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THE ROLE OF INTESTINAL DYSBACTERIOSIS IN THE GENESIS OF MICROBIAL ECZEMA IN CHILDREN

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Abstract. Recently there has been an increase in the incidence of eczema in the world. Up to 40% of all skin diseases are due to this pathology. A large proportion among various types of eczema is microbial eczema, which tends to be more severe with frequent, progressive relapses, a significant spread of the pathological process and is characterized by resistance to conventional methods of treatment. The available data on the important pathogenetic significance in the development and course of eczema of the pathology of the gastrointestinal tract are not well understood and often in practice they are not given much importance. The aim of this work was to analyze individual intestinal microbiota in children under 6 years of age suffering from microbial eczema. Comparison of laboratory indicators of stool analysis was made with the control group, consisted of patients with scleroderma. For various different between local games popular Fisher's exact criterion. An increase in the frequency of dysbiotic groups among children with microbial eczema was revealed, in particular, the detection of candidiasis, which requires the inclusion of relevant studies in the diagnostic search for the select the right therapy.

Key words: *microbial eczema; intestinal dysbacteriosis; microbial sensitization*

РОЛЬ ДИСБАКТЕРИОЗА КИШЕЧНИКА В ГЕНЕЗЕ МИКРОБНОЙ ЭКЗЕМЫ У ДЕТЕЙ

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Резюме. В последнее время отмечается увеличение заболеваемости экземой в мире. До 40% всех кожных заболеваний приходится на данную патологию. Большой удельный вес среди различных видов экзем составляет микробная экзема, имеющая тенденцию к более тяжелому течению с частыми, продолжительными рецидивами, значительным распространением патологического процесса и характеризующаяся резистентностью к общепринятым методам лечения. Имеющиеся данные о важном патогенетическом значении в развитии и течении экземы патологии желудочно-кишечного тракта недостаточно изучены, и часто на практике им не придается большого значения. Цель данной работы — анализ нарушений микробиоты кишечника у детей до 6 лет, страдающих микробной экземой. Производилось сравнение лабораторных показателей анализа кала с контрольной группой, которую составили пациенты со склеродермией. Для

выявления различий между двумя группами использовался точный критерий Фишера. Установлено достоверное увеличение частоты дисбиотических нарушений в группе детей с микробной экземой, в частности выявление кандидоза, что требует включения в диагностический поиск соответствующих лабораторных исследований для подбора рациональной терапии.

Ключевые слова: *микробная экзема; дисбактериоз кишечника; микробная сенсибилизация*

INTRODUCTION

Eczema (from the Greek *ekzeo* — I boil out) is a chronic recurrent allergic skin disease, formed under the influence of exogenous and endogenous trigger factors, characterized by the appearance of a polymorphic rash [9]. The disease occurs with itching, sleep disturbance and deterioration in quality of life. Recently, there has been an increase in the incidence of eczema in the world. Up to 40% of all skin diseases are due to this pathology. Urban residents get sick more often (60–65%) [10, 16]. Eczema appears at any age and can have an acute, subacute or chronic course [17].

Microbial eczema (ME) is one of the clinical forms of eczema. This is a polyetiological disease that develops as a result of the interaction of hereditary (polygenic multifactorial inheritance with pronounced expressivity and penetrance of genes), metabolic, neuroendocrine, vegetative-vascular, infectious-allergic and external factors [16]. In recent years, ME has acquired a tendency toward a more severe course with frequent, prolonged relapses, a significant spread of the pathological process, and is characterized by resistance to conventional treatment methods [2]. In the acute stage, ME is clinically manifested by asymmetrically located foci of edematous hyperemia with clear boundaries of different localization, the central part is covered with purulent and serous crusts, after removal of which an erosive surface with weeping in the form of "wells" is exposed. Secondary lesions (eczematids) may appear on large areas of the skin [16]. The clinical types of ME found in children include numular (coin-shaped) and post-traumatic. When skin scrapings from skin lesions in patients with eczema, *S. aureus* is detected in 80% of cases, *S. haemolyticus* in 14%, and yeast of the genus *Candida* in 40.7% [3, 7, 8, 11, 15]. In the pathogenesis of the disease, the leading role is given to bacterial sensitization, which is promoted both directly by microbial allergens and by skin autoantigens formed under the influence of bacterial and fungal flora [11].

An important pathogenetic significance in the development and further course of eczema, especially in children, is the pathology of the gastrointestinal tract and hepatobiliary system [4–6, 14, 17, 18], accompanied by enzymopathies, dyskinesias, intestinal dysbacteriosis, leading to impaired membrane digestion and malabsorption syndrome, which in turn creates additional antigenic stimulation of the body. Contrary to popular belief, gut microflora affects not only the metabolism of the body as a whole, but also the shaping of skin microbiome. It has been established that patients with ME have pronounced skin dysbiosis both in lesions and on unaffected skin [7, 12, 16]. Against this background, the microflora is transformed into a more pathogenic one, which contributes to the chronicization of dermatoses [12]. A direct connection between the state of the intestinal biocenosis and the course of allergic skin diseases was discovered. In particular, an increase in the frequency of seeding of *S. aureus* has been established, as well as a close relationship between its proliferation of the skin and intestines in patients with an acute form of ME, and a decrease in representatives of the autochthonous intestinal bacterial flora (bifidobacteria and lactobacilli) in the chronic course [12]. It has also been proven that the inclusion in therapy of probiotic drugs leads to a significantly faster resolution of clinical symptoms, a decrease in the frequency of exacerbations and relapses of the disease [1, 12, 18]. However, standards of medical care do not include the use of drugs to correct dysbiosis [13].

