

IL-10 AND IFN- γ GENES POLYMORPHISM IN HTLV-1 INFECTED INDIVIDUALS AND THEIR POSSIBLE RELATIONSHIP WITH HAM/TSP DEVELOPMENT

Lima A C M M¹, Araujo T H², Gois L L^{1,2}, Rego F F A^{1,2}, Castro Filho B G^{2,4}, Santos L A^{1,2,3,4}

¹Universidade Católica do Salvador

²Escola Bahiana de Medicina e Saúde Pública

³Programa de Pós-graduação em Ciências da Saúde, Faculdade de Medicina da Bahia, Universidade Federal da Bahia

⁴Instituto Gonçalo Moniz - Fundação Oswaldo Cruz

Background:

Human T-lymphotropic virus type 1 (HTLV-1) is an etiological agent of the HTLV-1-associated myelopathy/tropical spastic paraparesis (HAM/TSP), characterized by a chronic and progressive inflammation of central nervous system (CNS). The literature describes that the interleukin-10 (IL-10) and interferon-gamma (IFN- γ) expression is unbalanced in HAM/TSP patients, corroborate with the maintenance of the CNS exacerbated inflammation. Therefore, this study was developed to evaluate the presence of IL-10 and IFN- γ genes polymorphisms and their possible relationship with the HAM/TSP.

Methods:

This is a cross-sectional study of 60 HTLV-1 carriers (among asymptomatic and HAM/TSP individuals). Blood samples, clinical and epidemiological data were collected from these patients. DNA were extracted from PBMCs for IL-10 and IFN- γ amplification by PCR assay, using specific primers for each gene region. The PCR products will be then purified and sent for sequencing by the ABI 3500XL automatic sequencer. The sequences obtained will be aligned and the presence of genetic mutations will be estimated by direct counting of nucleotides, visualizing the alignment using the Geneious R9.1 tool. The presence of mutations and their frequencies in HAM/TSP and asymptomatic groups will be used to build a network of possible mutation associations identified with clinical and epidemiological data using the HIT-BAY methodology.

Results:

Based on the data that will be generated, it is expected to identify the presence of polymorphisms or mutations related to the host immune response and its relationship with the development of inflammatory diseases such as HAM/TSP.

Conclusions:

This study will enable the identification of genetic bases for the HTLV-1 pathogenesis mechanisms and the HAM/TSP development.

Disclosure of interest statement:

None.

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