HUMAN GENETICS

Genes May Link Ancient Eurasians, Native Americans

Anthropologists have long assumed that the first Americans, who crossed into North America by way of the Bering Strait, were originally of Asian stock. But recently they have been puzzled by surprising features on a handful of ancient American skeletons, including the controversial one known as Kennewick Man—features that resemble those of Europeans rather than Asians (*Science*, 10 April, p. 190). Now a new genetic study may link Native Americans and people of Europe and the Middle East, offering tantalizing support to a controversial theory that a band of people who originally lived in Europe or Asia Minor were among the continent's first settlers.

The new data, from a genetic marker appropriately called Lineage X, suggest a "definite—if ancient—link between Eurasians and Native Americans," says Theodore Schurr, a molecular anthropologist from Emory University in Atlanta, who presented the findings earlier this month at the annual meeting of the American Association of Physical Anthropologists in Salt Lake City.

Researchers studying unusual "Caucasoid-like" physical features in early American skeletons were immediately excited by the results. "It's an intriguing study," says Richard Jantz, a biological anthropologist at the University of Tennessee, Knoxville. Because European peoples presumably must have passed through Asia to reach North America, "it suggests that there might have been a distribution of people 10,000 or more years ago throughout Asia who looked more European than [Asians] do now." But "it's far too early and far more data are needed" before researchers can be sure of such history, cautions evolutionary geneticist Emoke Szathmary, who is president of the University of Manitoba in Winnipeg.

The team, led by Emory researchers Michael Brown and Douglas Wallace, and including Antonio Torroni from the University of Rome and Hans-Jurgen Bandelt from the University of Hamburg in Germany, was searching for the source population of a puzzling marker known as X. This marker is found at low frequencies throughout modern Native Americans and has also turned up in the remains of ancient Americans. Identified as a unique suite of genetic variations, X is found on the DNA in the cellular organelle called the mitochondrion, which is inherited only from the mother.

Researchers had already identified four common genetic variants, called haplogroups A, B, C, and D, in the mitochondrial DNA (mtDNA) of living Native Americans (*Science*, 4 October 1996, p. 31). These haplogroups turned up in various Asian populations, lending genetic support for the leading theory that Native Americans descended primarily from these peoples. But researchers also found a handful of other less common variants, one of which was later identified as X.

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X marks the spots. The genetic variant called X is found in Native Americans and some Eurasian populations, but not in Asians.

Haplogroup X was different: It was spotted by Torroni in a small number of European populations. So the Emory group set out to explore the marker's source. They analyzed blood samples from Native American, European, and Asian populations and reviewed published studies. "We fully expected to find it in Asia," like the other four Native American markers, says Brown.

To their surprise, however, haplogroup X was only confirmed in the genes of a smattering of living people in Europe and Asia Minor, including Italians, Finns, and certain Israelis. The team's review of published mtDNA sequences suggests that it may also be in Turks, Bulgarians, and Spaniards. But Brown's search has yet to find haplogroup X in any Asian population. "It's not in Tibet, Mongolia, Southeast Asia, or Northeast Asia," Schurr told the meeting. "The only time you pick it up is when you move west into Eurasia."

Researchers are continuing to check for the marker in Asia, but if it never appears there, "then we have a big gap to explain," says Schurr. It's possible that the source X population began in Asia and then spread to both the Americas and Europe, but left no descendants in Asia. It may be somewhat more likely, however, "that a small Caucasian band with females migrated from Europe right across Asia and into North America," says Brown. This group might have left no genetic traces of the journey in Asia because of its small size, or because its Asian descendants went extinct—"which is not unlikely," says Schurr, given the high turnover rate of different peoples.

Physical anthropologists say that this connection between Eurasia and early Americans may explain the puzzling features they see in the remains of some of the earliest Americans, such as the 9300-year-old Kennewick Man and his contemporary, the Spirit Cave Mummy from Nevada (*Science*, 10 April, p. 191). The Spirit Cave skeleton, for example, "doesn't look like anyone from any modern human population," says Jantz, but rather has a mix of features, such as a long, narrow skull and moderately high but not widely flaring cheekbones. He and others think these features may reflect a more "generalized" human stock that spread across Europe and Asia and into North America more than 10,000 years ago.

Other geneticists are impressed by the finding, but they urge caution in interpreting the data at this stage. "The connection [between Europe and North America] looks pretty good," says David Glenn Smith, a molecular anthropologist at the University of California, Davis, whose team has also found X in some paleo-American remains. "But the Asian data, particularly those from Southwest Asia, need to be looked at very closely" before researchers can be sure X isn't present there.

Indeed, a few teams have identified roughly similar variants in certain Asian populations. But the Brown team says those variants are distinct from the true haplogroup X, which they have defined rigorously for the first time as including both certain sequence mutations and also mutations found by slicing the DNA with certain enzymes. By those criteria, there's no sign of an Asian X in their own data or any other published results, he says.

The team hopes its work will spur other labs to check their data for signs of X. "When that happens, we'll be able to see the true global distribution of X," says Brown—and perhaps get a clearer picture of the first Americans.

–Virginia Morell