

The nose knows in asthma

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It has become increasingly clear in recent years that asthma comes in several variations, with different causes, different pathologies and different responses to therapy. These subtypes of asthma can be identified by knowing which genes are expressed at higher and lower levels in patients' airways. That information can, in turn, help guide personalized treatment to more effectively manage asthma and inspire research to better understand, manage, and possibly prevent asthma.

The difficulty is that [tissue samples](#) necessary for this kind of genetic profiling are currently obtained from the airways, which requires bronchoscopy, an [invasive procedure](#) involving sedation. Concerns about safety, sedation, and expense limits the use of bronchoscopy, especially among children, and thus the asthmatic tissue samples needed for [genetic profiling](#)

Max Seibold, PhD, assistant professor of genetics at National Jewish Health, and his colleagues recently described a less invasive, less expensive and safer way to obtain genetic profiles of asthmatic patients. In the *Journal of Allergy and Clinical Immunology*, they recently demonstrated that genes expressed in the nasal passages can serve as accurate proxies for those expressed deeper in the airways. Tissue samples can be obtained from nasal passages with a small brush.

Dr. Seibold and his colleagues showed that gene expression in the nasal passages overlaps 90% with genes expressed in the lungs. The researchers were able to distinguish asthmatic from non-asthmatic patients based on genes expressed in the nasal passages. They were also

able to distinguish allergic [asthma](#) from non-[allergic asthma](#), and associate high levels of the IL-13 gene with asthma exacerbations.

If these findings are confirmed with additional research, genetic profiles of asthmatic patients could become more a more common and valuable tool to guide both therapy and research.

Provided by National Jewish Health

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