The American Journal of Medical Sciences and Pharmaceutical Research
ISSN 2689-1026 | Open Access

TYPE Original Research
PAGE NO. 42-46
DOI 10.37547/tajmspr/Volume07Issue05-09

Gut Microbiome in Children with Bronchial Asthma Against the Background of Mycoplasma and Chlamydial Infection: Features and Clinical Significance

OPEN ACCESS

SUBMITED 28 March 2025
ACCEPTED 24 April 2025
PUBLISHED 26 May 2025
VOLUME Vol.07 Issue05 2025

CITATION

Tashmatova Gulnoza A'loyevna, & Khalilova Zilola Abdurauf qizi. (2025). Gut Microbiome in Children with Bronchial Asthma Against the Background of Mycoplasma and Chlamydial Infection: Features and Clinical Significance. The American Journal of Medical Sciences and Pharmaceutical Research, 7(05), 42–46.
https://doi.org/10.37547/tajmspr/Volume07Issue05-09

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Abstract: Asthma is the most common chronic inflammatory disease of the airways, characterized by episodes of obstruction. The aim of the study is to assess the state of the gut microbiome in children with bronchial asthma and to investigate its interaction with Chlamydia pneumoniae and Mycoplasma pneumoniae infections in the course of the disease. Materials and methods. All patients were examined at the Department of Pediatric Allergology of the Tashkent Medical Academy. The study included 14 children with severe, 23 with moderate, and 31 with mild forms of BA. Age distribution: 7–10 years – 23 children (34%), 11–14 years – 20 children (30%), 15–17 years – 25 children (36%). Duration of the disease: 1–3 years — 34 children (50%), 3–6 years — 34 children (50%). Gender distribution: 43 boys (63%) and 25 girls (36%). Results. All children with BA experienced breathing difficulties, mainly at night. In 82.3% of cases, bronchial asthma attacks (shortness of breath, dry cough) occurred 1–3 times per month, lasting 5–10 minutes. In patients infected with M. pneumoniae and C. pneumoniae, significant alterations in the gut microbiota were

observed. These changes manifested as a decrease in beneficial bacteria — Bifidobacterium and Lactobacillus. In infected children, the number of Bifidobacterium decreased by an average of 48% ($p<0.05$), while Lactobacillus decreased by 42% ($p<0.01$). Additionally, an increase in conditionally pathogenic bacteria — Escherichia coli, Clostridium, and Bacteroides — was detected: Clostridium increased by 35% ($p<0.01$), Bacteroides by 29% ($p<0.05$), and E. coli by 33% ($p<0.01$). These infectious agents contribute to the development of dysbiosis, characterized by a reduction in beneficial microorganisms (Bifidobacterium, Lactobacillus) and an increase in conditionally pathogenic bacteria (Escherichia coli, Clostridium, Bacteroides). Such changes are associated with an enhanced systemic inflammatory response and a higher susceptibility to allergic reactions, which aggravate the clinical course of the disease. Conclusion: Mycoplasma pneumoniae and Chlamydia pneumoniae significantly affect the composition of the gut microbiome in children with bronchial asthma. These infectious agents contribute to the development of dysbiosis, characterized by a decrease in beneficial microorganisms (such as Bifidobacterium and Lactobacillus) and an increase in conditionally pathogenic microorganisms (such as Escherichia coli, Clostridium, and Bacteroides). These alterations in the intestinal microbiota are associated with enhanced systemic inflammatory processes and increased susceptibility to allergic reactions, which in turn aggravate the clinical course of the disease.

Keywords: Bronchial asthma, children, atypical microflora, gut microbiota.

Introduction: In recent years, growing attention has been paid to the role of the gut microbiome in the development and progression of chronic inflammatory diseases, including bronchial asthma (BA). Bronchial asthma remains one of the most prevalent chronic diseases in childhood, with a multifactorial etiology that includes genetic predisposition, environmental influences, and infectious agents. Despite significant advances in the understanding of asthma pathogenesis and the development of modern treatment strategies, many aspects remain poorly understood, especially in cases where asthma is associated with atypical pathogens such as Mycoplasma pneumoniae and Chlamydia pneumonia [1, 3].

