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+15878858911
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THE IMPORTANCE OF THE ROLE OF THE BREAST MILK MICROBIOTA IN THE DEVELOPMENT OF ASTHMA IN CHILDREN

Wojciech Plizga
J. Gromkowski Regional Specialist Hospital, Wrocław, Poland
ORCID ID: 0009-0005-9847-2026

Ivanna Lazarchuk *(Corresponding Author, Email: ivanna.lazarchuk@gmail.com)*
Regional Specialist Hospital, Wrocław, Poland
ORCID ID: 0009-0000-1104-0794

Mateusz Sydor
5th Military Clinical Hospital with Polyclinic SPZOZ, Kraków, Poland
ORCID ID: 0009-0007-0975-8060

Paulina Kalemba
Faculty of Medicine, Wroclaw Medical University, Wrocław, Poland
ORCID ID: 0009-0000-5856-1271

Patrycja Lipska
Faculty of Medicine, Wroclaw Medical University, Wrocław, Poland
ORCID ID: 0009-0002-3351-2312

Konrad Kochman
J. Gromkowski Regional Specialist Hospital, Wrocław, Poland
ORCID ID: 0009-0000-1570-1836

Greta Stołecka
J. Mikulicz-Radecki University Clinical Hospital, Wrocław, Poland
ORCID ID: 0009-0003-9195-9742

Valeriia Merzhuk
Volyn Regional Clinical Hospital, Lutsk, Ukraine
ORCID ID: 0009-0008-6938-7633

Antoni Majda
Regional Specialist Hospital, Wrocław, Poland
ORCID ID: 0009-0006-4357-513X

Kacper Kucharski
J. Mikulicz-Radecki University Clinical Hospital, Wrocław, Poland
ORCID ID: 0009-0004-5709-8974

ABSTRACT

Human breast milk, due to its rich composition that contains an optimal nutrient profile, essential vitamins and beneficial commensal bacteria, is considered the most important form of infant nutrition. In fact, research has demonstrated that breastfeeding confers numerous health benefits, including the stimulation of infants' immune system development and the attenuation of risk factors associated with allergic diseases. Certain components of breast milk, such as oligosaccharides, has been proven to promote the development of gut bacteria, immune tolerance and reduce inflammation. Bacteria such as Lactobacillus and Bifidobacterium have also been shown to support the intestinal barrier and enhance the immune system of newborns. However, the impact of other components of the breast milk microbiota on this process, and especially on the risk of developing allergic diseases, is poorly investigated. In this narrative review, we aim to summarize what is known so far about the impact of the breast milk microbiota and how changes in its composition affect the development of allergic diseases in the newborns. A more profound comprehension of the impact of these microorganisms on the maturation of the immune system could facilitate the establishment of more efficacious prevention strategies for asthma and other allergic diseases. This could contribute to the optimization of breastfeeding practices and potential microbiological interventions to support child health.

KEYWORDS

Asthma, Breast Milk, Infants, Microbiota, Oligosaccharides

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1. Introduction

Human breast milk (HBM) is a complex fluid produced by the mammary glands in women's breasts and is the most recommended method of infant nutrition, offering food rich not only in nutrients and essential vitamins, but also in commensal bacteria that support the baby's early growth and development (Bianco et al., 2024). Mature human milk consists of 87%-88% water, 7% macronutrients, 1% protein and 3.8% fat, and has an energy content ranging from 60 to 75 kcal per 100 ml (Kim & Yi, 2020). The HBM also comprises immune cells, immunoglobulin A (IgA), anti-inflammatory factors, cytokines and antimicrobial peptides, including bacteriocin and lactoferrin. These components are essential for the development of immunity to harmless antigens, such as nutrients and beneficial microorganisms, and for the establishment of an effective immune response against pathogens (Duale et al., 2022). Additionally, HBM contains hormones, growth factors and oligosaccharides (also referred to as human milk oligosaccharides (HMOs)), with the latter playing a pivotal role in the development and composition of a child's gut microbiota (Boudry et al., 2021; Duale et al., 2022).

