

For Immediate Release

Scientific consortium maps the range of genetic diversity in Asia, and traces the genetic origins of Asian populations

Several genome-wide studies of human genetic diversity have been conducted on European populations. Now, for the first time, over 90 scientists from the Human Genome Organisation's (HUGO's) Pan-Asian SNP Consortium have extended this study to 73 Southeast Asian (SEA) and East Asian (EA) populations. This human genetic mapping of Asia has important implications, especially in the further understanding of migratory patterns in human history, and for the study of genetics and diseases. The findings were published online in a report in **Science** on 10 December 2009.

The study, conducted within and between the different populations in the Asia continent, showed that genetic ancestry was highly correlated with ethnic and linguistic groups. There was a clear increase in genetic diversity from northern to southern latitudes. The study also suggested that there was one major inflow of human migration into Asia arising from Southeast Asia, rather than multiple inflows from both southern and northern routes as proposed before. This indicates that Southeast Asia was the major geographic source of East Asian and North Asian populations (see accompanying picture). Moreover, the geographical and linguistic basis of genetic subgroups in Asia clarifies the need for genetic stratification when conducting genetic and pharmacogenomic studies in this continent.

One of the corresponding authors, Professor Edison Liu, Executive Director at the Genome Institute of Singapore (GIS), and the President of the HUGO which initiated and coordinated this research, said, "This study was a milestone not only in the science that emerged, but the consortium that was formed. 10 Asian countries came together in the spirit of solidarity to understand how we were related as a people, and

we finished with a truly Asian scientific community. We overcame shortage of funds and diverse operational constraints through partnerships, good will, and cultural sensitivity.”

Professor Liu also added that, “Affymetrix, led by Dr. Giulia C. Kennedy and based in the US, is our primary technology partner in this endeavour. We greatly appreciate their support. Our next goal is to expand this collaboration to all of Asia including Central Asia and the Polynesian Islands. We also aim to be more detailed in our genomic analysis and plan to include structural variations, as well as over a million single nucleotide polymorphisms in the next analysis.”

Professor Suthat Fucharoen, Thalassemia Research Center, Institute of Molecular Biosciences, Mahidol University, Thailand said “this project reflects a spirit of the scientific co-operation of colleagues in the region. This is beyond the limitation of politics and economic constrain of member countries. All of this will lead to the betterment of mankind in the future.”

Also from Thailand, Assoc. Prof. Daoroong Kangwanpong, Genetic Diversity Research Unit, Chiang Mai University said “the genetic admixture among the geographical and linguistic closely related subgroup, as well as along their migration routes, should not be ignored in the next phase of the consortium, if the polygenic disease and pharmacogenomic studies are to be conducted in the Asia continent”.

The Thai research team led by Prof. Suthat Fucharoen, Assoc. Prof. Prasit Palittapongarnpim, Assoc. Prof. Daoroong Kangwanpong, and Dr. Sissades Tongsima were responsible for the tasks of DNA sample collections from thirteen hill tribes in northern Thailand, DNA extraction, and data analysis. To facilitate the human resource development of young researchers in Thailand, some post graduate students from Chiang Mai University were selected to join their Singapore counterparts at the Genome Institute of Singapore during the DNA extraction process. The experience provided the opportunity for the students to learn new approaches to DNA extraction and also build research network.

Notes to the Editor:

Research publication:

The research findings described in the press release can be found in a report in the December 10, 2009 online issue of **Science** under the title “**Mapping Human Genetic Diversity in Asia**”.

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About the Human Genome Organization

www.hugo-international.org

Human Genome Organisation (HUGO) is an international organisation formally established in 1988 to foster collaboration between genome scientists around the world. It is entering the 20th year of its history by making an inflection in its direction. Now that the human genome has been sequenced, we are seeking the biological meaning of its information content. To this end, it is focusing on the medical implications of genomic knowledge. Moving forward, HUGO is also working to enhance the genomic capabilities in the emerging countries of the world. The excitement and interest in genomic sciences in Asia, Middle East, South America, and Africa are palpable and the hope is that these technologies will help in national development and health.

The HUGO Pan Asian SNP Consortium began in 2004 when a group of like-minded geneticists and genomicists from Asia decided to develop a collaborative programme to address the genetic architecture of Asian populations. The consortium was unique in the breadth and depth of involvement of Asian genetics communities and the engagement of so many Asian populations in the analysis.

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