

Background: The HTLV-I seroprevalence in the indigenous population of KwaZulu-Natal, South Africa, is 2.6%. This prevalence rate is higher than the 1.8% observed in Salvador, Bahia, Brazil.

Methods: We screened samples from 1,436 individuals from KwaZulu-Natal (South Africa) and performed phylogenetic analysis in ten of them and ten from Brazil.

Results: We obtained an HTLV seroprevalence of 1.8%. Phylogenetic analysis of the HTLV-I env partial and entire LTR regions showed that African and Brazilian isolates belonged inside the Transcontinental subgroup, but separately each other with distinct subclusters. Two of the Brazilian isolates clustered with an isolate from Mozambique. Molecular clock analysis of the LTR region, demonstrated that this virus was present in South Africa before it appeared in Mozambique and Brazil. The diversity of the LTR and env genes was 1.8% and 0.8%, respectively, for the Brazilian sequences, and 0.7% and 0.7%, respectively, for the South African sequences. The evolutionary rate for a family (mother and child) from African cohort was 4.48×10^{-4} nucleotide/site/year for the LTR and 1.26×10^{-4} nucleotide/site/year for the env genes. The diversity of these genes was 0.6% and 0.2%, respectively.

Conclusions: We demonstrate a higher divergence in Brazilian HTLV-I sequences and suggest that HTLV-I may have been introduced into Salvador from southern Africa during the slave trade.

P8
Novel Highly Divergent HTLV-1 Strains of the Melanesian Subtype C in Natives of Ambae Island, Vanuatu Archipelago.

O. Cassar¹, C. Capuano², E. Chungue¹, L. Meertens³ and A. Gessain⁴

¹Laboratoire de Microbiologie et Environnement, l'Institut Pasteur de Nouvelle-Calédonie, Nouméa, Nouvelle-Calédonie; ²WHO/OMS Vanuatu; ³EPVO, Institut Pasteur, Paris, France; ⁴Institut Pasteur, Paris, France

Background: HTLV-1 strains of the Melanesian subtype C, which represent the most highly divergent HTLV-1, have been reported in Papua New Guinean, Solomon Islanders and Australian Aborigines.

Methods: During a STD survey in women from Ambae island, (North edge of Vanuatu), we performed, in 2001, an epidemiological study using an EIA to detect plasma anti HTLV antibodies. All EIA sero-positive samples were tested by Western blot (HTLV I/II-2.4). Among 391 women investigated (mean age 36 years), we identified 4 HTLV-1 seropositive. Buffy coats DNAs were subjected to nested PCR to amplify the complete LTR (750 bp) and 522 bp of the gp21 env gene.

Results: The four novel HTLV-1 sequences were closely related to each other, both in the env and the LTR, exhibiting more than 99% of nucleotide homology. Furthermore, these sequences belong to the Melanesian subtype as demonstrated both by comparative sequences analyses and phylogenetic studies. Among the subtype C strains, 4 slightly different clusters now exist, each of them being geographically related (PNG, Solomon Island, Australia, Vanuatu). Novel field and molecular studies are ongoing to get new insights on the origin, evolution and modes of dissemination of such highly divergent HTLV-1 strains in Melanesian populations.

P9
HTLV-I Proviral Load Is Strongly Correlated with the HTLV-I Disease Status but not with the Presence or Absence of HLA-A*02 in Jamaica.

H. Li¹, M. Hisada¹, Y. Yamano², E. Maloney¹, K. Yao², B. Hanchard³, O. Morgan³ and S. Jacobson²

¹Division of Cancer Epidemiology and Genetics, National Cancer Institute, Viral Epidemiology Branch, Rockville, MD, USA; ²Neuroimmunology Branch, National Institute of Neurological Disorders and Stroke, Viral Immunology Section, Bethesda, MD, USA; ³University of the West Indies, Kingston, Jamaica

Background: HTLV-I is a causal agent of adult T-cell leukemia (ATL) and HTLV-associated myelopathy/tropical spastic paraparesis (HAM/TSP). HTLV-I proviral load and host genetic background represented by human leukocyte antigen (HLA) genes are thought to predict the risk of these diseases among HTLV-I carriers. A previous report indicates that HLA A*02 is associated with a lower proviral load and risk of HAM/TSP.

Methods: We quantified HTLV-I proviral load in 103 HTLV-I-positive persons (38 asymptomatic carriers [AC], 26 HAM/TSP and 39 ATL) by real-time quantitative PCR method. Proviral loads were compared between persons with and without the HLA-A*02 allele.

Results: The overall mean HTLV-I proviral load was 77.9% in ATL, 21.1% in HAM/TSP and 5.6% in AC, respectively (P < 0.01). However, proviral loads were not significantly different between persons with HLA-A*02 and those without it (Table).

Conclusions: HTLV-I proviral load is strongly correlated with HTLV-I disease status but not with the presence or absence of HLA-A*02. Other host and viral markers related to susceptibility and pathogenesis of HTLV-I infection warrant investigation.

Table. HTLV-I proviral load (mean ± SD, copies/100 PBMC) in persons with or without HLA-A*02 allele

	AC (n = 38)	HAM/TSP (n = 26)	ATL (n = 39)
HLA-A*02+	5.47 ± 3.95	20.74 ± 15.75	58.80 ± 57.20
HLA-A*02-	5.77 ± 8.58 (P = 0.89)	21.43 ± 17.26 (P = 0.92)	87.50 ± 73.81 (P = 0.23)

P10
Comparative Trends of HTLV-1 and HIV-1 Seroprevalence and Incidence Rates in Various Ethnic Groups Sharing the Same Environment in French Guiana.

P. Tortevoye¹, P. Tuppin², G. Carles³, C. Penaud³ and A. Gessain¹

¹Institut Pasteur, Paris, France; ²Etablissement Francais des Greffes, Paris, France; ³Service de Gynecologie-Obstetrique, Centre Hospitalier Frank Joly, Saint Laurent du Maroni, Guyane Francaise, Guyane Francaise

Background: To investigate comparative trends of HIV-1 and HTLV-1 seroprevalence and incidence in pregnant women from various ethnic groups in French Guiana.