Associations of the ITGB3 gene rs5918T>C and the APOA1 gene rs1799837C>T markers with serum lipid metabolism in coronary artery disease patients

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Funding Acknowledgement: Type of funding sources: Public grant(s) – National budget only. Main funding source(s): Near East University

Aim: The relationship between hypercholesterolemia, particularly elevated low density lipoprotein-cholesterol (LDL-C) levels and coronary artery disease is recognized by the evidence from previous epidemiologic studies. Importantly, genetic polymorphisms on different genes have been reported to be associated with plasma lipid levels. In this particular study, we aimed to investigate the relationship between the ITGB3 gene rs5918 T>C and APO-A1 gene rs1799837 C>T markers and serum lipid metabolism.

Patients and methods: A total of 100 subjects with CAD and 250 healthy subjects were involved in the current study. A basic biochemical analysis, including serum glucose, total serum cholesterol, HDL-C, LDL-C and triglycerides, was performed for each participant. Genotyping for the ITGB3 gene and APO-A1 gene polymorphisms was performed by polymerase chain reaction followed by restriction fragment length polymorphism (RFLP) analysis.

Results: With respect to the genotype and allele distributions of ITGB3 rs5918 T>C polymorphism, the frequency of the C allele was higher in the coronary artery disease (CAD) group compare to control group (p=0.001). Moreover, there was a statistically significant association detected between ITGB3 rs5918 CC genotype and serum total cholesterol (TC) and high-density lipoprotein cholesterol (HDL-C) (p=0.0006, p=0.016 respectively) in CAD group. However there was no statistically significant association was identified between the APOA1 rs1799837 C>T polymorphism and biochemical parameters in control and CAD group.

Conclusion: The results demonstrated that rs5918 T>C variant within the ITGB3 gene might have a clinical importance as a genetic marker which increases the susceptibility to CAD. Therefore, the ITGB3 gene rs5918 C allele may be offered as a screening option for CAD in Turkish Cypriot population who come in for medical check-up.