The Role Of Maternal Microbiota And The Quality Of Breast Milk

[1]Prof. Uma Devi T., [2]Dr Prema Krishnan

[1]PhD Scholar (Nursing), Department of Obstetrics and Gycaecological Nursing, Shri Sathya Sai College of Nursing, Sri Balaji Vidyapeeth (Deemed to be University), Chennai, India.
[2]Professor cum Principal, Department of Pediatric Nursing, Shri Sathya Sai College of Nursing, Sri Balaji idyapeeth (Deemed to be University), Chennai, India.
Address for correspondance:
Prof Uma Devi T., PhD Scholar,
Department of Obstetrics and Gycaecological Nursing, Shri Sathya Sai College of Nursing, Sri Balaji Vidyapeeth (Deemed to be University), Chennai, India

ABSTRACT

It is becoming more widely acknowledged that the content of breast milk and the health of the newborn are significantly influenced by the mother's microbiota. The intricate relationships among early-life immunological and metabolic development, breast milk bioactive components, and maternal microbial communities are examined in this review. It emphasizes how the microbiota of the mother's gut, skin, vagina, and surroundings help to seed good bacteria in milk, influencing the gut microbiota of the baby and promoting immunological development. Maternal microorganisms have a crucial role in child nutrition and disease prevention through their modulation of breast milk contents, such as immunoglobulins, cytokines, human milk oligosaccharides, fatty acids, vitamins, and antimicrobial peptides. The effects of factors affecting maternal microbiota on milk quality and microbial diversity are investigated. These factors include the mode of delivery, food, probiotic intake, antibiotic exposure, stress, and mother health.Clinical and scientific implications are also covered in the article, with a focus on methods for preserving a healthy mother microbiome for the best lactation results and the long-term health of the infant.

KEYWORDS: Maternal microbiota, Breast milk microbiome, Infant gut colonization, Human milk oligosaccharides (HMOs), Immunoglobulin A (IgA), Maternal diet, Probiotics and prebiotics, Antibiotic exposure, Early-life immune development.

How to Cite: Prof. Uma Devi T, Prema Krishnan, (2025) The Role Of Maternal Microbiota And The Quality Of Breast Milk, Vascular and Endovascular Review, Vol.8, No.5s, 162-167.

INTRODUCTION

The complex community of bacteria, viruses, and fungithat live in a woman's body, especially in her stomach, vagina, skin, and mammary glands, is known as the maternal microbiota.Pregnancy outcomes, postnatal infant development, and maternal health are all significantly impacted by these microbes.Breast milk considered as a sterile fluid, is understood to include a rich and dynamic microbiome that is influenced by the environment, nutrition, health, and microbial status of the mother that influences the neurodevelopmental outcomes and newborn health. The interaction of maternal and newborn microbiota, environmental exposures, and genetic predispositions can influence the immunological and metabolic development of the infant during the critical stages of fetal development, infancy, and early childhood, hence affecting the risk of chronic diseases in adulthood. Long-term health outcomes are impacted by the makeup and function of the mother's microbiota, which is passed on throughout pregnancy and lactation and is crucial in forming the infant's gut microbiome.

SOURCES OF BREAST MILK MICROBIOTA

The development of the newborn's gut microbiome and the stimulation of immune development depend on the diverse microbial community present in breast milk. Numerous maternal and environmental factors impact this milk microbiome, and each one enters the mammary gland or is transferred to the nursing infant via a distinct biological mechanism. The primary sources are the baby's mouth cavity (by direct mechanical transfer during eating), the mother's skin, the mother's gut (through the entero-mammary pathway), and the mother's vaginal and ambient microbiota. The method the baby was delivered, their personal hygiene practices, and their living environment all have an impact on these.

Entero-mammary pathway: Intestinal immune cells, mostly dendritic cells and macrophages, sample some beneficial gut bacteria (Bifidobacterium, Lactobacillus, and Enterococcus). After internalizing the microorganisms, these immune cells proceed to the mammary glands through the circulation and lymphatic system. After entering the mammary tissue, the bacteria are released into breast milk, which allows the baby to get commensals from the gut vertically. Anaerobic and HMO-using bacteria, which are otherwise challenging to transfer directly, can be delivered via this method.

