

# Findings with Paleogenomic Data Derived from 12,000 Year Old Human Remains Unearthed in North America

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**The combination of archaeological and paleogenomic data clearly establish that Native Americans were not only present in North America prior to any European migration, but also had a unique culture that still endures today denoting common cultural and genetic origins.**

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Genetic evidence obtained by mitochondrial DNA sequencing of the child from the Anzick-1 site in Montana<sup>1</sup> and the adolescent female from Hoyo Negro<sup>2</sup> in Mexico support a Beringian origin of the aboriginal peoples of North America. Both sets of remains date from the time of the Clovis Culture, which has previously been dated from 13,000 to 12,600 cal BP, that is calendar years before present. These are the earliest human remains DNA sequenced in North America to date. However, human coprolites dated as pre-Clovis (13,990-14,400 cal BP) from the Paisley Caves<sup>3</sup> in Oregon yielded DNA that was also Native American in origin and was over one thousand years older than the skeletal remains from the Anzick-1 and Hoyo Negro sites. In the study of early North American human skeletons including the Kennewick man, distinctive craniofacial morphology emerged which suggested a European origin to the early inhabitants of North America. This European migration was hypothesized by the Solutrean theory.<sup>4</sup> With DNA sequencing of the Anzick -1 child and the Hoyo Negro individual, along with the Paisley coprolites, this theory has now been refuted since all three genetic studies predate both Kennewick man and the Solutrean material culture. In addition to the DNA genome sequencing data from human organic material, there are also a number of archaeological sites that have been dated as being much older than the Clovis period, yielding material culture and in some cases biological material. These sites place human occupation of North America arguably up to or greater than 50,000 RCYBP as evidenced by the Topper site along the Savannah River in Allendale County, South Carolina, USA.<sup>5</sup>

The East Wenatchee site in Washington State as well as the Anzick-1 site offered a rich cache of Clovis material culture including some bone sticks carved from purported mastodon bones.<sup>6</sup> While anthropologists attempted to establish the intended use of these bone sticks, Marvin Kempf, hereditary chief of the Snoqualmie tribe in Northwest Washington, upon seeing the mastodon(?) bone artifacts, hypothesized the relics as being consistent in appearance and

markings with gaming pieces currently used in the Native American “stick game”. The “stick game”, or Sla-Hal as it is called in Snoqualmie tribal stories, and variants of it are still widely played in today’s Native American culture. In the Snoqualmie tribe and many others, the stick game had its origins in their creation story according to oral tradition.<sup>7</sup> The discovery of these ancient bone sticks is highly relevant since it ties the majority of the Native American tribes in North America to a single cultural origin, dating from the time of the Clovis culture. Though arranged intermarriage between the tribes kept them connected for a period of time, they eventually diverged as they migrated across the Americas. Over thousands of years, it is remarkable how the stick game has endured in the Native American culture across a timespan greater than 12,000 years and in spite of divergence of the original population into numerous tribes.<sup>7</sup> This common genetic origin established by the Anzick-1 and Hoyo Negro sequencing coupled with the material culture already unearthed from the time of the Clovis culture further support that Native American tribes were once one people with one culture, the remnants of which comprise most of the tribes in North America today. How long the Native Americans have actually inhabited North America prior to 12,000 cal BP remains an unanswered question.

Different theories have recently emerged in light of inconsistencies within the time frame of the first purported Beringial migration. The DNA sequencing of the human coprolites from the Paisley caves pushes the occupation by early Native Americans back by a thousand years or more. This, coupled with the possibility that the Topper site dated 50,000 RCYBP, that is radio carbon years before present, along with numerous other pre-Clovis sites across North America vastly pre-date the currently accepted timeline established for migration of the people from Beringia brings the theory that the peopling of North America occurred during the Clovis period via Beringial migration into question. The genetic data from Anzick-1 and Hoyo Negro confirm that the majority of Native American populations did originate from a fairly homogenous group that left Beringia more than 15,000 years ago. This homogeneity supports the Beringian Incubation Model which argues that Beringia was a habitable tundra plain, isolated from Siberia and the Americas by glaciers during OIS2, between 29,000 and 18,500 cal BP. It supports the possibility that the ancestors of the first Native Americans occupied this region for potentially as long as 10,000-20,000 years. But even this revised theory falls short considering there appears to have been human occupation of the Americas much earlier than previously believed.

Native American creation stories support the idea of an older human presence in North America. Many of the oral stories and songs state that the people have been here since “time immemorial”.<sup>8</sup> Native American elders promote the idea that their presence was in the Americas prior to the currently supported Beringian migration and that their ancestors were here well before the Clovis culture. Though, at this time, there is no DNA evidence to support these claims outside of the Oregon coprolites which are only marginally older than the Anzick and Hoyo Negro sites, the fact remains that there are numerous sites currently being excavated that are yielding material culture that predates the Clovis culture by thousands of years.<sup>9</sup> The existence of these sites is consistent with tribal claims of prior occupation. This could be from a previous

migration though some Native Americans believe their ancestors were already present in North America and migrated to Beringia and then back into North America later during the Clovis Cultural period. It is just a matter of time until older skeletal remains are either allowed to be sequenced by the tribes or new discoveries of older remains in conjunction with these pre-Clovis sites will occur which might potentially affect these migration theories. There will, however, need to be expanded cooperation from the Native American tribes to allow DNA testing of any new skeletal remains in order to support or invalidate the origins of pre-Clovis material culture.

