

► participants through Facebook. Users of the social-networking service can download a Genes for Good app that guides them through a series of health surveys to collect basic information, such as height, weight and whether a person uses tobacco. Users who complete 15 of these surveys can receive a ‘spit kit’ to collect saliva for DNA sequencing, and are encouraged to continue providing health information afterwards.

“We wanted to do something that would give us the possibility of capturing very large numbers of people in a way that is more engaging than the traditional types of study,” says Gonçalo Abecasis, a statistical geneticist at the University of Michigan in Ann Arbor who is leading the study.

WIDENING THE NET

Drawing on 23andMe’s example, the project will return genetic information to users — such as hints about ancestry drawn from a user’s genetic markers. The project also hopes to share the information it collects with other academic scientists,

“They’re smart to tether their research to a platform that has a much broader market base of people.”

or even companies developing new therapies, after removing identifying information such as names and addresses.

So far, Genes for Good has recruited 4,200 potential participants of the 20,000 it seeks, and hundreds of those have already sent back their spit kits. That is a relatively small number of genomes compared to the amount of genetic information contained in private databases. And it is dwarfed by the amount of data being amassed by public projects, such as one run by the UK Department of Health that aims to sequence the genomes of 100,000 patients.

Such efforts, in theory, could compete for participants with commercial ventures such as Ancestry.com DNA and 23andMe, which ask customers to pay for testing similar to the type that Genes for Good will offer for free. It is not clear whether that will affect the companies’ ability to attract customers and expand their data sets, given their significant head start.

Genes for Good is tapping the power of Facebook, with its 1.44 billion active monthly users. Given this potential, the project could become more massive than any previous genetic study, says Michelle Meyer, a bioethicist and legal scholar at the Icahn School of Medicine at Mount Sinai in New York. “They’re smart to tether their research to a platform that has a much broader market base of people than we’re used to seeing in research studies,” she adds. ■



DNA from humans who lived in the Andes 9,000 years ago gives clues to how South America was peopled.

ARCHAEOLOGY

South America settled in one go

Tests of human remains from a cave high in the Peruvian Andes point to a single early migration.

BY EWEN CALLAWAY

Humans settled in South America in a single wave of migration not long after their ancestors first crossed from Siberia into the Western Hemisphere during the last ice age, genetic evidence suggests. The finding, based on DNA from the remains of five ancient humans who lived high in the Peruvian Andes, also hints at how ancient Andeans evolved to thrive at altitudes of more than 4,000 metres.

Presented on 16 April at the annual meeting of the Society for American Archaeology (SAA) in San Francisco, California, the research sheds light on the last major continental migration in human prehistory — and one of the least understood.

South America’s oldest-known human occupation site — the 14,600-year-old Monte Verde settlement in Chile — suggests that people quickly reached the continent after crossing the Bering land bridge one or two thousand years earlier, perhaps skirting the Pacific coast. But some argue for a second migration. They use skeletal evidence to propose that the long, narrow skulls of South Americans living more than about 5,000 years ago differ too much from the rounder heads of more-recent

inhabitants, and of living indigenous people, to represent one continuous population¹.

In the 1950s and 1960s, Peruvian archaeologist Augusto Cardich discovered human remains bearing the characteristic ancient skull shape in a rock shelter perched high in the Andes in a region called Lauricocha. Carbon dating put the site at around 9,000 years old, making it a classic archaeological example of early high-altitude living. Later researchers dated remains from Lauricocha closer to 5,000 years old, greatly diminishing its appeal for researchers interested in the early prehistory of South America. “People simply forgot about this site. Nobody was interested any more,” says Lars Fehren-Schmitz, a biological anthropologist at the University of California, Santa Cruz.

More than half a century after the site’s discovery, Fehren-Schmitz’s team got permission to look at five human skeletons excavated from Lauricocha and held at the National Museum of the Archaeology, Anthropology and History of Peru in Lima. The team redated the remains, remeasured the skulls and extracted DNA.

Their work, presented by Fehren-Schmitz at the SAA meeting, paints a complicated picture of Lauricocha. Two of its residents, a woman and a 2-year-old child, died nearly 9,000 years ago. The third, a man, perished around 2,500 years later and another man died

CHRISTIAN KAPTEIN/ROBERT HARDING

about 2,300 years later still. The fifth specimen was not dated because of its condition. Only the woman's skull had a long, narrow shape, which is known as dolichocephaly.

To gauge whether the Lauricocha residents were descended from members of more than one migration, the team sequenced the DNA from their mitochondria, cellular organelles that are passed directly from mother to child, and thus trace maternal ancestry. All five people were found to be descended from maternal lines that are common among modern and ancient indigenous people of North and South America. The males' Y chromosomes put them on a lineage that arose in the region around the Bering Strait some 17,000 years ago — the most widely accepted time and place for the original human migration into the Americas. These and other DNA data suggested that all the Lauricocha humans are descended from the first humans to reach the Americas, supporting one migration into South America.

Not everyone accepts the argument. Such a wide-ranging conclusion cannot be drawn from a handful of remains found at a single site, says Tom Dillehay, an archaeologist at Vanderbilt University in Nashville, Tennessee. He argues that the 5,000-year gap between the earliest inhabitants at Monte Verde, which Dillehay excavated, and the earliest Lauricocha skeletons leaves the door open for earlier migrations.

“There may well be a single migration — they don't have the evidence for it,” he says.

Ancient human DNA from other parts of South America, such as the Amazon, may yet point to a second migration into the continent, agrees Fehren-Schmitz. His team is now analysing full genomes from Lauricocha and other South American sites to obtain a fuller picture of the continent's past.

Deborah Bolnick, a biological anthropologist at the University of Texas at Austin, accepts the argument for a single migration. But regardless of the number of waves, there would have been further population movements after that initial, southbound founding trek, she says, adding that analysis of full genomes from ancient South Americans will give a more nuanced picture of the continent's prehistory. Researchers studying ancient DNA have found evidence for a massive migration from present-day Russia and Ukraine into western Europe around 4,500 years ago², and Bolnick says that similar upheavals are bound to have happened in the Americas. In a 2014 paper, for instance, Fehren-Schmitz documented a migration into the Central Andes about 1,400 years ago, possibly driven by drought in lower-lying areas³.

Ancient South American genomes may also show how humans adapted to the New World. In a separate study, Fehren-Schmitz and his colleagues looked at a gene variant that protects

against altitude sickness. Between around 8,500 and 600 years ago, the presence of the variant increased markedly among the Andeans.

Fehren-Schmitz says that the finding is merely suggestive of local adaptation. But with full, ancient genomes in hand, researchers will be able to look more thoroughly for signs of adaptation to high altitude, says Bolnick. With that question in mind, her team is sequencing DNA from remains of mountain residents of Argentina. Ancient genomes from the Americas may also reveal how humans adapted to shifts in diet — early Americans domesticated maize (corn), potato and other crops — and to diseases imported from Europe, such as smallpox. South American prehistory, it seems, is about to get a lot more complicated. ■

1. Walter, A., Neves, W. A. & Hubbe, M. *Proc. Natl Acad. Sci. USA* **102**, 18309–18314 (2005).
2. Callaway, E. *Nature* **518**, 284–285 (2015).
3. Fehren-Schmitz, L. *et al. Proc. Natl Acad. Sci. USA* **111**, 9443–9448 (2014).

CORRECTION

The Editorial ‘Highway to health’ (*Nature* **520**, 407; 2015) stated that the African Centres for Disease Control and Prevention would need at least \$300 million and 60 staff members. This should have read \$60 million and 300 staff.