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Understanding gut microbiota in new-onset Crohn's disease

New researched published in *Cell Host & Microbe* outlines key changes in the diversity of the gut microbiota in the context of new-onset Crohn's disease (before treatment is initiated), which strongly correlated with disease status. The findings also show that exposure to antibiotics increases Crohn's-disease-associated dysbiosis and that, in fact, assessment of the mucosa-associated microbiota, rather than faecal microbiota, might be the best marker of disease.

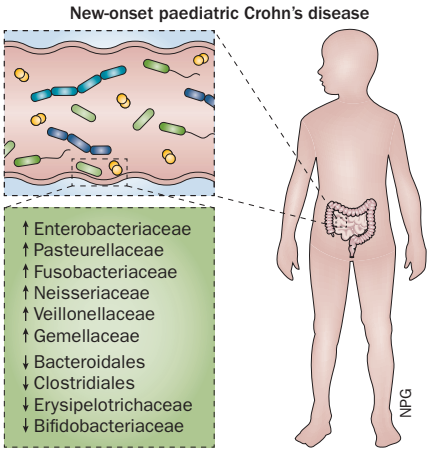
Crohn's disease is complex, with previous studies linking aberrant immune responses and host–microbe pathways in its development, but the findings have been inconsistent. Now, Dirk Gevers and colleagues have investigated the composition of the gut microbiota in a large cohort of paediatric patients with new-onset Crohn's disease ($n = 447$ versus 221 individuals with noninflammatory gastrointestinal conditions as controls) using a variety of next-generation sequencing approaches to deeply characterize the disease-associated microbiota.

Importantly, they examined samples at the time of diagnosis of Crohn's disease before treatment had been initiated, and across multiple locations in the gut (faecal, rectal tissue and ileal tissue samples). Gevers explains: "We used an exceptional sample set homogeneously collected across 28 clinics, a state-of-the-art combination of next-generation sequencing (including 16S rRNA gene sequencing with deep shotgun metagenomic sequencing), and a well-established multivariate analysis method to account for a wide range of demographic and clinical covariates".

The researchers found that, compared with controls, new-onset Crohn's disease was associated with an overall decrease in species richness of the mucosal microbiota, with shifts in abundance of several taxa (for instance, increased abundance of Fusobacteriaceae, with decreased abundance of Bacteroidales and Clostridiales). Notably, this imbalance was not observed in the microbiome profiles from stool samples.

A small subset of the paediatric patients with Crohn's disease (57 of 447) were treated with antibiotics during sample collection, enabling comparisons of the microbiota with and without antibiotic exposure. Interestingly, although antibiotics only weakly affected the overall species diversity, they strongly affected microbial composition, amplifying the dysbiosis observed.

Finally, the study authors explored the potential of gut microbial signatures as predictive markers of disease. "We found that the bacterial communities found in biopsy samples taken from rectal tissue, regardless of the location in which the inflammation is dominant, serves as a good [disease] predictor," notes Gevers, creating an "opportunity to use a minimally invasive approach to collecting patient samples for biomarker discovery".



Katrina Ray

Original article Gevers, D. *et al.* The treatment-naive microbiome in new-onset Crohn's disease. *Cell Host Microbe* **15**, 382–392 (2014)