

Natural and after colon washing fecal samples: the two sides of the coin for investigating the human gut microbiome

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Background:

The human gastrointestinal (GI) tract harbors a complex population of microorganisms which changes along its compartments. The selection of a sampling matrix fully representative of the GI microbial biodiversity is still challenging. Hence, we present a comparative study between two sampling matrices, feces (F) and colon washing feces (CWF).

Methods and Results:

The NGS metabarcoding approach targeting the V4 hypervariable region of the 16S rDNA was applied on the DNA, extracted from paired F and CWF of 30 volunteers and absolute quantified by ddPCR. Alpha diversity analysis showed a slightly higher biodiversity of CWF compared to F matched samples. However, beta diversity analysis, using the UniFrac distance, highlighted that the observed variability was mainly dominated by individual peculiarities, although paired samples generally tended to co-cluster. A relevant overlap between community composition among samples was also confirmed by the taxonomic analysis. Firmicutes, Bacteroidota, Proteobacteria and Actinobacteriota were the main phyla in both matrices.

Conclusions and Significance:

We report here the first comparative study on F and CWF matrices to investigate the human gut microbiome. We show that both matrices may be used equally and their combined use could lead to a more complete overview of the human gut microbiota for addressing different biological and clinical questions.

Keywords:

Human gut microbiome, metagenomics, NGS, 16S metabarcoding, matrices.

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Thematic Area:

- Microbiome: from Research to Clinics

Infrastructures:

This project took advantage of the omics and computational facilities provided by the Italian Node of ELIXIR (ELIXIR-IT), the European Research Infrastructure for Life Science, including the advanced equipment acquired by the CNR BiOmics infrastructural project (PIR01_00017) for carrying sequencing and subsequent bioinformatics analysis.