

Genetic characterization and phylogeny of human T-cell lymphotropic virus type I from Chile

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Infection with Human T-Cell Lymphotropic Virus type I (HTLV-I) have been associated with the development of the HTLV-I associated myelopathy/tropical spastic paraparesis (HAM/TSP).

Phylogenetic analyses of HTLV-I isolates have revealed that HTLV-I can be classified into three major groups: the Cosmopolitan, Central African and Melanesian. In the present study, we analyzed the tax, 5' Itr, gag, pol, and env sequences of proviruses of PBMC from ten HAM/TSP patients to investigate the phylogenetic characterization of HTLV-I in Chilean patients. HTLV-I provirus in PBMC from ten Chilean patients with HAM/TSP were amplified by PCR using primers of tax, 5' Itr, gag, pol, and env genes. Amplified products of the five genes were purified and nucleotide sequence was determined by the dideoxy termination procedure. DNA sequences were aligned with the CLUSTAL W program. The results of this study showed that the tax, 5' Itr, gag, pol, and env gene of the Chilean HTLV-I strains had a nucleotide homo