Identification of Type 2 Diabetes Mellitus Related Single Nucleotide Polymorphisms in the Middle East with Comparative and Epigenetic Analysis

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Type 2 diabetes mellitus (T2DM) is considered one of the top comorbidities in the Middle East. WHO reported in 2010 that the average prevalence of diabetes in this region is 9.3%. Variations in genes that control glucose homeostasis and insulin secretion might play a role in the development of this disease. Since genomic data about T2DM in this population are limited, this research aims to study Single Nucleotide Polymorphisms (SNPs) that might contribute to the development of T2DM and compare them with the ones in the United States. The Middle East population and genetic variation data were compiled from ClinVar, HGDP and dbSNP databases. 53 T2DM related SNPs were extracted from ClinVar database. Then the genotypes were retrieved from HGDP. After combining both datasets and performing analysis by Microsoft Excel, 8 SNPs were overlapping. After performing G-test and cross-referencing with dbSNP database, a similar methodology was used to evaluate variations in SNPs in the United States' population. 2 SNPs located in the TCF7L2 gene were found to be significantly associated with T2DM in both populations. 3 SNPs located in IGF2BP2, UCP2 and SLC30A8 were significantly associated with T2DM in the Middle East only. On the other hand, 3 other SNPs located in HFE, CDKAL1 and CAPN 10 genes were found to be significant in the United States. The findings may improve the ability to predict the risk of T2DM by implicating them into different modern methods for prediction of high risk for genetic diseases, such as the SNP chip.

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