Genetic factors and the presence of coronary collaterals in patients with stable coronary artery disease

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Background: The coronary collateral circulation (CCC) varies in patients with coronary artery disease (CAD). Although many studies were provided to detect factors associated with collateral development, genetic factors are still studied insufficiently. The goal of this study was to assess the association of single nucleotide polymorphisms (SNP) in genes involved in vascular growth with CCC in patients with stable CAD.

Purpose: To assess if genetic variations in hepatocyte growth factor (HGF), vascular endothelial growth factor (VEGF), urokinase-type plasminogen activator (gene PLAU) are associated with the presence of coronary collaterals in patients with stable CAD.

Methods: A single-centered study was performed between March 2012 and December 2017. In 579 patients with stable CAD who underwent coronary angiography and had at least 50% stenosis in at least one major coronary artery collaterals were assessed by the use of the Rentrop score (0–3) during coronary angiography. SNPs PLAU rs4065, VEGF rs1570360, rs2010963 and rs699947, HGF rs5745752 were genotyped, multivariate logistic regression was carried out to determine the association of genotypes with CCC.

Results: 337 patients had visible coronary collaterals (Rentrop grade 1, 2 and 3) and 236 patients didn't have visible collaterals (Rentrop grade 0). Beside traditional risk factors of poor CCC - diabetes, smoking and arterial hypertension – patients without visible coronary collaterals (Rentrop 0) showed a higher frequency of the HGF rs5745752 CC genotype than those with visible coronary collaterals (Rentrop 1–3; p=0.001). (Fig. 1) The odds ratio of having CCC Rentrop 0 in patients with genotype CC was statistically significant (odds ratio = 1.94 [95% confidence interval: 1.38–2.76]; p=0.001). Statistical analysis showed that the PLAU rs4065 and VEGF rs1570360, rs2010963 and rs699947 polymorphisms were not associated with CCC ($p<0.05$).

Conclusion: An association was found between the HGF rs5745752 polymorphism and the CCC in patients with stable CAD. Patients with the CC genotype are at greater risk of developing poor coronary collaterals.

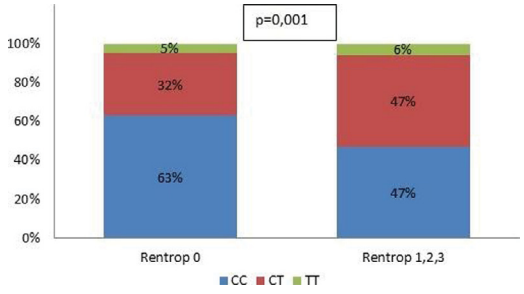

Figure 1