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Microbiome landscape and disease duration role in allergy in adult patients with bronchiectasis

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Abstract

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primarily neutrophilic, but the participation of allergies in the pathogenesis requires further research. The aim of the study was to determine the interconnection between allergy and microbiome landscape and the DD in pts with B.

Methods: The study included cohort of pts with confirmed by HRCT B. Total serum (TS) IgE was evaluated by using conventional electrochemiluminescence immunoassay. Isolation and identification of pathogens were conducted by classical bacteriological methods of inoculation on nutrient media. DD was calculated by the pts medical history. The methods of descriptive and non-parametric statistics were used to process the results.

Results: 21 pts were examined. Mean age 49.1±14.1years, 33.3% men; mean DD - 12.5±14.9 years. Pathogens were detected in 15(71.4%) samples (s), the combination of pathogens - in 2(9.5%) pts. *Pseudomonas aeruginosa (PA)* was identified in 7(33.3%) s, *Haemophilus influenza (HI)* in 7(33.3%) s, *Klebsiella pneumoniae* in 1(4.7%) s. The elevation of TS IgE was found in 7(33.3%) pts; median level 66.23 [24.8;107.2]. There was found moderate positive

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G1 the level of IgE is statistically significantly higher ($p=0,019$ by the Mann-Whitney test).

Conclusions: 1) The study showed that a longer DD and chronic colonization by pathogens are associated with higher levels of TS IgE in pts with B. 2) The most common pathogens are *PA* and *HI* in pts with B in Dnipro.

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