PREHISTORY, SCIENCE

The longest prehistoric journey undertaken by humans lasted thousands of years and spanned several generations

by **Guillermo Carvajal** May 16, 2025

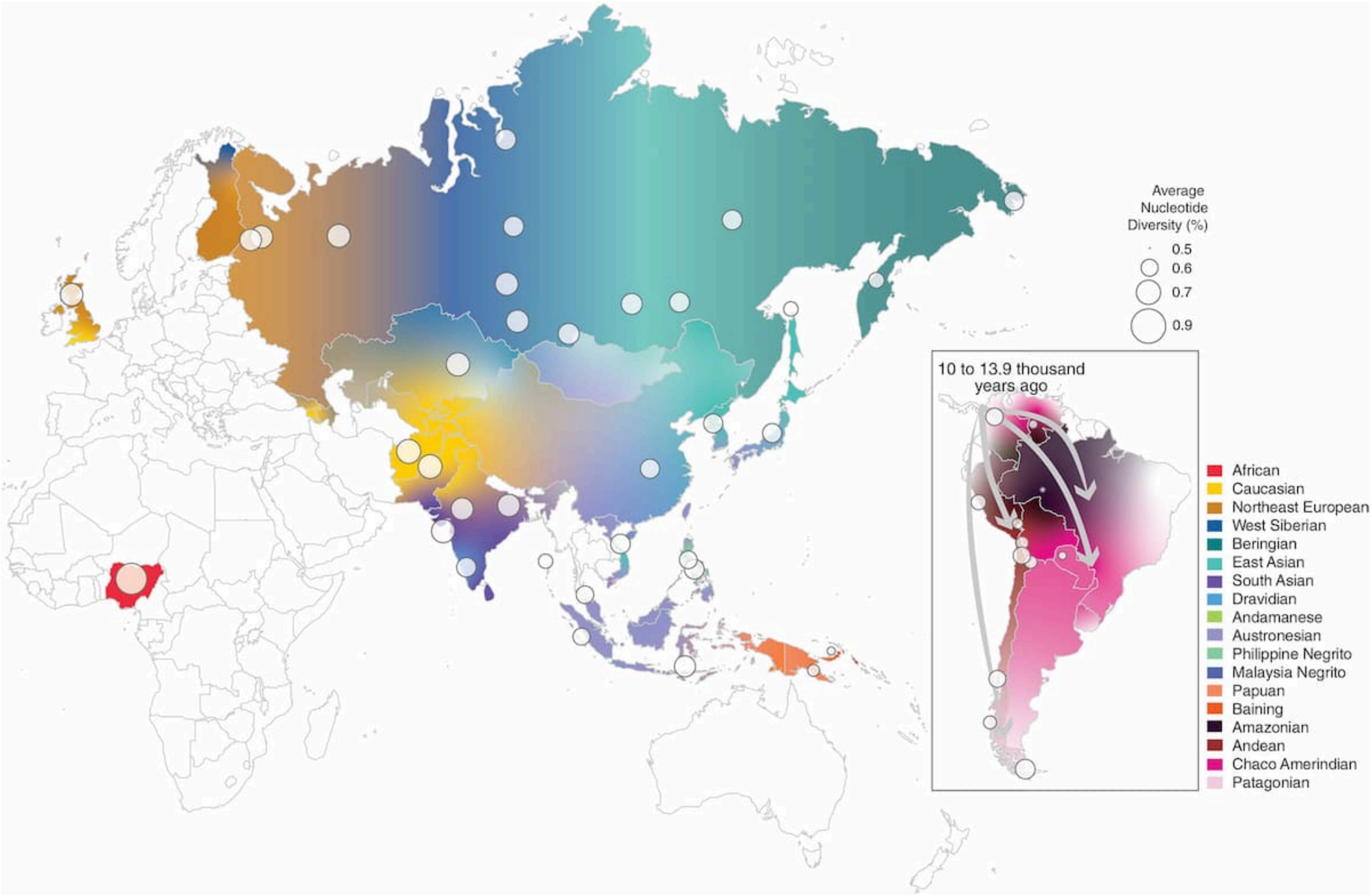
The greatest journey in human history was not made in a row, or perhaps it was. Credit: Google Gemini / labrujulaverde.com

An international team of scientists has managed to reconstruct the **longest prehistoric journey ever undertaken by humans**, carried out by the first Asians as they embarked on a journey of more than 20,000 kilometers on foot that took them from northern Asia to the southernmost tip of South America.

The research, published in the journal *Science* by scientists from Nanyang Technological University (NTU Singapore) in collaboration with the Singapore Centre for Environmental Life Sciences Engineering (SCELSE) and the Asian School of the Environment (ASE), succeeded in detailing this ancestral migration by analyzing the DNA sequences of 1,537 individuals belonging to 139 different ethnic groups. The results traced a **migratory route that began in Africa**, crossed northern Asia, and ended in Tierra del Fuego, in present-day Argentina.

The journey **lasted thousands of years and spanned numerous generations**, and it was made possible because, in the past, ice masses existed that connected regions that are now separated by oceans. These human groups had to face many other extreme natural obstacles and managed to adapt to drastically different environments along the way.

The study involved 48 authors from 22 institutions across Asia, Europe, and the Americas. Their genetic analyses enabled them to reconstruct patterns of shared ancestry and accumulated variations over time, which facilitated the identification of divergence points, displacement, and adaptation of various human populations.



Genetic ancestry and nucleotide diversity. Colors represent genetic ancestries estimated by whole-genome sequencing data of contemporary human populations. Countries having no data remained empty. Circle size indicates the average nucleotide diversity of each population. Credit: Elena S. Gusareva et al.

They found that the arrival of these ancient migrants to northwestern South America, specifically the region now shared by Panama and Colombia, occurred **approximately 14,000 years ago**. From there, the populations split into **four major groups**: one remained in the Amazon basin, while the others moved eastward to the dry Chaco and southward, crossing the valleys of the Andes Mountains to reach Patagonia.

According to the researchers, this migration had significant evolutionary consequences by reducing the genetic diversity of the migrants. As explained by Associate Professor Kim Hie Lim, corresponding author of the study and deputy director of the

GenomeAsia100K project, *those emigrants carried only a subset of the genetic pool of their ancestral populations during their long journey. Thus, the lower genetic diversity also led to a lower diversity of genes related to the immune system, which may limit a population's flexibility in fighting various infectious diseases. This could help explain why some Indigenous communities were more susceptible to diseases introduced by later immigrants, such as European settlers. Understanding how past dynamics have shaped the current genetic structure of populations can help us better understand human genetic resistance.*

Dr. Elena Gusareva, principal investigator at SCELSE and first author of the article, stated that *our findings highlight the extraordinary adaptability of early Indigenous groups, who successfully settled in very different environments. Thanks to SCELSE's high-resolution whole-genome sequencing technology, we can now uncover the deep history of human migrations and the genetic footprints left by the first settlers.*

The study also highlights the historical underrepresentation of Asian populations in major sequencing projects. Professor Stephan Schuster, chief scientific officer of the GenomeAsia100K consortium and senior author of the article, emphasized that *our study shows that the greatest diversity of human genomes is found in Asian populations, not in European ones, as has long been assumed due to sampling bias in large-scale genome sequencing projects.*

SOURCES

Nanyang Technological University

Elena S. Gusareva et al., *From North Asia to South America: Tracing the longest human migration through genomic sequencing*. Science388, eadk5081(2025). **DOI:10.1126/science.adk5081**