

**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
присвяченої 80-річчю БДМУ
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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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4. The magnitude of any effort is determined by incentives, incentives – the value of the goal, and the time and opportunity to achieve it. Unfortunately, health often becomes the goal when death becomes a near reality. However, even death cannot frighten a weak-willed person for long.

5. Four conditions are necessary for health: physical activity (at least for 20-30 minutes, but so that you sweat and your heart rate doubles), dietary restrictions, hardening, time and the ability to rest. And the fifth is a happy life!

Numerous physiological studies indicate that exercises that train the cardiovascular system should be isotonic (dynamic) rather than isometric (static), aerobic rather than anaerobic, intermittent rather than continuous, submaximal rather than maximal.

Physical activity affects all organs and systems, but the training effect develops at different rates in different organs. Therefore, the pace of increasing loads and duration should be chosen with a margin and focus on «slow» organs.

Conclusions. Doctors treat diseases, and health needs to be acquired independently through training. Because health is the «reserve power» of organs, of our entire physiology. They are necessary to maintain normal functional indicators at rest and during stress - physical and mental, as well as not to get sick, and if possible, not to die.

Semianiv M.M.

ASSOCIATION BETWEEN SPECIFIC GENETIC VARIATIONS IN THE AGTR1 AND VDR GENES AND THE RISK OF ESSENTIAL HYPERTENSION

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Introduction. Essential hypertension (EH) affects about 25-43% of the world population. Experts estimate that EH is the global most common disease: from 1 billion people in 2000 to 1,6 billion in 2025. As well, EH is one of the most important risk factors for death from cardiovascular diseases. EH, as a polygenic disease, develops as a result of the interaction of environmental factors, genetic factors and epigenomic structures. Most of genetic variations that are associated with normal or pathological conditions, including EH collected in Genome-wide association studies, where SNPs play the role of possible biomarkers for screening of EH predisposition.

The aim of this study was to establish the role of 1166A>C polymorphism of the AGTR1 gene (rs5186) and A/G polymorphism of the VDR gene (rs2228570) in risk prediction of essential hypertension (EH).

Materials and methods. The study included patients with EH and hypertensive-mediated organs damage (2nd stage), moderate, high/very high cardiovascular risk. 100 individuals were involved in the case-control study. There were 70.84% females, 29.16% males among them, the mean age was 57.86±7.81 y.o. Age- and gender-matched controls (n=60) whose blood pressure measurements were in normal range and without any apparent diseases were randomly selected to compare with the patient data. In order to detect AGTR1 (rs5186) and VDR (rs2228570) gene polymorphism the qualitative real-time polymerase chain reaction was done. AGTR1 gene genotyping was performed for 72 patients and 48 healthy individuals and VDR gene – for 100 patients and 60 healthy subjects.

Results. The distribution of genotypes and alleles AGTR1 (rs5186) and VDR (rs2228570) in the study and control groups did not differ significantly ($p>0.05$). C-allele of AGTR1 gene (rs5186) increases the risk of EAH more than 2 times [OR 2.31; 95% CI OR:1.19–4.47; $p = 0.011$], as well as AC- and the combination of AC- + CC-genotypes [OR–2.09; 95% CI OR:1.03–4.25; $p = 0.038$ and OR–2.30; 95% CI OR:1.14–4.64; $p=0.017$]. The epidemiological analysis showed that polymorphic variants VDR (rs2228570) genes are not the risk factors of EH in the observed. Although, combination of wild alleles of both genes in the homozygous state (AA_{AGTR1}/AA_{VDR}) makes a protective effect [OR=0,42; OR 95%CI:0,18-1,0; $\chi^2=3,74$; $p=0,05$], the combination of minor alleles (C-allele AGTR1 /AA_{VDR}+C-allele AGTR1/AG_{VDR}) increases the risk of EH more than threefold [OR=3,36; OR 95%CI:1,24-9,09; $\chi^2=5,88$; $p=0,015$].

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].

Sydorchuk L.P.

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% ($\chi^2=4.50$; p=0.034) and 41.66% ($\chi^2=50.0$; p<0.001), in the control – by 25.0% ($\chi^2=12.0$; p<0.001) and 40.0% ($\chi^2=33.33$; 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.