Microbiome Disharmony: A Catalyst in Breast Cancer Progression and Influencing Surgical Outcomes

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Abstract

As stated in the World Health Organisation (WHO) report of 2022, Breast cancer (BC) ranked as the most prevalent cancer among women in 157 countries, with approximately 0.5-1 per cent of BC in men and 670,000 mortality recorded. Among various other risk factors, in the past decade, the human microbial composition, viz. microbiota, has been the centre of attention in cancer biology, whose dysbiosis, which is the imbalance or disruption of the microbiome in the breast tissue and gut, can lead to BC as one of the causative factors. Once thought to be sterile, the breast tissue harbours a diverse population of microorganisms which can lead to the progression of BC. Administration of probiotics that claim to control the microbial community in the gut, which can be employed to prevent or even treat BC. This review delves into multiple studies that have advanced in this field, with an attention towards the roles of both the mammary tissue microbiome as well as its relation to the gut microbiome. Recent studies have revealed the complex communication between the gut-breast axis, immune regulation, and tumour microenvironment in BC. The gut microbiota, especially in its effect on the estrobolome and estrogen metabolism, constitutes an important modulator of BC risk, for the reason that dysbiosis could lead to a state of increased circulating estrogen levels, which would then favour and aid tumour growth. Microbial elements, which include lipopolysaccharides (LPS) and various short-chain fatty acids (SCFAs), aid in the contribution towards chronic inflammations along with immune suppressions, leading to a microenvironment that supports tumour development, which is tumour-permissive. The breast microbiome, in contrast to the gut microbiome, is gradually identified as one of the leading determinants of BC development, with certain bacterial taxa (e.g., *Methylobacterium* and *Sphingomonas*) being differentially abundant in the tumours vs healthy tissues. DNA damage by pathogenic bacteria, e.g., *Escherichia coli* and *Staphylococcus epidermidis*, has been associated with the application of genotoxins, which further substantiates the role of microbial factors in carcinogenesis. In addition, antibiotic, probiotic, and dietary manipulation of microbial composition is a promising therapeutic option. Additionally, we discuss the role of the microbiome in aesthetic and reconstructive surgeries. Knowledge of these microbially mediated interactions at the mechanistic level could help to open the door for microbiome-based biomarkers, as well as precision medicine strategies to BC prevention and treatment. Surgical interventions, including mastectomy with immediate or delayed reconstruction, implant-based or autologous tissue reconstructions, can interact with both systemic and local microbiota. Some factors matter quite a bit in recovery after surgery, such as infections that originate at the operative site where the operation took place, how the body responds to tiny foreign things left behind during surgery, and how healing progresses afterwards. Turns out the body's bacteria mix, or microbiome, plays a big role in all this too. Understanding how reconstructive choices modulate or are modulated by the breast microbiome could play a critical role in improving long-term outcomes and minimising complications.

Keywords

Breast Cancer, Microbiome, Plastic Surgery, Breast Surgery, Microbial Imbalance, Surgical Outcomes, Implants.

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