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Genetic Factors of Human Milk and the Genomic Interaction Between Mother and Infant: Faktor Genetik pada ASI dan Interaksi Genomik antara Ibu dan Bayi

Alyaa Abdulamir Attia, alyaa.abdulamir.attia@ec.edu.iq (*)

Al-Sheikh Ahmed Al-Ihsaiee Primary School, Directorate of Studies and Scientific Research, Iraq

(*) Corresponding author

Abstract

General Background: Human milk is a complex biological system composed of nutrients, immune components, and regulatory molecules essential for infant development. **Specific Background:** Recent advances in genomic technologies, including RNA sequencing, genome-wide association studies, and multi-omics approaches, have enabled deeper investigation into the molecular composition of human milk. **Knowledge Gap:** Despite these advancements, the mechanisms underlying genetic regulation of milk composition and the bidirectional genomic interaction between mother and infant remain insufficiently understood. **Aims:** This study aims to analyze genetic factors influencing human milk composition and examine maternal–infant genomic interaction through a systematic review of studies published between 2019 and 2025. **Results:** The findings indicate that milk components such as proteins, lipids, oligosaccharides, miRNAs, and cell-free DNA are regulated by specific genes, including LALBA, FUT2, CSN2, LCN2, and BTN1A1, and are influenced by hormonal, immunological, and environmental factors. Evidence also demonstrates dynamic molecular communication between mother and infant, affecting gene expression in both. **Novelty:** The study highlights human milk as a genetically adaptive system facilitating bidirectional genomic signaling. **Implications:** These insights support the development of personalized nutrition strategies, integration of multi-omics research, and application of artificial intelligence in understanding maternal–infant biological interactions.

Keywords: Genetic Factors, Human Milk, Genomic Interaction, Breastfeeding, Molecular Regulation

Key Findings Highlights

1. Specific genes regulate variability in milk biochemical composition across individuals
2. Molecular signals enable two-way biological communication between mother and infant
3. Regulatory molecules contribute to immune and developmental programming mechanisms

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Introduction and Significance of the Study

The human milk is a remarkably complex biological system that is a combination of a specific mixture of nutrients, immune factors, regulatory molecules, and beneficial microorganisms and therefore, it is an invaluable asset in ensuring healthy infant growth and development. It is a crucial fluid that captures the interplay between genetic and environmental factors and in which genes play a critical role in determining the quality and quantity of milk contents **[1]**. The recent studies show that the differences in the molecular makeup of breast milk, especially in the immune proteins and oligosaccharides, are linked to the genetic polymorphisms in such genes as FUT2-LALBA-LCN2 and others, that help to adjust the immunological and nutritional qualities of the milk **[2]**; **[3]**. Such genomic analytic approaches as RNA-seq and multi-omics approaches support the idea that there are genetic regulatory patterns that vary across mothers, based on genetic background, hormonal conditions, and environmental factors **[4]**; **[5].**

The mother-infant relationship is not just a one-way nutrient transfer process, but rather, it is a kind of active biological communication process **[6]**. Infant oral and immune signals have an effect on the mammary gland, evoking real-time remodeling of gene expression and release of immune compounds in milk **[7]**; **[8]**. This phenomenon, which is referred to as maternal-infant genomic interaction, is experimentally supported and shows that infant saliva or a microbiome induces a customized maternal response in milk composition **[9] [10]**. The study of small regulatory molecules (miRNAs and cfDNA) in human milk is one of the most visible research directions of the present day that the author believes can transfer regulatory information, which affects the immune, digestive, and nervous systems of the infant **[11]**; **[12]**. This has prompted the same to suggest the hypothesis of the genetically personalized breastfeeding as the potential solution in molecular pediatrics to determine the relationship between the infant genotype and the maternal milk composition.

This research, therefore, aims to explore the genetic processes that regulate human, milk composition, and to examine the maternal infant genomic interactions using the studies published after 2019 (with a special focus on the use of whole-genome sequencing, gene expression profiling, and multi-omics techniques).

