

Childhood asthma explained with gene mapping

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An international research team, including researchers from Karolinska Institutet, Sweden, has found six gene variants that can explain nearly 40 percent of all cases of asthma in children. The findings, presented in top-ranked New England Journal of Medicine (NEJM), are based on a genetic survey of 10 365 asthmatics and 16 110 control subjects.

"As high as 40 percent in the influence of genetic factors is very unusual when compared to other common diseases", says Professor Goran Pershagen at the Institute of Environmental Medicine, Karolinska Institutet, who led the Swedish part of the study. "The identified genes are involved in communication of epithelial damage to the [adaptive immune system](#) and activation of airway inflammation."

From earlier research it is known that asthma is caused by an interaction between genetic factors, lifestyle and environmental exposures. In children, asthma is often associated with allergic sensitization, but the risk is significantly elevated if the disease affects the parents. Although a number of genes previously have been associated with asthma and allergy development, no sufficiently large study has been conducted to map the entire human genome identifying "asthma genes" among both adults and children. The present study is the first that can claim a comprehensive screening of the link between specific genes and risk of [asthma](#).

The study was conducted within the GABRIEL consortium and funded mainly by the European sixth framework program. Corresponding

author is Professor William Cookson at the Imperial College in London, UK. The Swedish data that was used in the study came from the BAMSE-study, containing more than 4000 [children](#) from Stockholm county area that were followed during a twelve-year period.

More information: Moffatt M.F., Gut I.G., Demenais F. et. al; A large-scale, consortium-based genome-wide association study of asthma, *NEJM*, online 22 September 2010

Provided by Karolinska Institutet

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