

First published in [BBC News](#)



An international scientific effort has revealed the genetics behind Asia's diversity.

The Human Genome Organisation's (HUGO) Pan-Asian SNP Consortium carried out a study of almost 2,000 people across the continent.

Their findings support the hypothesis that Asia was populated primarily through a single migration event from the south.

The researchers described their findings in the journal [Science](#).

They found genetic similarities between populations throughout Asia and an increase in genetic diversity from northern to southern latitudes.

The team screened genetic samples from 73 Asian populations for more than 50,000 single-nucleotide polymorphisms (SNPs).

These are variations in pieces of the DNA code, which can be compared to find out how closely related two individuals are genetically.

The study found that, as expected, individuals who were from the same region, or who shared a common language also had a great deal in common genetically.

But it also answered a question about the origin of Asia's population. It showed that the continent was likely populated primarily through a single migration event from the south.

Previously, there has been some debate about whether Asia was populated in two waves - one to South East Asia, and a later one to central and north-east Asia, or whether only a single migration occurred.

Diversity explained

Edison Liu from the Genome Institute of Singapore was a leading member of the consortium.

He explained that the age of a population has a much bigger effect on genetic diversity than the population size.

"It seems likely from our data that they entered South East Asia first - making these populations older [and therefore more diverse]," he said.

"[It continued] later and probably more slowly to the north, with diversity being lost along the way in these 'younger' populations.

"So although the Chinese population is very large, it has less variation than the smaller number of individuals living in South East Asia, because the Chinese expansion occurred very recently, following the development of rice agriculture - within only the last 10,000 years."

Dr Liu said that it was "good news" that populations throughout Asia are genetically similar.

This knowledge will aid future genetic studies in the continent and help in the design of medicines to treat diseases that Asian populations might be at a higher risk of.

And the discovery of this common genetic heritage, he added, was a "reassuring social message", that "robbed racism of much biological support".

Shuhua Xu from the Chinese Academy of Sciences, who was a member of the consortium, said that this was "the first comprehensive study of genetic diversity and history of Asian populations".

"This is the first study to give a clear answer to the question on the origin of East Asian populations," Dr Xu added.

Vincent Macaulay, a statistical geneticist at the University of Glasgow in the UK told Science magazine that the team had produced "a fabulous data set".

The evidence for the southern coastal migration route, he said seemed "very strong".

The consortium involved 90 scientists from 11 countries including China, India, Indonesia, Japan, Korea, Malaysia, Philippines, Singapore, Taiwan, Thailand and the US.

Peter Underhill, a geneticist from Stanford University who was not involved in this study said that it represented an investment of a "tremendous amount of time, work and inter-institution collaboration".

He told BBC News: "This provides another important piece to the jigsaw puzzle of global human diversity."