Microbial and metabolic gut profiles across seven malignancies unveil fecal *Faecalibacillus intestinalis* and formic acid as commonly altered in cancer patients

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INTRODUCTION

The gut microbiota is considered a potential environmental factor associated with different human pathologies, including cancer, acting through endogenous metabolites and microbial products. Aim of the study was to define common changes in the composition of the gut microbiota and targeted fecal metabolomics profiles in seven different types of human malignancies.

METHODS

Patients: newly diagnosed at any disease stage. Sex- and age-matched healthy controls (HC) assigned separately to each of the studied patient groups. Fecal samples: collected from patients before system oncological treatment. Bacterial DNA and metabolites: whole genome shotgun sequencing (WGS) and gas chromatography/mass spectrometry (GC/MS).

RESULTS

**I.** Three hundred forty mix-case neoplasm patients were recruited, including 40 colorectal (CRC), 45 stomach, 71 breast, 34 lung, 50 melanoma cancers, 60 lymphoid neoplasms and 40 acute myeloid leukemia (AML). The HC group consisted of 178 individuals.

**II.** The Shannon index showed a lower a-diversity of the gut microbiota only between the lymphoid neoplasm and AML samples and the corresponding HC samples.

**III.** β-diversity of all cancer’s groups was significantly different from HC.

![Figure 1: Shannon index of the gut microbiota between malignancies and control group.](image)

*Faecalibacillus intestinalis* was underrepresented in each of the seven groups studied, *Anaerostipes hadrus* was underrepresented in all but the stomach cancer group.

**IV.** The relative concentration of formic acid was significantly higher in each of the case groups than in HC, and the abundance of seven species of *Faecalibacterium* correlated negatively with most amino acids and formic acid, and positively with the levels of acetic, propanoic, and butanoic acid.

![Figure 2: β-diversity of the gut microbiota between selected malignancies and control group.](image)

![Figure 3: Heat map derived from pairwise correlations (Spearman’s coefficient) between the abundance of bacterial species and metabolites identified in healthy controls and case-mixed cancer patients.](image)

CONCLUSION

Results demonstrated trends rather than objective differences correlated with different types of malignancy. *Faecalibacillus intestinalis* was underrepresented in each of the seven studied groups.

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