



CHANGES IN THE COLON MICROFLORA OF SCHOOL-AGE CHILDREN WITH BRONCHIAL ASTHMA

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ABSTRACT

The article deals with quantitative and qualitative changes in the colon microflora of school-age children with bronchial asthma.

It is known that colon microflora is protective against pathogenic and relatively pathogenic bacteria inhibiting their growth and providing for colonization resistance. It actively participates in the regulation of cholesterol and bile acids exchange, this making for stool formation, determining macroorganisms metabolism and forming its immunological responsiveness. Any derangement of intestinal microbiocenosis of various degrees may result in metabolic disturbance leading to deficiency of micronutrients, vitamins, trace elements and minerals, able to cause irreversible processes in macro-organism organs and systems, as well as immune status reduction.

Interrelated dysbiotic changes in the intestine, having reached a certain level, can be clinically manifested and influence the course of the underlying disease. In these conditions, patient's condition gets worse, clinical symptoms transpire, become more acute, duration of the disease increases, the treatment indices and the quality of patient's life deteriorate. And it is important to point out that, if we fail to optimize intestinal microflora, complications of underlying disease and relapses may become more frequent.

Eighty five children aged 12 to 18 with bronchial asthma of varying severity comprised the study group and were monitored. The comparison group consisted of 40 relatively healthy children. They were tested for fecal bacteria overgrowth on the first day in hospital during the acute illness period and then during remission after standard basic therapy on the 10-14th day.

According to these studies, it was determined that in the context of the basic treatment of patients with bronchial asthma, disorder of colon microbiocenosis was observed, which manifested its quantitative and qualitative changes, specifically, low content of bifido- and lactobacteria. It was also determined that the treatment of bronchial asthma using standard basic therapy does not lead to normalization of dysbiotic processes in the colon.

These results indicate that there is a need for new treatment methods capable to achieve a positive effect on the gut flora. This, in its turn, will improve a child's health in the presence of bronchial asthma as well as reduce the risk of the underlying disease complications and frequent relapses.

KEYWORDS: colon microflora, children, bronchial asthma.

INTRODUCTION

Colon microflora is protective against pathogenic and relatively pathogenic bacteria inhibiting their growth and providing for colonization resistance. It actively participates in the regulation of cholesterol and bile acids exchange, this making for stool formation, determining macroorganisms metabolism and forming its immunological responsiveness. Any intestine microbiocenosis disorder results in various metabolic disorders

leading to deficiency of micronutrients, vitamins, trace elements and minerals, this deficiency being able to cause irreversible processes in macro-organism organs and systems, as well, as immune status reduction [Gigante G et al., 2011; Guarino A et al., 2012].

Microflora is an important component of intestine protective barrier, which regulates immune responses on the local and systemic levels. It acts as an antigenic stimulus for gut lymphoid tissue, having constant antigenic effect on the immune system by the inducing the production of antibodies interferons, cytokines and complement [Gigante G et al., 2011; Li A et al., 2011].

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However, most authors consider intestinal dysbiosis a secondary process, pointing out that a variety of adverse effects influencing a child, such as stress, physical and psycho-emotional strains, unbalanced diet, unfavourable conditions environmental, and numerous pathological states cause changes in immune response and thereby may affect the qualitative and quantitative characteristics of the normal intestine flora. In the case of intestinal dysbacteriosis a sick child may show clinical symptoms associated with decreased colonization resistance, digestive disorders, trophic disorders, dysfunction of the intestinal microflora and changes in immune response [Mrázek J et al., 2008; Saulnier D et al., 2009].

Having reached a certain level interrelated dysbiotic changes in the intestine can be manifested clinically and influence the course of the underlying disease. In these conditions, patient's condition gets worse, clinical symptoms transpire, become more acute, duration of the disease increases, the treatment indices and the quality of patient's life

deteriorate. It is important to point out that, if we fail to optimize intestinal microflora, complications of the underlying disease and relapses may become more frequent [Antipkin Y et al., 2010; Iebba V et al., 2011].

The objective of our study was to investigate the qualitative and quantitative changes in intestinal microbiocenosis of school-age children with bronchial asthma.

MATERIALS AND METHODS

Eighty five children aged 12 to 18 with bronchial asthma of varying severity were monitored. These children were placed at the Pulmonology Department of Sumy Children's Clinical Hospital. The comparison group consisted of 40 relatively healthy children.

They were tested for fecal bacteria overgrowth on the first day in hospital during the acute illness period and then during remission after standard basic therapy on the 10-14th day.

Statistical processing of the results was carried

TABLE.

