

Breast Microbiota and Breast Cancer: Current Evidence and Clinical Implications

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Abstract—Breast microbiota refers to the microorganisms living in breast tissue, and current research focuses on the changes in this microbial community that influence breast cancer development in accordance with breast microbiota and its relation to cancer, and relevant biomarkers. Breast cancer remains the most frequently diagnosed malignancy among women worldwide and is a leading cause of cancer-related mortality. While genetic, hormonal, and environmental factors have long been recognized as key contributors to breast carcinogenesis, growing evidence highlights the breast microbiota as a potential modulator of breast health and disease. Once considered sterile, the breast tissue is now known to harbor a diverse microbial community comprising bacteria, fungi, viruses, and other microorganisms that interact with the host immune system and local tissue microenvironment. Alterations in the composition and diversity of this microbial ecosystem commonly referred to as dysbiosis, have been associated with breast cancer initiation, progression, metastasis, and response to therapy. Emerging studies have identified distinct microbial signatures in healthy and malignant breast tissues, suggesting that specific microbial taxa may influence carcinogenesis through mechanisms including chronic inflammation, immune modulation, estrogen metabolism, DNA damage, and the production of microbial metabolites. Furthermore, advances in high-throughput sequencing and multi-omics technologies have expanded our understanding of host–microbe interactions and their potential role in precision oncology. This review summarizes current knowledge on the composition of the breast microbiota, its proposed mechanisms in breast cancer development, and the differences observed across breast cancer subtypes. It also discusses the influence of microbiota on therapeutic efficacy and treatment-associated toxicity, as well as the emerging potential of microbiome-based biomarkers and interventions, including probiotics, prebiotics, and microbiota modulation strategies. Despite promising findings, significant challenges remain regarding methodological standardization, causality, and clinical translation. Continued research is essential to elucidate the functional role of the breast microbiota and to establish its utility as a diagnostic, prognostic, and therapeutic target in breast cancer management.

***Index Terms*—Breast microbiota; Breast cancer; Microbiome dysbiosis; Host–microbe interactions; Precision oncology**

I. INTRODUCTION

Breast cancer is the most commonly diagnosed malignancy among women worldwide and remains one of the leading causes of cancer-related morbidity and mortality despite substantial advances in screening, diagnosis, and treatment. According to recent global cancer statistics, breast cancer accounts for a significant proportion of new cancer cases and cancer-associated deaths, highlighting the urgent need to identify novel biomarkers and therapeutic targets that can improve patient outcomes. Traditionally, breast cancer has been regarded as a multifactorial disease driven by genetic predisposition, hormonal influences, lifestyle factors, environmental exposures, and immune dysregulation [1]. Mutations in genes such as BRCA1, BRCA2, TP53, and PIK3CA, together with prolonged estrogen exposure, obesity, aging, alcohol consumption, and reproductive factors, are well-established contributors to breast carcinogenesis. However, accumulating evidence over the past decade suggests that these factors alone cannot fully explain the heterogeneity of breast cancer development, progression, and treatment response. Consequently, attention has shifted toward understanding the role of the human microbiota as a previously underappreciated component of breast health and disease [2]. The human microbiota comprises a complex and dynamic community of bacteria, fungi, viruses, archaea, and other microorganisms that colonize various body sites, including the skin, gastrointestinal tract, oral cavity, respiratory tract, and urogenital tract. These microbial communities contribute to numerous physiological processes, including immune system maturation, nutrient metabolism, maintenance of epithelial integrity, and protection against pathogenic microorganisms. Advances in culture-independent techniques, particularly next-generation sequencing (NGS), metagenomics, meta transcriptomics, and metabolomics, have revolutionized our understanding of host–microbe interactions and revealed that tissues once believed to be sterile possess distinct microbial communities. Among these, breast tissue has emerged as a unique microbial niche containing diverse microorganisms that may influence both normal mammary physiology and pathological processes [3].

