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Metabolomics of UC bacterial ecosystem compared to the healthy donors.


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Introduction
Ulcerative colitis (UC) is an idiopathic inflammatory bowel disease (IBD), which is characterized by chronic inflammation of the colonic mucosa. As the etiology of IBDs remains still unknown, it has been shown in many studies that patients with UC have an altered bacterial microbiota. Thus, the bacterial and/or host-bacterial interactions may play role in the pathogenesis of UC. This study focus on the metabolic interactions, corresponding to the fecal microbiota derived from UC patients and healthy subjects, colonizing a dynamic in vitro gut model.

Materials and methods
Fecal samples came from 4 healthy volunteers and 8 UC patients (4 in remission and 4 in relapse state). Studies have been done in a dynamic in vitro gastrointestinal model, the M-SHIME1,3. For metabolic analyses mucus and lumen samples were taken from the M-SHIME after 42 hours. In order to extract metabolites cold MeOH was used. Metabolites were detected by LCMS as follow: a Dionex Ultimate 3000 RS liquid chromatigraph coupled to a Bruker maXis time of flight mass spectrometer. Analytes were separated on a Kinetex PFP column 50 x 2.10 mm, 2.6 µm, 100Å, using solvents: 10 mM NH4HCO3 and C2H3N as a linear gradient from 0 to 90% C2H3N over 8 min. Scan range was from 50 to 800 m/z. The differences in metabolite profiles4 were evaluated by principal component analysis (PCA) using Profile Analysis 2.0 by Bruker Daltonics.

Results and discussion
PCA showed a distinctive separation between UC in relapse and healthy donors, which confirmed the data, describing bacterial differences between two types of microflora, made for the same samples. The same result was observed for the lumen samples. Metabolites separating those two groups are e.g. bile acids, fatty acids and tryptophan. These results will be further studied and combined with the qPCR data, describing the changes in the bacterial community for the healthy donors and UC patients.

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