It is important to note that the composition of HBM varies according to the stage of lactation. HBM can be categorized into three distinct types: colostrum, transitional milk and mature milk. Each of these types is responsible for different infant nutritional needs. Colostrum is the first milk secreted between 48 and 72 hours after birth. This milk is characterized by its high concentration of immunoglobulins, antimicrobial peptides and growth factors, which contribute to the enhancement of the infant's immune system and the progression of their gastrointestinal development (Playford & Weiser, 2021). Transitional milk is characterized by the gradual replacement of colostrum with mature breast milk, a process that typically occurs within the first 20 days postpartum. During this transition, the composition of breast milk undergoes a significant change, with a concomitant increase in the levels of fats and lactose (Divedi et al., 2020). Approximately 20 days after birth, the mammary glands begin to produce mature milk that can be further divided into two distinct fractions: foremilk and hindmilk. Foremilk is more watery, providing mainly lactose and protein, while hindmilk is richer in fat, thus providing the baby with calorie-rich nourishment (Takumi et al., 2022). Furthermore, the composition of the mother's HBM is influenced by a number of additional factors, including the time of day, the mother's geographical and genetic background, the length of her pregnancy and her dietary habits. Of these, dietary habits have the greatest impact on fat content, immunomodulatory components and microbiota (Boudry et al., 2021). The variability of breast milk is of significance in this regard, as it provides infants with key nutrients, as well as with essential microorganisms, such as *Lactobacillus* and *Bifidobacterium*, and bioactive compounds (Notarbartolo et al., 2022).

The first exposure of the infant to the maternal microflora occurs during birth, with the ingestion of microorganisms from the mother's vagina and intestine. Subsequently, the bacteria are transmitted from the mother’s skin during the process of breastfeeding and also with the consumed milk, providing the infant with essential bioactive ingredients and bacteria (Cervantes-Monroy et al., 2024; Notarbartolo et al., 2022). Alterations in the intestinal microbiota, resulting from disturbances during intestinal colonization, have the potential to induce dysbiosis, a condition characterized by an imbalance between microbial species, modifications of their functional structure, and fluctuations in their metabolic activity (DeGruttola et al., 2016). Violation in the gut microbiota at such an early stage of life, in conjunction with an undeveloped immune system, have the potential to generate long-term consequences for the child in the form of impaired immune regulatory mechanisms. This has been associated with an increased risk of chronic inflammatory diseases, such as asthma and allergies (Boudry et al., 2021; Gajewski et al., 2020; Russell et al., 2012).

The Global Initiative for Asthma (GINA) indicates that asthma is one of the most prevalent chronic non-communicable diseases, resulting from chronic inflammation of the airways (Mims, 2015). GINA reports that 260 million individuals suffer from asthma, with over 14% of these cases occurring in children globally (*World Asthma Day 2024 - Global Initiative for Asthma - GINA*). This condition significantly affects the lives of millions of children, leading to recurrent symptoms, reduced physical activity and school participation. A growing number of studies suggest a correlation between breastfeeding and a reduced risk of childhood asthma and allergies, with some indicating a protective effect against their future occurrence. It has been demonstrated that breastfeeding can mitigate the negative effects of exposure to asthma triggers, such as air pollution and psychosocial stress. Furthermore, it has been shown to promote lung growth and improve lung function (Moossavi et al., 2018). Therefore, it is recommended that breastfeeding be continued for a period of four to six months (Hou et al., 2024). Moreover, it has been revealed that children who had never been breastfed were found to have an elevated risk of developing asthma symptoms within the initial four years of life (Sonnenschein-van der Voort et al., 2012).

The objective of this review is to facilitate a more profound comprehension of the immunological function of human milk-associated microflora and its impact on neonatal well-being. The work aims to elucidate the role of breast milk components such as microflora, HMOs, immunoglobulins and cytokines in immunological and microbiological processes, placing particular emphasis on the impact of dysbiosis and feeding duration on the development of asthma in children.

