

First 'genetic map' of Han Chinese may aid search for disease susceptibility genes

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The first genetic historical map of the Han Chinese, the largest ethnic population in the world, as they migrated from south to north over evolutionary time. was published online today by the *American Journal of Human Genetics* by scientists at the Genome Institute of Singapore (GIS).

Based on genome-wide DNA variation information in over 6,000 Han Chinese samples from 10 provinces in [China](#), this new map provides information about the population structure and evolutionary history of this group of people that can help scientists to identify subtle differences in the genetic diversity of Asian populations.

Understanding these differences may aid in the design and interpretation of studies to identify genes that confer susceptibility to such [common diseases](#) as diabetes in ethnic Chinese individuals. Understanding these differences also is crucial in exploring how genes and environment interact to cause diseases.

With the genetic map, the GIS scientists were able to show that the northern inhabitants of China were genetically distinguishable from those in the south, a finding that seems very consistent with the Han Chinese's historical migration pattern.

The genetic map also revealed that the genetic divergence was closely correlated with the geographic map of China. This finding suggests the persistence of local co-ancestry in the country.

"The genome-wide [genetic variation](#) study is a powerful tool which may be used to infer a person's ancestral origin and to study population relationships," said Liu Jianjun, Ph.D., GIS [Human Genetics](#) Group Leader.

"For example, an ethnic Chinese born and bred in Singapore can still be traced back to his or her ancestral roots in China," Dr. Liu said. "By investigating the genome-wide [DNA variation](#), we can determine whether an anonymous person is a Chinese, what the ancestral origin of this person in China may be, and sometimes which dialect group of the Han Chinese this person may belong to.

"More importantly, our study provides information for a better design of genetic studies in the search for genes that confer susceptibility to various diseases," he added.

Of particular interest to people in Singapore are the findings that while the majority of Singaporean Chinese hail from Southern China as expected, some have a more northern ancestral origin.

GIS Executive Director Edison Liu, M.D., said, "Genome association studies have provided significant insights into the genes involved in common disorders such as diabetes, high cholesterol, allergies, and neurological disorders, but most of this work has been done on Caucasian populations.

"More recently, Dr. Liu Jianjun from our institute has been working with his Chinese colleagues to define the genetic causes of some of these diseases in Asian populations," the GIS Executive Director added. "This work refined those tools so that the results will not be obscured by subtle differences in the genetic diversity of Asian populations. In the process, Dr. Liu has reconstructed a genetic historical map of the Chinese people as they migrated from south to north over evolutionary time."

"There are definite differences in genetic architecture between populations," noted Chia Kee Seng, M.D., Head, Department of Epidemiology & Public Health, National University of Singapore (NUS), and Director, NUS-GIS Centre for Molecular Epidemiology.

"We have seen this in the Singapore Genome Variation Project, a Joint NUH-GIS effort. Understanding these differences is crucial in exploring how genes and environment interact to cause diseases," he added.

The research results published in [American Journal of Human Genetics](#) is part of a larger ongoing project on the genome-wide association study of diseases among the Chinese population. The project is a collaboration between GIS and several institutions and universities in China.

In Jan. 2009, *Nature Genetics* published the findings of researchers at the GIS and Anhui Medical University, China, on psoriasis, a common chronic skin disease. In that study, led by Dr. Liu Jianjun at the GIS and Dr. Zhang Xuejun at the Anhui Medical University, the scientists discovered a genetic variant that provides protection against the development of psoriasis. The collaboration's recent discovery of over a dozen genetic risk variants for systematic lupus erythematosus (SLE) in the Chinese population was published in *Nature Genetics* in Oct. 2009.

Source: Agency for Science, Technology and Research (A*STAR)

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