

**МІНІСТЕРСТВО ОХОРОНИ ЗДОРОВ'Я УКРАЇНИ
ВИЩИЙ ДЕРЖАВНИЙ НАВЧАЛЬНИЙ ЗАКЛАД УКРАЇНИ
«БУКОВИНСЬКИЙ ДЕРЖАВНИЙ МЕДИЧНИЙ УНІВЕРСИТЕТ»**



МАТЕРІАЛИ

101 – ї

підсумкової наукової конференції

професорсько-викладацького персоналу

Вищого державного навчального закладу України

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Матеріали 101 – ї підсумкової наукової конференції професорсько-викладацького персоналу вищого державного навчального закладу України «Буковинський державний медичний університет» (м. Чернівці, 10, 12, 17 лютого 2020 р.) – Чернівці: Медуніверситет, 2020. – 488 с. іл.

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У збірнику представлені матеріали 101 – ї підсумкової наукової конференції професорсько-викладацького персоналу вищого державного навчального закладу України «Буковинський державний медичний університет» (м. Чернівці, 10, 12, 17 лютого 2020 р.) із стилістикою та орфографією у авторській редакції. Публікації присвячені актуальним проблемам фундаментальної, теоретичної та клінічної медицини.

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by a surrogate test with cefoxitin. In all strains, sensitivity to β -lactam antibiotics, aminoglycosides (gentamycin, amikacin), fluoroquinolones (ofloxacin, ciprofloxacin, levofloxacin), macrolides (erythromycin, clarithromycin, azithromycin), clindromycin and trithromycin, clindromycin, and trithromycin, and clitromycin were also determined. Technique for antibiotic sensitivity determination was conducted according to the CLSI recommendations, 2017. Discs with antibiotics, manufactured by Oxoid, were used.

Human upper respiratory tract mucous membrane in standard is normally colonized by various microorganisms, among which gram-positive cocci occupy a leading place. Therefore, the detection of a significant amount of *Staphylococcus aureus* from this biotope was expected. The results obtained are presented in table 69 strains of *Staphylococcus aureus* were isolated from the oral mucosa in 2018, and 149 strains - in 2019. The percentage of methicillin-resistant among them was 2.90 and 3.36, respectively. 10 and 20 strains of *Staphylococcus aureus* were isolated from the nasal mucosa, respectively (2018-2019). It is noteworthy that a significant proportion of the methicillin-resistant MRSA is 15% in the last year, while none of the 10 *S.aureus* strains isolated in 2018 were methicillin-resistant.

Table

Isolation frequency of *S. aureus* methicillin-resistant strains

	2018 year			2019 year		
	Number of isolated <i>S. aureus</i>	Number of MRSA	%	Number of isolated <i>S. aureus</i>	Number of MRSA	%
Oral mucosa	69	2	2,90	149	5	3,36
Nasal mucosa	10	0	0,00	20	3	15,00

When studying the antibiotic sensitivity of the isolated MRSA strains, it has been detected that resistance to antibiotics, which do not belong to β lactams occurs very often among them. The isolated strains were resistant to 3-7 antibiotics, which could belong to both one group and several groups. Compared to 2018 the percent of MRSA poly-resistant strains have almost doubled in 2019. The results obtained by the authors coincide with the data given by other scientists in their works. MRSA prevalence should be monitored continuously.

Dzhuryak V.S.

**ASSOCIATION OF ALDOSTERONE SYNTHASE CYP11B2 (-344C/T) GENE
POLYMORPHISM OF CHRONIC KIDNEY DISEASE IN PATIENTS WITH ARTERIAL
HYPERTENSION**

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Renin-angiotensin aldosterone system (RAAS) plays a major role in the blood pressure regulation. Aldosterone, synthesized in the adrenal cortex by aldosterone synthase is encoded by the cytochrome 11B2 aldosterone synthase gene (CYP11B2).

The aim of the study was to analyze the association of aldosterone synthase gene (CYP11B2) biallelic polymorphism in the promoter at position -344 (-344C/T) with Chronic Kidney Disease (CKD) in patients with essential arterial hypertension (EAH) in Bukovina region.

