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ETHNIC DIFFERENCES IN THE DISTRIBUTION OF INTERLEUKIN-10 POLYMORPHISMS AMONG THREE BRAZILIAN ETHNIC GROUPS AND INVESTIGATION IF INTERLEUKIN-10 POLYMORPHISMS COULD BE INVOLVED WITH DISEASE IN HTLV-1 INFECTED INDIVIDUALS FROM SALVADOR, BAHIA, BRAZIL.

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The majority of HTIV-1 infected individuals remain asymptomatic, indicating that only the infection is not sufficient to cause the disease. Interleukin-10 (IL-10) is a regulatory cytokine, and its principal role in vivo is to limit inflammatory response. IL-10 has been shown to influence both the susceptibility and course of various diseases, and the different polymorphisms in the IL-10 gene promoter have been associated with disease prevalence and severity. In addition, differences in the allele distribution of cytokines gene variants have been found in diverse ethnic groups. We tend to analyze the polymorphism -592 (C®A) in the interleukin-10 gene promoter in HTIV-1 non-infected individuals from 3 ethnic Brazilian groups and in infected individuals from Salvador/Bahia/Brazil and to verify its correlation with the risk of TSP/HAM development. We investigated *IL-10* promoter polymorphism by RFLP in 280 healthy individuals from three Brazilian ethnic groups (101 from Salvador, 102 from Tiriyó aboriginal and 77 German descendants from Joinville), and in 114 HTIV-1 infected individuals from Salvador (73 asymptomatic, 24 with TSP/HAM and 17 oligosymptomatic). We identified a tendency to a higher frequency of A allele in HTIV-1 infected individuals and to a raiser of C/C genotype in asymptomatic patients, suggesting that this polymorphism could be important to the development of HTIV-1 infection associated symptoms. Besides, we observed a significant difference in the allele frequency among Individuals from Tiriyó and Joinville, but it was absent among individuals from Salvador and the other populations.

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