Association analysis of the common genetic variant of PPARG gene with Type 2 Diabetes Mellitus

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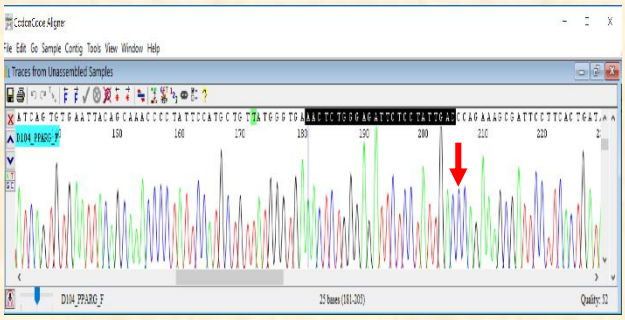

Figure 1: Result of sequencing rs1801282 SNP for CC genotype (wild).

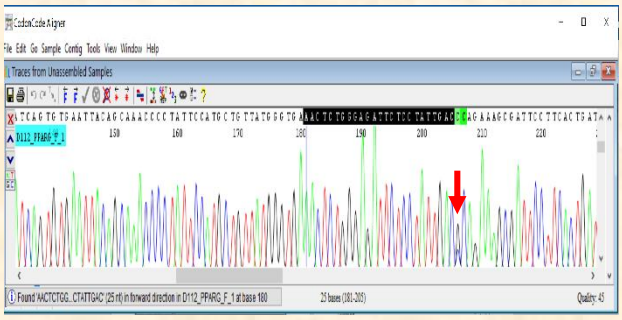

Figure 2: Result of sequencing rs1801282 SNP for CG genotype (heterozygote).

Figure 3: Result of sequencing rs1801282 SNP for GG genotype (mutant).

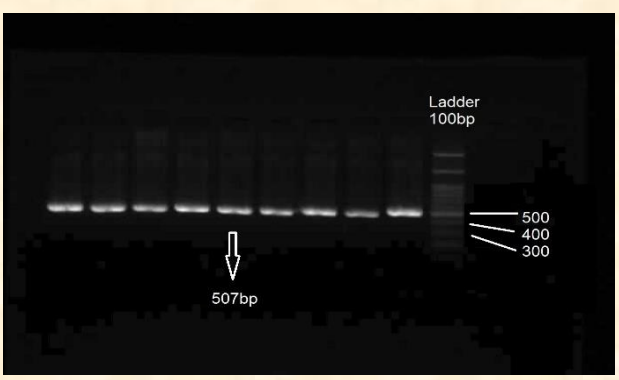

Figure 4: PCR product on 1% agarose gel electrophoresis.

ABSTRACT

Type 2 diabetes mellitus is characterized by chronic hyperglycemia associated with insulin resistance and relative insulin deficiency. Peroxisome proliferator activated receptor gamma (PPARG) is a nuclear hormone receptor of the ligand-dependent transcription factor with a key role in adipocyte differentiation, and glucose homeostasis; and It is one of the main candidate genes that are implicated in T2DM.

The aim of this study was to investigate the association of PPARG polymorphism rs1801282 with T2DM in Iranian population.

METHODS

This case-control study included 149 type 2 diabetic patients and 96 healthy individuals, Genotyping of PPARG common polymorphism (rs1801282) were determined by PCR and sequencing.

RESULTS

The frequencies of CG and GG genotypes of PPARG polymorphism among diabetic and non-diabetic groups were 12.75% vs 18.75% respectively for CG and zero vs 1.04% respectively for GG (p=0.17). Allelic analysis showed no difference of G allele between diabetic(6.37%) and non-diabetic subjects (10.42%) respectively (p=0.11). The odds ratio for G allele was 0.58 which was not statistically significant (p=0.11).

Although presence of PPARG polymorphism slightly decreased the odds of developing ophthalmic complications, the observed association was not statistically significant. In addition, presence of this polymorphism caused 27% increase in the risk of renal complication, but this association was not significant.

CONCLUSIONS

It seems that PPARG polymorphism was not associated with diabetes mellitus and its renal and ophthalmic complications. Longitudinal studies with larger sample sizes are suggested to show the exact effect of this polymorphism on developing diabetes mellitus.

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