RETROVIROLOGY

MEETING ABSTRACT Open Access

Viral caracterisation of "zoonotic" Foamy viruses

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From 15th International Conference on Human Retroviruses: HTLV and Related Viruses
Leuven and Gembloux, Belgium. 5-8 June 2011

Background

Simian Foamy Virus is a widespread retrovirus infecting non-human primates (NHP). It is latent in PBMCs but replicates efficiently in saliva. It can be transmitted to humans mainly by bites, giving rise to a lifelong infection. Little is known about FV replication in humans. Genomic changes and quasi-species variability in human PBMCs and saliva have not been extensively studied yet.

Materials and methods

In South Cameroon, a series of hunters bitten either by an African Green Monkey (AGM), a chimpanzee (cpz) or a gorilla (ggo) were found to be SFV-infected. Viral isolation was performed by co-cultivation of their PBMCs with BHK cells. We also analyzed quasi-species (in a 425pb-Pol fragment) from PBMCs and saliva of 9 SFVggo-infected hunters.

Results

5 viral strains (1 SFVagm, 2 SFVcpz and 2 SFVggo) were isolated and sequenced. They are about 5-15% divergent from the corresponding prototypical sequences. Their divergence is s(ub)pecies-specific and no common genomic feature was found between the "zoonotic" strains. Quasi-species variability ranges from 0,3% in saliva to 0,5% in PBMCs. In only 2/9 cases, FV clones are clustered in two groups: PBMCs versus saliva.

Conclusions

In contrast with previous studies, no deletion or specific mutations have been observed in the 5 "zoonotic" FV, suggesting that FV restriction in humans is not due to genetically impaired viruses. Preliminary data indicate that quasi-species variability in saliva seems not higher than in PBMCs, which might be explained by a low replication in human saliva.

Published: 6 June 2011

doi:10.1186/1742-4690-8-S1-A240
Cite this article as: Rua *et al.*: Viral caracterisation of "zoonotic" Foamy viruses. *Retrovirology* 2011 **8**(Suppl 1):A240.

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