

Bats or Rodents, Who Started it? Short History of the Gibbon Ape Leukaemia Virus–Koala Retrovirus Clade

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ABSTRACT. The close genetic relationship between gibbon ape leukaemia virus (GALV) and koala retrovirus (KoRV) has puzzled scientists since its discovery. As the two hosts are separated geographically and taxonomically, it was hypothesized that cross-species transmission of an ancestor virus from another host into gibbons and koalas had occurred. The relatively recent introduction of KoRV into the koala genome and the apparent absence of GALV in wild gibbons suggest that this ancestor virus or a close relative may still be in circulation. Investigation into the nature of this ancestor virus may provide insights on the impact of KoRV on declining koala populations and will also broaden our understanding of host-virus coevolution. A variety of mammalian species have been identified to harbor GALV-like viruses, but the true host of the ancestral virus of KoRV and GALV remains uncertain. Here we provide a short history of the most prominent candidates: rodents and bats.

Introduction

The isolation of koala retrovirus (KoRV) in 2000 instigated one of the most intriguing mysteries in retrovirology (Hanger *et al.*, 2000). The virus had a very high sequence identity and phylogenetic relationship with gibbon ape leukaemia virus (GALV), which had been identified in captive white-handed gibbons (*Hylobates lar*) in the 1970s. The close relationship between these viruses indicated that cross-species transmission had likely occurred. However, the two species (koalas and gibbons) are evolutionarily and geographically distant (Fig. 1), thus the direct transmission of virus between the species seemed improbable. Researchers hypothesized that these viruses were introduced into each species via another host. The debates over identifying the precursor virus and the original reservoir host continue.

Based on published phylogenetic analysis of the GALV-KoRV clade, both bats and rodents are host to viruses in basal and crown positions (Greenwood *et al.*, 2018). However, what makes the rodent reservoir more prominent is the fact that 53% of all gammaretroviral-derived endogenous retroviruses (ERVs) are shown to have rodent origins (Hayward *et al.*, 2013). It has been proposed that while bats are highly capable recipients of cross-species retrovirus transmission events, rodents are more commonly the originator of these events (Cui *et al.*, 2015); for example, murine retrovirus transmission to porcine endogenous retrovirus (PERV) (Denner, 2007) and the likely tree shrew origin of *Rhinolophus ferrumequinum* retrovirus (RfRV) found in the greater horseshoe bat (Cui *et al.*, 2015).

Here we summarize the history of GALV and look into two prominent candidates for the “ancestor” of the GALV-KoRV clade: rodents and bats.

Keywords: endogenous retrovirus (ERV), cross-species transmission, koala retrovirus (KoRV), gibbon ape leukemia virus (GALV), woolly monkey virus (WMV), flying fox retrovirus (FFRV)

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Submitted: 6 April 2022 **Accepted:** 5 May 2023 **Published:** 21 June 2023 (online only)

Publisher: The Australian Museum, Sydney, Australia (a statutory authority of, and principally funded by, the NSW State Government)

Citation: Mottaghinia, Saba, Lee McMichael, and Joanne Meers. 2023. Bats or rodents, who started it? Short history of the gibbon ape leukaemia virus–koala retrovirus clade. In *Proceedings of the Second Koala Retrovirus Workshop*, ed. D. E. Alquezar-Planas, D. P. Higgins, C. L. Singleton, and A. D. Greenwood. *Technical Reports of the Australian Museum Online* 38: 15–18.

<https://doi.org/10.3853/j.1835-4211.38.2023.1834>

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