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Characterization of Microbiocenosis in Adults

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Abstract
In order to study the microbiocenosis 1694 clinical samples have been investigated and determined that dysbiotic disorders were evident in 68% of cases. In category II (patients from 60 years above) dysbiotic disturbance were 12% more, than in category I (patients from 17 up to 60 years) and dominant role belongs to lacto flora. In 88% the dysbiosis were characterized with the presence of conditionally pathogenic bacteria, their frequency of isolation in category II were 12% less, than in category I. Mono infections were presented by the bacteria of genus *Escherichia, Klebsiella, Proteus* and other. As for mixed infections two and three-member associations consisted mainly of representatives of the family *Enterobacteriaceae* and *Enterococcus spp*. and in single cases in combination with *S.aureus* and *P.aeruginosa*. It was found out that adverse indicators of dysbiotic disorders associated with the role of conditionally pathogenic microorganisms are the formation of microbial associations.

Keywords: monoinfection, mixed infection, dysbiosis.

Introduction

The human intestinal microbiota is made up of trillions of microorganisms most of which are of bacterial and viral that are considered to be non-pathogenic. The microbiota functions in tandem with the host's defenses and the immune system to protect against pathogen colonization and invasion. It also performs an essential metabolic function, acting as a source of essential nutrients and vitamins and aiding in the extraction of energy and nutrients, such as short-chain fatty acids (SCFA) and amino acids, from food. Ultimately, the host depends on its intestinal microbiota for a number of vital functions and thus the intestinal microbiota may contribute to health. [1, 2]

In a healthy person, the gastrointestinal tract represents a balanced ecological system that has evolved and is represented by a large number of beneficial bacteria for the body. The healthy, adult-like GI microbiota has been usually regarded as relatively stable throughout adulthood, until ageing and its related pathophysiological processes start to affect its homeostasis. [2] The ageing process affects the human gut microbiota phylogenetic composition and its interaction with the immune system. Furthermore, reduced biodiversity and compromised stability of the intestinal microbiota with respect to younger individuals have often been reported in the elderly. [3, 4]

The violation of the qualitative and quantitative composition of the intestinal microflora and the disruption of the biological balance between the pathogenic and beneficial microflora in the body as a whole and in the intestine in particular is termed the dysbacteriosis.

It was shown that the disruption of the composition and quantitative ratio in the intestinal microbiocinosis occurs from a variety of causes: the nature of nutrition, age, antibiotic, hormonal, radiation and / or chemotherapy, the presence of chronic diseases of the digestive tract and etc. Their development is based on changes in living conditions in biotope, as a result of which populations of one or several species get advantages for growth and reproduction in front of their competitors and acquire an unusual dominant polo microbiocenosis. [5, 6]

New quantitative and qualitative relationships will only become a dysbiosis when the autostabilization mechanisms that are inherent in all evolutionarily developed systems are violated.

With dysbacteriosis, the balance between microorganisms is disturbed, the putrefactive or fermenting flora develops abundantly, the opportunistic microorganisms that are usually found in the intestinal contents in small quantities are actively developed and more pathogenic strains are often found instead of nonpathogenic *E.coli* strains.

Thus, knowledge of the detrimental changes to the microflora in is becoming increasingly important. Objective of the present investigation is the study of microbiocenosis in adults.

Material and method

While studying enteral microflora, the sowing incidence of separate microorganism species and their quantitative indices per 1 g of feces were determined. As a health standard the following indices were accepted: *Bifidobacteria* – 10^8-10^9 microbial cell per 1g, *Lactobacteria* – 10^6-10^7, *Enterococcus* – 10^5-10^6, number of typical *Escherichia* – 10^7-10^8, *Staphylococcus spp.*, conditionally-pathogenic enterobacteria $\leq 10^4$, fungi of *Candida* genus $\leq 10^4$. Bacteriological examination of 1694 clinical material (feces) isolated from children was made according to methodological recommendations. Morphological and biochemical properties of strains were studied by standard methods using different selected media (1,5% nutrient agar, nutrient broth, Endo medium, 5% Blood agar, Kligler agar, Manitol-salt agar and etc.) and Api-test systems.[8, 9]

Result and Discussion

Total of 1694 clinical material (feces) isolated from adults were examined during 2014-2015. Adults were divided in two categories: I –from 17 up to 60 years (996); II – from 60 years above (698).