100 subjects with EAH and target-organ damaging (2nd stage), moderate, high or very high cardiovascular risk were involved in the case-control study. Among them 79.0% (79) females and 21.0% (21) males, mean age 59.87±8.02 years; disease duration from 6 to 25 years. Diabetes Mellitus type 2 (DM 2) was in 28 persons, duration from 3 to 15 years. CKD was determined by the National Kidney Foundation recommendations (Kidney Disease: Improving Global Outcomes (KDIGO), 2012)¹ after glomerular filtration rate (GFR) decline <60 ml/min/1,73m² for ≥3 months (by Cockcroft-Gault formula and CKD-EPI for Cystatin-C and Creatinine serum levels depending on gender). CKD was diagnosed in 29 persons. All enrolled / screened patients signed the Informed



Consent to participate in the research. Control group included 48 practically healthy persons of relevant age. Gene polymorphism of aldosterone synthase gene CYP11B2 (-344C/T) was examined by polymerase chain reaction (PCR).

The probability of EAH in observed population increased 1.49 times in T-allele carriers of CYP11B2 gene, but only in females [OR=1.90; 95%CI:1.02-3.54; p=0.029], with contrary decreasing in C-allele women (p=0.041). No relevant dependences were observed in hypertensive males. T-allele increased probability of CKD (GFR<60 ml/min/1,73m²) in hypertensive population 1.48 times [OR=1.86; 95% CI: 1.01-3.58; p=0.049], especially in T-allele females 1.53 times [OR=6.51; 95%CI:1.39-30.60; p=0.007] with low CKD risk in T-allele males [OR=0.15; 95%CI:0.03-0.72; p=0.009], respectively as well. Some predictors like DM2, the 2nd and 3rd grades of Obesity, and the 3rd grade level of Blood Pressure elevation escalated the risk of CKD 2.4, 2.08-2.32 and 2.91 times, accordingly (p<0.05).

Thus, aldosterone synthase gene CYP11B2 (-344C/T) associated with EAH in Bukovina region. T-allele increased risk of CKD in hypertensive population, especially in females.

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DISBACTERIOSIS: THE MODERN VIEW ON THE PROBLEM AND POSSIBLE CORRECTION

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The most urgent issue in recent years is intestinal dysbiosis. By the term "dysbiosis" we mean changes in the microflora of the gastrointestinal tract (GIT) which normally populate non-sterile cavities, which in its turn leads to the appearance of qualitative and quantitative changes in the microbial impression of the intestine. We can also meet the term Bacterial overgrowth syndrome - a syndrome bacterial growth excess, which is often used in foreign literature.

Gastrointestinal tract microflora is known to play an important role in our body. For example: participates in the metabolism and synthesis of substances, water-salt metabolism, regulates the gas composition of the intestine, serves as a source of energy for the host cells, and also performs endocrine and immune functions. The weakening of one of these parts leads to an increase in the possibility of microbiocenosis of the gastrointestinal tract, bacterial translocation, the risk of sepsis, multiple organ failure.

The intestinal microflora protects people from colonization by exogenous pathogenic microorganisms, and suppresses also the growth of those pathogenic microorganisms that already exist in the intestine. Dysbacteriosis is not a major disease of the gastrointestinal tract, it manifests itself as a concomitant condition. Dysbiosis can be offset and uncompensated. In contrast to the compensated dysbiosis, which can be suspected only in a patient with manifestations of the disease of the gastrointestinal tract, uncompensated is accompanied by frustration disorders - diarrhea or constipation.

Treatment for dysbiosis begins primarily with the search for the disease, which led to a disturbance of the microbial composition of the intestine, as well as nutrition correction. The diet should be designed in such a way as to meet completely the needs of this organism. In the diet it is necessary to take products without preservatives, fresh vegetables and fruits, as well as sour-milk products, which contain the necessary lactobacillus and bifidobacteria.

In recent years, the following groups of drugs are used for the correction of the gastrointestinal tract microflora: probiotics, prebiotics, symbiotics, synbiotics and antimicrobial agents.

So, although the heading "dysbiosis" is absent in ICD-10, this does not diminish the essence of the problem. Correction of intestinal dysbiosis requires identification of the source of the disease and many associated factors. A general practitioner, using modern means of correcting the composition of the intestinal microflora, determines the combination for each individual patient.