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Abstract Topic: - Evolutionary and population genetics

Abstract Title: - Frequency of genetic variants associated with type 2 diabetes mellitus (T2DM) in a pilot study and their correlation with HBA1C levels.

Presenting author name: - Smita Kulkarni

Presenting author institute: - HaystackAnalytics Pvt. Ltd

Co-authors name: - Nandini Khona, Ashlesha Pradhan, Dr. Anu Prabha, Dr. Aparna Bhanushali, Dr, Anirvan Chatterjee

Co-authors institute: - HaystackAnalytics Pvt. Ltd, HaystackAnalytics Pvt. Ltd, HaystackAnalytics Pvt. Ltd, HaystackAnalytics Pvt. Ltd, HaystackAnalytics Pvt. Ltd

Aims: - Introduction: The risk of developing type 2 diabetes mellitus (T2DM) is significantly influenced by a combination of genetic and environmental factors. Numerous genes have been associated with the onset of T2DM, making genetic variations within these candidate genes a central focus for molecular investigation. Genome-wide association studies (GWAS) have revolutionised our understanding of the genetic basis of complex traits and diseases by identifying single nucleotide polymorphisms (SNPs) associated with various phenotypes.

AIM: In this study, we investigate the genetic associations of five SNPs, namely IGF2BP2 (rs1470579), KCNK16 (rs1535500), KCNQ1 (rs2237895), PTPRD (rs17584499) and SDHAF4 (rs1048886) with T2DM. Furthermore, we aim to explore potential links between these genetic variations and the HbA1C levels.

Methods: - Methodology: A total of 225 apparently healthy participants were included in this study. We conducted genotyping for five chosen SNPs using probe hybridization-based capture of all coding exons and exon-intron junctions of the targeted genes, followed by massively parallel sequencing. Statistical tests were employed to assess the relationship between these selected SNPs and T2DM.

Results: - Results: Allele and genotype frequencies were calculated for 5 SNPs. In IGF2BP2 (rs1470579A/C) the C allele - 29% with genotype distribution of AA/AC/CC: 55%, 32% and 13% respectively. In KCNK16 (rs1535500G/T) the T allele - 50% with genotype distribution of GG/GT/TT: 24%, 52% and 24% respectively. In KCNQ1 (rs2237895A/C) the C allele - 40% with genotype distribution of AA/AC/CC: 37%, 46% and 17% respectively. In KCNQ1 (rs2237895A/C) the C allele - 40% with genotype distribution of AA/AC/CC: 37%, 46% and 17% respectively. In PTPRD (rs17584499C/T) the T allele - 20% with genotype distribution of CC/CT/TT: 64%, 32% and 4% respectively. Lastly, in SDHAF4 (rs1048886A/G) the G allele - only 15% with genotype distribution of AA/AG/GG: 73%, 24% and 3% respectively.

Conclusions: - Conclusion: In our study the KCNK16 (rs1535500) T allele was seen in almost 50% of the samples followed by 40% of C allele of the KCNQ1 gene (rs2237895). We included SDHAF4 (rs1048886A/G) in our study as the Indian GWAS identified this SNP showing genome-wide significance (OR = 1.54, 95% CI = 1.32 – 1.80, P = 3.48×10−8). However, the frequency of C allele was seen to be only 15%. The MAFs for rs1535500G/T and rs17584499C/T are higher than reported in dbSNP with 50% and 20% in our study v/s 1.8% 9% in dbSNP. No significant association was identified between the genotypes and the HbA1C levels in our study. Evaluation of these samples with blood sugar levels is being undertaken.

Keywords: - Results: Allele and genotype frequencies were calculated for 5 SNPs. In IGF2BP2 (rs1470579A/C) the C allele - 29% with genotype distribution of AA/AC/CC: 55%, 32% and 13% respectively. In KCNK16 (rs1535500G/T) the T allele - 50% with genotype distribution of GG/GT/TT: 24%, 52% and 24% respectively. In KCNQ1 (rs2237895A/C) the C allele - 40% with genotype distribution of AA/AC/CC: 37%, 46% and 17% respectively. In KCNQ1 (rs2237895A/C) the C allele - 40% with genotype distribution of AA/AC/CC: 37%, 46% and 17% respectively. In PTPRD (rs17584499C/T) the T

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