

# African rhinos share retroviruses not found in Asian rhinos or other related species

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Southern white rhino in South Africa. Credit: Nicole Wreyford/Unsplash

Rhinoceros belong to a mammalian order called odd-toed ungulates that also include horses and tapirs. They are found in Africa and Asia. Until recently, evidence suggested that throughout their evolutionary history,

gammaretroviruses such as Murine leukemia virus had not colonized their genomes, unlike most other mammalian orders.

The colonization process is called retroviral endogenization and has resulted in most mammalian genomes being composed of up to 10% retroviral-like sequences. An analysis of modern and extinct rhino genomes headed by the German Leibniz Institute for Zoo and Wildlife Research (Leibniz-IZW) now found that African rhinos have dozens of gammaretroviruses in their genomes absent from the genomes of Asian rhino species, such as the Sumatran and Javan rhino, and that the African black rhino has two related groups, one missing from the white rhinos.

The restriction of gammaretroviruses to African rhinos and the close relatedness of the viruses to rodent viruses, particularly those of African rodents, suggests that African rhinos were infected by an exogenous viral variant and their genomes colonized in Africa. The work is published in the *Journal of Virology*.

Retroviruses such as the causal agent of aids, HIV-1, are unique among viruses in that they have to integrate into the DNA of the host as part of their replication cycle. If this happens in the germline in spermatocytes or oocytes, they can become a part of the host [genome](#) that is inherited by the following generation and then are present in every cell of offspring bodies.

This evolutionary process has happened so often that on average up to 10% of the mammalian genome is made up of retroviruses or their remnants. A previous study of available genomes from horses and their relatives suggested that they, along with rhinos and tapirs, had not been invaded by gammaretroviruses, a group of viruses related to mouse and bird viruses that have successfully colonized most [mammalian genomes](#).

"We had data from several rhino species where we kept finding large

portions of gammaretroviruses. When we used much newer and more complete reference genomes from modern and extinct rhinos we found that only African rhinos had been colonized," says Dr. Kyriakos Tsangaras lead author of this study.

Together with colleagues from Australia and Germany the scientific team found that in fact two different viral groups had colonized African rhinos. One of them had only colonized the black rhino (*Diceros bicornis*) and not the white rhino (*Ceratotherium simum*) and was evolutionarily younger than the one shared by both. As both groups are restricted to African rhinos the study suggests that the African rhino lineage was infected and their genomes colonized in Africa, and that is why the respective gammaretroviruses are not found in Asian rhinoceros and other rhino relatives.

"This ultimately comes down to lack of high-quality reference sequences of wildlife," says Prof Alex Greenwood, head of the Wildlife Disease Department at the Leibniz-IZW. "While things have improved a lot since the first human genome was sequenced, you miss things such as viral history when the databases lack so many species or high-quality reference genomes from many species. It is really another example of why we need more genome reference sequences from wildlife because we don't know what other things we are missing and which conclusions we draw about presence and absence of [sequences](#) that may turn out to be a consequence of too little information."

**More information:** Kyriakos Tsangaras et al, Evolutionarily Young African Rhinoceros Gammaretroviruses, *Journal of Virology* (2023).  
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