

The maternal microbiota connection: Insights from feces and breast milk

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Abstract

Maternal gut microbiota and breast milk play a critical role in developing the infant's gut microbiota, influencing early health outcomes. Dysbiosis in early life is associated with an increased risk of chronic conditions, including allergies, asthma, and obesity, emphasizing the need for a balanced microbiota for optimal health. Breast milk is a vital source of beneficial microorganisms such as *Lactobacillus* and *Bifidobacterium*, which support the infant's immune and metabolic functions. Advances in metagenomic next-generation sequencing (mNGS) have significantly deepened our understanding of microbiota composition and its functional implications. The interplay between maternal and infant microbiota presents potential opportunities for probiotic-based interventions to improve infant health outcomes. This highlights the importance of further research into microbiota-centered health strategies to mitigate the long-term effects of dysbiosis. The findings offer valuable insights that could guide public health initiatives and lay the groundwork for future interventions to enhance maternal and infant health through effective microbiota management.

Keywords: Breast Milk; Dysbiosis; Health Outcomes; Infant Gut Microbiota; Maternal Microbiota

1. Introduction

Gut microbiota dysbiosis during early life has been associated with the development of chronic diseases such as allergies, asthma, and obesity, affecting both children and adults. Dysbiosis, characterized by an imbalance in microbial composition, triggers a pro-inflammatory state that disrupts digestion, metabolism, and immune responses (1,2). Emerging evidence highlights that maternal gut microbiota influences infant gut microbiota composition, with factors such as delivery mode, breastfeeding patterns and maternal diet shaping the infant's microbial ecosystem (3).

Breast milk (BM) is crucial for transferring functional microbiota, primarily *Lactobacillus* and *Bifidobacterium*, from mother to infant. These probiotics are pivotal in colonizing the infant's gut and promoting health (4,5). Studies using 16S rRNA sequencing have identified dominant species like *Lactobacillus ruminis* and *Bifidobacterium longum subsp. infantis* across maternal feces, BM and infant feces (5,6).

However, the resolution of 16S rRNA sequencing is limited at the species level. Metagenomic next-generation sequencing (mNGS) offers a more comprehensive approach by analyzing entire microbial genomes within a single sample, providing detailed insights into microbial profiles (7,8). Comprehensive profiling of microbiota in BM and maternal feces could pave the way for probiotic development, enhancing infant health and mitigating disease risks (9).

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Given these insights, this review aims to summarize current knowledge on microbiota composition and potential functions in maternal feces and breast milk. By integrating existing findings, this article highlights their role in shaping infant health and provides a foundation for future research and probiotic interventions.

2. Material and methods

2.1. Study Design

This study employed a narrative review approach to collect, analyze, and synthesize information about maternal fecal microbiota and human breast milk microbiota from various literature sources.

2.2. Literature Source Identification

Relevant literature was identified through systematic searches in electronic databases such as PubMed and Google Scholar, as well as official health organization websites, including those of the World Health Organization (WHO).

2.3. Inclusion and Exclusion Criteria

Articles were included if they addressed topics related to the definition, prevalence, health implications, and other relevant aspects of maternal fecal microbiota and breast milk microbiota. Only articles published within a specified timeframe (e.g., the last ten years) were selected. Articles deemed irrelevant or not available in English were excluded.

2.4. Data Collection

Information regarding the definition, concept, laboratory profiles, prevalence, and health implications of maternal fecal microbiota and breast milk microbiota was extracted from the selected articles. The data was organized and synthesized to draw coherent conclusions.

2.5. Data Analysis

The extracted data was qualitatively analyzed to identify patterns, trends, and emerging insights from the literature. Relationships between findings were explored to gain a comprehensive understanding of the topic.

2.6. Report Compilation

The findings were compiled into a structured narrative review comprising an introduction, methodology, key findings, discussion, and conclusion. The report was reviewed and revised to ensure accuracy, clarity, and completeness.

3. Results and discussion

3.1. Breast Milk Microbiota

The breast milk microbiota refers to the diverse microbial population in human milk, including bacteria, viruses, fungi, parasites, and archaea. Over 800 bacterial species have been identified, predominantly facultative anaerobes and obligate aerobes (10,11). Core genera, such as *Staphylococcus*, *Streptococcus*, *Serratia*, and *Pseudomonas*, represent around 50% of the microbiota, though their abundance varies (12,13). Breast milk, the second major microbial source for infants after vaginal delivery, is influenced by maternal mammary glands, areolar skin, and infant oral microbiota. Breastfed infants consume 1×10^5 – 1×10^7 bacteria daily, contributing to 30% of their microbiota (14). Two main mechanisms shape this microbiota: the entero-mammary pathway, involving bacterial transfer from the maternal gut to the breast, and retrograde flow, where microorganisms are exchanged between the breast and the infant's oral cavity (15,16).

