

tistically different from the results of the non-seroconverters. Bands of low intensity ("weak bands") of precursors of gp21 were found in 12/20(60%) ($p < 0.001$, when compared with non-seroconverters). The risk factors identified in the 20 individuals were: positive family member (35%), blood transfusion (25%), illegal drug use (15%), risky sexual behavior (30%). In four cases (20%) the possible risk factor was unknown.

Conclusions: Although most seroindeterminate donors are probably not infected with HTLV, delayed seroconversion makes counseling very difficult in this population. The seroconversion rate must be considered and long term cohort studies are necessary to better understand the meaning of WB indeterminate results. Supported by Fapemig

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Molecular Characterization of HTLV Coinfecting HIV-1 Patients.

M. O. Ishak¹, A. C. Vallinoto², V. N. Azevedo², L. F. Machado², L. Lobato³ and R. Ishak²

¹Universidade Federal do Para, Belem, Para, Brazil; ²UFPA, Belem, Para, Brazil; ³SESPA

Background: HTLV/HIV-1 coinfection is common in Brazil and it is associated to risk factors such as multiple sex partners and IVDU. The present study used serological and molecular methods to further pursue the molecular epidemiology of HTLV among HIV-1 patients from two urban areas of the Amazon region of Brazil

Methods: Samples collected from 147 patients from Belem and 51 from Macapa were serologically tested for HTLV-I/II (OrthoDiagnostic Inc., USA). PBMC DNA of the positive samples were subjected to nested PCR of pX, env and LTR to confirm infection and subtyping. RFLP on the products was performed using TaqI, DraI, SacI, ApaI e XhoI.

Results: Six samples (3%, all from Belem) were reactive to HTLV-I/II. Amplification of a pX fragment of 159bp and TaqI digestion confirmed that 4 (66.7%) were HTLV-II and 2 (33.3%) were HTLV-I. The amplification of 630bp region of env and digestion with XhoI, suggested the molecular subtypes HTLV-IIa and HTLV-IIc. Sequencing of 5'LTR confirmed the subtype HTLV-IIc. Amplification of a fragment (765bp) of HTLV-I 5'LTR and digestion with ApaI, SacI and DraI, suggested the virus to be of the Cosmopolitan group, subtype A.

Conclusions: The results confirm the higher frequency of HTLV-II, molecular subtype IIc, coinfecting HIV-1 patients as a unique situation in Belem, Brazil, and the absence of the virus in Macapa, a large urban setting 350 km apart.

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HTLV I and II Infections in England and Wales 1988–2001.

L. J. Payne¹, J. H. Tosswill², G. P. Taylor³ and I. Simms¹

¹Communicable Disease Surveillance Centre, London, United Kingdom; ²Central Public Health Laboratory, London, United Kingdom; ³Department GU Medicine & Communicable Diseases, Imperial College, London, United Kingdom

Background: Screening of blood donations in the UK commenced during August 2002 and numbers of HTLV diagnoses are likely to rise. A review of cases reported prior to 2002 was conducted.

Methods: Laboratory reports of HTLV diagnoses in England and Wales received at a national surveillance centre and serological diagnoses made at a national reference laboratory between 1988–2001 were collated.

Results: Six-hundred and fifty reports were identified in this time period, with an average of 46 new diagnoses per year (range 30–59). Where gender was recorded ($n = 619$) the ratio of females to male was 2:1. Median age at diagnosis in both sexes ($n = 532$) was 57 years. Of the 314 HTLV-positive individuals with reported ethnic origin or country of birth, over 80% were associated with the Caribbean. Clinical information provided ($n = 480$) indicated a greater numbers of cases were diagnosed with a presentation of Tropical Spastic Paraparesis (TSP) ($n = 173$) than Adult T-Cell Lymphoma/Leukaemia ($n = 131$). 53% of TSP cases were reported in the first 5 years of the 14-year period.

Conclusions: Most cases in England & Wales are diagnosed amongst individuals with origins in the Caribbean. Decreasing reports of TSP suggest that earlier reports included prevalent cases. Updated information collated for this review will be presented.

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Evaluation of Viral Markers in Families with HTLV-I-Associated Diseases in the Caribbean.

M. Hisada¹, L. LaGrenade², A. Manns³, E. M. Maloney¹, M. Dotrang⁴, T. Sawada⁵, H. Li¹, N. Jack⁶, O. Morgan⁷, B. Hanchard⁷, C. F. Bartholomew⁶ and R. J. Wilks⁷

¹Viral Epidemiology Branch, Division of Cancer Epidemiology and Genetics, National Cancer Institute, Rockville, MD, USA; ²Food and Drug Administration, Rockville, MD, USA; ³Department of Clinical Practice, Kensington, MD, USA; ⁴Computer Sciences Corporation, Rockville, MD, USA; ⁵Diagnostic Department, Eisai Co., Ltd., Tsukuba, Ibaraki, Japan; ⁶University of the West Indies, Port of Spain, Trinidad, Trinidad and Tobago; ⁷University of the West Indies, Kingston, Jamaica

Background: Reports of "high risk" families for HTLV-I-associated diseases, i.e., the presence of familial clustering of HTLV-I associated illnesses has led to the hypothesis that genetic factor may be in part responsible for susceptibility to ATL, HAM/TSP and ID.

Methods: We evaluated provirus load, antibody titer and presence of anti-Tax antibody among 235 HTLV-I carriers and their 1st degree relatives. Comparisons were made between 37 ATL cases and their 73 relatives, 12 HAM/TSP cases and their 21 relatives, and 28 ID cases and their 64 relatives.

Results: The mean log₁₀ provirus load was higher in ATL ($P < 0.0001$), HAM/TSP ($P < 0.007$) and ID ($P = 0.003$) cases as compared to their respective relatives. The mean log₁₀ antibody titer was not different by disease status in ATL ($P = 0.20$) and ID ($P = 0.23$) families, but was higher in HAM/TSP cases as compared to their relatives ($P = 0.002$). Presence of anti-Tax antibody was similar by disease status in ATL families ($P = 0.39$), but was higher among HAM/TSP ($P = 0.03$) and ID ($P = 0.05$) cases than their relatives.

Conclusions: Provirus load is a strong predictor of HTLV-I associated diseases in high risk families, but high antibody responses distinguish HAM/TSP from ATL. Immune response in ID cases is a composite of those of ATL and HAM/TSP.