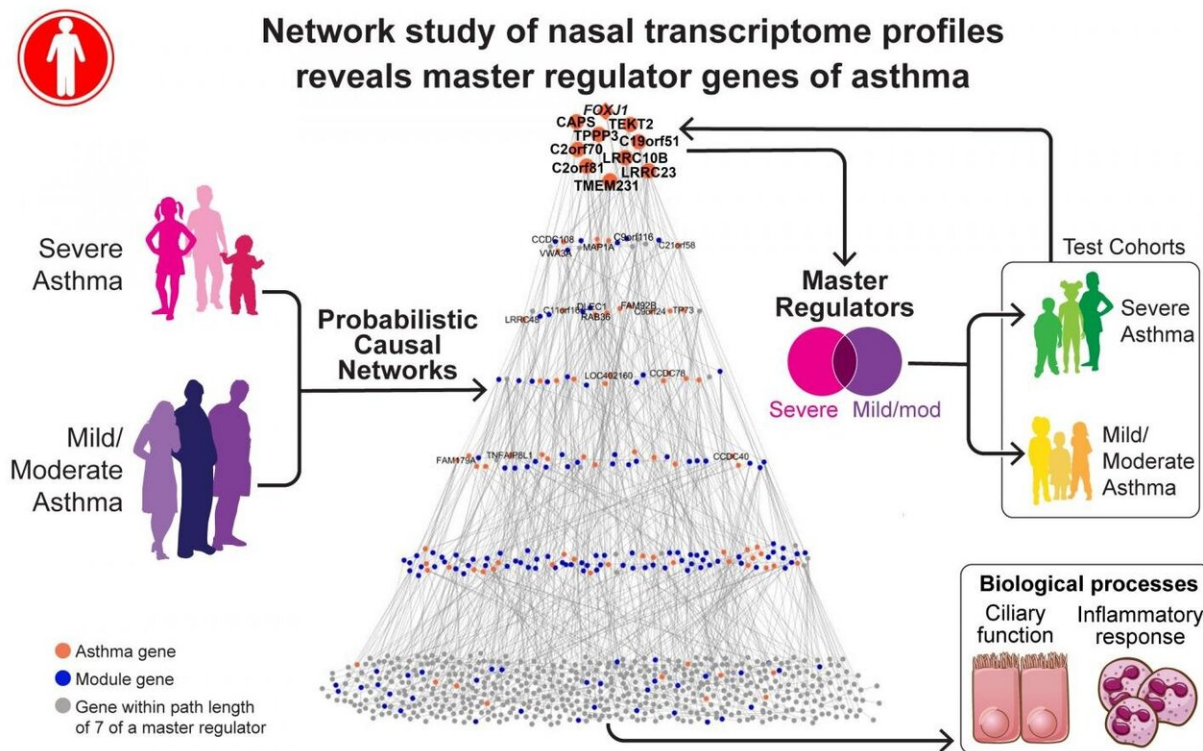


# Researchers identify master regulator genes of asthma

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Network study of nasal transcriptome profiles reveals master regulator genes of asthma Credit: Mount Sinai

Researchers identify master regulator genes of asthma, provide new path forward in the study of asthma and the development of novel therapies. Identification of these master regulator genes provides a new path

forward in the study of asthma and the development of novel therapies and treatments.

After identifying nasal gene signatures for mild, moderate, and severe persistent [asthma](#), the researchers applied probabilistic causal methods to identify master regulator genes and validated their results in independent cohorts. Researchers identified a master regulator gene common to asthma across severity and ages (FOXP1); master regulator genes of severe persistent asthma in children (LRRC23, TMEM231, CAPS, PTPRC FYB); and master regulator genes of mild/moderate persistent asthma in children and adults (C1orf38, FMNL1). The identified master regulators causally regulate the expression of downstream genes that modulate ciliary function and [inflammatory response](#) to influence asthma.

156 children were recruited at Mount Sinai Health System in New York with severe persistent asthma as well as controls for nasal transcriptome profiling. Network-based and probabilistic causal methods were applied to identify severe asthma genes and their master regulators. The same approach was then taken in an independent cohort of 190 adults with mild/moderate asthma and controls to identify mild/moderate asthma genes and their master regulators. Comparative analysis of the master regulator genes followed by validation testing in independent children with severe asthma (n=21) and mild/moderate asthma (n=154) was then performed.

Said Mount Sinai's Dr. Supinda Bunyavanich of the research: "Asthma is a common disease that affects people of all ages around the world. We studied nasal samples from [children](#) and adults with varying asthma severity not only to identify nasal signatures of mild, moderate, and severe asthma, but also to decipher master [regulator genes](#) that causally regulate key biological processes such as inflammatory response and ciliary function that underlie asthma. The master regulators we identified

provide a novel path forward for uncovering mechanisms and novel therapy for asthma."

**More information:** Anh N. Do et al, Network study of nasal transcriptome profiles reveals master regulator genes of asthma, *Journal of Allergy and Clinical Immunology* (2020). [DOI: 10.1016/j.jaci.2020.07.006](https://doi.org/10.1016/j.jaci.2020.07.006)

Provided by The Mount Sinai Hospital

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