

TO-03

POLYMORPHISMS IN THE INTERLEUKIN-6 PROMOTER AFFECTS THE RISK OF HUMAN T LYMPHOTROPIC VIRUS TYPE I-ASSOCIATED MYELOPATHY/TROPICAL SPASTIC PARAPARESIS.

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SNP in the human IL-6 promoter at -634, -597, -572 and -174 have been associated to the gene function and disease susceptibility. In addition, it has been suggested that these polymorphism could lead to different production of IL-6 (inflammatory cytokine). This effect might help to keep the status asymptomatic or HAM/TSP development in HTLV-I infected individuals. Objective: To analyze polymorphisms in the interleukin-6 gene promoter in HTLV-1 infected individuals from Salvador/Bahia/Brazil and to verify its correlation with the risk of HAM/TSP development. Materials and Methods: We had analyzed the cytokine promoter gene polymorphism using RFLP (-634) and Real Time PCR (-597, -572 and -174). We studied 133 infected individuals (84 asymptomatic, 26 with HAM/TSP and 23 oligosymptomatic), and 100 non-infected individual from general population. The provirus load measurement was performed by real time PCR method in 67 individuals (53 asymptomatic and 14 with HAM/TSP). Results: We identified a significant association between possession of a C residue at -634 position and a increased risk of HAM/TSP. In addition, the IL-6 -174G/C showed a higher frequency of G allele in HAM/TSP patients. The nucleotide at position -572 was nonpolymorphic, while at -597 only three were polymorphics. The median provirus load was significantly higher in patients with HAM/TSP than in asymptomatic. However, in these patients we not found a correlation with allele distribution. Conclusion: The IL-6 polymorphisms can be important in the development of symptoms. These studies can contribute to better understanding of the complex association between IL-6 promoter variability and disease susceptibility.

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