

PREDICTING CLOSTRIDIODES DIFFICILE INFECTION IN PAEDIATRIC INFLAMMATORY BOWEL DISEASE PATIENTS ACCORDING TO GUT MICROBIAL COMPOSITION AND SHORT CHAIN FATTY ACIDS PRODUCTION

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A prospective study of pediatric inflammatory bowel disease patients found that baseline microbiome composition predicted protection from Clostridioides difficile infection and that CDI was associated with worse clinical outcomes and long-term microbiome alterations.

KEY POINTS

- Pediatric IBD patients who developed CDI had significantly more surgeries (HR 3.15, $P=0.019$), hospitalizations (RR 2.20, $P<0.001$), and were more likely to progress to biologic therapy (HR 1.85, $P=0.06$).
- Patients who did not develop CDI had higher baseline abundance of several bacterial taxa including Bifidobacterium bifidum, Blautia hydrogenotrophica, Eubacterium, Ruminococcus torques group, and Lachnospirillum, many of which were associated with higher stool short-chain fatty acid levels.
- A random forest classification model successfully predicted patients protected from CDI based on baseline microbial composition.
- Patients in remission after CDI had significantly lower beta diversity and reduced abundance of Oscillospira taxa (CAG 352, NK4A214 group, UCG 002) that were associated with short-chain fatty acid production, indicating persistent microbiome changes.
- This study addresses the gap in understanding microbiome features that predispose pediatric IBD patients to CDI and the long-term microbiome impacts of CDI in this population.

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