



## RESEARCH REPOSITORY

*This is the author's final version of the work, as accepted for publication following peer review but without the publisher's layout or pagination.  
The definitive version is available at:*

<https://doi.org/10.1111/mam.12142>

Cripps, J.K., Pacioni, C., Scroggie, M.P., Woolnough, A.P. and Ramsey, D.S.L. (2018)  
Introduced deer and their potential role in disease transmission to livestock in Australia.  
Mammal Review

<http://researchrepository.murdoch.edu.au/id/eprint/42934/>

Copyright: © 2018 The Mammal Society and John Wiley & Sons Ltd  
It is posted here for your personal use. No further distribution is permitted.

1 **REVIEW**

2 **Introduced deer and their potential role in disease transmission to**  
3 **livestock in Australia**

4 Jemma K. CRIPPS\* *Arthur Rylah Institute for Environmental Research, Department of Environment,*  
5 *Land, Water and Planning, Heidelberg, Victoria, 3084, Australia and School of BioSciences, University*  
6 *of Melbourne, Victoria, 3010, Australia. Email: jemma.cripps@delwp.vic.gov.au*

7 Carlo PACIONI *Arthur Rylah Institute for Environmental Research, Department of Environment, Land,*  
8 *Water and Planning, Heidelberg, Victoria, 3084, Australia and School of Veterinary and Life Sciences,*  
9 *Murdoch University, Murdoch, WA 6009, Australia. Email: carlo.pacioni@delwp.vic.gov.au*

10 Michael P. SCROGGIE *Arthur Rylah Institute for Environmental Research, Department of*  
11 *Environment, Land, Water and Planning, Heidelberg, Victoria, 3084, Australia and School of*  
12 *BioSciences, University of Melbourne, Victoria, 3010, Australia. Email:*  
13 *michael.scroggie@delwp.vic.gov.au*

14 Andrew P. WOOLNOUGH *Department of Economic Development, Jobs, Transport and Resources, 475*  
15 *Mickleham Road, Attwood, Victoria, 3049, Australia. Email: andrew.woolnough@ecodev.vic.gov.au*

16 David S. L. RAMSEY *Arthur Rylah Institute for Environmental Research, Department of Environment,*  
17 *Land, Water and Planning, Heidelberg, Victoria, 3084, Australia. Email:*  
18 *david.ramsey@delwp.vic.gov.au*

19 \* Correspondence author

20 **ABSTRACT**

21 1. The transmission of pathogens between wildlife and livestock is a globally recognised threat  
22 to the livestock industry, as well as to human and wildlife health. Wild cervids are  
23 susceptible to many of the diseases affecting livestock. This presents a challenge for wildlife  
24 and domestic animal disease management, because the frequent use of agricultural areas by  
25 wild cervids may hamper the effectiveness of disease control strategies.

- 26        2. Six deer species have established wild populations in Australia and are expanding in range  
27            and abundance. A comprehensive literature review of diseases impacting deer and livestock  
28            was undertaken, resulting in consideration of 38 pathogens. A qualitative risk assessment  
29            was then carried out to assess the overall risk posed by the pathogens to the livestock  
30            industry.
- 31        3. Five diseases (bovine tuberculosis, foot and mouth disease, malignant catarrhal fever, surra  
32            and screw-worm fly infestation) ranked highly in our risk assessment. Of these five diseases,  
33            only one (malignant catarrhal fever) is currently present in Australia, but all five are  
34            notifiable diseases at a national level. Data on these diseases in deer are limited, especially  
35            for one of the most abundant species, the sambar deer *Rusa unicolor*, highlighting a further  
36            potential risk attributable to a lack of understanding of disease epidemiology.
- 37        4. This paper provides a detailed review of the pathogens affecting both cervids and livestock  
38            in Australia, and applies a qualitative framework for assessing the risk posed by deer to the  
39            livestock industry. The qualitative framework used here could easily be adapted to assess  
40            disease risk in other contexts, making this work relevant to scientists and wildlife managers,  
41            as well as to livestock industry workers, worldwide.

42    Keywords: Cervidae, disease, livestock, spillover, wildlife-livestock interface.

43    Running head: Potential disease risk from introduced deer in Australia

44    Submitted: 7 March 2018

45    Returned for revision: 8 May 2018

46    Revision accepted: 20 July 2018

47    Editor: DR

48

## 49 INTRODUCTION

50 The transmission of pathogens between wildlife and livestock is globally recognised as a threat to  
51 the livestock industry, as well as to human and wildlife health. The frequency of emerging (and re-  
52 emerging) infectious diseases in wildlife reservoirs has increased, posing new questions about  
53 disease pathogenesis and epidemiology (Rhyan & Spraker 2010). Human-driven changes in land use,  
54 encroachment into wildlife habitat, increasing distribution and abundance of invasive alien species,  
55 climate change and intensified livestock production practices are all factors that can increase the  
56 potential for disease outbreaks. Anthropogenic landscape modifications create new interfaces  
57 between livestock and wildlife, potentially exacerbating processes that favour pathogen  
58 transmission (Miller et al. 2013). The transmission of an infectious agent at the wildlife/livestock  
59 interface may occur directly, through interspecies contact, or indirectly, through shared space or  
60 vectors. Overabundance of native or invasive exotic species may exacerbate the risk of transmission  
61 through increased population densities and increases in host contact rates (Gortázar et al. 2006).

62 Multi-host pathogens are very prevalent among the infectious agents of domestic mammals;  
63 estimates suggest that 77% of pathogens infecting mammalian livestock are generalists that can  
64 infect multiple host species (Cleaveland et al. 2001). For parasites, the incidence of host sharing is  
65 variable but can be high: between 14 and 76% of nematode species found in various taxa of wild  
66 hosts also infect domestic hosts, and between 42 and 77% of nematode species in various domestic  
67 hosts are recorded as infecting wild hosts (Walker & Morgan 2014). As deer (family Cervidae) are  
68 ungulates, closely related to economically important livestock species including cattle *Bos taurus*,  
69 sheep *Ovis aries* and goats *Capra hircus*, it is unsurprising that they share many pathogens, including  
70 several of major agricultural importance. Wild cervids present a unique challenge for wildlife disease  
71 management, as they frequently share habitats and resources with domestic livestock. Previous  
72 reviews by Conner et al. (2008) in North America and Böhm et al. (2007) in the UK have covered  
73 many of these shared cervid-livestock infectious diseases in detail, but with a focus on the  
74 implications for those local contexts. The potential role of deer as vectors of diseases and pathogens  
75 in Australia was highlighted by Davis et al. (2016) but has not been examined in depth. Australian  
76 agriculture currently experiences substantial benefits due to its freedom from many epidemic  
77 diseases that impact livestock industries in other parts of the world. The issue of cervid-transmitted  
78 disease in Australia is highly significant, as exotic disease incursion or outbreaks of emerging or  
79 endemic disease could cause serious production losses, resulting in substantial economic impacts.  
80 Transmission of disease by cervids could also prevent effective control, management or eradication  
81 of a livestock disease, resulting in prolonged epidemics.

82 Globally, deer have been introduced to many countries and have become established in multiple  
83 areas outside their native range (Clout & Russell 2008). Australia is no exception - in the mid-1800s,  
84 multiple species were introduced to Australia from Europe and Southeast Asia, and now populations  
85 of six deer species, chital *Axis axis*, hog deer *Axis porcinus*, red deer *Cervus elaphus*, fallow deer  
86 *Dama dama*, Javan rusa *Rusa timorensis*, and sambar deer *Rusa unicolor*, are well-established and  
87 increasing in geographic range and abundance (Davis et al. 2016). There are no reliable estimates of  
88 deer abundance in Australia, but populations appear to be increasing in size. For example, deer  
89 harvest statistics in the state of Victoria show that the reported number of deer harvested has  
90 increased by an average of 15% per year since 2009, despite reduced harvest effort over this time  
91 (Moloney & Turnbull 2018). There are several issues associated with population increases of deer  
92 (reviewed by Burgin et al. 2015, Davis et al. 2016), including the expansion of deer into new areas  
93 and consequent increases in disease risk, especially as these species have not yet reached their  
94 maximum potential geographic ranges in Australia. Currently, wild deer are most commonly found in  
95 south-eastern Australia, however Davis et al. (2016) showed that deer have the potential to occupy  
96 many parts of Australia from which they are currently absent, including parts of the arid interior  
97 (Figure 1). In northern Australia, 75% of land is devoted to livestock production. This land contains  
98 almost 50% of Australia's cattle population (PricewaterhouseCoopers 2011). If pathogens of  
99 agricultural significance become established in wild deer populations, they will present a significant  
100 threat to livestock production and markets.

