New genetic study sheds light on serious childhood disease

January 9 2009

Genetic variations that can predispose children to a serious disease that damages the heart have been identified in a genome-wide association study of Kawasaki Disease, published today in *PLoS Genetics*.

The disease, the cause of which is currently unknown, is a rare and severe childhood disorder that occurs mainly in young children. It is the most common cause of childhood acquired heart disease in developed countries.

The disease is more common in Japanese children and those of Asian descent, but it is found in all ethnic groups, affecting around 1 in 10,000 children of Caucasian descent.

The new study identifies variations in 31 genes which appear to increase a child's risk of developing Kawasaki Disease.

The findings will enable scientists to develop more effective ways of tackling the disease, by revealing new targets for treatment, say the researchers, from Imperial College London, the University of Western Australia, the Genome Institute of Singapore, Emma Childrens Hospital, Netherlands, and the University of San Diego California.

Some of the variations identified appear in genes that work together to control signalling between immune cells and heart cells. The researchers are planning to carry out further work to understand how these mutations contribute to the disease.

Epidemiological studies suggest that Kawasaki Disease is triggered by an as yet unidentified infection. It is currently treated using pooled antibodies from healthy donors. This treatment shortens the period of illness and most children recover after two to three weeks. It reduces but does not eliminate the risk of heart disease.

Professor Michael Levin, one of the authors of the study from the Department of Paediatrics at Imperial College London said: "Sadly, all the hospitals in the UK frequently see children with Kawasaki Disease. A child whose coronary arteries are damaged in early childhood faces a lifetime of uncertainty and risk, and we desperately need better treatments to prevent long term heart problems in those affected. We hope our new study will help us to reach this goal."

Dr Victoria Wright, another author of the study from the Department of Paediatrics at Imperial College London said: "Kawasaki Disease was identified less than fifty years ago so it is a relatively new disease. We still have a long way to go with this research but this is an important step in understanding the disease better."

For the new study, the international consortium combined their patients to perform a genome-wide association study in 119 Caucasian KD cases and 135 matched controls from Australia, Holland, USA and the UK. They looked at 250000 genetic variants in each patient and uncovered the most significant genes that appeared to be involved in Kawasaki Disease. They then replicated this in an independent cohort of a total of 893 KD cases plus population and family controls.

The researchers are now planning to analyse an Asian cohort of people with Kawasaki Disease, to see if their results can be replicated in this population.

Source: Imperial College London