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Dynamics of the microbiota in right-sided colon cancer patients: pre- and post-tumor resection

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Recent research has underscored the significant role of gut microbiota in colorectal cancer (CRC) progression, with dysbiosis emerging as a hallmark feature. In CRC patients, dysbiosis is characterized by reduced microbial diversity, depletion of protective bacteria, and an increase in pathogenic taxa. These changes disrupt host–microbe interactions, lead to metabolic imbalances, and trigger inflammatory responses that contribute to carcinogenesis [1]. Although previous studies generally report lower microbial diversity in CRC patients compared to healthy individuals, some have suggested that CRC-associated dysbiosis may also result in increased microbial richness due to the expansion of specific pathogenic bacteria [2].

Among the pathogenic bacteria enriched in CRC patients, *Fusobacterium nucleatum* is particularly implicated in tumor progression by promoting inflammation, immune evasion, and treatment resistance [3]. Increased levels of *Prevotella* have also been observed; however, its role in CRC remains debated, with some studies suggesting it may even have a protective effect against disease progression [4]. Meanwhile, beneficial bacteria such as *Faecalibacterium prausnitzii*—known for their anti-inflammatory properties and role in maintaining gut homeostasis—are significantly reduced in CRC patients [5, 6]. Structural shifts in the microbial composition, including a decrease in Firmicutes and an increase in *Bacteroidetes*, further highlight the distinct microbiome alterations associated with CRC [7].

The present study offers a focused perspective on the gut microbiota dynamics in patients with right-sided colon cancer (RCC) before and after tumor resection, distinguishing it from previous research that did not differentiate between right- and left-sided CRC. Given that microbial composition varies with tumor location within the colon, concentrating on RCC provides valuable insights into disease-specific microbial changes and their potential clinical implications [8].

A key strength of the study is its investigation of microbiome changes before and after tumor resection in RCC patients. Prior to surgery, RCC patients exhibited a significantly higher proportion of *Proteobacteria* (52.97%) compared to healthy controls (9.16%, $P<0.001$), while *Bacteroidetes*—a dominant phylum in healthy individuals (56.34%)—was markedly reduced. After tumor resection, *Proteobacteria* levels dropped to 19.87% ($P<0.001$) and *Bacteroidetes* increased to 50.90% ($P<0.001$), suggesting that surgical intervention contributes to a partial restoration of microbial balance. Nevertheless, the microbiota composition in RCC patients remained distinct from that of healthy controls, indicating that tumor resection alone does not fully restore eubiosis. This finding highlights the potential role of adjunctive therapies, such as probiotics, prebiotics, and dietary modifications, in promoting microbial recovery and improving patient outcomes.

Several limitations of the study must be acknowledged. One major concern is the potential bias introduced by demographic differences between the healthy control group and RCC patients. Variables such as age, sex distribution, comorbidities, dietary hab-

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its, and smoking history can influence microbiome composition, and these factors were not fully controlled in the study. Consequently, some of the observed microbial differences might stem from these demographic disparities rather than being directly attributable to RCC. Another limitation is that the study analyzed microbiota composition only at the phylum and genus levels, without exploring metabolic functional changes. Because microbial metabolites play a crucial role in host immunity, inflammation, and tumor microenvironment modulation, future research should incorporate metagenomic and metabolomic analyses to achieve a more comprehensive understanding of microbiota-driven mechanisms in CRC progression.

Despite these limitations, the study's design—comparing each patient's microbiota before and after tumor resection—adds significant value. Rather than merely contrasting CRC patients with healthy controls, this approach evaluates the direct impact of surgical intervention on microbial composition. It provides a clearer picture of how tumor presence influences gut microbiota and how its removal alters microbial dynamics. Further research with larger cohorts and longitudinal follow-up is needed to determine whether these microbiota shifts persist over time and to assess their potential impact on disease recurrence and patient prognosis.

In summary, the study represents a crucial step in identifying microbiota-based signatures specific to RCC and underscores the need for targeted interventions to restore microbial homeostasis after surgery. Although further refinement in study design and analytical methods is necessary, the findings contribute to the growing body of evidence linking gut microbiota to CRC pathogenesis and highlight the potential of microbiome-targeted strategies in CRC management and prevention.

ARTICLE INFORMATION

Conflict of interest

Youn Young Park is an editorial board member of this journal, but was not involved in the peer reviewer selection, evaluation, or decision process of this article. No other potential conflict of interest relevant to this article was reported.

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