

**МІНІСТЕРСТВО ОХОРОНИ ЗДОРОВ'Я УКРАЇНИ
БУКОВИНСЬКИЙ ДЕРЖАВНИЙ МЕДИЧНИЙ УНІВЕРСИТЕТ»**



МАТЕРІАЛИ

**105-ї підсумкової науково-практичної конференції
з міжнародною участю
професорсько-викладацького персоналу
БУКОВИНСЬКОГО ДЕРЖАВНОГО МЕДИЧНОГО УНІВЕРСИТЕТУ
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Матеріали підсумкової 105-ї науково-практичної конференції з міжнародною участю професорсько-викладацького персоналу Буковинського державного медичного університету, присвяченої 80-річчю БДМУ (м. Чернівці, 05, 07, 12 лютого 2024 р.) – Чернівці: Медуніверситет, 2024. – 477 с. іл.

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У збірнику представлені матеріали 105-ї підсумкової науково-практичної конференції з міжнародною участю професорсько-викладацького персоналу Буковинського державного медичного університету, присвяченої 80-річчю БДМУ (м. Чернівці, 05, 07, 12 лютого 2024 р.) із стилістикою та орфографією у авторській редакції. Публікації присвячені актуальним проблемам фундаментальної, теоретичної та клінічної медицини.

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identified in 27,0% (10) of people. Hereat, there were 45.9% (17) of the cases of homozygous carriers of the "wild" NN-genotype (N34), NS-heterozygous (N34S) - 51,4% (19) of the cases. One (2,7%) patient was a homozygous carrier of the mutant S- allele (SS-genotype, 34S).

On distributing all the patients according to the etiological agent it was found out that the frequency of the NN and NS-genotypes in patients with biliary pancreatitis made up 52,6% (10) and 47,7% (9), respectively and did not differ statistically from that in patients with pancreatitis of nonbiliary genesis – 33,3% (6) and 61,1% (11) respectively ($\chi^2 = 0,003$, $p = 0,95$ and $\chi^2 = 0,68$, $p = 0,4$ respectively).

While analyzing the group of patients with acute edematous biliary pancreatitis, it was established that the homozygous carriers of the favourable "wild" N allele and heterozygous occurred with the same frequency - 50% (5) and 50% (5), respectively. However, a tendency towards a domination of the NS-genotype was established in patients with edematous pancreatitis of nonbiliary genesis as compared with the NN-genotype whose frequency of detection made up 85,7% (6) and 14,3% (1), respectively. However, such differences were not significant statistically ($\chi^2 = 2,00$, $p = 0,16$). No homozygous carriers of the mutant S-allele were detected in patients with acute edematous pancreatitis.

In patients with acute destructive pancreatitis of biliary and nonbiliary genesis the frequency of detecting genotypes NN (N34) and NS (N34S) did not differ significantly: 55,5% (5) and 44,5% (4) versus 45,5% (5) and 45,5% (5) respectively ($\chi^2 = 0,001$, $p = 0,97$ and $\chi^2 = 0,114$, $p = 0,74$ respectively).

Conclusions. Thus, the frequency of the NN and NS-genotypes of the SPINK1 gene in the patients examined did not differ significantly from patients with various forms of acute pancreatitis. The carriage of the unfavourable SS-genotype, in our opinion, may be a contributory factor for the onset of the disease and a potentiation of its further progression, as well as a prognostic marker of a severe clinical course of acute pancreatitis with the development of necrotic lesions of the pancreas.

Mazur O.O.

MICROBIOTA OF THE MAXILLARY SINUSES OF CHRONIC PURULENT RHINOSINUSITIS IN PATIENTS WITH TYPE 1 DIABETES MELLITUS

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Introduction. Understanding the microbiota of the maxillary sinuses in chronic rhinosinusitis is important for developing new treatment strategies, such as targeted antibiotics or probiotics, that can restore a healthy bacterial balance and alleviate symptoms.

The aim of the study was to determine the species and population composition of the microbiota of chronic purulent maxillary rhinosinusitis in patients with type 1 diabetes mellitus of moderate severity type 1 diabetes mellitus (DM) and 10 patients with CPRS of the same age without concomitant pathology.

Material and methods. Bacteriological and mycological methods were used to study the species, population level quantitative characteristics of the microbiota of the maxillary sinus biotope in 38 patients with chronic purulent rhinosinusitis (CPRS) with type 1 diabetes mellitus (DM) and 10 patients without CPRS of the same age pathology.