A rather unique study involving two variants of archaic human head lice also supports pre-Clovis human occupation of the Americas and the isolation of the inhabitants thereof.<sup>10</sup> Genetic studies confirm two ancient louse lineages diverged ca. 1.18 million years ago. One lineage spread worldwide while the other was found exclusively in the Americas. The study suggests that an extinct archaic hominin, possibly *Homo erectus*, was most likely the host for this variant in the Americas and apparently interacted with Native Americans as early as 30,000 to 50,000 cal BP allowing the lice to transfer to them, presumably by jumping onto them during fights, sex, sharing of clothes or perhaps cannibalism.

Through their oral histories and songs, Native Americans also claim they are a unique people in addition to being ancient. There are several genetic studies that lend support to this claim of uniqueness. One such study involves Y haplogroup mapping and clearly indicates a high frequency of the Q haplogroup distinctive to Native Americans.<sup>11</sup> Additionally, a high-frequency private allele, the 9-repeat allele at microsatellite D9S1120, has been reported in Native American and Western Beringian populations.<sup>12</sup> The presence of this allele has been suggested as evidence that all modern Native Americans descended primarily from a single founding population. Yet another study used hierarchical clustering to divide the world into regions, each of which represented a unique genetic family within the human species.<sup>13</sup> These regions were characterized using distinctive patterns of allele frequencies generated by a panel of STRs which formed families and super-families. The Native American regions formed their own super-family which was distinct from all other super-families worldwide. HLA genes have also been found to be unique in Amerindians and do not relate with any other worldwide population, according to their HLA genetic profile.<sup>14</sup> These findings support either an autochthonous origin for the Amerindians or a very long Amerindian isolation, neither of which fit well with the Beringial migration model and are therefore controversial.

With the current controversy surrounding the formerly accepted “Out of Africa” theory coupled with recent genetic data proving that many human populations contain an admixture of one or more extinct hominin species as well as an admixture from an undiscovered species, standardly held scientific beliefs as to the geographical origins of various human populations as well as the origin of modern humans in general are now in question. Additionally, some genetic variants that are rare today were more common in the past while other variants that are abundant today may

have increased in frequency only in the past few thousand years because of mutations, population genetics and genetic drift.

These recent genetic data suggest that the current distribution of genetic lineages may not correctly reflect the geographic areas upon which they were found thousands of years ago. This inconsistency in genetic variation supports the finding that some lineages clearly had a different or wider range in the past. With Next Generation whole genome sequencing (NGS) becoming more widespread and affordable along with improved techniques enabling ancient DNA to be extracted and successfully sequenced, NGS has emerged as a critical tool to investigate human paleogenomics. Resultantly, the origins of ancient human populations throughout the world as well as our relationship with extinct hominins, genetic remnants of which are found in many existing human populations worldwide, are now able to be successfully investigated.

It has been proven that Native American populations contain admixtures from both Neanderthal and Denisovan hominins.<sup>15</sup> Furthermore, Native Americans have more Denisovan and Neanderthal DNA than Europeans and the Denisovan and Neanderthal DNA that they carry is different than that carried by Europeans. Finding a substantial admixture of both of these extinct hominins in a population is uncommon and adds yet another layer of mystery as to their origins. Since it is unknown whether any Neanderthal or Denisovan individuals inhabited North America in the past, these admixtures currently support a potential ancient Siberian origin for Native Americans since it has been established that Neanderthals and Denisovans interbred in Siberia well before the Beringians inhabited the land bridge.<sup>15</sup> It seems that the further back human remains are sequenced, the more complex the interrelationships between different groups of people and the more muddled their geographic origins become.

In the case of the Sla-Hal sticks found buried with the Anzick-1 child and the bone sticks unearthed at the East Wenatchee Clovis site coupled with the extant existence of similar sticks still utilized by the majority of today's Native American tribes, insight can be provided into a surviving culture that arose from a common source dating over 12,000 cal BP. The paleogenomic data from the Anzick-1 child and the Hoyo Negro skeletal remains also support these cultural findings since their lineages are consistent with individuals that migrated from Beringia into North America, thereby establishing a common genetic origin from which modern Native Americans descended.

The combination of these archaeological and paleogenomic data clearly establish at this time that Native Americans were not only present in North America prior to any European migration, but also had a unique culture that still endures today. It is important not to isolate the various scientific disciplines when investigating the origin of human populations such as this one since oftentimes these disciplines support one another, thus creating a more comprehensive understanding of these ancient people. Furthermore, in light of ever-changing theories in the geographic origin of various human populations, one must be careful about assuming that all current genetic patterns are representative of the past.

Considering archaeological and anthropologic findings concurrently often supports the genetic studies. Hopefully, the scientific community will embrace the newer datasets that are in some cases contradictory to established theories via this new generation of scientific study. It is exciting that science can now delve into the mysteries of ancient cultures and genetic origins in depth with emerging modern technologies. It is only a matter of time until the enigma surrounding the appearance of people in North America and any remaining questions of their origins are resolved.

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