

of sebum, humidity and acidity of the environment. The secretion of sweat glands, neutral pH and heat increase the degree of seeding by microorganisms. The most common representatives of the skin microflora are various species of the genera *Corynebacterium*, *Staphylococcus*, *Micrococcus* and *Propionibacterium*.

Sometimes the representatives of the normal microflora can be dangerous to the immunosuppressive organism or in the background of quantitative and qualitative disorders in the microbiocenosis, becoming pathogens. Thus, a representative of the normoflora of human skin *Propionibacterium* may have pathogenicity in excessive colonization in the background of disorders in the skin microbiome. A typical species of the genus *Propionibacterium* is *P. freudenreichii*.

Our skin is in constant contact with clothing, that is open areas have a more volatile microflora, and closed areas are dependent on textiles and conditions of its use. The purpose of our study is to determine the effect of substances for fabric sorting on the representative of the normal microflora of human skin *P. freudenreichii*.

The aim of the study was to determine the sensitivity of *P. freudenreichii* to substances treated with the studied flaps of different textures. The task of the study was to determine the effect of the studied flaps on the number and viability of *P. freudenreichii* and to establish the ability of the culture of *P. freudenreichii* to recover after interaction with the sample examined.

12 samples of different textile flaps were taken for the study treated with different substances to organize them. All the samples were coded. Flaps 1 cm<sup>2</sup> were cut from the fabric under aseptic conditions. The experimental study is aimed at determining the effect of substances the textile flaps are treated with on the representative of the normal microflora of the human body *P. freudenreichii*. The study is divided into two stages: the first aims to determine the impact of the studied flap on the number and viability of *P. freudenreichii*, the second - to determine the ability of the culture of *P. freudenreichii* to recover after changing the nutrient medium. *P. freudenreichii* reference strain of the microorganism is a member of the family of propionic acid bacteria. Thioglycol sterility control medium was used for its cultivation.

Thus, the experimental study found the effect of the studied flaps of fabrics treated with various substances on the number and viability of *P. freudenreichii*. The test culture was mostly affected by 10<sup>7</sup> CFU/ml 3, 5 and 9, which reduced the number of bacteria on 5 orders, with the recovery of cultures was at a minimum level - 10<sup>2</sup>-10<sup>3</sup> cells/ml, which indicates irreversible changes in the vital processes of *P. freudenreichii*. The experiment with 10<sup>8</sup> CFU/ml *P. freudenreichii* also isolated samples 3, 5 and 9, namely substances with which these samples were treated were effective even at an order of magnitude higher microbial load. The most promising was the sample 9, because it acted equally in the first and second microbial load, and significantly disturbed the vital activity of the reference culture and limited the opportunities for its recovery. The next step was to determine the toxicity of substances for textile treatment and to determine the sensitivity of other test cultures of microorganisms to the studied tissue samples. The obtained results are of practical importance in the manufacture of medical textiles and patient care products.

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## **TAXONOMIC COMPOSITION AND MICROBIOLOGICAL INDICATORS OF MICROBIOTA OF INFECTIOUS-INFLAMMATORY PROCESSES OF SOFT TISSUES**

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Microbiological examination was performed in III patients with infectious-inflammatory processes of the soft tissues: post-infectious abscess (32.43 %), carbuncle (16.21 %), panaritium (10.81 %), appendicular filtrates, purulent cyst and phlegmon (8.11 %), mastitis (7.21 %) and others. The test material was purulent-serous exudate of the focus, in some patients with their consent, the wall of the inflammatory focus was selected to determine the concentration of microbiota in the exudate and tissue.