The breast microbiota consists of microorganisms residing within breast tissue, nipple ducts, breast skin, and breast milk. These microbial populations are thought to originate from multiple sources, including the skin microbiota, maternal gastrointestinal tract via immune cell trafficking, hematogenous dissemination, breastfeeding, and environmental exposure. Studies have consistently identified bacterial genera such as *Staphylococcus*, *Streptococcus*, *Corynebacterium*, *Lactobacillus*, *Cutibacterium* (formerly *Propionibacterium*), *Micrococcus*, and *Pseudomonas* as common members of the healthy breast microbiome [4]. These microorganisms are believed to contribute to tissue homeostasis by modulating local immune responses, maintaining epithelial barrier function, producing antimicrobial compounds, and participating in metabolic pathways that influence mammary gland physiology. Disturbances in this balanced

microbial ecosystem, commonly referred to as dysbiosis, have increasingly been implicated in inflammatory breast disorders and breast cancer [5]. Recent investigations have demonstrated significant differences in microbial diversity and composition between healthy breast tissue and breast tumors, suggesting that alterations in the breast microbiota may contribute to tumor initiation and progression. Several studies have reported increased abundance of potentially pathogenic bacteria, including species belonging to *Escherichia*, *Fusobacterium*, and *Bacillus*, in breast tumors, whereas beneficial commensal bacteria such as *Lactobacillus* and *Sphingomonas* are often depleted [6].

These microbial alterations may promote carcinogenesis through multiple mechanisms, including chronic inflammation, immune evasion, production of genotoxic metabolites, oxidative DNA damage, modulation of estrogen metabolism, activation of oncogenic signaling pathways, and remodeling of the tumor microenvironment. Furthermore, microbial metabolites such as short-chain fatty acids, secondary bile acids, and other bioactive compounds may influence cellular proliferation, apoptosis, angiogenesis, and metastatic potential [7]. The interaction between the breast microbiota and systemic microbiomes, particularly the gut microbiota, has also emerged as an important area of investigation because of its role in regulating estrogen circulation, immune function, and therapeutic responses. Beyond its potential involvement in cancer initiation, the breast microbiota has gained attention as a determinant of clinical outcomes. Emerging evidence indicates that microbial composition may influence susceptibility to chemotherapy-related toxicity, radiotherapy responses, endocrine therapy effectiveness, and immunotherapy efficacy [8]. Consequently, modulation of the microbiota through probiotics, prebiotics, dietary interventions, antibiotics, fecal microbiota transplantation, and other microbiome-targeted approaches is being explored as a promising adjunct to conventional breast cancer treatment. Moreover, microbial signatures identified in breast tissue, breast milk, nipple aspirate fluid, or blood may serve as novel non-invasive biomarkers for early diagnosis, prognosis, risk stratification, and prediction of therapeutic response. Recent advances in microbiome research have transformed the understanding of the breast as a biologically active microbial ecosystem rather than a sterile organ [9]. The application of culture-independent technologies, including 16S rRNA gene sequencing, whole-genome metagenomic sequencing, meta transcriptomics, metabolomics, and proteomics, has enabled researchers to characterize microbial communities with unprecedented accuracy and identify functional interactions between microorganisms and host tissues. These technological developments have revealed that the breast microbiota is highly dynamic and influenced by numerous intrinsic and extrinsic factors, including age, hormonal status, reproductive history, lactation, diet, obesity, antibiotic exposure, geographic location, and genetic background. Such factors contribute to interindividual variability in microbial composition and may influence susceptibility to breast diseases, including cancer [10].

Furthermore, increasing evidence suggests that the breast microbiota does not function independently but interacts closely with the gut microbiota through the gut–breast axis, whereby microbial metabolites, immune mediators, and circulating hormones influence mammary gland

physiology and tumor biology. Understanding these complex host–microbe interactions may provide valuable insights into the mechanisms underlying breast cancer initiation and progression [11]. Consequently, integrating microbiome research with genomics, immunology, and clinical oncology offers promising opportunities for identifying novel diagnostic biomarkers, improving risk prediction, and developing personalized therapeutic strategies that enhance treatment efficacy while minimizing adverse effects, ultimately contributing to more effective precision medicine approaches for breast cancer management [12]. Despite these advances, many aspects of the breast microbiota remain poorly understood. Considerable variability exists among published studies because of differences in sample collection, sequencing methodologies, contamination control, bioinformatic analyses, and patient characteristics. Furthermore, it remains unclear whether microbial dysbiosis is a causal factor in breast carcinogenesis or a consequence of tumor development [13].

