

Oncogenic retrovirus, chronic infection and cancer: Viral strategies that favor viral persistence in humans

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Human T-cell leukemia/Lymphoma virus type 1 (HTLV-1) infects about twenty million people worldwide. HTLV-1 is more frequent in some area of the world; for example 1% of the inhabitants of Kyushu, an island of Japan, are infected by HTLV-1. The virus was first isolated in the late Seventies at the National Cancer Institute from a patient that had Adult T-cell leukemia/Lymphoma (ATLL). HTLV-1 causes not only ATLL but also a neurological disease that results in paralysis of the lower limbs, designated Tropical Spastic Paraparesis/ HTLV-1 associated Myelopathy (TSP/HAM). However, disease occurs only in approximately 2% of the infected individuals in their life time. HTLV-1 is the first oncogenic retrovirus found in humans. Like the other known human retroviruses, such as the Human Immune Deficiency Virus type 1 and 2 (HIV-1 and HIV-2) that cause Acquired Immune Deficiency (AIDS), HTLV-1 has a complex genome that encodes several structural and non structural proteins. HTLV-1 associated oncogenicity does not appear to be due to insertional mutagenesis. Rather, the expression of viral proteins in the virus-infected T-cells increases their survival and their ability to escape immune recognition. A current hypothesis for HTLV-1 leukemogenesis is that HTLV-1, by prolonging the life of the infected T-cells, may favor the accumulation of genetic lesions that ultimately cause the uncontrolled growth of T-cell and leukemia. Thus, the identification of the viral genetic determinant that prolong the life of the infected T-cells and favors viral persistence is important because it may provide several targets to inhibit virus spreading in the host and the subsequent cancer development.