

The Origins and Ecological Impact of Koala Retrovirus

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ABSTRACT. The genome of koala retrovirus (KoRV) has striking similarity to the gibbon ape leukemia virus (GALV) genome, suggesting the two viruses may share a common ancestor. Screening of DNA from a range of potential hosts of this putative ancestor virus revealed retroviral sequence from a grassland melomys (*Melomys burtoni*) that was closely related to sequence of both KoRV and GALV. This novel virus has been named *Melomys burtoni* retrovirus (MbRV). As grassland melomys and koalas share habitat, it is possible that there has been cross-species transmission of virus in the past.

Although a causative relationship between KoRV infection and disease in koalas is yet to be confirmed, koala populations with a high prevalence of KoRV infection have a higher incidence of diseases characteristic of retroviruses (cancer and immunosuppression) than populations with low KoRV-prevalence. Not all KoRV-infected koalas develop clinical disease. This variation in disease expression may result from differences in proviral (DNA) insertion sites among koalas, genetic variability of KoRV in different individuals or from variation in host genetics.

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Gammaretroviruses (RV) infect a large range of vertebrate hosts, and are causative agents of a number of diseases including lymphoid tumours and immunosuppression (Bendinelli *et al.*, 1985; Rosenberg & Jolicoeur, 1997). Koala retrovirus (KoRV) is a relatively newly discovered retrovirus which is widespread throughout wild koala (*Phascolarctos cinereus*) populations in Australia (Hanger *et al.*, 2000; Simmons *et al.*, 2012). KoRV is of particular interest because it is the only known retrovirus currently undergoing a process of active endogenization in its host (Tarlinton *et*

al., 2006). Koalas are known to suffer a high incidence of both chlamydiosis and cancer, and the high prevalence of KoRV has been suggested as a possible aetiological agent for immunosuppression and cancer in these animals (Tarlinton *et al.*, 2008). Koala numbers in the wild have declined alarmingly since the beginning of European colonization and their geographic range has been significantly reduced. While the reasons for this decline are multi factorial, the high prevalence of KoRV and its apparent association with other diseases in koalas is a serious cause for concern.

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