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# The Role of Gut Microbiota in Modulating Immune Responses to Cancer Therapies

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## Introduction

Over the past decade, cancer therapy has undergone a paradigm shift from conventional chemotherapeutics to precision-based strategies such as Immune Checkpoint Inhibitors (ICIs), adoptive cell transfer, and cancer vaccines. Despite these advances, treatment responses vary widely among patients, and immune-related adverse effects remain significant challenges. Emerging evidence highlights the gut microbiota—the trillions of microorganisms residing in the gastrointestinal tract—as a critical determinant of therapeutic efficacy and toxicity in cancer treatments. These microbial communities not only regulate systemic immune responses but also influence the pharmacodynamics and pharmacokinetics of anti-cancer drugs. Understanding the interplay between gut microbiota and host immunity has opened new opportunities to enhance cancer therapy outcomes through microbiome-targeted interventions [1].

## Description

The gut microbiota exerts profound effects on the immune system by shaping both innate and adaptive responses. Microbial metabolites such as Short-Chain Fatty Acids (SCFAs), particularly butyrate and propionate, modulate regulatory T cell (Treg) development, maintain epithelial barrier integrity, and regulate cytokine production. In the context of cancer, these metabolites influence the tumor microenvironment by either promoting anti-inflammatory conditions or enhancing cytotoxic T lymphocyte activity. Specific microbial taxa, including species of *Akkermansia*, *Bifidobacterium*, and *Faecalibacterium*, have been linked to improved responses to ICIs such as anti-PD-1 and anti-CTLA-4 therapies. These bacteria are thought to enhance dendritic cell activation, increase antigen presentation, and promote interferon-gamma (IFN-γ)-secreting T cells, all of which are crucial for robust anti-tumor immunity. Conversely, dysbiosis—characterized by reduced microbial diversity or enrichment of pathogenic bacteria—can impair immune surveillance, promote chronic inflammation, and diminish therapeutic efficacy [2].

Clinical and preclinical studies have demonstrated that gut microbiota composition strongly correlates with patient responses to ICIs. For example, patients with higher abundance of *Akkermansia muciniphila* were shown to have improved progression-free survival when treated with PD-1 inhibitors. Fecal Microbiota Transplantation (FMT) from responders into germ-free or antibiotic-treated mice restored anti-tumor immunity and enhanced checkpoint blockade efficacy, underscoring the causal role of microbiota in therapy response. On the other hand, broad-spectrum antibiotic use prior to or during ICI therapy has been associated with poor clinical outcomes, likely due to the depletion of beneficial commensals essential for immune modulation. Beyond ICIs, microbiota have also been implicated in shaping responses to chemotherapeutics such as cyclophosphamide, which requires microbial-mediated translocation of bacterial products to secondary lymphoid organs to elicit Th17 responses that augment anti-tumor effects. These findings highlight the microbiome as a predictive biomarker of therapeutic response and as a modifiable factor in cancer treatment strategies [3].

The gut microbiota also influences the toxicity profile of cancer therapies, particularly immune-related adverse events. For instance, colitis induced by anti-CTLA-4 therapy has been linked to distinct microbial signatures characterized by low abundance of Bacteroides fragilis. Supplementation or restoration of such bacteria in preclinical models mitigated colitis severity by inducing regulatory T cells and anti-inflammatory cytokines. Similarly, the gut microbiota has been implicated in chemotherapy-induced mucositis and radiotherapy-associated enteropathy, where dysbiosis exacerbates mucosal damage and inflammation. Manipulating microbial communities to restore homeostasis therefore presents a promising strategy to reduce adverse events while preserving therapeutic efficacy. These observations not only underscore the dual role of gut microbiota in modulating both efficacy and toxicity but also emphasize the potential of microbiome-informed patient stratification in clinical oncology. Given the pivotal role of the gut microbiome in cancer therapy outcomes, numerous therapeutic strategies are being developed to manipulate microbial composition and function [4,5].

## Conclusion

The gut microbiota represents a critical mediator of immune responses to cancer therapies, influencing both treatment efficacy and adverse effects. By shaping systemic immunity and modulating the tumor microenvironment, specific microbial taxa and their metabolites act as key determinants of therapeutic success. Advances in microbiome research are paving the way for novel adjunctive strategies that can enhance current cancer treatments, ranging from FMT and probiotics to engineered microbial therapies. Future directions will require integration of multi-omics technologies, including metagenomics, metabolomics, and immunogenomics, to unravel the complex host-microbiota interactions underlying cancer therapy responses. Ultimately, leveraging the gut microbiome as a therapeutic ally holds immense potential to revolutionize cancer treatment paradigms, enabling more personalized, effective, and safer interventions for patients worldwide. Integration of microbiome profiling into precision oncology frameworks also holds promise for developing personalized treatment regimens based on individual microbial signatures.

## Acknowledgement

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## Conflict of Interest

None.

## References

1. Fang H, Rodrigues e-Lacerda R, Barra NG, Kukje Zada D, Robin N, et al. (2025). Postbiotic impact on host metabolism and immunity provides therapeutic potential in metabolic disease. Endocr Rev 46: 60-79.

2. Mititelu M, Lupuliasa D, Neacșu SM, Olteanu G, Busnatu ȘS, et al. (2024). Polyunsaturated fatty acids and human health: A key to modern nutritional balance in association with polyphenolic compounds from food sources. Foods 14: 46.

3. Cuciniello R, Di Meo F, Filosa S, Crispi S, Bergamo P (2023). The antioxidant effect of dietary bioactives arises from the interplay between the physiology of the host and the gut microbiota: Involvement of short-chain fatty acids. Antioxidants 12: 1073.

4. Raghav K, Siena S, Takashima A, Kato T, Van den Eynde M, et al. (2024). Trastuzumab deruxtecan in patients with HER2-positive advanced colorectal cancer (DESTINY-CRC02): primary results from a multicentre, randomised, phase 2 trial. Lancet Oncol 25: 1147-1162.

5. Varayathu H, Sarathy V, Thomas BE, Mufti SS, Naik R (2021). Combination strategies to augment immune check point inhibitors efficacy-implications for translational research. Front Oncol 11: 559161.