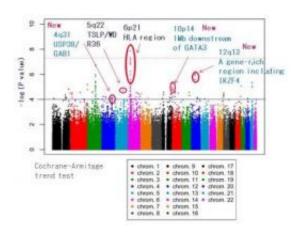


Genome-wide study reveals 3 new susceptibility loci for adult asthma in Japanese population

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This chart shows the results of a genome-wide association study on adult asthma (1,532 patients, 3,304 controls) Credit: RIKEN

Researchers at the RIKEN Center for Genomic Medicine (CGM), together with colleagues at Kyoto University, Tsukuba University, Harvard University, and other medical institutions have identified three new loci associated with susceptibility to adult asthma in the Japanese population. The findings appear in *Nature Genetics* and derive from a genome-wide study of 4836 Japanese individuals.

Around the world, hundreds of millions of people suffer from bronchial asthma, a <u>chronic inflammatory disease</u> characterized by symptoms of



wheezing, shortness of breath and coughing. In adults, death caused by asthma is by far most prevalent among the elderly, with 90% of cases afflicting those aged 60 or older. Treatment techniques remain ineffective in severe cases, resulting in chronic suffering and a heavy economic burden for patients and their families.

To clarify the genetic origins of adult asthma, the research group conducted a genome-wide association study on 1532 adult patients and 3,304 controls. Among a total of roughly 460,000 genetic variants (called Single Nucleotide Polymorphisms or SNPs), the group identified five genetic regions associated with susceptibility to adult asthma, three of which had not previously been connected to the disease. The associations were confirmed in a separate replication study on a population of 5,639 patients and 24,608 controls.

The regions identified contain SNPs previously associated with the FEV1/FVC ratio, a calculated ratio crucial to the diagnosis of obstructive and restrictive diseases, as well as numerous genes that play a role in immunity response to infection and inflammation. One of these genes encodes the protein thymic stromal lymphopoietin (TSLP), which plays a critical role in sensing environmental agents and triggering immune response. The SNP in the region containing this gene was reproduced in a separate study on non-Hispanic individuals of European ancestry, suggesting that region may be a common hereditary factor for asthma across ethnic groups.

Together, the findings of this extensive study shed light on the genetic factors contributing to asthma susceptibility, pointing the way to more effective treatment techniques and a better future for millions of asthma sufferers around the world.

Provided by RIKEN



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