

Genetic roots of the first Americans

The whole-genome sequence of a human associated with the earliest widespread culture in North America confirms the Asian ancestry of the Clovis people and their relatedness to present-day Native Americans. [SEE LETTER P.225](#)

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Advances in genetics and archaeology over recent decades have transformed our understanding of the ancestry and migration history of indigenous Americans^{1–5}. However, limited genetic information from the earliest inhabitants of the Americas (those living more than 5,000 years before present) has made it difficult to test many hypotheses about the settlement and early history of this continent. On page 225 of this issue, Rasmussen *et al.*⁶ describe the complete genome sequence of an infant boy, Anzick-1, who was interred between 12,707 and 12,556 years ago at the Anzick site in Montana. Anzick-1 is the only known human burial associated with the Clovis culture — the oldest widespread archaeological complex in North America⁷, which is dated to 13,000 to 12,600 years ago. His genome is the first from an ancient American individual to be fully sequenced.

Anzick-1's mitochondrial DNA (maternally inherited extra-nuclear DNA located in cell mitochondria) belongs to the D4h3a lineage, a pan-American lineage thought to be one of the 'founder' lineages carried by the first people to enter the Americas. It is rare among present-day Native Americans (found in 1.4% of individuals) but more common in the oldest inhabitants of the Americas^{8,9}. Anzick-1's paternally inherited Y-chromosome lineage (Q-L54*(xM3)) is common in Native Americans¹. Comparisons of his nuclear genome with genetic data from Eurasian and Native American populations show that he is most closely related to Native American populations and more genetically similar to Siberians than to other Eurasians.

These genetic affinities between Anzick-1 and other Native Americans are not a surprise, because there is ample evidence that contemporary Native Americans are descended from the ancient inhabitants of the Americas^{1–3,10}. However, debate has persisted about this relationship because some of the earliest American skeletons exhibit distinctive craniofacial features¹¹ and because of continued attention to the Solutrean hypothesis, which proposes that the Clovis complex was derived from a transatlantic migration of Europeans who used Solutrean tools between 21,000 and

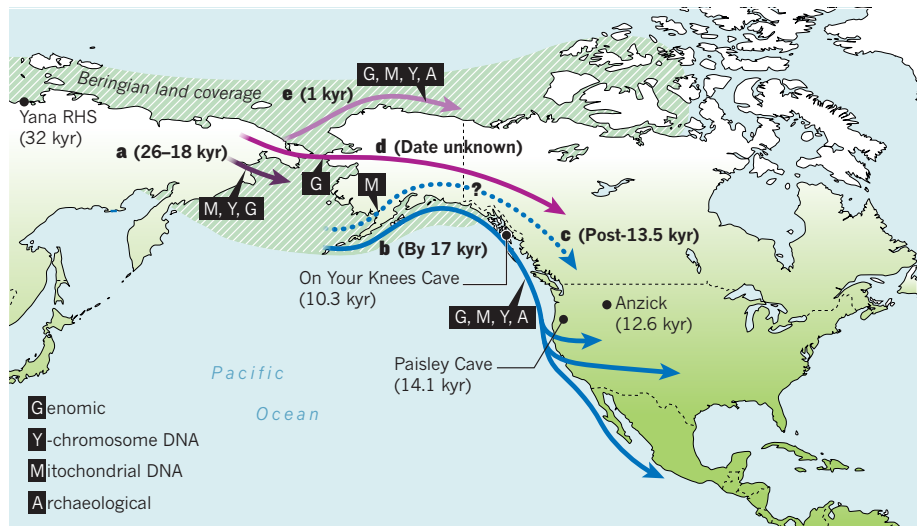


Figure 1 | Populating a continent. A hypothetical scenario for the peopling of the Americas, showing possible migration events (a–e) as described in the main text, coloured according to putative region of origin (Beringia, blue; Siberia, shades of purple). Also shown are some key archaeological sites in North America and Siberia, and the type of evidence (genomic, mitochondrial DNA, Y-chromosome DNA and archaeological) currently supporting each hypothesized migration. Shading depicts the extent of Beringia during the Last Glacial Maximum. (kyr, thousand years ago.)

17,000 years ago¹². The fragmentary nature of Anzick-1's remains means that they cannot be used to address questions about whether ancient Americans with distinctive craniofacial morphology were related to modern Native Americans. However, this genome contributes to a large body of genetic and archaeological research to lay the Solutrean hypothesis to rest once and for all. It shows that Anzick-1 indisputably had Asian ancestors and is related to contemporary Native Americans. Unless proponents offer evidence of direct European ancestry in other securely dated ancient American genomes, the Solutrean hypothesis can no longer be treated as a credible alternative for Clovis (or Native American) origins. It is time to move on to more interesting questions.

Rasmussen and colleagues' analysis of the Anzick-1 genome highlights some such questions. They find support for the proposal that Native Americans are descended from three 'streams' of gene flow from Asia, with some North Americans tracing their ancestry to multiple independent migrations from Siberia⁵. Intriguingly, their study reveals additional genetic substructure in North America — some

Native North American populations are genetically differentiated from Central and South Americans and from Anzick-1, indicating ancient divergences between Native American populations. The authors rule out additional migration from Eurasia as the cause of these patterns, but more North American genomes are needed to elucidate the evolutionary history that produced this structure.

