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DNA study 'fills gaps' in Indigenous Americans' ancestry

Story by Fred Schwaller • 1d • 3 min read



A genetic analysis of modern day and ancient Indigenous Americans DNA has traced how people migrated through the Americas over thousands of years

The first people to colonize the Americas migrated from modern-day Russia about 20,000-30,000 years ago, a new study has found.

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The study also found the early settlers split into groups that became isolated in different environmental settings. The findings provide a new genetic and cultural understanding of present-day South American communities, said the researchers.

"[It fills] key gaps in our understanding of how the diverse populations of present-day South America came to be," said Elena Gusareva, the study's lead author, who is based at Nanyang Technological University, Singapore.

Gusareva said the participants in the study had been "deeply motivated" to uncover their people's history. This showed the importance of ancestral knowledge for people's identities, Gusareva said.

The researcher cited an "urgent case" involving the Kawésqar people of Patagonia, whose population and 6000-year-old cultural heritage is in danger of disappearing: "This genetic record is one of the last chances to preserve their legacy."

Eurasian roots of Indigenous Americans

Gusareva and colleagues sequenced the genomes of 1,537 individuals from 139 ethnic groups in northern Eurasia and the Americas.

They compared these with millions of tiny variations in modern-day Indigenous people's genes to ancient DNA from the first peoples to arrive in the Americas. They said this created a genomic dataset from people previously underrepresented in ancestral science.

Tracing how these genetic codes changed in people from different geographical regions and various Indigenous groups allowed them

to study patterns of population history, migration, and adaptation over thousands of years.

"Our genetic analysis of Indigenous groups is crucial because their genomes carry unique insights into the earliest human history in the region," said Gusareva's colleague, Hie Lim Kim, a geneticist at Nanyang Technological University.

Their analysis appears to corroborate existing archeological evidence, showing the first peoples in the Americas diverged from North Eurasians between 19,300 and 26,800 years ago.

The dates are "consistent with a large body of archeological evidence," said Francisco Javier Aceituno, an archeologist at the University of Antioquia, Colombia, who was not involved in the new study.

By comparing genetic datasets, the researchers said they had been able to find the closest living relatives of Indigenous North Americans are west Beringian groups, such as the Inuit, Koryaks, and Luoravetlans. Beringia was an ice bridge between modern-day Russia and North America the last ice age.

The foundation of South America's Indigenous groups

Gusareva and Kim's study found that after the early settlers had arrived in South America and then split into four distinct groups — Amazonian, Andean, Chaco Amerindian and Patagonian — they each became isolated in different environments.

Aceituno told DW these groups of hunter-gatherers probably divided "to occupy new territories, generate new family groups and avoid isolation."

Gusareva believes the new genetic data shows natural barriers, such as the Amazon rainforest and the Andes mountain range, led to the isolation of these Indigenous groups.

"This made their genetic makeup more uniform, similar to what is seen in island populations," Gusareva said.

Ancient gene mutations affect modern South Americans' health

The study also found Indigenous groups have distinct genetic traits, which may have evolved through their adapting to extreme environments and long-term isolation from other groups.

For instance, a group of Andean highlanders carries a gene mutation that helps them adapt to low levels of oxygen.

Mutations in the gene *EPAS1* stimulate new blood vessel formation and produce more red blood cells. *EPAS1* mutations have also been found in people from Tibet.

"As people adapted to diverse and often extreme environments — like high altitudes or cold climates — their genomes evolved accordingly," said Kim.

Previous studies have found genetic variations among Brazil's Indigenous groups may cause them to respond differently to medication for blood clots or high cholesterol.

Kim said the new research had revealed more than 70 gene variations that could increase [people's] vulnerability to emerging infectious diseases: "Many of these populations are already small. It's critical to provide tailored healthcare and disease prevention efforts to support their well-being."

Edited by: Matthew Ward Agius

Source:

Gusareva ES, et al., Science (2025). From North Asia to South