Prevalence of CXCR4-tropic viruses in clustered transmission chains at the time of primary HIV-1 infection

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Abstract

During 2003–2010, 555 strains isolated from sexually-infected patients at the time of primary HIV-1 infection (PHI) were characterized. Tree topology revealed that 11.7% of PHIs segregated into transmission clusters. CXCR4-usage was identified in 27 strains (4.9%) and was significantly associated with subtype B (p 0.003) and low CD4 cell count (p 0.01). In clustered and unique PHIs, the prevalence of CXCR4-tropic strains was 1.5% and 5.3%, respectively (p 0.35). Our results are in line with the hypothesis of a mucosal bottleneck contributing to the high prevalence of CCR5 variants during PHI.