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Oral presentation

Evidence for replication of human endogenous retroviruses type-K (HERV-K) in HIV-1 positive patients

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Background

The infectious capacity of particle-coding human endogenous retrovirus type-K HERV-K(HML-2) virions is still questionable.

Materials and methods

The full-length RNA env gene, necessary for cell-to-cell transmission, was amplified from plasma samples (three time-points) of six HIV-1 seropositive individuals and sequenced in order to track the phylogenetic evolution of HERV-K.

Results

Type-1 and Type-2 HERV-K(HML-2) were co-amplified. Phylogenetic analyses revealed frequent detection of inter and intra-subtype HERV-K(HML-2) recombinant env sequences. Type-1 but not type-2 env sequences were mostly edited at specific sites, originating a unique hypermutated consensus sequence (K111), which cluster in a unique phylogenetic branch. HERV-K sequences less than 98% similar to known proviruses suggest that these proviruses are unfixed. dN/dS ratios < 1 strongly suggested that HERV-K replicated by reinfection, which may explain the finding of putative HERV-K recombinant and hypermutated sequences.

Conclusion

Our data suggest that the HERV-K(HML-2) family code for infectious viral particles. RNA recombination could serve to efficiently remove mutated HERV-K alleles by combining intact parts of different genomes