

Research team defines genetic subtypes of asthma

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A Yale-led analysis of gene expression in asthma patients identified three major clusters of the disease. The finding could lead to a personalized approach to asthma management.

The study was published March 12 in the *American Journal of Respiratory Critical Care Medicine*.

Senior author Dr. Geoffrey Chupp, associate professor of medicine

(pulmonary) at Yale School of Medicine (YSM), and his team analyzed genes in the sputum and blood of children and adults with asthma. They identified three major genetic subtypes that they called transcriptomic endotypes of asthma, or "TEA" clusters. The clusters divide asthmatics into three subgroups—those at risk of having near-fatal asthma attacks, those with severe symptoms of the disease, and those with milder asthma. The TEA cluster to which a patient belongs can be identified with a blood test.

While more research is underway to confirm the findings, the study may help identify those individuals at risk for the most severe asthma attacks, such as those requiring hospitalizations. The findings could also lead to more personalized treatment and better outcomes.

More information: "Non-invasive Analysis of the Sputum Transcriptome Discriminates Clinical Phenotypes of Asthma." *Am J Respir Crit Care Med*. First published online 12 Mar 2015 as [DOI: 10.1164/rccm.201408-1440OC](https://doi.org/10.1164/rccm.201408-1440OC)

Provided by Yale University

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