Addressing these challenges will require standardized methodologies, large multicenter studies, longitudinal investigations, and functional experiments to establish causal relationships and elucidate the molecular mechanisms underlying host–microbe interactions. This review aims to provide a comprehensive overview of the current understanding of the breast microbiota and its relationship with breast cancer. It summarizes the composition and origins of the breast microbiota, examines the mechanisms through which microbial communities may influence breast carcinogenesis, discusses microbial alterations associated with different breast cancer subtypes, and evaluates the potential clinical applications of microbiome-based biomarkers and therapeutic interventions. Finally, the review highlights current challenges, knowledge gaps, and future research directions that may facilitate the integration of microbiome science into precision medicine for breast cancer prevention, diagnosis, and treatment.

II. BREAST MICROBIOTA

The human breast was traditionally considered a sterile organ except during lactation or in the presence of infection. However, advances in next-generation sequencing (NGS) and culture-independent molecular techniques have fundamentally changed this perception by demonstrating that healthy breast tissue harbors a unique and diverse microbial community, collectively referred to as the breast microbiota. This microbial ecosystem comprises bacteria, fungi, viruses, and archaea that coexist with host tissues and contribute to the maintenance of mammary gland homeostasis [14]. Unlike pathogenic microorganisms that cause infection, commensal microbes establish a symbiotic relationship with the host by regulating immune responses, maintaining epithelial integrity, competing with opportunistic pathogens, and producing bioactive metabolites that influence tissue physiology. Although the breast microbiota is less abundant than the gut microbiota, its biological significance has gained increasing attention because of its potential role in breast development, lactation, inflammation, and carcinogenesis [15]. Growing evidence suggests that alterations in microbial composition, diversity, and function may influence breast

health and contribute to the initiation and progression of breast diseases, particularly breast cancer.

The breast microbiota consists of a relatively low-biomass but taxonomically diverse microbial population distributed throughout breast tissue, nipple ducts, the areolar skin, adipose tissue, and breast milk. Several studies have consistently identified bacterial phyla including Proteobacteria, Firmicutes, Actinobacteria, and Bacteroidetes as dominant members of the healthy breast microbial community. At the genus level, microorganisms such as *Staphylococcus*, *Streptococcus*, *Cutibacterium* (formerly *Propionibacterium*), *Corynebacterium*, *Lactobacillus*, *Micrococcus*, *Pseudomonas*, *Sphingomonas*, and *Acinetobacter* are frequently detected in normal breast tissue [16]. The composition of this microbial community varies considerably among individuals owing to differences in age, ethnicity, hormonal status, menopausal state, body mass index, dietary habits, antibiotic exposure, geographic location, pregnancy, breastfeeding history, and genetic background. These microorganisms interact with epithelial cells, immune cells, and stromal components of the mammary gland to maintain tissue homeostasis through a variety of mechanisms, including immune regulation, production of antimicrobial peptides, modulation of inflammatory pathways, and metabolism of endogenous compounds such as estrogens [17].

