



POSTER PRESENTATION

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Analysis of HIV-1 gp120 quasispecies suggests high prevalence of intra-subtype recombination

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From AIDS Vaccine 2012

Boston, MA, USA. 9-12 September 2012

Background

Recombination between viruses of the same HIV-1 subtype has been understudied primarily due to the lack of reference sequences, as well as appropriate bio-informatics tools. The introduction of recombination detection program (RDP3) made the detection of HIV-1 intra-subtype recombination feasible.

Methods

This study determined the prevalence and patterns of HIV-1 intra-subtype recombinants among female bar and hotel workers in Moshi, Tanzania. The HIV-1 env gp120 V1-C5 quasispecies from 45 subjects classified as pure HIV-1 subtypes A1, C, or D were analyzed for recombination events by RDP3.

Results

HIV-1 quasispecies with evidence for recombination were found in 89% of subjects infected with pure HIV-1 subtypes A, C, and D. Recombinant viruses were observed at both the baseline and the 12 month visits in 88% of the subjects; in 12% of subjects recombination was identified only at the later time point. Two major patterns were observed: 70% of subjects had unique recombination breakpoints without dominance of any particular variant, while in 30% of subjects a specific recombinant variant dominated in the pool of viral quasispecies.

Conclusion

A large proportion of female bar and hotel workers were infected with intra-subtype recombinant viruses. These results suggest that HIV-1 co- and super-infections are common in this population, and occur more frequently than previously thought. Intra-subtype recombination

contributes to the increased viral diversity which poses a challenge to HIV-1 vaccine design.

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Published: 13 September 2012

doi:10.1186/1742-4690-9-S2-P146

Cite this article as: Kiwelu et al.: Analysis of HIV-1 gp120 quasispecies suggests high prevalence of intra-subtype recombination. *Retrovirology* 2012 **9**(Suppl 2):P146.

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