3.2. Factors Influencing the Composition of Breast Milk Microbiota

3.2.1. Lactation Stage

The microbiota composition in breast milk changes with lactation stages, including colostrum, transitional, and mature milk. Colostrum typically contains more immune-regulating bacteria, while mature milk has a more diverse microbiota profile. Components such as human milk oligosaccharides (HMOs) and glycosylation patterns change with lactation stages. These alterations help to support the infant's gut microbiota development and immune system. However, some studies report inconsistent findings on the impact of the lactation stage on breast milk microbiota (14).

3.2.2. Maternal Health

Maternal health conditions, including obesity, allergies, and celiac disease, significantly impact breast milk microbiota. Obesity is associated with a decrease in *Bifidobacterium* spp. and an increase in *Staphylococcus* levels in breast milk. Allergies also contribute to reduced microbial diversity and richness. Celiac disease is linked to decreased *Bifidobacterium* abundance and higher *Verrucomicrobia* proportions. These changes could influence infant health outcomes, such as immune system development (14).

3.2.3. Delivery Mode and Gestational Age

The mode of delivery affects microbial diversity in breast milk. Vaginal delivery is associated with a higher abundance of *Lactobacillus* and *Bifidobacterium*, reflecting exposure to the maternal vaginal microbiota. Cesarean sections, especially non-emergency ones, often produce a milk microbiota composition similar to maternal skin or oral microbiota. Emergency cesarean deliveries, however, tend to have a profile closer to vaginal births. Physiological stress, hormonal signals, and gestational age also play roles in shaping breast milk microbiota (14).

3.2.4. Antibiotic Use and Medical Treatments

Antibiotic exposure during pregnancy or lactation reduces beneficial bacteria like *Lactobacillus* and *Bifidobacterium* in breast milk. This may affect the establishment of the infant's gut microbiota and immune system. Additionally, antibiotics can lead to the presence of antibiotic-resistance genes in breast milk, which may be transmitted to infants. Chemotherapy has been linked to increased *Acinetobacter* levels and reduced *Bifidobacterium*, *Staphylococcus*, and *Eubacterium* spp. The timing and type of medical treatment may influence these effects (14).

3.2.5. Geographical Location

Geographical differences in environment, climate, diet, and lifestyle contribute to variations in breast milk microbiota. Regions with diverse climates and dietary patterns show distinct microbial profiles in breast milk. Environmental exposure also impacts HMO profiles, immune markers, lipid content, and metabolic pathways in breast milk. These factors interact with local microbial populations, further diversifying breast milk microbiota. Studying these variations can inform region-specific strategies for maternal and infant health (14).

3.2.6. Dietary Intake

Maternal diet influences the composition of breast milk microbiota, affecting both microbial diversity and abundance. For example, saturated and monounsaturated fatty acids, proteins, and fiber intake have been linked to specific taxa. Vitamin C intake during pregnancy is correlated with higher *Staphylococcus* abundance, while polyunsaturated fatty acids and linoleic acid during lactation increase *Bifidobacterium* levels. Interestingly, maternal diet during pregnancy may have a more significant impact than lactation. These findings highlight the interplay between nutrition and microbial transfer through breast milk (14).

3.2.7. Maternal Infections

Maternal infections, including mastitis and viral infections, can alter the microbial composition of breast milk. Acute mastitis reduces microbial diversity and results in different microbiota profiles compared to healthy mothers. HIV-positive mothers have higher *Lactobacillus* levels and lower *Staphylococcus* abundance in their milk. The impact of other infections, such as Human Papillomavirus (HPV), on breast milk microbiota remains unclear due to limited studies. Research on the long-term effects of maternal infections on infant microbiota and health is still needed (14).

3.2.8. Genetics

Maternal genetics, particularly the FUT2 gene, influence the production of HMOs and the associated microbiota composition. HMOs stimulate the growth of beneficial bacteria such as *Staphylococcus* and *Bifidobacterium* in breast milk and the infant's gut. Variations in FUT2 activity affect the levels of 2'-fucosyllactose (2FL), a key HMO, in breast milk. Non-secretor mothers who produce less 2FL have milk associated with reduced *Bifidobacterium* colonization in their infants. Genome-wide studies targeting breast milk microbiota are needed to uncover further genetic influences (14).