The origin of the breast microbiota remains an active area of investigation. Several routes of microbial colonization have been proposed. One mechanism involves direct migration of microorganisms from the skin through the nipple and lactiferous ducts into deeper breast tissue. Another hypothesis suggests hematogenous dissemination, whereby microbes originating from the gastrointestinal tract or oral cavity reach breast tissue through the bloodstream or lymphatic circulation [18]. During pregnancy and lactation, immune cells may transport beneficial bacteria from the maternal intestine to the mammary gland through an entero-mammary pathway, thereby contributing to the microbial composition of breast milk. Environmental exposure, breastfeeding practices, maternal diet, and host immune status may further shape the microbial community within breast tissue. The interaction between the gut microbiota and breast microbiota, often referred to as the gut–breast axis, has emerged as an important area of research because microbial metabolites, circulating immune mediators, and estrogen metabolism may influence mammary gland physiology and susceptibility to disease [19]. Under normal physiological conditions, the breast microbiota contributes to maintaining tissue homeostasis by supporting immune surveillance and preventing colonization by pathogenic microorganisms. Commensal bacteria stimulate innate and adaptive immune responses through interactions with pattern-recognition receptors, including Toll-like receptors, resulting in controlled cytokine production and balanced immune activation. Beneficial microorganisms also produce antimicrobial compounds and metabolites that inhibit pathogen growth while promoting epithelial barrier integrity [20]. Furthermore, certain microbial species participate in estrogen metabolism through the activity of the estrobolome, a collection of microbial genes involved in estrogen biotransformation. Because estrogen is a major regulator of mammary gland development and an established risk factor for hormone receptor-positive breast cancer, alterations in microbial regulation of estrogen metabolism may influence breast cancer susceptibility [21].

In addition, microbial metabolites such as short-chain fatty acids, secondary bile acids, and indole derivatives may regulate cellular proliferation, apoptosis, oxidative stress, and immune responses, thereby contributing to tissue health. Despite the growing recognition of the breast microbiota, significant challenges remain in accurately characterizing its composition and function. Breast tissue contains relatively low microbial biomass, making studies susceptible to contamination during sample collection, DNA extraction, sequencing, and laboratory processing. Variations in sampling methods, sequencing platforms, bioinformatic pipelines, and patient characteristics have contributed to inconsistent findings across studies. Consequently, standardized protocols and larger multicenter investigations are needed to establish a definitive microbial profile of healthy breast tissue and to distinguish true resident microorganisms from contaminants [22]. Nevertheless, accumulating evidence supports the existence of a distinct breast microbiota that plays an important role in mammary gland biology. Continued research integrating microbiology, immunology, genomics, metabolomics, and clinical oncology is expected to provide a deeper understanding of host–microbe interactions and their implications for breast health, ultimately paving the way for microbiome-based biomarkers and therapeutic strategies in breast disease management [23].

III. BREAST MICROBIOTA AND ITS RELATIONSHIP WITH BREAST CANCER

The discovery of a distinct microbial community within breast tissue has introduced a new dimension to understanding breast physiology and carcinogenesis. Historically, the mammary gland was considered a sterile environment, and the presence of microorganisms was primarily associated with pathological conditions such as mastitis. However, advances in molecular sequencing technologies have demonstrated that healthy breast tissue contains a diverse and dynamic microbial ecosystem, collectively referred to as the breast microbiota [24]. This microbial community consists mainly of bacteria belonging to the phyla Proteobacteria, Firmicutes, Actinobacteria, and Bacteroidetes, with commonly identified genera including *Staphylococcus*, *Streptococcus*, *Corynebacterium*, *Cutibacterium*, *Lactobacillus*, and *Sphingomonas*. Increasing evidence suggests that alterations in the composition and functional activity of these microbial communities may contribute to breast cancer development, progression, and therapeutic responses [25]. The concept of microbial dysbiosis, characterized by reduced microbial diversity or an imbalance between beneficial and potentially harmful microorganisms, has become an important area of investigation in breast cancer biology. Several studies have reported significant differences between the microbiota of healthy breast tissue and malignant breast tissue. Breast tumors have been associated with distinct microbial signatures, including enrichment of certain bacterial species and depletion of commensal organisms. For example, some studies have identified increased abundance of bacteria belonging to *Bacillus*, *Enterobacteriaceae*, *Fusobacterium*, and *Staphylococcus* species in tumor tissues, whereas beneficial bacteria such as *Lactobacillus* and *Sphingomonas* appear to be reduced [26].

