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The state of the skin microbiome in patients with acne

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Introduction & Objectives: Acne (acne vulgaris) is a chronic relapsing skin condition, which occupies one of the leading places in the structure of dermatopathology, especially in young people of working age; it is a common cause of persistent scarring and negatively affects the psycho-emotional state of patients, their quality of life and performance at work. In the scientific works of domestic and foreign authors, there are indications of the relationship between the development, clinical course and severity of acne with the state of microbiota of the skin.**

Objective. To study and evaluate the degree of changes in the microbiocenosis of the skin in patients with acne, depending on their clinical course.

Materials & Methods: We examined 85 patients with acne aged 18 to 45 y/o, 49 (57.32%) women and 36 (43.87%) men, and 35 apparently healthy persons who made up the control group. The study of skin microbiocenosis was carried out by the method of microbiological study of the composition of the skin microbiota by the rinse test.

Results: According to the clinical classification of acne, 45 (51.8%) patients were diagnosed with papular acne, 31 (35.3%) with comedonal acne and 11 (12.9%) with nodular acne. 39 (44.7%) persons had acne for up to 1 year, and in 48 (55.3%) patients the duration of the disease was from 1 to 5 years.

In the microbiocenosis of the skin in patients with acne, an increase in seeding with associations of Streptococcus ά Haemolyticus + Staphylococcus Haemolyticus + Micrococcus was observed in 23 (27.05%) patients, Streptococcus β Haemolyticus + Staphylococcus Aureus + E.Coli + Candida albicans in 39 (45.88%) patients, especially in patients with papular acne and presence of Demodex folliculorum, and none of them was detected in the control group. Compared to the control group, where associations with the predominance of Staphylococcus Epidermidis were more often sown and there were no pathogenic cocci, a certain part belonged to monocultures of Staphylococcus haemolyticus and Staphylococcus aureus in patients with acne in the microbiocenosis. There was a significant increase in the growth of Streptococcus ά Haemoliticus (in 11 (12.94%) patients), Staphylococcus Haemoliticus (in 12 (14.12%) patients), Staphylococcus aureus (in 28 (32.94%) patients). In 13 (15.29) patients with acne, fungi of the Candida genus were cultured, and all of the above microorganisms were not cultured in the patients of the control group. The skin microbiocenosis disorders were observed in 20 (66.66%) patients with comedonal acne, in 37 (84.09%) patients with papular acne and in all patients with nodular acne.

Conclusion: In the examined patients with acne, the qualitative and quantitative changes in the parameters of microbiocenosis of the skin were determined, which depend on the clinical course of dermatosis. The most significant changes in the qualitative and quantitative composition of microbiota of the skin were found in patients with a chronic, severe and extremely severe acne and the presence of Demodex folliculorum. The different degrees of changes in the indicators of microbiota of the skin in patients with acne indicate the expediency of bacteriological and cultural studies of microbiocenosis of the skin in such patients for the purpose of timely informative diagnosis and prescription of a combination, differentiation and pathogenetically substantiated therapy.