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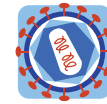
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MEETING ABSTRACT

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HTLV-2 in Central Africa: HTLV-2 subtype B strains similar to those found in Amerindian tribes are endemic in Bakola Pygmies from south Cameroon but not in surrounding Bantus and Baka Pygmies

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Background

Presence and origin of endemic foci of HTLV-2 infection in Africa remain a matter of debate.

Material and methods

To better appreciate the epidemiological and molecular determinants of HTLV-2 infection in Central Africa, we performed a survey in 3903 inhabitants of a South Cameroon forest area, including 1051 Bakola Pygmies, 815 Baka Pygmies and 2037 Bantus living in their neighboring. HTLV-1 and HTLV-2 infection was determined by both specific serological (IFA and WB) and molecular (different generic and specific PCR) methods.

Results

HTLV-1/2 prevalence was of 3% (117/3903) with 90 HTLV-1 (2.3%) and 27 HTLV-2 (0.7%). Surprisingly, HTLV-2 infection was restricted to Bakola Pygmies (27/1051 2.5%) with no HTLV-2 infection in any of the 2852 Baka or Bantus individuals. In Bakola Pygmies, HTLV-2 seroprevalence increased with age, reaching 6.5% in the elder persons. Ongoing intrafamilial HTLV-2 transmission was evidenced. Lymphoid T cell lines (CD8+ or CD4+, CD25+) producing HTLV-2 antigens, were established from PBMCs cultures of HTLV-2

infected individuals. Sequences of a 672 nucleotide LTR fragment, obtained from 7 HTLV-2 samples, showed a very high degree of homologies among samples (< 1% nucleotide divergence) but also surprisingly with Amerindian HTLV-2 B strains. Complete sequence (8954 bp) of one isolate confirmed a typical HTLV-2 B strain.

Conclusion

This study demonstrates clearly a HTLV-2 endemic population, with ongoing transmission, in Central Africa. Furthermore, it gives insights into several central questions regarding the origin and evolution rate of HTLV-2 and the migrations of infected populations.

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