

For millennia, people on the Mongolian steppes have milked their animals despite being lactose intolerant.

away the soil along with pot fragments and trash pits, archaeological evidence for diet is scarce. So Warinner's Max Planck colleague Shevan Wilkin took dental calculus—the hard plaque that builds up on teeth—from nine skeletons and tested it for key proteins.

The calculus yielded milk proteins from sheep, goats, and bovines such as yak or cow. Yet DNA from teeth and leg bones showed the herders were lactose intolerant. And they carried only a trace of DNA from the Yamnaya, the team reports this week in the *Proceedings of the National Academy of Sciences*. “They’re exploiting these animals for dairying even though they’re not lactase persistent,” Collins says.

That disconnect between dairy and DNA isn't limited to Mongolia. Researchers recently found milk proteins on pots at Çatalhöyük in Turkey, which at 9000 years old dates to the beginnings of domestication, 4 millennia before lactase persistence appears. “There seem to be milk proteins popping up all over the place, and the wonderful evolution we expected to see isn't happening,” Collins says.

Modern Mongolians digest dairy by using bacteria to digest lactose for them, turning milk into yogurt and cheese, along with a rich suite of dairy products unknown in the Western diet. Ancient pastoralists may have adopted similar strategies. “Control and manipulation of microbes is core to this whole transformation ... that enables them to have a dairying culture,” Warinner says.

Geneticists are going back to the drawing board to understand why lactase persistence is common—and apparently selected for—in some dairying populations but absent in others. “Why is there a signal of natural selection if there was already a cultural solution?” asks Joachim Burger, a geneticist at Johannes Gutenberg University in Mainz, Germany.

How dairying reached Mongolia is also a puzzle. The Yamnaya's widespread genetic signature shows they replaced many European and Asian Bronze Age populations. But they seem to have stopped at the Altai Mountains west of Mongolia. “Culturally, it's a really dynamic period, but the people themselves don't seem to be changing,” Warinner says. She thinks even though the Yamnaya didn't contribute their genes to East Asia, they did spread their culture, including dairying. “It's a local population that has adopted the steppe way of life.”

Given these surprising results, Warinner has a new goal: To figure out just which microbes helped Mongolians digest milk. ■

Andrew Curry is a journalist in Berlin.

## HUMAN EVOLUTION

# Ancient DNA tracks migrations around Americas

### Trove of new samples reveals expansion of Clovis hunters and mysterious 9000-year-old population turnover

By Lizzie Wade

For decades, scientists could describe the peopling of the Americas only in broad strokes, leaving plenty of mysteries about when and how people spread across the continents. Now, state of the art ancient DNA methods, applied to scores of new samples from around the Americas, are filling in the picture. Two independent studies, published in *Cell* and online in *Science*, find that ancient populations expanded rapidly across the Americas about 13,000 years ago. They also emphasize that the story continued in the thousands of years since, revealing previously undocumented, large-scale movements between North and South America.

The data include 64 newly sequenced ancient DNA samples from Alaska to Patagonia, spanning more than 10,000 years of genetic history. “The numbers [of samples] are just extraordinary,” says Ben Potter, an archaeologist at the University of Alaska in

Fairbanks. Prior to these studies, only six genomes older than 6000 years from the Americas had been sequenced. As a result, says Jennifer Raff, an anthropological geneticist at the University of Kansas in Lawrence, “The [genetic] models that we've been using to explain the peopling of the Americas have always been oversimplified.”

