

Poster presentation

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## Use of HIV-1 LTR Sequence Variants as Prognostic Indicators of HIV Dementia

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To date, no prognostic viral markers exist for the onset of human immunodeficiency virus type 1 (HIV-1)-associated dementia (HIVD). The long terminal repeat (LTR) regulates HIV-1 viral gene expression via its interaction with multiple viral and host factors, including CCAAT/enhancer binding protein (C/EBP) and Sp transcription factor families. We have examined sequence variation at C/EBP sites I and II, and Sp sites I, II, and III in peripheral blood (PB)-derived LTRs from HIV-1-infected patients for potential signature sequences. The 3T configuration of C/EBP site I (C to T at position 3) and 5T configuration of Sp site III (C to T at position 5) were the only variants examined that were found in low frequencies in PB-derived LTRs derived from patients at early stages of HIV-1 disease, and at increasing frequencies in patients representing later stages of disease. Sequence variation at these sites was also examined in LTRs derived from autopsied brain tissue of patients both with and without HIVD. The 3T C/EBP site I was identified in 25% of brain-derived LTRs from patients with HIVD, but was absent in patients without HIVD. This suggests that 3T C/EBP site I, and possibly 5T Sp site III may prove valuable in assessing the likelihood of an HIV-1-infected individual developing HIVD.