2. Breast milk as a source of microorganisms and bioactive components

HBM is widely regarded as the optimal nutritional source for infants up to six months of age. The practice of breastfeeding for the first six months of an infant's life has been demonstrated to reduce infectious disease mortality by 88% in comparison to infants who were not breastfed (Mosca & Giannì, 2017). Numerous epidemiological studies have demonstrated the benefits of breastfeeding, including a reduced risk of respiratory infections, atopic dermatitis and asthma (Demmelmair et al., 2020). HBM is being optimally adapted to the nutritional requirements of the infant. Its composition fluctuates daily, in accordance with the menstrual cycle and the lactation period (Łubiech & Twarużek, 2020). In addition to supplying the infant with essential nutrients, it provides the infant with commensal bacteria (Lyons et al., 2020). Łubiech K and Twarużek M state that the absorption of commensals by a child consuming 800 ml of milk per day can range from $8x10^4$ to $8x10^8$ (Łubiech & Twarużek, 2020). It has been demonstrated that the presence of these bacteria has a beneficial effect on the health of the child, with the capacity to prevent the adhesion of pathogens to the intestinal walls and to promote colonization by beneficial microbiota (Lyons et al., 2020).

A study of the composition of HBM revealed the presence of bacteria such as *Lactobacilli*, *Lactococci*, *Enterococci* and *Leuconostoc spp.* in the milk of healthy women. Of the *Lactobacilli* genus present in breast milk, the following have been identified: *Lactobacillus gasseri*, *Lactobacillus rhamnosus*, *Lactobacillus plantarum*, *Lactobacillus fermentum* and *Enterococcus faecium* (Łubiech & Twarużek, 2020). Gavin A and Ostovar K isolated bacterial species belonging to five families (i.e. *Micrococcaceae*, *Streptococcaceae*, *Corynebacteriaceae*, *Lactobacillaceae* and *Neisseriaceae*) from the HBM of five breastfeeding women. In a series of subsequent studies, additional potentially probiotic *Bifidobacterium* strains were isolated, which, in conjunction with probiotic *Lactobacillus* strains, have been shown to prevent pathogenic bacteria such as *Shigella spp.*, *Salmonella spp.* and *Escherichia coli* from adhering to the intestinal wall (Gavin & Ostovar, 1977). In the review by Zimmermann P and Curtis N, a total of 44 studies with 3105 breast milk samples from 2655 women were analyzed. In addition to bacteria, DNA was isolated from fungi, archaea, eukaryotes and viruses. The most common genera identified were *Staphylococcus, Streptococcus, Lactobacillus, Pseudomonas, Bifidobacterium, Corynebacterium, Enterococcus, Acinetobacter, Rothia, Cutibacterium, Veillonella* and *Bacteroides* (Zimmermann & Curtis, 2020). Furthermore, HBM has been shown to contain a variety of *Lactobacillus* species, including *Lactobacillus casei, Lactobacillus salivarius, L. plantarum, L. fermentum, L. rhamnosus*, and *L. gasseri*. In contrast, the most commonly isolated and detected *Lactobacillus* species in infant feces were *Lactobacillus brevis, L. fermentum, Lactobacillus reuteri, L. rhamnosus*, and *L. plantarum* (Zhang et al., 2020).

Albarracin L et al. conducted a study on mouse infants that involved the oral administration of certain *Lactobacillus* strains, including *L. rhamnosus* CRL1505 and *L. plantarum* MPL16. The study confirmed that Lactobacilli enhance the immunity of mice against respiratory tract infections by modulating alveolar macrophages and improving interferon production (Albarracin et al., 2024). The results of a study by Chen CM et al. are of particular interest. The study suggested that intranasal administration of *Lactobacillus johnsonii* to neonatal mice exposed to hyperoxia enhances lung development, improves weight gain and rebalances the gut microbiota after lung injury (Chen et al., 2023). Additionally, Yu J et al. demonstrated that oral administration of *L. rhamnosus* to mice resulted in a reduction in airway inflammation, hyperresponsiveness, and IgE production (Yu et al., 2010). In a study by Huang CF et al., the severity of asthma symptoms in children was evaluated by administering probiotics separately as well as together with *Lactobacillus paracasei* and *Lactobacillus fermentum*. The results highlighted that the utilization of these probiotics not only reduced the severity of asthma, but also improved symptom control and quality of life. Of particular interest was the observation that the concomitant administration of these two probiotics resulted in a substantial reduction in IgE levels, accompanied by an enhancement in peak expiratory flow (Huang et al., 2018).

