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Comparison of oral and intestinal human microbiota and association of *Fusobacterium nucleatum* infection in patients with colorectal cancer: A pilot study

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The study used next-generation sequencing (NGS) to analyze and compare human microbiota from three different environments, saliva, feces, and cancer tissue (CT), of a selected cohort of 10 Italian patients with colorectal cancer (CRC) vs. 10 healthy controls (saliva and feces). Furthermore, the *Fusobacterium nucleatum* (*F. nucleatum*) abundance in the same districts was investigated through quantitative polymerase chain reaction (RT-qPCR) to assess the association with CRC. The difference of bacterial taxonomic composition, *F. nucleatum* abundance between CRC and healthy controls and the relationship of *F. nucleatum* presence with clinical variables were evaluated. Taxonomic analysis revealed the presence of three main bacterial phyla, which comprises ca. 80% of reads: Firmicutes (39.18%), Bacteroidetes (30.36%), and Proteobacteria (10.65%). The three examined environments showed different bacterial assemblages; in particular, we observed the enrichment of members of Bacteroidetes within fecal samples of CRC patients, while Firmicutes were over-represented in the fecal samples of healthy controls. The CT samples show the highest alpha diversity values. *F. nucleatum* in patients was shown to be more abundant in saliva samples than in feces samples and, notably related to the presence of metastases. These results highlight a different taxonomic composition of feces from CRC compared to healthy controls and that the *F. nucleatum* presence is positively associated with the clinical course of CRC patients (metastasis). So, our results could be useful to promote the development of novel bacteria-related diagnostic tools and therapeutic interventions in CRC patients.

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