

New inherited retroviruses identified in the koala genome

June 13 2022



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Historic virus infections can be traced in vertebrate genomes. For millions of years, these genomes have been repositories for retroviruses that incorporated their code into germline cells and were inherited as

endogenous retroviruses (ERVs). Researchers from Uppsala University now provide new findings about retroviral establishment in the koala genome. The findings are being published in the journal *PNAS*.

The researchers examined the koala [genome](#) and found new ERV lineages, in addition to the previously known koala retrovirus (KoRV). KoRV has been associated with illness in koalas, such as cancer, and is in the process of becoming established as ERVs in the population. This has contributed to the koala being seen as a potential model for the establishment of retroviruses in real time and their [health effects](#), a potential now reinforced by the unexpected distribution pattern of new ERV lineages.

"By screening available koala genomes, we have identified novel ERV lineages. One of these is related to the squirrel monkey retrovirus, which is normally found in South/Central America. Many ERVs of this type are only found in a few koala individuals, which indicates that they are relatively new. It may even indicate an ongoing establishment in the population," says Mette Lillie, lead author of the study.

Large-scale sequencing of entire genomes from species populations enables researchers to draw parallels between the novel ERVs and retroviruses that are currently establishing themselves, such as KoRV. Based on the distribution pattern of ERVs in the population and comparisons of how ERV lineages differ, the researchers conclude that additional active retroviruses may be discovered in koalas and other [animal species](#) that share the same environment. The observations are a driving force in the search for potentially active retroviruses in the Australian fauna, which have not yet been identified.

"The ERVs that have been left behind after retrovirus infections in the past now make it possible to uncover historical interactions between [retroviruses](#) and animal species, such as mapping how virus transmission

has taken place. Variations in ERV distribution patterns within host populations can also be valuable as genomic markers, for example in management and protection of endangered species," says Patric Jern, who headed the study.

More information: Expansion of a retrovirus lineage in the koala genome, *Proceedings of the National Academy of Sciences* (2022). [DOI: 10.1073/pnas.2201844119](https://doi.org/10.1073/pnas.2201844119).

Provided by Uppsala University

Citation: New inherited retroviruses identified in the koala genome (2022, June 13) retrieved 23 May 2024 from <https://phys.org/news/2022-06-inherited-retroviruses-koala-genome.html>

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