



News Asia

Early Asians made prehistoric migration to South America

Study explores how different populations respond to diseases and how their immune systems have evolved



Paul Carey
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[Asians](#) made humanity's longest [prehistoric migration](#) and shaped the genetic landscape in the Americas, finds NTU Singapore-led study

Tracing the impact of migration on genetic characteristics, the study offers insights into how different populations respond to diseases and how their immune systems have evolved. Early Asians made humanity's longest prehistoric migration, travelling 20,000km on foot – over several generations – to the southernmost tip of South America, a study has found.

The migration took place over 100,000 years ago, and would have played out over thousands of years, when land masses were different – ice bridged certain portions that made the route passable. Scientists analysed DNA sequence data from 1,537 individuals representing 139 diverse ethnic groups, to reach their conclusions. The study, published in the journal *Science*, involved 48 authors from 22 institutions across Asia, Europe and the Americas, led by scientists from Nanyang Technological University.

The researchers traced an ancient migratory journey that began in Africa, proceeded through Central and North Asia – headed through Beringia (between modern day Russia and Canada)

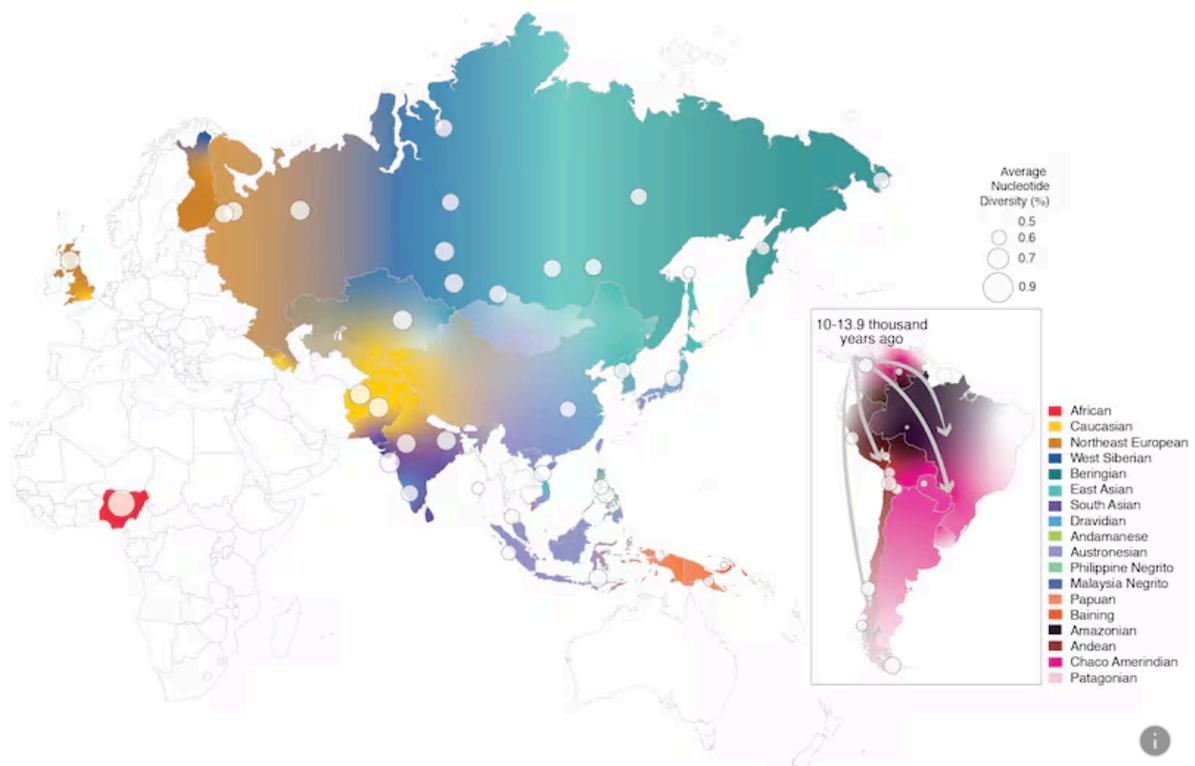
and Alaska, before ending at Tierra del Fuego in modern-day Patagonia in Argentina and Chile, which is considered the final boundary of human migration on Earth.



