



**COMPARISON OF THE CLINICAL COURSE OF OSLT WITH THE NATURE
OF DISORDERS OF THE MICROFLORA OF THE UPPER RESPIRATORY
TRACT IN CHILDREN**

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Abstract: Acute respiratory diseases are the most common in childhood. Together with influenza, they account for at least 70% of all morbidity in children. Acute stenosing laryngotracheitis is one of the most serious manifestations of acute respiratory diseases in young children, requiring hospitalization of the child and intensive care [15].

Keywords: OSLT, dysbiotic disorders, gram-positive and gram-negative flora, Candida.

Annotatsiya: O'tkir respirator kasalliklar bolalik davrida eng ko'p uchraydi. Ularning ulushi gripp bilan birgalikda bolalardagi barcha kasallanishlar tarkibida kamida 70% ni tashkil qiladi. O'tkir stenozli laringotraxeit yosh bolalardagi o'tkir respirator kasalliklarning eng xavfli ko'rinishlaridan biri bo'lib, bolani kasalxonaga yotqizishni va intensiv terapiyani talab qiladi [15].

Kalit says: OSLT, disbiyotik kasalliklar, gramm-musbat va gramm-manfiy flora, Candida.



Introduction

In recent years, many countries have seen an increase in resistance of respiratory pathogens. It is obvious that changes in the sensitivity of microorganisms require changes in empirical antibacterial therapy, which is only possible if there are data obtained from continuous monitoring of resistance not only in the country as a whole, but also, above all, at the regional level [7, 14].

It is believed that respiratory viruses not only have a high affinity for certain parts of the respiratory tract, but also contribute to the colonization of the respiratory tract mucosa by bacteria [1, 2, 3, 10].

Viral-bacterial associations lead to complicated course of laryngotracheitis, formation of recurrent forms [5, 6, 8]. Most domestic pediatricians note that the main bacteria detected during LT are opportunistic pneumotropic microorganisms, which are representatives of normal flora of the respiratory tract [11,16].

As studies have shown, the risk group for developing croup syndrome in viral and viral-bacterial infections includes children with allergic diathesis, food allergies, patients with atopic dermatitis, hay fever, frequently and long-term ill children, sensitized by previous infections, medications, as well as those in the post-vaccination period. Patients with a burdened history of allergic and some other diseases show a particular tendency to recurrence of laryngitis/laryngotracheitis and a protracted course of the disease [13].

Materials and methods of research

The upper respiratory tract microbiocenosis was determined using bacteriological testing. For this purpose, material was collected using a docron swab, then placed in an enrichment medium (Eagle's medium or 199 Parker's medium). This achieved the accumulation of the pathogen in the epithelial cells of the mucous membrane of the posterior wall of the larynx, which significantly increases the probability of isolating the pathogen. The cultures in the accumulation medium were incubated at $t - 37^{\circ}C$ for 18-24 hours, then seeded with a swab on nutrient media. Identification of the isolated



microorganisms was carried out in accordance with the tests recommended in the "Bergie's bacterial identifier" [J. Hoult].

In 275 children aged 6 months to 7 years with established recurrent stenosing laryngotracheitis, the microbial landscape of the mucous membranes of the upper respiratory tract (URT) was studied using conventional bacteriological research methods, including cultures of nasopharyngeal and laryngopharyngeal secretions on nutrient media with subsequent identification. In our studies, the microflora of the respiratory tract was assessed in primary and recurrent SLT in the acute period (from day 1 to day 5 of the disease) and in the period of remission (from day 6 of the disease).

The microbial landscape was assessed in cases of newly developed laryngeal stenosis and its recurrence against the background of acute respiratory viral infection in the acute period (from the 1st to the 7th day of illness) before the start of antibacterial therapy and in the period of complete health (at least 10-14 days after the respiratory viral and/or bacterial infection). Not only the qualitative microbiological landscape was taken into account, but also its quantitative content.

Discussion and results

During the acute period of viral infection, only 87 (31.6%) children had a normal microflora composition in the nasopharynx and 52 (18.1%) in the laryngopharynx.

Dysbiotic processes were characterized by the colonization of the mucous membranes of the upper respiratory tract by pathogenic and opportunistic gram-positive and gram-negative flora, and a decrease in the secretion of saprophytic and normal microflora. *Staphylococcus aureus* is the undoubted leader in this process. It occurs both as a monoculture and in associations - in combination with other pathogenic pathogens. Along with gram-positive bacteria, *Candida* fungi were detected, as well as *Klebsiella*, *E. coli*, *Enterobacter*, *Moraxella*, which formed complex associations [4].

