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KoRV and *Chlamydia*: Are they Co-culprits?

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Abstract. There are two main infectious disease threats for the koala; *Chlamydia* and KoRV. A major question is whether or not KoRV predisposes koalas to more severe chlamydial disease. In the only study to date that has examined co-infections, KoRV load (as determined by qPCR) and chlamydial load (as determined by qPCR) and chlamydial disease were examined in wild koalas. While there was a statistically significant correlation between *Chlamydia* infection load and *Chlamydia* clinical disease score, there was no significant correlation between KoRV load and either *Chlamydia* infection load or *Chlamydia* clinical disease score, however the groups were not ideally constructed and hence additional comparisons are needed. If KoRV does predispose koalas to more severe chlamydial disease, one would expect it to do this via an effect on the koala immune system. A series of *Chlamydia* vaccine trials in captive as well as wild koalas are showing that koalas in fact appear to make perfectly normal antibody and cytokine responses to vaccine antigens, even if they have high circulating KoRV loads, arguing against an immune suppressive effect by KoRV.

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In Australia, wild koala (*Phascolarctos cinereus*) populations in many areas, particularly Queensland and NSW, are declining for many reasons. One of the main causes of these declines is infection and disease due to *Chlamydia* (Polkinghorne et al., 2013). While *Chlamydia* cause similar disease syndromes in their non-koala hosts, the koala seems to have a higher than expected level of disease. This raises the question as to whether or not KoRV is somehow contributing to chlamydial disease. This brief overview will focus first on what we know about *Chlamydia* in koalas and then look at the very limited data regarding KoRV and *Chlamydia*.

Overview of *Chlamydia*

Chlamydia is an obligate intracellular bacterium with a unique two-phase developmental cycle. Immunity to chlamydial infections requires both a strong, neutralising antibody response as well as an interferon-gamma directed T cell response. Of the nine species present in the genus *Chlamydia*, two, *C. pecorum* and *C. pneumoniae*, cause infections in koalas (Jackson *et al*., 1999; Deveraux *et al*., 2003). The frequency of chlamydial infections (measured by a range of techniques, but utilizing PCR mostly of late) varies between populations, ranging from nil (on just a few island populations) to 90% in several populations (Polkinghorne *et al*., 2013). Disease levels also vary, but usually represent 25% or so of the infection level at any time point sampled. Animals are infected at ocular and urogenital sites mainly. Of the two chlamydial species, *C. pecorum* is by far the most common and is thought to be the species responsible for the symptoms observed (Glassick *et al*., 1996).

Even though it is *C. pecorum* that is responsible for most infection and disease in koalas, there is considerable genetic diversity between sub-strains (Jackson *et al*., 1997). A range of gene markers have been used to assess *C. pecorum* strain diversity and while there are some minor differences, they all show that the various koala *C. pecorum* genotypes cluster together, but show considerable strain diversity.