

New tales told by old infections

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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 [retroviruses](#), 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 [host organism](#)'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

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