We analyzed the composition of the respiratory tract microbiocenosis depending on the number of episodes of laryngeal stenosis suffered against the background of a viral infection. In patients with 3 episodes of stenosing laryngotracheitis (SLT), the normal



composition of the nasopharynx microflora was recorded in 136 (49.4%) examined children, in the laryngopharynx - in 82 (29.8%). In other cases, gram-positive bacteria were most often detected in 91 (33.1%) in the nasopharynx and in 85 (30.1%) in the laryngopharynx and Staphylococcus aureus in monoculture (45 (16.3%) and 86 (31.3%)), that is, microbial communities were formed that characterize the first degree of dysbiosis. Associations of gram-positive with gram-negative microbes (grade II dysbiosis) were rare - in 18 (6.5%) cases in the nasopharynx and in 27 (9.8%) in the laryngopharynx.

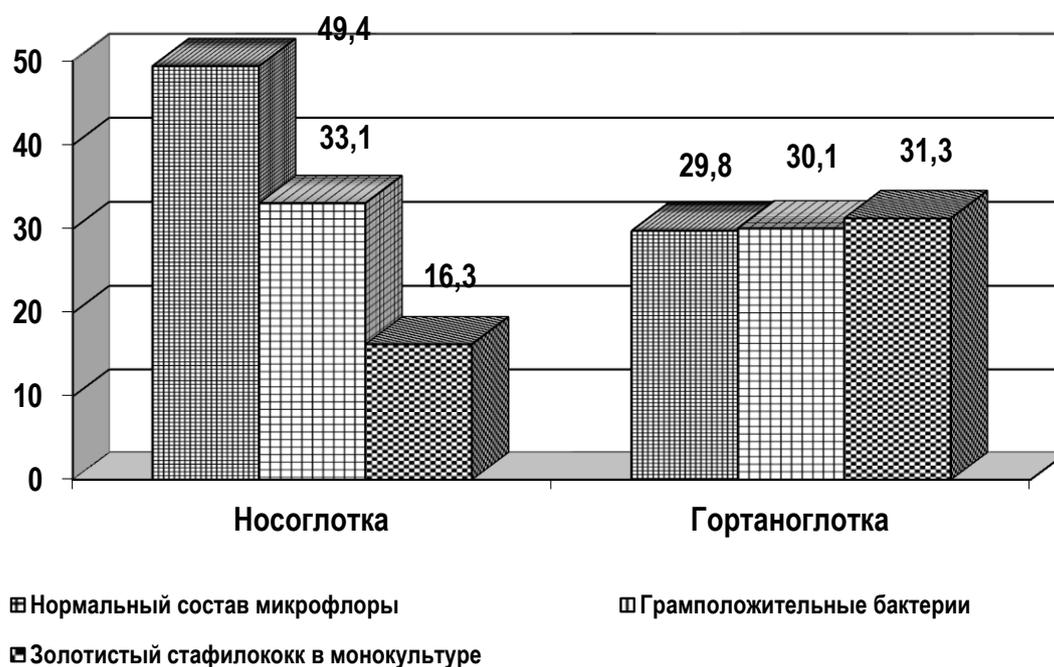


Fig. 1. The composition of the microbiocenosis of the respiratory tract depending on from the number of episodes (3 episodes) of laryngeal stenosis

In children with 4-5 cases of laryngeal stenosis in the acute period of viral infection, normal microflora in the upper respiratory tract was determined in one third of patients. Pathogenic flora of the nasopharynx in the acute period is mainly represented by associations of gram-positive bacteria 158 (57.5%), monoculture of Staphylococcus aureus is quite often detected - in 81 (29.5%) cases. Complex associations of microorganisms are registered in 29 (10.5%) children. In the laryngopharynx of these same patients, the composition of the microbiocenosis slightly changes - the proportion of gram-positive



flora 102 (37.1%) and staphylococcus monoculture 22 (8.0%) decreases, the number of patients with complex associations of microbes significantly increases - up to 112 (40.7%), gram-negative microorganisms, unusual for this econiche, appear in monoculture - in 29 (10.5%) of the examined. In the period of convalescence of ARVI, the microbiocenosis in the nasopharynx is represented mainly by Staphylococcus aureus in monoculture in 162 (58.9%), there are almost no complex associations - 15 (5.5%). In the laryngopharynx, complex associations were more often recorded, the percentage of children with S. aureus in monoculture on the mucous membranes remains high - 98 (35.6%).

