МІНІСТЕРСТВО ОХОРОНИ ЗДОРОВ'Я УКРАЇНИ
БУКОВИНСЬКИЙ ДЕРЖАВНИЙ МЕДИЧНИЙ УНІВЕРСИТЕТ»

М А Т Е Р І А Л И

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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Conclusions. Consequently, genotypes and alleles of *VDR* (rs2228570) gene are not associated with the risk of developing EH in the examined. *C*-allele of *AGTR1* gene (rs5186) increases the risk of hypertension more than 2 times [OR–2.31; p=0.011]. Combination of minor *C*-allele of *AGTR1* gene and *A*-allele of *VDR* gene (*C*-allele $_{AGTR1}$ /AA_{VDR}+*C*-allele $_{AGTR1}$/AG_{VDR}) escalates the risk of EH more than 3 times [OR=3,36; p=0,015].

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LINKAGE OF BLOOD PRESSURE VALUES WITH NOS3 (rs2070744) AND GNB3 (rs5443) GENES POLYMORPHISMS IN THE NORTH-BUKOVINIAN POPULATION

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Introduction. Essential arterial hypertension (EAH) is one of the most common cardiovascular disease worldwide (4.3 million / person / year). Therefore, early detection and correction of risk factors including elevated blood pressure (BP) is important for effective secondary prevention of EAH.

The aim of the study: was to investigate the association of EAH severity with genes polymorphism of the endothelial nitric oxide synthase (NOS3, rs2070744) and guanine nucleotide-binding protein beta-3 (GNB3, rs5443) in Bukovina region.

Materials and methods. One hundred patients with EAH and target-organ damaging (2nd stage), moderate, high or very high cardiovascular risk were involved in the case-control study. Among them were 79.0% (79) women and 21.0% (21) men. Their average age was 59.87±8.02; disease duration from 6 to 25 years. All participant underwent clinical and laboratory examinations. Blood pressure (BP), Creatinine, glucose, lipids panel were studied. *GNB3* (rs5443) and *NOS3* (rs2070744) genotyping performed by TaqMan probes (CFX96™Real-Time PCR). Risk assessed by Relative Risk, Odds Ratio and 95% Confidential intervals. All enrolled /examined patients signed the Informed Consent to participate in the study. Control group included 48 practically healthy individuals of relevant age.

Results. A mutation of the *NOS3* gene (*786T>C*, rs2070744) and the *GNB3* gene (*825C>T*, rs5443) in the homozygous state in the West-Ukrainian population suffers from EAH occurs with a frequency of 16.67% and 8.33%, with no differences with the control subjects (p>0.05). In both groups dominate the *T*-allele of the *NOS3* gene and the *C*-allele of the *GNB3* gene: in patients by 12.5% (χ^2=4.50; p=0.034) and 41.66% (χ^2=50.0; p<0.001), in the control – by 25.0% (χ^2=12.0; p<0.001) and 40.0% (χ^2=33.33; p<0.001), respectively. The results of the binary logistic regression analysis did not confirm the prediction of the EAH appearance by polymorphic variants of the *NOS3* (rs2070744) and *GNB3* (rs5443) genes. However, the *TT* genotype of the GNB3 gene (rs5443) increases unreliably the EAH risk almost twice as likely [OR=2.0; OR 95%CI:0.40-10.82; p>0.05]. Epidemiological analysis did not confirm the association of the *NOS3* gene with the EAH severity. But *T*-allele of the *GNB3* gene increases the probability of high normal BP almost 5 times [OR=4.86; OR 95%CI:0.99-24.75; p=0.042].

Conclusion. Thus, the *NOS3* (rs2070744) and *GNB3* (rs5443) genes polymorphisms are not associated with blood pressure values and EAH severity as well.

Vasiuk V.L.

