

Poster presentation

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P20-17. Evolution of multiple transmitted viruses during the early stage of HIV-1 infection

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Background

Multiple transmitted viruses have been detected in about 20% of acute HIV-1 infected individuals. However, the evolution of these viruses during the early infection stage has not been fully studied.

Methods

Longitudinal plasma samples were collected from 16 subtype C infected individuals. Multiple full-length HIV-1 genomes were obtained by SGA from the first HIV-1+ plasma sample (screening) and one or more later time point samples.

Results

Analysis of SGA sequences showed 10 subjects were infected with a single transmitted virus while the other six were infected with two or more transmitted viruses. In two cases (CH0275 and CH0078), only one and two sequences representing additional transmitted viruses were identified after analyzing 24 and 57 SGAs, respectively. To better estimate frequencies of such minority transmitted viral populations at screening, a large number of viral genomes (937 and 359 for CH0275 and CH0078, respectively) were analyzed by parallel allele-specific sequencing (PASS) and these rare transmitted viruses were found at low frequencies (4.2% and 6.8%) in both individuals. In all six individuals infected with multiple transmitted viruses, only one transmitted virus (often the minority population) became the predominant viral pop-

ulation in the later time points. Since all six screening samples were collected at the acute infection stage (antibody negative), the viral population may not yet be affected by immune selection pressure.

Conclusion

The data suggests prior to immune selection the proportion of each transmitted virus may be related to replicative capacity, while the survival or elimination of one transmitted viral population at later infection stages may be determined by the immune selection pressure. Further studies are required to identify factors that determine dynamic changes of viral populations over time.