Results. In patients with CPRS, combined with type 1 diabetes mellitus with moderate severity, bacteria of the genus *Bifidobacterium* and *Lactobacillus*, as well as bacteria of the genus *Streptococcus* (*S.salivarius*, *S.sanguis*, *S.mitis*, *L.lactis*), *Corynebacterium*. Against this background, the contents of the maxillary sinus cavity are contaminated with pathogenic and opportunistic bacteria of the genus *Prevotella*, *Fusobacterium*, *Streptococcus* (*S.pneumoniae*, *S.pyogenes*, *S.viridans*), *Staphylococcus* (*S.aureus*, *S.epidermidis*), *H.influenzae .catarrhalis*, *E.coli* and yeast fungi of the genus *Candida*. Such changes have led to violations of the dominance of indigenous obligate bacteria in the microbiocenosis.

CPRS in patients with type 1 diabetes disrupts microbial associations. In patients with HCV, the number of associations consisting of 3 species increases 2.7 times, but the number of

associations consisting of 4 species of microorganisms decreases 1.4 times. The number of associations consisting of 5 species in patients decreases by 3.5 times.

Among the most numerous associations consisting of 3 species of pathogenic and conditionally pathogenic autochthonous facultative microorganisms, the associations of the following representatives are more common: *M.catarrhalis*, *S.aureus* and *Bacteroides spp.*; *Prevotella spp.*, *S.viridans* and *S.salivarius*; *M.catarrhalis*, *Prevotella spp.* and *S.epidermitis*; *H.influenzae*, *Prevotella spp.* and *S.epidermitis*. Associations consisting of 4 species were found in 34% of patients and consist of *S.pneumoniae*, *M.catarrhalis*, *S.pyogenes*, *Fusobacterium spp.*; *S.pneumoniae*, *E.coli*, *S.aureus* and *Candida spp.*; *S.pneumoniae*, *E.coli Hly+*, *S.viridans* and *Candida spp.*

The dominant pathogens of the chronic inflammatory process in the maxillary sinuses are *S.pneumoniae*, *H.influenzae*, *M.catarrhalis*. Other bacteria (*S.pyogenes*, *S.aureus*, *E.coli Hly+*, *B.fragilis*) are additional or accidental (*E.coli Hly+*, *B.fragilis*) pathogens. All leading pathogens persist in the habitat in the association.

Conclusions. In patients with CPRS combined with type 1 diabetes mellitus of moderate severity an imbalance of autochthonous obligate, facultative and allochthonous microorganisms is formed in the contents of the maxillary sinus cavity due to the elimination or formation of a pronounced deficiency of autochthonous obligates, genus *Balibacterus .sanguis*, *S.mitis*, *S.mutans*, *L.lactis*, etc.) and a significant increase in the number and dominant role of pathogenic and opportunistic *S.pneumoniae*, *Bacteroides spp.*, *S.epidermidis*, *M.catarrhalis*, *H.influenzae*, *Prevotella spp.*, *S.viridans*, *S.pyogenes*, *S.aureus* and others. Therefore, the severity of type 1 diabetes in patients with CPRS negatively affects the species composition, population level, qualitative and quantitative dominance of autochthonous obligate and facultative, as well as allochthonous for the habitat of microorganisms and their associations.

Melnyk I.M.

PERSONALIZED APPROACH TO THE TREATMENT OF PURULENT WOUNDS

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Introduction. The problem of effective treatment of purulent wounds is one of the most pressing issues in surgery, the importance of which increased significantly during the war period. Despite the numerous developments of methods of local impact on the surface of the wound, the synthesis of new drugs for disinfection, stimulation of regenerative regeneration, it is not always possible to achieve a quick positive result of treatment. This is due to the multifaceted pathogenesis of wound healing processes, the mechanisms of which are far from fully revealed, the expressed individual feature of inflammatory reactions and regeneration processes, which are genetically determined, and this requires a personalized approach to treatment. It can be done through various genetic studies that reveal the individual characteristics of these processes and make it possible to predict their course. All this will be the basis for the choice of personalized treatment tactics.

The aim of the study is to increase the effectiveness of purulent wound treatment by researching the primary mechanisms of inflammation and regeneration as well as their genetic determination and on this basis to develop personalized treatment tactics.

Material and methods. The subject of the study was 8 patients with purulent wounds of the extremities, who underwent a comprehensive laboratory examination with an assessment of the activity of peroxide oxidation processes, proteolytic and fibrinolytic activity, markers of the severity of inflammation and regeneration processes. All patients were analyzed for polymorphism of the matrix metalloproteinase (MMP1) gene by Real Time PCR.

Results. A clear dependence of the nature of the pro- and antioxidant systems on the phase of the wound process was revealed. Excessive activation of peroxide oxidation processes in the inflammatory phase is accompanied by pronounced activity of antioxidant protection enzymes. In the regeneration phase, there is an advantage of antioxidant systems over the activity of peroxide oxidation. In the third phase, an unstable balance between pro- and antioxidant systems is observed.