From the clinical material taken from III patients, 171 strains of opportunistic bacteria belonging to 11 different taxonomic groups were isolated and identified. According to the constancy index, frequency of occurrence, Margalef species richness index, Whittaker species diversity and Simpson and Birger-Parker species dominance, the leading pathogens of infectious-inflammatory processes in modern conditions are *Staphylococcus aureus* (constancy index 68.47 % 0.6 index, diversity 14.15, species dominance of Simpson 0.467 and Berger - Parker 0.685). *Streptococcus pyogenes* (persistence index 20.72 %), *Escherichia coli* (19.82 %), and *Proteus mirabilis* (persistence index 15.32 %) are important in the formation of infectious and inflammatory processes in the soft tissues. In addition to anaerobic facultative and aerobic bacteria, obligate anaerobic bacteria (*Bacteroides fragilis*, *Peptostreptococcus prevoti*, *Prevotella melaninogenica*) are isolated in 8.10 % of patients. In 50 (45.05 %) patients the infectious-inflammatory process was formed by monoculture of *S. aureus* in 19.33 patients, *E. coli* in 13.46 %, *S. pyogenes* in 11.54 % of patients and rarely *S. epidermidis* and *P. mirabilis*. Associations consisting of two taxa were found in 61 (54.95 %) patients. The most frequent associations were *S. aureus*, *P. mirabilis* (11.54 %), *S. aureus* and *P. aeruginosa* (8.65 %), *S. aureus* and *S. pyogenes*, and *S. aureus* and *E. coli* (7 each), 69 %). *S. aureus* and *E. cloacae* (6.73 %). Infectious and inflammatory processes caused by the association of different taxa had a more severe course.

The localization of the causative agent of the infectious-inflammatory process of the soft tissues (in the exudate or in the tissue of inflammatory process) is of key importance for the development of treatment tactics. *S. aureus* and *E. coli* were found to be mainly localized in tissue ( $6.81 \pm 0.37$  lgCFU / g and  $5.31 \pm 0.41$  lgCFU / g) and to a lesser extent in exudate ( $5.27 \pm 0.47$  lgCFU / g and  $3.87 \pm 0.29$  lgCFU / g), respectively; *P. mirabilis* is localized in the soft tissues in a concentrate of 4.90 lgCFU / g, and in exudate only 3.00 lgCFU / g. *S. pyogenes* and *S. epidermidis* are found in higher concentrations in the exudate ( $6.17 \pm 0.49$  lgCFU / g and  $3.78 \pm 0.17$  lgCFU / g). However,  $4.78 \pm 0.31$  lgCFU/g and  $3.08 \pm 0.16$  lgCFU / g, respectively. In patients, the etiological agent is *S. aureus*, *E. coli* and *P. mirabilis*. It is advisable to use galvanization to deliver the antimicrobial agent to the tissue.

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## **DESTABILIZATION OF COLONIC LUMINAL MICROBIOME IN CHRONIC OBSTRUCTIVE BRONCHITIS**

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The state of dynamic equilibrium between the organism, its microbiome and the environment, which has developed evolutionarily, and due to which the human body is at the optimal level, is called eobiosis (normobiosis). Disturbance of eobiosis, which is expressed in the development of destabilization in different biotopes and is associated with changes in the normal taxonomic composition and function of the symbiotic microbiota, means dysbiosis or dysbacteriosis. Chronic obstructive bronchitis is one of the most common inflammatory human diseases. Close anatomical location, physiological relationships, and general systemic immune responses suggest that changes in the respiratory microbiota should be associated with destabilization of the colon microbiome.

In 63 patients with chronic obstructive bronchitis by bacteriological and mycological methods the taxonomic composition and population level of the colonic microbiome were studied, its microecological indices in the "host-microbiome" ecosystem was established. The control group consisted of 20 practically healthy individuals.

Obligate anaerobic bacteria of the genus *Bifidobacterium* (in 20 (31.75 %) patients), *Propionibacterium* – (in 5 (7.94 %) were found to be the most important in the colon microbiome in patients with chronic obstructive bronchitis concerning representation and multifunctional role. Under such conditions, the colonic biotope is contaminated and colonized by pathogenic enterobacteria: enteropathogenic *E. coli* - in 5 (7.94 %) patients, enterotoxigenic *E. coli* - in 4 (6.35 %), enteroinvasive *E. coli* – in one (1.59 %) patient, *E. coli* Hly + - in 12 (19.05 %), *E. coli*