Retrovirology

Poster presentation

Identification of C/EBP Binding Sites Within the Clade C LTR

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from 2005 International Meeting of The Institute of Human Virology
Baltimore, USA, 29 August – 2 September 2005

Published: 8 December 2005

Retrovirology 2005, **2**(Suppl 1):P56 doi:10.1186/1742-4690-2-S1-P56

Human immunodeficiency virus type 1 (HIV-1) has been transmitted worldwide and regional viral clades have been designated as subtype A through K. Subtype C, which is concentrated in southeast Asia and sub-Saharan Africa, is the most prevalent subtype worldwide. To date, no studies have examined the role of CCAAT/enhancer binding proteins (C/EBP) in LTR-directed viral gene expression in the clade C LTR. Within clade B viruses, two functional C/EBP sites upstream of the TATA box have been shown to be required for efficient viral replication in cells of monocyte/macrophage lineage. In order to assess the role of the C/EBP sites within the subtype C viral LTR, 211 HIV-1 subtype C LTR sequences were collected and aligned via the Clustal V method. From these analyses, three potential C/EBP sites were identified: two upstream binding sites and one downstream binding site. Interestingly, the putative downstream site was highly conserved between clades B and C, suggesting the presence of a functionally important cis-acting element that has yet to be characterized. Electrophoretic mobility shift analyses demonstrated that two of the three sites within the HIV-1 subytpe C were able to bind C/EBP factors. Additional studies focused on examining relative binding affinities of naturally occurring variants of these two sites. Future studies will examine the roles of these sites in the regulation of LTR activity.