The gut-lung axis constitutes a bidirectional communication pathway between the gut microbiota and the respiratory system, whereby there is a reciprocal active exchange of microorganisms and/or their metabolites and immunomodulatory signals (Haldar et al., 2023). There is an increasing body of evidence from the scientific community that suggests a link between the gastrointestinal tract and the respiratory system. However, the precise mechanism by which this connection occurs remains to be fully elucidated. Two explanatory hypotheses have been put forward to attempt to explain this phenomenon. The first is the gut-lymphatic theory, which posits that the gut microbiota and its associated products can modulate the immune response in the lungs via the lymphatic system. The second is the common mucosal immune system hypothesis, which suggests that the gut and lung mucosa share an integrated immune system (Trivedi & Barve, 2020). The influence of the maternal milk microbiota on the functioning of the gut-lung axis is an important area of research. This is because both the immunological components of milk and microbial imbalances have the capacity to modulate the development of the child's immune system. The following sections examine how these components contribute to shaping the risk of developing asthma.

3. Immunomodulatory properties of breast milk bacteria

The bacteria contained in human breast milk, such as *Lactobacillus* and *Bifidobacterium*, play a role in supporting the infant's gut barrier and overall immune system. These bacteria interact with intestinal epithelial cells to enhance the production of tight junction proteins, therefore reducing intestinal permeability and protecting against the translocation of harmful pathogens. Moreover, it is evident that bacterial metabolites, such as short-chain fatty acids (SCFAs), play a pivotal role in modulating the gut environment, thereby creating favorable conditions for beneficial microbes and maintaining intestinal integrity (Matar et al., 2024). The microbiota also exerts influence through epigenetic mechanisms, contributing to local and systemic changes in the host phenotype. Alterations in the intestinal microbiota can affect tight junction-related protein expression, impacting intestinal permeability. Additionally, it has been proven that SCFAs can inhibit histone deacetylases, leading to changes in transcriptional activity, chromatin structure, and DNA methylation. This epigenetic regulation can activate genes necessary for intestinal barrier repair and immune modulation (Matar et al., 2024). The transient intestinal microbiota acquired from breast milk is crucial in shifting the newborn's immune profile from a Th2-dominant state to a more balanced Th1/Th2 response, which is essential for optimal immune function, enabling the immune system to efficiently combat diverse pathogens, prevent overreaction, and maintain immune homeostasis (Toscano et al., 2017). Specific strains of *Lactobacillus* present in breast milk have been shown to stimulate macrophages to produce Th1 cytokines, including interleukin 2 (IL-2), IL-12, and tumor necrosis factor alpha, thereby promoting a stronger Th1 response therefore enhancing protection against infections, lowering allergy risk, and supporting long-term immune health (Díaz-Ropero et al., 2007). Studies indicate that breastfed children exhibit stronger Th1 responses compared to formula-fed counterparts, with the immunomodulatory effects of breastfeeding persisting beyond weaning. Furthermore, bacteria from breast milk promote B cell development in Peyer's patches and stimulate IgA production through Toll-Like Receptor signaling, such as Lipopolysaccharide-induced Inducible Nitric Oxide Synthase upregulation in Peyer's Patch Dendritic Cells. This process, involving Transforming Growth Factor Beta (TGFβ) as well as B-Cell Activating Factor and a Proliferation-Inducing Ligand, enhances the immune system's capacity, by promoting the differentiation of B cells to guard the mucosal surface, thereby providing the first protective barrier against pathogens (Massacand et al., 2008; Toscano et al., 2017).