These microbial alterations may not simply represent a consequence of tumor development but may actively contribute to carcinogenesis through multiple biological mechanisms. The interaction between microbial communities and mammary epithelial cells can influence inflammatory pathways, immune responses, cellular metabolism, and genomic stability, all of which are critical processes involved in cancer initiation and progression [27]. One of the major mechanisms linking breast microbiota to cancer development is chronic inflammation. Persistent microbial stimulation can activate immune cells and promote the production of pro-inflammatory cytokines, including interleukin-6 (IL-6), tumor necrosis factor-alpha (TNF- α), and other inflammatory mediators. Chronic inflammation creates a tumor-promoting microenvironment by enhancing oxidative stress, DNA damage, angiogenesis, and cellular proliferation. Certain microorganisms may also produce metabolites or enzymes capable of inducing genomic instability and altering host cell signaling pathways [28]. For example, microbial-derived reactive oxygen species and genotoxic compounds may contribute to DNA mutations, while bacterial metabolites can influence pathways involved in apoptosis, epithelial–mesenchymal transition, and metastatic behavior. The breast microbiota may also influence breast cancer risk through regulation of estrogen metabolism. Estrogen is a key hormonal factor involved in the development of hormone receptor-positive breast cancers. Microorganisms associated with the human microbiome possess genes encoding enzymes involved in estrogen transformation, collectively known as the estrobolome. Alterations in microbial composition may affect estrogen circulation and availability by modifying estrogen reactivation and metabolism, potentially influencing hormone-dependent breast cancer risk. In addition, microbial communities can regulate immune surveillance within the breast microenvironment.

Beneficial bacteria may enhance anti-tumor immune responses, whereas dysbiotic microbial populations may promote immune suppression, allowing tumor cells to evade immune detection [29]. The breast microbiota may also interact with the tumor microenvironment, which consists of cancer cells, immune cells, fibroblasts, extracellular matrix components, and signaling molecules. Microorganisms present within tumor tissues can influence immune cell infiltration, metabolic activity, and response to anticancer treatments. Recent studies have demonstrated that intratumoral bacteria may reside within cancer cells or immune cells and potentially affect tumor behavior [30]. These findings suggest that the microbiota may serve not only as a marker of disease but also as an active participant in tumor biology. Furthermore, differences in microbial composition among breast cancer subtypes, including estrogen receptor-positive, HER2-positive, and triple-negative breast cancers, indicate that microbial patterns may contribute to disease heterogeneity and clinical outcomes. Beyond disease development, the breast microbiota has potential implications for breast cancer diagnosis, prognosis, and treatment [31]. Microbial signatures identified in breast tissue, nipple aspirate fluid, blood, or other biological samples may serve as novel biomarkers for early detection or risk assessment.

Additionally, microbiota composition may influence the effectiveness and toxicity of anticancer therapies, including chemotherapy, endocrine therapy, and immunotherapy. Modulation of microbial communities using probiotics, prebiotics, dietary interventions, or other microbiome-

targeted strategies represents an emerging approach to complement existing cancer treatments. However, further research is required to determine whether specific microbial changes directly cause breast cancer or occur as a result of tumor-associated environmental changes [32]. Although current evidence strongly supports an association between breast microbiota alterations and breast cancer, several challenges remain. Differences in sample collection methods, sequencing platforms, contamination control procedures, and analytical approaches have contributed to variability among studies. The relatively low microbial biomass of breast tissue also presents technical challenges in accurately identifying resident microorganisms. Future investigations using standardized methodologies, longitudinal study designs, and integrated multi-omics approaches will be essential to clarify the functional role of breast microbiota in carcinogenesis [33]. Understanding the complex relationship between microorganisms and mammary tissue may ultimately provide new opportunities for microbiome-based biomarkers, preventive strategies, and personalized therapeutic approaches in breast cancer management.

