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Asians have at least 10 ancestral lineages, northern Europeans just one: NTU-hosted genetic study

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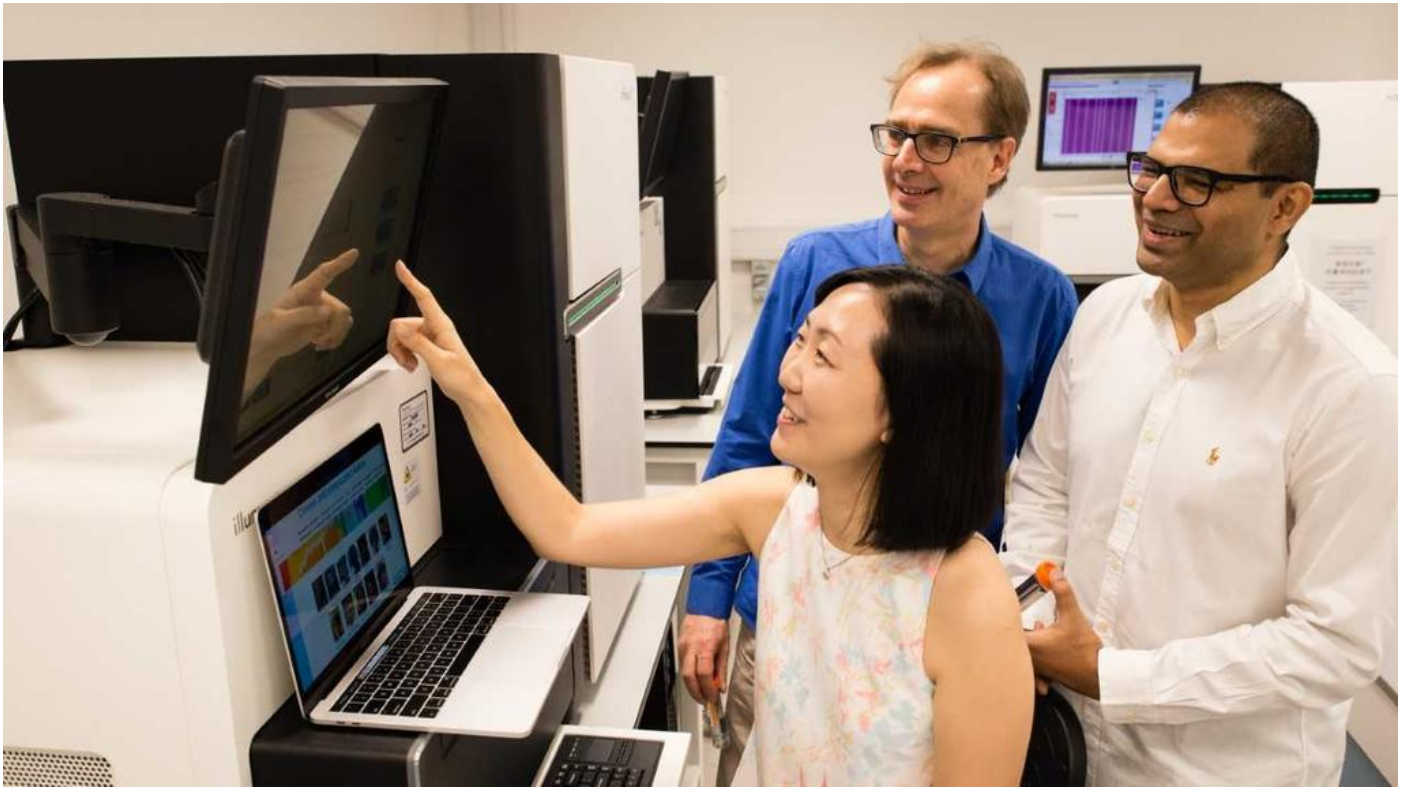

NTU

(L-R) NTU Asst Prof Kim Hie Lim, GenomeAsia 100K scientific chairman and NTU Professor Stephan Schuster and executive chairman of GenomeAsia 100K Mr Mahesh Pratapneni.

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SINGAPORE — A ground-breaking genetic study has found that Asians, who form over 40 per cent of the world's population, can be traced to at least 10 different ancestral groups or lineages. In contrast, northern Europeans can be grouped into just one.

Despite this broad diversity, Asians are hugely under-represented in human genetic studies, accounting for only 6 per cent of the world's recorded genome sequences previously. Broadly speaking, a genome is a genetic code containing all of an organism's hereditary information.

This research gap is now being plugged by the GenomeAsia 100K project, a pilot study that aims to better understand the genome diversity of Asian ethnicities by sequencing 100,000 genomes of people living in Asia.

A non-profit global consortium, hosted by Nanyang Technological University (NTU), is conducting the project. It also comprises: United States and Indian genetic diagnostics company MedGenome, US biotechnology corporation Genentech and South Korean precision medical and biotechnology firm Macrogen. The National Supercomputing Centre Singapore (NSCC) helped analyse the data.

The initial findings of the ongoing study, which started in 2016, were published as the cover paper for the scientific journal Nature on Thursday (Dec 5), and are based on an analysis of the genomes of 1,739 people of 219 population groups and 64 countries across Asia.

The researchers involved in the project said in a press release issued by NTU on Thursday that their findings represent not only the widest coverage of genetic diversity in Asia to date, but are also the continent's first comprehensive genetic map.

WHAT IS A GENOME?

According to the National Human Genome Research Institute (NHGRI), the genome represents an organism's complete set of Deoxyribonucleic acid (DNA).

For the genomes of any two people, 99.9 per cent of this code is the same, the NTU media statement said.

On average, the remaining 0.1 per cent, or three million nucleotides, are different between the two people, it added.

"This genetic variance helps humankind colonise the most diverse environments on the planet and makes it resilient to disease," it said. "But it also results in a differential response to many medicines."

To better understand this variance among Asians, the study included genomes from several countries including India, Malaysia, South Korea, Papua New Guinea and Russia.

NTU's Assistant Professor Kim Hie Lim, who is leading the project's efforts in population genetics, told TODAY that no samples were taken from Singapore as there is a separate group doing a similar study to create Singapore's first genetic databank.

TODAY previously reported in October that a team from the Genome Institute of Singapore of the Agency for Science, Technology and Research (A*Star) collected the blood samples of close to 5,000 Singaporeans — 2,780 Chinese, 903 Malays and 1,127 Indians.

WHY IS IT IMPORTANT?

Asst Prof Kim, who specialises in population genomic analyses at NTU's Asian School of the Environment, said genome sequencing helps to not only reveal a person's ancestry, but his genetic background too

“Doctors commonly always ask: ‘Do you have any drug allergies?’” she said. “But you won’t know till you actually use it.”

She noted that different groups could be harmed by a particular medication.

For instance, she said that people with a North Asian ancestry – such as Japanese, Korean, Mongolian or Chinese – have a higher than usual risk of an adverse response to the drug Warfarin, which is a common anticoagulant drug prescribed to treat cardiovascular diseases.

As the database of information on Asian genomes grows, Asst Prof Kim said it will provide a useful reference for medical researchers to create the right medicine for different groups of people.

The next phase of the study will involve sequencing patients with “known diseases”, she said, though the specifics of which diseases they will focus on are still under discussion.

Regardless, she said the research will allow scientists to have a better understanding of what causes the diseases, and how to treat them.