Research Square

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Association of *APOAI* rs670 and *APOB* rs693 Gene Polymorphisms and Risk Factors for Cardiovascular Diseases in Young Brazilians and Africans.

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Abstract

Background and objectives: Single Nucleotide Polymorphisms (SNP) are promising atherosclerosis indicators. The *APOAI* gene polymorphism variant rs670 shows that G (Guanine) allele is the most frequent and the A (Adenine) allele is the rarest, with both being associated with HDL-c variations in different ethnicities. In the *APOB* variant rs693, the C (Cytosine) allele is the most frequent, while the T (Timine) allele is the rarest and associated with dyslipidemia and cardiovascular risk. This study aims to evaluate biochemical and genetic risk factors for CVD development in young Brazilians and Africans.

Methods: Anthropometric parameters were used for measurement. Blood Samples were collected to evaluate Total cholesterol, triglycerides, HDL-cholesterol, LDL-cholesterol, Apolipoproteins A-I and B, ApoB/ApoA-I ratio, and high-sensitive C-reactive protein (hs-CRP) quantification. The antioxidant capacity of HDL was evaluated by the LagTime assay and the serum enzyme Paraoxonase 1 (PON1) activity. Genetic Analysis was made through DNA extraction from whole blood leukocytes and genotyping of the rs670 and rs693 polymorphisms using the real-time PCR (q-PCR) technique.

Results: G allele and homozygous GG genotype of rs670 were the most frequent in both ethnicities. Among Brazilians, the A allele and GA genotype were associated with higher cardiovascular risk. Regarding the rs693 polymorphism, the C allele was the most frequent in both ethnicities, and the T allele was more frequent between Africans. Also, the CC genotype was the most frequent among Brazilians, and the CT genotype the most frequent among Africans, which presented higher TT frequency. T allele and TT genotype were associated with higher cardiovascular risk factors in both populations.

Conclusion: Brazilians are doubly affected by these variables, while Africans are more susceptible to risks due to changes in the rs693 polymorphism.

Full Text

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