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ABSTRACT

Diabetes is a worldwide health concern that is one of the leading causes of healthcare spending, mortality, morbidity, and economic growth loss. In our results, we have found significant association of JAZF1 (rs864745) variant with T2D. JAZF1 (rs864745) showed high percentage of Homozygous mutant GG 55 (27.5%) in patients as compared to controls GG 10 (10%). 2% difference was observed in case of heterozygous AG in patients (28%) as compared to control (26%). In our results, WFS1 (rs10010131) showed less percentage of Homozygous mutant GG 32 (16.33%) in patients as compared to controls GG 9 (9%). The OR and p- values show no association between WFS1 with T2D in Delhi population. In our study, SLC30A8 (rs13266634) showed high percentage of Homozygous mutant CC 22 (11%) in patients as compared to controls CC 3 (3%). There is a significant difference was observed between the two groups under the dominant and recessive models (p value < 0.001). The study concludes that *JAZF1 rs864745*, and *SLC30A8 rs13266634* genes were found to be related with risk of T2D and risk related to heterozygosity and mutant homozygosity.. Based on these findings, we propose that each population examine its unique genomic make-up for T2D risk analysis.