ADIPOKINES DISBALANCE IN PATIENTS WITH COMORBIDITY OF TYPE 2 DIABETES AND ESSENTIAL HYPERTENSION DEPENDING ON GENETIC POLYMORPHISM OF AGTR1 GENE

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It is known that polymorphism of angiotensin II receptor type 1 gene (AGTR1) in many populations leads to the changes of the regulation of vascular tone and cardiovascular remodeling.

The aim of the study was to investigate the associations of AGTR1 polymorphism with adipokines disbalance in comorbidity of essential hypertension (EH) and type 2 diabetes (DM2) in Ukrainian population.

The main group consisted of 320 patients with EH and DM2, the comparison group consisted of 90 patients with EH without DM2, the control group consisted of 31 healthy individuals.

We determined levels of adiponectin and leptin, conducted genotyping of polymorphic marker A1166C of AGTR1.

It was established that more than half of patients with EH both as in presence and absence of DM2 had A/C and C/C genotypes of AGTR1. As to the spectrum of these genotypes main group and comparison group significantly differ from control group ($p<0.01$). It was found that allele C was present in 33.1% of main group patients and in 31.1% of comparison group patients; in control group it was present significantly much less frequently (in 19.4%, $p<0.01$). Main group with A/C and C/C genotypes of AGTR1 gene was characterized by significantly lower levels of adiponectin and higher levels of leptin as compared to A/A genotype ($p<0.01$). It can be explained by the influence of angiotensin II activation to the change of expression of gene encoding adipokines. In comparison group AGTR1polymorphism did not affect adipokines levels. The absence of differences of adipokines levels depending on the polymorphism in comparison group, unlike the main group, can indicate that the association of metabolic parameters with AGTR1polymorphism is more pronounced in presence of DM2.

Conclusions: In Ukrainian population of patients with comorbidity of EH and DM2 A/C and C/C genotypes of AGTR1 gene were associated with more pronounced adipokines disbalance as compared to A/A genotype of specified gene.