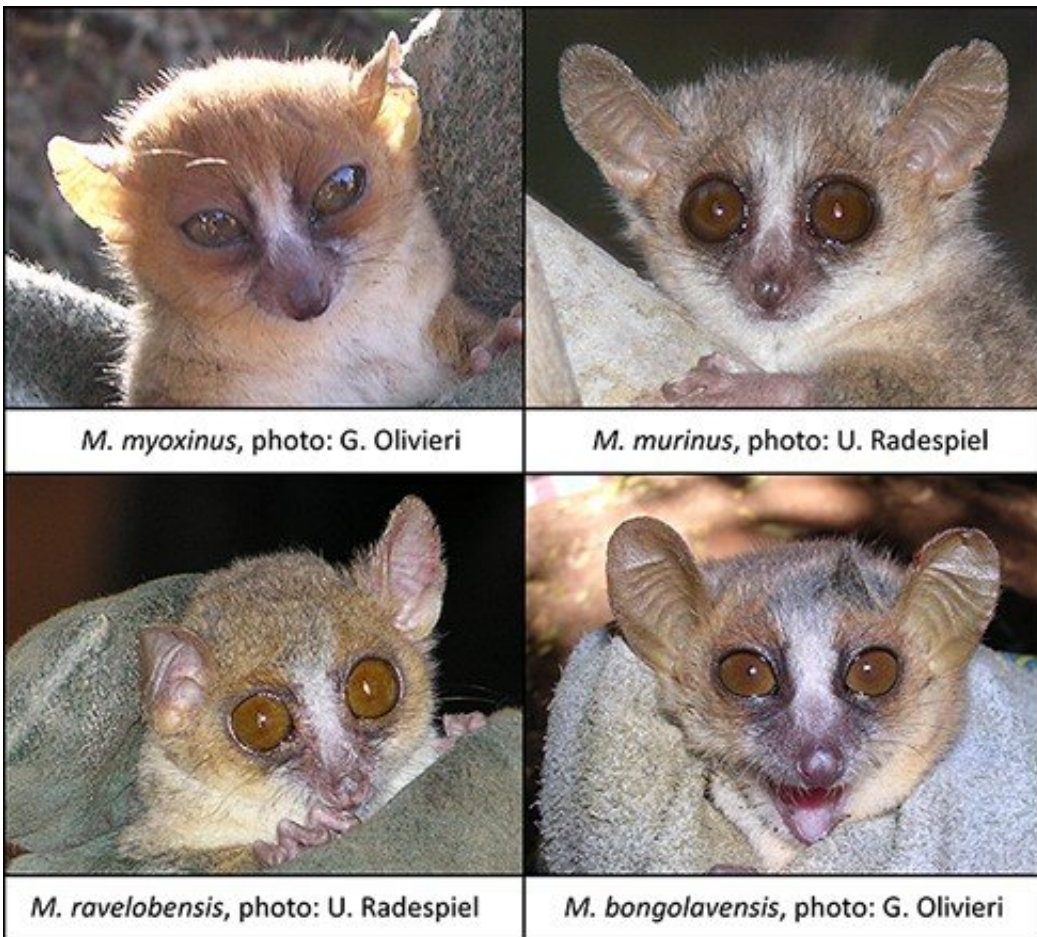


Madagascar mouse lemur retroviruses are diverse, similar to ones found in polar bears or domestic sheep

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Photos of the four studied mouse lemur species: *M. myoxinus*, photo: G. Olivieri, 2003; *M. murinus*, photo: U. Radespiel, 2013; *M. ravelobensis*, photo: U. Radespiel, 2004; *M. bongolavensis*, photo: G. Olivieri, 2003. Credit: *Virus Evolution* (2022). DOI: 10.1093/ve/veac117

Madagascar is home to a unique biodiversity with a large number of endemic species, among those many lemur species, including the mouse lemurs. This diversity is also found in their retroviruses, a team led by scientists from the Leibniz Institute of Zoo and Wildlife Research (Leibniz-IZW) and the University of Stirling reports in the journal *Virus Evolution*.

They analyzed the mouse lemur genome and identified [viruses](#) of two classes that represent ancient infections of the mouse lemur germline. The viruses now behave similarly to lemur genes and are thus called [endogenous retroviruses](#) (ERVs). It was surprising that some of the identified [retroviruses](#) are closely related to viruses found in other, very different mammals such as [polar bears](#) or [domestic sheep](#). This suggests an intriguing and complex pattern of host switching of retroviruses, much more complex than previously thought.

For their analysis, the team collected [blood samples](#) from four species of Malagasy mouse lemurs and screened them using high throughput sequencing. The scientists identified two gamma and three beta retrovirus sequences in the lemurs' genomes, representing ancient infections of the mouse lemur germlines. Since then, the virus DNA has been incorporated in the host genomes and the viruses are no longer active or infectious.

"We were surprised to find that one of the two identified gamma retroviruses was related to an ERV described in polar bears," states Dr. Sharon Kessler, a German Academic Exchange Service (DAAD) supported scientist and Assistant Professor at the University of Stirling. The polar bear virus is young from an evolutionary point of view whereas the lemur virus is old. "How these related viruses infected such geographically separated species is unclear," Kessler says.

There were further surprises among the beta retroviruses. A virulent

retrovirus that infects domestic sheep called Jaagsiekte sheep retrovirus (JSRV), which also forms ERVs in domestic sheep, is thought to be a virus confined to domestic sheep, goats and their relatives—the first cloned sheep "Dolly" had to be euthanized after a JSRV infection and subsequent illness. The mouse lemurs have a closely related JSRV-like virus in their genome.

"This suggests that JSRV-like viruses have been more widespread among mammals and are considerably older than previously thought. Why they only show up in such disparate species and in such a punctuated way is curious," says Prof Alex Greenwood, head of the Leibniz-IZW Department of Wildlife Diseases, where the sample screening was conducted. Similarly, the team also identified a virus in the [mouse lemurs](#) related to retroviruses found in squirrel monkeys, vampire bats and marsupials.

"This group of viruses is becoming more interesting over time as more and more examples of similar viruses are being found in many places including very young ones that may still have currently infectious exogenous counterparts in nature," says Greenwood.

Much of the mouse lemur retroviral diversity observed is associated with non-primate viruses, suggesting a complex pattern of viral host switching around the time the ancestors of lemurs colonized Madagascar. Further studies of viral diversity will help to clarify the complex history of retroviral transmission among mammals.

Retroviruses are viruses that replicate by incorporating their genetic material into the genome of a host cell. If the [infected cell](#) is a germ cell, the retrovirus can subsequently be passed on as an "endogenous" retrovirus and spread throughout a population as part of the host genome.

Repeated infections have resulted in endogenous retroviruses being ubiquitous in mammalian genomes, sometimes making up significant portions of the host genome. However, most [retrovirus](#) integrations are very old and already degraded and therefore inactive—their initial impact on host health reduced by millions of years of evolution.

More information: Sharon E Kessler et al, Long-term host–pathogen evolution of endogenous beta- and gammaretroviruses in mouse lemurs with little evidence of recent retroviral introgression, *Virus Evolution* (2022). [DOI: 10.1093/ve/veac117](https://doi.org/10.1093/ve/veac117)

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