Retrovirology

Poster presentation

Evolution of viruses and antiviral defense

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from Frontiers of Retrovirology: Complex retroviruses, retroelements and their hosts
Montpellier, France. 21-23 September 2009

Published: 24 September 2009

Retrovirology 2009, **6**(Suppl 2):P59 doi:10.1186/1742-4690-6-S2-P59

This abstract is available from: http://www.retrovirology.com/content/6/S2/P59

Contemporary viruses can be organized in an evolutionary tree ranging from the RNA world to the DNA world, from ribozymes, via viroids, DNA-ribozymes, Influenza, retro-and para-retroviruses to DNA viruses - supporting a „virus-first" hypothesis. Retroviruses have shaped or may have even built the human genome, where up to 50% are retrovirus-related sequences to which increasing and decreasing complexities contributed. Rudimentary reverse transcription from RNA to DNA is still ongoing today in telomeres during embryogenesis and cancer [1]. Sequence analysis of the human genome witnesses our past, indicating how long HIV-like viruses, reverse transcriptase and RNases H have been around. Endogenization of retroviruses is actively ongoing in animal models and may allow a prediction on the future of HIV in people. Evolution of HIV takes place during antiretroviral therapies. An HIV suicide approach circumvents mutagenesis and escape mutants [2,3]. Co-evolution or crossing arms, also known from phage and bacteria, can be deduced from structural and functional similarities of retroviral replication and the siRNA-mediated antiviral defense machineries [4]. An evolutionary relationship between siRNA and interferon can be constructed by comparing their pathways. SiRNA involving dicer as well as inter-feron are active antiviral defense mechanisms in mammalian cells, tested by dicer and interferon knockdown analyses [5,6]. The systems differ in strength and sequence specificities.

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