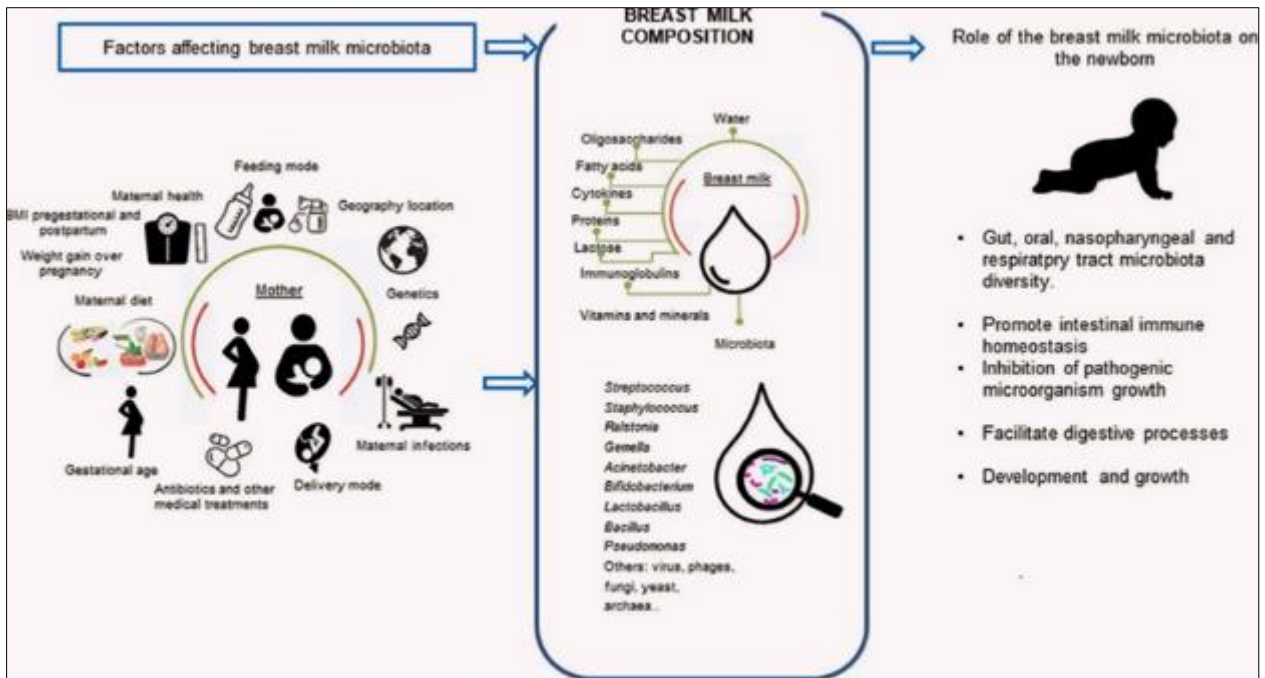


Figure 1 Factors Influencing the Composition of Breast Milk Microbiota (14)

3.3. The Benefits of Human Milk Microbiota for Infants

Breastfeeding plays a crucial role in shaping the infant gut microbiota through direct exposure to human milk microbiota and bioactive components that influence bacterial growth and metabolism (17). The significance of breast milk microbiota has been increasingly recognized in maternal and infant health within the microbiome context. Breastfeeding reduces infant mortality and morbidity and provides long-term health benefits. It protects infants against gastrointestinal infections, necrotizing enterocolitis, respiratory infections, and sudden infant death syndrome. Furthermore, it lowers the risk of chronic diseases such as allergies, asthma, diabetes, obesity, irritable bowel syndrome, and Crohn’s disease (18,19).

