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Prevalence of CCR5-tropic HIV-1 among treatment-experienced individuals in South Africa infected with Clade C virus

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Purpose of the study

HIV-1 enters target cells by binding to the CD4 molecule and a co-receptor (CCR5 [R5] and/or CXCR4 [X4]). HIV-1 may be classified as R5-tropic, X4-tropic, or dual/mixed (D/M) tropic depending on the co-receptor(s) used. Little is known about the prevalence of R5-tropic HIV-1 in regions of the world where non-clade B virus predominates. The objectives of this study were to determine the prevalence of R5-tropic HIV-1 amongst treatment-experienced (TE) individuals in South Africa infected with Clade C virus (the predominant Clade in South Africa) and to ascertain variables associated with R5 tropism.

Methods

At a single study visit, in this cross-sectional study conducted at three sites in South Africa, a brief questionnaire elicited information on demographics, HIV clinical history, and antiretroviral regimens. Blood was drawn from subjects and analyzed for CD4 cell count, HIV-1 RNA load (VL), and HIV-1 genotype to ascertain clade. Clade C samples with a VL of >1,000 copies/mL were tested for tropism via the original phenotypic Trofile™ assay.

Summary of results

Of the 353 subjects recruited for this study, 294 (84.2%) had a VL of >1,000 copies/mL; 276 (93.9%) of these were infected with Clade C HIV-1. Tropism results were obtained for 206 (74.6%) subjects with Clade C HIV-1. Mean age at study entry was 37 years; 40.8% of subjects were male, and the majority (97.6%) were of African race/ethnicity. Most (98.1%) subjects reported a heterosexual mode of HIV-1 transmission. Mean VL was 122,978 copies/mL and mean CD4 cell count was 208 cells/μL. R5, D/M and X4-tropic HIV-1 was present in 146 (70.9%), 52 (25.2%) and 8 (3.9%) of TE subjects, respectively. A multivariate logistic model was fitted including age, sex, CD4 cell count, VL, time since HIV diagnosis, and mode of HIV transmission. Backward selection from a saturated model with all two-way interactions yielded three variables significantly associated with R5 tropism: age, VL, and CD4 cell count.

Conclusion

R5-tropic HIV-1 was the predominant variant detected in this TE South African population infected with Clade C HIV-1. In a multivariate model, older age, higher CD4 cell count, and higher VL were all associated with the presence of R5 co-receptor usage.