101 We set out to review the global literature on diseases of agricultural significance known to occur in  
102 wild deer populations, or to have documented potential to be transmitted to, and hosted by, any of  
103 the six Australian deer species, as well as economically important livestock species, predominantly  
104 sheep and cattle, but also pigs *Sus scrofa domestica*, goats and horses *Equus caballus*. We do not  
105 review the impact on farmed deer, as they comprise only a small percentage (<0.05%) of livestock. In  
106 2010–11 (the latest year for which data are available) 45 073 deer were farmed in Australia (Animal  
107 Health Australia 2017). In comparison, there are over 25 million cattle and 67.5 million sheep across  
108 the continent (Meat and Livestock Australia, 2017). A large number of pathogens are theoretically  
109 hosted by both deer and livestock; it has been necessary to restrict this review to those diseases that  
110 have been relatively well studied or are of major economic importance. We conducted a qualitative  
111 risk assessment by compiling information to assess the potential risks of each disease to the  
112 Australian livestock industry, based on current understanding. The information we provide from our  
113 risk assessment could assist decision-making around disease prioritisation, management and  
114 surveillance, both in Australia and elsewhere in the world where deer and domestic livestock

115 interact. Hence, this disease risk assessment framework could easily be adapted and used within  
116 other contexts.

117 Figure 1.

118 Current (red; West 2011) and potential distribution (greyscale) of the six deer species established in  
119 the wild in Australia (republished from Davis et al. 2016). The potential distributions were estimated  
120 using the Climatch algorithm (Invasive Animals CRC 2011).

## 121 **METHODS**

### 122 **Literature review**

123 We identified peer-reviewed and grey literature from studies worldwide that have reported  
124 pathogens infecting wild deer (Cervidae) populations and known or have potential transmission risks  
125 to economically important ungulate livestock in Australia. Our assessment, out of necessity, included  
126 pathogens not known to occur in Australia, but known to infect both livestock and wild Cervidae  
127 elsewhere. We briefly report on important literature regarding each parasite or pathogen fulfilling  
128 these criteria. Our intention was to cast the widest possible net and to identify pathogens that fulfil  
129 the stated criteria for inclusion, without providing a thorough assessment for arrival or  
130 establishment risks in Australia. We also consulted earlier reviews on this topic from within Australia  
131 (Animal Health Australia 2011, Davis et al. 2016) and elsewhere (Simpson 2002, Böhm et al. 2007,  
132 Conner et al. 2008) to identify pathogens of interest. Previous reviews on this topic from Australia  
133 have been relatively brief - our work expands on these by conducting a thorough assessment of the  
134 literature to compile potential diseases shared by deer and livestock, and then prioritising the risk to  
135 the livestock industry through a risk assessment process.

136 We searched online databases (Web of Science, Scopus, Google Scholar) for references using  
137 combinations of the following search strings: 'deer', 'cervidae', 'spillover', 'disease', 'livestock',  
138 'pathogen', 'parasite', 'source', and 'infection'. We also used the terms 'deer ("pathogen name")'  
139 and 'cervidae ("pathogen name")'. Full search strings are provided in Appendix S1.

140 We use the term 'maintenance hosts', for directly transmitted pathogens only, to describe hosts in  
141 which the disease persists by vertical transmission (mother to offspring) or by horizontal  
142 transmission (from one individual to another) within the species, without the need for any external  
143 source of reinfection. We use 'spillover hosts' to describe where the occurrence of the disease  
144 within a host population requires an external source of reinfection. Spillover hosts may further be  
145 characterised as 'dead-end' hosts if they play no further role in disease transmission (Coleman &

146 Cooke 2001). Disease in spillover and dead-end hosts typically disappears, as disease is eliminated  
147 from the maintenance host. However, in some cases spillover hosts can act as amplifying hosts,  
148 increasing the transmission risk to other wildlife hosts or to livestock. The transmission of infection  
149 across the wildlife/livestock interface tends to occur predominantly through a spillover effect  
150 (livestock infect wildlife) or via a spillback effect where wildlife reinfect livestock (Conner et al.  
151 2008).

## 152 **Disease risk assessment**

153 We evaluated several criteria (likelihood of deer being susceptible, being infected, transmitting the  
154 disease to livestock, and being infected by livestock) to rank the overall risk posed by the selected  
155 pathogens to the livestock industry, using a similar approach to Hartley et al. (2013). We expressed  
156 these qualitative 'likelihood scores' as high, medium or low. With the first category ('susceptible'),  
157 we evaluated the degree to which there is certainty that the six deer species we considered are  
158 susceptible to the pathogen. With 'infected' we evaluated the likelihood of the deer species  
159 acquiring the infection, given that they are exposed to the pathogen. The 'transmitting the disease  
160 to livestock' criterion was used to express the likelihood that, once it was present in deer  
161 populations, the pathogen would be transmitted to livestock species. We used a gradient of  
162 likelihood scores, where we considered pathogens that are transmitted exclusively by direct physical  
163 contact to have a lower score than pathogens that are transmitted indirectly (for example by  
164 environmental contamination, which only requires shared habitat to spread the infection), which in  
165 turn were considered to have a lower likelihood than infections that are spread by vectors (where  
166 the assumption was made that suitable vectors exist in Australia). Our reasoning for this is that we  
167 consider very close physical contact of deer and livestock to be rarer (although anecdotal evidence  
168 indicates that it does sometimes occur) than situations where pasture or supplemental food is  
169 shared, for example, the use of feed troughs by deer. The category 'being infected by livestock'  
170 reported the likelihood of deer becoming infected, given that a disease is present in livestock.  
171 Factors that we took into consideration included whether management actions would be put in  
172 place to control infection in livestock, that may consequently also reduce the risk of infection to  
173 deer.

174 In contrast to Hartley et al. (2013), we separated the category 'infected' into three intermediate  
175 steps to allow a more transparent assessment, as well as to facilitate an update of our assessment  
176 when new information becomes available. The three steps were then combined to obtain an  
177 average 'infected' score. We detail these intermediate steps as follows:

178 Presence: whether the pathogen is present in Australia (or alternatively, the likely risk of it being  
179 introduced and becoming established). For pathogens not yet present, likely risks were assessed (as  
180 described in Appendix S2) using information that is publicly available through Biosecurity Import Risk  
181 Analyses (Australian Department of Agriculture and Water Resources 2018).

182 Distribution: we considered the geographical distribution (based on detected cases) of pathogens  
183 already present in Australia, or, alternatively, the likelihood of them becoming widespread should  
184 they arrive in Australia. We paid particular attention to whether the known (or potential)  
185 distribution of the pathogen would match the known and potential distribution of deer.

186 Transmission: the route of transmission plays an important role in the probability of transmission of  
187 diseases, as well as in disease management. We focussed on transmission within each deer species  
188 (i.e. intra-species transmission) and its influence on the epidemiology of the disease (e.g. highly  
189 contagious diseases were given higher scores).

190 In addition to the criteria used by Hartley et al. (2013), we included 'impact', where we attempted to  
191 predict the potential additional economic impact that a disease would have on livestock farming (in  
192 this case, the economic impact on the predominant livestock farmed in Australia, sheep and cattle),  
193 should deer become an additional route of transmission to those already recognised. The impact  
194 depends on the clinical consequences of the disease, the management actions (e.g. containment,  
195 stamping out, slaughter, vaccination), and the costs resulting from these. Generally speaking,  
196 diseases that are currently common, and whose management would not dramatically change if deer  
197 were implicated in their transmission, were scored as having a low impact, while exotic diseases that  
198 would require extensive intervention or cause dramatic loss were scored as high.

