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Longitudinal Changes of HTLV-I Viral Markers in Asymptomatic Carriers in Jamaica.

P. C. Van Veldhuisen¹, T. Sawada², B. Hanchard³, R. J. Wilks³ and M. Hisada⁴

¹The George Washington University and The EMMES Corporation, Rockville, MD, USA; ²Diagnostic Department, Eisai Co., Ltd., Tsukuba, Ibaraki, Japan; ³University of the West Indies, Kingston, Jamaica; ⁴Viral Epidemiology Branch, Division of Cancer Epidemiology and Genetics, National Cancer Institute, Rockville, MD, USA

Background: HTLV-I provirus load, antibody titer and anti-Tax antibody are associated with disease pathogenesis, but changes in levels within individual over time among asymptomatic carriers have not been well described in population studies.

Methods: A total of 192 asymptomatic HTLV-I carriers (159 female, 33 male) in Jamaica were prospectively evaluated for virus markers between 1985 and 1994.

Results: The mean antibody titers were greater in those 40 years or older compared with those <40 (p = 0.03). Within each individual, titers increased slightly over time (p = 0.26) among those <30 years old, but progressively decreased over time among those >40 years old (p < 0.001). Prevalence of anti-Tax was higher in those 40 years or older (p = 0.05). Five of 65 subjects developed detectable anti-Tax antibody (19.8 per 1,000 PY), and 10 of 104 subjects lost the anti-Tax antibody (19.8 per 1,000 PY) over follow-up. The mean provirus load did not differ by age and was stable within individual over time.

Conclusions: Antibody responses to HTLV-I may wane with older age while the amount of provirus remains stable. These changes may correlate with age-specific risks of diseases among HTLV-I carriers.

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HTLV-I/II in South America as a Public Health Challenge: How to Advance Research?

A. E. Carneiro-Proietti¹, B. C. Catalan-Soares², F. A. Proietti³ and I. GIPH¹

¹Fundação Hemominas, Belo Horizonte, Minas Gerais, Brazil; ²Ensino e Pesquisa, Fundação Hemominas, Belo Horizonte, Minas Gerais, Brazil; ³Departamento de Medicina Preventiva e Social, Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil

Background: The presence of the human T-cell lymphotropic viruses (HTLV-I/II) infection in South America is well established, but its origin, spectrum in the continent and impact in population health are still unclear.

Methods: South America has close to 350 million inhabitants in its 13 countries. HTLV-I/II presence has been reported with impressive numbers in most of them and may be considered endemic in the continent. The distribution of HTLV I/II among native Amerindian populations has shown a geographic clustering of type I in the Andes highlands and Brazilian coast, while type II predominant in lowlands of South America.

Results: Although comparability between studies conducted among blood donors in different countries may be difficult, the data indicate that the viruses are also circulating among otherwise healthy individuals.

Conclusions: HTLV-I/II infection and its related diseases

should be considered a public health concern in South America and measures to prevent the infection's spread and reduce the related morbidity should be emphasized. Accordingly, advancement of the diverse fields of HTLV research should be encouraged and means to obtain support should be pursued, applying to government and corporate granting agencies. Regional meetings could foster collaborative actions, avoiding duplication of actions and optimizing the scarce resources.

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Molecular Characterization of Tax Region in HTLV-I Patients from Brazil.

S. Kashima¹, O. M. Takayanagu², E. M. Hachiya¹, R. Carreto³, L. C. Alcantara⁴, B. Galvão Castro⁴, M. Pombo de Oliveira⁵ and D. T. Covas¹

¹Blood Center of Ribeirão Preto, Ribeirão Preto, São Paulo, Brazil; ²School of Medicine of Ribeirão Preto, Ribeirão Preto, São Paulo, Brazil; ³Molecular Biology Laboratory, Blood Center of Ribeirão Preto, Ribeirão Preto, São Paulo, Brazil; ⁴Centro de Pesquisas Gonçalo Moniz, Salvador, Bahia, Brazil; ⁵National Institute of Cancer, Rio de Janeiro, Brazil

Background: Epidemiological and molecular aspects of HTLV-I isolates from Brazil were investigated in patients with asymptomatic, HAM/TSP and ATL profile, in order to determine characteristic patterns for tax region since it comprises an important regulatory protein.

Methods: We collected 122 samples of patients from distinct clinical groups. These samples belonged to different parts of the country where different ranges of HTLV-I/II frequencies are observed. We amplified the whole tax region (~1000 bp) and submitted the nucleotide sequences to molecular analysis.

Results: The results showed that tax region of the Brazilian HTLV-I isolates had a nucleotide similarity of 99% respect to ATK-1. Analysis of the pattern of those substitutions showed that 5 specific nucleotide substitutions at positions 7401 (C-T), 7914 (T-C), 7920 (C-T), 7982 (C-T) and 8231 (G-A) were highly conserved among Brazilian isolates (79,6% of the samples). Those substitutions showed a frequency ranging from 81.6% to 100% in the sample group, and 18,4 to 24,1% in the references.

Conclusions: Also it could be seen that these changes were not correlated to a specific clinical status of the patients and seems to be a geographic characteristic since the molecular phylogeny analysis using LTR region resulted that 98,3% of HTLV-I sequences clustered inside the Cosmopolitan subtype (Ia). Financial Support: CTC, FUNDHERP, FAPESP

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HTLV-I and HTLV-II Proviral Sequences in Argentinean Blood Donors with Indeterminate Western Blot (WB) Patterns.

A. M. Mangano¹, M. Remesar², A. M. del Pozo² and L. Sen¹

¹Lab. Biología Celular y Retrovirus, Hospital de Pediatría "J.P. Garrahan", Buenos Aires, Argentina; ²Hemotherapy Unit, Hospital de Pediatría "J.P. Garrahan", Buenos Aires, Argentina

Background: In Buenos Aires ~4/10,000 blood donors (BD) have indeterminate (Ind) WB. We conducted an 8-year