



MEETING ABSTRACT

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# Analysis of temporal expression of HTLV-2 reveals similarities and functional differences from HTLV-1

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In the present study, we developed a robust splice site-specific real-time RT-PCR method to quantitate all HTLV-2 transcripts. Results of this analysis conducted on three different infected cell lines (HTLV-2A Mo-T, C344 and HTLV-2B BJAB-Gu) showed that the most abundant mRNA was gag/pol followed by the accessory transcript 1-3, coding for the p28 and for p22/p20 proteins. The third most abundant mRNA was tax/rex.

To investigate if different mRNAs produced by HTLV-2 are expressed at different levels upon viral reactivation, we studied the kinetics of viral expression in PBMCs from three subjects infected with HTLV-2B and cultured *in vitro* for 48 hours. The level of expression of the full length gag/pol transcript was the highest in all samples. The tax/rex mRNA was detected already at time zero and increased very rapidly following *in vitro* culture, reaching the highest copy number between zero and 2-4 hours. The minus-strand APH-2 mRNA, was expressed at high level. As observed in the infected cell lines, the 1-3 mRNA was expressed at high levels in all subjects. This finding is particularly intriguing, as it encodes two proteins that were shown to exert a powerful control on Tax and Rex function. This peculiar pattern of expression, which is in striking contrast with that of HTLV-1, might in part explain the differential pathogenicity of the two viruses.

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