It remains unclear whether changes in the composition of the gut microbiome precede the development of ME or whether changes in the gastrointestinal (GI) tract are secondary. The most probable is the assumption about the existence of a so-called "vicious circle" in the relationship between allergic diseases and GI pathologies [4–6].

AIM

The aim of this study is to analyze disturbances of the gut microbiota in children with microbial eczema and assess its effect on the underlying condition.

MATERIALS AND METHODS

The study is based on a comparative analysis of laboratory data characterizing the state of gut microbiota of two groups of patients who were examined and treated in the dermatovenerological department of the clinic of Saint Petersburg State Pediatric Medical University for 6 years from 2011 to 2023. The first group consisted of children (n=12) with an average age of 3 years 5 months, who were

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diagnosed with ME based on complaints and clinical and anamnestic data. The control group included children with localized scleroderma (n=12) with an average age of 4 years 8 months. All subjects underwent stool analysis for conditionally pathogenic microflora and/or stool analysis for dysbacteriosis. Statistical data analysis was carried out using the Excel program. Differences in proportions independent variables were assessed by Fisher's exact test. The criterion of reliability at $p < 0.05$ was considered statistically significant for indicators.

RESULTS AND DISCUSSION

A comparative analysis of identified deviations in gut microbiota in two groups of children is presented in Table 1.

Intestinal dysbacteriosis due to the proliferation of pathogenic or opportunistic bacteria and/or fungi of the genus *Candida* was detected in 83% of cases when analyzing the stool of children with ME, which is 2 times more frequent than in patients with scleroderma (42%). In particular, proliferation of fungi of the genus *Candida* was detected significantly more often (in 58% of cases versus 8%, respectively). Another important pathogen, which was more common in the children of the first group, was *Staphylococcus aureus* (33% versus 8%), but the difference in the two groups was not statistically significant. Among the less common pathogens in the group of children with ME, *Proteus mirabilis, Citrobacter freundii, Klebsiella oxytoca, and hemolytic Escherichia coli* were identified. It was not possible to conduct a comparative analysis of disturbances of the normal autochthonous microbiota, including bifidobacteria and lactobacilli, since a detailed stool analysis for dysbacteriosis was not carried out for all subjects. However, a decrease in lacto- and/or bifidobacteria was detected in 100% of cases when performing this analysis in children with ME, which was not observed in the second group.

The results obtained confirm the presence of dysbiotic changes in the intestines of patients with ME and their direct relationship with the disease, which allows us to talk about disorder of the intestinal microbiocenosis as one of the links of pathogenesis. At the same time, the etiological structure of pathogens that we identified does not differ qualitatively from that in previously conducted studies, however, the largest share was made up of *Candida*, and not the coccal flora. It should be noted that the species composition may differ depending on the region of residence and the age group of patients.

CONCLUSION

Dysbiotic disorders in the intestine are an important component of the pathogenesis of ME. Changes in the intestinal microbiocenosis in children with ME under 6 years of age are characterized by an increase in the number of various pathogenic flora; fungi of the genus *Candida* are most often identified. The polyetiological disease requires a comprehensive approach, including diagnosis and correction of the intestinal dysbacteriosis.

ADDITIONAL INFORMATION

Author contribution. Thereby, all authors made a substantial contribution to the conception of the study, acquisition, analysis, interpretation of data for the work, drafting and revising the article, final approval of the version to be published and agree to be accountable for all aspects of the study.

Competing interests. The authors declare that they have no competing interests.

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Table 1. Pathological deviations in the intestinal microbiocenosis in in the main and control groups of children

Таблица 1. Патологические отклонения в микробиоценозе кишечника в основной и контрольной группах детей

Identified pathological deviations in the intestinal microbiocenosis / Выявленные патологические отклонения в микробиоценозе кишечника	Children with microbial eczema, n=12 / Дети с микробной экземой, n=12	Control group, n=12 / Контрольная группа, n=12	Reliability of differences, p / Достоверность различий, p
Yeast-like fungi of the genus *Candida* / Дрожжеподобные грибы рода *Candida*	7*	1	0,01
Staphylococcus aureus	4	1	0,14
Proliferation of pathogenic or opportunistic bacteria and/or fungi of the genus *Candida* / Пролиферация патогенных или условно-патогенных бактерий и/или грибов рода *Candida*	10*	5	0,04

*Statistically significant differences / * Статистически значимые различия.

Consent for publication. Written consent was obtained from the patient for publication of relevant medical information within the manuscript.

ДОПОЛНИТЕЛЬНАЯ ИНФОРМАЦИЯ

Вклад авторов. Все авторы внесли существенный вклад в разработку концепции, проведение исследования и подготовку статьи, прочли и одобрили финальную версию перед публикацией.

Конфликт интересов. Авторы декларируют отсутствие явных и потенциальных конфликтов интересов, связанных с публикацией настоящей статьи.

Источник финансирования. Авторы заявляют об отсутствии внешнего финансирования при проведении исследования.

Информированное согласие на публикацию. Авторы получили письменное согласие пациентов на публикацию медицинских данных.

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