IV. MICROBIOME-BASED BIOMARKERS FOR BREAST CANCER

The emergence of microbiome research has provided new opportunities for identifying innovative biomarkers for breast cancer diagnosis, prognosis, and treatment prediction. Conventional breast cancer biomarkers, including estrogen receptor (ER), progesterone receptor (PR), human epidermal growth factor receptor 2 (HER2), and genomic signatures, have significantly improved patient classification and therapeutic decision-making. However, these markers do not completely explain the biological complexity and heterogeneity of breast cancer [34]. Increasing evidence suggests that microbial communities associated with breast tissue, tumors, gut, oral cavity, and systemic circulation may provide additional molecular information that can improve risk assessment and personalized cancer management. Microbiome-based biomarkers refer to specific microbial taxa, microbial gene profiles, metabolic products, or host–microbe interaction patterns that are associated with disease presence, progression, or response to therapy. The identification of such signatures has become an emerging area of interest in breast cancer research due to the ability of microorganisms to influence tumor biology, immune regulation, inflammation, and treatment outcomes. Studies investigating the breast microbiome have demonstrated distinct microbial patterns between healthy breast tissue and malignant lesions, suggesting that microbial composition may serve as a potential diagnostic marker [35]. Several investigations have reported reduced microbial diversity and altered abundance of specific bacterial groups in breast tumors compared with normal tissues. Enrichment of certain microorganisms, including members of *Staphylococcus*, *Bacillus*, *Enterobacteriaceae*, and *Fusobacterium*, has been observed in association with breast cancer, whereas beneficial commensals such as *Lactobacillus*, *Sphingomonas*, and other protective bacterial groups may be decreased. These microbial signatures could potentially complement existing diagnostic approaches by providing additional information about tumor-associated changes [36]. Furthermore, analysis of microbial DNA, RNA, or metabolites from minimally invasive samples

such as nipple aspirate fluid, breast milk, blood, stool, or oral samples may offer opportunities for developing non-invasive biomarkers for early cancer detection. The gut microbiome has also emerged as an important source of biomarkers due to its influence on systemic metabolism, immune regulation, and hormone balance. The gut–breast axis represents a critical pathway through which intestinal microorganisms may affect breast cancer risk and progression. Alterations in gut microbial composition can modify estrogen metabolism through regulation of the estrobolome, influence circulating hormone levels, and affect immune responses involved in tumor surveillance [37]. Specific microbial patterns associated with increased estrogen reactivation or chronic inflammation may indicate higher susceptibility to hormone-dependent breast cancers.

Additionally, microbial metabolites such as short-chain fatty acids, bile acid derivatives, indole compounds, and other bioactive molecules have potential value as biomarkers because they can regulate immune cell activity, epithelial proliferation, oxidative stress, and tumor-promoting pathways. Microbiome-based biomarkers may also contribute to breast cancer prognosis and prediction of treatment response. The tumor-associated microbiome can influence the tumor microenvironment by affecting immune cell infiltration, inflammatory signaling, angiogenesis, and metastatic potential. Differences in microbial profiles among breast cancer subtypes, including ER-positive, HER2-positive, and triple-negative breast cancers, suggest that microbial signatures may provide additional information for molecular classification [38]. Furthermore, emerging evidence indicates that the microbiome may influence the effectiveness of anticancer therapies. For example, gut microorganisms can modulate immune checkpoint inhibitor responses by regulating immune activation, while microbial enzymes may affect the metabolism and toxicity of chemotherapeutic agents. Therefore, microbiome profiles may serve as predictive biomarkers to identify patients who are more likely to benefit from specific therapeutic approaches or who may require microbiota-targeted interventions [39]. Advances in high-throughput sequencing, metagenomics, metabolomics, and artificial intelligence-based bioinformatics have accelerated the discovery of microbiome-derived biomarkers. Multi-omics approaches integrating microbial composition, functional genes, metabolites, immune markers, and host genomic information may provide a more comprehensive understanding of breast cancer biology. Machine learning algorithms are also being explored to identify complex microbial patterns that can distinguish cancer patients from healthy individuals or predict treatment outcomes [40].