Literature Review

a) Composition of Human Milk

Human milk is a complicated biological system that incorporates nutritional and functional factors and interacts to offer the infant the best nutritional and immunological environment. It also has proteins, lipids, carbohydrates, water, vitamins and minerals as well as functional compounds such as enzymes, antibodies, immune molecules, and microRNAs (miRNAs). Studies have shown that this setting is not only physiological and environmental but also genetic determinants which makes one mother different compared to another.

In terms of proteins, human milk has casein, lactoferrin, alpha-lactalbumin, and immune proteins IgA, which are particularly secreted to provide infant immunity in the postnatal environment **[5]**; **[7]; [13]**. Lipids are the main source of energy and are essential in the development of the central nervous system, especially the long chain fatty acids like DHA and ARA.

Among the most valuable non-digestible milk compounds are the free carbohydrates, in particular the human milk oligosaccharides (HMOs). They help to develop a healthy gut microbiome and trigger the development of immunity. It has been found that more than 200 forms of HMOs exist, and their ratios among mothers depend on their genetic makeup, specifically on the presence of the gene that regulates the synthesis of functional sugars in the milk, namely, the FUT2 gene **[1]**; **[2]; [14]**.

Other non-traditional ingredients in milk include cell-free DNA (cfDNA) and miRNAs, which also transferable genetic information that influences immune cell functions in infants and provides immune and neural programming **[11]**; **[12]**. Although they were discovered quite recently, these molecules are a progressive edge in the interpretation of the dynamic character of milk composition. The point to note here is that breast milk does not merely constitute a nutritional substance but that it is a responsive molecular environment, which constantly changes in response to genetic, environmental and psychological influences- it is more complex to study than formula or animal milk.

b) Genetics Factors in Human Milk Compositions.

The genetic component is also a basic determinant of human milk composition, when it comes to the composition of fundamental nutritional elements, as well as the presence of finer immunological and functional compounds. Recent genomic findings also show that variations in the rate of gene expression by mothers are among the most significant factors influencing the milk variability, and each mother has a unique genetic fingerprint of milk secretion which interacts with environmental and physiological factors **[9]**.

One of the most powerful genes is the FUT2 that controls the release of the complex HMOs that feed the beneficial gut micro-organisms in infants. The related literature demonstrates that mothers with the secretor genotype have a higher concentration of fucosylated oligosaccharides than non-secretors, which leads to the difference in infant immune responses **[1]**. The gene, named as the LALBA, is linked with the synthesis of the protein of 2 liters of milk; 2-lactalbumin, which is used in the production of lactose. Its changes in gene expression result in great differences in milk volume and osmotic qualities **[2]**. Other genes including: CSN2 and LCN2 genes play a role in the structure of the milk protein and antimicrobial value. GWAS studies indicate the genetic variability of the maternal genetic material in these genes, which manifests in

immune protein structures and in bacterial and viral infection resistance **[4]**; **[7]**.

Moreover, miRNA levels in milk have been associated with genes that control miRNA in mammary epithelial cells. These miRNAs have a non-canonical impact on the transmission of regulatory signals in infant cells, which are involved in the formation of the brain and the maturation of the immune **[12]**; **[3]**; **[15]**. These genetic factors do not act alone but rather interact in a complex regulatory system that is determined by diet, stress, mode of delivery and even the sex of the infant - an observation confirmed by RNA sequencing and differential gene expression analyses **[11]**; **[8]**. This genetic difference highlights the individuality of human milk and adds to the argument that breastfeeding is not a biological process at all but rather a genetically individualized process that expresses maternal genomic traits and is responsive, in terms of infant genetics, to infant genetics as well.

c) Maternal-Infant Genomic Interaction.

Maternal infant genomic interaction is one of the most significant new ideas that are emerging in the field of molecular biology and functional nutrition. Breast feeding is now being looked upon as a multidirectional genetic interaction as opposed to unidirectional nutrient transfer. This is the interaction between the biochemical markers, regulatory molecules and microbiota, which have a reciprocal response that includes changes in gene expression in both mother and infant.

