Faecal microbiota composition in adult, newly diagnosed, treatment-naïve IBD patients

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INTRODUCTION

The intestine represents an interface where host tissues come in contact with microbiota in a balanced state of homeostasis. Mounting knowledge on gut microbiota led to many important findings associating the composition of bacterial taxa in the human gastrointestinal tract with many human disorders including the Inflammatory Bowel Disease (IBD). Ulcerative Colitis (UC) and Crohn's Disease (CD) as the most prevalent forms of IBD are characterized by chronic relapsing inflammation affecting the intestinal mucosa. Despite both diseases having an unknown aetiology, there is increasing evidence that intestinal microbial dysbiosis has a role in the pathogenesis (1).

AIM

One of the main objectives of the Minute for IBD study is to investigate the contribution of the faecal microbiota composition to the disease specific phenotype in newly diagnosed and treatment naïve IBD patients.

MATERIALS & METHODS

The study included willing adult individuals without prior diagnosis of intestinal disease and willing to participate. Prior to diagnosis and disease-specific therapy, faecal samples were collected from 58 patients using OMNIgene.Gut collection system. 32 patients, 18 IBD (7 CD and 11 UC) and 14 Irritable Bowel Syndrome (IBS), were age-stratified and their faecal microbiota composition was determined by amplification and sequencing of bacterial 16S rRNA gene using Illumina MiSeq (V3-V4 region).

MP Biomedicals Fast DNA spin commercially available kit for DNA extraction was employed. Raw sequencing files were processed using QIIME pipeline and Operational Taxonomic Units (OTUs) were assigned using the vsearch algorithm and PyNast alignment against the GreenGenes database (version 13_8, May 2013). The diversity within sample was ascertained using alpha diversity index PD whole tree, as implemented in the QIIME pipeline, with rarefaction from 5000-25000 sequences. Overrepresentation of taxa is determined using generalised linear model and Kruskal Wallace test on centre-log ratio (clr) transformed counts, as implemented in the ALDeX2 R package (2).

CONCLUSION

Preliminary results of our study demonstrated differences in faecal bacterial populations between adult, newly diagnosed, treatment-naïve IBD and IBS patients.

RESULTS

Demographic data of included patients: 15 females (F) and 17 (M) males (4F and 3M in CD, 5F and 6M in UC, 6F and 8M in IBS group) with mean age of 46, 37 and 35 for CD, UC and IBS group, respectively. Relative abundance data on family level revealed substantial inter-individual differences among patients at all levels (Fig. 1). PCA analysis showed a certain level of grouping according to diagnosis, and UC group displayed lower richness using phylogeny-sensitive alpha diversity (Fig 2). Taxon analysis confirmed significance between groups in size effects (>0,5) and in Kruskal Wallace test ($p<0,05$) analyses but not after applying BH correction. Mainly, the number of taxa differing between groups was higher when comparing CD vs. IBS than UC vs. IBS. On the family level, of the taxa that had effect size >0,5 in CD vs. IBS comparison higher medians were seen for *Erysipelotrichaceae, Bifidobacteriaceae, Coriobacteriaceae, Enterobacteriaceae, Pasteurellaceae, Turicibacteraceae,* and *Fusobacteriaceae* but lower for *Verrucomicrobiaceae.* UC compared to IBS group had lower medians for *Rikenellaceae* and *Verrucomicrobiaceae* and higher median for *Turicibacteraceae.* These data demonstrate differences in bacterial content, both in terms of richness and contributions by individual taxa, pertinent to disease pathology in different types of IBD.

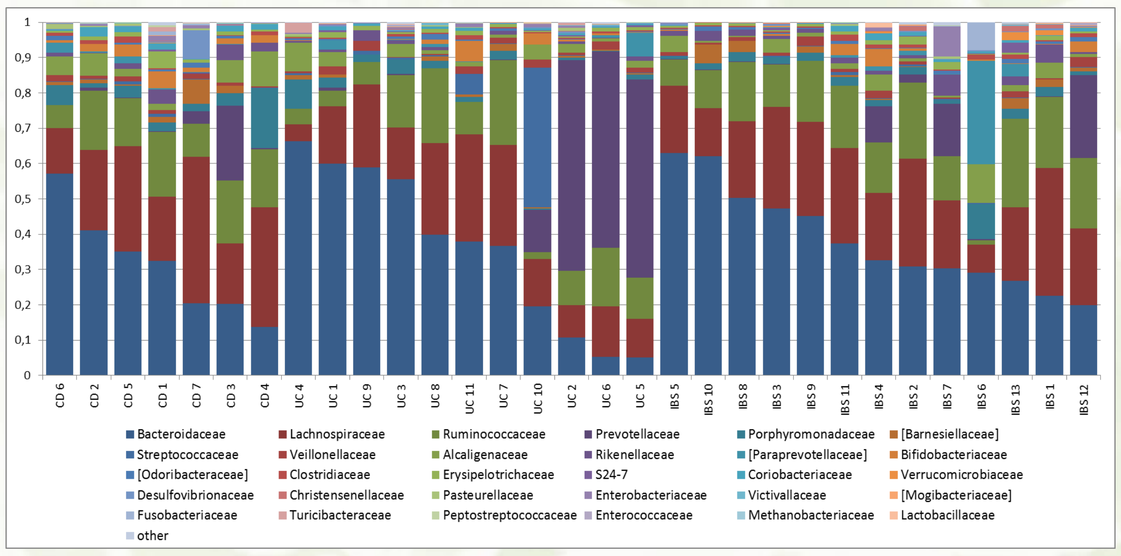

Figure 1. Relative abundance data for all patients from CD, UC and IBS groups at family level.

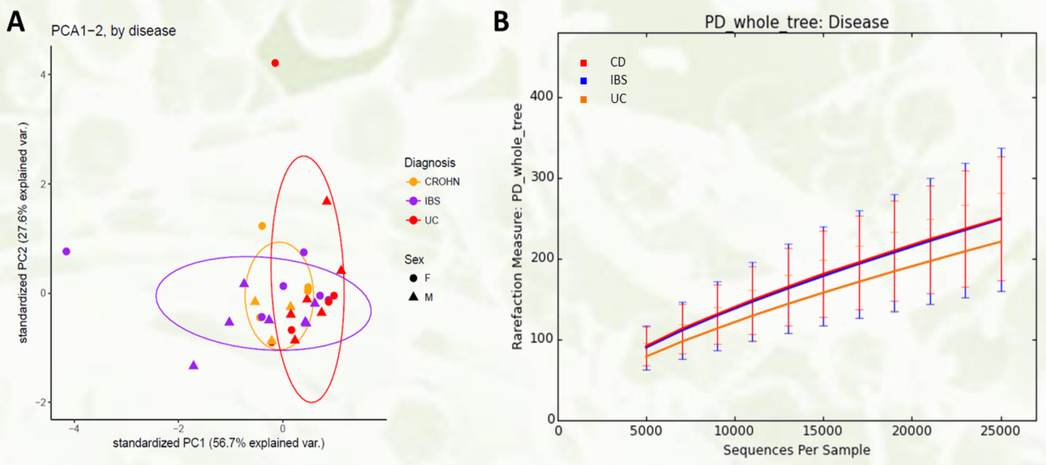

Figure 2. (A) Principle component analysis (PCA) of families detected with ffirst two components covering 84,3 % of total variance. (B) Alpha diversity analysis for CD, UC and IBS groups after rarefaction: PD_whole_tree index.

REFERENCES

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