gastrointestinal growth conditions. This study indicated also that bacterial virulence factors act in concert to elicit their pathogenic potential whereas the host immune system evolved strong mechanisms to detect and target bacteria regardless of their bacterial surface arming.

P667 Low prevalence of Blastocystis sp. in active ulcerative colitis patients

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Background: Ulcerative colitis (UC) is supposed to originate from a disbalance in the interplay between the gut microbiota and the innate and adaptive immune system. Apart from the microbiota, there might be other members; such as parasites, that could play a role in UC. The prevalence of Blastocystis in industrialised countries is decreasing whereas in the developing world chronic infestation is much more common, while the prevalence of ulcerative colitis shows the opposite. The primary objective of this study is to compare Blastocystis prevalence in a well-defined cohort of active ulcerative colitis patients compared to extensively ascertained healthy controls.

Methods: Clinically and endoscopically active UC patients, participating in a clinical trial and extensively tested healthy subjects, participating in the same trial as faecal donors were included. Healthy subjects did not have gastrointestinal symptoms, did not travel to an underdeveloped country within 6 months before inclusion and were extensively screened for infectious diseases by a screenings questionnaire, as well as serology and stool cultures. Diagnosis of intestinal parasites was performed with the Triple Faeces Test (TFT), a reliable method for detection of intestinal parasites; especially also Blastocystis sp. Healthy subjects did not use medication. UC patients were not allowed to use anti-TNF medication or Prednisolone >10mg daily. Both groups did not use antibiotic treatment within 6 weeks before inclusion.

Results: 169 subjects were included; 45 UC patients (median age 39.0 years (IQR 29–46), 49% male) and 124 healthy subjects (median age 37 years (IQR 22–38), 54% male). Healthy subjects were significantly younger than UC patients (P < 0.001). Median disease duration of UC was 9 years (range 0–27), 64.4% of UC patients used oral mesalamine, 29% used rectal mesalazine or corticosteroids, 29% used thiopurines and 20% used systemic corticosteroids. The prevalence of Blastocystis sp was 40/124 (32%) in healthy subjects and 6/45 (13%) in UC patients (P < 0.05). There was no association between the use of mesalamine, immunosuppressants or corticosteroids and the presence of parasites in UC patients.

Conclusions: Infection with Blastocystis is significantly less frequent in ulcerative colitis patients as compared to healthy controls.

P668 Interspace microbiome profiling (IS-pro) enables to differentiate IBD subclasses and disease activity by specific loss of bacterial diversity

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Background: Supposedly, intestinal microbiota plays a major role in IBD pathogenesis. Differences in its composition have been observed between and within patients with Crohn’s disease (CD) and ulcerative colitis (UC), varying with disease activity. This opens diagnostic potential in IBD. To date no standard laboratory techniques for microbiota analysis, suitable for daily clinical practice, are available, the more when using sample types like faeces and mucosal biopsies. As sampling method, storage and processing of samples have been shown to affect microbiota analysis, limitations in standardisation and accessibility arise. Therefore, we aimed to collect rectal swabs from IBD patients during consultation in an outpatient clinical setting and analyse these with IS-pro.

Methods: Rectal swabs were collected from consecutive IBD patients at a referral, third-line IBD outpatient clinic. Disease activity was determined with clinical indices. Total DNA was isolated by standard laboratory isolation procedures. Subsequently, microbial DNA was analysed with IS-pro, a within 8 hours performed, automated, high-throughput molecular fingerprinting method identifying composition of intestinal microbiota based on the ribosomal DNA (rDNA) interspace (IS) region combined with phylum specific sequence variation of the 16S rDNA. Combined with the proprietary IS-pro software suite, final output consists of profiles giving relative quantification of bacterial species within the most prominent phyla, Bacteroidetes, Firmicutes, Actinobacteria, Proteobacteria, Fusobacteria and Verrucomicrobia. From these data, Shannon diversity indices were calculated for all samples.

Results: In total 144 rectal swabs were collected (CD n = 85; UC n = 59). Lower species diversity in the Firmicutes/Actinobacteria phyla was observed in CD as compared to UC (p 0.02).

Species diversity in the Proteobacteria phylum was lower in active disease, both for CD (p 0.02) and UC (p 0.05). Loss of species in Bacteroidetes phylum in active CD versus quiescent CD was observed (p < 0.01).

Total species diversity was lower in active disease, both in CD and UC (p 0.05 and p 0.05, respectively). Within each phylum no specific species was typically associated with disease type or degree of activity.

Conclusions: Rectal swabs analysed with IS-pro is a feasible means of microbiota determination in an outpatient clinical setting. Differences in species diversity were observed in IBD; disease subtype differed when analysing diversity in the Firmicutes/Actinobacteria phyla whereas disease activity was associated with lower diversity in Proteobacteria (in IBD) and in Bacteroidetes (in CD). These data suggest that diagnosis and stratification of IBD by microbial profiling (IS-pro) may be feasible.