



Asians made humanity's longest prehistoric migration and shaped the genetic landscape in the Americas

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An international genomics study led by scientists from Nanyang Technological University, Singapore (NTU Singapore) at the Singapore Centre for Environmental Life Sciences Engineering (SCELSE) and Asian School of the Environment (ASE) has shown that early Asians made humanity's longest prehistoric migration.

These prehistoric humans, roaming the earth over a hundred thousand years ago, would have traversed more than 20,000 kilometres on foot from North Asia to the southernmost tip of South America.

This journey would have taken multiple generations of humans, taking thousands of years. In the past, land masses were also different, with ice bridging certain portions that made the route possible.

Supported by the GenomeAsia100K consortium [1], the study was published this week in *Science*, which analyses DNA sequence data from 1,537 individuals representing 139 diverse ethnic groups.

The study involved 48 authors from 22 institutions across Asia, Europe and the Americas.

The researchers traced an ancient migratory journey that began in Africa, proceeded through North Asia and ended at Tierra del Fuego in modern-day Argentina, which is considered the final boundary of human migration on Earth.

By comparing patterns of shared ancestry and genetic variations that accumulate over time, the team was able to trace how groups split, moved, and adapted to new environments.

These patterns allowed the team to reconstruct ancient migration routes and estimate when different populations diverged.

The reconstructed routes gave a detailed picture of how early humans reached the far edge of the Americas, and the findings suggested that this pioneering group overcame extreme environmental challenges to complete their journey across millennia.

A key insight was that these early migrants arrived at the northwestern tip of South America, where modern-day Panama meets Colombia, approximately 14,000 years ago.

From this critical point of entry, the population diverged into four major groups: one remained in the Amazon basin, while the others moved eastward to the Dry Chaco region and southward to Patagonia's ice fields, navigating the valleys of the Andes Mountains, the highest mountain range outside of Asia.

By analysing the genetic profiles of indigenous populations in Eurasia and South America, researchers from the GenomeAsia100K project have, for the first time, mapped the unexpectedly large genetic diversity of Asia.

Understanding migration and genetic resilience

The study also sheds light on the evolutionary consequences of such a vast migration.

Associate Professor Kim Hie Lim from NTU's Asian School of the Environment, the study's corresponding author, explained that the arduous journey over thousands of years had reduced the genetic diversity of the migrant population.

"Those migrants carried only a subset of the gene pool in their ancestral populations through their long journey. Thus, the reduced genetic diversity also caused a reduced diversity in immune-related genes, which can limit a population's flexibility to fight various infectious diseases," explained Assoc Prof Kim, a Principal Investigator at SCELSE and Vice-Director of GenomeAsia100K.

"This could explain why some Indigenous communities were more susceptible to illnesses or diseases introduced by later immigrants, such as European colonists. Understanding how past dynamics have shaped the genetic structure of today's current population can yield deeper insights into human genetic resilience."

SCELS Senior Research Fellow Dr Elena Gusareva, the study's first author, said that these early groups settled into new ecological niches, and over hundreds of generations, their bodies and lifestyles evolved in response to the unique challenges of each region.

“Our findings highlight the extraordinary adaptability of early, diverse indigenous groups who successfully settled in vastly different environments. Using high-resolution whole-genome sequencing technology at SCELS, we can now uncover the deep history of human migration and the genetic footprints left behind by the early settlers.”

Importance of Asian representation in genetic studies

NTU Professor Stephan Schuster, the study's senior author of the paper and the Scientific Director of the GenomeAsia100K consortium, said: “Our study shows that a greater diversity of human genomes is found in Asian populations, not European ones, as has long been assumed due to sampling bias in large-scale genome sequencing projects.”

“This reshapes our understanding of historical population movements and lays a stronger foundation for future research into human evolution. Our new insights underscore the importance of increasing the representation of Asian populations in genetic studies, especially as genomics plays a critical role in personalised medicine, public health, and the understanding of human evolution,” added Prof Schuster, who is the President's Chair in Genomics at NTU's School of Biological Sciences, and the Deputy Centre Director at SCELS.

By tracing the impact of migration and isolation on genetic characteristics, the study offers insights into how different populations respond to diseases and how their immune systems have evolved.

The findings also help scientists better understand the genetic makeup of Native American populations and help policymakers to better protect and conserve native communities.

It also demonstrates how advanced genomic tools and global collaboration can deepen humanity's understanding of human evolution and inform future medical and scientific breakthroughs.

[1] GenomeAsia100K is a non-profit consortium focused on sequencing and analysing 100,000 Asian genomes to drive population-specific medical advancements and precision medicine.