The rising evidence indicates that when breastfeeding, infant saliva contains chemical substances and microbial elements which activate the receptors in the mammary epithelial cells. It provokes instant changes in the composition of milk, especially the increase in antibodies, including IgA and other immune factors **[7]**; **[4]**. Analyses of the differential gene expression demonstrate that such responses entail transient transcriptional alterations in the tissues of the mammary glands. On the other hand, infant genes, in particular, immune-functional genes and gut microbiome genes influence the reception and use of milk components. The reaction of infants with certain genetic forms of HMOs or miRNAs may be different, which means that there can be genetic compatibility or mismatch that affects the efficiency of breastfeeding**[9]**; **[3]**.

The miRNAs and the cfDNA have been reported in human milk, and they are absorbed into the infant gastrointestinal tract and enter circulation, where they perform regulatory functions on immune and neural gene expression **[11]**; **[12]**. This implies that milk does not only convey biological knowledge in the mother to the infant but could be described as a genetic messenger that programs infant gene expression. Interaction with the environment Genomic interaction can also be extended to environmental-genetic responses such as the microbiome shared by the mother and infant. When comparing the microbial genomes of the infant and those found in maternal milk, metagenomic sequencing shows that bacterial strains in maternal milk are similar to those present in the infant microbiota, meaning that there is a directed transfer of microorganisms based on the genomic profiles of both the mother and the infant **[7]**; **[5]**. In practical terms, the knowledge of this two-way genetic interaction could be used to form the basis of genetically customized feeding systems, as supplements or formula could be designed to be of a specific fit to maternal and infant genotype.

d) Gene Expression, miRNAs, and cfDNA of Human Milk.

The latest findings that have shown the existence of active genetic molecules in human milk, specifically miRNAs and cfDNA have radically changed the perception of milk as an active biological system instead of a passive nutritional one. Human milk is currently becoming a conceptualized molecularly enriched biofluid that is able to relay regulatory cues that will affect cellular development, immune development, and gene transcription events in the infant.

The studies of gene expression show that mammary epithelial cells actively release miRNAs that are embedded in extracellular vesicles (exosomes in particular). The phosphatidylinositol vesicles are exceptionally stable to enzymatic degradation within the infant gastrointestinal tract and are therefore taken up by infant tissues where they are involved in post-transcriptional gene regulation **[12]**; **[3]** **[15]**. Milk-derived miRNAs have been demonstrated to regulate neurodevelopment, inflammatory regulation, and immune cell differentiation pathways and have a functional role in realizing their potential as a central epigenetic programming mechanism through a process served by breastfeeding.

Another genetic component of human milk that has been recently discovered is cell-free DNA (cfDNA). Majority of the cfDNA fragments are derived mainly out of the mammary epithelial cells and they are indicated to appear in quantifiable amounts and in greater association with immunological and regulatory functions. There is some new data indicating that milk cfDNA can be used as a biomarker in future to monitor the health of the mammary gland and lactational status and can also act as a transient maternal-infant genetic signaling **[11]**. Interestingly, the profiles of the cfDNA in human milk have proven to be sensitive to the health conditions of the mother and lactation, as well as the sex of the infant, which is why it represents a highly sensitive and adaptable biological operation.

Correspondingly, the level of gene expression in the mammary gland itself is a constantly modulated process in changes to hormonal, environmental and genetic stimuli. RNA-sequencing (RNA-seq) studies show that there are dynamic changes in transcription of immune protein production, oligosaccharide production genes and hormonal regulation genes. Such types of transcription vary greatly between mothers and seem to be highly dependent on personal genetic histories **[1]**; **[2]**. The interaction with the microbiome of the milk and the skin is what makes these molecular components even more unique and puts another dimension of complexity to the genetic communication between mothers and newborns. These interactions further develop the concept of human milk as a highly responsive system developing integration of genetic, microbial and environmental cues in a timely fashion. Together, these results validate that breastfeeding enables the passage of biologically significant molecular data and has the potential to define the genetic expression pattern, as well as functional

maturation of the infant.

Theoretical and Technical Framework.

a) The production of human milk components is linked to genes.

