

New knowledge about retrovirus-host co-evolution

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A young rabbit looking through the grass. Credit: Ksd5/Wikipedia

Retroviruses have colonised vertebrate hosts for millions of years by inserting their genes into host genomes, enabling their inheritance through generations as endogenous retroviruses (ERVs). Researchers from Uppsala University now provide new knowledge about the long-term associations of retroviruses and their hosts by studying ERV

variation and segregation in wild and domestic rabbit populations. The findings are being published in *Proceedings of the National Academy of Sciences (PNAS)*.

Retroviruses, such as HIV in humans, must become part of the host cell's nuclear DNA to produce new viruses. Over timescales of millions of years, retroviral infiltrations of germ cells have been inherited by the host's offspring as ERVs, which make up large parts of vertebrate genomes today.

The researchers used recent technological advances for [population](#)-based analyses of whole genomes derived from wild and domestic hosts, which offer new insights into ERV-host genome variation. As a model, the researchers studied European rabbits, which diverged into two subspecies on the Iberian Peninsula about one million years ago and were domesticated in southern France about 1,000 years ago.

"By studying whole genome sequences from related host populations compared to the genome of a single individual, we can identify new ERVs to better understand retrovirus-host co-evolution," says Daniel Rivas, lead author of the study.

Using data from hundreds of individuals from many [rabbit](#) populations, the researchers were able to identify previously unknown retroviral insertions, as well as determine the spread of those that existed in the reference [genome](#). The ERV diversity mostly follows rabbit divergence and the results indicate substantial variation across ERV insertions in different rabbit populations. This new knowledge sheds light on how ERVs spread in host populations, and how that spread correlates with the evolution of the host species.

"The abundance and segregating variation we uncover from host populations demonstrate the genomic ERV record as a remarkable

source for an evolutionary perspective on retrovirus-[host](#) associations," says Patric Jern, who headed the study.

More information: Salvador Daniel Rivas-Carrillo et al. Whole-genome comparison of endogenous retrovirus segregation across wild and domestic host species populations, *Proceedings of the National Academy of Sciences* (2018). [DOI: 10.1073/pnas.1815056115](https://doi.org/10.1073/pnas.1815056115)

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