

Abstract

Introduction: Type 2 diabetes mellitus (T2DM) is a multifactorial disease with a strong genetic component interacting with environmental factors. Many genes have been significantly associated with developing type 2 diabetes mellitus. Most of these genes have been linked to beta-cell dysfunction, impaired glucose homeostasis and insulin secretion. Transcription factor-7-like 2 (TCF7L2) gene has been found as an unexpected suspect for type 2 diabetes. The strongest and most commonly associated alleles of the TCF7L2 gene in T2DM in many countries are rs7903146 and rs12255372.

Aim: The aim of this study was to evaluate the association between TCF7L2 gene in T2DM among Palestinian people. Two SNP's rs7903146C/T, rs12255372G/T alleles in the TCF7L2 gene were investigated in diabetic patients and control groups.

Methods: This is a case control study. A total of 326 participants were included in this study; 249 participants with T2DM and 77 normal glycemic controls. RFLP PCR was performed using two restriction enzymes *RsaI* and *BseGI* to identify the presence of the two specific mutations in the alleles of the TCF7L2 gene among the study population. Allele specific PCR was also performed to substitute for DNA sequencing on one hand and to genotype the TCF7L2 gene as homo or heterozygous. We used SPSS v.21 to compare the results obtained of the case and control groups.

Results: There was a strong association between the two SNP's rs7903146C/T, rs12255372G/T alleles and T2DM. Both alleles have statistically significant association with the disease. Each of the two alleles had stronger association with T2DM when tested alone than when both alleles were combined. We observed that several normal participants carried the SNP in one or both alleles. This indicates the possibility of future development of diabetes.

Conclusion: TCF7L2gene is strongly associated with T2DM. This important finding can be utilized in screening the population at risk of developing diabetes. Furthermore, genetic testing can also be applied to the normal population to determine who can be prone to develop diabetes in the future.