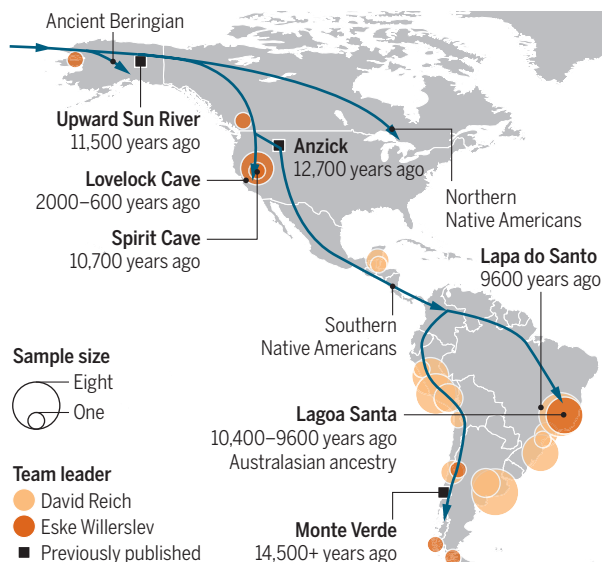
Eske Willerslev, an evolutionary geneticist at the University of Copenhagen who led the *Science* team, worked closely with the Fallon Paiute-Shoshone Tribe in Nevada to gain access to some of the new samples. The tribe had been fighting to repatriate 10,700-year-old remains found in Nevada's Spirit Cave and had resisted destructive genetic testing. But when Willerslev visited the tribe in person and vowed to do the work only with their permission, the tribe agreed, hoping the result would bolster their case for repatriation.

It did. Willerslev found that the remains from Spirit Cave are most closely related to living Native Americans. That strengthened the Fallon Paiute-Shoshone Tribe's claim to the bones, which were returned to them in 2016 and reburied. Willerslev's study validates that “this is our homeland, these are our ancestors,” says Rochanne Downs, the tribe's cultural coordinator.

Willerslev added the Spirit Cave data to 14 other new whole genomes from sites scattered from Alaska to Chile and ranging from 10,700 to 500 years old. His data join an even bigger trove published in *Cell* by a team led by population geneticist David Reich of Harvard Medical School in Boston. They analyzed DNA from 49 new samples from Central and South America dating from 10,900 to 700 years old, at more than 1.2 million positions across the genome. All told, the

## A trail of DNA

Two new papers add DNA from 64 ancient individuals to the sparse genetic record of the Americas. They show that people related to the Anzick child, part of the Clovis culture, quickly spread across both North and South America about 13,000 years ago.



data decisively dispel suggestions, based on the distinctive skull shape of a few ancient remains, that early populations had a different ancestry from today's Native Americans. "Native Americans truly did originate in the Americas, as a genetically and culturally distinctive group. They are absolutely indigenous to this continent," Raff says.

The two studies also provide an unprecedented view of how ancient Americans moved across the continent beginning about 13,000 years ago. Previous genetic work had suggested the ancestors of Native Americans split from Siberians and East Asians about 25,000 years ago, perhaps when they entered the now mostly drowned landmass of Beringia, which bridged the Russian Far East and North America. Some populations stayed isolated in Beringia, and Willerslev sequenced one new example of such an "Ancient Beringian," 9000-year-old remains from Alaska's Seward peninsula. Meanwhile, other groups headed south. At some point, those that journeyed south of the ice sheets split into two groups—"Southern Native Americans" and "Northern Native Americans" (also sometimes called Ancestral A and B lineages), who went on to populate the continents (see map, p. 627).

By looking for genetic similarities between far-flung samples, both papers add detail—some of it puzzling—to this pattern. The 12,700-year-old Anzick child from Montana, who is associated with the mammoth-hunting Clovis culture, known for their distinctive spear points, provided a key reference point. Willerslev detected Anzick-related ancestry in both the Spirit Cave individual—who is associated with western stemmed tools, a tradition likely older than Clovis—and 10,000-year-old remains from Lagoa Santa in Brazil. Reich's team found an even closer relationship between Anzick and 9300- to 10,900-year-old samples from Chile, Brazil, and Belize.

Those close genetic affinities at similar times but across vast distances suggest people must have moved rapidly across the Americas, with little time to evolve into distinct genetic groups. Reich's team argues that Clovis technology might have spurred this rapid expansion. But anthropological geneticist Deborah Bolnick of the University of Connecticut in Storrs notes the Anzick-related ancestry group may have been broader than the Clovis people, and doubts that the culture was a driver.

