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BACTERIAL MICROBIOME AND ALTERED IMMUNE STATUS IN PERENNIAL ALLERGIC RHINITIS PATIENTS IN UKRAINE

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Inflammatory disease of the nasal mucosa, including perennial allergic rhinitis (PAR) is increasing annually, perhaps related to the bacterial microbiome microflora of the upper respiratory tract. This study analyzes the microflora of the upper respiratory tract in patients with PAR.

METHODS: A prospective microbiological study was performed in 98 patients aged 25 to 69 years with PAR. The upper respiratory tract was examined with identification of bacterial isolates and immunological studies in the laboratories of the State University "Institute of Microbiology and Immunology named after I.I. Mechnikov" of the National Academy of Sciences of Ukraine.

RESULTS: Strains of *Streptococcus aureus* in 69/98 (67.62%); *Malassezia furfur* (*Pityrosporum ovale*, *P. orbiculare*) in 20/98 (20.41%); *Streptococcus pyogenes* in 7/98 (7.14%), and *Candida* in 6/98 (6.12%) were obtained on microbe isolation from the upper respiratory tracts of PAR patients. All patients with PAR had reduced secretion of IFN- γ and IL-12, which correlated with the severity of allergic disease and decreased lung function $r=0.69$ ($r<0.05$); $r=0.74$ ($r<0.05$). This was accompanied by decreased levels of humoral immunity: IgA 2.200 [1.98; 2,900] g/l; IgM 1.900 [1.600; 1.700] g/l; and IgG 12.00 [11.50; 12.33 g/l] and decreased T-lymphocytes and decreases in the number of immunoregulatory subpopulations (T-helpers and T-suppressors) relative to reference values ($p<0.05$). 63 (64.29%) in PAR patients who had increased total IgE, averaging 205.5 \pm 12.25 IU/ml.

CONCLUSIONS: The upper respiratory tract microbiome may influence the severity of perennial allergic disease being associated with defective bacterial defenses and altered immune status in PAR.