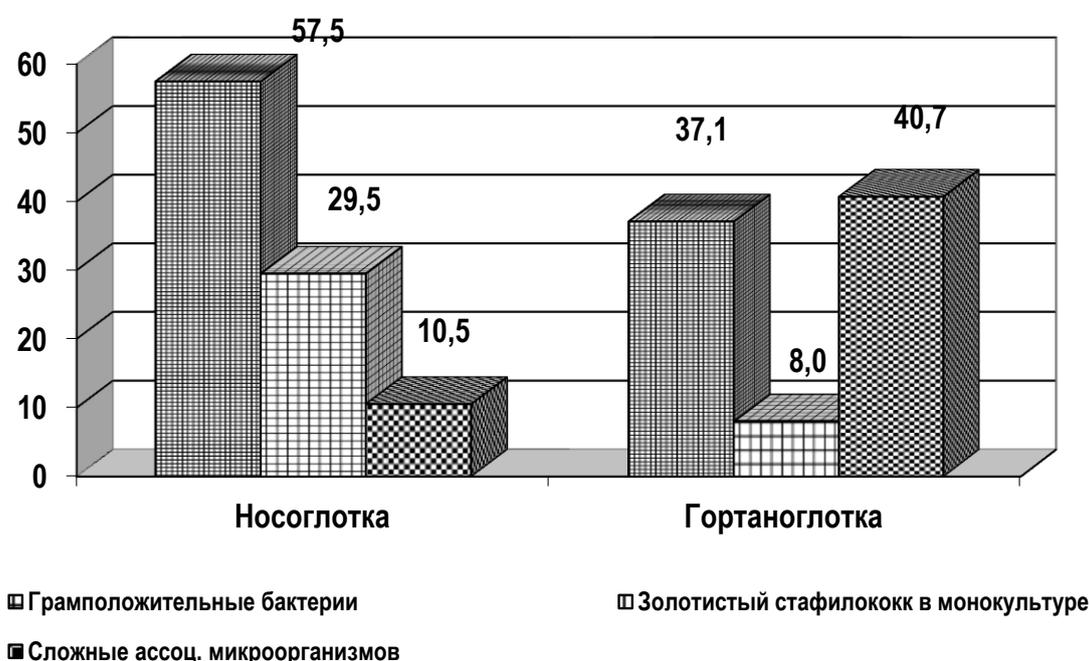


Fig. 2. The composition of the microbiocenosis of the respiratory tract depending on from the number of episodes of laryngeal stenosis suffered (4-5 episodes)

In children with 6 or more episodes of SLT against the background of ARVI, the normal composition of microflora in the period of acute infection was determined in the nasopharynx in 45 (16.4%) examined patients and in the laryngopharynx in 29 (10.5%), in the convalescence period in 55 (20.0%) and 42 (15.3%), respectively. Dysbiotic disorders in the nasopharynx in the acute period were expressed by an increase in the proportion of children with complex associations of microbes 75 (27.3%), and the preservation of the



leading role of gram-positive flora 112 (40.7%). In the laryngopharynx, there is a significant (12.5%) increase in allochthonous flora - *E. coli*, *Enterobacter*, *Moraxella*, *Candida* fungi and their associations with gram-positive microbes 121 (44.0%) with a decreasing role of gram-positive pathogens 72 (26.2%). During the convalescence period, gram-negative microorganisms in monoculture 17 (6.2%) also began to be detected in the nasopharynx of these children, the percentage of gram-positive microbes decreases 34 (12.4%), there is a significant increase in *Staphylococcus aureus* and complex bacterial associations by 42%. In the laryngopharynx, the microflora is represented by complex associations - in 125 (45.5%) children, a decrease in the role of gram-positive microbes and an increase in the percentage of allochthonous flora to 6.7%.

