

Poster presentation

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P07-09. Contemporaneous transmission of genetically distinct HIV variants from a single donor to two recipients

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Background

New infections are frequently seeded by a single viral strain. What determines which variant is successfully transmitted from the diverse donor quasispecies is not clear. In the SIV/macaque model it has been reported that different strains can be transmitted from one animal to multiple recipients. Here we show that this is also true for HIV infection.

Methods

We studied two MSM with a history of HIV-1 infection by a third party on 21/7/04 and presenting with symptoms of seroconversion 35 and 42 days later. Samples of plasma from both recipients were taken at presentation and after 24 weeks. No samples were available from the donor. Viral sequences of gag (P24 aa 20–231), RT (aa 32–293) and env were obtained by cloning. To minimise artefactual diversity, env sequences were also amplified by single genome amplification (SGA) and compared with sequences from other acutely infected patients and longitudinal datasets to model the diversity within the donor.

Results

The pol and gag clonal sequences from the two patients at both baseline and after 24 weeks clustered to the exclusion of all background sequences (bootstrap 100%, average pair-wise distance 3.4%) and support the clinical history of a single donor. However, the env sequences, although related, showed significant divergence (intra-

host vs inter-host distance <1% vs 7.4%, P value <0.0001). These data were supported by SGA, from which it was inferred that the transmitted env sequences were separated by at least 3.7 years of within-host evolution in the donor despite being transmitted on the same evening.

Conclusion

This is the first report and analysis of different HIV env variants being transmitted from one donor to two different recipients. As well as the challenge of population-wide variability, these data show that a successful vaccine must cover the additional – and possibly unpredictable – challenge of within-host diversity.