Such approaches may facilitate the development of precision medicine strategies in which microbiome information is incorporated alongside clinical, pathological, and molecular characteristics. Despite promising findings, several challenges must be addressed before microbiome-based biomarkers can be translated into routine clinical practice. The low microbial biomass of breast tissue increases the risk of contamination during sample processing, and variations in sequencing methods, sample collection procedures, patient characteristics, and analytical pipelines contribute to inconsistent results among studies [41]. Additionally, it remains difficult to determine whether microbial alterations are causes of breast cancer development or

consequences of tumor-associated environmental changes. Large-scale longitudinal studies with standardized methodologies are required to validate specific microbial signatures and establish their clinical reliability. Microbiome-based biomarkers represent a promising and rapidly developing field in breast cancer research. The ability of microbial communities to influence carcinogenesis, immune regulation, metabolism, and therapeutic response highlights their potential value as diagnostic, prognostic, and predictive tools [42]. Future integration of microbiome profiling with conventional biomarkers and molecular oncology approaches may improve early detection, risk stratification, and personalized treatment strategies, contributing to more effective management of breast cancer.

V. DISCUSSION

The emerging evidence on the breast microbiota has significantly expanded the understanding of breast cancer biology by revealing the complex interactions between microorganisms and the mammary microenvironment. Traditionally, breast cancer research has primarily focused on genetic alterations, hormonal regulation, environmental exposures, and immune mechanisms; however, recent advances in microbiome science indicate that microbial communities may represent an additional biological factor influencing breast cancer initiation, progression, and therapeutic response. The identification of distinct microbial patterns in healthy and malignant breast tissues suggests that the breast microbiota is not merely a passive component of the tumor environment but may actively participate in regulating cellular and molecular processes associated with carcinogenesis [43]. Although the field remains in its early stages, current findings highlight the potential of the breast microbiome as a novel area for biomarker discovery and therapeutic development.

Multiple studies have demonstrated that breast cancer is associated with alterations in microbial diversity and composition compared with non-malignant breast tissue. Tumor-associated microbial communities appear to exhibit enrichment of certain bacterial taxa and depletion of potentially protective microorganisms. These changes may contribute to tumor development through several mechanisms, including chronic inflammation, immune modulation, oxidative stress, DNA damage, and alteration of metabolic pathways [44]. The presence of specific bacteria within tumor tissues suggests that microorganisms may influence the tumor microenvironment by regulating immune cell recruitment, cytokine production, angiogenesis, and epithelial cell behavior. However, whether microbial dysbiosis is a driving factor in breast carcinogenesis or a consequence of tumor-associated changes remains an important question requiring further investigation.

One of the most promising aspects of breast microbiome research is its potential application in precision medicine. Microbial signatures from breast tissue, nipple aspirate fluid, blood, stool, and other biological samples may serve as diagnostic or prognostic biomarkers. Compared with conventional biomarkers, microbiome-based markers have the potential advantage of reflecting dynamic interactions between the tumor, host immune system, and metabolic environment.