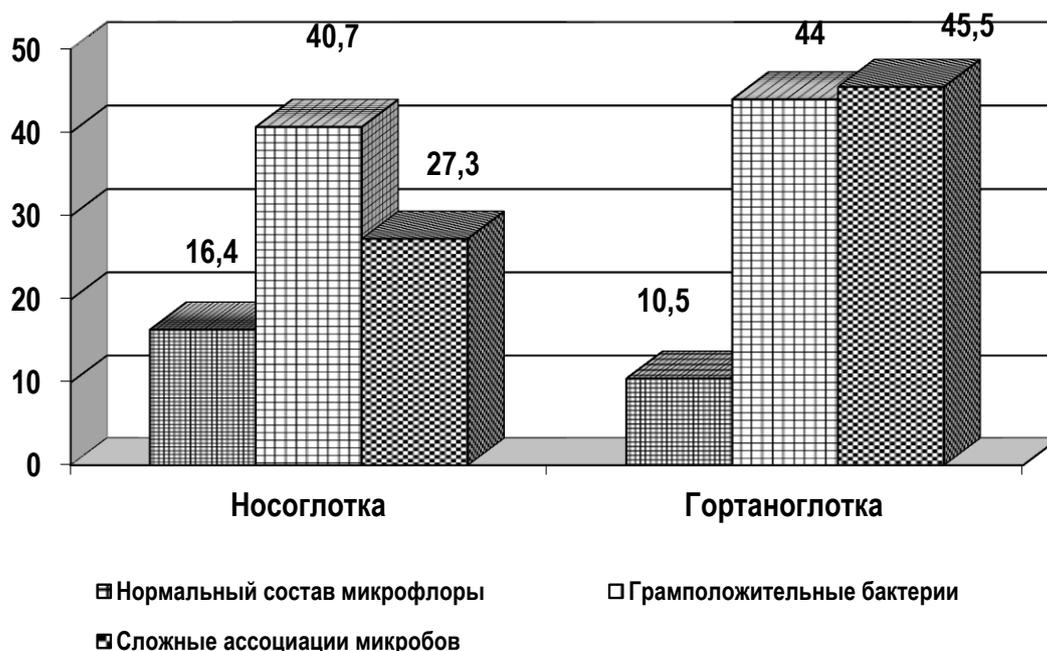


Fig. 3. Composition of the microbiocenosis of the respiratory tract depending on the number of episodes (6 or more episodes) of laryngeal stenosis

The indicators of the specific weight of different microorganisms in the overall structure of the isolated microflora do not quite adequately reflect their etiological role in the development and maintenance of the infectious process [9, 12]. A more illustrative indicator is the infectivity rate - the percentage of patients in whose material at any stage



of the examination (in any period of exacerbation) at least once a particular pathogen was detected. Thus, in patients with RSLT, *S. aureus*, β -hemolytic streptococcus, *Candida* fungi were isolated in 49.5%, 28% and 22.5%, respectively. The indicator of constancy - the proportion of samples containing a certain type of microorganism - is also a characteristic of the etiological significance of clinical isolates. In α -hemolytic streptococcus and *S. aureus*, the constancy index was 33.6% and 53.9%, while in *Candida* fungi it was 28.6%, which confirms their participation in the formation and maintenance of dysbiosis of the URT mucous membranes. When comparing the clinical course of SLT with the nature of dysbiotic disorders, it was found that the disease is characterized by a more pronounced fever and intoxication in children who do not have microflora disorders. With dysbiosis of grades I and II, the disease occurs against the background of mild or absent toxicosis at subfebrile or normal temperature. In children with dysbiosis of grade II on the URT mucous membranes, we noted frequent development of grade II laryngeal stenosis, a reliable increase in the duration of cough, severity of catarrhal syndrome, and a "rich" auscultatory picture in the lungs compared to children with a normal composition of the URT microflora. The frequency of recurrence of SLT was also in direct correlation with the nature of the identified dysbiotic disorders.

Dysbiotic disorders, maintaining a chronic inflammatory process in the mucous membranes of the upper respiratory tract, ensure an increase in the degree of laryngeal stenosis, an increase in the duration of cough, changes in the lungs and are a risk factor for the recurrence of stenosing laryngotracheitis.

