

Early Asians travelled over 20,000km from North Asia to South America

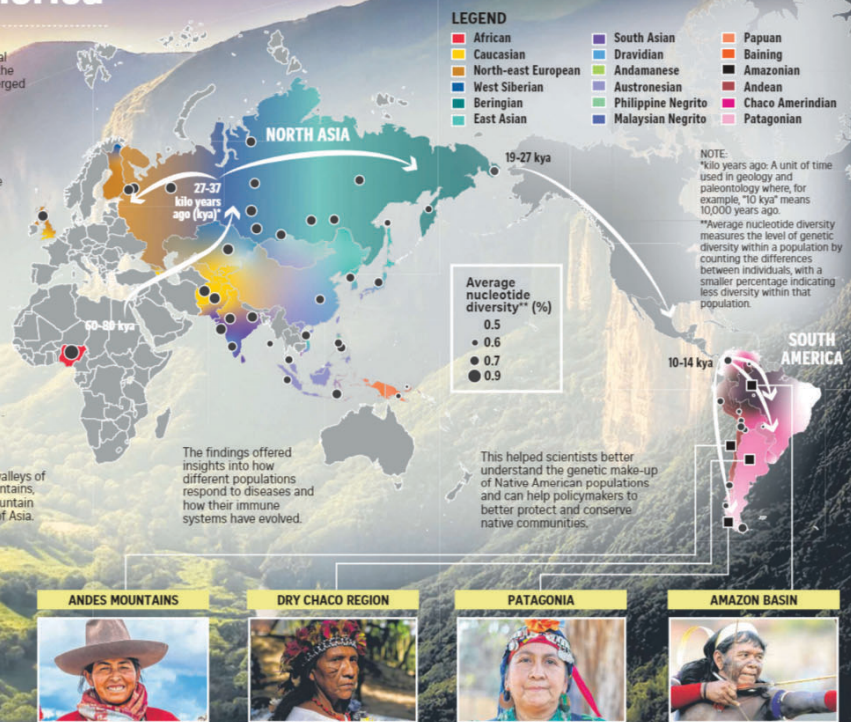
The researchers traced an ancient migratory journey that began in Africa, proceeded through North Asia and ended at Tierra del Fuego in modern-day Argentina, which is considered the final boundary of human migration on earth.

These early migrants arrived at the north-western 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:

- 1 One group remained in the Amazon basin.
- 2 One moved eastwards to the Dry Chaco region.
- 3 One went southwards to Patagonia's ice fields.
- 4 Another group navigated the valleys of the Andes mountains, the highest mountain range outside of Asia.

An international genomics study led by NTU scientists found that Asians made the longest prehistoric migration on foot and shaped the genetic landscape in the Americas. It mapped, for the first time, the large genetic diversity of Asians, who make up more than half the world's population.



Source: NTU-SCELSE. PHOTOS: AFP, ISTOCKPHOTO, NTU-SCELSE, REUTERS, AI-GENERATED ILLUSTRATION, STRAITS TIMES GRAPHICS

Study finds early Asians made humanity's longest prehistoric migration

Journey shaped genetic landscape in the Americas; first time migration tracked via DNA

Judith Tan
Correspondent

What does a modern-day Mongolian or a Siberian have in common with a Quechua from Peru, living almost 20,000km away?

They share a lot in their DNA, in fact, according to scientists from the Singapore Centre for Environmental Life Sciences Engineering (SCELSE) at Nanyang Technologi-

cal University.

Early Asians walked more than 20,000km from North Asia to South America, making the Asian and the South American closely related as the journey shaped the genetic landscape in the Americas from as far back as 14,000 years ago.

Known as humanity's longest prehistoric migration, the journey would have taken multiple generations of humans thousands of years.

It started from Asia to Beringia, a land bridge connecting Siberia and Alaska during the ice age, and crossing into South America through the Isthmus of Panama and eventually settling in Patago-

nia in Chile.

This is the first time migration has been tracked via DNA. Understanding such migration patterns can help explain differences in immune systems, said Associate Professor Kim Hie Lim from NTU's Asian School of the Environment.

The findings were published on May 16 in *Science*, a peer-reviewed academic journal of the American Association for the Advancement of Science and one of the world's top academic publications.

Prof Kim's team collaborated with a medical doctor from Japan, who had travelled to South America to collect blood samples from indigenous groups around 40 years ago, she said.

"It was from those samples that we took the DNA and sequenced (it)," she added.

