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Abstract Topic: - Complex traits and polygenic disorders

Abstract Title: - Analysis of MDM2, VEGFA and MCP-1 variants towards susceptibility of Diabetic Retinopathy in North West Indian population.

Presenting author name: - Manroop SIngh Buttar

Presenting author institute: - Guru Nanak Dev University

Co-authors name: - Kamlesh Guleria, Amarjit Singh Bhanwer, Vasudha Sambyal, , , , , ,

Co-authors institute: - Guru Nanak Dev University, Sri Guru Ram Das University of Health Sciences, Guru Nanak Dev University, , , , , ,

Aims: - Diabetic retinopathy (DR) is one of the major microvascular complications associated with Type 2 Diabetes (T2D) and is one of the leading causes of blindness worldwide. Vascular endothelial growth factor A (VEGFA) overexpression promotes vessel endothelial cell proliferation, migration, tube formation, and sprouting, thereby subserving as a contributing factor for DR. MDM2 is involved in various important biological functions, signaling pathways and its variants has been found to associated with eye diseases. It has been shown in studies that MDM2 and VEGFA works in correlation altering the normal functioning of endothelial cells, causing the progression of DR. VEGFA -2578C/A has shown to functionally effect mRNA. MDM2 rs3730485 has been shown to reduce the transcription of P1 promoter and has shown association with complex disorders. Following hyperglycemia, retinal pigmented epithelial (RPE) cells, endothelial cells, and Müller's glial cells are of utmost importance for MCP-1 production and vitreous MCP-1 levels rise in patients with DR. MCP-1 rs3917887 has shown association in T2D related complication in previous studies. The present study is an attempt to evaluate the association of selected variants of MDM2, VEGFA and MCP1 genes with Diabetic Retinopathy.

Methods: - In this case-control study 414 DR patients, 425 T2D patients (internal controls) and 402 healthy controls (CN) were analyzed. DNA samples were screened for MDM2 rs3730485, VEGFA -2578C/A and MCP-1 rs3917887 polymorphisms using PCR (polymerase chain reaction) based methods.

Results: - MDM2 rs3730485 DD genotype showed frequency of 6% in cases and 4.2% in controls, Majority subjects were wild type homozygous. VEGFA -2578 AA genotype showed frequency of 22.2% in cases and 23.4% in cases. MCP-1 rs3917887 DD genotype showed frequency of 10.5% in cases and 9.5% in controls. Majority subjects were of heterozygous genotype for both -2578C/A and rs3917887 variants. The genotypic and allelic frequencies showed no significant difference between all study groups in the investigated polymorphisms.

Conclusions: - The current study has furthered our knowledge about the understanding of DR genetics in the North-West Indian Population.

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