

New knowledge about host-virus coevolution unmasked from the genomic record

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Retroviruses are important pathogens, which have attacked vertebrate hosts for millions of years. Researchers from Uppsala University and Lund University, now provide new knowledge about the long-term interactions of retroviruses and their hosts by analyzing endogenous retroviruses (ERVs), retroviruses whose genes have become part of the host organism's genome. The findings are now being published in *Proceedings of the National Academy of Sciences (PNAS)*.

Retroviruses, including HIV in humans, must become part of the host cell's genome to produce new viruses. Occasionally retroviruses infiltrate germ cells and transmit vertically to the host's offspring as ERVs. Consequently, ERVs make up large portions of vertebrate genomes and represent a record of past host-retrovirus interactions.

"This study demonstrates the powerful resource presented by the genomic ERV record to better understand host-retrovirus coevolution", says Patric Jern, Research fellow at the Department of Medical Biochemistry and Microbiology, Uppsala University, who headed the study.

The researchers used recent technological advances in big-data analyses of whole genome sequences for new insights into retroviral evolution, diversity, host switching, and the factors influencing retroviral transmission. Around 36,000 ERVs recovered from 65 vertebrate genomes show that retroviruses are widespread across vertebrates and that retroviral lineages are either short-lived over evolutionary time or a



considerable number of retroviruses await discovery. No major vertebrate lineage studied has escaped retroviral activity and <u>retroviruses</u> appear to be extreme host generalists that frequently switch among distantly related <u>vertebrate</u> hosts.

"We hope that these methods will be helpful in future studies by generating additional knowledge about the evolutionary ecology of viruses and their host species", says Patric Jern.

More information: Pan-vertebrate comparative genomics unmasks retrovirus macroevolution , *PNAS*, www.pnas.org/cgi/doi/10.1073/pnas.1414980112

Provided by Uppsala University

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