The DNA sequence data of 1,537 individuals from 139 diverse ethnic groups was then analysed to help identify genetic markers related to certain diseases.

"The long migration resulted in the decline of genetic diversity (of four groups)," Prof Kim said.

One group settled in the high mountainous areas of the Andes, another in the Amazonian jungle, a third in the desert area in Chaco and the fourth in the frigid areas of Patagonia.

"If there is such a small immune genetic diversity, you may have (less adaptability) against emerging infectious diseases... If a population does not have the diversity, it can be easily wiped out by certain pathogens, emerging pathogens or unexposed pathogens. Such populations cannot survive," Prof Kim said.

She also highlighted the groups' genetic adaptation to extreme environments, pointing out how the genes of the people living in frigid areas adapted to their conditions with genetic variations related to the breakdown of fats and keeping warm. "Once outside the region, they would fall sick because they could not metabolise fat properly,"

she said.

Professor Stephan Schuster, scientific director of the GenomeAsia 100K consortium and senior author of the paper, said: "(It is) only after we know the entire genetic make-up of humanity that we can provide precision medicine that is specific to the needs of every ethnic group, in particular, those that have become endangered and are on the brink of going extinct."

The study was supported by the GenomeAsia 100K consortium, a non-profit group collaborating to sequence and analyse 100,000 Asian individuals' genomes to help accelerate medical advances and precision medicine specific to the Asian population.

With Russia being part of North Asia, SCELSE senior research fellow Elena Gusareva said there was a large collection of genomes in Tomsk, one of the oldest cities in Siberia.

"Knowing that we are working for future generations, people in Tomsk were very interested and very keen to work on the research," she added.

According to Prof Schuster, Asians make up more than 50 per cent of mankind, yet when it comes to big projects, Asian representation "is only 2 per cent to 6 per cent of the total participants".

"The GenomeAsia 100K study is like the equivalent of the Rosetta Stone for human population sequencing projects, uncovering an unprecedented genetic diversity that we did not know of when we started the project," he said.

The Rosetta Stone is a large stone tablet discovered in Egypt in 1799 that allowed researchers to translate ancient Egyptian hieroglyphic writing for the first time.

Yet, in some instances, people are worried about whether it is ethical to carry out such a DNA sequencing project if, for example, DNA was taken without permission.

"We have very good and strong protocols in place, and we are operating under... an institutional review board that sets the rules to protect the participants and researchers undertaking the research. Despite what some activists believe - that these groups need to be protected - many of these ethnic groups want to be known and represented in a global project," Prof Schuster said.

Apart from offering insights into how different populations respond to diseases and how their immune systems have evolved, the findings also help policymakers better protect and conserve native communities.

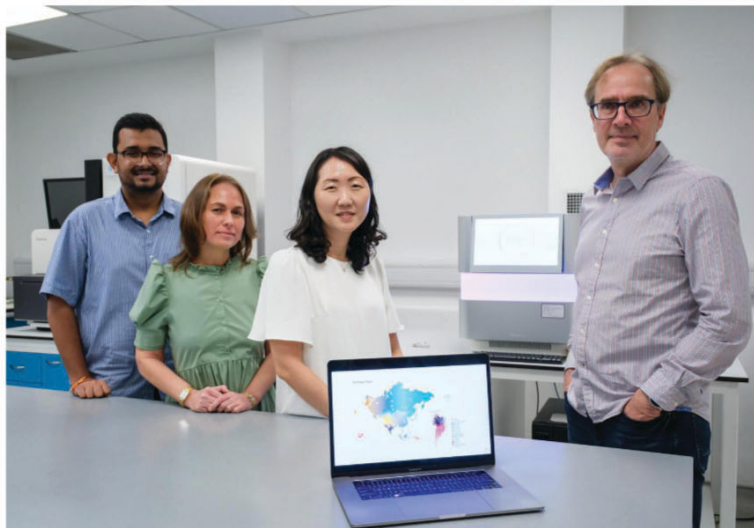
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MORE VULNERABLE TO DISEASES

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ASSOCIATE PROFESSOR KIM HIE LIM, from NTU's Asian School of the Environment.



(From left) Research fellow Amit Gourav Ghosh, senior research fellow Elena Gusareva, Associate Professor Kim Hie Lim and Professor Stephan Schuster from the NTU team who used DNA to track humanity's longest prehistoric migration. PHOTO: NTU