

Microbiome of the upper respiratory tract (URT) of children with atopic bronchial asthma (BA)

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Background:

The state of the microbiome is an important component of human health, however studies on the relationship of the microbiome and asthma in Russia a little.

Material:

Studied the microbiome of the URT in patients aged 5 to 17 years with atopic BA with the use of the culture method: at 174 children studied the microbiome of the mucous membrane of the nasal cavity, 170 children - mucous membrane of the posterior wall of the pharynx.

Results:

The mucous membrane of the nasal cavity: the 17.82% of patients (31/174) pathogenic and conditionally pathogenic flora is not selected; 45.40% (79/174) selected *Staphylococcus aureus*, 29.31% (51/174) of children – *Staphylococcus epidermidis*; in individual patients – other variants of pathogenic and conditionally pathogenic microorganisms, including *Haemophilus influenzae* (3 patients), *Klebsiella pneumonia* (3 patients) and *Streptococcus pneumonia* (4 patients), *Proteus* (2 patients).

The mucosa of the posterior pharyngeal wall: in 74.71% patients (127/170) of pathogenic and conditionally pathogenic flora is not selected; 4.71% (8/170) of the selected *Staphylococcus aureus*, 17.06% (29/170) children – fungi of the genus *Candida* (one receive therapy with the inclusion of corticosteroids 17 patients), children in single – *Escherichia coli* (1 patient), *Klebsiella pneumonia* (3 patients), *Staphylococcus epidermidis* (2 patients).

The level of total IgE in serum was: in group of patients with the mucous membrane of the nasal cavity which are pathogenic and conditionally pathogenic flora is not selected, 179 ± 143 U/ml in the group of patients with the mucous membrane of the nasal cavity which highlighted *Staphylococcus aureus*, 316 ± 283 U/ml, in the group of patients with the mucous membrane of the nasal cavity were selected *Staphylococcus epidermidis* – 353 ± 356 U/ml, in the group of patients with other variants of conditionally pathogenic and pathogenic flora – 163 ± 108 U/ml, $p=0.023$. Differences in the level of total Immunoglobulin E, depending on the characteristics of the microbiome of the throat in patients with asthma not established.

Conclusions:

Thus, the condition of the mucous upper respiratory tract microbiome, especially of the mucous membrane of the nasal cavity, the relationship with and typically the features of atopic bronchial asthma in children, and demonstrates the feasibility of a therapy aimed at the normalization of microbiome.