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Metabolomics of UC bacterial ecosystem compared to the healthy donors.

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Introduction

Ulcerative colitis¹⁾ (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 microbiota²⁾. 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-SHIME^{2),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 chromatograph 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 NH₄HCO₂ 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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