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Impact of the hypoxia inducible factor- 1α (HIF- 1α) pro582ser polymorphism and its gene expression on diabetic foot ulcers.

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Abstract

AIM:

Adaptation to low oxygen tension (hypoxia) in cells and tissues leads to the transcriptional induction of series of genes and the primary factor mediating this response is the hypoxia-inducible factor- 1α . This study was designed in order to examine the HIF- 1α gene polymorphism, p582s (rs11549465) in Exon-12 of HIF- 1α gene in diabetic subjects with and without foot ulcers (DFU) and to find its expression under these pathological conditions.

METHODS:

A total of 224 subjects from our tertiary care centre were included, which consists of healthy controls (N=66), type 2 diabetes mellitus (T2DM) (N=79) and T2DM withfoot ulcers (DFU) (N=79). Allelic and genotypic comparisons between the different groups were evaluated by PCR-RFLP. The gene expression studies on selected samples (N=15 of each group) were done by Semi-quantitative real time PCR.

RESULTS AND DISCUSSIONS:

Genotype analysis showed a significant increase in presence of 'T' allele in T2DM & DFU when compared to that of control subjects. Allele wise analysis showed a higher frequency of 'T' allele in the T2DM (62.03%) when compared to that of control subjects (53.79%). Interestingly, semi-quantitative RT-PCR results showed decreased expression of HIF-1α gene on DFU when compared to that of T2DM and control subjects.

CONCLUSION:

Our findings predict that there is an association of HIF-1 α gene polymorphism on foot ulcer patients when compare to that of healthy controls. Semi-quantitative real time studies showed decreased HIF-1 α gene expression on foot ulcer patients suggesting its possible role on the pathogenesis.

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KEYWORDS:

DFU; HIF-1α; Hypoxia; SNP; T2DM

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