J Mol Genet Med 2018, Volume 12
DOI: 10.4172/1747-0862-C1-025

Polymorphisms in selenoprotein P and S genes: Lack of association with metabolic syndrome in subjects with cardiovascular disease in Selenegene study

Mojgan Gharipour, Masoumeh Sadeghi, Khadija Ouguerram, El-Hassane Nazih, Mansoor Salehi and Mehrdad Behmanesh
Isfahan Cardiovascular Research Institute Isfahan, Iran

Introduction & Aim: The incidence of metabolic syndrome (MetS) is due to the interaction between environmental factors and genetic factors, some previous studies considered the role of selenium in developing MetS. Two selenoproteins SEPP1 and SEPS1 are responsible for anti-oxidative defense and susceptibility to MetS. Since the involvement of SNPs in SEPP1 and SEPS1 have not studied in MetS and its components, this study aims at investigating the associations between MetS risk and four selenoprotein genetic polymorphisms SEPS1 (rs28665122), SEPS1 (rs4965373), SEPP1 (rs7579) and SEPP1 (rs3877899) in an Iranian population.

Material & Method: The study sample of this case-control consisted of 136 Iranian patients with cardiovascular disease (71 MetS-affected individuals (MetS), 65 MetS un-affected individuals (control)) from December 2015 until March 2016. Demographic data, medical history, stress, physical activity, smoking habit, anthropometric measurements, FBS, total cholesterol, triglyceride, HDL, and LDL cholesterol determined. TaqMan probes used for allelic discrimination of two polymorphic variants of SEPP1 (rs7579) and (rs3877899) and SEPS1 (rs4965373). The strength of association was presented as odds ratio by using logistic regression model.

Results: TG is higher among MetS subjects (198.5±122.0 vs. 139.1±86.5, P=0.003). Systolic and diastolic blood pressure, BMI, WC, were higher among subjects with MetS (P=0.05). Non-significant differences were found in genotypic of the SNPs of SEPS1 (rs4965373), SEPS1 (rs28665122), SEPP1 (rs7579) and SEPP1 (rs3877899) between MetS and control group. The results of this case-control study showed no significant associations between components of MetS and polymorphisms in selenoprotein SEPS1 (rs4965373), (rs28665122), SEPP1 (rs7579) and SEPP1 (rs3877899) in an Iranian population.

Conclusion: In summary, the findings from the current study reveal no association of SEPS1 and SELPP1 variants with MetS in an Iranian population with CVD. It seems that post translational changes in this gene would be responsible for the relationship between the product of these genes and MetS.

mojgharipour@yahoo.com