4. Human milk oligosaccharides as prebiotics

Human milk oligosaccharides (HMOs) are complex carbohydrates composed of monosaccharides and derivatives, including glucose, galactose, N-acetylglucosamine, fucose, and sialic acid, that play a crucial role in shaping the newborn's intestinal microbiota, and supporting its immune system development (Plaza-Díaz et al., 2018). These compounds act as prebiotics, reaching the distal intestine undigested, where they selectively support the growth of beneficial mutualistic bacteria, particularly certain species of *Bifidobacterium* and *Bacteroides* (Triantis et al., 2018). By shaping the composition of the intestinal microbiota, HMOs promote the proliferation of these beneficial bacteria, which in turn inhibits the colonization of potentially harmful bacterial strains in the infant's gut. This selective influence underscores the importance of HMOs in fostering a healthy microbial environment during early life (Rousseaux et al., 2021). However, in a longitudinal study investigating the effects of HMO's on infant gut colonization, researchers collected breast milk and stool samples from mothers and infants from birth to one year. Stool samples were stored using eSwab with Amies medium, while breast milk was collected manually or via pump in sterile containers. This study analyzed the diversity of the infant gut microbiome and found no significant links to individual HMO's in mothers' milk. However, the dominant *Bifidobacterium* species in each sample strongly influenced microbiome variability. Although the composition of HMO's in breast milk remained stable over several weeks, the infant gut microbiome underwent significant changes during the same period, suggesting that even minor differences in breast milk composition, besides HMO's, could influence gut microbiome development (Ennis et al., 2024).

5. Immunoglobulins and cytokines in breast milk

Breast milk contains a variety of cytokines and chemokines that support immune system development and protection. Immunomodulatory cytokines in murine milk, including TGFβ have been shown to influence the development and maturation of the mucosal immune system in neonatal mice and are associated with the protection against allergic asthma and atopic dermatitis (Rajani et al., 2018). Maternal cytokines (TGFβ, IL-6, and IL-10) in milk could contribute to the development and differentiation of IgA-producing cells like naive B cells, plasmablasts and plasma cells, therefore enhancing mucosal immunity and protection against infections (Field, 2005). Secretory IgA (sIgA), derived from maternal IgA in mammary glands, supports neonatal gut health by preventing pathogen adherence, neutralizing toxins, and offering passive immunity (Nolan et al., 2019). Moreover, researchers have indicated that reduction of sIgA in breast milk theoretically may modulate the potential protective effects of breastfeeding (Meng et al., 2019). Interestingly, evidence from human immunization studies suggests that when women are orally immunized, there is a specific increase in plasma cells within the milk, but not in saliva or serum (Rajani et al., 2018). This finding supports the idea that IgA in breast milk mirrors the antigenic exposure of the mother's gut, including dietary proteins (Oddy, 2017). Furthermore, breast milk helps to modulate the infant's immune system by stimulating the production of protective IgA, encouraging the development of a balanced immune response, which may prevent allergies (Oddy, 2017; Rajani et al., 2018).

