Association of functional SNPs -1306 C/T and -1575 G/A in MMP-2 Promoter with the susceptibility of development of T2D.

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Abstract

Background: Diabetes mellitus (DM) is a group of metabolic disorders defined by hyperglycemia. Beside the environmental and behavioral factors, genetic predisposition has been shown to be a critical risk factor in the pathogenesis of T2D and its related complications. As part of the genetic risk factors, polymorphisms in the metalloproteinase genes have been gaining a wide attention in the pathophysiology of T2D and its complications. The aim of this study is to investigate whether the polymorphisms rs 243865 (-1306C/T) and rs 243866 (-1575 G/A) in metalloproteinase 2 gene are associated with T2D.

Methods: 310 normoglycemic control subjects and 791 T2D patients were enrolled in a retrospective case-control. Genotyping of MMP-2 variants was performed by real time PCR.

Results: A higher proportion of males in the T2D group compared to women was observed in the demographic and clinical characteristics of study participants. A significant statistical difference between controls and diabetic patients was obtained Minor allele frequencies (MAF) of rs 243865 (-1306C/T) and rs 243866 (-1575 G/A) MMP-2, were significantly different between T2D cases and controls. An inheritance hypothesis for this polymorphism was tested according to three models: codominant, dominant, and recessive. A significant association was shown under the dominant model of the rs243865 polymorphism CT, which revealed a 0.66-fold reduced risk within individuals with CT + TT versus individuals with a double homozygote CC genotype.

Moreover, according to the dominant model, individuals with GT＋TT genotypes of the rs243866 MMP-2 SNP had a 0.68-fold reduced risk of developing the T2D disease.

Conclusion: Our study suggests that rs243865/rs243866 in the MMP-2 gene are associated with protection for T2D.