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Letter to Editor

Gut microbiome influences incidence and outcomes of breast cancer by regulating levels and activity of steroid hormones in women

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ABSTRACT

This review comprehensively examines the role of the gut microbiome in breast cancer by regulating steroid hormones, emphasizing the impact of probiotics on gut diversity and metabolic health. The discussion could be enriched with more detailed mechanistic insights and longitudinal studies.

Key words: Gut microbiome, breast cancer, cellular pathways

Dear Editor,

I am writing to commend the authors on their review titled "Gut microbiome influences incidence and outcomes of breast cancer by regulating levels and activity of steroid hormones in women"[1]. This study presents a thorough investigation that makes a significant contribution to our understanding of the complex association between the composition of the gut microbiome and breast cancer. The authors have done an outstanding job of clarifying the complex roles gut microbiota play in immune modulation, metabolic functioning, and the control of steroid hormones (**Figure 1**). These functions are critical for understanding the course of breast cancer and the effectiveness of treatment. Particularly important is their description of how probiotics might improve gut microbiome diversity and metabolic health, pointing toward interesting paths for future therapeutic approaches. Furthermore, the incorporation of several factors such as age, menopause status, obesity, and ethnicity into the formation of gut microbiota is a beneficial approach[1].

The article offers a solid basis; however, it omits several important details that would have expanded the conversation. More thorough mechanistic insights into the interactions between certain microbial metabolites and the cellular pathways implicated in breast cancer would enhance the article. Although butyrate and lithocholic acid are mentioned in the study, the specific molecular processes by which these metabolites affect gene expression and the tumor microenvironment are not thoroughly explored. Clarifying these processes may enable us to cure or prevent breast cancer by manipulating the gut microbiota[2].

We may also gain a better understanding of the targets for therapeutic intervention. Additionally, the study would have been more comprehensive if it had focused more on clinical trials and longitudinal studies tracking the changes in the gut microbiome's composition over time in relation to the course of breast cancer and the effectiveness of therapy. Highlighting completed or ongoing longitudinal research could provide a more dynamic picture of these temporal correlations[3]. Findings would have greater translational significance if longitudinal data were used to determine causative links and patterns of interaction between gut microbiota and breast cancer.

Furthermore, while the article briefly mentions ethnicity in relation to the composition of the gut microbiome and the occurrence of breast cancer, it does not provide a detailed examination of how genetic, nutritional, and environmental factors vary among populations. More information from a wider range of demographic categories would offer a more comprehensive and inclusive picture[4]. The composition of gut microbiota is influenced by lifestyle, nutrition, and genetic background, and these factors have been shown to have a major impact on breast cancer risk and treatment outcomes. A thorough analysis of these factors across various ethnic groups may uncover significant differences and result in more specialized and effective solutions[5].

Recent technological advancements in microbiome research, such as multi-omics approaches and advanced bioinformatics tools, are also overlooked in this review. These technologies could be showcased to demonstrate how they are enhancing our understanding of microbiome interactions and opening up possibilities for personalized therapies. Metagenomics,

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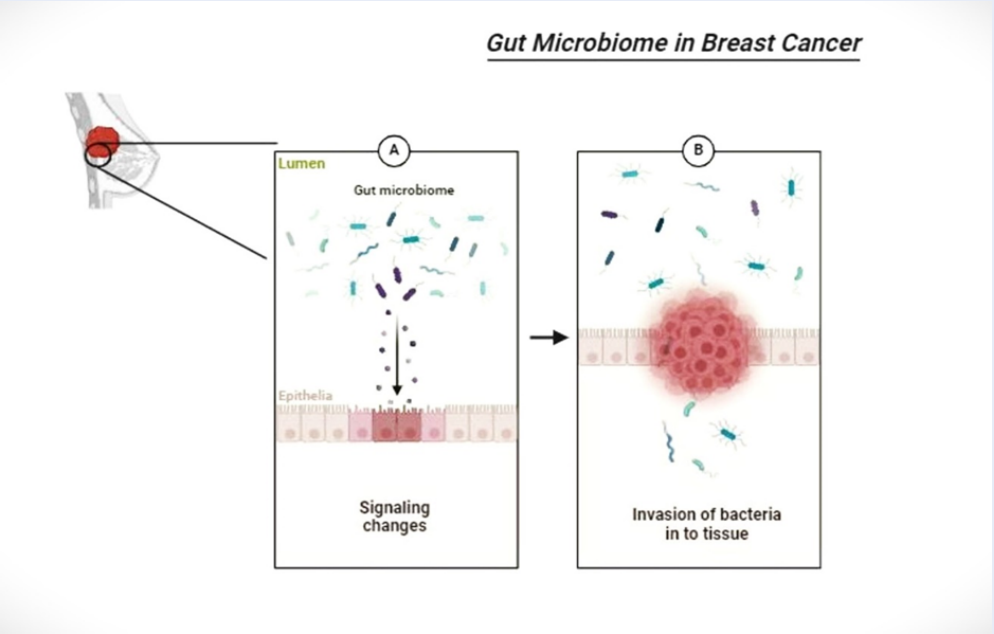

Figure 1: **Figure illustrates the gut microbiome, featuring various bacteria and enzymes interacting with steroid hormones and breast cancer cells, thereby conveying the complexity of the relationship between the gut microbiome and breast cancer**.

metatranscriptomics, and metabolomics are examples of multi-omics approaches that provide a comprehensive understanding of the functioning of the microbiome and its interactions with the host[6]. It would be highly valuable to discuss their potential in identifying new biomarkers for targeted therapy and early detection, as this would open up new research directions. Probiotics are included in the study, but other methods of microbiome manipulation such as prebiotics, synbiotics, and fecal microbiota transplantation (FMT) are not given ample attention. Analyzing the specific functions, mechanisms, and effectiveness of these strategies in altering gut microbiome composition and improving the prognosis for breast cancer patients could provide useful insights for therapeutic applications[7]. For instance, FMT has shown potential in reestablishing microbiome diversity and function under various conditions, but further research is needed in the context of breast cancer. Although brief, the discussion of phages' role in disease control is intriguing. The article's depth would increase with in-depth examinations of the mechanics and therapeutic applications of phage therapy. Phages, a type of bacteriophage, exhibit remarkable specificity. They have the ability to target pathogenic bacteria within the microbiome and reduce their numbers without disrupting beneficial microbial populations[8,9].

In conclusion, the article provides a solid foundation for understanding the connection between the gut microbiota and breast cancer; nevertheless, its comprehensiveness and utility could be greatly enhanced by addressing these overlooked opportunities and improving certain aspects. I appreciate the authors' efforts and eagerly await further works that will deepen our understanding of this vital intersection between cancer and microbiology.

ABBREVIATIONS

None.

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All authors equally contributed to this work, read and approved the final manuscript.

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The authors declare that they have no competing interests.

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