Microbiology

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disease behavior and location between these 8 patients and the others. Anti-glycan and anti-Candida antibodies status were stable during active versus quiescent disease and anti-glycan antibodies levels did not change significantly.

Conclusions: CD patients are frequently colonized by C. albicans and are more heavily colonized in active than in quiescent phase of the disease while the antiglycan antibodies status is not influenced by disease activity. Colonization by C. albicans may participate in triggering intestinal inflammation in CD.

Reference(s)

P698
Characterization of the tissue-associated microbiome in active and inactive IBD
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Background: Recent studies have suggested a role for microbes in the etiology of Crohn’s disease (CD) and ulcerative colitis (UC). The aim of this study was to evaluate the composition of the tissue-associated microflora obtained from a minimally medicated, well-characterized cohort.

Methods: Patients with UC and CD (not on antibiotics, steroids, immunomodulators or biologics) and non-IBD healthy controls (HC) were recruited from Mount Sinai Hospital, Toronto. Demographic and clinical data were collected and sigmoid biopsies obtained from all patients during standard of care endoscopic evaluation. Terminal ileum samples were available on a subset of subjects. Endoscopic appearance at biopsy site was recorded and clinical activity assessed by CDAI and Mayo scores. Microbial DNA was extracted and the V4-V5 hypervariable region of the 16s rRNA gene was sequenced using the Illumina MiSeq platform. Paired end reads were stitched, quality trimmed, assembled into OTUs with 97% sequence identity and assigned to a taxonomy using QIIME. Raw counts were converted to relative abundance, and statistical comparisons were conducted using non-parametric statistics in R with false discovery rate (FDR) correction for multiple testing, and LEfSe.

Results: In total 179 samples (115 sigmoid, 64 terminal ileum) from 115 individuals were included in this analysis (44 HC, 34 CD, 37 UC). 15 patients with UC and 11 with CD had endoscopically confirmed active colonic inflammation. 5 patients with CD had ileal inflammation. 108 genera were detected which met the inclusion criteria. Sigmoid samples from individuals with CD had decreased levels of genera previously associated with IBD compared to HC, including Ruminococcus, Roseburla and Clostridium (pFDR < 0.05). Small reductions in these organisms were also detected in UC.

Faecalibacterium was decreased among individuals with CD compared to HC (pFDR < 0.05). Additional organisms showed evidence of association with IBD, however with marginal significance. Several genera also demonstrated inflammation-specific changes, including Bifidobacteria, which were detected in higher frequency in samples taken from inflamed tissue of CD and UC patients compared to those from uninfamed tissue. No associations with outcome were seen in the terminal ileum.

Conclusions: Our results demonstrate that specific microbes including members of the Firmicutes, are associated with IBD outcome and inflammatory status. These results are further evidence for a role of microbial ‘dysbiosis’ in IBD.

P699
Temporal bacterial community dynamics vary among ulcerative colitis patients after faecal microbiota transplantation
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Background: Faecal microbiota transplantation (FMT) from healthy donors, which is an effective alternative for treatment of Clostridium difficile-associated disease, is being considered for several disorders such as inflammatory bowel disease, irritable bowel syndrome and metabolic syndrome. Disease remission upon FMT is thought to be facilitated by an efficient colonization of healthy donor microbiota, but knowledge of the composition and temporal stability of patient microbiota after FMT is lacking.

Methods: Five patients with moderately to severely active ulcerative colitis (Mayo score > 6) and refractory to standard therapy received FMT via nasojejunal tube and enema. In addition to clinical activity and adverse events, the patients’ faecal bacterial communities were monitored at multiple time points for up to 12 weeks using 16S rRNA gene-targeted pyrosequencing.

Results: FMT elicited fever and a temporary increase of C-reactive protein. Abundant bacteria from donors established in recipients but the efficiency and stability of donor microbiota colonization varied greatly. A positive clinical response was observed after 12 weeks in one patient whose microbiota had been effectively augmented by FMT. This augmentation was marked by successive colonization of donor-derived phyotypes including the anti-inflammatory and/or short-chain fatty acids-producing Faecalibacterium prausnitzii, Roseburla faecis, and Bacteroides ovatus. Disease severity (as measured by Mayo Score) was associated with an over-representation of Enterobacteriaceae and an under-representation of Lachnospiraceae.

Conclusions: This study highlights the value of characterizing temporally resolved microbiota dynamics for a better understanding of FMT efficacy and provides potentially-useful diagnostic indicators for monitoring FMT success in the treatment of ulcerative colitis.

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Evaluation of location-specific, tissue-associated microbiota in the ileal pouch, terminal ileum and colon in inflammatory bowel disease (IBD)
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Background: The microbiome has been evaluated separately in conventional IBD and post-ileal pouch-anal anastomosis (IPAA), however, a comparison of the microflora between these groups has not been conducted. The aim of this study was to compare and contrast the microbial profile of colonic and ileal tissue with that of pouch and afferent limb tissue.

Methods: Subjects with Crohn’s disease (CD), ulcerative colitis (UC) (with and without a pouch), familial adenomatous polyposis (FAP) (with a pouch) and healthy controls (HC) were recruited from Mount Sinai Hospital, Toronto. Biopsies were taken from the pouch and afferent limb of patients with pouches, and from the sigmoid and terminal ileum (TI) of those without, during standard of care endoscopy. Demographic, clinical and endoscopic data was recorded at the time of procedure. Microbial DNA was extracted and the V4-V5