Furthermore, the integration of microbiome profiles with genomic, transcriptomic, and metabolomic data may provide a more comprehensive understanding of individual tumor characteristics [45]. Such multi-dimensional approaches could improve early detection, risk stratification, and prediction of therapeutic responses in different breast cancer subtypes. The relationship between microbiota and cancer treatment response represents another important area of clinical interest. Increasing evidence indicates that microbial communities can influence the metabolism and effectiveness of anticancer drugs, including chemotherapy, endocrine therapy, and immunotherapy. Gut microorganisms, in particular, have been shown to regulate systemic immune responses and may affect the activity of immune checkpoint inhibitors by modifying immune cell function. Similarly, breast tissue-associated microbes may influence local immune activity within the tumor microenvironment [46]. These findings suggest that microbiome modulation through dietary interventions, probiotics, prebiotics, or targeted microbial therapies could potentially enhance treatment efficacy. However, clinical application of microbiome-based interventions requires careful evaluation to determine safety, specificity, and long-term effects. Despite the promising findings, several limitations currently restrict the translation of breast microbiome research into clinical practice. The breast microbiota is a low-biomass microbial ecosystem, making it highly susceptible to contamination during tissue collection, DNA extraction, and sequencing procedures. Differences in experimental design, sequencing platforms, bioinformatic pipelines, and patient characteristics have contributed to variability among published studies [47]. Additionally, many investigations are based on small sample sizes and cross-sectional designs, limiting the ability to establish causal relationships between microbial changes and cancer development. Standardized methodologies, larger multicenter studies, and longitudinal analyses are essential to validate microbial biomarkers and determine their clinical relevance. Future research should focus on understanding the functional role of specific microorganisms rather than simply identifying microbial differences between healthy and cancerous tissues [48]. Functional studies using metabolomics, microbial culture approaches, organoid models, and animal systems will be necessary to determine how individual microbial species influence breast cancer biology. Furthermore, investigating interactions between the breast microbiota, gut microbiota, immune system, and host genetics may provide deeper insights into the mechanisms underlying disease progression. The development of reliable microbiome-based diagnostic tools and therapeutic strategies will require integration of microbiology with oncology, immunology, and computational biology [49]. Breast microbiota represents a promising and rapidly developing field with significant implications for breast cancer research. Current evidence suggests that microbial communities contribute to breast cancer through complex interactions involving inflammation, immunity, metabolism, and tumor microenvironment regulation. Although several challenges remain, microbiome-based biomarkers and therapeutic approaches have the potential to complement existing breast cancer management strategies. Continued research will be essential to determine the clinical utility of the breast microbiome and to translate these discoveries into effective approaches for cancer prevention, diagnosis, and personalized treatment [50].

VI. CONCLUSION

The emerging field of breast microbiota research has provided a new perspective on the complex biological processes underlying breast health and breast cancer development. Once considered a sterile tissue, the breast is now recognized as a distinct microbial niche containing diverse microorganisms that interact continuously with mammary epithelial cells, immune components, and the surrounding tumor microenvironment. Increasing evidence indicates that alterations in the composition, diversity, and functional activity of the breast microbiota may influence multiple aspects of breast cancer biology, including tumor initiation, progression, metastasis, and response to therapy. These findings have expanded the traditional understanding of breast carcinogenesis by highlighting the importance of host–microbe interactions alongside genetic, hormonal, and environmental factors. The relationship between breast microbiota and breast cancer appears to be mediated through several interconnected mechanisms, including chronic inflammation, immune modulation, estrogen metabolism, oxidative stress, DNA damage, and regulation of cellular signaling pathways. Microbial dysbiosis may create a tumor-promoting environment by increasing inflammatory responses, altering immune surveillance, and producing metabolites that influence cancer cell behavior. Furthermore, differences in microbial profiles among breast cancer subtypes suggest that the microbiota may contribute to disease heterogeneity and could provide additional biological information beyond conventional molecular classifications. The identification of specific microbial signatures associated with healthy breast tissue, benign conditions, and malignant tumors highlights the potential of microbiota-based approaches for improving our understanding of breast cancer risk and progression.

The future of breast cancer research will likely involve a more comprehensive understanding of the interactions between the breast microbiota, gut microbiota, immune system, and host genetics. Advances in microbiome engineering, precision medicine, artificial intelligence-based microbial profiling, and targeted microbial interventions may provide new opportunities for breast cancer prevention, diagnosis, and therapy. Strategies involving probiotics, prebiotics, dietary modification, or other microbiome-directed approaches require further investigation to determine their safety and effectiveness in clinical settings. In conclusion, the breast microbiota represents a promising frontier in breast cancer research, offering valuable insights into disease mechanisms and potential opportunities for improved patient management. Although many questions remain regarding microbial causality, functional significance, and clinical translation, current evidence strongly supports the importance of incorporating microbiome science into modern breast oncology. Continued interdisciplinary research integrating microbiology, molecular biology, immunology, and clinical oncology will be essential to unlock the full potential of the breast microbiome and translate these discoveries into innovative approaches for breast cancer prevention, diagnosis, and personalized treatment.

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