

Oral presentation

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0A06-01. Multiplicity of infection by HIV-1 in injection drug users, men who have sex with men and heterosexuals

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Background

We have recently shown that transmitted/founder virus(es) can be identified unambiguously using single genome amplification (SGA) (Keele, PNAS, 2008; Salazar, JEM, 2009) and that in heterosexual transmissions approximately 80% of patients are infected by a single virus or infected cell (Keele, PNAS, 2008; Haaland, PLoS Pathogens, 2009; Abrahams, JVirol, 2009). Here we explore the characteristics of virus transmission in men who have sex with men (MSM) and injection drug users (IDU).

Methods

Full-length env sequences were derived by SGA from plasma vRNA from 30 acutely infected MSM and 11 IDU from North America. Modes of infection were determined by self-report. Unclassified amplicons were sequenced, aligned, and analyzed by neighbor-joining phylogenies and the Highlighter tool.

Results

Maximum within-patient diversity ranged from 0.08–7.12%. In the MSM group, 19 of 30 (63%) acutely infected subjects had evidence of a single transmitted/founder (t/f) virus and 11 of the 30 had evidence of transmission by a minimum of 2–10 viruses. In the IDU group, 4 of the 11 (36%) had evidence of a single t/f virus, while the remaining 7 demonstrated transmission by a minimum of 3–19 variants. In the subjects with multiple trans-

missions, the median number of t/f variants was 3 for MSM and 5 for IDU. Differences in single versus multiple virus transmissions among HSX, MSM and IDU were statistically significant ($p < 0.006$).

Conclusion

The HIV-1 transmission event is different in HSX, MSM and IDU. We see single variant transmission in approximately 80% of HSX, 60% of MSM and 40% of IDU. When multiple transmissions occur, they tend to have a higher number of variants in IDU than in MSM or HSX. These findings indicate that risk of HIV-1 acquisition correlates with numbers of transmitted viruses. This, along with the phenotypic properties of these viruses (especially Env), may be important in vaccine design and assessment.