ASSOCIATION OF MATRIX GLA-PROTEIN GENE ALLELIC POLYMORPHISMS WITH ACUTE CORONARY SYNDROME IN THE UKRAINIAN POPULATION

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Extracellular calcification is a common and clinically significant component of a number of important human diseases including atherosclerosis. Myocardial infarction in most instances is the consequence of a thrombus forming on a ruptured atherosclerotic plaque, which is frequently associated with calcification. Coronary calcification in asymptomatic patients is known to increase the risk of coronary heart disease (CHD), and mineral deposits are found in more than 90% of patients with CHD. Recent studies suggest that in addition to modifiable coronary risk factors, such as hypertension, hyperlipidemia, and cigarette smoking, there is a strong genetic background for development of arterial calcification. The role of genetic predisposition to coronary artery calcification has been estimated to be up to 50%. Matrix γ-carboxyglutamic acid protein (MGP) is known to be a potent inhibitor of calcification in blood vessels and is strongly expressed on calcified atherosclerotic plaques in humans; it could modify the calcification in such plaques and the risk CHD. The human gene *MGP* is located on chromosome 12p. At present, among the large amount of identified *MGP* single nucleotide polymorphisms (SNPs) 8 of them are under the most intensive investigation: 2 of them in exons, and 6 in the upstream region of the gene. In vitro studies suggest that SNPs in *MGP* are associated with altered promoter activity. In addition, there is some evidence that *MGP* SNPs are associated with arterial calcification, although these results are not consistent.The purpose of this study was to investigate the association of three variants of MGP SNPs (G-7A, T-138C, Thr83Ala) with acute coronary syndrome (ACS) in Ukrainian population. Polymerase chain reaction and restriction fragment length polymorphism (RFLP) analysis were used to detect the above mentioned variants of *MGP* gene in 115 patients with acute coronary syndrome and in 110 practically healthyindividuals.Distribution of major allele homozygotous, heterozygotes and minor allele homozygotes in control group while analyzing T^{-138}→Cpromoter polymorphism58,7%, 36,7%, 4,6 while analyzing G^{-7}→A polymorphism of the promoter was - 41,8%, 54,5%, 3,6% , while at the assay of Thr_{83}→Ala polymorphism (exon 4) these were – 43,9%, 45,9%, 10,2%. Distribution of major allele homozygotous, heterozygotes and minor allele homozygotes in group with acute coronary syndrome: while analyzing T^{-138}→CMGP promoter polymorphism were 59,8%, 32,7%, 7,5%, while analyzing G^{-7}→A promoter polymorphism were - 42,1%, 45,6%, 12,3% , while at the assay of Thr_{83}→Ala polymorphism (exon 4) these were– 42,6%, 43,5%, 13,9%. It was estimated that A/A genotype (G^{-7}→A polymorphism) was significantly (p=0,02) associated with acute coronary syndrome in Ukrainian population.