MICROBIOTA OF THE GUT, DYSBIOSIS AND IT'S CORRECTION: STATE OF THE PROBLEM

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Introduction. The complex interplay between the gut microbiota and IBD is an area of great interest for understanding disease pathogenesis and developing new treatments. Microbiota composition in the human's gut can be affected both by endogenous and exogenous factors. Interactions with the immune system and intestinal epithelial cells, influence of concomitant pathology are internal ones, second group includes medications, surgery, diet, harmful habits.

The aim of the study. The purpose of this review is to summarize the latest evidence on the importance of microbiota investigation and to explore possible future areas of research.

Material and methods. We performed bibliometric analysis for relevant publications in English and Ukrainian languages published after 2020 in Pubmed, Web of Science Core Collection and GoogleScholar. Altogether, around 600 articles on our topic were published within the mentioned period, of which 190 were analysed.

Results. Over time, dysbiosis has been reconsidered as a possible cofactor of multiple acute and chronic human diseases.The vicious cycles between gut dysbiosis and the GI tract diseases progression include impaired gut barrier, enrichment of circulating microbiota, toxicities of microbiota metabolites, a cascade of pro-inflammatory chemokines or cytokines, and augmentation in the generation of reactive oxygen species. Persistent oxidative stress, LPS infiltration and hepatocyte damage through the enterohepatic circulation may lead to hepatic stellate cell activation and hepatic fibrosis. Dysregulation of the gut flora is one of the factors connected to the onset of fatty liver disease. The pro- or anti-tumor effects of specific bacterial strains or gut microbiota-related metabolites, such as bile acids and short-chain fatty acids, have been highlighted in many human and animal studies. Dietary choices may alter constitution of the microbiome and cause gut microbiome dysbiosis, particularly due to the intake of food high in fructose sugars, animal products, and saturated fats.COVID-19 contributed to alcohol intake increase in some countries (folk medicine, social isolation), was accompanied by polypharmacy with using hepatotoxic drugs; medicamentous resistance; hypodynamia, decrease of physical activity and obesity frequency increase. Remarkable fact is that the problem is actual worldwide, and countries from all continents contributed the core collection of publications on this topic.

Preclinical and clinical studies have demonstrated that modulation of the gut microbiota can ameliorate liver function, reduce inflammation in liver and other portions of GI tract, underscoring the potential of this approach to improve HCC outcomes.Probiotics, prebiotics, synbiotics, fecal microbial transplantation (FMT), bioengineered bacteria, gut-restricted FXR agonists and others are promising therapeutic approaches that can alter gut microbiota composition.

Conclusions. The fine balance between symbiotic and potentially opportunistic and/or pathogenic microorganisms can undergo quantitative and qualitative alterations. A lot of economical, social, cultural factors are influencing microbiota of the gut. They are dynamic, depend on lifestyle of the individual and the population worldwide.

Voroniuk K.O.

ASSOCIATION OF GEOMETRIC MODELS OF LEFT VENTRICULAR HYPERTROPHY WITH CLINICAL, METABOLIC-HORMONAL PARAMETERS AND MINERAL METABOLISM IN HYPERTENSIVE PATIENTS

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Introduction. Hypertension is the leading cause of cardiovascular disease and premature death worldwide. Owing to widespread use of antihypertensive medications, global mean blood pressure (BP) has remained constant or decreased slightly over the past four decades. By contrast, the prevalence of hypertension has increased, especially in low and middle-income countries (LMICs). Estimates suggest that in 2010, 31.1% of adults (1.39 billion) worldwide had hypertension. The prevalence of hypertension among adults was higher in LMICs (31.5%, 1.04 billion people) than in high-income countries (HICs; 28.5%, 349 million people). Variations in the levels of risk factors for hypertension, such as high sodium intake, low potassium intake, obesity, alcohol consumption, physical inactivity and unhealthy diet, may explain some of the regional heterogeneity in hypertension prevalence. Despite the increasing prevalence, the proportions of hypertension awareness, treatment and BP control are low, particularly in LMICs, and few comprehensive assessments of the economic impact of hypertension exist. Future studies are warranted to test implementation strategies for hypertension prevention and control, especially in