

GENOMES

Ancient DNA Links Native Americans With Europe

SANTA FE—Where did the first Americans come from? Most researchers agree that Paleoamericans moved across the Bering Land Bridge from Asia sometime before 15,000 years ago, suggesting roots in East Asia. But just where the source populations arose has long been a mystery.

Now comes a surprising twist, from the complete nuclear genome of a Siberian boy who died 24,000 years ago—the oldest complete genome of a modern human sequenced to date. His DNA shows close ties to those of today's Native Americans. Yet he apparently descended not from East Asians, but from people who had lived in Europe or western Asia. The finding suggests that about a third of the ancestry of today's Native Americans

can be traced to “western Eurasia,” with the other two-thirds coming from eastern Asia, according to a talk at a meeting* here by ancient DNA expert Eske Willerslev of the University of Copenhagen. It also implies that traces of European ancestry previously detected in modern Native Americans do not come solely from mixing with European colonists, as most scientists had assumed, but have much deeper roots.

“I’m still processing that Native Americans are one-third European,” says geneticist Connie Mulligan of the University of Florida in Gainesville. “It’s jaw-dropping.” At the very least, says geneticist Dennis O’Rourke of the University of Utah in Salt Lake City, “this is going to stimulate a lot of discussion.”

Researchers have been trying to parse the origins of the first Americans for decades. Most agree that people moved across Beringia, via a vast ice age land bridge (see map p. 410), and began spreading through the Americas, reaching Chile by 14,500 years ago. But the origins of the source popula-

tions are not clear, and some archaeologists have even suggested that ancient Europeans crossing the Atlantic were part of the mix (*Science*, 16 March 2012, p. 1289). Others have contended that early skeletons found



Boy's bones. DNA from this ancient Siberian skeleton offers clues to the first Americans.

in the Americas, such as the 9000-year-old Kennewick Man, show some European features (*Science*, 10 April 1998, p. 190). In his talk, Willerslev argued that the ancient genome “can actually explain a lot of these inconsistencies,” by offering glimpses of prehistoric populations before more recent migrations and other demographic events blurred the picture.

The genome comes from the right upper arm bone of a boy aged about 4 years, who lived by Siberia's Belaya River. Those who buried him adorned his grave with flint tools, pendants, a bead necklace, and a sprinkling of ochre. In the 1920s, Russian archaeologists discovered the burial and other artifacts near a village called Mal'ta, which gave the celebrated site its name. Willerslev and co-author Kelly Graf of Texas A&M University in College Station, traveled to the State Hermitage Museum in St. Petersburg, Russia, where the boy's remains are housed, and took a bone sample.

Willerslev reported that the team was able to sequence the boy's genome, and also

to radiocarbon date the bone. The team then used a variety of statistical methods to compare the genome with that of living populations. They found that a portion of the boy's genome is shared only by today's Native Americans and no other groups, showing a close relationship. Yet the child's Y chromosome belongs to a genetic group called Y haplogroup R, and its mitochondrial DNA to a haplogroup U. Today, those haplogroups are found almost exclusively in people living in Europe and regions of Asia west of the Altai Mountains, which are near the borders of Russia, China, and Mongolia.

One expected relationship was missing from the picture: The boy's genome showed no connection to modern East Asians. DNA studies of living people strongly suggest that East Asians—perhaps Siberians, Chinese, or Japanese—make up the major part of Native American ancestors. So how could the boy be related to living Native Americans, but not to East Asians? “This was kind of puzzling at first,”

Willerslev told the meeting. But there seemed little doubt that the finding was correct, he said, because nearly all Native Americans from North and South America were equally related to the Mal'ta child, indicating that he represented very deep Native American roots.

The team proposes a relatively simple scenario: Before 24,000 years ago, the ancestors of Native Americans and the ancestors of today's East Asians split into distinct groups. The Mal'ta child represents a population of Native American ancestors

who moved into Siberia, probably from Europe or west Asia. Then, sometime after the Mal'ta boy died, this population mixed with East Asians. The new, admixed population eventually made its way to the Americas. Exactly when and where the

admixture happened is not clear, Willerslev said. But the deep roots in Europe or west Asia could help explain features of some Paleoamerican skeletons and of Native American DNA today. “The west Eurasian [genetic] signatures that we very often find in today's Native Americans don't all come from postcolonial admixture,” Willerslev

Online

sciencemag.org

Podcast interview with author Michael Balter (http://scim.ag/pod_6157).

* Paleoamerican Odyssey, Santa Fe, 16–20 October.

said in his talk. “Some of them are ancient.”

