

A Crohn's disease-associated gene expression profile and microbial community

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Crohn's and other inflammatory bowel diseases (IBDs) can be painful and debilitating. There are no known cures for these diseases, but the symptoms can be managed. It is widely thought that IBDs develop as a result of an individual's genetic make-up, their gut microbiota, and environmental cues, though it is not fully understood how these factors promote IBDs.

A new study in the *Journal of Clinical Investigation* identifies a specific gene expression profile and microbial community associated with Crohn's disease. Lee Denson and colleagues at Cincinnati Children's Hospital Medical Center compared the intestines of healthy patients to pediatric Crohn's disease patients.

Crohn's disease patients had altered expression of 2 genes, *DUOX2* and *APOA1*, as well as a distinct microbial community. Furthermore, *APOA1* expression and microbial abundance could be used to predict clinical outcomes in Crohn's disease patients.

More information: Pediatric Crohn disease patients exhibit specific ileal transcriptome and microbiome signature, *J Clin Invest.* [DOI: 10.1172/JCI75436](https://doi.org/10.1172/JCI75436)

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