Category I: Disbiotic disturbance of intestinal microbiocenosis were observed in 62% cases. 48% of dysbiosis were caused by significant decrease of *Lactobacillus*; 15% by *Bifidobacterium* and 37% of important reducing were mentioned at the same time with both *Lactobacillus + Bifidobacterium* microorganisms. Decreased of the number of typical *E.coli* was observed in 15% of cases. In 22% *E.coli* with reduced fermentative properties has been detected.

Approximately in 94% disbiotical disorders of intestinal microflora were characterized by the presense of conditionally-pathogenic bacteria of genus *Escherichia, Klebsiella, Proteus, Staphylococcus* and other. Monoinfections were observed in 70% cases. Leading position was held by hemolytic *E.coli* - 87%. At a lesser degree was isolated hemolytic *Enterococcus spp.* -10%, *Klebsiella spp.* – 2.3%. In single cases were found *Proteus spp., P.aeruginosa, Staphylococcus spp*. Mixed infection were mentioned in 30% of clinical material. Out of microbial associations were dominated the same combination: hemolytic *E.coli* + hemolytic *Enterococcus spp.* – 54%, hemolytic *E.coli* + *Proteus spp.* - 12%; hemolytic *E.coli*+ *Klebsiella spp.* -15%; hemolytic *E.coli* +*S.aureus* – 8%.

Category II: Disbiotic disturbance of intestinal microbiocenosis were observed in 74% cases. 48% of dysbiosis were caused by significant decrease of *Lactobacillus*; 19% by *Bifidobacterium* and 33% of important reducing were mentioned at the same time with both *Lactobacillus + Bifidobacterium* microorganisms.

Decreased of the number of typical *E.coli* was observed in 13,4% of cases. In 35% *E.coli* with reduced fermentative properties has been detected.

Approximately in 82% disbiotical disorders of intestinal microflora were characterized by the presence of conditionally-pathogenic bacteria of genus *Escherichia, Klebsiella, Proteus, Staphylococcus* and other. Monoinfections were observed in 73% cases. Leading position was held by hemolytic *E.coli* - 84%. At a lesser degree was isolated hemolytic *Enterococcus spp.* - 9%, *Proteus spp.* - 4%, *Klebsiella spp.* – 3.3%. In single cases were found *P.aeruginosa, Staphylococcus spp*. Mixed infection were mentioned in 27% of clinical material. Out of microbial associations were dominated the same combination: hemolytic *E.coli* + hemolytic *Enterococcus spp.* – 51%, hemolytic *E.coli* + *Proteus spp* -15,6%; hemolytic *E.coli* + *Klebsiella spp.* -11%; hemolytic *E.coli* +*S.aureus* – 7,2%

Conclusions

As a result of our work it was found that intestinal dysbiosis in adults were characterized with changes in the qualitative and quantitative composition of microflora in 68% of cases.

Studies have shown that, in the presence of a significant frequency of deviations in relation to obligate representatives, the dominant role belongs to the lacto flora. In category II (patients from 60 years above) dysbiotic disturbance were 12% more, than in category I (patients from 17 up to 60 years).

Characterizing the dysbiosis associated with a decrease in the fermentative function of *E.coli* we identified 2 types of disorders: the first were associated with a decrease in the number of typical *Escherichia* and second caused by replacement of typical *Escherichia* by *E.coli* with reduced lactase activity. In category II *E.coli* with reduced lactase activity were 13% more, than in category I.

In case of determining the dysbiotic conditions, attention was paid to the quantitative excess of the norm of conditionally pathogenic microorganisms. In 88% the dysbiosis were characterized with the presence of conditionally pathogenic bacteria, their frequency of isolation in category II were 12% less, than in category I. Our studies showed a high incidence of types of dysbiosis characterized by the presence of hemolytic strains of bacteria in the intestinal microflora. The strongly dominated by hemolytic *E.coli*. Hemolytic activity was also possessed by *Klebsiella spp*. and *Enterococcus spp.*

Adverse indicators of dysbiotic disorders associated with the role of conditionally pathogenic microorganisms are the formation of microbial associations. Two and three-member associations consisted mainly of representatives of the family *Enterobacteriaceae* and *Enterococcus spp.*, in single cases in combination with *S.aureus* and *P.aeruginosa.*

Thus, our investigations have shown that dysbiotic conditions were characterized by a variety of types of dysbiosis: the isolation of pathogenic microflora, replacement of typical representatives of microbiocenosis with atypical ones, significant decrease of *Bifidobacteria* and *Lactobacteria*, formation of microbial associations. A comparison of types of dysbiosis found out that there are differences in dysbiotic disorders in different age categories

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