Association of the rs7903146 and rs12255372 polymorphisms in the $TCF7L2$ gene with type 2 diabetes in a population from northeastern Brazil

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ABSTRACT. Approximately 200 million people suffer from type 2 diabetes (T2D) worldwide, and the rapid increase in the prevalence of this disease is likely a result of multiple environmental factors, such as increased food intake and decreased physical activity in genetically predisposed individuals. Different population studies have demonstrated a strong association of two polymorphic variations in the $TCF7L2$ gene, the noncoding single nucleotide polymorphisms
(SNPs) rs7903146 (C/T) and rs12255372 (G/T), with T2D. Herein, we analyzed the association of these SNPs with T2D in a population from northeastern Brazil. Our results showed that the genotype and allele frequencies in TCF7L2 rs7903146 and rs12255372 were similar in the patient and control groups (P > 0.05). In addition, the allele frequencies were not significantly associated with T2D risk [rs7903146: odds ratio (OR) = 0.95, 95% confidence interval (CI) = 0.52-1.76, P = 1.00, and rs12255372: OR = 1.38, 95%CI = 0.72-2.62, P = 0.41]. These data suggest that the TCF7L2 SNPs rs7903146 and rs12255372 may not significantly contribute to T2D susceptibility in this population. However, our results may reflect the small number of subjects. Alternatively, these results may be attributable to specific ethnic effects, as most of the previously reported associations were demonstrated with predominantly European populations. To reach a definitive conclusion on the role of such gene variants for T2D in mixed populations, additional efforts are necessary to replicate this study with larger populations from areas with more ethnic heterogeneity.

**Key words:** Type 2 diabetes; Genetic polymorphisms; TCF7L2; rs7903146; rs12255372; Mixed population