199 We did not carry out a separate disease risk assessment for each deer species. However, we report  
200 notable differences when we expect these to occur. Most deer species found in Australia are known  
201 to use agricultural land (Lindeman & Forsyth 2008), especially when this occurs adjacent to, or is  
202 interspersed with, native forest areas, which are preferred deer habitat. Disease susceptibility and  
203 social behaviour were the two main factors evaluated when assessing differences between species.  
204 With the exception of sambar and hog deer, the deer species in Australia are gregarious, which  
205 generally facilitates higher contact rates and the spread of highly transmissible pathogens (Sah et al.  
206 2018). In the absence of information on the relative abundance of deer, we therefore assumed that  
207 in situations of equivalent density, these gregarious species would pose a greater risk to livestock.

208 The overall risk assessment ranking was calculated using an average rating of the probability of  
209 occurrence (through combining the scores from the 'susceptible', 'infected', 'infecting livestock' and



210 'being infected by livestock' categories) and then ranking this against the potential 'impact' of the  
 211 pathogen, using the risk assessment matrix shown in Table 1.

212 **Table 1.** Risk assessment categories used for assessing the overall risk (a combination of the  
 213 probability of occurrence and the impact) posed by pathogens infecting wild deer for the livestock  
 214 industry in Australia. The probability of occurrence was a combined score from the 'susceptible',  
 215 'infected', 'infecting livestock' and 'being infected by livestock' categories (see text for details).

|                           | Impact <span style="float: right;">216</span> |        |        |
|---------------------------|---|--------|--------|
| Probability of occurrence | Low   | Medium | High   |
| Low                       | Low   | Low    | Medium |
| Medium                    | Low   | Medium | High   |
| High                      | Medium  | High   | High   |

## 217 **RESULTS**

### 218 **Literature review**

219 In total, we documented eight bacterial, eight viral and one prion disease known to infect both the  
220 deer species that occur in Australia and livestock. All species of deer host a wide range of parasites,  
221 and we documented 19 endoparasites (13 helminths and six protozoans) and two ectoparasites  
222 which are known to infect both livestock and the deer species of interest. For each disease, we  
223 documented the host species, the transmission routes, whether the disease is present in Australia,  
224 and a list of relevant references from the literature (Table 2).

### 225 **Disease risk assessment**

226 From the list of documented pathogens (Table 2), the overall risk assessment (combination of  
227 probability of occurrence and impact) was assessed as 'high' for five pathogens, 'medium' for 11  
228 pathogens and 'low' for 21 pathogens (Table 3). We describe below details on those diseases ranked  
229 as 'high', while comprehensive information and literature on the remaining pathogens (scored as  
230 'low' or 'medium') can be found in Appendix S3.

### 231 ***Mycobacterium bovis* (bovine tuberculosis)**

232 *Mycobacterium bovis*, the causative agent of bovine tuberculosis (bTB), has one of the broadest host  
233 ranges of all known pathogens (O'Reilly & Daborn 1995). Bovine tuberculosis is primarily a  
234 respiratory disease and a prominent disease of cattle. It is found in most livestock species (cattle,  
235 sheep, goats, pigs, deer and horses) and can become zoonotic. It is transmitted primarily by direct  
236 contact via infectious aerosols in farmed deer and livestock, but can also be spread through contact  
237 with urine and faeces in wild deer (Böhm et al. 2007). *Mycobacterium bovis*'s broad host range  
238 includes many wildlife species such as common brushtail possums *Trichosurus vulpecula* in New  
239 Zealand (Coleman 1988), European badgers *Meles meles* in the UK (Gallagher & Clifton-Hadley  
240 2000), bison *Bison bison* in Canada (Nishi et al. 2006) and African buffalo *Syncerus caffer* in southern  
241 Africa (Cross & Getz 2006). Epidemiological studies of bTB in wild deer populations have occurred in  
242 New Zealand (Nugent 2011), Europe (de Mendoza et al. 2006) and the USA (Schmitt et al. 1997).

243 There is evidence that *Mycobacterium bovis* strains can spillover from livestock into wild deer hosts  
244 (particularly fallow deer and red deer), and then spillback, reinfesting domestic livestock (Coleman &  
245 Cooke 2001, de Mendoza et al. 2006, Nugent 2011). There is also evidence that bTB can be  
246 maintained in free-ranging cervid populations without infected livestock involvement (Schmitt et al.  
247 1997, O'Brien et al. 2006), although there is a scarcity of data showing this for red, fallow, sambar or  
248 hog deer. Wild deer populations appear to have the capacity to act as maintenance hosts for

249 *Mycobacterium bovis*, particularly if they reach high densities (Coleman & Cooke 2001, Nugent  
250 2011), or are highly aggregated (Ramsey et al. 2014), leading to outbreaks of bTB in livestock  
251 (Schmitt et al. 1997, Ramsey et al. 2014). Evidence from New Zealand suggests that deer could play a  
252 role in initiating new outbreaks of bTB outside infection areas through dispersal, or can reinstate  
253 infection after it has been eliminated in other hosts by acting as a long-lived reservoir of infection  
254 (Ryan et al. 2006, Nugent et al. 2015).

255 Bovine tuberculosis formerly occurred in livestock in Australia, but was eliminated through an  
256 intensive test and slaughter program (Cousins & Roberts 2001). An integral part of the success of the  
257 eradication program was the culling of wild water buffalo *Bubalus bubalis*, which reduced this  
258 species to low numbers and eliminated it as a maintenance host and source of reinfection for cattle  
259 (Cousins & Roberts 2001). A lack of other established wildlife hosts was also seen as a crucial factor  
260 for this success. Failure to eradicate bTB elsewhere (New Zealand, the UK) has generally been  
261 attributed to the presence of a significant wildlife reservoir (i.e. possums and badgers) causing  
262 continual spillback of disease to livestock populations (Tweddle & Livingstone 1994, Palmer 2007).  
263 There has only been one known outbreak of *Mycobacterium bovis* in deer in Australia, which  
264 occurred in three farmed herds of fallow deer and was successfully eliminated through a test and  
265 slaughter program (Robinson et al. 1989).

266 Successful bTB control strategies tend to focus around test and slaughter or segregation of infected  
267 animals, although these strategies are complicated when there is a wildlife reservoir involved.  
268 Culling may decrease transmission by decreasing the population density of the reservoir host.  
269 However, it may not always be an effective method in controlling outbreaks, or be publicly  
270 supported (O'Brien et al. 2011). Vaccination of livestock against *Mycobacterium bovis* tends to occur  
271 when test and slaughter campaigns are not feasible, but the effectiveness of vaccination in wildlife  
272 hosts is yet to be proven (Siembieda et al. 2011). Any outbreak of bTB in wild deer populations  
273 would present a significant risk to the Australian livestock industry and would be costly to eradicate,  
274 resulting in substantial financial losses.

#### 275 ***Aphthae epizooticae* (foot and mouth disease)**

276 *Aphthae epizooticae*, causing foot and mouth disease (FMDV), is a highly contagious viral pathogen  
277 that spreads rapidly among livestock, particularly when animals are housed close together. It affects  
278 cattle, sheep, goats, pigs, and farmed deer, and is spread via the respiratory route, although small  
279 quantities of the pathogen are excreted in the faeces, urine, saliva and other fluids of infected hosts.  
280 There are seven different viral serotypes of FMDV that are disease-causing, and they can persist in  
281 the environment for long periods of time when conditions are favourable (Davies 2002). Although

282 most infected hosts can recover, outbreaks in livestock can have significant economic impacts  
283 (Knight-Jones et al. 2013). Infected animals can excrete the virus for up to four days before showing  
284 clinical signs. FMDV tends to have a higher transmission rate in cattle than in sheep, as cattle tend to  
285 be more susceptible to the disease (Keeling et al. 2001). Outbreaks have historically occurred in  
286 several parts of the world, including Europe, Africa, Asia and the Middle East, and attempts to  
287 control FMDV have a long history (Sutmoller et al. 2003).