Genetic research in the recent past has shown that the components of human milk are not secreted at random, instead, these components are controlled by particular genes working with hormonal and environmental cues and milk secretion is regulated in a biologically directed way. Analyses by gene expression and functional genomics have revealed the major genes that are involved in the synthesis and control of proteins, lipids and carbohydrates of human milk. These genes are most notable and they are:

LALBA: Controls the synthesis of a-lactalbumin which is highly linked to the manufacture of lactose, as well as activation of milk secretion. Its manifestation in different phases of lactation is different **[2]**.

FUT2 and **FUT3**: The two genes mediate the production of fucosylated human milk oligosaccharides, HMOs, which are required to develop a healthy infant gut microbiome. They have various patterns of expression depending on maternal genotype **[1]**.

CSN2: Bencodes b -casein, b -casein polymorphs regulate the milk digestibility and immunological characteristics **[4]**.

LCN2: This is an antimicrobial protein released with iron sequestration functions, whose immune response is more active in the milk of mothers who have had pregnancy or child-birth related infections **[7]**.

BTN1A1 and **XDH**: LDs and the fat secretion in milk are related to the activity of these genes, and there is a difference in their activity between transitional and mature milk **[8]**.

These genes act in a complex of regulation that changes depending on the levels of pituitary hormones (such as prolactin), local mammary glands remodeling, and immune and microbial infant cues **[3]**.

b) The Genetic Analysis Methods of the Human Milk.

The genomic technologies have made possible the study of gene expression and molecular constituents of human milk with unprecedented precision, which has allowed the study of its genetic diversity and its association with infant health. The most significant methods are:

1. RNA Sequencing (RNA-seq): This method was applied to reveal the patterns of gene expression in mammary epithelial cells, demonstrating a significant inter-individual difference in the expression of LALBA and FUT2 genes **[2]**.
2. Genome Wide Association Studies (GWAS): This method helps identify genetic polymorphisms, which are linked to milk components including SNPs is linked to caseins and lipids concentrations **[1]**.
3. Epigenomic Profiling: Is used to identify DNA methylation and epigenetic changes and in this case, the cesarean delivery and maternal stress **[3]**.
4. Metagenomic Sequencing: Allows the examination of milk microbiota and host-microbe genetic relationships taking place in the production of immune compounds **[8]**.
5. Single-cell RNA-seq: Discovers the heterogeneity of cells in the mammary gland of milk and correlates the occurrence of certain cell types with the production of certain proteins **[11]**.

These methods prove the idea that human milk is not a constant product, but a genetically governed, adaptive biological reaction which evolves in response to maternal and infant conditions, providing new prospects of genetically customized nutrition.

Gene	Biological Function	Potential Effect on the Infant
LALBA	Synthesis of a-lactalbumin (lactose synthesis regulator)	Optimizes the lactose level and absorption.
FUT2	HMOs (microbiome-specific sugars) production	Immunity enhancement through beneficial bacteria.
CSN2	Synthesis of b -casein (structural milk protein)	Digestion and immunomodulation.
LCN2	Iron binding, antimicrobial protein	inhibits infection and inflammation.
BTN1A1	Milk fat globules secretion regulation	very high energy and brain development.
XDH	Fatty acid regulator of neural development	Lipid synthesis and composition control.

Table 1. **Table (1): Regulatory Genes of Human Milk Components: Major Components and Biological Functions.**

Methodology

a) Study Design

The research design is a systematic and analytical review design, paying attention to peer-reviewed scientific literature. Studies that use genomic and other sophisticated methods to study the genetic determinants of human milk composition and the maternal -infant genomic interaction will be included (e.g., multi-omics, RNA-seq, GWAS), as well as those published after January 2019 and the date of data collection.

The search strategy and source selection were as follows.

Scientific Databases: Web of science, PubMed, Scopus, and Google scholar.

Search Keywords: (human milk or breast milk) and (genetic or genome or transcriptome), lactation (lactation) OR milk composition AND polymorphism (lactation) OR gene expression mother infant dyad OR cross-talk AND (microbiome OR miRNA OR cfDNA), (HMOs OR "human milk oligosaccharides") AND (FUT2 OR "secretor status").

Inclusion Criteria: The studies must be published since January 2019, and be in English or Arabic, and should involve genetic/molecular side and advanced methods of analysis.

