techman / May 21, 2011 09:52AM

[International Participation][BioMedical] Genetic Variants Associated with Blood Pressure Identified in East Asians

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Academia Sinica Newsletter (2011/05/20) The Asian Genetic Epidemiology Network Blood Pressure consortium, including four researchers from Academia Sinica, Academician and Distinguished Research Fellow Yuan-Tsong CHEN, Director of the National Center for Genome Medicine Jer-Yuarn WU, Assistant Research Scientist of the National Genotyping Center Chien-Hsiun CHEN and Research Assistant of the Institute of Biomedical Sciences Li-Ching CHANG, as well as 45 researchers from Japan, Korea, China, Singapore, and the United States, have recently identified five previously unknown genetic variants that influence blood pressure among populations of East Asian ancestry. The findings were published online in the journal Nature Genetics on May 15, 2011.

The group conducted three different types of studies to draw their conclusions: a meta-analysis of genome-wide association studies of systolic and diastolic blood pressure in 19,608 individuals of East Asian ancestry; de novo genotyping of top loci in 10,518 individuals; and replication in 20,247 independent East Asian samples.

The group identified five new "loci" (gene locations) that influence blood pressure among populations of East Asian ancestry. The strongest association was found at the locus 12q24.13. These findings provide new insights into blood pressure regulation for intervention in East Asian populations. The findings also suggest that the association between common genetic variants and blood pressure may vary among populations with differing ancestry. Up until now, most research into the genetic associations with blood pressure had been conducted in populations of European descent. The significant loci uncovered in this study demand further investigation and may be used to aid development of drugs for blood-pressure related conditions.

The Asian Genetic Epidemiology Network is a consortium which conducts genetic epidemiology studies of cardiovascular disease and related conditions such as blood pressure (or hypertension), diabetes and obesity in Asian populations. The Asian Genetic Epidemiology Network blood pressure data was collected from 19,608 individuals of East Asian descent who underwent standardized collection of blood pressure measurements in eight population- and family-based genome-wide association studies including: the Cardio-metabolic Genome Epidemiology (CAGE) Network, Genetic Epidemiology Network of Salt-Sensitivity (GenSalt), Korean Association Resource (KARE) Project, Shanghai Hypertension Study, Singapore Malay Eye Survey (SiMES), Singapore Prospective Study (SP2) Program, Suita Study, and Taiwan Super Control Study.

The whole article entitled "Meta-analysis of genome-wide association studies identifies common variants associated with blood pressure variation in east Asians" can be found online at the Nature Genetics website at:
http://www.nature.com/ng/journal/vaop/ncurrent/full/ng.834.html

Related Website:
http://agenconsortium.org/

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Reference:
Academia Sinica Newsletter 2011/05/20

National Science Council International Cooperation Sci-Tech Newsbrief
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Edited 1 time(s). Last edit at 05/21/2011 09:57AM by techman.