Escherichia coli B2 strains prevalent in inflammatory bowel disease patients have distinct metabolic capabilities that enable colonization of intestinal mucosa - DTU Orbit
(10/08/2019)

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Background: Escherichia coli is considered a leading bacterial trigger of inflammatory bowel disease (IBD). E. coli isolates from IBD patients primarily belong to phylogroup B2. Previous studies have focused on broad comparative genomic analysis of E. coli B2 isolates, and identified virulence factors that allow B2 strains to reside within human intestinal mucosa. Metabolic capabilities of E. coli strains have been shown to be related to their colonization site, but remain unexplored in IBD-associated strains.

Results: In this study, we utilized pan-genome analysis and genome-scale models (GEMs) of metabolism to study metabolic capabilities of IBD-associated E. coli B2 strains. The study yielded three results: i) Pan-genome analysis of 110 E. coli strains (including 53 isolates from IBD studies) revealed discriminating metabolic genes between B2 strains and other strains; ii) Both comparative genomic analysis and GEMs suggested that B2 strains have an advantage in degrading and utilizing sugars derived from mucus glycan, and iii) GEMs revealed distinct metabolic features in B2 strains that potentially allow them to utilize energy more efficiently. For example, B2 strains lack the enzymes to degrade amadori products, but instead rely on neighboring bacteria to convert these substrates into a more readily usable and potentially less sought after product.

Conclusions: Taken together, these results suggest that the metabolic capabilities of B2 strains vary significantly from those of other strains, enabling B2 strains to colonize intestinal mucosa. The results from this study motivate a broad experimental assessment of the nutritional effects on E. coli B2 pathophysiology in IBD patients.