Skin and newborn oral cavity: The infant's mouth and gut are colonized by the mother's areolar and skin bacteria when breastfeeding. On the other hand, a two-way exchange can occur when bacteria from the baby's oral cavity enter the nipple ducts. This process supports the diversity of the milk and newborn microbiomes while preserving regional microbial ecosystems.

Vaginal and environmental sources: The method of delivery affects the infant's first exposure to germs. While caesarean delivery favors skin-associated bacteria like Staphylococcus and Corynebacterium, vaginal birth exposes newborns to Lactobacillus and other vaginal bacterial species. The mother's milk microbiome is further shaped by environmental factors such as pets, nutrition, cleanliness habits, household microbiota, and local living conditions, all of which have an indirect impact on infant gut colonization.

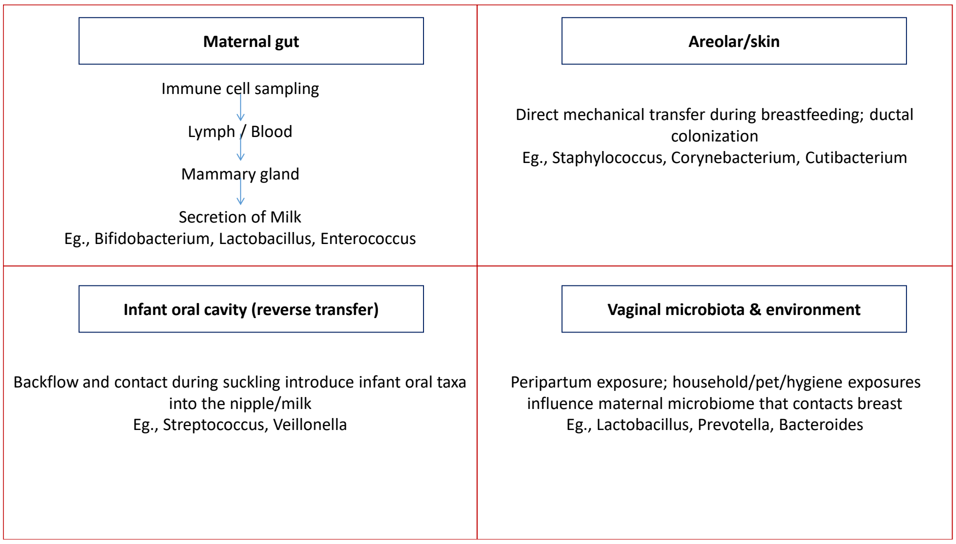

Figure 2 — Sources, Mechanisms & generations

But there are several maternal and environmental factors influence the composition and diversity of the breast milk microbiota, ultimately shaping the infant's microbial and immune development. Mode of delivery plays a pivotal role—infants born via vaginal birth are exposed to vaginal microbial taxa such as *Lactobacillus* and *Prevotella*, which may also be reflected in the mother's milk microbiota. In contrast, cesarean section delivery often leads to dominance of skin-associated microbes like *Staphylococcus* and *Corynebacterium*, reflecting altered microbial transfer patterns. Maternal diet and nutrient intake are also key determinants; diets rich in fiber, polyunsaturated fatty acids (PUFAs), and fermented foods have been shown to influence the milk's fatty acid profile and modulate the diversity and abundance of beneficial bacteria. Antibiotic exposure, whether during pregnancy, peripartum, or postpartum, can transiently disrupt microbial equilibrium, resulting in reduced bacterial diversity and dysbiosis in breast milk, which may subsequently affect the infant's gut colonization. Maternal body mass index (BMI) and metabolic health further contribute to microbial variation—obesity is associated with lower microbial diversity and distinct taxa distribution, often accompanied by altered lipid and metabolite profiles in milk. Probiotic supplementation during pregnancy or lactation can beneficially modify the milk microbiome, with certain administered strains (e.g., *Lactobacillus rhamnosus*, *Bifidobacterium*) being detected in milk and linked to improved infant gut health. Lastly, psychosocial stress has emerged as an influential, though less studied, factor; stress-related hormonal and immunological changes may alter the mammary microbial environment, suggesting a potential link between maternal emotional well-being and milk microbiota composition. Together, these factors highlight the dynamic and multifactorial nature of the human milk microbiome and its sensitivity to maternal physiology, behavior, and environment.

