

PROPERTIES OF INTESTINAL MICROFLORA OF CHILDREN WITH INFLAMMATORY DISEASE OF THE RESPIRATORY SYSTEM

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Abstract. *The progress in studying the microbiome in children and adolescents and its impact on maintaining health is considered one of the most significant achievements of modern medicine. In children with various diseases, the qualitative and quantitative indicators of the microflora of the intestinal tract change, which causes the development of dysbiosis? Study of changes in the state of intestinal microflora in children during treatment with anti-inflammatory drugs has retained its significance and relevance since there is insufficient research in this area, which requires a more detailed analysis of this problem.*

Keywords: *intestinal microflora in children, anti-tuberculosis treatment, intestinal dysbiosis, tuberculosis in children, microbiota, lactobacilli, bifidobacterial.*

Relevance: There are more than 300 species of different microorganisms in the intestines of a healthy person [3]. Intestinal microflora, due to its composition, can influence the functions of the gastrointestinal tract (GIT) and the formation of immunity [7,10]. In children with various diseases, both infectious and non-infectious, the qualitative and quantitative indicators of the intestinal microflora change tract [4].

The root causes of dysbiosis can be: diseases of the digestive system, acute intestinal infections, prolonged taking antibacterial drugs, diets and stressful situations [2, 5]. The clinical picture of an imbalance of intestinal microflora can be recognized by such complaints as flatulence, a feeling of heaviness in the abdomen, pain, unstable chair [1]. When the microbiota is disrupted, immune protection decreases, including against pulmonary infection [5].

Also, there is evidence in the literature about the negative impact of anti-inflammatory drugs (AEDs) on the intestinal microflora, which can cause deep and persistent dysbiosis [8,9]. The study of changes in the state of the intestinal microflora in children during treatment with anti-inflammatory drugs has retained its significance and relevance, since research in this area is insufficient; contradictory or performed without taking into account the anti-inflammatory therapy regimen.

Purpose of the study: to study the microbial landscape of colonic contents in children receiving antibiotics and sulfa drugs for inflammatory diseases of the respiratory system.

Materials and methods: The study included 22 children who received treatment at a clinical children's medical center. Patients aged 3 to 12 years inclusive, without infection. The gender composition is represented by 13 (59.1%) girls, and 9 (40.9%) boys, the average age is 6 years. The study of intestinal microflora was carried out using a quantitative bacteriological method. The research material was feces collected in a sterile disposable container, which was delivered to the bacteriological laboratory of the Department of Microbiology and Virology of TMA. Dilutions were carried out in sterile physiological solution, pH was determined, and cultures were performed on selective and differential diagnostic media. Biochemical properties were studied using

commercial test systems ANAEROTEST 23. The results were interpreted on the basis of regional norms and industry standards [6].

Results: According to bacteriological examination, all patients had disturbances in intestinal microflora. Dysbiotic disorders of grade III were observed in 9 (37.5%) children, grade II - in 10 (41.7%) people, grade I - in 3 (20.8%) patients. The composition of representatives of the intestinal microflora in children with respiratory inflammation was revealed: in patients, a decrease in the number of representatives of the genus *Bifidobacterium* spp. was 66.7%, compared with uniform standards. A decrease in the number of *Lactobacillus* spp was also detected. in 45.8% of patients. *Clostridium* and *Klebsiella* and *Proteus* were found in titers not exceeding the normal value in 95.8%. Among the opportunistic bacteria, representatives of the Enterobacteriaceae family predominated; an increase in lactose-positive *Escherichia coli* occurred in 12.5% of children, and a decrease in 20.8% of patients. The quantitative level of lactose-negative and hemolysin-producing *Escherichia coli* in 95.8% of patients was normal. Coccal opportunistic microflora was represented by bacteria of the genus *Staphylococcus* and *Streptococcus*. Among staphylococci, an increase in *S. simulans*, *S. lentus*, *S. epidermidis*, and the number of *S. aureus* corresponded to the norms. The content of enterococci was reduced in 54.2% of children; *E. faecalis* and *E. faecium* were identified. Disturbances in the composition of the microflora are evidenced by the appearance of *Providencia rettgeri* up to 3×10^5 (4.2%), *Citrobacter freundii* up to 4×10^6 (12.5%), *Citrobacter diversus* 3×10^6 (4.2%), *Enterobacter agglomerans* 1×10^8 (4.2%), *Hafnia alvei* 1×10^6 (4.2%). Fungi of the genus *Candida* were found in the intestinal contents of 66.7% of children.

A significant predominance of *C. albicans* has been established. When studying the pH of the material, a slightly acidic reaction with Me 6.5 (6.0; 6.63) was observed, which may indicate the activation of pathogenic microflora and malfunctions of the enzymatic system. A negative effect of PVP on the intestinal microflora was revealed, however, for the first time, such an effect was examined in children receiving therapy according to IV and V regimens with the inclusion of drugs included in these regimens.

The factors determining the development of dysbiosis are diverse. First of all, the reason for its development may be the use of antibacterial drugs for the treatment of inflammatory diseases of the respiratory system. The presence of the disease pneumonia creates the preconditions for the occurrence of pronounced disturbances of microbiocenosis. The dysbiotic state is aggravated by disorders of the immune system, contributing to the protracted course of the disease and the development of complications in children.

Results: Thus, maintaining a complete and active intestinal normobiota is possible by ensuring its dynamic control in patients with inflammatory diseases of the respiratory system during treatment. The results of studying the characteristics of the microbiota suggest that patients need probiotic therapy during treatment for a disease of the respiratory system.

Conclusion: Research by various authors has established that in the treatment of intestinal dysbiosis, preference is given to bifid-containing drugs, which have the property of restoring these parts of the microbiocenosis. This necessitates further research to study the possibilities of prevention and correction of intestinal microflora disorders in children receiving therapy for multidrug-resistant inflammatory disease of the respiratory system.

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