Letter to Editor

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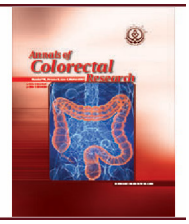

Oral and Colonic Microbiomes and Colon Cancer

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Dear Editor

The oral microbiota can include a wide range of bacteria, fungi, protozoa, and viruses, which translocate via the digestive tract and contribute to local disease (1-10). Recently, many studies have focused on the role of oral microbiota in intestinal tract pathologies (1, 5-10). Because of higher prevalence, most works are conducted on colorectal cancer (CRC); in addition to the oncology area, they focus on aspects of the coronavirus disease 2019 (COVID-19) scenario (6, 8). *Helicobacter pylori*, *Streptococcus gallolyticus*, and *Escherichia coli* are agents involved in CRC, though *Fusobacterium*, *Peptostreptococcus*, and *Porphyromonas spp.* also have a role (1). These oral microbes cause opposite effects to the beneficial *Bifidobacteria*, *Roseburia*, and *Faecalibacterium*, eliciting DNA epithelial damage and apoptosis in the bowel (1). Synergistic intrafungal and antagonistic bacterial-fungal associations are described in CRC, as well as higher Basidiomycota/Ascomycota rates, characterizing dysbiosis (4, 5).

Although not entirely clear, the pathogenic relationships of oral and intestinal microbiota and CRC development or COVID-19 manifestations are of interest (1-3, 5-10). An imbalance of the microbial ecosystem interfering with pH and micronutrients and predisposing to dysbiosis is considered a triggering factor of CRC (2, 3, 5, 9). The advent of new biomarkers to diagnose this tumor is also under consideration (2, 3, 5, 7, 9, 10).

We read with interest the review of Nair V related to oral bacteria and colorectal disorders, especially the agents of oral diseases also involved in dysbiosis and CRC (1). Orally-derived opportunistic bacteria reaching the colon favor CRC development by producing toxic factors and inhibitor factors that reduce the number of local beneficial bacteria (1). The routes of transport are swallowing and the bloodstream (while chewing or brushing the teeth). The author cited *Porphyromonas gingivalis* and *Actinobacillus actinomycetemcomitans* as oral bacteria related to colorectal pathologies, with biopsies in CRC showing reduced levels of *Blautia*, *Bifidobacterium*, and *Faecalibacterium*, and increased oral microbiota (1). Worthy of note, *Fusobacterium nucleatum* and *P. gingivalis* were emphasized among the most often oral microorganisms found increased in evaluations performed in CRC. Preventive care includes good oral hygiene, routine dentist evaluations, and probiotics (1).

In the setting of oral microorganisms and the development of malignancy in the digestive tract, it seems of some interest the Brazilian case study on the concomitance of oral paracoccidioidomycosis in a male with an esophageal spinocellular carcinoma (4). The authors commented on the possibility of the causal coexistence of these conditions, which could be due to alcohol and tobacco use as predisposing

factors of dysbiosis (4, 9). In fact, *P. gingivalis*, *Tannerella forsythia*, *Capnocytophaga gingiv*alis, and *Prevotella melaninogenica* can be associated with oral and esophageal cancers (9). Oral bacterial dysbiosis gives origin to a favorable milieu for mycosis development, and bacteriome, mycobiome, or their interaction can contribute to cancer pathogenesis (9).

Besides oral mycobiome and cancer, we comment on relations between the intestinal microorganisms and dysfunctional immune responses in COVID-19 (6, 8). As commensals with immunomodulatory potential, *Eubacterium rectale, Faecalibacterium prausnitzii, and bifidobacteria* were reduced in numbers up to 30 days after cure (6). Gut microbiota seem to be in concordance with the severity of COVID-19 and the magnitude of inflammatory cytokines, chemokines, and plasma marker levels of tissue damage (6). Based on more recent data, the authors highlighted the need to understand the specific roles of gut microorganisms in human immune function and systemic inflammation (6). SARS-CoV-2 infection can impact the intestinal microbiota homeostasis as well as antiviral drugs, plasma or immunoglobulin administration, and diet supplementation (8). There are few studies of correlations between intestinal microbiota and COVID-19, but microbial diversity and homeostasis, including the presence or absence of beneficial microorganisms in the gut, may have a major role in determining the disease course (8).

As a whole, the interest in the exact role played by microbiota and mycobiome in the earliest phenomena of human oncology and infectious pathology is growing. The studies herein commented yielded the necessary basis for further research in the field of prevention and management both of common malignancies and the current pandemic.

Conflicts of interest: None declared.

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