THE MATERNAL MICROBIOTA AND ITS LINK TO BREAST MILK MICROBIOME

The broad and intricate ecology of bacteria, viruses, and fungi that inhabit different parts of the mother's body, including the gastrointestinal tract, vagina, skin, oral cavity, and mammary glands, is known as the maternal microbiota. By promoting nutrition metabolism, immunological regulation, endocrine balance, and defense against pathogenic invasion, these microbial communities work together to maintain homeostasis. (Rinninella et al., 2019).

Due to hormonal, metabolic, and immunological changes that prime the mother and fetus for optimal development, the maternal microbiome experiences significant alterations throughout pregnancy. For instance, in late pregnancy, the gut microbiota tends to become less diversified but more energy-harvesting, reflecting the mother's elevated metabolic needs.(Koren et al., 2012). Similarly, the vaginal microbiota, dominated by *Lactobacillus* species, plays a significant role in maintaining the pH and preventing ascending infections, thereby protecting the fetus.

It is also known that the mammary gland is a microbial habitat with a resident microbiota that can come from a variety of maternal origins. The long-term belief that breast milk is a sterile fluid has been disproved by the revelation that it contains living microbes.(Cabrera-Rubio et al., 2012; Pannaraj et al., 2017). Modern genomic and RNA sequencing techniques have identified more than 700 bacterial species in human milk, though their abundance and diversity vary according to maternal health, diet, mode of delivery, lactation stage, and geographical factors.

The entero-mammary route theory, which postulates that specific maternal intestinal bacteria, including Bifidobacterium longum and Lactobacillus rhamnosus, are selectively transferred from the maternal gut to the mammary gland via immune cell-mediated translocation, is supported by new data. (Rodríguez, 2014; Jost et al., 2014). This mechanism ensures the vertical transfer of microbes from mother to infant during breastfeeding, supplying the newborn's intestines with beneficial commensals that are necessary for immunological and metabolic development.

Breast milk microbiota interacts synergistically with human milk oligosaccharides (HMOs), antimicrobial peptides, immunoglobulins, and cytokines, creating a bioactive matrix that influences the development of the infant's immune system and gut ecology. For instance, *Bifidobacterium infantis*uses particular HMOs as a substrate to produce short-chain fatty acids (SCFAs), which improve the integrity of the intestinal barrier and control inflammatory reactions. (Milani et al., 2017).

Additionally, it has been shown that the mother's dietary habits and the composition of her gut microbiota affect the lipid, protein, and micronutrient profiles of breast milk. Diets rich in fiber, polyphenols, and fermented foods, which promote the growth of beneficial species like Bifidobacterium and Lactobacillus, further strengthen the anti-inflammatory and immunoregulatory properties of milk. However, maternal obesity, high-fat diets, and antibiotic exposure are associated with lower microbial diversity and higher pro-inflammatory cytokines in milk. (Collado et al., 2012; Kumar et al., 2016).

From a developmental and clinical standpoint, the maternal microbiota–milk axis is now viewed as a critical determinant of infant health. The early colonization of the infant's stomach by maternal commensal microbes is associated with a lower risk of allergies, necrotizing enterocolitis, obesity, and metabolic illnesses in late periods of life(Fitzstevens et al., 2017). Thus, maternal microbial balance is not merely a reflection of health but an active biological interfacetransmitting microbial, immune, and metabolic signals from mother to child during the lactational period.

Table 1: Key Aspects of Maternal Microbiota and Their Scientific Evidence

Features	**Observations**
Maternal gut microbiotica changes pregnancy	Reduced diversity, increased Proteobacteria and Actinobacteria for energy harvest
Presence of microbes in milk	Milk contains >700 bacterial species
Entero-mammary pathway	Gut - origin bacteria translocate to milk via dentritic cells
Effect of maternal diet on milk microbiome	Fiber-and probiotic rich diets enhance beneficial bacteria in milk