288 Although FMDV has been detected in many wildlife species, it appears to cause clinical disease  
289 almost exclusively in livestock (Weaver et al. 2013). Experimental studies in the 1970s showed that  
290 all deer species in the UK, including red and fallow deer, were susceptible to FMDV transmission  
291 when exposed to infected cattle, and could transmit the disease within their own species as well as  
292 to sheep and cattle (Sutmoller et al. 2003). Susceptibility of deer species to FMDV can vary and,  
293 while infection in red and fallow deer is generally subclinical (Simpson 2002), disease persistence can  
294 be high in these two species, increasing transmission risk to livestock. Red deer, for example, shed  
295 similar amounts of the virus to sheep and cattle (Haigh et al. 2002). FMDV infection has been  
296 recorded in six deer species including red and fallow deer (Haigh et al. 2002), and in captive sambar  
297 deer (Weaver et al. 2013). While there is clear experimental evidence of disease transmission  
298 between wild cervids and domestic livestock and vice versa, there is however limited evidence of  
299 this occurring under natural conditions (Weaver et al. 2013, Dhollander et al. 2016). Outside of  
300 Africa, where African buffalo are maintenance hosts, FMDV is maintained mainly in domestic  
301 ruminants, and wildlife occasionally become infected accidentally by spillover (Bengis et al. 2002).  
302 Epidemiological modelling of FMDV spread in deer in Europe has concluded that cervid populations  
303 are unlikely to be able to maintain FMDV for long periods of time without reinfection from domestic  
304 hosts (Dhollander et al. 2016). However, virus circulation may be prolonged when cervid population  
305 densities are high. Disease transmission between deer and domestic livestock is most likely to occur  
306 through direct contact between hosts.

307 Australia is currently free of FMDV and it is a notifiable disease in all states and territories. The  
308 introduction of this disease would have enormous economic impacts, with the costs of an outbreak  
309 of FMDV in Australia estimated to be up to A\$5.2 billion (Buetre et al. 2013). Due to concerns around  
310 these economic impacts, epidemiological modelling for FMDV spread in feral pigs in Australia has  
311 been undertaken (Pech & Hone 1988, Doran & Laffan 2005), and suggests that very high culling rates  
312 of pigs would be required for eradication of FMDV. No literature could be located documenting  
313 comparable modelling of FMDV infection in deer in Australia. FMDV excretion can peak before  
314 clinical signs occur, which means the disease would be very difficult to contain or eradicate if there  
315 was an incursion into Australia, as its spread is rapid.

316 In livestock, FMDV control methods are normally focused around intensive culling (slaughter and  
317 disposal of susceptible livestock) on infected farms and surrounding farms, vaccination, and strict  
318 biosecurity controls for personnel who have contact with infected animals (Sutmoller et al. 2003).  
319 There has been widespread use of vaccination programs in Europe to control the disease, which can  
320 be effective if maintained. As different serotypes are dominant in different parts of the world,  
321 control through vaccination can be difficult because vaccines that are effective against one serotype  
322 will not protect against others. Epidemiological modelling has been used to support decision-making  
323 processes during FMDV outbreaks in livestock, particularly in the UK (Keeling 2005), and could be a  
324 useful tool for modelling similar outbreaks in wildlife. Control strategies for FMDV outbreaks in  
325 wildlife are varied. Culling programs to remove infected animals and reduce density have been used  
326 in Mongolian gazelles *Procapra gutturosa*, while fencing has been successfully used to manage  
327 FMDV transmission between African buffalo and livestock (Weaver et al. 2013).

### 328 **Herpesviruses (malignant catarrhal fever)**

329 Malignant catarrhal fever (MCF) is an infectious viral disease in the gammaherpesvirus group, often  
330 affecting domestic cattle and deer. Three types of the MCF herpesvirus have been identified as  
331 causing disease, with sheep and wildebeest *Connochaetes* spp. identified as asymptomatic carriers  
332 or natural hosts (Heuschele et al. 1984). These two natural hosts act as reservoirs, causing spillover  
333 infection in other species that then experience severe clinical disease. A feature of MCF in cattle is  
334 that outbreaks are unpredictable and sporadic, and infection typically occurs following close contact  
335 with sheep that are actively shedding (Callan & Van Metre 2004). Transmission is predominantly  
336 respiratory, and direct contact with a natural host is not necessarily required - wind-borne infection  
337 has also been documented (Haigh et al. 2002). Vertical transfer of infection between a female and  
338 her offspring (transplacentally) can also occur. All herpesviruses can establish latent infections  
339 (where there is a dormant phase to their life cycle, Engels & Ackermann 1996), which allows the  
340 virus to persist in a population for long periods, with periodic reactivation then posing a risk for  
341 transmission to domestic or wild animals.

342 Wildlife hosts infected with MCF include mostly wild ruminants (Heuschele et al. 1984) and there is  
343 abundant evidence that MCF occurs in free-ranging cervids (Heuschele et al. 1984, Li et al. 1996).  
344 Indeed, MCF is considered one of the most important diseases of farmed deer due to its high  
345 mortality rates (Reid & Buxton 1984). MCF has been reported in 14 species of deer, including five of  
346 the Australian species – red, fallow, chital, sambar and hog deer (Heuschele et al. 1984, Semiadi et  
347 al. 1994, Haigh et al. 2002). Stress seems to play a significant role in disease outbreaks, with  
348 infection peaking when conditions are crowded and during winter and spring, when deer may be in

349 poorer condition (Haigh et al. 2002). Deer appear to be particularly susceptible and death often  
350 occurs within 48 hours of the first clinical signs (Jesser 2005). However, the evidence suggests that  
351 deer are not significant maintenance hosts, but tend to be spillover hosts, acquiring the infection  
352 primarily from sheep (Reid et al. 1979).

353 MCF occurs sporadically in Australia and mainly in cattle. Outbreaks in captive deer have been  
354 documented in Australia (Tomkins et al. 1997), and lesions consistent with MCF were described by  
355 Presidente (1978) in captive Javan rusa deer in Victoria, but the virus could not be isolated and  
356 confirmed as that causing MCF. No effective treatment or vaccine for MCF has been described. In  
357 the absence of a vaccine, the best strategy appears to be limiting contact between susceptible  
358 species, for example, deer and the natural host, sheep (Callan & Van Metre 2004).

### 359 ***Trypanosoma evansi* (surra)**

360 *Trypanosoma evansi* is a protozoan that causes the disease trypanosomiasis or surra in vertebrate  
361 animals. *Trypanosoma evansi* is transmitted mechanically by various species of tabanid flies  
362 (horseflies). It is found over a wide range of climates, but is more common in the tropics. The main  
363 host species affected by *Trypanosoma evansi* depends on the predominant mammalian species in a  
364 region, as it has a wide host range (Reid 2002). *Trypanosoma evansi* has become established in wild  
365 reservoirs all over the world, mostly as a consequence of moving infected livestock. Deer, including  
366 sambar and hog deer (Desquesnes et al. 2013), are susceptible to *Trypanosoma evansi*, however  
367 reports of surra in deer are not particularly common. As deer may tolerate a heavy burden  
368 of *Trypanosoma evansi* without showing any clinical signs, they can be an efficient reservoir of the  
369 pathogen (Reid et al. 1999).

370 The only known introduction of *Trypanosoma evansi* into Australia was in camels *Camelus*  
371 *dromedarius* and *Camelus bactrianus* imported from India to Port Hedland, Western Australia, in  
372 1907 (Reid 2002), and this incursion was rapidly eradicated through the slaughter of infected  
373 animals. Today, the likely route of introduction would be via eastward spread into Papua New  
374 Guinea and then across the islands of the Torres Strait (Reid 2002). *Trypanosoma evansi* is a  
375 substantial threat for Australia and has the potential to become endemic, firstly because tabanid  
376 vectors are common, and secondly because there are large populations of potential reservoir hosts,  
377 such as feral pigs, in many areas where livestock occur (Reid 2002). It is a notifiable disease in all  
378 states and territories. Although small outbreaks of surra have been eradicated in Australia and  
379 elsewhere, no country is known to have eliminated the disease once it has become well established  
380 (Desquesnes et al. 2013). Increasing populations of feral deer would be likely to act as reservoirs and  
381 could contribute to disease establishment, should it reach Australia.

