A distinctive human genetic lineage persisted in central Argentina for 8,500 years

The DNA of ancient individuals dating to between 10,000 and 150 years ago reveals the existence of a long-standing, yet previously uncharacterized, lineage in the Southern Cone of South America — a region comprising what is now Argentina, Chile and Uruguay. People with this ancestry produced offspring with other, pre-existing groups in surrounding regions. Genomic data from present-day inhabitants attest to the genetic continuity of the lineage in central Argentina.

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The question

The peopling of South America is thought to have been a two-stream migration process, along the Pacific and Atlantic sides of the continent. Genetic differences cluster ancient-human genomes dating to 9,000 years before present (BP) or later into at least three Native South American ancestry groups: central Andes (found in the west of the continent); tropical and subtropical forest or lowlands (including Amazonia; found to the east of the Andes); and central Chile, Patagonia and Pampas (found in the south)[1,2]. However, owing to the limited number of samples available, there are currently substantial gaps — in time and space — in South America's genetic record. The genetic ancestries of people in the Southern Cone (that is, territories south of the Tropic of Capricorn) are particularly under-studied.

The discovery

We analysed genetic data from 238 ancient individuals from present-day Argentina dating to as long ago as 10,000 BP, using statistical-analysis techniques to learn about the region's population history. For example, if two sets of individuals from distinct regions share more genetic variants than expected by chance[3], the ancestors of these groups probably had offspring together at some point in the past. We used statistical comparisons of several groups to build trees of how these populations were related (Fig. 1a), and mapped them onto a low-dimensional representation to visualize their genetic structure. We applied a method[4] called hapROH to find low-diversity genomic regions that indicate small community sizes or reproductive unions between close kin.

Genetic differentiation between populations in the Southern Cone and other South American regions began at least 10,000 years ago. The earliest individual from the Pampas region (the central eastern grasslands stretching from the Atlantic coast to central Argentina) was dated to that period and showed genetic similarity to other people from the Southern Cone, but not to contemporary individuals from the central Andes and central-east Brazil. In central Argentina, a genetic analysis involving a person from 8,500 BP revealed a previously unknown lineage from which all sampled individuals from this region, dating to between 4,600 and 150 BP, mainly descended. We inferred that this central Argentine ancestry was involved in three interregional migration events (Fig. 1b): in northwest Argentina; in the Pampas (where it seems to have become the main lineage after 800 BP); and in the Gran Chaco region (which extends across northern Argentina, western Paraguay, southeastern Bolivia and border areas of southwestern Brazil). This central Argentine lineage has persisted for more than eight millennia and remains present today in modern individuals from the region, who also have European and African ancestry. In northwest Argentina, close-kin unions were more common than in other regions of the central Southern Cone, probably reflecting differences in cultural practices.

The implications

The discovery of a previously unknown South American genetic lineage shows that our understanding of the peopling of the Americas is still limited compared with that of other regions. We expect that studies that address the remaining gaps in the continent's ancient genetic record will bring further surprises. Meanwhile, the picture emerging from this and previous work suggests that South America has a rather distinctive population history, in that people often remained in the same place for many millennia. In other parts of the world, rapid population turnover seems to have been more common[5].

Our study could only roughly investigate the history of the Gran Chaco region, owing to limited sample sizes and low data quality. Furthermore, we were able to obtain data from only a limited number of very early individuals, increasing the uncertainty of events in deep time.

Our data set was also not sufficient to fill the gap in the genetic record for the northern part of Patagonia — the region between central Argentina and the southernmost tip of South America. North Patagonia's genetic history is completely unknown, and future studies should aim to complete that picture.

Rodrigo Nores is at the National University of Córdoba and CONICET, Córdoba, Argentina, and **Javier Maravall-López** is at Harvard University, Cambridge, Massachusetts, USA.

