Complete genome of all strains of the gibbon ape leukemia virus sequenced
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Scientists of the Berlin Leibniz Institute for Zoo and Wildlife Research (IZW) have sequenced the complete genomes of all five identified GALV strains using target enrichment and next-generation sequencing. GALVs have to date only been isolated from captive primates, primarily gibbons, although it is strongly suspected that the natural host is a rodent or bat species. The phylogenetic analysis based on the newly generated genomic sequences has revealed that the four strains of GALV isolated from gibbons are closely related to the woolly monkey sarcoma virus, which is a GALV strain that likely originated in a gibbon host. All together the GALVs constitute a sister taxon of the well-known koala-retroviruses (KoRVs). Using an evolutionary approach, it was discovered that GALV and KoRV demonstrate selective pressure on the proteins specifically involved in the interaction with the host suggesting that the host immune system forces the viruses to adapt. Of particular note, such selective pressures were detected on the particularly pathogenic viruses, which are GALV strains that are more oncogenic and the KoRV strains that are potentially exogenous.

GALV is part of a large group of disease-associated gammaretroviruses found in a wide variety of Australasian mammals. Viruses related to GALV are regularly found in wildlife species particularly rodents and bats. Understanding their diversity and evolution is critical to understand the origin and the spread of a major group of pathogenic viruses.


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