


RESEARCH ARTICLE

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Genetic diversity of *Escherichia coli* in gut microbiota of patients with Crohn's disease discovered using metagenomic and genomic analyses

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Abstract

Background: Crohn's disease is associated with gut dysbiosis. Independent studies have shown an increase in the abundance of certain bacterial species, particularly *Escherichia coli* with the adherent-invasive pathotype, in the gut. The role of these species in this disease needs to be elucidated.

Methods: We performed a metagenomic study investigating the gut microbiota of patients with Crohn's disease. A metagenomic reconstruction of the consensus genome content of the species was used to assess the genetic variability.

Results: The abnormal shifts in the microbial community structures in Crohn's disease were heterogeneous among the patients. The metagenomic data suggested the existence of multiple *E. coli* strains within individual patients. We discovered that the genetic diversity of the species was high and that only a few samples manifested similarity to the adherent-invasive varieties. The other species demonstrated genetic diversity comparable to that observed in the healthy subjects. Our results were supported by a comparison of the sequenced genomes of isolates from the same microbiota samples and a meta-analysis of published gut metagenomes.

Conclusions: The genomic diversity of Crohn's disease-associated *E. coli* within and among the patients paves the way towards an understanding of the microbial mechanisms underlying the onset and progression of the Crohn's disease and the development of new strategies for the prevention and treatment of this disease.

Keywords: Gut microbiota, Crohn's disease, *Escherichia coli*, Gene content, Inflammatory bowel diseases, Metagenomics, Pangenome

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