The Anzick-1 genome, together with other genetic and archaeological evidence^{1–10}, helps to build a possible scenario for the peopling of the Americas. We know that humans had moved into northwestern Beringia from Siberia by 32,000 years ago¹³. Sometime between 26,000 and 18,000 years ago, these people expanded into eastern Beringia (Fig. 1a) and evolved genetic characteristics unique to Native American populations¹⁴. By 17,000 years ago, deglaciation of the Pacific coastline allowed a southward coastal migration (Fig. 1b), bringing the first Americans to Monte Verde in Chile by 14,600 years ago^{15,16}. Because Anzick-1's mitochondrial lineage is primarily found along the Pacific coast, this migration may have included his ancestors,

the ancestors of Central and South Americans, and those of other D4h3a-bearing populations (although we note that Rasmussen *et al.* may not agree with this interpretation). Descendants of these migrants who moved eastward, south of the Cordilleran and Laurentide ice sheets, could have developed the Clovis culture³. Some mitochondrial DNA studies also suggest a second wave of migration through the interior ice-free corridor that opened after 13,500 years ago¹⁷ (Fig. 1c), but this hypothesis is not yet supported by other evidence.

Genome-wide (and possibly mitochondrial) evidence^{5,7} shows that a second group of Siberians subsequently moved into North America (Fig. 1d), contributing to the ancestry of modern Chipewyans and perhaps other North American groups. Another expansion from Siberia brought Neo-Eskimo ancestors to North America (Fig. 1e) sometime before their expansion eastward around 800–1,000 years ago^{1,10,18}. Thousands of years of subsequent gene flow and other evolutionary forces, as well as region-specific cultural histories, contributed to the population structure of indigenous Americans.

The Anzick-1 study — similar to earlier studies of the 4,000-year-old Saqqaq genome from Greenland¹⁸, the 24,000-year-old Mal'ta genome from Siberia¹⁹ and the 7,000-year-old Mesolithic genome from Spain²⁰ — demonstrates that ancient genomes can yield insights into prehistoric population histories. However, the conclusions that can be drawn from a single genome are limited. Genome sequencing is not yet cost-effective for population-scale sampling of ancient remains, and many ancient samples do not contain enough DNA for complete genome sequencing. Studies of targeted DNA regions are therefore still needed. Furthermore, there are limitations on what we can learn from genetics alone, necessitating models that account for all available palaeoclimatological, genetic and archaeological data.

The Anzick-1 genome confirms many predictions from archaeological and genetic studies, and moves us closer to a nuanced and comprehensive model for the population history of the Americas. However, this genome, similar to the Mal'ta¹⁹ and European Mesolithic²⁰ genomes, shows that patterns of genetic diversity have changed dramatically over time. Some genetic variants that are rare today were more common in the past, and variants that are ubiquitous today may have increased in frequency only in the past few thousand years. Moreover, the current distribution of genetic lineages may not reflect the geographic areas in which they were found thousands of years ago — some lineages clearly had a different or wider range in the past^{6,19}. Perhaps the most important lesson from palaeogenomic studies, then, is that we must be cautious about assuming that present-day genetic patterns are representative of the past. Analyses of ancient human genomes are making it clear that

thousands of years of evolutionary processes have drastically reshaped the genetic landscape within any given geographic region. ■

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COSMOLOGY

Cool start to hydrogen ionization

Simulations of the cosmos cast doubt on assumptions about the temperature of primordial hydrogen gas when it was ionized by the first stars and galaxies, complicating the interpretation of ongoing observations. SEE LETTER P.197

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Not long after the Big Bang, the Universe cooled sufficiently for electrons and protons to become bound into hydrogen atoms. Over the next few hundred million years, the primordial hydrogen gas continued to cool as the Universe expanded. For astrophysicists, the excitement starts at this point, when the first stars, galaxies and black holes are believed to have released X-rays and ultraviolet light that initially heated and later 'reionized' the primordial hydrogen. This period of reionization ended about one billion years after the Big Bang. On page 197 of this issue, Fialkov and colleagues¹ report simulations that challenge existing theoretical expectations about the final stages in this sequence.

In their simulations, the authors use improved models of X-ray emission driven by the accretion of mass in binary star systems from early cosmic epochs, and find that it may have taken much longer than previously projected to heat the primordial hydrogen between nascent galaxies. The improved models come from studies^{2,3} of the evolution of binary systems throughout cosmological time, and predict more energetic X-rays than previous models, which favoured low-energy emission. High-energy X-rays are able to travel farther before being absorbed by primordial gas. This results in a more uniform heating

of the gas, but also means that, counter-intuitively, less energy is deposited into the gas overall, owing to effects associated with the Universe's expansion.

Whereas X-rays are primarily responsible for heating the primordial gas, ultraviolet light from early stars drives its ionization. Hence, although heating is prolonged in the authors' simulations, ionization proceeds at the same pace as in previous simulations, because the model for ultraviolet emission has not changed. The result is that ionization commences before the gas is hot. This outcome is contrary to earlier expectations and has significant consequences for a new branch of observational astrophysics.

Over the past decade, astrophysicists around the world have constructed pioneering radio telescopes to detect the 21-centimetre-wavelength radio emission of neutral atomic hydrogen from the reionization era. Instruments include the Low Frequency Array (LOFAR)⁴, the Precision Array for Probing the Epoch of Reionization (PAPER)⁵ and the Murchison Widefield Array (MWA)⁶. These telescopes do not observe at 21-cm wavelengths, but rather at metre wavelengths. Owing to the Universe's expansion, 21-cm radiation from the early Universe is highly stretched (redshifted) on its way to Earth. The intensity and distribution of the redshifted 21-cm emission on the sky can be used to map the temperature, density and