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Taiwan Scientists Published Results in *NATURE-Genetics* on Chromosome Regions Linked to Kawasaki Disease

Hsinchu, April 11, 2012. Researchers from the Institute of Biomedical Sciences (IBMS), Academia Sinica, National Tsing Hua University, along with 15 physicians from 8 hospitals around Taiwan have identified two new chromosomal regions (susceptibility loci) that could predispose individuals to Kawasaki disease.

This important achievement, which leads to a better understanding of immune and inflammation activation in Kawasaki disease, was published in the leading genetics journal *Nature Genetics* on March 25, 2012.

According to the first author of the paper, Assistant Professor Yi-Ching Lee who joined the Institute of Molecular Medicine, National Tsing Hua University in August of 2011, “*Kawasaki disease is an acute, self-limiting vasculitis (disease that centers around inflammation of blood vessels) that affects infants and young children under 5 years old.*”

Professor Lee further elaborated that *“The cause of Kawasaki disease is currently unknown. Symptoms include prolonged fever, skin rash, swollen glands, red eyes, mouth inflammation, and swollen hands and feet. Kawasaki disease can be hard to diagnose, because there is not a test for it. Coronary aneurysms develop in 15%–25% of untreated Kawasaki disease children, and it is the leading cause of acquired heart disease among children in industrialized countries. Treatment of Kawasaki disease in the acute phase is directed at reducing inflammation in the coronary artery wall and preventing coronary thrombosis through intravenous administration of high doses of immunoglobulin.”*

Genetic determinants have been suggested to contribute to susceptibility to Kawasaki disease among children. Asian countries have higher incidences of Kawasaki disease than Western countries; Japan has the highest annual incidence, followed by Korea and Taiwan. The annual incidence in Taiwan was 69 cases per 100,000 children under 5 years old age. Although the cause of Kawasaki disease is unknown, clinical and epidemiological findings suggest that in genetically predisposed individuals an infectious agent triggers an inflammatory response which leads to host immune dysregulation.

To find novel candidate loci that could predispose individuals to Kawasaki disease, a genome-wide association study led by Drs. Jer-Yuarn Wu, Fuu-Jen Tsai and Yuan-Tsong Chen, and managed by Dr. Yi-Ching Lee was conducted at the Institute of Biomedical Science in Academia Sinica in collaboration with hospitals around Taiwan. The study involved 622 Kawasaki disease patients and 1,107 controls from a Han Chinese population residing in Taiwan, and replicated in an independent Han Chinese cohort of 261 cases and 550 controls. The gene encoding for the B lymphoid tyrosine kinase (BLK) is contained in one of the loci identified and the gene encoding for the CD40 is contained in second loci. Both candidate loci are known to be involved in immune and inflammatory responses.

Dr. Lee managed the study during the period when she worked as a group leader of SNP genotyping by Sequenom at National Center for Genome Medicine, Institute of Biomedical Sciences, Academia Sinica, from November 2006 to July 2011. After joining National Tsing Hua

University, Dr. Lee continued working on the project. She communicated with the collaborated doctors involved in the patient recruitment and gave progress reports in the regularly meetings of Taiwan Pediatric ID Alliance. She organized and supervised the GWAS and replication genotyping pipeline and devised the overall analysis plan, analyzed the data, produced the figures and tables, wrote the manuscript, submitted the manuscript, replied to reviewers' comments, and revised the manuscript.

“The findings of the study may lead to a better understanding of immune and inflammation activation in Kawasaki disease, and also suggest potential diagnostic and treatment strategies for Kawasaki disease,” concluded Dr. Lee

The article entitled: **“Two new susceptibility loci for Kawasaki disease identified through genome-wide association analysis”** can be found at the Nature Genetics website at:

<http://www.nature.com/ng/journal/vaop/ncurrent/full/ng.2227.html>

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