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.

**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.