

Researchers discover new retroviruses in polar bear 'Knut' and panda 'Bao Bao'

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Credit: Zoo Wuppertal

Endogenous retroviruses (ERVs) are viruses that at some point in the past inserted themselves into the nuclear genome of a host's germ cell. Once integrated in a germ cell the virus would be passed on from one generation to the next and the endogenous retroviral genome would therefore be inherited to new species that evolve from the original host. 'ERV sequences and fragments make up about eight per cent of the human genome,' explains Professor Jens Mayer from the Department of Human Genetics at Saarland

University. Endogenous retroviruses are found not only in humans, but also in other mammals such as horses, cattle, apes, koalas and, as has now been shown, in polar bears and giant pandas.

Working in collaboration with Professor Alex D Greenwood and Kyriakos Tsangaras from the Leibniz Institute for Zoo and Wildlife Research in Berlin, Jens Mayer has been taking a closer look at the DNA sequences from polar bears and great pandas. 'We have characterised endogenous retroviral sequences in both bear species and found a strong similarity between the two, which indicates that these two [virus species](#) are closely related,' says human geneticist Mayer. The researchers also identified ERV sequences in other bear species such as the brown bear, the black bear and the spectacled bear. 'Using molecular dating methods we have now been able to show that the retrovirus became integrated into the genetic material of an ancestor of today's bear species around 45 million years ago,' explains Greenwood. The research team also showed that the original retrovirus was closely related to those found in the genomes of bats and cattle. Interestingly, the viruses found in bears exhibit strong similarity with several endogenous retroviruses found in the [human genome](#). 'Some of these sequences are suspected of playing a role in the occurrence of cancer, neurodegenerative or autoimmune diseases,' says Mayer.

The sort of extensive [genome analysis](#) of different species of wildlife carried out in this study helps scientists gain a better insight into the evolution of retroviruses by learning which retroviruses infected which groups of animals millions of years ago. The data can also provide valuable information on the evolutionary development of mammals. The researchers make use of a variety of techniques to analyse DNA sequences, including very recent high-throughput ('next generation') sequencing methods that facilitate highly efficient DNA sequencing.

In addition to research scientists from Saarland University and the Leibniz Institute for Zoo and Wildlife Research, scientists from the following institutions were also involved in the study: the Berlin Center for Genomics in Biodiversity Research, the Natural History Museum of Denmark, the Department of Biochemistry and Biophysics at the University of California (San Francisco), the Berlin Institute for Medical Systems Biology and the Institute of Virology at Freie Universität Berlin.

More information: Mayer J, Tsangaras K, Heeger F, Avila-Arcos M, Stenglein MD, Chen W, Sun W, Mazzoni CJ, Osterrieder N, Greenwood AD (2013): A novel endogenous betaretrovirus group characterized from polar bears (*Ursus maritimus*) and giant pandas (*Ailuropoda melanoleuca*). *Virology* 443, 1-10. [doi: 10.1016/j.virol.2013.05.008](https://doi.org/10.1016/j.virol.2013.05.008).

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