### 382 ***Chrysomya bezziana* (screw-worm fly infestation)**

383 The Old World screw-worm fly *Chrysomya bezziana* is a parasitic insect pest that is endemic to the  
384 tropical regions of Asia, the Middle East and Africa. The insect reproduces by laying its eggs in open  
385 wounds and mucus membranes of mammals. Upon hatching, the fly larvae eat the living flesh of the  
386 host, causing injury (cutaneous myiasis), secondary infections and in extreme cases, death.  
387 *Chrysomya bezziana* has been found in free-ranging sambar deer in India (Radhakrishnan et al. 2012)  
388 and in captive Persian fallow deer (*Dama dama mesopotamica*, Mombeni et al. 2014). In Papua New  
389 Guinea, Javan rusa deer are likely to be maintenance hosts of *Chrysomya bezziana* (Spradbery &  
390 Tozer 2013). No literature on its occurrence in other wild deer species could be located. Currently  
391 the Australian mainland is free of *Chrysomya bezziana*, and although its distribution is relatively  
392 static, its range includes Australia's tropical northern neighbours such as Indonesia, Malaysia and  
393 Papua New Guinea. Due to the close geographical location of *Chrysomya bezziana* range and the  
394 shipping traffic to and from Australian ports, there is a risk of introduction of this species to Australia  
395 through importation of the insect, particularly in northern Australia (Welch et al. 2014). Increasing  
396 populations of wild deer would be likely to act as reservoirs and further contribute to spread of the  
397 parasite, should it reach Australia.

## 398 **DISCUSSION**

### 399 **Diseases of deer and potential threats to Australian livestock**

400 In total, we considered eight bacterial, eight viral, one prion, 13 helminth, six protozoan, and two  
401 ectoparasitic diseases (Table 2, Appendix S3) affecting deer and livestock species. Many of the  
402 pathogens are zoonoses and pose a risk of disease in humans as well. There is substantial literature  
403 describing infectious diseases in deer, but very little of this is focused on deer in Australia. Indeed,  
404 there is a scarcity of recent information describing basic screening of diseases in deer found in  
405 Australia. Also of note was the deficiency of information available in the literature about the  
406 pathogens infecting Asian deer species, such as sambar deer or hog deer, which makes it difficult to  
407 assess their susceptibility and their potential contribution to disease risk in Australia. By far the  
408 overwhelming majority of studies of cervid diseases relevant to Australia have come from research  
409 in the UK on red and fallow deer (reviewed by Böhm et al. 2007).

410 We focused this review on a range of infectious agents that have the potential to be shared between  
411 domestic livestock and wild deer and are likely to be of economic importance to livestock farming.  
412 Given the current paucity of information, we found it particularly difficult to estimate the impact of  
413 diseases that are currently present within Australia, and for which an increase in deer abundance or

414 range may affect their incidence. The overall disease risk for the majority of pathogens was found to  
415 be low, which was supported by the lack of evidence for clinical infection in deer to date. However,  
416 some diseases, such as anthrax and bluetongue, which are currently present in Australia, are  
417 considered to be medium risk based on a relatively low risk of transmission to or from livestock and  
418 the moderate potential economic impacts they could have if wild deer were to play a role in future  
419 outbreaks. Risk may be greatly underestimated if there is significant uncertainty around diseases  
420 scored as 'medium' or 'low' due to limited knowledge of these diseases. The impact of variation in  
421 knowledge and disease ranking would be worthy of further investigation.

422 Of the pathogens we considered, the majority are transmitted by contact with, or ingestion of,  
423 contaminated excretory products in the environment, mostly via the faecal-oral route. Experimental  
424 and natural transmission studies in deer have provided disease-specific evidence for the  
425 transmission of many of the pathogens we examined. However, common susceptibility to a disease  
426 does not necessarily equate to shared infection. Few studies have examined the natural  
427 transmission of pathogens between livestock and deer, and modes of transmission are still not fully  
428 understood in many cases (Frölich et al. 2002). The existence of a pathogen in either wild deer or  
429 domestic ruminants is irrelevant to establishment of the disease in the other if the two populations  
430 do not interact, either directly or indirectly (Hartley et al. 2013). A recent review by Pruvot et al.  
431 (2014) also suggests that transmission route can be important when assessing the risk of pathogens  
432 spreading between domestic and wild animals; indirectly transmitted pathogens are more easily  
433 shared between species than directly transmitted ones, because they do not require a strict  
434 temporal or spatial sympatry. Future work in Australia should focus on quantifying contact rates  
435 between deer and livestock, in order to improve estimates of infection likelihood. This can be done  
436 by using proximity loggers or animal-borne cameras, as demonstrated by Lavelle et al. (2014), or by  
437 using molecular markers (Streicker et al. 2010, Allison et al. 2013, Faria et al. 2013).

#### 438 **Influence of deer ecology and density on disease risk**

439 The behavioural ecology of each deer species influences its exposure risk to different diseases.  
440 Sharing of habitat with livestock, as has been reported in sambar deer in Victoria, Australia  
441 (Lindeman & Forsyth 2008), increases the risk of transmission via fomites, vector and aerosol spread.  
442 Riparian habitat within agricultural regions can exacerbate disease risk, as deer may concentrate in  
443 these areas, increasing between-group contact rates and spatial overlap (Nobert et al. 2016). Social  
444 behaviour affects transmission between wild deer, as the number of contacts between conspecific  
445 individuals influences the ability of a disease to become established (Hartley et al. 2013). Most deer  
446 species present in Australia are gregarious (with the exception of sambar deer and hog deer),



447 forming large groups and thus increase the probability of disease spread (Animal Health Australia  
448 2011, Sah et al. 2018). This may be especially relevant for two of the highly ranked diseases, bovine  
449 tuberculosis and foot and mouth disease. Male cervids may contribute disproportionately to the risk  
450 of transmission, through contact with multiple females during the breeding season across a range of  
451 spatial scales; or through contact with infectious agents at scent stations (Conner et al. 2008).  
452 Moreover, breeding interactions may leave male deer in poor condition and susceptible to disease.

453 The size of the host's home range influences the potential for disease transmission to livestock and  
454 other deer herds, as it indicates the likely extent of movement of individual infected animals, and  
455 therefore the geographical range over which each animal could transmit disease. In cervids, juvenile  
456 males disperse from their natal home range, which could also contribute to the spread of disease  
457 and movement of infection into new areas (Conner et al. 2008). Seasonal changes in food availability  
458 may result in animals frequently making short-distance movements to more suitable habitats or  
459 food sources (Conner et al. 2008), which may bring them into contact with livestock or cause them  
460 to transmit disease to deer in uninfected areas. Unfortunately, little is known about the home range  
461 sizes and seasonal movements of any of the deer species in Australia.

462 Current and future range expansions of deer into new locations may result in disease establishment  
463 there, as these new environmental conditions may be more suitable for certain diseases. Range  
464 expansions will also increase the risk of deer encountering other cervid species, livestock and farmed  
465 deer. If deer expand into areas of high livestock density, disease establishment and maintenance in  
466 the host deer population and spillback to livestock will become more likely (Böhm et al. 2007). The  
467 risk of both direct and indirect disease transmission will be influenced by host density, and there is  
468 likely to be a greater risk of transmission in areas of both high livestock density and high deer  
469 density. Increasing deer abundance means an increased number of hosts available for the  
470 transmission of disease, and a higher contact rate between hosts. These issues are likely to be  
471 particularly relevant for three of the highly ranked diseases, bovine tuberculosis, foot and mouth  
472 disease and malignant catarrhal fever, because high host densities can result in the disease  
473 becoming established in the deer population. When sympatric host species share the same  
474 infectious disease, multiple transmission pathways are possible (Woolhouse et al. 2001, Barron et al.  
475 2015). Under such circumstances, multiple hosts can act as one large heterogeneous host  
476 population, potentially exacerbating disease transmission and spread (Dobson 2004). Consequently,  
477 increases in deer abundance may exacerbate the potential for disease persistence and spread in  
478 livestock-deer communities.