Changes in the colon microflora of school-age children with bronchial asthma

Genus and species of microorganisms	Practically healthy children, CFU/g (n=40)	Study groups	
		Children suffering from asthma	
		Before treatment, CFU/g (n=85)	After treatment, CFU/g (n=85)
	1	2	3
Bifidobacteria	7.23±0.13	3.56±0.16 p _{1,2} <0.001	3.55±0.16 p _{1,3} <0.001 p _{2,3} >0.05
Lactobacteria	7.76±0.12	3.54±0.19 p _{1,2} <0.001	3.41±0.18 p _{1,3} <0.001 p _{2,3} >0.05
The total number of E. coli	6.33±0.21	5.17±0.1 p _{1,2} <0.001	5.01±0.11 p _{1,3} <0.001 p _{2,3} >0.05
Relatively pathogenic microflora	1.72±0.52	3.38±0.15 p _{1,2} <0.01	3.3±0.16 p _{1,3} <0.01 p _{2,3} >0.05
Staphylococcus	0	1.42±0.21 p _{1,2} <0.001	1.45±0.22 p _{1,3} <0.001 p _{2,3} >0.05
Fungi of Candida genus	1.14±0.29	4.27±0.16 p _{1,2} <0.01	4.16±0.17 p _{1,3} <0.001 p _{2,3} >0.05

NOTES: p - reliability of differences; p_{1,2}, p_{1,3} - comparison of indicators to those of the control group before and after treatment; p_{2,3} - comparison of indicators before and after treatment for children with asthma.

out using a number of variations to count arithmetic mean value of the standard error of the arithmetic mean. A significant difference of two samples was evaluated by Student's *t*-test. For the treatment of the material used software package Microsoft Office Excel, adapted for biomedical research.

RESEARCH

Children, suffering from asthma, showed significant quantitative changes of anaerobic flora, which were characterized by lower contents of *Bifidus* and *Lactobacillus*. Thus, the number of bifidobacteria during exacerbation of the disease was significantly lower – 3.56 ± 0.16 CFU/g, than in healthy subjects 7.23 ± 0.13 CFU/g ($p < 0.001$). The content of lactobacilli amounted to 3.54 ± 0.19 CFU/g against 7.76 ± 0.12 CFU/g in comparison group ($p < 0.001$). There were also qualitative and quantitative changes in the population of *Escherichia coli*, which were characterized by reliable reduction in the total number of *E. coli* (5.17 ± 0.11 CFU/g) as compared to that of the control group – 6.33 ± 0.21 CFU/g ($p < 0.001$). The study showed a significant increase in relatively pathogenic flora in the stool (*Enterococcus faecalis*, *Enterobacter cloacae*, *Citrobacter*, *Klebsiella pneumoniae*, etc.) – 3.38 ± 0.15 CFU/g (comparison group children had – 1.72 ± 0.52 CFU/g) ($p < 0.01$). The species of relatively pathogenic flora for patients with asthma differed from that of healthy individuals. The most often detected fungi was of the genus *Candida*, with microbial quantity 4.27 ± 0.16 CFU/g, while for healthy individuals it comprises 1.14 ± 0.29 CFU/g ($p < 0.01$). The content of *staphylococcus* (*aureus* and hemolytic) amounted to 1.42 ± 0.21

CFU/g, whereas for healthy children in the stool it was missing ($p < 0.001$) (Table).

Following the standard basic therapy for children with bronchial asthma the level of bifidobacteria remained almost unchanged – 3.55 ± 0.16 CFU/g (3.56 ± 0.16 CFU/g – before treatment) ($p > 0.05$), the number of lactobacilli remained fairly low – $3,41 \pm 0.18$, as compared to the rate before treatment ($p > 0.05$). There was also a tendency of decrease in the total number of *E. coli* up to $5.01 \pm 0,1$ CFU/g as compared to the data before treatment – 5.17 ± 0.1 CTU/g ($p > 0.05$). Treatment dynamics did not show a tendency to reduce the number of relatively pathogenic flora ($p < 0.05$). There remained a high titer of *Candida* fungi that amounted to 4.16 ± 0.17 CFU/g ($p < 0.05$), and *Staphylococcus* – 1.45 ± 0.22 CFU/g, in comparison with the data in the period of asthma exacerbation ($p > 0.05$) (Table).

CONCLUSIONS

Thus, the data obtained from this study demonstrates the presence of intestinal microbiocenosis disorders with school-age children suffering from bronchial asthma, while these disorders transpire with qualitative and quantitative changes of microflora.

It was also found that while treating asthma the use of standard basic therapy alone does not lead to normalization of dysbiotic processes in the colon. There is a need for new treatment methods that can bring about a positive effect on intestinal microflora, which, in its turn, will improve a child's health in the presence of bronchial asthma as well as reduce the risk of the underlying disease complications and frequent relapses.

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