

META-ANALYSIS OF THE GENETIC FACTORS THAT PREDISPOSED ASIAN WOMEN TO GESTATIONAL DIABETES MELLITUS

ABSTRACT

A meta-analysis was conducted to determine the significant risk alleles which increase the risks of gestational diabetes mellitus (GDM) in Asian to help in decision-making for genotyping of women at risk. PubMed, Science Direct and HuGE navigator were used to identify relevant studies from January 2000 to November 2018. Data extraction was done by five reviewers. Using Review Manager 5.3, association between 11 SNPs and risks of GDM was determined. Odds ratios (ORs) with 95% confidence intervals (95% CI), test of heterogeneity and publication bias were calculated. The result was considered significant if $p\text{-value} \leq 0.05$. Twenty-one studies were identified based on the inclusion and exclusion criteria. From 11 genetic variants studied, 9 were found to have significant association with GDM susceptibility with different heterogeneity. Allelic, dominant and recessive genetic models show MTNR1B (rs138753, rs10830963) and CDKAL1 (rs7754840) are significantly associated with GDM. IGF2BP2 (rs4402960) was found to have significant association with GDM using allelic and recessive models. For TCF7L2 (rs7903146), significant association was found using allelic, dominant and over dominant models. KCNQ1 (rs2237892) showed association with GDM in dominant model only. Strong associations with increased susceptibility for GDM were also found for GSTM1 (deletion), GSTT1 (deletion) and GSTP1 (rs1695). However, MTNR1B (rs10830962) and PPAR γ 2 are lack of association with GDM risk in Asian population. Nine genetic variants were associated with increased GDM risk in Asian population. Screening of these polymorphisms to identify pregnant women at risk is recommended for prevention and personalised intervention.

Keywords: Gestational diabetes mellitus, Single nucleotide polymorphism, Odds ratio, Confidence interval, Meta-analysis