

Genetic influence on pulmonary function: Six further genes identified

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In an analysis of several genome-wide association studies, an international team of scientists has identified six novel gene regions that are associated with the function of the lungs. Their results have been published in the current issue of the *Nature Genetics* scientific journal.

In their investigations or so-called genome-wide association studies, the team of researchers compared the genetic profile of study [participants](#) to the forced vital capacity (FVC), a volume parameter of [lung function](#). Six gene loci here displayed a clear association with the FVC values. Involvement in [lung development](#) or certain pulmonary diseases is furthermore suspected for these genes.

Better understanding of the association between genes, lung function and lung diseases

The identified genes open up new molecular biological approaches for a better understanding of lung development and of the repair and remodelling processes during disease pathogenesis. "The results supply the foundation for detailed research into [lung diseases](#) and clarification of the association between genetics, lung function and susceptibility to respiratory disorders", reports Prof. Dr. Holger Schulz, head of the Pulmonary Epidemiology research group at the Helmholtz Zentrum München (HMGU). "Against the background of these findings, we can, for example identify possible risk groups and develop new therapeutic approaches", adds Dr. Christian Gieger (HMGU).

Comprehensive genome analysis: more than 85,000 participants from 35 studies

Under the direction of the National Institute of Environmental Health Sciences in the United States, the team of international scientists analyzed the data from a total of 85,170 participants from 35 study cohorts. Also included were participants in the German KORA cohort studies, which were evaluated by HMGU scientists. The Institutes of Epidemiology I and II (EPI I, EPI II), the Institute of Genetic Epidemiology (IGE) and the Comprehensive Pneumology Center (CPC) at the HMGU were involved.

More information: Loth, D. et al. (2014): Genome-wide association analysis identifies six new loci associated with forced vital capacity, *Nature Genetics* (2014). | [DOI: 10.1038/ng.3011](https://doi.org/10.1038/ng.3011)

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