The talk sparked lively exchange, and not everyone was ready to buy the team’s scenario, at least until they can read the full paper, which is in press at *Nature*. “This is a lot to hang on one skeleton,” Mulligan says. Willerslev said during the discussion that his group is now trying to sequence the genomes of skeletons “further west.”

The new findings are consistent with a report published in *Genetics* last year (and almost entirely ignored at the time) that used modern DNA to conclude that Native Americans have significant—and ancient—ties to Europeans. “Our group is very excited to see this,” says Alexander Kim, who works with geneticist David Reich at Harvard Medical School in Boston and represented the group at the meeting. Reich’s team found that populations they identified as Native American ancestors in Asia apparently also contributed genes to populations in northern Europe.



Headed east. The Mal’ta boy was related to people who later migrated across Beringia to the Americas.

Thus, both studies suggest a source population in Asia whose genes made their way east all the way to the Americas, and west, all the way to Europe.

“Mal’ta might be a missing link, a representative of the Asian population that admixed

both into Europeans and Native Americans,” Reich says. If so, he adds, it shows “the value of ancient DNA in peeling back history and resolving mysteries that are difficult to solve using only present day samples.”

—MICHAEL BALTER

SCIENCE FUNDING

U.S. Shutdown Ends, but Not Budget Anxiety

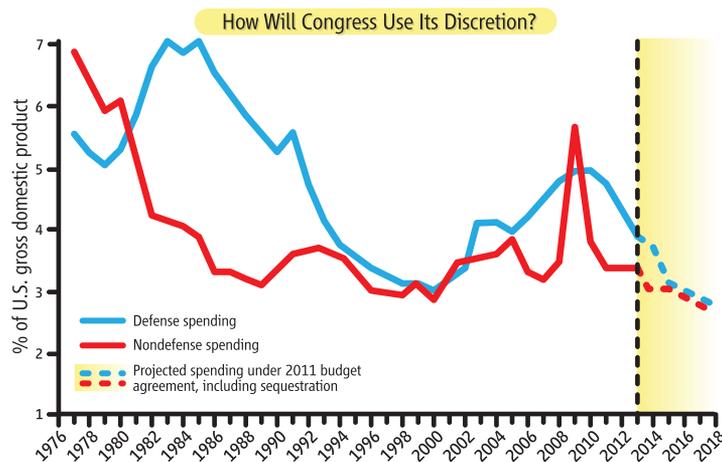
And now for the main event.

The reopening of the U.S. government last week after a 16-day shutdown has allowed most federal researchers to get back to work and has restarted the grantmaking machinery at key science funding agencies. But the anxiety isn’t over.

Business as usual means Congress must again confront the unpleasant political reality that the federal government spends hundreds of billions of dollars more each year than it takes in. Legislators have given themselves 2 months to come up with at least the outline of a plan to begin reducing the deficit, starting with a budget for the 2014 fiscal year that began on 1 October. And as that effort unfolds, scientists need to know that the rules of the federal budget game have changed.

The good news for research advocates: The rigid, across-the-board budget cuts that shrunk most agency budgets by 5% in the 2013 fiscal year are gone. The mechanism that spawned them, sequestration, remains in effect. However, instead of applying a meat ax to every federal agency, sequestration has morphed into a ceiling on all federal discretionary spending—outlays for every-

thing other than mandatory programs such as Medicare and Social Security, and interest on the national debt. And that ceiling is likely to remain flat in 2014 for the pot of federal funding that includes fundamental research.



Fear of falling. The budget agreement squeezes civilian discretionary funding, which spiked because of the 2009 stimulus package after holding steady for decades as a share of GDP.

That change means Congress and the White House will have more flexibility to decide where to make any cuts. So researchers will have a chance to make the case that research is a long-term investment, that it generates the innovations needed for sustained economic growth and prosperity, and

that its ultimate payoff can’t be predicted. The bad news, however, is that science is back to competing against every other special interest for a bigger slice of a federal funding pie that isn’t growing. “It will be up to the research community to make the case that science is essential within the constraints that legislators are facing,” says Samuel Rankin, head of the Coalition for National Science Funding and head of the Washington, D.C., office of the American Mathematical Society.

The temporary budget agreement approved last week, which funds the government until 15 January at 2013 levels, sets overall discretionary spending at \$986 billion. Defense spending accounts for \$518 billion, leaving \$468 billion for civilian programs.

Absent a new agreement, in January the discretionary total for 2014 will shrink by nearly \$20 billion, to \$967 billion.

Defense spending, which was protected from deeper cuts in 2013, would absorb the entire blow, dropping by 4% to \$498 billion. Spending for civilian programs would stay essentially level, at \$469 billion.

The lower 2014 spending limits are part of a 2011 budget agreement to reduce the