

## Infant Gastrointestinal the State as a Disease Motive: Programming Considerations

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### Abstract

The gut microbiota consists of trillions of bacteria, viruses, and fungi that form a perfect symbiosis with their host. They perform immunological, metabolic, and endocrine functions in the body. Microflora is formed in the uterus. Dysbiosis is a microbiome disorder characterized by an imbalance in the composition of the microbiota and alterations in its function and metabolic activity. Causes of intestinal dysbiosis include maternal nutritional deficiencies, hormonal therapy, medication, especially antibiotic use, and lack of contact with the maternal vaginal flora during spontaneous childbirth. Alterations in the gut microbiota are increasingly found in a variety of diseases and persist from early neonatal to adulthood. In recent years, it has become increasingly clear that components of the gut microbiota are important for proper development of the immune system, and that their disruption leads to disease.

**Keywords:** Intestinal microbiota; Dysbiosis; Neonates; Diseases; Biomarkers of inflammation

### Introduction

The human microbiota consists of different types of microorganisms such as bacteria, viruses and fungi. They enter into symbiosis with the host and have important metabolic, immune, and endocrine functions in the human body [1]. The composition of the gut microbiota varies between individuals, changes during development, and depends on host-environment interactions. The intestinal flora is constantly exposed to various external influences. In the intestinal tract, bacteria, viruses and fungi are in a dynamic equilibrium [2]. The presence of viruses as part of the gut microbiome has long been neglected. 90% of them are in the form of bacteriophages and about 10% of the viruses are plant or animal viruses ingested with food [3]. A swarm of bacteria, viruses and fungi colonize the intestinal tract before birth, contribute to nutrient metabolism, stimulate the immune system and protect the host against pathogens. Comparing the gut microbiota of term and preterm infants, significant differences were found in gut microbiota colonization. Bacteroidetes in the 1st year of life, Parabacteroides and Christensenellaceae in the 2nd year, Lactobacillus, Streptococcus (2nd year), Carnobacterium (4th year) in the 1st year of prematurity [4]. These differences disappear after he is four years old. When this balance is disrupted and the 'good' bacteria can no longer control the 'bad' bacteria, it is called dysbiosis. Gut dysbiosis is a condition of neonatal and early adulthood (gluten enteropathy, intolerance to food ingredients, allergies, asthma, metabolic disorders, autism, cancer, and many other autoimmune diseases). are related. Relevant and newborn adapted. It adapts to the extrauterine environment by developing intestinal immunological homeostasis. Adequate bacterial colonization is required to achieve proper development of intestinal immunological homeostasis [5]. Close contact with the mother's breast provides emotional security to the newborn, especially for sick or preterm babies, so breastfeeding is the most important factor for proper colonization. ,contains a variety of substances, including simple sugars and complex hormones. They are referred to as breast milk bioactive complexes due to their pronounced biological activity in infants. Breast milk is mainly composed of water and nutrients dissolved in it.

Proteins, fats, carbohydrates, vitamins, minerals and trace elements. Other factors with specific immune functions are known to exist. Findings in the maternal bronchial-mammary circuit and intramammary circuit indicated that pathogenic microorganisms that

threatened the mother via the gastrointestinal tract or respiratory tract produced specific antibodies in breast milk. It is contained and cannot replicate, but is sufficiently antigenic to develop specific antibodies in infants. In this way, they participate in the maturation of the child's immune system [6].

Formation and proliferation of the gut microbiota begin at birth, but changes in its composition are highly dependent on various genetic, dietary, and environmental factors. A major obstacle to the proper development of the intestinal microbiota is inadequate nutrition (excessive intake of processed foods of animal origin, inadequate intake of fresh fruit, especially vegetables and vegetable juices, unnecessary excess of antibiotics). Consumption, inadequate intake of breast milk, or short lactation period). ), increasing the potential for inflammation that increases the intestinal microbiota. Prenatal maternal gut composition influences the formation of fetal immunity [7]. Although the function of the placental microbiome is unknown, it is known that the gut microbiota is the most important factor in the health of offspring during pregnancy. The passage of bacteria from the gut of pregnant women and their colonization at extra-intestinal sites during pregnancy explains the presence of bacteria in breast milk. However, IgG-associated bacteria can also be transmitted postnatally, and transplacental IgG-mediated bacterial transmission is also possible, potentially compromising immune system development. , suggesting that it is partially dependent on IgG-mediated transmission of bacterial components. Transplacental immunomodulation is mediated not only by bacterial components such as lipopolysaccharides, but also by cytokines and hormones [8].