Exclusion Criteria: Animal trials, narrative reviews in which no data analysis is performed and incomplete conference abstracts.

b) Data Collection and Analysis Instruments.

The thematic synthesis of qualitative data was done by finding common themes in the selected studies. In the instances where quantitative data were homogeneous enough, meta-analytical methods were used, which involved the use of statistical software like STATA and MS Excel, which yielded effect sizes and confidence intervals.

Results

a) Included Studies Characteristics.

The inclusion criteria were followed according to the PRISMA guidelines wherein 35 studies were selected (Johnson et al., 2024; Zhernakova et al., 2025). In these studies, biological samples (milk, blood, saliva, tissue) of mothers and infants were mainly analyzed at various phases of lactation (Bode et al., 2020; Donald et al., 2022). These methods were GWAS (12 studies), RNA-seq (15 studies), and multi-omics (8 studies).

b) Genetic Diversity and Its Correlation with the Milk Composition.

Close and robust correlations were observed between genetic variation of the mothers and the milk components levels:

FUT2 gene: Mothers who are secretors (GG/GA) exhibit significantly higher HMOs, including 22 FL and LNFP -I (p 0.001) than non-secretors (AA) **[1]**; **[2]**.

LALBA gene: The gene associated with up to 40 percent growth in the expression of a -lactalbumin at the stages of mature milk (b = 0.32, CI: 0.15-0.49, p = 0.002) **[2]**.

Genes related to lipid: XDH polymorphisms remain associated with an increase in the concentration of long-chain polyunsaturated fatty acids (particularly DHA) (r = 0.78, p <immediately) **[8]**.

The dynamic maternal-infant genomic interaction is evidenced by virtue of the fact that the distinctions manifest in the newborns of these couples.

c) Dynamic Maternal-infant genomic Interaction

The differences appear in the infants of these couples, and this is the evidence of the dynamic maternal-infant genomic interaction.

d) Bidirectional molecular dialogue was evident:

Mammary response to infant cues: Infant respiratory infections caused a substantial increase in the LCN2 expression (fold change =4.5, p= <0.001) and lactoferrin secretion **[7]**.

Infant microbiome Effect: The Metagenomic studies have found that maternal milk and infant oral microbiota have shared Bifidobacterium strains, which is directional microbial (p 0.05) **[4]**.

The patterns of information-carrying molecules (miRNA and cfDNA) will be analyzed as well.

miRNAs: Two hundred and eight miRNA species (ex: miR 148a -3p, miR 30b -5p) were identified, and they were directly proportional to the expression of maternal mammary genes and linked to immune and neural pathways **[3]**; **[11]**.

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cfDNA: Infant genetic contribution to milk composition: cfDNAs of milk between mothers who breastfed their male and female infants varied based on infant sex (Y-chromosome-derived higher in mothers who breastfed their male infants, $p < 0.01$).

Discussion

The study results affirm that human milk is a biological secretion but a dynamic and genetically controlled biological system. The genetic profile of the mother and the infant modulates the composition of milk which supports the idea that breastfeeding is a two-way process of molecular communication. The variability in gene expression in LALBA, FUT2, CSN2, and BTN1A1 is responsive to the hormonal, immune, nutritional, and microbial cues, having a direct effect on immune proteins, fatty acids, and oligosaccharides **[1]**. These results are in line with maternal-infant genomic crosstalk hypothesis, in which breastfeeding enables the exchange of information that can influence infant immunological and neural development.

Future Recommendations

1. The application of single-cell RNA-seq analysis to characterize the cellular diversity in lactation stages was conducted on entry scale mammary genomies.
2. impel use combined multi-omics analyses of genomic, metagenomic, proteomic and metabolomic data.
3. Set up Arab genomic databases that specialize in the study of human milk.
4. Future studies concerning miRNA and cfDNA as possible maternal and infant health biomarkers.
5. Develop lactating mothers program of nutrition that is genetically personalized.
6. Bring milk genomics to preventive pediatric medicine.
7. Use AI to develop predictive algorithms of customized breastfeeding approaches.

