

Were there two migration routes into North America? Genetics meets archaeology

P

opular accounts of the peopling of North America paint a picture of a lone long-ago trek across the Bering Land Bridge and then south along the Pacific coast, a view based largely on DNA evidence. But other clues point to people also traversing “ice-free corridors” that emerged from melting glaciers like terrestrial tentacles.

A new paper in [Science Advances](#) reviews the evidence for more than one way into North America. It concludes that people followed at least two routes, coastal and interior, and that the view over the land bridge “commonly disseminated in the popular press is a prematurely narrow interpretation of current evidence.” The journal held a news conference with three of the investigators.

“We’ve seen conflicting narratives about the timing and the nature of the peopling of the Americas. We wanted to evaluate this claim and provide a framework to discuss the process – not based on speculation but on a critical review of current evidence. Rather than confusion, there is growing congruence of the archeological, paleoecological, and genetic records,” said co-author and archaeologist Ben Potter, professor of anthropology at the University of Alaska, Fairbanks.



People likely came to the northern U.S. and Canada through more than one route.

More philosophically, the report beautifully illustrates scientific inquiry, operating in a blind-man-and-the-elephant sort of way, revealing not alternate facts, but multiple solutions to a shared challenge – a search for habitable land. It also touches on ways to avoid so-called [“helicopter research,”](#) in which wealthy nations send expeditions to probe the health and lives of poorer people, without involving them in the work.

Over the Bering Land Bridge

The 1000-mile Bering Land Bridge appeared between Siberia and Alaska 15,000 to 25,000 years ago, when winds blew away snow from the retreating glaciers. The areas for several hundred miles on either side of the bridge, and the bridge itself, are called Beringia.

Ancestors of Native Americans left Siberia from 18,400 to 23,000 years ago, according to calculations derived from comparisons of [mitochondrial DNA sequences](#), which represent the maternal lineage. The gene pool of the travelers was in flux, with some alleles (gene variants) vanishing as people died, while new ones arose from mutations occurring during the journey. As a result, the genomes of modern Native Americans differ a bit from those of their Asian, and even older European, forebears.

Over time the ancestral Native American genome changed as people from other populations added their genes, and genetic diversity fell due to infectious diseases like smallpox, and, later, the genocidal activities of colonists, said co-author Ripan Malhi, Romano professor of Anthropology at the Carl R. Woese Institute for Genomic Biology at the University of Illinois Urbana-Champaign.

5-31-2018 2-mitochondria (1)

Image not found or type unknown

Mitochondria house only a few genes, whose sequence differences considered with mutation rates can reveal long-ago genetic divergence. Image credit: Northwestern University

Tracking mitochondrial DNA illuminates only a handful of a person's hundreds or thousands of ancestors; it is the lineage extending backward from one's mother's mother's mother. And because the few genes in the mitochondrial genome encode mostly proteins that function in basic cellular energy reactions, and don't endow visible traits, tracing it doesn't reveal much about what the people were like.

"Mitochondrial DNA is a relatively good marker for deep time studies, especially in the case of the Americas where we have a very structured population and relatively low genetic diversity, but it is limited in terms of information. It will not inform about adaptation to the environment or to pathogens, for example" said geneticist and co-author Bastien Llamas, of the Australian Research Council at the University of Adelaide.

Rapid reproduction

From about 14,000 to 16,000 years ago, as the massive ice sheets melted, a tiny founding human population in North America underwent a time of rapid expansion. The burst of reproduction amplified the alleles brought in by the survivors and their offspring, as some gene variants from those who had perished vanished from the population. The people spread south and east as the first Native Americans, a migration that took about 2,000 years. Genetic and archeological evidence was lost from parts of the coastal migratory path under water today – that is, the story of Native American origins may be missing some chapters.

[potter HR](#)

Image not found or type unknown

A closer look at the area of interest. (Potter et al, Sci. Adv. 2018; eaat5473)

The harsh environment and the chance sampling of genetic drift whittled away at the original human genetic diversity of those who traveled over the land bridge. Today, Native American genomes reflect the long-ago exodus in five sets (haplogroups) of mitochondrial alleles, two haplogroups on the Y chromosome (tracking the paternal lineage), and a few rare autosomal gene variants. The presence of these markers in all modern indigenous populations in southern Siberia and some in northern Siberia suggests a single migration to North America.

Dates assigned to events like migrations using DNA data are ranges, rather than precise times. Researchers derive the ranges by extrapolating backwards using the mutation rates of known genes and the number of genetic differences (due to mutations in those genes) among modern peoples from different places and populations. The more alike the sequence between two individuals, the more recently they shared an ancestor – the basis of building genetic family trees. The time estimates represent the most recent span.

