

# Koala Retrovirus Infection and Disease in South Australian Koala (*Phascolarctos cinereus*) Populations

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**ABSTRACT.** Koala retrovirus (KoRV) infection, endogenous in all northern koalas (*Phascolarctos cinereus*), has been found to occur at lower, but increasing, prevalence in the Kangaroo Island and Mount Lofty Ranges koala populations in South Australia. Proviral and viral loads are also lower than in Queensland koalas, which may be due to exogenous spread of infection, or may be related to the variable presence of viral genes and fragmented expression that has been found in positive Mount Lofty Ranges koalas. However, high proviral loads and full expression across the KoRV genome in South Australian koalas has been found in individuals with neoplasia, particularly lymphoma, which can be as extensive and as severe as that observed in northern koalas. KoRV-A is the predominant subtype and no association with chlamydial status has been found except that high viral loads correlate with severity of chlamydiosis. Based on the complexity of KoRV infections in South Australian koalas, further research is needed to understand the differences in transmission and pathogenesis that occur.

## Introduction

The understanding of koala retrovirus (KoRV) in koala (*Phascolarctos cinereus*) populations in South Australia (SA) has gradually increased over the past 15 years. Previous KoRV studies have focussed on Kangaroo Island, which holds one of the five geographically separated SA koala populations, the others being the Mount Lofty Ranges, Eyre Peninsula, the Riverland, and the lower southeast of the state. Kangaroo Island, at least prior to the 2019/2020 bushfires, and the Mount Lofty Ranges represent two of the largest SA populations and have generally been regarded as healthy, though genetically restricted. Recent KoRV research has been conducted with koalas from both of these populations, however the KoRV status of the other SA koala populations remains unknown.

## Kangaroo Island

The Kangaroo Island koala population was founded from a small translocated group of koalas from French Island, Victoria, in the 1920s (Robinson, 1978), which subsequently

expanded in numbers to the point of requiring population control measures (Duka & Masters, 2005). Their fecundity may be partly attributed to the recent finding that Kangaroo Island koalas are free of infection with *Chlamydia pecorum*, based on 170 koalas tested between 2014–2017 and analysis of over 13,000 veterinary records from a sterilization program (Fabijan *et al.*, 2019). The total koala population, which was estimated at 50,000 in 2016, has now been reduced by approximately 80% in the recent bushfires to an estimated current population of 5,000–10,000 animals (DEW, 2020; Dunstan *et al.*, 2021).

The earliest study of KoRV on Kangaroo Island in 2004 ( $n = 26$ ) found no evidence of infection by end-point PCR (Tarlinton *et al.*, 2006); however, a subsequent end point PCR based study conducted in 2007 found 15% prevalence within the animals sampled ( $n = 162$ ) (Simmons *et al.*, 2012). This low proportion of infected koalas, in conjunction with low proviral load, led researchers to conclude that transmission was exogenous, rather than endogenous, in this population (Simmons *et al.*, 2012). However, a 2013 publication reported an updated prevalence of 30–35%

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