479

**480 Conclusion**

481 Deer have the potential to play a significant role in the epidemiology of multiple livestock diseases,  
482 both those that are currently present in Australia, and those that are absent, but have the potential  
483 to become established in the future. Of the 38 pathogens we reviewed, five of these classify as of a  
484 high risk for transmission by deer to Australian livestock. Of these five diseases, only one (malignant  
485 catarrhal fever) is currently present in Australia, but all five are notifiable diseases at a national level.  
486 Our review has revealed that there is little understanding or discussion of disease risks in deer within  
487 the Australian literature. This is especially concerning as deer populations are large and expanding,  
488 and it is likely that the eradication of exotic diseases through culling would be very challenging.  
489 Furthermore, sambar deer and hog deer pose potential risks due to the dearth in understanding of  
490 the ecology and disease epidemiology of these two species.

491 Our disease risk assessment can assist decision-makers by outlining high, medium and low risks of  
492 diseases of concern. However, improvements in disease monitoring of Australian deer are required  
493 to provide timely knowledge on disease incursion and spread, in order to minimise the risk of  
494 impacts on both humans and livestock. At present, there are no disease surveillance programs  
495 targeting deer in Australia. Hence, the feasibility of large-scale surveillance strategies for detecting  
496 incursions of exotic disease or outbreaks of endemic disease in Australian deer populations should  
497 be investigated. Large-scale surveillance programs of wild deer could be based on hunter-harvested  
498 deer or on other forms of passive surveillance (e.g. public reporting of moribund or dead deer).  
499 Successful examples of such passive surveillance programs utilising hunter-harvested deer include  
500 bovine tuberculosis surveillance programs in France (Rivière et al. 2015) and in lower Michigan, USA  
501 (O'Brien et al. 2006). These programs could serve as models for a surveillance program in Australia.

502 We apply the disease risk assessment to the Australian context, and provide a framework that can  
503 easily be adapted to different contexts. For example, in other locations where livestock farming is  
504 less extensive than in Australia, the three categories ('presence', 'distribution' and 'transmission')  
505 which are used to calculate the 'infected' score, can be altered as required. Our review highlights  
506 how a qualitative risk assessment can be used to ascertain which diseases pose the highest risk and  
507 where gaps in knowledge inhibit our understanding and risk of disease transmission, making our  
508 approach relevant to scientists, wildlife managers, and livestock industry workers worldwide.

**509 ACKNOWLEDGEMENTS**

510 This review was commissioned and funded by the Department of Economic Development, Jobs,  
511 Transport and Resources, Victoria, Australia (DEDJTR). We thank Nicky Buller and Sam Hair

512 (Department of Agriculture and Food, Western Australia) and Peter Menkhorst and Lindy Lumsden  
513 (Department of Environment, Land, Water and Planning, Victoria, Australia) for comments on an  
514 early version. The suggestions of two anonymous referees greatly improved the first draft of the  
515 manuscript.

516

## 517 **SUPPORTING INFORMATION**

518

519 Additional supplemental material may be found online in the Supporting Information section at the  
520 end of the article.

521

522 **Appendix S1.** Web of Science, Scopus and Google Scholar search terms used to review the literature  
523 on the pathogens of deer and livestock and disease risk.

524 **Appendix S2.** Notes on the process of assessing the risk of disease entry into Australia.

525 **Appendix S3.** Summary details on diseases ranked as 'low' or 'medium' in the disease risk  
526 assessment.

527

## 528 **REFERENCES**

529 Allison AB, Kohler DJ, Fox KA, Brown JD, Gerhold RW, Shearn-Bochsler VI, Dubovi EJ, Parrish CR,  
530 Holmes EC (2013) Frequent cross-species transmission of parvoviruses among diverse carnivore  
531 hosts. *Journal of Virology* 87: 2342-2347.

532 Andrews JRH (1973) A host-parasite checklist of helminths of wild ruminants in New Zealand. *New*  
533 *Zealand Veterinary Journal* 21: 43-47.

534 Animal Health Australia (2011) *Wild Animal Response Strategy (Version 3.3)*. Australian Veterinary  
535 Emergency Plan (AUSVETPLAN), Edition 3, Primary Industries Ministerial Council, Canberra, Australia.  
536 <https://www.animalhealthaustralia.com.au/our-publications/ausvetplan-manuals-and-documents/>

537 Animal Health Australia (2017) *Animal Health in Australia 2016*. Animal Health Australia, Canberra,  
538 Australia.

539 [https://www.animalhealthaustralia.com.au/wp-content/uploads/AHIA-Document\\_digital\\_FA.pdf](https://www.animalhealthaustralia.com.au/wp-content/uploads/AHIA-Document_digital_FA.pdf)

540 Barré N, Bianchi M, de Garine-Wichatitsky M (2002) Effect of the association of cattle and rusa deer  
541 *Cervus timorensis rusa* on populations of cattle ticks (*Boophilus microplus*). *Annals of the New York*  
542 *Academy of Sciences* 969: 280-289.

- 543 Barron DG, Gervasi SS, Pruitt JN, Martin LB. (2015) Behavioral competence: how host behaviors can  
544 interact to influence parasite transmission risk. *Current Opinion in Behavioral Sciences* 6: 35-40.
- 545 Barth D, Matzke P (1984) Gastrointestinal nematodes of fallow deer (*Dama dama* L.) in Germany.  
546 *Veterinary Parasitology* 16: 173-176.
- 547 Bengis RG, Kock RA, Fischer J (2002) Infectious animal diseases: the wildlife/livestock interface.  
548 *Revue Scientifique et Technique (International Office of Epizootics)* 21: 53-66.
- 549 Bisset SA (1980) Species involved in ostertagiasis in calves. *New Zealand Veterinary Journal* 28: 54.
- 550 Böhm M, White PC, Chambers J, Smith L, Hutchings M (2007) Wild deer as a source of infection for  
551 livestock and humans in the UK. *The Veterinary Journal* 174: 260–276.
- 552 Buetre B, Wicks S, Kruger H, Millist N, Yainshet A, Garner G et al. (2013) *Potential Socio-economic*  
553 *Impacts of an Outbreak of Foot-and-mouth Disease in Australia*. Research report, Australian Bureau  
554 of Agricultural and Resource Economics and Sciences, Canberra, Australia.  
555 <http://apo.org.au/system/files/35972/apo-nid35972-14146.pdf>
- 556 Burgin S, Mattila M, McPhee D, Hundloe T (2015) Feral deer in the suburbs: an emerging issue for  
557 Australia? *Human Dimensions of Wildlife* 20: 65-80.
- 558 Callan RJ, Van Metre DC (2004) Viral diseases of the ruminant nervous system. *Veterinary Clinics of*  
559 *North America: Food Animal Practice* 20: 327-362.
- 560 Chintoan-Uta C, Morgan ER, Skuce PJ, Coles GC (2014) Wild deer as potential vectors of  
561 anthelmintic-resistant abomasal nematodes between cattle and sheep farms. *Proceedings of the*  
562 *Royal Society of London B: Biological Sciences* 281: 20132985.
- 563 Cleaveland S, Laurenson MK, Taylor LH (2001) Diseases of humans and their domestic mammals:  
564 pathogen characteristics, host range and the risk of emergence. *Philosophical Transactions of the*  
565 *Royal Society of London B: Biological Sciences* 356: 991-999.
- 566 Clout MN, Russell JC (2008) The invasion ecology of mammals: a global perspective. *Wildlife*  
567 *Research* 35: 180-184.
- 568 Coelho AC, Matos A, Matos M, de Lurdes Pinto M, dos Anjos Pires M (2013) *Mycobacterium avium*  
569 *Complex in Domestic and Wild Animals*. Insights from Veterinary Medicine. *INTECH Open Access*  
570 *Publisher*. DOI: 10.5772/54323. Available from: [https://www.intechopen.com/books/insights-from-](https://www.intechopen.com/books/insights-from-veterinary-medicine/mycobacterium-avium-complex-in-domestic-and-wild-animals)  
571 [veterinary-medicine/mycobacterium-avium-complex-in-domestic-and-wild-animals](https://www.intechopen.com/books/insights-from-veterinary-medicine/mycobacterium-avium-complex-in-domestic-and-wild-animals)