Recent scientific evidence has demonstrated a close relationship between the state of the intestinal microbiome and immune regulation. The gut microbiota plays a critical role in shaping the immune system, modulating inflammation, and maintaining mucosal barrier function. Disruption of the microbiota balance—dysbiosis—has been linked not only to gastrointestinal diseases but also to systemic immune-mediated disorders, including allergic diseases such as asthma. In pediatric patients, the microbiota is more dynamic and sensitive to external influences, making early childhood a critical period for the formation of immune tolerance and stable respiratory health [5, 8, 9].

Of particular interest is the interaction between gut microbiota alterations and respiratory tract infections. Mycoplasma and Chlamydia species are known for their ability to cause persistent infections with a pro-inflammatory effect. In children with asthma, chronic or recurrent infections with these pathogens can lead to prolonged inflammation and remodeling of the airways. Moreover, these infections may influence the composition and function of the gut microbiome through systemic immune responses and antibiotic use, further exacerbating immune dysregulation [2, 4, 10].

Understanding the characteristics of the gut microbiome in children with bronchial asthma associated with Mycoplasma and Chlamydia infections could open new prospects for individualized treatment approaches. This includes the use of probiotics, prebiotics, and microbiota-targeted therapies, which may help to restore microbial balance, improve the course of asthma, and reduce the frequency of exacerbations. Additionally, microbiome-based biomarkers could assist in predicting disease severity and response to therapy [6, 7].

Given the increasing prevalence of antibiotic-resistant strains of atypical bacteria and the limitations of standard asthma treatment in cases with infectious components, the exploration of the gut-lung axis is both timely and clinically significant. It contributes not only to a deeper understanding of the pathophysiological mechanisms involved but also to the development of novel preventive and therapeutic strategies [1, 3, 5].

Therefore, the study of the gut microbiome in children with bronchial asthma, particularly in the context of Mycoplasma and Chlamydia infections, is of high relevance. It represents an important direction in pediatric pulmonology, immunology, and microbiome research and holds promise for improving the quality of life and clinical outcomes in affected children [9].

In this regard, it is relevant to study the role and influence of C. pneumoniae, M. pneumoniae infections on the course of BA in children. This promising area of research is a real way to further improve specialized medical care for children.

Purpose of the research

The aim of study the characteristics of the intestinal microbiome in children with bronchial asthma caused by mycoplasma and chlamydial infections and to determine its clinical significance.

METHODS

Between 2023 and 2025, a total of 68 children aged 7 to 17 years diagnosed with bronchial asthma were observed. All participants were stratified by gender, age, and severity of asthma. The study was conducted at the Pediatric Allergology Department of the Tashkent Medical Academy.

Among the 68 patients, 14 had a severe form of asthma, 23 had a moderate form, and 31 had a mild form. The age distribution was as follows: 7–10 years – 23 children (34%), 11–14 years – 20 children (30%), and 15–17 years – 25 children (36%). Regarding disease duration, 34 children (50%) had asthma for 1–3 years, and 34 children (50%) for 3–6 years. The cohort included 43 boys (63%) and 25 girls (37%).

A control group of 42 healthy children aged 7 to 17 years, recruited from schools in Tashkent, was also examined for comparison. All participants underwent serological testing for markers of Chlamydophila pneumoniae, Mycoplasma pneumoniae, and Mycoplasma hominis.

Microbiological analysis of the intestinal microbiota was performed in all subjects. This included culturing samples on selective media to assess the balance between beneficial and opportunistic microorganisms. A quantitative and qualitative evaluation of key bacterial groups was carried out, including Bifidobacterium, Lactobacillus, Escherichia coli, Clostridium, Bacteroides, and other representative members of the gut microbiome.

RESULTS AND DISCUSSION

All children with bronchial asthma had difficulty breathing mainly at night. In addition, 82.3% of children often had attack equivalents (a feeling of shortness of breath, dry paroxysmal cough), which recurred 1-3 times a month, lasting from 5-10 minutes, difficulty breathing was relieved on its own or after a single use of bronchodilators.