We also compared the nature of dysbiotic changes in the respiratory tract in the acute period of the disease depending on the age of our patients and noted frequent damage to the mucous membranes by *Staphylococcus aureus* in all age periods. In the acute period of PSLT in children over 3 years old, the most pronounced disturbances in the microbiocenosis of the mucous membranes of the respiratory tract are determined, both in the nasopharynx and in the laryngopharynx (normal microflora composition is present in 9.5% and 9% of the examined, respectively). We did not find such a pattern in the acute



period of RSLT. During the remission period of PSLT, the normal microbiological composition of the respiratory tract is restored only in half of the examined children aged 0 to 3 years; at an older age, the normal flora composition in the nasopharynx is in 33% of children aged 3-6 years and in 22% aged 6 years and older. The normal microbial landscape of the laryngopharynx in children under 3 years of age during the remission period with PSLT was determined in 50% of cases, in the other two groups - only in 25%. With RSLT during the remission period, the restoration of normal flora from 0 to 3 years was noted only in 16%, over 3 years - in 50% of cases the microflora remains normal.

In the acute period, significant shifts in the microbiocenosis of the respiratory tract were noted in both primary and recurrent SLT. Dysbiotic processes were characterized by the colonization of the mucous membranes of the upper respiratory tract with pathogenic and opportunistic gram-positive and gram-negative flora, a decrease in the release of saprophytic and normal microflora. *Staphylococcus aureus* is the undoubted leader in this process in the acute period of the disease. It occurs both as a monoculture and in the form of associations - in combination with other pathogenic pathogens. The incidence of *Staphylococcus aureus* in the respiratory tract in the acute period is high both in PSLT and in RSLT. In PSLT in the acute period, *Staphylococcus aureus* was isolated from the nasopharynx of 28% of the examined children, and from the laryngopharynx in 25%. In RSLT, this microbe was detected in 39% of cases in the nasopharynx and in 23% of children in the laryngopharynx. In associations, *S. aureus* was more often isolated from the laryngopharynx in patients with RSLT - in 22% of cases.

In the acute period of the disease, α -hemolytic streptococcus is most often detected in the laryngopharynx of patients with PSLT (17%), while in RSLT it was detected extremely rarely (in 2% of cases). In both PSLT and RSLT, *E. coli* is detected on the mucous membranes of the upper respiratory tract in the acute period (6 and 8%, respectively). Fungi of the genus *Candida* were detected in the laryngopharynx in PSLT in 25% of cases, and in RSLT - in 18%; mycelia of the fungus were also isolated from the nasopharynx, both in PSLT and RSLT. Complex associations of microorganisms were not



observed only in the nasopharynx of patients with PSLT, while in RSLT they were detected both in the nasopharynx (15%) and in the laryngopharynx (23% of those examined). Gram-positive pathogens in the acute period of SLT are found mainly in the form of associations, mainly with *Staphylococcus aureus*, and do not have such a high representation in the URT as *S. aureus*.

In acute period of RSLT, complex pathogen associations were more common in older children in the laryngopharynx (43%). The presence of such changes in the microbiocenosis characterizes the severity of dysbiotic processes and the duration of their existence. In acute period of PSLT, the above patterns are not detected, although pathogens such as *Candida*, *E. coli*, *Klebsiella* are more often isolated in older children. The incidence of respiratory mucosa by *Staphylococcus aureus* in the remission period is very high, both in primary and recurrent SLT. But in RSLT, the process of colonization of the mucous membranes by this pathogen is expressed to a greater extent. In PSLT, the level of *S. aureus* isolation from the nasopharynx is at the level of 32%, in RSLT it reaches almost 50%. (β -hemolytic streptococcus is found in RSLT only in the form of associations, and only in the laryngopharynx - up to 17% of cases, in PSLT β -hemolytic streptococcus is found in the nasopharynx as a monoculture - up to 7%, in the laryngopharynx in the form of associations - up to 20% of those examined. Pneumococcus in PSLT is detected in the respiratory tract during remission in 13%), in RSLT only in the laryngopharynx in 12% of those examined. Complex associations of pathogens during remission are found in the nasopharynx in RSLT almost 2 times more often than in PSLT. In the laryngopharynx, complex combinations of pathogens in PSLT during remission are detected quite often - in 33%, in RSLT - in 26%. Both in the acute period and during remission, phenomena of deepening of dysbiotic processes in the nasopharynx are detected during RSLT.

Conclusion

Thus, the identification of complex associations of microorganisms, long-term persistence of pathogens in RSLT demonstrates a certain degree of dysbiotic disorders of



the respiratory tract in this disease. In ASLT, we noted an aggravation of the process of dysbiocenosis of the respiratory tract, characterized by the colonization of the respiratory tract mucosa first by pathogenic gram-positive flora, then the addition of gram-negative microflora, and even microorganisms that are not typical for this econiche.

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