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# Longest early human migration was from Asia, and it shaped the Americas

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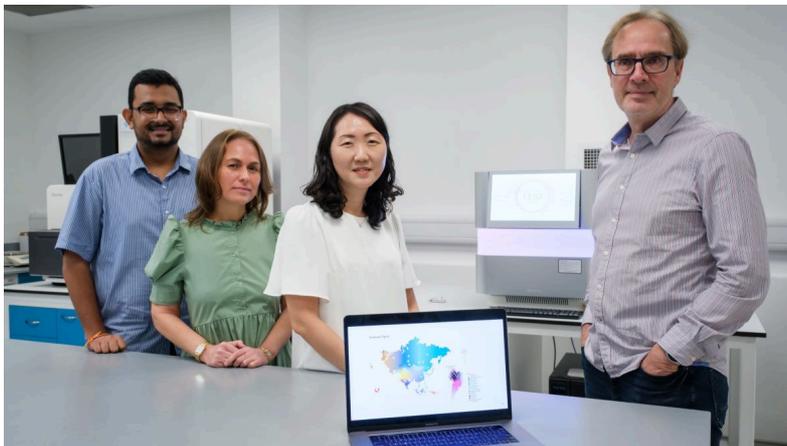
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A new genomics study has revealed that the longest migration of early humans was from Asia more than 100,000 years ago, covering more than 20,000km on foot.

The researchers say understanding this migration and modern genetic diversity can assist in developing better tools to deal with medicine and public health problems in modern populations.

The journey took the ancient people from North Asia across the ice bridge that once spanned the Bering Strait to North America, all the way down to the southern tip of South America. The trip would have taken thousands of years.



NTU and SCELSE researchers, comprising Research Fellow Dr Amit Gourav Ghosh, Senior Research Fellow Dr Elena S. Gusareva, Assoc Prof Kim Hie Lim, and Prof Stephan Schuster, with the advanced DNA sequencing machines in SCELSE. Credit: NTU Singapore.

The study, [published](#) in *Science*, is based on DNA sequencing of 1,537 modern human individuals from 139 different ethnic groups.

Comparing shared genetic traits and ancestry allowed the researchers to reconstruct the ancient journey, mapping out when different populations diverged.

One contentious result of the study is the finding that early humans made it to South America about 14,000 years ago. The arrival of humans to South America has been subject to [debate](#) for decades. Some studies suggest that human-made artefacts have been found in South America dating to [25,000 years ago](#).

If the new study is right, the artefacts must be younger than previously thought.

Once in South America, the genetic research shows that early human migrants split into 4 major populations: a group in the Amazon basin, others in the dry Chaco region in the east, some south to Patagonia's ice fields, and others in the valleys of the Andes Mountains.

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The researchers also believe their findings help explain the genetic diversity of Asia which is higher than in other parts of the world, including those who settled in the Americas.

“Those migrants carried only a subset of the gene pool in their ancestral populations through their long journey,” says corresponding author Kim Hie Lim from the Nanyang Technological University (NTU), Singapore. “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.”

“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,” Kim adds.

“Our findings highlight the extraordinary adaptability of early, diverse indigenous groups who successfully settled in vastly different environments,” says first author Elena Gusareva from the Singapore Centre for Environmental Life Sciences Engineering (SCELSE). “Using high-resolution whole-genome sequencing technology at SCELSE, we can now uncover the deep history of human migration and the genetic footprints left behind by the early settlers.”

“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,” says senior author Stephan Schuster from NTU. “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.”

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