

THE ROLE OF INTESTINAL AND VAGINAL MICROBIOME IN PRE- GRAVITY PREPARATION OF WOMEN WITH ANEMIA

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Abstract. A review of publications devoted to the study of the microbiome composition of the vagina and intestines of a woman during pregnancy and the postpartum period was conducted, as well as a search for and description of the results of studies examining the mechanisms of transmission of maternal microbiota to the newborn in order to assess these changes and determine their role in the homeostasis of the female body, the impact on the newborn, the course of pregnancy and the postpartum period.

Keywords: microbiota, vaginal microbiome, intestinal microbiota, opportunistic microorganisms.

INTRODUCTION

The human microbiome is a complex ecosystem that occupies various biotopes – skin, mucous membranes, organ tissues. The microbiome and the body as a whole exist in symbiotic relationships [1]. The microbiome composition is dynamic and is influenced by a number of factors, such as lifestyle, race, age, hormonal status, and nutrition. To date, a large number of studies have been published demonstrating not only the active role of the microbiota in physiological processes in the body, but also its direct participation in pathological metamorphoses. The intestinal microbiota is considered a microecosystem, which is an important link in ensuring a number of physiological functions, such as protection of the intestinal mucosa, systemic immunomodulation of the host, protection against the attachment of pathogenic bacteria to epithelial cells, and limitation of the absorption of pathogenic metabolites by these cells [1].

MATERIALS AND METHODS

Pregnancy is a complex process accompanied by hormonal, metabolic and immunological changes. A number of authors have proven a decrease in the immunological protective properties of the body to ensure the processes of implantation and subsequent development of the embryo. A decrease in immunity is reflected directly in a decrease in the barrier functions of the mucous membranes and in a change in the microbiotic balance in certain biotopes. These changes contribute to the growth of UPM due to a shift in its balance of quantitative and qualitative relationships with the normal microbiota. This serves as a trigger in the mechanism of occurrence of such conditions as bacterial vaginosis (BV), aerobic vaginitis (AV), candidal vulvovaginitis.

RESULTS AND DISCUSSION

A certain barrier is the vaginal mucosa, which provides protection from the effects of pathogenic microorganisms due to their interaction with epithelial cells, immune system cells and microorganisms colonizing the vaginal mucosa [4]. The vaginal microbiome contains about 10% of all female microbiota and plays an important role in ensuring the physiological norm of the genitourinary system, preventing the development of pathological changes. It is necessary to take into account the relationship of local biocenoses of the body, united into a single microbial ecological system, which functionally and metabolically interacts with other organs and systems, ensuring the maintenance of homeostasis. The microbial composition of the female genital tract changes depending on the production of estrogen [2]. It is known that estrogens promote the deposition of glycogen in the vaginal epithelium, progesterone promotes the cytolysis of epithelial cells with the release of glycogen, and lactobacilli metabolize glycogen into lactic acid, maintaining an acidic environment of the vagina (pH 3.8-4.5). During ovulation, against the background of increasing estrogen saturation, the vaginal microbiome is characterized by the dominance of *Lactobacillus* and maximum acidity of the environment. During menstruation, a decrease in glycogen concentration associated with a drop in estrogen levels leads to an increase in pH and the risk of

dysbiotic disorders. It has been established that with an increase in the pH of vaginal discharge above 4.5, elimination or a sharp decrease in the concentration of normal microflora and a significant increase in the level of OM are observed, which significantly increases the risk of vaginal infections [1]. The use of innovative methods for identifying bacteria of the genus *Lactobacillus* (sequencing of the 16S rRNA gene region, MALDI-TOF mass spectrometry) showed that more than two dozen species of lactobacilli are found in the vaginal microbiota [2]. The four most frequently detected species are *Lactobacillus crispatus*, *L. gasseri*, *L. iners* and *L. jensenii* [3], less frequently – *L. acidophilus*, *L. fermentum*, *L. plantarum*, *L. brevis*, *L. casei*, *L. vaginalis*, *L. delbrueckii*, *L. salivarius*, *L. reuteri* and *L. rhamnosus* [4]. The vaginal microbiota may contain either one or several species of lactobacilli, often in equal proportions, which can significantly enhance the protective potential of the vaginal ecosystem.

In particular, this study showed that differences in the microbiome of newborns depending on the method of delivery were present at the age of 1 month and disappeared by the age of 4-6 months. According to the authors, breastfeeding is the only source of a number of biologically active elements that contribute to the development of the intestinal microbiome, systemic metabolism and the immune system [3]. The establishment of intestinal microbiota at an early age has a significant impact on subsequent human health. The main sources of intestinal microorganisms of the infant are the mother's microorganisms inhabiting her skin, vagina, and the microbiome of the mother's breast milk. There is a close relationship between the intestinal microflora of the infant and the microflora of the mother's breast milk, oligosaccharides included in its composition. Breast milk oligosaccharides not only act as the sole carbon sources for the *Bifidobacterium longum infantis* culture, leading to the proliferation of these bacteria, but also stimulate bacterial genes, which has a major impact on enterocyte protection. Indeed, recent studies have shown that breast milk microbiota can directly affect the infant's gut microbiota, and the effect of breast milk on the infant's gut microbiota depends on the duration of breastfeeding [4]. A study published in the

journal *Microbiome* in 2024 demonstrated a relationship between the transmission of fungal microflora and the subsequent establishment of the early intestinal microbiota of the newborn and the maternal intestinal microbiome. The results support the idea that the fungal microflora phenotype is transmitted from mother to offspring [2]. Breastfeeding also had consistent associations with individual taxa previously associated with feeding type and influencing overall infant health (e.g. *Bifidobacterium*).

CONCLUSION

The data available today on the maternal microbiome prove the key role of balance in the organism-host relationship both at the pre-pregnancy stage, during pregnancy, and in the post-natal period. The leading role of the maternal microbiota in the formation of the newborn's microbiome is absolutely indisputable. The microbiological composition of various biotopes of the female body serves as a certain regulatory mechanism in immunological, physiological and pathological processes.

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