

Parasites and gut microbiota: is there a link?

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Background and aims: The impact of infections on gut microbiota is complex and not well defined. Several factors are involved in changing of the gut microbiota composition at the occurrence of a bacterial infection whereas little is known on the impact of parasites. The aim of this study was to assess the gut microbiota composition in patients with imported malaria and Chagas disease (CD) hospitalized at the National Institute for Infectious Diseases, INMI "Lazzaro Spallanzani", Rome, Italy.

Materials and Methods: Thirty-one subjects (20 with imported malaria, 7 with CD and 6 healthy donors (HD)) were enrolled. The V3–V4 hypervariable region of the bacterial 16S rRNA gene was amplified from total DNA according to the Illumina 16S Metagenomic Sequencing Library Preparation instructions. Paired-end sequencing (2 × 300 cycles) was carried out on an Illumina MiSeq device (Illumina Inc., San Diego, CA, USA) according to the manufacturer's specifications. Sequence data generated as FASTQ files, were analyzed using the 16S Metagenomics GAIA 2.0 software which performs the quality control of the reads/pairs (i.e., trimming, clipping and adapter removal steps) through FastQC and BBDuk. The reads/pairs are mapped with BWA-MEM against the custom databases (based on NCBI).

Results: Differences in microbiota were observed among subjects with malaria or CD compared to HD. In detail, imported malaria population showed an over-expression of *Nitrospinae*, *Synergistetes*, *Nitrospirae* and *Fusobacteria* phyla, *Sphingobacteriaceae*, *Selenomonadaceae*, *Flavobacteriaceae*, *Desulfohalobiaceae*, *Paenibacillaceae* familia and *Massiliprevotella*, *Oribacterium*, *Dysgonomonas*, *Catenibacterium*, *Paludibacter* genera, whereas *Nautiliaceae*, *Nocardiaceae* and *Lachnospiraceae* familia and *Anaerobium*, *Lactococcus*, *Acidaminococcus*, *Wigglesworthia* and *Gorbachella* genera were under-represented than HD. Conversely, in the CD population, *Synergistetes*, *Fusobacteria* and *Candidatus Saccharibacteria* phyla, *Selenomonadaceae*, *Synergistaceae*, *Succinivibrionaceae*, *Sphingobacteriaceae* and *Oxalobacteraceae* familia and *Alloprevotella*, *Catenibacterium*, *Massiliprevotella*, *Duodenibacillus* and *Howardella* genera were the most enriched taxa compared to HD. *Verrucomicrobia* and *Firmicutes* phyla, *Vibrionaceae*, *Pseudomonadaceae*, *Nocardiaceae*, *Lachnospiraceae* and *Ruminococcaceae* familia, and *Acidaminococcus*, *Lactococcus*, *Vibrio*, *Fenollaria* and *Wigglesworthia* genera were decreased in CD patients versus HD.

Discussion: Relevant perturbations in the gut microbiota of patients affected by either malaria or Chagas disease were observed compared to healthy donors. Particularly, the lactic acid producer *Lactococcus*, and the butyrate producers *Lachnospiraceae* (and *Ruminococcaceae* only in CD patients) decreased only in affected patients. In conclusion, as already known for bacterial infections, also parasites could play a potential role on gut microbiota composition. Further analysis are needed to better define the interaction between parasites and gut microbiota.