MODULATION OF BREAST MILK BIOACTIVE COMPONENTS

The nutritional and immunological qualities of breast milk are influenced by the mother's microbiota. Human milk oligosaccharides (HMOs) serve as prebiotics for baby Bifidobacteria and are regulated by genes from gut microbes. SCFAs control anti-inflammatory cytokines like IL-10 and TGF-β, which promote tolerance, whereas maternal microbial exposure increases IgA and IgG secretion, which offers immunological protection. Lipids and fatty acids, such as CLA and omega-3s, which assist brain and retinal development, are also impacted by microbial metabolism. Lactoferrin and lysozyme, two antimicrobial peptides that shield milk from infections and further improve newborn health, are increased by a balanced microbiome.The maternal microbiota influences the nutritional and immunological quality of breast milk through biochemical signaling:

Table 2: Components of Breastmilk anf It's Functions

Milk component	***Microbiota - Linked Functions***
Human Milk Oligosaccharides	Their synthesis and profile are partially regulated by maternal gut microbial genes, and they serve as prebiotics for the infants' stomach.
Immunoglobulins (IgA, IgG)	Secretary IgA in milk rises as a result of mucosal immune priming triggered by maternal microbial exposure.
Cytokines (IL - 10 and TGF - Beta)	SCFAs produced by the mother's gut microbes control anti-inflammatory cytokines, aiding in the development of the infant's immune system.
Lipids and Fatty Acids	The production of conjugated linoleic acid and omega-3 fatty acids in breast milk is influenced by the maternal microbiome, which promotes infants' neurodevelopment and retinal maturation.
Antimicrobial Peptides (Lactoferrin and Lysozyme)	A healthy maternal microbiota prevents pathogen colonization in breast milk by enhancing antimicrobial expression.

MATERNAL MICROBIOTA'S INFLUENCE ON BREAST MILK QUALITY

The maternal microbiota—especially that of the gut, mammary glands, skin, and vaginal tract—plays a crucial role in shaping the immunological, biochemical, and microbial composition of breast milk. This, in turn, directly influences infant health, growth, and disease resistance.

Immune and Anti-inflammatory Properties

Through microbial metabolites and structural elements like lipopolysaccharides and peptidoglycans, the maternal gut microbiota interacts with the immune system, triggering immunological signaling that affects the composition of breast milk. The secretory immunoglobulin A (IgA) in milk, which coats the infant's gut and inhibits pathogen attachment, is higher when the gut microbiota is healthy because it improves mucosal immunity. Mothers with healthy gut flora had higher levels of milk IgA and anti-inflammatory cytokines, according to Gómez-Gallego et al. (2016). In a similar vein, a healthy mother's microbiota encourages the release of lactoferrin and anti-inflammatory cytokines (IL-10, TGF-β), which strengthens immunological tolerance and lowers inflammation in babies. Le Doare et al. (2018) also noted that a higher risk of infections in babies and a decrease in cytokine variety in milk were linked to dysbiosis in the maternal microbiome.

Prebiotic Components – Human Milk Oligosaccharides (HMOs)

Complex, indigestible carbohydrates known as human milk oligosaccharides (HMOs) are produced in the mammary gland under the control of microbes and genes. They act as specific substrates for Lactobacillus reuteri and Bifidobacterium infantis, two helpful bacteria that are found in the infant's stomach. The diversity and concentration of HMOs in milk are influenced by the maternal gut microbiota, which also affects HMO production via modifying the activity of associated enzymes. According to Korpela et al. (2018), moms who had a more varied gut microbiota produced a greater range of HMOs, which encouraged children to have a gut colonization dominated by Bifidobacterium. In the newborn gut, HMOs serve as prebiotics, immunological signaling modulators, and decoy receptors that prevent pathogen adherence (e.g., E. coli, Campylobacter).

Nutritional and Metabolic Quality

The nutritional profile of breast milk is shaped by the maternal gut microbiota, which is essential for nutrient production and metabolism. The composition of milk fatty acids, especially short-chain fatty acids (SCFAs) like acetate, propionate, and butyrate, which even in trace amounts support immunological homeostasis and gut development in infants, is influenced by gut microorganisms that control lipid metabolism. The availability of long-chain polyunsaturated fatty acids in milk is influenced by the metabolism of maternal microbes. Furthermore, the synthesis of vital vitamins like B2, B6, B12, and K is influenced by gut flora, which also affects the amount of these vitamins in breast milk. The antibiotic-induced disturbance of the microbiota can lower the micronutrient content of milk and identified 'Bifidobacterium adolescentis' and 'Lactobacillus plantarum' as important vitamin-producing microorganisms.