- 572 Coleman JD (1988) Distribution, prevalence, and epidemiology of bovine tuberculosis in brushtail  
573 possums, *Trichosurus vulpecula*, in the Hohonu Range, New-Zealand. *Wildlife Research* 15: 651-663.
- 574 Coleman JD, Cooke MM (2001) *Mycobacterium bovis* infection in wildlife in New Zealand.  
575 *Tuberculosis* 81: 191-202.
- 576 Conner MM, Ebinger MR, Blanchong JA, Cross PC (2008) Infectious disease in cervids of North  
577 America. *Annals of the New York Academy of Sciences* 1134: 146-172.
- 578 Corbel MJ (1997) Brucellosis: an overview. *Emerging Infectious Diseases* 3: 213-221.
- 579 Cousins D, Roberts J (2001) Australia's campaign to eradicate bovine tuberculosis: the battle for  
580 freedom and beyond. *Tuberculosis* 81: 5–15.
- 581 Cross PC, Getz WM (2006) Assessing vaccination as a control strategy in an ongoing epidemic: bovine  
582 tuberculosis in African buffalo. *Ecological Modelling* 196: 494-504.
- 583 Dauschies A, Najdrowski M (2005) Eimeriosis in cattle: current understanding. *Journal of Veterinary*  
584 *Medicine, Series B* 52: 417-427.
- 585 Davies G (2002) Foot and mouth disease. *Research in Veterinary Science* 73: 195-199.
- 586 Davis NE, Bennett A, Forsyth DM, Bowman DM, Lefroy EC, Wood SW et al. (2016) A systematic  
587 review of the impacts and management of introduced deer (family Cervidae) in Australia. *Wildlife*  
588 *Research* 43: 515-532.
- 589 de Lisle GW, Mackintosh CG, Bengis RG (2001) *Mycobacterium bovis* in free-living and captive  
590 wildlife, including farmed deer. *Revue Scientifique et Technique (International Office of Epizootics)*  
591 20: 86-111.
- 592 de Mendoza JH, Parra A, Tato A, Alonso JM, Rey JM, Pena, J et al. (2006) Bovine tuberculosis in wild  
593 boar (*Sus scrofa*), red deer (*Cervus elaphus*) and cattle (*Bos taurus*) in a Mediterranean ecosystem  
594 (1992–2004). *Preventive Veterinary Medicine* 74: 239-247.
- 595 Australian Department of Agriculture and Water Resources (2018). Biosecurity Import Risk Analysis.  
596 Australian Department of Agriculture and Water Resources, Canberra, Australia.  
597 <http://www.agriculture.gov.au/biosecurity/risk-analysis/conducting>
- 598 Desquesnes M, Holzmuller P, Lai DH, Dargantes A, Lun ZR, Jittaplapong S (2013) *Trypanosoma evansi*  
599 and surra: a review and perspectives on origin, history, distribution, taxonomy, morphology, hosts,  
600 and pathogenic effects. *BioMed Research International* 2013: 1-22.

- 601 Dhollander S, Belsham GJ, Lange M, Willgert K, Alexandrov T, Chondrokouki E et al. (2016) Assessing  
602 the potential spread and maintenance of foot-and-mouth disease virus infection in wild ungulates:  
603 general principles and application to a specific scenario in Thrace. *Transboundary and Emerging*  
604 *Diseases* 63: 165-174.
- 605 Dobson A (2004) Population dynamics of pathogens with multiple host species. *The American*  
606 *Naturalist* 164: S64-S78.
- 607 Donahoe SL, Lindsay SA, Krockenberger M, Phalen D, Šlapeta J (2015) A review of neosporosis and  
608 pathologic findings of *Neospora caninum* infection in wildlife. *International Journal for Parasitology:*  
609 *Parasites and Wildlife* 4: 216-238.
- 610 Doran RJ, Laffan SW (2005) Simulating the spatial dynamics of foot and mouth disease outbreaks in  
611 feral pigs and livestock in Queensland, Australia, using a susceptible-infected-recovered cellular  
612 automata model. *Preventive Veterinary Medicine* 70: 133-152.
- 613 Dubey JP (1999) Recent advances in *Neospora* and neosporosis. *Veterinary Parasitology* 84: 349-367.
- 614 Ellis WA (2015) Animal leptospirosis. In: Adler B (eds) *Leptospira and Leptospirosis, Current Topics in*  
615 *Microbiology and Immunology*, 99-137. Springer Berlin Heidelberg, New York, USA.
- 616 Engels M, Ackermann M (1996) Pathogenesis of ruminant herpesvirus infections. *Veterinary*  
617 *Microbiology* 53: 3-15.
- 618 Faria NR, Suchard MA, Rambaut A, Streicker DG, Lemey P (2013) Simultaneously reconstructing viral  
619 cross-species transmission history and identifying the underlying constraints. *Philosophical*  
620 *Transactions of the Royal Society B: Biological Sciences* 368: 20120196.
- 621 Frölich K, Thiede S, Kozikowski T, Jakob W (2002) A review of mutual transmission of important  
622 infectious diseases between livestock and wildlife in Europe. *Annals of the New York Academy of*  
623 *Sciences* 969: 4-13.
- 624 Gallagher J, Clifton-Hadley RS (2000) Tuberculosis in badgers; a review of the disease and its  
625 significance for other animals. *Research in Veterinary Science* 69: 203-217.
- 626 George JE (1990) Wildlife as a constraint to the eradication of *Boophilus* spp. (Acari: Ixodidae).  
627 *Journal of Agricultural Entomology* 7: 119-125.
- 628 Gortázar C, Acevedo P, Ruiz-Fons F, Vicente J (2006) Disease risks and overabundance of game  
629 species. *European Journal of Wildlife Research* 52: 81-87.

- 630 Haigh JC, Mackintosh C, Griffin F (2002) Viral, parasitic and prion diseases of farmed deer and  
631 bison. *Revue Scientifique et Technique (International Office of Epizootics)* 21: 219-248.
- 632 Handeland K, Gibbons LM, Skorping A (2000) Experimental *Elaphostrongylus cervi* infection in sheep  
633 and goats. *Journal of Comparative Pathology* 123: 248-257.
- 634 Hartley M, Voller F, Murray T, Roberts H (2013) Qualitative veterinary risk assessment of the role of  
635 wild deer in the likelihood of incursion and the impact on effective disease control of selected exotic  
636 notifiable diseases in England. *European Journal of Wildlife Research* 59: 257-270.
- 637 Heuschele WP, Oosterhuis J, Anderson MP, Swansen M, Fletcher HR (1984) Malignant catarrhal  
638 fever in wild ruminants. In: Ryder OA, Byrd ML (eds) *One Medicine*, 296-308. Springer Berlin  
639 Heidelberg, New York, USA.
- 640 Horner GW, Robinson AJ, Hunter R, Cox BT, Smith R (1987) Parapoxvirus infections in New Zealand  
641 farmed red deer (*Cervus elaphus*). *New Zealand Veterinary Journal* 35: 41-45.
- 642 Jenkins DJ (2005) Hydatid control in Australia: where it began, what we have achieved and where to  
643 from here. *International Journal for Parasitology* 35: 733-740.
- 644 Jerrett IV, Slee KJ, Robertson BI (1990) Yersiniosis in farmed deer. *Australian Veterinary Journal* 67:  
645 212-214.
- 646 Jesser P (2005) *Deer in Queensland: Pest Status Review Series – Land Protection*. Report. Department  
647 of Natural Resources and Mines, Queensland: Brisbane, Australia.  
648 [https://www.daf.qld.gov.au/data/assets/pdf\\_file/0004/72454/IPA-Deer-PSA.pdf](https://www.daf.qld.gov.au/data/assets/pdf_file/0004/72454/IPA-Deer-PSA.pdf)
- 649 Johnson M, Mackintosh CG, Labes RE, Taylor MJ, Wharton DA (2003) *Dictyocaulus* species: cross  
650 infection between cattle and red deer. *New Zealand Veterinary Journal* 51: 93-98.
- 651 Keeling MJ (2005) Models of foot-and-mouth disease. *Proceedings of the Royal Society of London B:*  
652 *Biological Sciences* 272: 1195-1202.
- 653 Keeling MJ, Woolhouse ME, Shaw DJ, Matthews L, Chase-Topping M, Haydon DT et al. (2001)  
654 Dynamics of the 2001 UK foot and mouth epidemic: stochastic dispersal in a heterogeneous  
655 landscape. *Science* 294: 813-817.
- 656 Knight-Jones TJD, Rushton J (2013) The economic impacts of foot and mouth disease – what are  
657 they, how big are they and where do they occur? *Preventive Veterinary Medicine* 112: 161-173.