6. Early life gut microbiota and its role in atopy and asthma risk

Current research indicates a strong connection between dysbiosis, reduced microbial diversity in the infant gut microbiota, and the risk of developing atopy and asthma. The first three months of life appear to be particularly important in establishing a healthy microbiome (Arrieta et al., 2015). Fujimura KE et al. analyzed stool samples from 298 neonates and identified three distinct microbiota composition states (neonatal gut microbiota (NGM) - NGM1, NGM2, NGM3) using Dirichlet multinomial mixture modelling. These states differed in bacterial diversity and the relative abundance of taxa. NGM3, characterized by a reduction in *Bifidobacterium*, *Faecalibacterium* and *Akkermansia* species, alongside increased abundance of fungi such as *Candida* and *Rhodotorula*, was associated with a significantly elevated risk for multisensitised atopy (54.5%) and asthma (40%) by ages two and four (Fujimura et al., 2016). Furthermore, a study conducted by Arrieta MC et al. highlighted significant differences in microbiota composition between healthy children and those at high risk of asthma based on the Asthma Predictive Index. Infants at risk exhibited microbial dysbiosis characterized by reduced abundance of four bacterial genera: *Faecalibacterium, Lachnospira, Veillonella* and *Rothia*. Notably, these differences were more pronounced in early infancy compared to samples collected at one year of age (Arrieta et al., 2015). Similarly, Sjögren YM et al. observed that infants who later developed allergies were significantly less frequently colonized by *Lactobacillus* species, *Bifidobacterium adolescentis*, and *Clostridium difficile* during the first two months of life (Sjögren et al., 2009). However, contrasting findings were reported by Penders J et al., as the researchers did not observe any differences in the prevalence of *B. adolescentis* or other *Bifidobacterium* species between children who developed atopy and those who remained healthy. The only bacteria for which the presence was observed to be considerably higher in children with atopy was *E. coli*. Interestingly, the prevalence of *B. adolescentis* in one-month-old infants differed markedly between those two studies: 75% versus 6% in healthy infants and 57% versus 0% in allergic infants (Penders et al., 2006). In another study, Bisgaard H et al. examined 411 children born to mothers with asthma to evaluate the impact of microbial diversity at 1 and 12 months of age on the occurrence of atopic disorders, with a follow-up assessment at six years. This study found that reduced bacterial diversity in the infant gut microbiota was associated with an increased risk of allergic sensitization, allergic rhinitis and peripheral blood eosinophilia. However, no significant associations were found with asthma or atopic dermatitis during the first six years of life (Bisgaard et al., 2011).

7. Differences in gut microbiota and asthma risk between breastfed and formula-fed children

The composition of the gut microbiota plays a pivotal role in determining the immune system, metabolism and susceptibility to allergic and chronic diseases. A comparative analysis of the gut microbiota of breastfed and formula-fed infants revealed significant differences that can influence long-term health outcomes. The results of a meta-analysis conducted by Ho NT et al. examining the impact of exclusive breastfeeding on the gut microbiota of infants across diverse populations indicate a correlation between the absence of exclusive breastfeeding or a shorter duration of exclusive breastfeeding during the first six months of life and an increased diversity of the infant's gut microbiome. Furthermore, the microbiome displayed increased levels of age-related modifications, a composition of bacteria more akin to that observed in adults, and an elevated proportion of functional bacterial pathways involved in carbohydrate metabolism and a reduction in those associated with lipid metabolism, detoxification, and the metabolism of vitamins and cofactors. Additionally, exclusive breastfeeding, particularly for a duration exceeding two months post-partum, was linked with a more stable profile of gut bacterial taxa and a reduced incidence of diarrheal-associated microbial dysbiosis. The pronounced alteration in the gut microbiota of infants observed with non-breastfeeding practices may exceed the developmental trajectory of the infant's age-appropriate immunological and biological processes (Ho et al., 2018). The findings of a systematic review conducted by Inchingolo F et al. indicate that infants fed with modified milk compared to breastfed infants exhibited notable differences in their gut microflora composition. The number of beneficial bacteria, such as *Lactobacillus* and *Bifidobacterium*, were found to be higher in infants who were regularly breastfed. In contrast, infants fed with modified milk have been observed to exhibit an increase in the prevalence of potentially pathogenic bacteria, including *Enterobacteriaceae* and *Clostridium difficile*. The microbial composition of infants fed with modified milk has undergone alteration, which can result in an elevated risk of infection and other health complications (Inchingolo et al., 2024).

