



Ancient Skeleton Sheds Light on Native American Roots

Analysis of approximately 12,000-year-old human remains supports the idea that modern Native Americans evolved from ancestors who migrated out of Asia.

By Anna Azvolinsky | May 15, 2014

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Divers transport Hoyo Negro skull.
PAUL NICKLEN/NATIONAL GEOGRAPHIC

The uncovering of an almost completely intact, 12,000-year-old skeleton of a 15- or 16-year-old girl—found in an underwater cave near Mexico—lends support to the idea that modern Native Americans originated from an ancient population that came from Beringia, not from distinct migrations of peoples from different parts of Asia and Europe. The discovery of this remarkably well-preserved specimen by divers has, for the first time, allowed researchers to perform both genetic and morphological analyses from a single, ancient individual. Washington-based archaeologist and paleontologist [James Chatters](#) and his colleagues today (May 15) published in *Science* their analysis of the ancient individual.

The well-preserved ancient skeleton, which includes facial bones and teeth, helps to resolve the debate among scientists of whether ancient Native Americans arrived in the Americas from Asia through Beringia in a single migration sometime between 26,000 and 14,000 years ago. Genetic analyses to date have supported the idea that ancient people from Beringia were the ancestors of today's Native Americans, who eventually spread south and populated the Americas. Yet morphological analyses showed that the oldest available American skeletons do not have the same facial features of modern Native Americans, or even indigenous Siberian populations. Rather, these early American inhabitants resembled people from Eurasia.

"With this specimen, we have evidence that the physical differences between the ancient and modern Americans came about through evolution that occurred after the Beringia migration," said Chatters.

The teenage girl, who the researchers named Naia, is thought to have lived between 12,000 and 13,000 years ago. "This skeleton is one of the oldest to be found in America," said [Theodore Schurr](#), a biological anthropologist specializing in human evolutionary genetics at the University of Pennsylvania who was not involved in the work. "This analysis provides a perspective on both the morphological and genetic diversity of the Americas at an important time point."

According to Chatters, there are only five other ancient-human specimens discovered in the Americas that are at least 12,000 years old. "It's a very small club," he said. Two of these also had intact skulls, but Naia is the only one yet found with near-full set of teeth, which are helpful for analyzing ancestry.

The skull and teeth of the ancient teenage girl are thought to be representative of those of the earliest Americans, and are unlike those of modern Native Americans—findings consistent with previously found specimens of the same age.

But sequencing Naia's maternally inherited mitochondrial DNA (mtDNA), extracted from one of her molars, the researchers uncovered evidence to suggest that she belongs to the sub-haplogroup D1—a genetic lineage that only occurs in the Americas but originated in Asia. This particular lineage is thought to have risen in Beringia after the ancient Beringian population separated from other Asian populations. And the team's genetic analysis on Naia did not uncover evidence of European, Australian, or southern Asian ancestry.

"That we see the D1 haplogroup from this ancient skeleton indicates that this girl's maternal ancestry traces to the same source population as that of modern Native Americans," said molecular anthropologist [Deborah Bolnick](#) at the University of Texas at Austin. "About 11 percent of Native Americans today exhibit this haplogroup."

The recent analysis of the 12,600-year-old "Anzick-1" skeleton found in central Montana also showed that early Native Americans descended from an ancient Asian population from Beringia. While researchers sequenced the entire genome of Anzick-1, his facial skeleton was not intact—the child, estimated to be about 12 to 18 months old when he died, would have been too young for facial morphology comparison, said Chatters.

Unlike Anzick-1, Naia was uncovered on accident. A group of divers, which included study coauthor Alberto

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Nava Blank from the Bay Area Underwater Explorers in California, were exploring an underwater cave called Hoyo Negro in the Yucatán Peninsula when they found her bones. The divers reported the site to Mexico's National Institute of Anthropology and History, which spearheaded the analysis. Besides Naia, the explorers also identified more than 20 animals including seven cave bears, Saber Tooth tigers, and giant ground sloths. "This project had everything you could ask for in science—excitement, danger, beauty—and even extinct animal bones!" said Chatters.