Willerslev also finds traces of this Anzick-related ancestry in later samples

from South America and Lovelock Cave in Nevada. But in Reich's data it fades starting about 9000 years ago in much of South America, suggesting "a major population replacement," he says.

After that population turnover in South America, both teams see striking genetic continuity in many regions. But that doesn't mean no one moved around. Reich's group sees a new genetic signal entering the central Andes about 4200 years ago, carried by people who are most closely related to ancient inhabitants of the Channel Islands, off Southern California. Meanwhile, Willerslev's team detects ancestry related to the present-day Mixe, an Indigenous group from Oaxaca in Mexico, spreading to South America about 6000 years ago and North America about 1000 years ago. Neither of these migrations replaced local communities, but rather mixed with them. Both teams say

they could be seeing the same signal, but "without comparing the data, it's really hard to tell," says archaeogeneticist Cosimo Posth of the Max Planck Institute for the Science of Human History in Jena, Germany, the first author of the *Cell* paper.

Just as mysterious is the trace of Australasian ancestry in some ancient South Americans. Reich and others had previously seen hints of it in living people in the Brazilian Amazon. Now, Willerslev has provided more evidence: telltale DNA in one person from Lagoa Santa in Brazil, who lived 10,400 years ago. "How did it get there? We have no idea," says geneticist José Víctor Moreno-Mayar of the University of Copenhagen, first author of the Willerslev paper.

The signal doesn't appear in any other of the team's samples, "somehow leaping over all of North America in a single bound," says co-author and archaeologist David Meltzer of Southern Methodist University in Dallas, Texas. He wonders whether that Australasian ancestry was confined to a small population of Siberian migrants who remained isolated from other Native American ancestors throughout the journey through Beringia and the Americas. That suggests individual groups may have moved into the continents without mixing.

Delighted as they are with the data in the new studies, scientists want more. Meltzer points out that none of the new samples can illuminate what's happening at pre-Clovis sites such as Chile's Monte Verde, which was occupied 14,500 years ago. And Potter notes that, "We have a huge, gaping hole in the central and eastern North American [sampling] record. ... These papers aren't the final words." ■

## INFECTIOUS DISEASES

## Indonesian fatwa causes immunization rates to drop

Clerics declare measles and rubella vaccine made with pork components impure

By Dyna Rochmyaningsih,  
in Sungai Karang, Indonesia

**A**s the bell rang on a recent morning at an elementary school here and pupils filled the classrooms, anxious adults crowded the corridors outside. It was vaccination day, but many parents in this North Sumatra village did not want their children immunized with a new measles-rubella (MR) vaccine. Some told the teacher their children were at home, not feeling well. Others were there to make sure their kids didn't get the jab. They whispered the reason with disgust: The vaccine "contains elements of pork." By the time the vaccination team left, only six out of 38 students had been immunized.

Millions of parents around Indonesia have eschewed the vaccine in recent months, after Islamic clerics declared the MR vaccine "haram," or forbidden under Islamic law because pig components are used in its manufacturing. Vaccine coverage has plummeted as a result, alarming public health experts who worry that the world's largest Muslim-majority country could see new waves of measles and more miscarriages and birth defects resulting from rubella infections during pregnancy.

Indonesia has long used a locally produced measles vaccine as part of its childhood vaccination scheme, but coverage has been patchy, and until recently, the country had one of the highest measles burdens in the world, according to the World Health Organization (WHO). Last year, as part of a WHO-led plan to eliminate measles and rubella globally by 2020, Indonesia switched to a combined MR vaccine, produced by the Serum Institute of India in Mumbai. The Ministry of Health launched an ambitious catchup campaign targeting 67 million children aged 9 months to 15 years. The first phase, in 2017 on the island of Java, was a success; all six provinces

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**Rochanne Downs.**  
Fallon Paiute-Shoshone Tribe

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