8. Effect of breastfeeding duration on child's risk of developing asthma

In recent years, there have been many systematic reviews and meta-analyses of the effect of breastfeeding duration on the incidence of asthma in children. According to Güngör D et al., there is moderate evidence to suggest a correlation between a shorter duration of breastfeeding and an increased risk of asthma in childhood and adolescence. In 20 independent studies (mostly observational), 8 demonstrated statistically significant associations, and in all but one of these studies, a shorter duration of breastfeeding was associated with a higher risk (Güngör et al., 2019). Moreover, the meta-analysis conducted by Dogaru CM et al. strongly suggests that breastfeeding plays a protective role in the prevention of childhood asthma. Researchers found that the duration of breastfeeding is also a significant prevention factor, with longer periods of breastfeeding being associated with a reduced risk of asthma. The strongest correlation was observed in children aged 0–2 years, with a subsequent decline in the strength of the association with increasing age. It is crucial to acknowledge that the occurrence of wheezing during this period is likely attributable to viral respiratory infections and should not be conflated with atopic asthma. Consequently, the observed correlation is substantiated by the established protective effect of breastfeeding against infections during this age range. As the child matures, an increasing number of factors exert influence over respiratory morbidity, thereby rendering it challenging to ascertain the precise impact of breastfeeding. Nevertheless, some evidence of a reduction in risk persists among school-aged children. The proposition that the emergence of later asthma is precipitated by respiratory infections in early life offers a rationale for why the protective impact of breastfeeding in infants remains evident in older children (Dogaru et al., 2014). Nonetheless, meta-analyses by Brew et al. revealed an absence of evidence indicating that any duration of breastfeeding provides protection against the onset of wheezing in children aged five years and above. This underscores the distinctions in the phenotype of asthma or wheezing in early childhood compared to that observed in children aged five and older (Brew et al., 2011). Conversely, Lodge CJ et al. demonstrated that longer durations of breastfeeding were correlated with a reduced risk of asthma in children and adolescents (5-18 years), particularly in middle/low-income countries. However, this estimate was characterized by substantial heterogeneity and a low quality of evidence (Lodge et al., 2015). The observed discrepancy in findings between the two meta-analyses conducted on children aged 5-18 years may be attributed to the inclusion of a greater number of studies in the meta-analysis conducted by Lodge et al. In contrast to the Brew et al. analysis, the Lodge et al. meta-analysis categorized studies as either 'more or less' breastfeeding.

9. Conclusions

Human breast milk is an invaluable source of essential nutrients, bioactive components and microorganisms that play a crucial role in the development of an infant's immune system and gut microbiota. The diverse composition of human breast milk provides both nutritional support and immune protection, ensuring early defense against pathogens. Various factors, including maternal diet, maternal origin, and gestational length, significantly influence the composition of the milk microbiota and, consequently, the infant's health outcomes. Moreover, bacteria derived from HBM support the intestinal barrier and exhibit immunomodulatory properties, which involve balancing the immune response to optimally protect the body against infectious agents. As has been previously outlined, human milk oligosaccharides act as prebiotics, fostering beneficial gut microbiota and influencing the immune system's maturation. Consumption of breast milk stimulates the production of protective IgA, encouraging harmonized immune response, which may prevent allergies. In light of the strong connection between dysbiosis, reduced microbial diversity in the infant intestinal bacteria species and the risk of developing atopy and asthma, it is important to highlight how pivotal the impact of human milk oligosaccharides on the infant's gut microbiota is, particularly during the early stages of life. Additionally, a comprehensive analysis revealed significant differences in the gut microbiota of breastfed and formula-fed infants, favoring the former due to the increased prevalence of potentially pathogenic bacteria in formula-fed newborns. Breastfeeding has been shown to reduce the incidence of infections, allergies, and asthma, especially in the first two years of life, and an extended duration of breastfeeding further amplifies this protective effect. In conclusion, breastfeeding serves as a critical intervention in the early establishment of the infant’s immune system, offering protection against various diseases, including asthma and allergies. The ongoing research into the microbiota and immune modulation by breast milk underscores its importance in promoting neonatal well-being and shaping long-term health outcomes. Certainly, further studies are required to thoroughly elucidate the underlying mechanisms and optimize breastfeeding practices to ensure the best possible start for infants.

Ethical approval: The study was a descriptive one. No humans or animals were a subject of examinations.

Conflict of Interest: No conflicts of interest to declare.

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