"This was brilliant science," said prehistoric archaeologist [Dennis Jenkins](#) of the University of Oregon, who was not involved in the work. "The way [the team] used radiocarbon dating and mineral formation analysis to establish the skeleton's age was very innovative."

The researchers are now working to sequence Naia's nuclear genome and to extract additional DNA from another tooth to confirm their genetic findings.

J.C. Chatters et al., "Late Pleistocene human skeleton and mtDNA link Paleoamericans and modern Native Americans," *Science*, doi:10.1126/science.1252619, 2014.

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princess
Posts: 1

May 16, 2014

so sorry, I dont think 1 body is enough conclusive evidence to support your claim.
scientist have been to wrong too many times.

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LeeH
Posts: 30

May 16, 2014

As a scientist of more than 30 years let me reaffirm that an "n" of one is not statistically significant.

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derBear
Posts: 1

May 16, 2014

This doesn't have to be statistically correct to be scientifically significant. If we were sorting through the bones of 5000 individuals in a WalMart parking lot in Boston, I would say the DNA evidence was not statistically significant.

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Doug Easton
Posts: 10

May 17, 2014

The basic haplogroups are well defined. Their evolutionary and geographical associations are worked out. What this paper suggests is that a particular skeleton belongs to a particular mitochondrial haplogroup common to northern asian populations. This is not a statistical inference.

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The possibilities for error would lie in the sequencing. The sequencing done these days is done by oversampling, meaning many reads of the mitochondrial DNA are done. Not only that, but there are key signs in the sequence which allow for internal checking. Sequencing error is highly unlikely.

The paper is saying that one particular individual belonging to a particular "family of people" lived in Mexico 12,000 years ago. That is not dependent on a statistical argument.

Of course one would like other individuals to sequence. You then would be asking if there were people from other haplogroups living there at that time. Say, for argument's sake that another specimen is found belonging to another unrelated haplogroup, that would not be evidence that this one is "wrong." All it says is that there may be other groups that colonized the Americas. If there are markers in the nuclear DNA that indicate there are sequences typical of other populations in her DNA this would indicate that she had ancestors that lived in other places as well.

The fact that she is from a time so close to the earliest known human habitation of the Americas strongly suggests that her people were the ancestors of Native Americans. In no place in the article does it say that there are no alternative scenarios. It only this is the best explanation to date. That is what all Science does.

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James V. Kohl
Posts: 120

May 17, 2014

The fact that [Large Numbers of Novel miRNAs Originate from DNA Transposons and Are Coincident with a Large Species Radiation in Bats](#) suggests that differences in the skull and teeth result from ecological variation, which is manifested in morphological and behavioral phenotypes as nutrient-dependent pheromone-controlled ecological adaptations.

See for example: [A Cluster of Olfactory Receptor Genes Linked to Frugivory in Bats](#) and the model of cause and effect via conserved molecular mechanisms across all species: [Nutrient--dependent / pheromone--controlled adaptive evolution: a model](#).

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mightythor
Posts: 37

May 17, 2014

If I read the article correctly, only the mitochondrial DNA sequence has been reported, which sheds light only on maternal inheritance. Mom might have been Beringian, while Naia inherited her (skeletal) facial features from her Eurasian Dad.

If this pattern is confirmed in other skeletons, it may lend support to the Ugly Girl Hypothesis: when any two populations mingle, the males of both populations will prefer to mate with the females of the cuter population, and the maternal DNA of the ugly population will be lost.

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RobL
Posts: 1

May 19, 2014

Yes the n factor of 1 could easily skew the assumptions here with air travel and diversification 12000 years ago. Sacram by the way.

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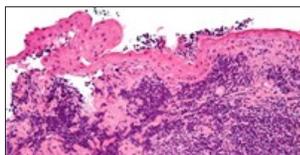
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