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Some issues of the formation of microbial Cenosis in infants

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Abstract

Human microbiota performs and regulates a multitude of functions, which ensures the maintenance of microbial homeostasis and creates a unified ecosystem. Microbiota is an important component of the human body and is closely linked to both human health and disease. Study results raise the suggestions of possibility that the infant may be first seeded in utero. Here is discussed some of the current and key issues surrounding these issues.

Keywords: Human Microbiota; Microbiome;Caesarian Delivery; Normal Vaginal Delivery; Placental microbiome

1. Introduction

Human microbiota is a relatively stable ecological system that has evolved through evolution and is an indicator of health. Understanding the process of microbial composition in different ages plays an important role in the study of human development and physiology.

The findings of several studies indicate increasing possibility of prediction in the development of the human microbiome in utero [1,2].

After birth, the microorganisms that make up the normal microbiota develop in a particular order, forming stable populations of bacteria that subsequently become part of the normal adult microbiota. The main factor determining its composition in a particular part of the body is the local environment created by pH, temperature, oxygen, water and nutrient content. Other factors such as peristalsis, secretion of saliva and lysozyme and secretion of immunoglobulins also play a role in the formation of the microbiota.

Bacteria are found in the meconium of newborns. This probably indicates the presence of microorganisms in the intestines of the newborn before birth (e. i. colonisation occurs in the intrauterine period) [3]. However, factors related to delivery process also influence the initial stage of colonisation of the neonatal microbiome. Studies show that there is a significant difference between the microbiome profiles of caesarian delivery *and* normal vaginal delivery neonates. Antibiotics may alter the microbial profile of the mother, which in turn will also affect the gut microbial profile of the newborn [4].

In addition, at two months, the salivary microbiome of children born by caesarean section is significantly more diverse than that of children born vaginally, but again these differences disappear after 12 months. The salivary microbiome is dynamic during the first two years of life, and age-related factors appear to be the strongest determinant. Colonization by species such as Candida albicans is a good example of age-related changes in exposure [5].

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The placental microbiome is poorly understood, although it has been found to contain bacteria with diverse metabolic and immunoregulatory functions. A unique niche of the placental microbiome has been identified, consisting of non-pathogenic commensal microorganisms (*Proteobacteria, Firmicutes, Tenericutes, Fusobacteria, and Bacteroidetes phyla)*. In addition, the placental microbiome has been found to be similar to the oral microbiome [6].

The mode of delivery (physiological, caesarean section) as well as the completion of natural nutrition are critical factors in the formation of the gut microbiota. Microbial density changes dramatically in the first year of life [7].

The contact of the newborn with microorganisms also occurs during passage through the birth canal. During breastfeeding the gastrointestinal tract is dominated by gram-positive bacteria (bifido- and lactobacilli). Immunoglobulins and other elements are also important. During formula-feeding this bacterial population decreases as the number of gram-negative bacteria (e.g. *Enterobacteriaceae*) increases. Physiological, immunological and hormonal changes in a woman's body during pregnancy increase her susceptibility to infections (including oral and periodontal infections) [8.9].

Also, normal changes in oestrogen and progesterone affect the composition of the oral microbiota, which contributes to the development of gingivitis and periodontal disease[10].

In the gut of newborns, complex microbial associations develop in the first week of life, in which the bacterial composition undergoes dynamic and important changes and appears in a relatively well-established form at 1 to 3 years of age [11].

What factors form these early microbial associations and exactly when microbial exposure and colonization of the newborn occurs are still unclear [12].

In the first week of life, the gut microbiota is abundantly colonised by including *Bifidobacterium, Proteobacterium, Bacteroides* and, much less frequently, *Firmicutes* (*Lactobacillus spp*., including the dominant representative of the vaginal microbiota), which dominate the vaginal microbiota [13].

Prior to this, *Firmicutes* and *Tenericutes* phyla and, to a lesser extent, *Actinobacteria* dominated in neonates weighing less than 1200 g [14].

It is well known that the colonisation of the open body cavities of the newborn with normal flora and the subsequent formation of its eubiosis are closely related to the microbiocenosis of the newborn. The formation of microbial cenosis begins in the first days after birth. In the first three days of breastfeeding many species, including putrefactive bacteria, multiply in the large intestine, and when the baby is fed mother's milk putrefactive bacteria disappear and a constant flora gradually forms. Bifidobacteria colonize in the colon (10^9-10^{10} microorganisms in 1 g of faeces) and their proportion in the biocoenosis is 82-95%. The proportion of other obligate microorganisms (*E.coli, Lactobacter, Streptococcus, Enterococcus and Staphylococcus)* is low and does not exceed 10-15% in total.

Human microbiota as the self-regulating open system strongly influences the morphofunctional properties of the host organism. Development of microbiome in different ages is a focus of intense studies.

2. Conclusion

Related to food digestion and metabolism, immune system development and activation, and the production of neurotransmitters that influence behaviour and cognitive functions.

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