11 new genetic associations for asthma-with-hay fever

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23andMe has participated in the first ever genome-wide association study of the combined asthma-with-hay fever phenotype. Led by researchers at the QIMR Berghofer Medical Research Institute, the study identified 11 independent genetic markers associated with the development of asthma-with-hay fever, including two associations reaching a level of significance with allergic disease for the first time.

Previous research has shown that both asthma and hay fever share 50-90 percent of their genetic susceptibility and 20-50 percent of their environmental susceptibility. ([1,2]) 23andMe has collected information on both conditions through its asthma symptoms survey, and in this analysis used data contributed by 15,072 of its customers. Data was also collected from three additional studies conducted in Australia and the United Kingdom, with cases defined as persons who reported a physician diagnosis of asthma and also hay fever (total N=6,685). This group was compared to a control group of individuals who reported neither a diagnosis of asthma or hay fever (total N=14,091).

"While previous analyses provided evidence of a stronger genetic association of this combined phenotype, there has not been a genome-wide association study exploring the connection in further detail," said David Hinds, Ph.D., study author and 23andMe principal scientist, statistical genetics. "In this first-of-its-kind study, we've identified new genetic associations that can provide the means to identify people at risk for allergic disease with greater efficiency."

By considering the phenotype of asthma-with-hay fever, 11 independent variants with genome-wide significant associations with disease risk were identified, amongst which were variants in the 8q21 and 16p13 regions, which have now been established as containing genetic risk factors for allergic disease. The study also found that genetic risk factors for allergic disease are located in or near variants ZBTB10 and CLEC16A. Further investigations of the entities underlying both associations may help identify previously unrecognized pathways in the development of asthma and hay fever.

The study, titled "Genome-wide association analysis of the phenotype asthma-with-hay fever for 20,000 persons identified 11 risk loci, including variants near ZBTB10 and CLEC16A" was published on January 2, 2014 in the *Journal of Allergy and Clinical Immunology*.

More information: www.jacionline.org/article/S00… (13)01643-6/fulltext

Related:

1. Duffy DL, Martin NG, Battistutta D, Hopper JL, Mathews JD. Genetics of asthma and hay fever in Australian twins. Am Rev Respir Dis 1990; 142:1351-8.

2. Thomsen SF, Ulrik CS, Kyvik KO, Ferreira MA, Backer V. Multivariate genetic analysis of atopy phenotypes in a selected sample of twins. Clin Exp Allergy 2006; 36: 1382-90.

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