yucatan Peninsula may have looked different due to evolutionary adaptation. Unfortunately, there are no DNA studies conducted on these early skeletons. It is possible that the DNA is too degraded, but conducting such a test may lead to more convincing explanations of the morphological differences. The DNA studies that have been conducted (Fagundes et. al., 2008; Chatters et. al., 2014; Rasmussen et. al., 2014) yield strong evidence that Native Americans are East Asian in ancestry, with a haplogroup that occurred as a result from divergence from the larger population. It is unlikely that this odd haplogroup is evidence of South Asian ancestry because the haplogroup is so rare except in the modern day Native American population. This evidence, coupled with the DNA evidence from the Clovis boy, creates a strong argument that East Asians were the first to populate the Americas. It is unlikely that another population would exist and not show up in the DNA evidence, so a two migration hypothesis is unlikely.

Beringia is the most likely mode of peopling the Americas. A water migration is not plausible because crossing the ocean would have required technology much more advanced than South Asians and Australians possessed at that time. No other land bridges linked the Eurasian continent to the North and South American continents. Therefore, there is currently no feasible mechanism that could support the idea of two separate migration events. It is possible the morphometric similarities between the skeletons found off the coast of the Yucatan Peninsula and modern Southern Asians and Australians is circumstantial. There is no marker indicated how closely these similarities are related, so the term is ambiguous and therefore cannot be quantified.

Due to the lack of quantifiable evidence and the absence of a mechanism for travelling, the two migration hypothesis does not seem possible.

CONCLUSION:

It seems most likely that there was a single migration event across Beringia that took place earlier than the original timeline suggested that populated the Americas. The migration occurred 13,000+ years ago. The group spread across the continent rapidly, and the rise of Clovis was widespread. Morphological changes were a result of adjusting evolutionarily to new and diverse environments. DNA analysis and the presence of certain haplogroups supplements this hypothesis. More research is necessary on existing Paleoamerican and Native American remains to confirm the presence of these haplogroups in all remains.

FIGURES:

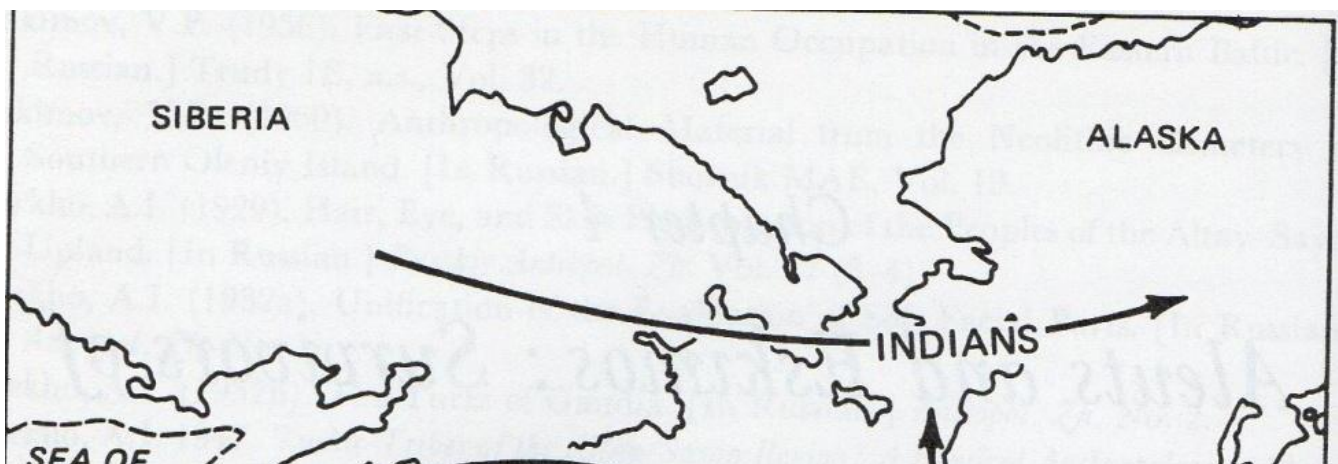


Figure 1: Beringia Migration Route (Laughlin and Harper, 1979)



Figure 2: Possible Migration Routes to populate the Americas (Gonzalez Gonzalez et. al., 2008)

REFERENCES

- Chatters, J. C., 2014, Late Pleistocene human skeleton and mtDNA link Paleoamericans and modern Native Americans: *Science*, v. 344, n. 6185, pp. 750—754
- Dewar, E., 2002, *Bones: discovering the first Americans*: Carroll & Graf, pp. 11—26
- Dixon, E. J., 1993, *Quest for the origins of the first Americans*, University of New Mexico Press, pp. 2—24
- Fagundes, N. J. R., Kanitz, R., Eckert, R., Valls, A. C. S., Bogo, M. R., Salzano, F. M., Smith, D. G., Silva, W. A. Jr., Zago, M. A., Ribeiro-dos-Santos, A. K., Santos, S. E. B., Petzl-Erier, M. L., Bonatto, S. L., 2008, Mitochondrial population genomics support a single Pre-Clovis origin with a coastal route for peopling of the Americas: *American journal of human genetics*, v. 82, n. 3, pp. 58—592

- Fiedel, S. J., 2000, The peopling of the New World: Present Evidence, New Theories, and Future Directions: *journal of archaeological research*, v. 8, n. 1, pp. 39—103
- Flannery, T., 2001, *The eternal frontier*: Atlantic Monthly Press, pp. 173—185
- Gonzalez Gonzalez, A. H., Sandoval, C. R., Mata, A. T., Sanvicente, M. B., Stinnesbeck, W., O., A. J., de los Rios, M., and Acevez, E., 2008, The arrival of humans on the Yucatan Peninsula: evidence from submerged caves in the state of Quintana Roo, Mexico: current research in the Pleistocene: *Special Report*, v. 25, pp. 1—24
- Hoffecker, J. F., Powers, R. W., and Goebel, T., 1993, The colonization of Beringia and the peopling of the new world, *Science*, v. 269
- Laughlin, W. S. and Harper, A. B., 1979, *The first Americans: origins, affinities, and adaptations*: Wenner-Gren Foundation for Anthropological Research, pp. 1—56
- Lovgren, S., 2003, Who were the first Americans?: *National Geographic*, Online Special Article
- Rasmussen, M., Anzick, S. L., Waters, M. R., Skoglund, P., DeGiorgio, M., Stafford, T. W. Jr., Rasmussen, S., Moltke, I., Albrechtsen, A., Doyle, S. M., Poznik, G. D., Gudmundsdottir, V., Yadav, R., Malaspinas, A., White V. S. S., Allentoft, M. E., Cornejo, O. E., Tambets, K., Eriksson, A., Heintzman, P. D., Karmin, M., Korneliussen, T. S., Meltzer, D. J., Pierre, T. L., Stenderup, J., Saag, L., Warmuth, V. M., Lopes, M. C., Malhi, R. S., Brunak, S., Sicheritz-Ponten, T., Barnes, I., Collins, M., Orlando, L., Balloux, F., Manica, A., Gupta, R., Metspalu, M., Bustamante, C. D., Jakobsson, M., Nielsen, R., Willerslev, E., 2014, The genome of a Late Pleistocene human from a Clovis burial site in western Montana: *Nature*, v. 506, pp. 225—229
- Waters, M. R. and Stafford, T. W. Jr., 2007, Redefining the age of Clovis: implications for peopling the Americas: *Science*, v. 315 n. 5815, pp. 1122—1126

Willerslev, E., 2014, Americas only Clovis skeleton had its genome mapped: University of
Copenhagen: Online Special