DNA sequence data can guess at times and relationships, but not where people came from. So we know

that some Native Americans descended from the folks who crossed the land bridge, but not precisely where those ancestors lived. Potter suggested that they may have separated from others somewhere in northeast Asia as far back as 25,000 years ago, ushering in thousands of years of “genetic isolation” that sculpted what would become the Native American ancestral genome.

Follow the latest news and policy debates on sustainable agriculture, biomedicine, and other ‘disruptive’ innovations. Subscribe to our newsletter.

[SIGN UP](#)

The vegetated corridor emerges

The Beringians must have faced obstacles. Drowning as their pathway became submerged is obvious, but they also likely encountered drifting ice chunks, volcanic eruptions, and the ebb and flow of the rich “kelp highways” that supported the robust food web that may have sustained the early migrants. “We haven’t fully evaluated human ecology for this region,” said Potter.

Meanwhile, people could have also come through [ice-free corridors](#) that formed between the two major ice sheets that covered the northern U.S. and most of Canada, the researchers contend. The clues to that scenario aren’t telltale DNA sequences, but more environmental: signs of salmon fishing in the interior of Alaska and the Yukon, charcoal in remains of hearths, and evidence of butchering large mammals such as horses, bison, and camels.

Ancient meals suggest a “vegetated corridor” in the northern US and Canada, such as carbon-14 dates on the stomach contents of voles from at least 14,870 years ago. Remains of bison and horses date to about 13,100 years ago. Evidence of trees hails from Boone Lake in northwestern Alberta from at least 13,500 years ago and from Charlie Lake, British Columbia, from about 12,600 years ago. These times predate the [Clovis](#) Paleo-Indians, known for their leaf-shaped “Clovis point” tools from 12,900 to 13,200 years ago.

The rich vegetated corridor evidence contrasts with the scarcity of signs of a coastal lifestyle among Native American ancestors. “All antecedent cultures in Siberia and far northeast Asia are clearly terrestrial, not maritime; they were hunting mammoth, bison, and horse. The earliest Beringians were doing the same, as were the earliest widespread Paleo-Indian group, Clovis,” explained Potter.

potter HR

Image not found or type unknown

A map of northwest North America indicates archeological sites older than 10,000 years and sites of possible vegetated corridors. (Potter et al., Sci. Adv. 2018;4: eaat5473)

Reconciling evidence and “helicopter research”

Human DNA studies support a Pacific Coastal route, while DNA from other species suggests an inland ice-free corridor. “I think we’re in a very exciting time where we can’t exclude either coastal or interior route. I suspect both probably were used. Geologically informed surveys and paleoecological work needs to take place in both regions,” said Potter. What’s also needed are DNA data, on a genomic scale, representing people who came along the vegetated corridor. And that introduces the issue of genetic testing of indigenous populations.

[“Community-based participatory research”](#) is the goal, rather than “helicopter research,” defined as “a clinical or epidemiologic research project conducted by foreign scientists who use local contacts to gain access to a population group and obtain samples.” “To do this, researchers must work with linked present-day communities,” said Malhi. Such efforts can quickly grow contentious when the visitors are wealthy and their subjects not, as the case of the [Havasupai](#) people of the Grand Canyon reportedly illustrates. A more recent example is investigation of the diving prowess of Indonesia’s [Bajau](#) people.

“We need to partner and work with these communities in an approach where we address questions that non-indigenous and indigenous researchers are interested in, and involve them more completely in research. In my experience many of these community members are interested in using genomics as a tool

to learn about their history,” said Malhi, who helped organize the Summer internship for Indigenous Peoples in Genomics ([SING](#)). He suggests starting the conversation by identifying tribal councils in linked communities using data from the [Native American Graves Protection and Repatriation Act](#). “In Alaska, many indigenous peoples are not on reservations. They’re in villages on the landscape where their ancestors were,” Potter added.



Excavation of early site in Beringia.

Image credit: Ben A. Potter

Research projects involving indigenous communities should go beyond DNA to include “traditional life ways like salmon fishing, caribou hunting, and the relationships of humans and the environment,” Potter suggested, and “connecting with indigenous peoples, particularly at primary school age and working with organizations and programs, to identify opportunities for advanced training and to develop curriculum.”

Llamas agreed that the convergence of disciplines presents opportunities for indigenous communities, “from ecology to genetics and archeology field work, or analyzing genetic data, or making sure that results are communicated properly and displayed in museums. It would be great if the indigenous communities would take charge and make sure the message is transmitted widely and correctly.”

Ricki Lewis is the GLP’s senior contributing writer focusing on gene therapy and gene editing. She has a PhD in genetics and is a genetic counselor, science writer and author of *The Forever Fix: Gene Therapy and the Boy Who Saved It*, the only popular book about gene therapy. [BIO](#). Follow her at her [website](#) or Twitter [@rickilewis](#)