

New tales told by old infections

November 25 2013

Retroviruses are important pathogens capable of crossing species barriers to infect new hosts, but knowledge of their evolutionary history is limited. By mapping endogenous retroviruses (ERVs), retroviruses whose genes have become part of the host organism's genome, researchers at Uppsala University, Sweden, can now provide unique insights into the evolutionary relationships of retroviruses and their host species. The findings will be published in a coming issue of *Proceedings of the National Academy of Sciences (PNAS)*.

All <u>retroviruses</u>, including HIV in humans, must become part of the host cell's genome in order to produce new viruses. When a germ line cell is infected there is a chance for the virus to be passed on to the <u>host</u> <u>organism</u>'s offspring, and for millions of years retroviruses have colonized vertebrate hosts, leaving traces in their genetic make-up as endogenous retroviruses (ERVs).

Using large-scale computer analyses, researchers in Patric Jern's research team at Science for Life Laboratory, Department of Medical Biochemistry and Microbiology at Uppsala University, uncover new depths in retroviral diversity and find evidence for a host reservoir of one group of retroviruses, with rampant host switching throughout history. The computer screening identified nearly 90,000 ERVs from 60 host genomes sampled across vertebrate diversity, making it possible for the researchers to map host distribution, origin, and transmission of these viruses.

"Our results indicate that current infectious retrovirus diversity may be



underestimated, adding credence to the possibility that many additional retroviruses may remain to be discovered in vertebrate species," says Alexander Hayward, the lead author of the new study.

The researchers find evidence of frequent host-switching by one group of retroviruses throughout history, pointing to a rodent host reservoir and that rats may have acted as facilitators of retroviral spread across diverse mammalian hosts.

"This study demonstrates the potential of the genomic record as an important resource for improving understanding of the long term coevolution among retroviruses and host species," says Patric Jern.

The genomic record provided by ERVs offers improved knowledge of the evolution and frequency of past retroviral spread to evaluate future risks and limitations for horizontal transmission between different <u>host</u> <u>species</u>. This is relevant given the emergence of prominent diseases linked with retroviral infection, such as HIV, which switched hosts to humans from monkey species.

More information: Hayward A., Grabherr M., and Jern P. (2013) Broad-scale phylogenomics provides insights into retrovirus-host evolution. *Proceedings of the National Academy of Sciences* <u>www.pnas.org/cgi/doi/10.1073/pnas.1315419110</u>

Provided by Uppsala University

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