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Stromal cell- derived factor (SDF-1 ß) gene polymorphism and their association with DFU: An Asian Indian population study Vijay Viswanathan[1], Dhamodharan.U[1], Ezhilarasi.K[1], Parthiban.M[1], Indira Padmalayam[2], RamaRajaram[3]
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Several environmental and genetic factors are believed to influence the onset of type 2 diabetes and its complications, but its cause has yet to be clarified. Cytokines have recently been the focus of several studies due to their crucial roles in diabetes and its complications and the impact of cytokine imbalance in diabetic foot ulcer (DFU), has been reported earlier. Stromal cell-derived factor-1 (SDF-1) a member of CXC chemokine family is constitutively produced by bone marrow stromal cells. SDF-1 (which is also called as CXCL-12) plays a key role in the recruitment of leukocytes to the sites of injury/infection and inflammation, angiogenesis, and has angiostatic properties as well. The key roles of SDF-1 as an inhibitory chemokine in autoimmunity and inflammations raise questions concerning the impacts of this cytokine in the pathogenesis of DFU. Further a single nucleotide polymorphism in SDF-1 gene has been shown to regulate its expression. In this study we investigate a potential correlation between a SNP, G801A in the SDF-1 gene in an Asian Indian population with T2DM and DFU who attended our tertiary care hospital in Chennai, India. This is the first study which correlates a genetic polymorphism in SDF-1ß gene with complications of T2DM. The study population consisted of total 406 subjects, divided into three groups. Group I with 140 healthy volunteers, Group II with 135 T2DM patients without complications, and Group III with 131 Diabetic foot ulcer patients. Peripheral blood genomic DNA was subjected to PCR-RFLP and analyzed for the presence of 302, 202 & 100 bps bands. The results showed a significantly increased frequency of the homozygous wild genotype GG in the diabetic groups (groups II and III) compared to healthy subjects (group I) suggesting an association of this genotype with diabetes. Further, the relative risk for GG genotype was higher in Group III 6.368(2.358-17.195) suggesting an association with DFU ($p<0.001$). We conclude that the homozygous wild genotype GG of SDF-1ß gene is significantly associated with increased risk in DFU patients.