МІНІСТЕРСТВО ОХОРОНИ ЗДОРОВ'Я УКРАЇНИ
БУКОВИНСЬКИЙ ДЕРЖАВНИЙ МЕДИЧНИЙ УНІВЕРСИТЕТ

М А Т Е Р І А Л И

106-ї підсумкової науково-практичної конференції
з міжнародною участю
професорсько-викладацького колективу
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Матеріали підсумкової 106-ї науково-практичної конференції з міжнародною участю професорсько-викладацького колективу Буковинського державного медичного університету (м. Чернівці, 03, 05, 10 лютого 2025 р.) – Чернівці: Медуніверситет, 2025. – 450 с. іл.

У збірнику представлені матеріали 106-ї науково-практичної конференції з міжнародною участю професорсько-викладацького колективу Буковинського державного медичного університету (м. Чернівці, 03, 05, 10 лютого 2025 р.) зі стилістикою та орфографією у авторській редакції. Публікації присвячені актуальним проблемам фундаментальної, теоретичної та клінічної медицини.

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discharge from the conjunctival cavity are possible. Long-term observations (1-5 years) confirmed a satisfactory cosmetic and functional effect on the operated eyelids, no lacrimation and no xerosis of the eye.

Conclusions. The application of a wraparound suture to the medial third of the everted eyelid is an easy to perform, anatomically accessible way to achieve the proper cosmetic and functional effect. The author's technique is a rational addition to the classical reconstructive methods of blepharoplasty, which in combination gives a stable corrective effect along the entire length of the pathologically altered eyelid.

Maksymyuk V.V.

GENOTYPES OF THE SPINK1 GENE IN PATIENTS WITH VARIOUS FORMS OF ACUTE PANCREATITIS

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Introduction. One of the fundamental mechanisms is the neutralizing effect of the secretory pancreatic trypsin inhibitor (the serine protease inhibitor of Kazal's type I - SPINK1). This particular peptide is composed of 56 amino acids and plays the role of an irreversible links between the trypsin serine and the lysine of its active center. SPINK1 is able to neutralize up to 20% of the total amount of trypsin, which is formed in the acinar cell.

The aim of the study. Study of genetically determined defense mechanisms aimed at preventing intrapancreatic enzyme activation.

Material and methods. The research involved 37 people with different forms of acute pancreatitis. Among them were 25 (67.6%) men and 12 (34.2%) women. The average age of the patients made up 48 ± 14,4 years. The patients were divided into 2 groups. The first group was made up of 17 patients with acute edematous pancreatitis. The second group comprised 20 patients with acute necrotizing pancreatitis.

Results. The presence of the favourable "wild - type" N-allele ("wild - type", Wt) - 73,0% (27) of the people was detected in the majority of the subjects. The pathological "mutant" S-variant was identified in 27,0% (10) of the people. As a result, there were 45.9% (17) of the cases of homozygous carriers of the "wild" NN genotype (N34), NS heterozygotes (N34S) - 51,4% (19) of the cases. One (2,7%) patient was a homozygous carrier of the mutant S - allele (SS - genotype, 34S). A distribution of the genotypes according to the polymorphic N34S variant of the SPINK1 gene among the examinees corresponded to expected Hardy – Weinberg's equilibrium ($p > 0,05$).

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 ($\chi2 = 0,003$, $p = 0,95$ and $\chi2 = 0,68$, $p = 0,4$ 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 heterozygotes occurred with the same frequency - 50% (5) and 50% (5), respectively.

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 ($\chi2 = 0,001$, $p = 0,97$ and $\chi2 = 0,114$, $p = 0,74$ respectively).

The homozygous mutation SS-genotype was detected in one person of the specified group. It should be noted that the initiation of the disease was associated with the nonbiliary factor in a female patient with the SS-genotype. The course of the disease was characterized by particular "aggressiveness" with the development of acute suppurative subtotal pancreatonecrosis which became complicated by the formation of abscesses of the omental bursa and the right subdiaphragmatic space, retroperitoneal phlegmon, external pancreatic and duodenal fistulae, left-side exudative pleuresy and toxicobacterial shock. The length of the patient's hospital stay made up

118 bed days 10 step-by-step surgical interferences, having been performed during this period. The development of the painful form of chronic pancreatitis with a predisposition to frequent recurrence was certified in the patient in the process of a follow-up. Taking into account the adduced analysis of the patient's case history with the SS-genotype, as well as the nonbiliary and nonalcoholic etiology of the disease, in our opinion, it is reasonable to believe that one of the main reasons for such a severe clinical course of acute pancreatitis in a particular case was its hereditary nature.

Conclusions. Thus, the frequency of the NN and NS-genotypes of the SPINK1 gene in the patients examined by us, 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 disease onset 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.

CHARACTERISTICS OF THE BACTERIAL ASSOCIATIONS OF THE PARANASAL SINUSES IN CHRONIC PURULENT RHINOSINUSITIS IN PATIENTS WITH TYPE 1 DIABETES MELLITUS

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Introduction The problem of chronic purulent rhinosinusitis (CPRS) in patients with type 1 diabetes mellitus (T1DM) is relevant due to the increased risk of infections, complicated course of the disease, impact on quality of life, frequency of relapses, economic burden and the need for a multidisciplinary approach to treatment.

The aim of the study. It was to count the number of pathogen associations of the microbiota of chronic purulent paranasal rhinosinusitis in patients with type 1 diabetes mellitus of moderate severity T1DM and 10 patients with HPRS 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 paranasal sinuses biotope in 38 patients with CPRS with T1DM and 10 patients without CPRS of the same age pathology.

Results. The dominant pathogens of the chronic inflammatory process in the maxillary sinuses are S.pneumoniae, H.influenzae, M.catarrhalis. Other bacteria are additional or accidental pathogens. All leading pathogens persist in the habitat in the association.

In patients with HPRS, combined with T1DM of moderate severity in the contents of the sinuses cavity, an imbalance of autochthonous obligate, facultative and allochthonous microorganisms is formed due to the elimination or formation of a pronounced deficiency of autochthonous obligates, 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.

In patients with HPRS, combined with T1DM 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 sinuses cavity are contaminated with pathogenic and opportunistic bacteria of the genus Prevotella, Fusobacterium, Streptococcus (S.pneumoniae, S.pyogenes, S.viridans), Staphylococcus (S.aurens, 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.

HPRS in patients with T1DM disrupts microbial associations. In patients with HPRS, 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