Protection Against Pathogens

The maternal microbiota functions as a biological defense system that preserves the microbial stability of breast milk by preventing pathogen overgrowth. Through competitive exclusion, commensal species such as Staphylococcus epidermidis and Lactobacillus gasseri inhibit pathogenic microbes like Staphylococcus aureus and Candida albicans by competing for nutrients and adhesion sites within the mammary ducts. Lactobacillus strains isolated from breast milk effectively suppresses the growth of these pathogens. Additionally, the production of antimicrobial peptides (AMPs) and metabolites such as bacteriocins and lactic acid by beneficial milk bacteria helps maintain a mildly acidic environment, further restricting pathogen proliferation. It was reported that Lactobacillus salivarius from human milk produces bacteriocins with potent activity against mastitis-causing pathogens, highlighting the protective role of the maternal microbiota in maintaining milk safety and infant health.

FACTORS AFFECTING MATERNAL MICROBIOTA AND MILK QUALITY

Mode of Delivery

More maternal vaginal and gut bacteria are transferred during birth when a baby is delivered vaginally, which seems to foster a milk microbiota that is more diverse and rich in beneficial bacterias. Compared to vaginal births, cesarean section deliveries were substantially linked to modifications in the microbial makeup of breast milk. On the other hand, the milk microbiota seems to be skewed by C-section in favor of the micriobiomes that are more commonly found in the skin or mouth (such Staphylococcus and Corynebacterium) and less common in the mother's gut or vagina. The trajectory of gut colonization in infants and even the results of immune development may be impacted by this changed microbial seeding.

Maternal Dietary Habits

It has been demonstrated that the composition of the mother's diet, particularly the amount of fiber, plant versus animal protein, complex carbohydrates, and fatty acid profile, shapes the diversity (richness & evenness) and taxonomy of the milk microbiota. Mothers in diet clusters with higher intakes of plant-based proteins, fiber, and carbs, for example, had richer and more diverse taxa in their breast milk microbiota than mothers in clusters with higher intakes of animal protein and lipids. Furthermore, when combined with additional stressors (such as C-section or antibiotics), diets high in fat or animal protein tended to correspond with decreased abundances of beneficial genera (such as Lactobacillus and Bifidobacterium) in milk. As a result, nutrition becomes a variable that can affect the ecology of milk microbes and subsequent newborn colonization.

Probiotic / Prebiotic Intake

There is evidence that probiotics (such as Lactobacillus rhamnosus or Bifidobacterium longum strains) and prebiotic fibers taken by women can affect the composition of the milk microbiota (by boosting the presence of beneficial taxa) and, in turn, the gut microbiota of the newborn. According to a systematic analysis, probiotic supplements given to mothers during pregnancy and breastfeeding frequently caused the provided strains to colonize the breast milk microbiome. Although impact sizes and consistency vary, this shows that probiotic/prebiotic intake by mothers may be a feasible way to favorably alter the milk microbiota.

Antibiotic Exposure (Maternal/Peripartum)

Antibiotic use has a significant impact on the milk microbiota by reducing diversity and changing taxonomic composition, whether it is through intrapartum prophylaxis, postpartum treatment for mothers, or peripartum antibiotic exposure. For instance, significant alterations in milk microbial diversity and abundance were associated with just one day of antibiotic exposure in mothers of preterm children. Furthermore, the reduction of beneficial genera (such as Lactobacillus and Bifidobacterium) in both milk and the infant's gut is linked to the mother's exposure to antibiotics during breastfeeding. The effects of antibiotic exposure are complex since they impact the microbiota of the mother's gut and vaginal/skin, which are the reservoirs for milk bacteria, as well as horizontal transmission during delivery and lactation.

Stress and Hormonal Factors

There is growing evidence that the composition of the microbiota in breast milk can be influenced by maternal psychosocial stress, hormonal changes (such as cortisol and catecholamines), and associated alterations in gut physiology (such as altered microbiota and increased intestinal permeability). An RCT supported the idea of a gut–brain–mammary axis of microbial transmission by revealing that a stress-reduction intervention changed the mother's gut microbiome and breast milk microbiota. According to another study, moms who experienced more early postpartum stress had milk microbiomes with different beta-diversity than mothers who experienced less stress. For instance, their milk microbiomes had higher levels of Staphylococcus, Corynebacterium, and Acinetobacter and lower levels of Streptococcus, Gemella, and Veillonella. Thus, through gut, immunological, and hormonal pathways, mother emotional and physiological stress may indirectly alter the milk microbiota, which could have an impact on the microbial seeding of the newborn.