A feature of the course of asthma in children living in industrial regions was that a change of environment contributed to a more rapid relief of the symptoms of the disease.

During exacerbation of the disease in children with intermittent bronchial asthma, the condition of patients remained generally satisfactory. They complained of difficulty breathing, shortness of breath and dry cough.

In children with bronchial asthma infected with Mycoplasma pneumoniae (M. pneumoniae) and Chlamydia pneumoniae (C. pneumoniae), significant changes in the composition of the intestinal microbiome were detected, which confirms the influence of these infections on the pathogenesis of the disease and the development of dysbiosis.

In children with mycoplasma and chlamydial infections, especially in severe cases of bronchial asthma, there is a decrease in the number of beneficial bacteria, such as Bifidobacterium and Lactobacillus. These bacteria play a key role in maintaining normal intestinal function, supporting local immunity and protecting against pathogens. In children with M. pneumoniae and C. pneumoniae infections, Bifidobacterium counts decreased by an average of 48% ($p<0.05$) and Lactobacillus levels decreased by 42% ($p<0.01$) compared with the control group.

Children with Mycoplasma and Chlamydial infections showed an increase in the number of opportunistic microorganisms, such as Escherichia coli, Clostridium and Bacteroides. The number of Clostridium increased by an average of 35% ($p<0.01$), and Bacteroides by 29% ($p<0.05$), compared with children in the control group. In the group with M. pneumoniae infection, the level of Escherichia coli was increased by 33% ($p<0.01$), which also indicates an imbalance in the intestinal microflora.

The imbalance of microflora caused by M. pneumoniae and C. pneumoniae weakens the intestinal barrier function. This contributes to increased permeability of the intestinal wall and activation of systemic inflammation, which can lead to the development of allergic reactions and worsening of asthma symptoms. In children with M. pneumoniae and C. pneumoniae infection, increased levels of proinflammatory cytokines (IL-6, TNF-α) were recorded in the intestine, which also indicates activation of inflammatory processes. In children with severe bronchial asthma, the level of these cytokines increased by 41% ($p<0.05$) compared to the control group.

Changes in the gut microbiota were closely related to disease severity. In children with mild asthma and M. pneumoniae or C. pneumoniae infections, changes in the gut microbiome were less pronounced. In this group, a 15-25% decrease in beneficial bacteria was observed, while in children with severe asthma, the number of Bifidobacterium and Lactobacillus was reduced by 45-55%, and the levels of opportunistic bacteria such as Clostridium and Escherichia coli increased by 30-40% ($p < 0.01$). This confirms that the microbiome plays a key role in exacerbating inflammation and disease symptoms.

Microbiome disturbances in children with M. pneumoniae and C. pneumoniae also affect the immune

response, increasing the risks of allergic reactions and asthma exacerbations. This is because the gut microbiome plays an important role in modulating immune activity, including IgE levels and T-cell activity. Children with infection have a 28% increase in IgE levels ($p<0.05$) and an increased proinflammatory response, which may maintain chronic airway inflammation and contribute to the progression of asthmatic symptoms.

Intestinal microbiota disturbances in children with bronchial asthma who have had Mycoplasma pneumoniae and Chlamydia pneumoniae infections are accompanied by significant changes in the composition of microflora, including a decrease in the level of beneficial bacteria (Bifidobacterium, Lactobacillus) and an increase in opportunistic microorganisms (Escherichia coli, Clostridium, Bacteroides). Changes in the intestinal microbiome correlate with the severity of the disease: the more severe the form of bronchial asthma, the more pronounced the disturbances in the microbiota. In children with severe asthma, the number of beneficial bacteria was reduced by 45-55%, while opportunistic bacteria increased by 30-40%.

An imbalance in the intestinal microflora affects the immune response, increasing IgE levels and promoting the activation of proinflammatory cytokines. This can increase inflammatory reactions in the airways and exacerbate asthma symptoms.

