

## The Evolution of Koala Retroviruses: Insights from other Endogenous Retroviruses

ALFRED L. ROCA\*<sup>1</sup> AND ALEX D. GREENWOOD<sup>2</sup>

<sup>1</sup> Department of Animal Sciences, University of Illinois at Urbana-Champaign,  
Urbana, IL 61801, United States of America

<sup>2</sup> Head of Department of Wildlife Diseases,  
Leibniz Institute for Zoo and Wildlife Research, 10315 Berlin, Germany  
[roca@illinois.edu](mailto:roca@illinois.edu)

**ABSTRACT.** The koala retrovirus (KoRV) is associated with outbreaks of *Chlamydia* and leukemia in wild and zoo koalas (*Phascolarctos cinereus*). Although endogenous retrovirus-like elements (ERVs) are common in the genomes of all vertebrates (comprising ca 8% of the human genome), KoRV is the only retrovirus known to be currently in the process of transitioning from exogenous to endogenous form. Here, we examine how other host-pathogen interactions, including other host-ERV systems, can inform our understanding of KoRV in koalas. We note that as an exogenous retrovirus becomes endogenous, there would be a dramatic reduction in mutation rates, which may shift the process of accommodation from the pathogen to the host. The low genetic diversity present in koalas may be in part responsible for the failure of the species to develop genetic resistance to KoRV. Isolation between koala populations may have hindered the geographic spread of the virus, but may also hinder selective sweeps of beneficial host alleles or beneficial proviral mutations, thereby precluding rapid increases in host fitness. In humans, some ERVs are involved in normal host functions such as placentation, or in the pathogenesis of diseases such as Hodgkin's lymphoma. However, ERVs present in humans and other species are ancient, precluding prospective studies of germ line invasions. By contrast, the ongoing invasion of the koala germ line by KoRV provides a singular opportunity to study retroviral endogenization as it is occurring. This research can benefit the health of both humans and koalas.

ROCA, ALFRED L., AND ALEX D. GREENWOOD. 2014. The evolution of koala retroviruses: insights from other endogenous retroviruses. In *The Koala and its Retroviruses: Implications for Sustainability and Survival*, ed. Geoffrey W. Pye, Rebecca N. Johnson and Alex D. Greenwood. *Technical Reports of the Australian Museum, Online* 24: 5–10.

Endogenous retroviruses are common elements present in the genomes of all vertebrates examined, with ca. 8% of the human genome comprised of retrovirus-like elements (Bromham, 2002; Weiss, 2006; Pontius *et al.*, 2007; Blikstad *et al.*, 2008). Although some ERVs play a functional role in host health and disease in humans and other species (Roy-Burman, 1995; Mi *et al.*, 2000; Lamprecht *et al.*, 2010), most ERVs exist as “junk DNA” with highly disrupted coding regions and no functional role (Roca *et al.*, 2004; Roca *et al.*, 2005; Pontius *et al.*, 2007). Comparisons across

the genomes of humans and other primates, and of other vertebrate lineages, have shown that ERVs have resulted from multiple invasions of and proliferations in the host germ line by retroviruses (Johnson & Coffin, 1999; Blikstad *et al.*, 2008; Polani *et al.*, 2010). Despite being ubiquitous, almost all known ERVs endogenized many thousands or millions of generations ago, making it difficult to infer the events that occur during and shortly after the invasion of a host germ line by an endogenizing retrovirus (Weiss, 2006; Blikstad *et al.*, 2008).

\* author for correspondence