### Intestinal microbiome of newborns

The gastrointestinal (GI) tract is perhaps the largest and most

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important immune system organ in the body and plays a central role in the body's immune response. The intestinal epithelial barrier is in constant interaction with the intestinal microbiota and cells of the immune system. Communication between epithelial cells, immune cells and the microbiome is of paramount importance, as specific immune responses to antigens depend on this communication. Alterations in the intestinal flora (dysbiosis) trigger an immune response and increase the body's susceptibility to most childhood and adult diseases [9].

At birth, the neonatal gut microbiota is dominated by the family Enterobacteriaceae and the genera Staphylococci. After that, Lactobacillus and Bifidobacterium dominate. Until the introduction of solid foods, bacteria of the genus Bifidobacterium predominate. After the weaning period, the genera Bacteroides, Prevotella, Ruminococcus, Clostridium, and Veillonella predominate. While the pre-weaning microbiota is rich in bacteria that facilitate lactic acid utilization, post-weaning solid foods contain bacteria containing genes encoding carbohydrate breakdown, vitamin synthesis, and xenobiotic breakdown. Facilitating fertility mode growth is one of the factors influencing microbiota development during early childhood. The gut flora of vaginal-born infants resembles that of the maternal vagina, with Lactobacillus, Prevotella, and Sneathia spp. Similar to, Corynebacterium and Propionibacterium predominate. Several studies have shown that colonization with Bacteroides and Bifidobacterium begins in the first month of life and that Clostridium difficile concentrations are very high. It has also been reported that the presence of Bacteroidetes in children born by cesarean section decreased after 3–4 months, and the diversity of the microbiota in these children decreased [10].

In the first 2-3 years of life, the intestinal flora develops intensively. After the age of three, the microflora resembles that of an adult. To establish a stable gut microbiome, he needs two important changes during childhood. The first occurs immediately after birth and during lactation when the predominant microorganism is Bifidobacterium. Another change occurs when you introduce solid foods into your child's diet. During this period, bacteria of the genera Bacteroides and Firmicutes predominate.

### Impact of antibiotics on gut microbiota

Given the disruption of the gut microbiota in infants receiving antibiotics, the following questions arise: Until what age are antibiotics effective? Some studies have looked at how antibiotics work immediately after birth (children) or before birth (mothers).

In a study of 15 preterm infants, short-term administration of antibiotics (up to 3 days) immediately after treatment reduced intestinal bifidobacteria in infants up to 3 weeks of age.

With long-term treatment (more than 5 days), the number of bifidobacteria remained reduced until 6 weeks of age. Despite the initial changes, the microbiota eventually recovered. In conclusion, the duration of antibiotic use was the main factor in microbiota changes. Early in the neonatal period, the bacterial community of infants of mothers receiving intrapartum antibiotic prophylaxis (IAP) against group B streptococci (GBS) differed from unexposed infants. Within 1 hour of her administration of antibiotics during vaginal delivery, her bifidobacteria decreased by 7.2% of hers and the Clostridium overgrowth was positive. They also had low numbers of Actinomycetes and Bacteroidetes and an excess of Proteobacteria.

### Therapeutic directions of treatment of Intestinal Dysbiosis

Development of the fetal gut microbiota begins during life in the womb, and a microbial imbalance in the maternal gastrointestinal tract may contribute to the fetal gut microbiota. The composition of the gut microbiota determines the appropriate type of immune response and the strength of intercellular connections in the gut epithelium. One of the basic types of intercellular junctions in the gut is tight junctions (TJs). TJs are multipotent complexes of integral membrane proteins (claudins and occluding) and cytoplasmic membrane proteins. They are key regulators of intestinal permeability and maintain cell polarity by restricting protein movement across the cell membrane. Impaired intestinal colonization can compromise the intestinal barrier and loosen intercellular junctions by affecting the expression and function of TJ-forming proteins. There is evidence that disruption of the intestinal epithelial barrier increases the movement of bacteria and bacteria-associated products across the epithelium.

### Conclusions

The gut microbiota of newborns is highly diverse. Therefore, its composition influences delivery methods, nutrition, maternal antibiotic and probiotic use, environment, maternal socioeconomic status, geographic location, infection with pathogenic microorganisms, and many other factors. All of these factors can lead to intestinal dysbiosis that predisposes to the development of the disease from childhood to adulthood. This period in the newborn is critical in reducing the risk of chronic disease by correcting gut microbiota abnormalities through gut microbiota interventions.

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