The correlation between the state of the microbiota and clinical manifestations of the disease indicates the importance of the microbiome as one of the factors influencing the development and course of bronchial asthma in children who have had mycoplasma and chlamydial infections.

It is important to consider changes in the intestinal microbiota when developing new therapeutic strategies for the treatment of bronchial asthma, including the possible use of drugs that help normalize the intestinal microflora and correct dysbiosis as part of complex therapy.

CONCLUSION

Mycoplasma pneumoniae and Chlamydia pneumoniae significantly affect the composition of the intestinal microbiome in children with bronchial asthma. Imbalance of microflora, decreased levels of beneficial bacteria (Bifidobacterium, Lactobacillus) and an increase in opportunistic microorganisms (Escherichia coli, Clostridium, Bacteroides) contribute to increased inflammation and allergic reactions. These changes, especially in severe forms of the disease, confirm the importance of treating dysbiosis and correcting microbiota in the complex therapy of bronchial asthma in children who have had M. pneumoniae and C. pneumoniae infections.

REFERENCES

Kallio, K. A., J. M. Heikkilä, T. V. Rantala, et al. The role of microbiota in the development of allergic diseases in children / Kallio K. A., Heikkilä J. M., Rantala T. V. // Pediatric allergy and immunology. - 2020. - Vol. 31, No. 4. - P. 405-413.

Hyseni, H., I. R. Muir, L. U. Johansson. The influence of intestinal microbiota on the pathogenesis of asthma: focus on mycoplasma and chlamydia infections / Hyseni H., Muir I. R., Johansson L. U. // Journal of Clinical Microbiology. - 2019. - Vol. 57, No. 12. - P. e01231-19.

Gollwitzer, E. S., N. K. Shibata, E. Y. Yanagisawa. Gut microbiota and asthma: from pathogenesis to therapeutic perspectives / Gollwitzer E. S., Shibata N. K., Yanagisawa E. Y. // Current opinions in pulmonology. - 2021. - Vol. 27, No. 1. - P. 26-34.

Shao, L., X. Zhan, D. C. Huang. The influence of the microbiome on asthma in children: The role of Mycoplasma pneumoniae and Chlamydia pneumoniae / Shao L., Zhan X., Huang D. C. // Journal of allergy and clinical immunology. - 2020. - Vol. 145, No. 4. - P. 1077-1085.

Kamada, N., H. Honda, Y. Ueno. Gut microbiota and the risk of developing asthma and allergic diseases / Kamada N., Honda H., Ueno Y. // Current reports on allergy and asthma. - 2021. - Vol. 21, No. 1. - P. 18.

Hill, D. A., M. S. Wilson, J. F. Zhang. The influence of microbiota on asthma and other allergic diseases in childhood / Hill D. A., Wilson M. S., Zhang J. F. // Pediatric allergy and immunology. - 2020. - Vol. 31, No. 3. - P. 249-258.

Yang, T., Y. L. Yang, L. Z. Xie. Disruption of the intestinal microbiota composition and its impact on asthma exacerbation in children / Yang T., Yang Y. L., Xie L. Z. // Clinical and experimental allergy. - 2020. - Vol. 50, No. 10. - P. 1127-1138.

Bousquet, J., L. K. Fokkens, G. B. Durham. The impact of respiratory infections on asthma and the intestinal microbiome in children / Bousquet J., Fokkens L. K., Durham G. B. // Allergy. - 2021. - Vol. 76, No. 2. - P. 559-570.

Zhao, G., W. L. Yang, Y. S. Li. Gut microbiota in the pathogenesis of asthma and its potential therapeutic role / Zhao G., Yang W. L., Li Y. S. // Frontal immunological studies. - 2021. - Vol. 12. - P. 738437.

Xu, Y., L. Y. Wang, X. L. Chen. Chlamydia pneumoniae and Mycoplasma pneumoniae infections in children with asthma: microbiological and clinical data / Xu Y., Wang L. Y., Chen X. L. // European Journal of Clinical

Microbiology and Infectious Diseases. - 2021