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FEATURES

Study traces 20,000km prehistoric migration linking Asians and South Americans

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SINGAPORE – A historic DNA study has uncovered strong genetic links between modern-day Asians and indigenous South American groups, shedding new light on humanity's longest-known prehistoric migration spanning over 20,000 kilometres.

The findings, led by researchers from the Singapore Centre for Environmental Life Sciences Engineering (SCELSE) at Nanyang Technological University (NTU), show that early Asians – including those from regions like Mongolia and Siberia – are genetically connected to South American populations such as the Quechua of Peru.

The research traced a prehistoric migration route that began in North Asia during the Ice Age, where ancient humans crossed the now-submerged Beringia land bridge into Alaska. They continued through the Isthmus of Panama before finally settling in southern Chile's Patagonia region – a journey that unfolded over thousands of years and multiple generations.

First DNA evidence of migration

Published in the prestigious journal *Science* on May 16, the study marks the first time this ancient migration has been mapped using DNA.

"Understanding how ancient populations moved and settled not only helps us understand human history, but also explains how their immune systems adapted to different environments," said Associate Professor Kim Hie Lim of NTU's Asian School of the Environment.

(From left) Research fellows Amit Gourav Ghosh and Elena Gusareva, Associate Professor Kim Hie Lim and Professor Stephan Schuster from the team that used DNA to track humanity's longest prehistoric migration. PHOTO: ANN via NANYANG TECHNOLOGICAL UNIVERSITY/THE STRAITS TIMES

The study was made possible through decades-old blood samples collected from South American indigenous groups by a Japanese medical doctor more than 40 years ago. DNA was extracted and sequenced from these samples, alongside genetic data from 1,537 individuals across 139 ethnic groups.

Implications for immune systems and disease resistance

The data revealed that the long migration led to a decrease in genetic diversity among four groups that settled in distinct regions – the Andes mountains, Amazon rainforest, Chaco desert, and icy Patagonia.

“This reduced genetic variation can have serious implications for disease resistance,” said Prof Kim. “Populations with low immune gene diversity are less equipped to fight emerging diseases and may be more vulnerable to extinction.”

Researchers also observed how certain groups genetically adapted to extreme climates. For example, inhabitants of cold regions developed genetic traits related to fat metabolism and thermoregulation. “If they move out of their native environment, their bodies may struggle to function properly,” Prof Kim added.

Advancing precision medicine in Asia

The study is part of the GenomeAsia 100K project, a non-profit consortium aiming to sequence 100,000 Asian genomes to promote medical research tailored to Asian populations.

Professor Stephan Schuster, senior author of the study and scientific director of GenomeAsia 100K, stressed the need for inclusive research. “Asians make up over 50 per cent of the global population, yet they are vastly under-represented in genomic studies,” he said.

“This project is like the Rosetta Stone of human DNA – unlocking new insights into our shared ancestry and supporting future breakthroughs in personalised medicine, especially for endangered or overlooked ethnic groups.”

Ethical safeguards in genetic research

Addressing concerns over the ethical collection of DNA, Prof Schuster noted that the study adhered strictly to international review protocols. “While some critics claim these communities need protection, many indigenous groups were eager to participate and be recognised in global scientific efforts.”

Policy and conservation benefits

Beyond medicine, the research also has implications for preserving indigenous communities. By understanding how specific populations are genetically vulnerable or adapted, governments and organisations can better protect their health and cultural heritage.

The study underscores the deep, genetic connections shared across continents – and highlights the importance of representing Asian populations in global scientific conversations.

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