

# **The *tax* Gene Sequences Form Two Divergent Monophyletic Lineages Corresponding to Types I and II of Simian and Human T-Cell Leukemia/Lymphotropic Viruses<sup>\*1</sup>**

Adriana Giri<sup>a</sup>, Jill Pecon Slattery<sup>b</sup>, Walid Heneine<sup>c</sup>, Antoine Gessain<sup>d</sup>, Emilia Rivadeneira<sup>a</sup>, Ronald C. Desrosiers<sup>e</sup>, Leon Rosen<sup>f</sup>, Ronald Anthony<sup>g</sup>, Joko Pamungkas<sup>h</sup>, Diah Iskandriati<sup>h</sup>, Allen L. Richards<sup>i</sup>, Vincent Herve<sup>i</sup>, Harold McClure<sup>k</sup>, Stephen J. O'Brien<sup>b</sup> and Genoveffa Franchini<sup>a,\*</sup>

<sup>a</sup> Basic Research Laboratory, National Cancer Institute, Bethesda, Maryland, 20892

<sup>b</sup> Laboratory of Genomic Diversity, National Cancer Institute, Frederick Cancer Research and Development Center, Frederick, Maryland, 21702

<sup>c</sup> Retrovirus Diseases Branch, Division of Viral and Rickettsial Diseases, Center for Infectious Diseases, Centers for Disease Control and Prevention, Atlanta, Georgia, 30333

<sup>d</sup> Unité d'Epidémiologie des Virus Oncogènes et Service d'Informatique Scientifique, Institute Pasteur, 28 rue du Dr. Roux, 75724, Paris Cédex 15, France

<sup>e</sup> Division of Microbiology, Harvard Medical School, Southborough, Massachusetts, 01772

<sup>f</sup> Pacific Biomedical Research Center, University of Hawaii, Honolulu, Hawaii, 96816

<sup>g</sup> American University of the Caribbean, P.O. Box 1695, Belize City, Belize

<sup>h</sup> Primate Research Center, Bogor Agricultural University, Bogor, Indonesia

<sup>i</sup> Department of Immunology, U.S. Naval Medical Research Unit N2, Jakarta, Box 3, APOAP, 96520-8132

<sup>j</sup> Pasteur Institute, Bangui, Central African Republic

<sup>k</sup> Yerkes Regional Primate Research Center in Atlanta, Georgia, 30322

## **Abstract**

Evolutionary associations of human and simian T-cell leukemia/lymphotropic viruses I and II (HTLV-I/II and STLV-I/II) are inferred from phylogenetic analysis of *tax* gene sequences. Samples studied consisted of a geographically diverse assemblage of viral strains obtained from 10 human subjects and 20 individuals representing 12 species of nonhuman primates. Sequence analyses identified distinct substitutions, which distinguished between viral types I and II, irrespective of host species. Phylogenetic reconstruction of nucleotide sequences strongly supported two major evolutionary groups corresponding to viral types I and II. With the type I lineage, clusters were composed of strains from multiple host species. A genetically diverse, monophyletic lineage consisting of eight new viral strains from several species of Asian macaques was identified. The second lineage consisted of a monophyletic assemblage of HTLV-II/STLV-II strains from Africa and the New World, including an isolate from a pygmy chimp (*Pan paniscus*) as an early divergence within the lineage. High levels of genetic variation among strains from Asian STLV-I macaque suggest the virus arose in Asia. Evidence of the origin of the type II virus is less clear, but diversity among HTLV-II variants from a single isolated population of Mbatı villagers is suggestive but not proof of an African origin.