EXPERT OPINION

"This is a notable contribution to South American palaeogenomics. The authors report genome-wide data from 238 ancient individuals from central and northern Argentina, spanning nearly 10,000 years — the largest ancient-DNA data set from this region to date. They identify a deeply divergent genetic lineage in central Argentina, detectable from 8,500 years ago to at least 150 years ago, that remained stable geographically and temporally — a rare case of long-term isolation-by-distance in human populations." (CC BY 4.0)

A reviewer

FIGURE

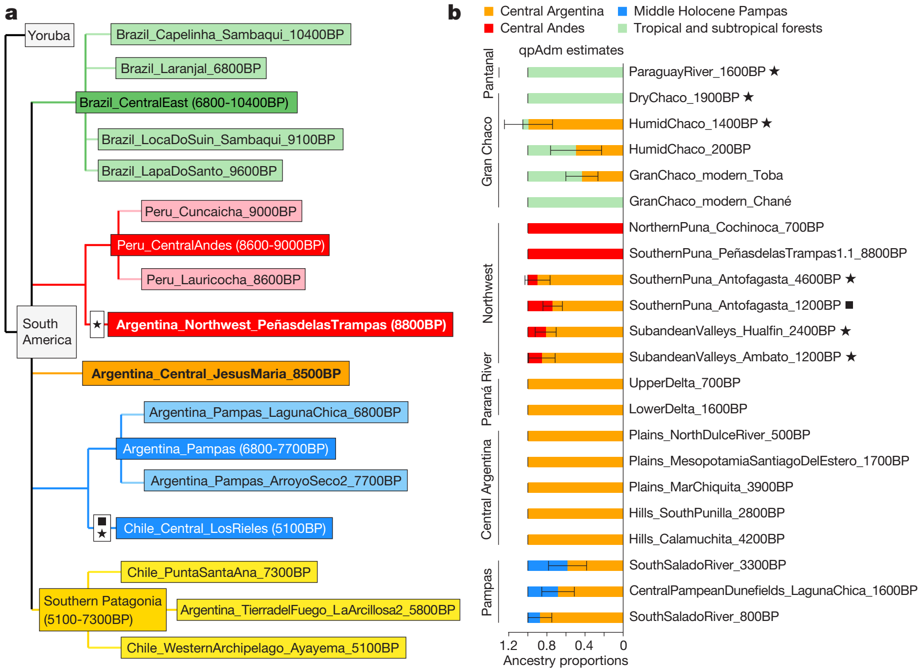

Figure 1 | Distinct early genetic lineages in South America and ancestry composition of later individuals. **a**, Reconstructed relationships of early ancient individuals in South America. Modern countries, archaeological sites (for single individuals) and dates (in years before present; BP) are indicated. The orange lineage, represented by an ancient individual from central Argentina, was previously unknown. **b**, Genetic ancestry of select ancient individuals, with estimates of contributions (calculated using a program called qpAdm) from the central Argentine ancestry (orange), from people from the Argentine Pampas (the central eastern grasslands stretching from the Atlantic coast to central Argentina) around 7,000 BP (blue), from individuals from the central Andes since around 9,000 BP (red) and from modern Native South Americans from the lowlands (green). Newly reported individuals are indicated in bold, and lineages for which the evidence is weak are indicated by a star. The square indicates that affinity with Mesoamerican-related populations was detected. Data for 73 ancient individuals are not shown due to space constraints; 67 of them are from central Argentina and carry 100% of the newly described ancestry.

BEHIND THE PAPER

Our study started in 2017, through a National Geographic Society initiative, with 29 teeth from Córdoba province in central Argentina. We later expanded the study area by including 125 samples from northwest, northeast and east Argentina. After building collaborations and collecting samples, we finalized our data set in 2024 with 344 samples from 310 individuals across 133 archaeological sites, representing decades of work by more than 30 Argentine archaeologists.

A common way to analyse ancient-DNA data sets is to use modern individuals' DNA as a high-quality reference. In the Americas, however, data sets of modern Native American groups might be missing key representatives. In our case, the previously unknown lineage was the majority ancestry in our data set, yet was completely absent from modern reference panels, and so it was initially difficult to glean patterns from the data. We eventually analysed ancient individuals in a reference-free way: that work seeded all our subsequent conclusions.

R.N. and **J.M.-C.**

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FROM THE EDITOR

Although ancient DNA has taught us a lot about the population history of western Eurasia, thanks to the thousands of data sets available at this point, very few genomic data sets for ancient populations from South America have been reported. This study provides a considerable number of genome-wide data sets for individuals found at archaeological sites in central and northern Argentina. The analysis reveals the genetic continuity of one lineage in the region over thousands of years.

Michelle Trenkmann, Senior Editor, *Nature*