O096
Oral Session
Microbiome and microbiota: new "M's" in microbiology

CORE GUT MICROBIOME AND TEMPORAL STABILITY IN CHILDREN

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Objectives:

The human intestinal microbiota is considered to have major functions in maintaining human health. Dysbiosis is thought to be associated with various diseases, including inflammatory bowel disease, metabolic syndrome, obesity, functional abdominal pain and immune disorders. To understand the role of intestinal microbiota in the pathogenesis and disease course, normal microbiota composition and temporal stability should be defined. While these parameters have been evaluated for adults, information on this topic for children is limited.

Here we describe describe microbial composition, short-term and long-term stability of the intestinal microbiota in healthy children aged 2-17 years.

Methods:

In this prospective study, fecal samples of 60 children (median age 9,3 years, IQR 5,7-12,3) were collected weekly for 6 weeks. Long-term stability was assessed by collecting one more fecal sample one year later. All samples (including T=0) were analysed by means of IS-pro, a validated high-throughput, PCR-based profiling technique. Additionally, all T=0 samples were analyzed by 454 pyrosequencing. For one sample long-read sequences were analysed by Pacific Biosciences sequencing to identify core microbiota to species level

Results:

While composition of the microbiota was highly variable between subjects, a core microbiome consisting of Bacteriodetes species which were present in most children could be identified. Moreover, there was a clear within-family clustering of microbiota composition.
A total of 60 children were included (median age 9,3 years, IQR 5,7-12,3). Both short-term and long-term stability was highly phylum-specific. Bacteriodetes showed a median correlation coefficient (R) at one-week-interval (R1) of 0,87 (Q1: 0,81, Q3: 0,91) at 5-week-interval (R5) of 0,86 (Q1: 0,80, Q3: 0,88) and at 1-year-interval (R12) of 0,80 (Q1: 0,73, Q3: 0,84). Firmicutes showed a more variable pattern: R1 0,69 (Q1: 0,57, Q3: 0,78), R5 0,61 (Q1: 0,50, Q3: 0,73) and R12 0,49 (Q1: 0,38, Q3: 0,61). Proteobacteria: R1 0,67 (Q1: 0,52, Q3: 0,77), R5 0,67 (Q1: 0,48, Q3: 0,72) and R12 0,48 (Q1: 0,37, Q3: 0,55). In addition, we observed a common core microbiome, consisting of 3 species within the phylum Bacteriodetes (Bacteroides vulgatis, Alistipes Putredinis and Alistipes finegoldii). Intra-individual diversity was stable through time on phylum level (Shannon diversity index Bacteriodetes 3,1; Firmicutes 2,9; Proteobacteria 2,5).
Conclusion:
Short-term and long-term stability in healthy children showed a highly phylum-specific pattern. Bacteriodetes were more stable compared to Firmicutes and Proteobacteria. Intra-individual microbiotal diversity remained stable through time for all phyla. Finally, our results suggest the existence of a common core microbiome in healthy children within the phylum Bacteriodetes, consisting of at least the species Bacteroides vulgatis, Alistipes Putredinis and Alistipes finegoldii.