Gestational Age & Maternal Health Status

Changes in milk microbiota patterns are linked to preterm birth, maternal obesity, or metabolic dysregulation (such as gestational diabetes). For instance, the milk microbiota of mothers of preterm infants (less than 1,250 g) showed temporal alterations and was highly personalized; these dynamics were linked with maternal BMI, delivery style, and antibiotic exposure. Additionally, there is a lack of particular large-scale human milk microbiome investigations, but other literature links changed gut microbiota to obesity and poor maternal metabolic health, which may thus affect milk microbiota. Thus, the environment during pregnancy and the health of the mother create an environment that encourages the growth of microbiota in milk and, in turn, increases the risk of colonization in the newborn.

THE MATERNAL MICROBIOTA–BREAST MILK–INFANT HEALTH AXIS

The maternal microbiota, including gut, vaginal, oral, and skin communities, forms the primary microbial reservoir influencing maternal and infant health. Gut microbes produce short-chain fatty acids (SCFAs) that regulate immunity, metabolism, and hormonal signaling, while vaginal microbiota (*Lactobacillus crispatus*, *L. jensenii*) and skin microbes (*Staphylococcus*, *Corynebacterium*) contribute to the infant's initial microbial colonization and milk microbiome. Maternal factors such as diet, BMI, hormones, and antibiotics shape these communities and milk composition.

