

Diabetes Mellitus (DM) is a complex metabolic illness characterized by hyperglycemia and insulin resistance which has a genetic and environmental component. This study aimed to establish the connection between the polymorphism of *HNF1B* genes, especially through their two single nucleotide polymorphisms (SNPs), rs4430796 and rs11651052, and the production of insulin in T2D by examining the genetic variant of the two SNPs in Pakistani population. As per the inclusion and exclusion criteria of WHO, 15 families comprising of diabetes and non-diabetic individuals were taken to draw blood samples. The genomic DNA that had been isolated in the samples was assessed using Sanger sequencing, Polymerase Chain Reaction, (PCR), and restriction Fragment Length Polymorphism, (RFLP) techniques using *TaqI* and *MspI* enzymes respectively. Clinical data were recorded such as blood pressure, Body Mass Index (BMI), and family history. It was observed that females in this cohort had a higher tendency to T2D compared to males in this cohort. The GG genotype, or SNP rs4430796, was significantly associated with T2D ($P < 0.05$). At this location, the Mega 12 software projected an arginine-to-lysine substitution, which could be a factor in the changed synthesis of insulin. Affected people also had a high frequency of SNP rs11651052, which has the GT genotype. Histidine-to-arginine substitution was seen in this SNP, which may have an effect on insulin regulation. A possible generational risk factor for T2D was identified by pedigree analysis as rs4430796 (GG). In this cohort, rs4430796 has a greater connection with the genetic propensity to T2D than the other SNP. According to these results, rs4430796 and rs11651052 in particular may be important genetic variants in *HNF1B* that affect insulin synthesis and the pathogenesis of T2D. Investigating these SNPs further may enhance preventative and early diagnosis methods.