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Meta-analysis: Genetic Polymorphisms associated with Gestational Diabetes Mellitus

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CONTEXT: The Gestational Diabetes Mellitus (GDM) is a metabolic condition characterized by impaired glucose tolerance of varying degrees that develops or first recognized during pregnancy. Using genome wide association analysis, multiple studies have been performed to identify genes showing polymorphism and association with the GDM. However, markers these studies reported mostly fail to show similar association when replicated by other countries in their population. In this study, we aim to identify markers which showed statistically significant positive association with GDM consistently in different countries and populations

OBJECTIVE: To identify genetic polymorphisms consistently associated with gestational diabetes mellitus across multiple ethnicities

METHOD: An exhaustive search of literature was done from January 1st 1980 to February 28th 2017 using terms as Single nucleotide polymorphisms (SNPs), genome-wide association study (GWAS), Gestational diabetes mellitus (GDM) in MEDLINE, EMBASE, CDSR and Google scholar by two independent researchers.

RESULTS: We have found several genes showing genetic polymorphisms and association with GDM. Among them top genes include Transcription factor 7 like 2 (TCF7L2); Melatonin Receptor 1B (MTNR1B), Hepatocyte Nuclear factor 4 alpha (HNF4A); Potassium voltage-gated channel subfamily Q member 1 (KCNQ1), insulin like growth factor 2 mRNA binding protein 2 (IGF2BP2), CDK5 regulatory sub unit associated protein 1 like 1 (CDKAL1), calpain 10 (CAPN10) which showed statistically significant positive association with GDM in multiple population

CONCLUSION: The metaanalysis conducted here identified markers consistently reported to be associated with GDM in multiple ethnicities and provides a base work for further screening and validation of these markers in a large cohort of our Pakistani population.

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