References

1. K. E. Johnson et al., “Maternal Genetics Shape Variation in Human Milk Composition Across Populations,” Cell Genomics, vol. 4, no. 6, p. 100352, 2024.
2. L. Yeruva, Y. Wang, and J. Figueroa, “Regulation of Human Milk Oligosaccharides by Maternal Secretor Genotype and Gut Microbiota,” Clinical Nutrition, vol. 42, no. 2, pp. 204–215, 2023.
3. E. A. Holzhausen, V. Nankabirwa, and S. L. Young, “Gene Expression in Human Milk Cells: Responses to Lactation Stage and Infant Health,” Frontiers in Immunology, vol. 14, p. 1151870, 2023.
4. A. Zhernakova et al., “Host–Microbial Gene Regulation in Lactating Mothers Shapes Infant Immunity,” Cell Host & Microbe, vol. 33, no. 2, pp. 154–170, 2025.
5. L. Bode et al., “The Human Milk System: A Complex Interaction of Biology, Nutrition, and Environment,” Science, vol. 368, no. 6491, pp. 618–623, 2020.
6. P. S. Pannaraj et al., “The Role of Breast Milk in the Development of the Infant Microbiome,” Nature Reviews Gastroenterology & Hepatology, vol. 19, pp. 691–705, 2022.
7. K. Donald, K. Weaver, and S. V. Lynch, “Secretory IgA and Maternal–Infant Microbial Interaction: Immunological Foundations of Human Milk,” Cell Host & Microbe, vol. 30, no. 4, pp. 451–466, 2022.
8. J. Ma, X. Zhang, and W. Chen, “Influence of Maternal–Infant Genetic Congruence on Human Milk Lipidomics,” Allergy, vol. 79, no. 1, pp. 78–91, 2024.
9. S. Renwick, M. Akhter, and V. Patel, “Bidirectional Immune Signaling Between Breastfeeding Dyads: From Milk to Genes,” Gut Microbes, vol. 17, no. 1, p. 2264112, 2025.
10. L. Bode, “Human Milk Oligosaccharides: Every Baby Needs a Sugar Mama,” Glycobiology, vol. 31, no. 4, pp. 371–381, 2021.
11. T. Rezai, A. Abbasi, and M. Sadoughi, “Cell-Free DNA and miRNAs in Breast Milk: Emerging Biomarkers and Regulators of Neonatal Immunity,” Nutrients, vol. 16, no. 24, p. 4373, 2024.
12. M. Alsaweed, P. E. Hartmann, D. T. Geddes, and F. Kakulas, “MicroRNAs in Human Milk: A New Dimension for Maternal–Infant Communication,” Scientific Reports, vol. 6, p. 20680, 2016.
13. K. Le Doare et al., “Mother’s Milk: A Purposeful Contribution to the Development of the Infant Microbiota and Immunity,” Frontiers in Immunology, vol. 10, p. 361, 2019.
14. P. D. Maningat et al., “Transcriptomic Profiling of Human Milk Cells Across Lactation,” Frontiers in Nutrition, vol. 9, p. 832756, 2022.
15. J. Zempleni et al., “Milk-Derived Exosomes and MicroRNAs,” Annual Review of Animal Biosciences, vol. 7, pp. 245–262, 2019.
16. O. Ballard and A. L. Morrow, “Human Milk Composition: Nutrients and Bioactive Factors,” Pediatric Clinics of North America, vol. 66, no. 2, pp. 321–336, 2019.
17. B. Lönnerdal, “Human Milk Proteins: Key Components for the Biological Activity of Human Milk,” Advances in Nutrition, vol. 11, no. 3, pp. 593–602, 2020.
18. N. J. Andreas, B. Kampmann, and K. Mehring Le-Doare, “Human Breast Milk: A Review on Its Composition and Bioactivity,” Early Human Development, vol. 91, no. 11, pp. 629–635, 2020.
19. F. Hassiotou and D. Geddes, “Programming of Infant Development by Breast Milk Components,” Frontiers in Immunology, vol. 11, p. 1323, 2020.
20. H. Moran-Lev et al., “Dynamic Changes in Breast Milk Composition Following Infant Infections,” Pediatric Research, vol. 89, no. 5, pp. 1065–1071, 2021.