

**O1049 Gut microbiome analysis in common variable immunodeficiency patients and paired healthy controls sharing the same household**

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**Background:** In recent years, our understanding of a human microbial composition and its implication in health and disease has been completely changed. A rise in a new technologies development, mainly high-throughput sequencing platforms and new bioinformatic approaches, has enabled us to read out the human microbial communities at a previously unimaginable scale. We also have gained knowledge of IgA antibodies regulating microbial growth and epithelial adhesion and their lack causing increased microbial translocation and local inflammation. These processes might significantly contribute to the CVID pathology. The current study aims to analyse gut microbiome composition in CVID patients and healthy controls sharing the same household, and to assess whether gut microbiome can influence the CVID phenotype.

**Materials/methods:** A group of 16 pairs composed of CVID patients and their healthy counterparts sharing the same household were recruited into the study. All participants provided stool samples for gut microbial profiling using targeted 16S rRNA next generation sequencing performed on the Illumina Miseq platform. Data processing and analysis were performed using the QIIME pipeline. Group differences in taxa relative abundance were determined by non-parametric statistical tests implemented in online tool Calypso.

**Results:** Despite a high inter-individual variability, pair analysis revealed lower alpha-diversity ( $p < 0.05$ ) in the CVID group as was previously found in other similar pathological conditions. Beta-diversity visualized by PcoA plots based on UniFrac and Bray-Curtis distances revealed distant clustering according to health status. These observations were confirmed by independent redundancy analysis, where health-status was the only significant factor ( $p = 0.002$ ). Further, pair analysis revealed microbial dysbiosis in CVID patients, characterised by significantly increased Proteobacteria, Enterobacteriaceae, Lactobacillaceae, Gemellaceae, Streptococcaceae, Porphyromonaceae counts and decreased Erysipelotrichaceae and Paraprevotellaceae counts.

**Conclusions:** We suppose that some of these detected shifts in taxa abundance in either group might have a biological significance. For example, phylum Proteobacteria harbours many pathogens and can contribute to local inflammation in CVID while Lactobacillaceae could be increased as a result of inflammation since this taxon is microaerophilic. A possible relationship between observed shifts and the CVID phenotype needs to be further investigated.