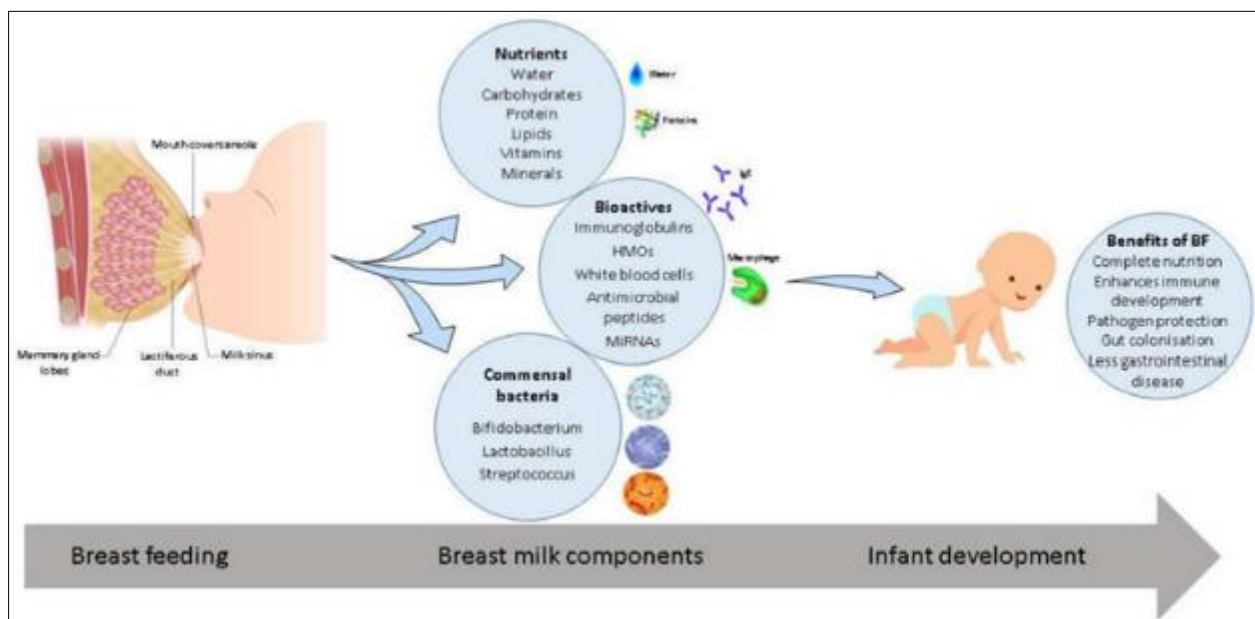


Figure 2 Composition and Benefits associated with Breastfeeding (4)

Recent studies have explored how breast milk bacteria function in the infant’s gut. Breast milk microbiota prevents infections through antimicrobial compound production, competitive exclusion, pathogen adhesion inhibition, and

enhanced mucin production (4,20). Moreover, it supports immune system maturation by shifting intrauterine Th2-dominant immune responses to balanced Th1/Th2 immunity and inducing regulatory T-cell differentiation. Metagenomic analyses reveal immunomodulatory DNA motifs in breast milk microbiota that reduce inflammatory responses. Additionally, breast milk bacteria metabolize oligosaccharides to produce short-chain fatty acids, promoting beneficial bacterial growth. These processes enhance gut immune homeostasis and nutrient absorption, inhibiting pathogens like *Salmonella enterica* and *Escherichia coli* (14).

3.4. Factors Influencing Maternal Gut Microbiota Composition

3.4.1. Pre-Pregnancy Factors

In humans and mice, environmental factors have been shown to dominate host genetics in shaping the overall structure of the gut microbiota. Key factors that influence the adult gut microbiota include anthropometric measures (e.g., Body Mass Index (BMI)), medications (e.g., antibiotics, proton pump inhibitors (PPI)), diseases (e.g., type-2 diabetes), lifestyle (e.g., smoking), and diet (e.g., Mediterranean diet). Early life factors, such as diet, physical activity, urban living, and pet exposure, can have long-lasting effects on the gut microbiota. Previous smoking habits can even influence the microbiota long after cessation. These factors can continue to affect the gut microbiota during pregnancy. Research using 16S rRNA sequencing of fecal samples from pregnant women has shown that pre-pregnancy BMI affects 20 operational taxonomic units (OTUs). Diseases like hyperthyroidism and inflammatory bowel disease (IBD) have been linked to changes in OTUs during pregnancy (21,22).

3.4.2. During Pregnancy

Studies in mice indicate that pre-pregnancy and dietary factors influence pregnancy-related shifts in maternal gut microbiota. Diet during pregnancy significantly impacts maternal microbiota, as demonstrated in a cohort study of 86 mother-infant pairs, where maternal macronutrient intake was strongly linked to neonatal gut microbiota (23). Pre-pregnancy weight and weight gain during pregnancy have also been shown to affect the maternal gut microbiota. A cohort study of 169 overweight/obese women found lower alpha diversity and changes in microbial composition, with excessive gestational weight gain further altering gut microbiota composition. The impact of pre-pregnancy BMI and weight gain during pregnancy on infant gut microbiota is still unclear, though some studies suggest a correlation depending on the delivery mode (24,25).

