

PRELIMINARY RESULTS AND DISCUSSION

Four (4) candidate genetic variants associated with response to gliclazide were revealed. The two most significant single nucleotide polymorphisms (SNP) are variants of the gene 5-hydroxytryptamine receptor 2C (*HTR2C*) (CC > GC > GG: OR 28.20, 95% CI 2.59, 1,464.13; *p-value* 0.0015 and AA vs. GG + AG: OR 0.04, 95% CI 0.00069, 0.389; *p-value* 0.0015 respectively). The third SNP is a variant of the gene high mobility group 20A (*HMG20A*) (AA > AG > GG: OR 3.70, 95% CI 1.50, 10.03; *p-value* 0.0018).

CONCLUSION

The study revealed SNPs that were not previously associated with response to gliclazide. These may be further investigated and validated to identify markers for response to this medication. This will be the basis for matching of patients with the appropriate medications and hence provide improved outcomes.

KEY WORDS

pharmacogenetics, diabetes mellitus, type 2, gliclazide

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CORRELATION OF CANDIDATE GENETIC VARIATIONS FOR SUSCEPTIBILITY AND RISK ASSESSMENT OF TYPE 2 DIABETES MELLITUS AMONG FILIPINOS

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OBJECTIVES

The study aims to determine genetic variants associated with type 2 diabetes mellitus (T2DM) that can help in the development of personalized care for Filipinos.

METHODOLOGY

A total of 201 unrelated adult Filipinos were enrolled in this matched case-control study (67 cases with T2DM to 134 controls). DNA from blood was genotyped via customized Illumina (GoldenGate Genotyping and Infinium iSelect) microarray beadchips, investigating 357 candidate genetic variants associated with T2DM. Correlation with T2DM was done via permuted Pearson chi-square tests of allelic/genotypic association, Bonferroni correction for multiplicity, and Efron conditional logistic regression analysis.

RESULTS AND DISCUSSION

Three (3) candidate variants exhibited significant association with T2DM among Filipinos. A *CDKAL1* (cyclin-dependent kinase 5 regulatory subunit-associated protein 1 like 1 gene) variant showed the greatest risk in association (AA > AC > CC: OR 10.08, 95% CI 5.21, 19.53; *p* 0.0145). Other variants showed significance, namely a *SERPINF1* (serpin family member 1 gene) variant (CC > CT > TT: OR 5.43, 95% CI 2.84, 10.38; *p* 0.0164) and a *GPR45* (G protein-coupled receptor 45 gene) variant (CC > CT > TT: OR 2.56, 95% CI 1.43, 4.59; *p* 0.0206).

CONCLUSION

Preliminary results present variations in *CDKAL1*, *SERPINF1*, and *GPR45* significantly associated with T2DM which may be further investigated through clinical validation to develop diagnostic/prognostic markers for T2DM in Filipinos. Though Philippine genetic studies for T2DM are limited, the emergence of genetic research and genotyping technology presents the opportunity to better optimize T2DM management and treatment in the Filipino individual.

KEY WORDS

diabetes mellitus, type 2, genetic susceptibility, genotyping