Evolutionary Dynamics of HIV-1 Subtype C Accessory and Regulatory Genes in Primary Infection

The Harvard community has made this article openly available. Please share how this access benefits you. Your story matters

Citation

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

Citable link
http://nrs.harvard.edu/urn-3:HUL.InstRepos:10483963

Terms of Use
This article was downloaded from Harvard University’s DASH repository, and is made available under the terms and conditions applicable to Other Posted Material, as set forth at http://nrs.harvard.edu/urn-3:HUL.InstRepos:dash.current.terms-of-use#LAA
Evolutionary dynamics of HIV-1 subtype C accessory and regulatory genes in primary infection

R Rossenkhan1*, 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 quasispecies 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 rev exon 1 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 (BHP), 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.