Exposure to factors like smoking during pregnancy can influence the maternal microbiota—a study by Zubcevic et al. (26) on mice found that prenatal nicotine exposure affects maternal gut microbiota, potentially mediating changes in gene expression and influencing fetal exposure to short-chain fatty acids (SCFA) and circulating leptin during in-utero development. Furthermore, maternal pregnancy history, such as parity, can accelerate gut microbiota changes during pregnancy, as observed in a longitudinal study on pigs. Medications such as antibiotics, PPIs, laxatives, metformin, and pre- and probiotics modulate the gut microbiota during pregnancy. Thus, numerous factors shape the maternal gut microbiome throughout pregnancy (22,27,28).

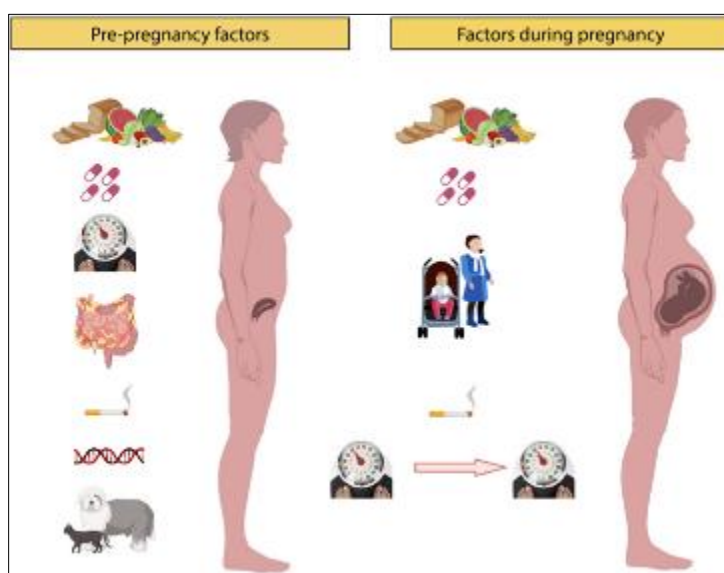


Figure 3 Factors that shape the maternal gut microbiota before and during pregnancy (22)

3.5. The Role of Maternal Gut Microbiota in Infant Health

Maternal gut microbiota has significant implications for maternal and infant health, influencing various aspects such as fetal neurodevelopment. Vuong et al. (29) demonstrated in rodent models that maternal gut microbiota promotes thalamocortical axonogenesis through microbial modulation of metabolites that signal to neurons during embryonic brain development. This process may have long-lasting effects on infant behavior. A cohort study involving 213 mothers and 215 children revealed that the alpha diversity of maternal gut microbiota during the third trimester correlates with internalizing behaviors in children at two years of age. However, the sample size was relatively small. Beyond neurodevelopment, maternal gut microbiota also shapes the infant's metabolic system via metabolites such as SCFAs, as shown in rodent studies (30,31). Furthermore, specific gut bacteria, such as *Prevotella copri*, have been linked to a reduced risk of food allergies in children. These findings emphasize the importance of further research on the relationship between maternal gut microbiota composition and infant health, given its short- and long-term health consequences (22,32).

Maternal gut microbiota is crucial in regulating metabolism and immunity during pregnancy. It aids in the digestion of carbohydrates, producing essential metabolites like vitamins, amino acids, and SCFAs, which are vital for fetal development (33). Studies on mice indicate that dietary changes can impact fetal growth and development through the gut microbiota, with malnutrition or high-fat diets impairing metabolic function and growth. Specific maternal gut bacteria, such as segmented filamentous bacteria, are key in maintaining immune responses and fetal neurodevelopment. Thus, maternal gut microbiota and its metabolites are closely associated with prenatal fetal development (33,34).

4. Conclusion

In summary, this review highlights the significant role of maternal gut microbiota and breast milk in shaping the infant's gut microbiota and influencing early health outcomes. Dysbiosis in the early stages of life is associated with the development of chronic diseases such as allergies, asthma, and obesity. The transfer of beneficial bacteria, including *Lactobacillus* and *Bifidobacterium*, through breast milk is crucial in supporting the infant's immune system and metabolic health. Advances in sequencing technologies, particularly metagenomic next-generation sequencing (mNGS), provide deeper insights into the complexity of microbiota composition and their functional roles. This research underscores the importance of understanding maternal-infant microbiota interactions to develop potentially targeted probiotic interventions. By improving infant health through better microbiota management, this study offers valuable contributions to public health and provides a foundation for future research into microbiota-based health interventions.

Compliance with ethical standards

Disclosure of conflict of interest

No conflict of interest is to be disclosed.

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