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 findings suggested that this pioneering group overcame extreme environmental challenges to complete their journey across millennia. Migrants arrived at the northwestern tip of South America, where modern-day Panama meets Colombia, approximately 14,000 years ago.

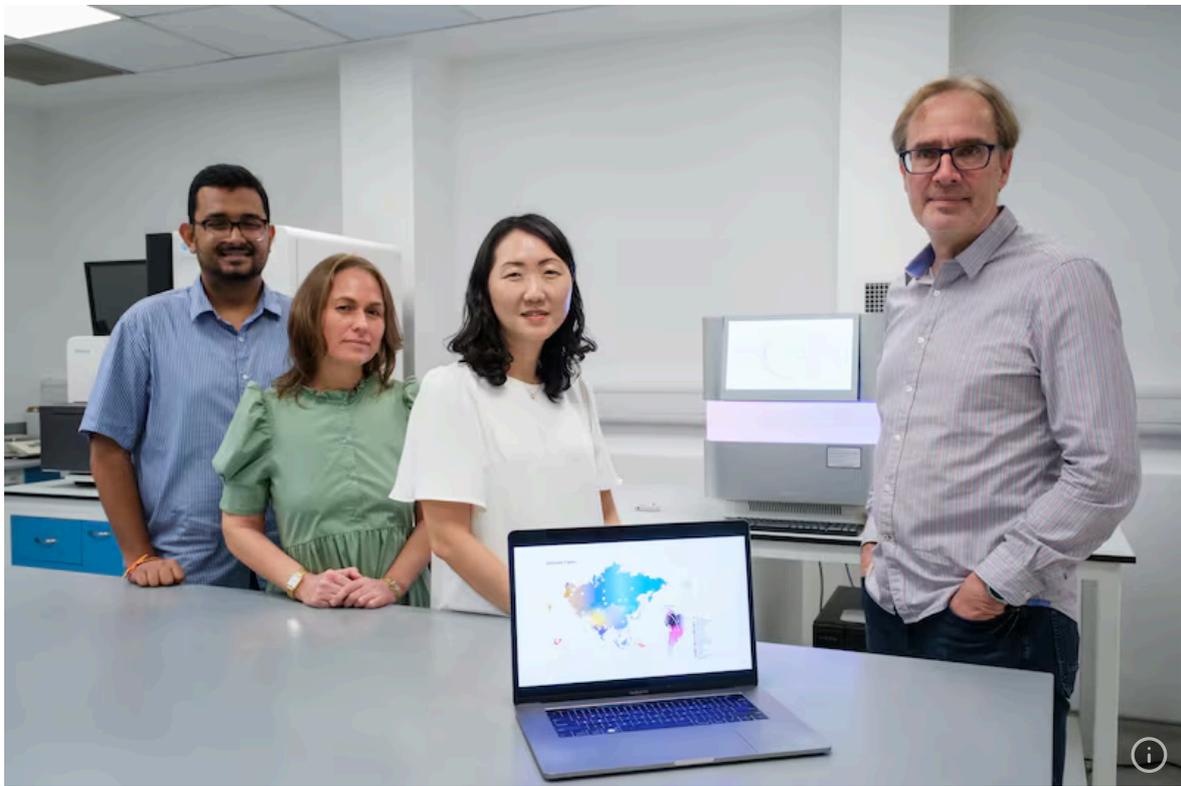
The population diverged into four major groups: one remained in the Amazon basin, while the others moved eastward to the Dry Chaco region and southward to Patagonia's ice fields, navigating the valleys of the Andes Mountains, the highest mountain range outside of Asia. The study also sheds light on the 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 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," she said.

"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."



NTU Professor Stephan Schuster, the study's senior author, said the study showed 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. He pointed out that Asians make up 50 per cent of mankind but are only involved in up to 6 per cent of scientific studies.

"This reshapes our understanding of historical population movements and lays a stronger foundation for future research into human evolution," he said. 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."

The study was supported by GenomeAsia100K consortium, a non-profit consortium focused on sequencing and analysing 100,000 Asian genomes to drive population-specific medical advancements.

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