R. gnavus

Background: The mucosa-associated gut microbiota directly modulates epithelial and mucosal function. In this study, we investigated the mucosa-associated microbial community in patients with inflammatory bowel disease (IBD) using endoscopic brush samples.

Methods: This study was approved by the ethics committee of the Shiga University of Medical Science (permission No. 28-111). Samples were obtained by gentle brushing of mucosal surfaces while avoiding bleeding using cytology brushes (COOK® CCB-7-240-3-S, Bloomington, IN). In total, 174 mucus samples from 26 ulcerative colitis (UC), 43 Crohn’s disease (CD) and 14 non-IBD controls were obtained by gentle brushing of mucosal surfaces using endoscopic cytology brushes. The gut microbiome was analysed using 16S rRNA gene sequencing.

Results: There were no significant differences in the microbial structure between different anatomical sites (the ileum, cecum and sigmoid colon) within the individual. There was a significant difference in the microbial structure between CD, UC and non-IBD controls. The difference between CD and non-IBD controls was more remarkable than that between UC patients and non-IBD controls. alpha-diversity was significantly lower in UC and CD patients compared with non-IBD controls. When comparing CD patients with non-IBD controls, the phylum Proteobacteria was significantly increased, and the phyla Firmicutes and Bacteroidetes were significantly reduced. These included a significant increase of the genera Escherichia, Ruminococcus (R. gnavus), Cetobacterium, Actinobacillus, and Enterococcus and a significant decrease of the genera Faecalibacterium, Coprococcus, Prevotella, Roseburia. Comparison between CD and UC patients revealed that the genera Escherichia, Ruminococcus (R. gnavus), Clostridium, Cetobacterium, Peptostreptococcus were more abundant in CD patients and that the genera Faecalibacterium, Blautia, Bifidobacterium, Roseburia, Cito bacter were more abundant in UC patients.

Conclusions: Our novel findings are as follows: (a) inter-individual uniformity of the gut microbial structure at different anatomical sites of the colon and ileum, (b) no difference in the microbial structure between inflamed and non-inflamed mucosa, (c) mucosa-associated dysbiosis is more evident in CD patients than UC patients. There is a possibility that collection methods of mucus samples such as biopsy or brushing might strongly affect the results of 16S rDNA sequencing. A comparative study of methods of sample collection should be considered in the future.

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Faecal microbiota in treatment-naive ulcerative colitis and its relation to treatment escalation

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Background: Ulcerative colitis (UC) is a chronic inflammatory disease affecting the large intestine. The disease course varies from an indolent disease to an aggressive disease, requiring early introduction of biologics and colectomy in treatment refractory individuals. There is a clinical need of biomarkers that can be used to predict the future disease course already at diagnosis. Microbiota signatures might be of help in this respect and could potentially become a tool for the implementation of personalised medicine.

Methods: Fecal samples were collected at diagnosis from 47 treatment-naive UC patients in the IBD-character cohort. Extent of inflammation was defined according to the Montreal classification. Fecal microbiota composition was assessed using the GA-map™ Dysbiosis Test [Casén et al., 2015]. Patients were followed prospectively for up to 5 years and information on treatment escalation and surgery was collected. Patients were categorised into two groups based on need of treatment escalation, defined as introduction of biologics and/or colectomy during the study period. Differences between groups were compared by using the Wilcoxon test.

Results: Among 47 UC patients, 38 (81%) were classified as dysbiotic (12 mild and 26 severe). A total of 6 (13%) patients required treatment escalation. Patients with extensive colitis (E3) seemed to be more likely to require treatment escalation than patients with left-sided colitis (E2) or proctitis (E1) (OR = 4.8, 95% CI (0.78–30.0); p = 0.09). No significant association was found between the severity of dysbiosis and treatment escalation during follow-up (p > 0.05).

The total abundance of bacteria (p = 0.008) as well as the abundance of Ruminococcus gnavus (p = 0.03), Lactobacillus spp. (p = 0.03), Mycoplasma hominis (p = 0.04), and Streptococcus spp. (p = 0.04) was significantly lower in patients who required treatment escalation compared with patients who did not require escalation (p = 0.008).

Conclusions: Decreased abundance of Ruminococcus gnavus, Lactobacillus spp., Mycoplasma hominis, and Streptococcus spp. at diagnosis of UC seems to be associated with a more aggressive disease, requiring the introduction of biological therapies or colectomy.

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Successful detection of dysbiosis and altered short-chain fatty acids levels in in vitro colonic microbiota culture system using faecal samples of ulcerative colitis

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Background: Ulcerative colitis (UC) involves chronic and recurring inflammation of the intestinal tract. It is widely recognised that the composition of gut microbiota and intestinal metabolites are altered in UC patients. There is increasing number of clinical studies which supports the idea that imbalance of gut microbiota (dysbiosis) plays a role in pathogenesis and/or progression of UC. We previously reported single-batch fermentation system (Takagi et al., PLoS One, 2016) which can approximately recapitulate the microbiota of fecal sample in vitro, and could detect the change of microbiota and metabolites when prebiotics were supplemented to the system. It prompted us to test if this system could actually detect the unbalanced fecal microbiota and metabolites of UC patients; which may suggest the potential usefulness of this system for preclinical evaluation of effect of probiotics and prebiotics before administration to patients.