



POSTER PRESENTATION

Open Access

Evolutionary dynamics of HIV-1 subtype C accessory and regulatory genes in primary infection

R Rossenkhan^{1*}, V Novitsky², TK Sebunya³, R Musonda⁴, BA Gashe³, M Essex²

From AIDS Vaccine 2012

Boston, MA, USA. 9-12 September 2012

Background

Studies addressing the dynamics of accessory and regulatory viral gene diversity and selection during early stage of HIV-1 infection are limited but crucial for progress towards vaccine research.

Methods

Intra-patient diversity and evolution was assessed during primary HIV-1C infection, viral quasiespecies were obtained by single genome amplification (SGA) at multiple sampling time points up to one year post-seroconversion (p/s).

Results

The mean intra-patient diversity was found to be 0.11% (95%CI; 0.02 to 0.20) for *vif*, 0.23% (95%CI; 0.08 to 0.38) for *vpr*, 0.35% (95%CI; -0.05 to 0.75) for *vpu*, 0.18% (95%CI; 0.01 to 0.35) for *tat* exon 1 and 0.30% (95%CI; 0.02 to 0.58) for *rev* exon 1 during the time period 0 to 90 days p/s. The intra-patient diversity increased gradually in all non-structural genes over the first year of HIV-1 infection, which was evident from the *vif* mean intra-patient diversity of 0.46% (95%CI; 0.28 to 0.64), *vpr* 0.44% (95%CI; 0.24 to 0.64), *vpu* 0.84% (95%CI; 0.55 to 1.13), *tat* exon 1 0.35% (95%CI; 0.14 to 0.56) and 0.42% (95%CI; 0.18 to 0.66) for *rev* exon 1 during the time period of 181 to 500 days p/s. Statistically significant increases in viral diversity were observed for *vif* ($p=0.013$) and *vpu* ($p=0.002$). Weak and sporadic associations between levels of viral diversity within the non-structural genes and HIV-1 RNA load during primary infection were found. Positive and negative selection

patterns over the first year post-seroconversion were assessed in each of these genes, providing insight into the selection pressures on these genes which are crucial for viral replication in-vivo.

Conclusion

Our study highlights differential diversity and slower diversification across these HIV-1 genes. The most likely cause is different selection pressure imposed by host immune response to the encoded viral gene products that may result in different evolutionary rates.

Author details

¹HSPH/UB/BHP, Boston, MA, Botswana. ²Harvard School of Public Health (HSPH)/ BHP, Boston, MA, USA. ³University of Botswana (UB), Gaborone, Botswana. ⁴Botswana Harvard AIDS Institute Partnership (BHIP), Gaborone, Botswana.

Published: 13 September 2012

doi:10.1186/1742-4690-9-S2-P142

Cite this article as: Rossenkhan *et al.*: Evolutionary dynamics of HIV-1 subtype C accessory and regulatory genes in primary infection. *Retrovirology* 2012 **9**(Suppl 2):P142.

¹HSPH/UB/BHP, Boston, MA, Botswana

Full list of author information is available at the end of the article