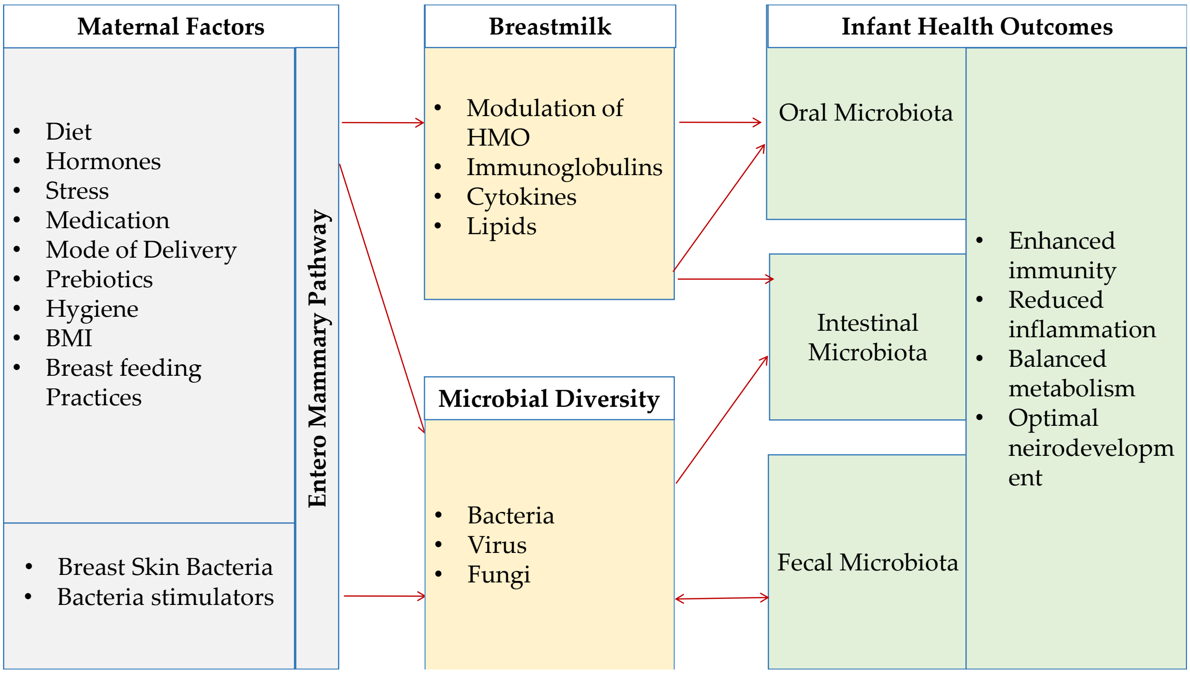

Figure 1 : Maternal Microbiotica- Breastmilk-Infant Health Axis

Vertical transmission occurs via the entero-mammary pathway, where intestinal immune cells transport commensal bacteria (e.g., *Bifidobacterium longum*, *Lactobacillus rhamnosus*, *Enterococcus faecium*) to the mammary glands. Breast milk delivers microbial and molecular signals that guide infant gut colonization, immune maturation, and epithelial development. Beneficial microbes (*Bifidobacterium breve*, *Lactobacillus gasseri*, *Streptococcus salivarius*) and SCFAs promote barrier integrity, regulate inflammation, and support regulatory T-cell differentiation. This microbiota–milk–infant interplay shapes long-term outcomes, lowering risks of necrotizing enterocolitis, allergies, obesity, metabolic disorders, and enhancing neurodevelopment via microbial metabolites such as tryptophan and GABA.

CONCLUSION

The nutritional, immunological, and microbiological quality of breast milk is largely determined by the mother's microbiota, which also affects the infant's gut colonization, immune programming, and long-term health. Maternal microorganisms aid in the production of bioactive substances including immunoglobulins, cytokines, and human milk oligosaccharides that shield the baby from infections and inflammation through processes of microbial transmission, immunological modulation, and metabolic regulation. A healthy infant gut environment is fostered by the presence of helpful bacteria like *Lactobacillus* and *Bifidobacterium* in milk, which are guaranteed by a balanced maternal microbiome. On the other hand, changes in milk microbial diversity and composition brought on by stress, poor diet, overuse of antibiotics, or metabolic problems may have an impact on baby immunity and metabolism.Therefore, to maximize the quality of breast milk and encourage resilience and lifelong health in newborns, it is crucial to maintain a healthy maternal microbiome through a nutrient-rich diet, probiotic and prebiotic supplements, prudent antibiotic use, and stress management.

REFERENCE

1. Cabrera-Rubio, R., Collado, M. C., Laitinen, K., Salminen, S., Isolauri, E., & Mira, A. (2012). The human milk microbiome changes over lactation and is shaped by maternal weight and mode of delivery. *American Journal of Clinical Nutrition, 96*(3), 544–551.
2. Collado, M. C., Isolauri, E., Laitinen, K., & Salminen, S. (2012). Effect of mother’s microbiota on the newborn colonization process. *Current Opinion in Clinical Nutrition and Metabolic Care, 15*(5), 583–588.
3. Fitzstevens, J. L., Smith, K. C., Hagadorn, J. I., Caimano, M. J., & Matson, A. P. (2017). Systematic review of the human milk microbiota. *Nutrition in Clinical Practice, 32*(3), 354–364.
4. Jost, T., Lacroix, C., Braegger, C. P., Rochat, F., & Chassard, C. (2014). Vertical mother–neonate transfer of maternal gut bacteria via breastfeeding. *Environmental Microbiology, 16*(9), 2891–2904.
5. Koren, O., Goodrich, J. K., Cullender, T. C., et al. (2012). Host remodeling of the gut microbiome and metabolic changes during pregnancy. *Cell, 150*(3), 470–480.
6. Milani, C., Duranti, S., Bottacini, F., Casey, E., Turroni, F., Mahony, J., ... & Ventura, M. (2017). The first microbial colonizers of the human gut: Composition, activities, and health implications of the infant gut microbiota. *Microbiology and Molecular Biology Reviews, 81*(4), e00036-17.
7. Pannaraj, P. S., Li, F., Cerini, C., Bender, J. M., Yang, S., Rollie, A., ... & Aldrovandi, G. M. (2017). Association between breast milk bacterial communities and establishment and development of the infant gut microbiome. *JAMA Pediatrics, 171*(7), 647–654.
8. Rinninella, E., Raoul, P., Cintoni, M., Franceschi, F., Miggiano, G. A. D., Gasbarrini, A., & Mele, M. C. (2019). What is the healthy gut microbiota composition? A changing ecosystem across age, environment, diet, and diseases. *Microorganisms, 7*(1), 14.
9. Rodríguez, J. M. (2014). The origin of human milk bacteria: Is there a bacterial entero-mammary pathway during late pregnancy and lactation? *Advances in Nutrition, 5*(6), 779–784.