Sixteen new genetic regions for allergies discovered

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(Medical Xpress)—In two of the largest genetic studies ever conducted on common allergies, including pollen, dust-mite and cat allergies, 16 new genetic regions related to the condition have been discovered. Together they are responsible for at least 25 per cent of allergy in the population. Eight of the genetic variations have previously been associated with asthma. The discoveries, published today in *Nature Genetics*, are a major step towards understanding the biological basis of common allergies.

Allergies are very common. According to Allergy UK, around 21 million adults in the UK suffer from at least one allergy. The numbers are increasing every year and, in the UK, it is estimated that 50 per cent of

all children are diagnosed with an allergic condition.

The first study, undertaken by the Early Genetics and Lifecourse Epidemiology research cohort (EAGLE), which includes Children of the 90s (ALSPAC) at the University of Bristol, involved almost 32,000 individuals from 16 studies worldwide.

The EAGLE study was conducted in two stages. The first compared 5,809 allergy sufferers with 9,875 non-allergy sufferers (controls). Allergy was assessed objectively by measuring allergen levels in blood or by a skin-prick test. The second phase replicated the study in 6,145 independent allergy sufferers and 10,137 controls.

Ten of the genetic locations were associated with self-reported allergy symptoms in an independent companion study of 53,000 individuals conducted by 23andMe, the American personal genetics company, and Children of the 90s.

Professor John Henderson from Children of the 90s, who was involved in the EAGLE study, said: "Allergy is an important component of many diseases, including asthma, eczema and hay fever, which together account for a huge burden on patients and the health services. This is a very exciting time for allergy research. Genetic discoveries have identified specific pathways of allergy development that are not shared with allergic diseases like asthma. Understanding these pathways could lead to eventual development of drugs that cure or prevent allergy rather than just suppressing its symptoms."

Dr David Hinds, 23andMe principal scientist who was involved in the 23andMe study said: "We've seen some substantial increases in prevalence of allergies and asthma. Although environmental factors certainly play a role, our study reinforces the genetic link between common allergens and a person's susceptibility to experiencing an

allergic reaction.

"Additionally, current estimates of the heritability of allergies are high, which suggests that understanding the genetic factors underlying allergic conditions may be key to understanding who might be most likely to suffer from allergies and how the condition might best be treated."

Dr Nic Timpson from Children of the 90s, who was involved in both studies, added: "One of the key features of this work is the demonstration that with a suitably sized study, the analysis of medically relevant questionnaire data alongside genetic variation has the potential to yield important information concerning the underlying biology of a complex outcome.

"Indeed, through a collaborative interaction with colleagues from EAGLE where specific tests of allergic sensitization were available, we were able to independently replicate many of the findings made here."

The papers, Klaus Bønnelykke et al, 'Meta-analysis of genome-wide association studies identifies 10 loci influencing allergic sensitization', doi 10.1038/ng.2694 and David A Hinds et al, 'A genome-wide association meta-analysis of self-reported allergy identifies shared and allergy-specific susceptibility loci', doi:10.1038/ng.2686 will be published online in *Nature Genetics* on 30 June 2013.

More information: dx.doi.org/10.1038/ng.2686
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