- 658 Lavelle MJ, Fischer JW, Phillips GE, Hildreth AM, Campbell TA, Hewitt DG, Hygnstrom SE,  
659 Vercauteren KC (2014) Assessing risk of disease transmission: direct implications for an indirect  
660 science. *BioScience* 64: 524-530.
- 661 Levine ND, Tadros W (1980) Named species and hosts of *Sarcocystis* (Protozoa: Apicomplexa:  
662 Sarcocystidae). *Systematic Parasitology* 2: 41-59.
- 663 Li H, Shen DT, Jessup DA, Knowles DP, Gorham JR, Thorne T, O'Toole D, Crawford TB (1996)  
664 Prevalence of antibody to malignant catarrhal fever virus in wild and domestic ruminants by  
665 competitive-inhibition ELISA. *Journal of Wildlife Diseases* 32: 437-443.
- 666 Lindeman MJ, Forsyth DM (2008) *Agricultural Impacts of Wild Deer in Victoria*. Arthur Rylah Institute  
667 for Environmental Research Technical Report Series No. 182. Department of Sustainability and  
668 Environment, Heidelberg, Victoria, Australia.
- 669 Mackintosh CG (1992) Observations on the relative susceptibility to disease of different species of  
670 deer farmed in New Zealand. In: Brown RD (eds) *The Biology of Deer*, 113-119. Springer Berlin  
671 Heidelberg, New York, USA.
- 672 Mackintosh CG, De Lisle GW, Collins DM, Griffin JFT (2004) Mycobacterial diseases of deer. *New  
673 Zealand Veterinary Journal* 52: 163-174.
- 674 Mackintosh C, Haigh JC, Griffin F (2002) Bacterial diseases of farmed deer and bison. *Revue  
675 Scientifique et Technique (International Office of Epizootics)* 21: 249-264.
- 676 Maclachlan NJ, Zientara S, Savini G, Daniels PW (2015a) Epizootic haemorrhagic disease. *Revue  
677 Scientifique et Technique (International Office of Epizootics)* 34: 341-351.
- 678 Maclachlan NJ, Mayo CE, Daniels PW, Savini G, Zientara S, Gibbs, EP (2015b) Bluetongue. *Revue  
679 Scientifique et Technique (International Office of Epizootics)* 34: 329-340.
- 680 Mair NS (1973) Yersiniosis in wildlife and its public health implications. *Journal of Wildlife Diseases* 9:  
681 64-71.
- 682 Malcicka M (2015) Life history and biology of *Fascioloides magna* (Trematoda) and its native and  
683 exotic hosts. *Ecology and Evolution* 5: 1381-1397.
- 684 McKenzie RA (1985) *Deer Farming Techniques and Diseases of Deer in Queensland*. Report,  
685 Queensland Department of Primary Industries, Brisbane, Queensland, Australia.



- 686 Meat and Livestock Australia (2017). *Beef and Sheepmeat Fast Facts*. Meat and Livestock Australia  
687 Limited, Australia. <https://www.mla.com.au/prices-markets/Trends-analysis/fast-facts/>
- 688 Miller RS, Farnsworth ML, Malmberg JL (2013) Diseases at the livestock–wildlife interface: status,  
689 challenges, and opportunities in the United States. *Preventive Veterinary Medicine* 110: 119-132.
- 690 Mohamad KY, Rodolakis A (2010) Recent advances in the understanding of *Chlamydophila pecorum*  
691 infections, sixteen years after it was named as the fourth species of the Chlamydiaceae family.  
692 *Veterinary Research* 41: 27.
- 693 Moloney PD, Turnbull JD (2018) *Estimates of the 2017 Deer Harvest in Victoria: Results from Surveys*  
694 *of Victorian Game Licence Holders in 2017*. Unpublished report for the Game Management  
695 Authority. Arthur Rylah Institute for Environmental Research, Department of Environment, Land,  
696 Water and Planning, Heidelberg, Victoria.
- 697 Mombeni EG, Mombeini MG, Khalaj M, Garavand MM, Rezaei AA, Lahijan-zadeh A, Kenarkohi M,  
698 Mola SA, Hosseini SK (2014) Management and control of an outbreak of fatal traumatic myiasis due  
699 to *Chrysomya bezziana* in a herd of Persian fallow deer (*Dama dama mesopotamica*). *Journal of*  
700 *Veterinary Science and Technology* 5: 157.
- 701 Nandi S, Negi BS (1999) Bovine ephemeral fever: a review. *Comparative Immunology, Microbiology*  
702 *and Infectious Diseases* 22: 81-91.
- 703 Nettleton PF, Thiry E, Reid H, Pastoret PP (1988) Herpesvirus infections in Cervidae. *Revue*  
704 *Scientifique et Technique (International Office of Epizootics)* 7: 977-988.
- 705 Nishi JS, Shury T, Elkin BT (2006) Wildlife reservoirs for bovine tuberculosis (*Mycobacterium bovis*) in  
706 Canada: strategies for management and research. *Veterinary Microbiology* 112: 325-338.
- 707 Nobert BR, Merrill EH, Pybus MJ, Bollinger TK, Hwang YT (2016) Landscape connectivity predicts  
708 chronic wasting disease risk in Canada. *Journal of Applied Ecology* 53: 1450-1459.
- 709 Nugent G (2011) Maintenance, spillover and spillback transmission of bovine tuberculosis in multi-  
710 host wildlife complexes: a New Zealand case study. *Veterinary Microbiology* 151: 34-42.
- 711 Nugent G, Gortazar C, Knowles G (2015) The epidemiology of *Mycobacterium bovis* in wild deer and  
712 feral pigs and their roles in the establishment and spread of bovine tuberculosis in New Zealand  
713 wildlife. *New Zealand Veterinary Journal* 63: 54-67.
- 714 O'Reilly LM, Daborn CJ (1995) The epidemiology of *Mycobacterium bovis* infections in animals and  
715 man: a review. *Tubercle and Lung Disease* 76: 1-46.

- 716 O'Brien DJ, Schmitt SM, Fitzgerald SD, Berry DE, Hickling GJ (2006) Managing the wildlife reservoir of  
717 *Mycobacterium bovis*: the Michigan, USA, experience. *Veterinary Microbiology* 112: 313-323.
- 718 O'Brien DJ, Schmitt SM, Rudolph BA, Nugent G. (2011) Recent advances in the management of  
719 bovine tuberculosis in free-ranging wildlife. *Veterinary Microbiology* 151: 23-33.
- 720 O'Toole A, Browne JA, Hogan S, Bassière T, DeWaal T, Mulcahy G, Zintl A (2014) Identity of rumen  
721 fluke in deer. *Parasitology Research* 113: 4097-4103.
- 722 Palmer MV (2007) Tuberculosis: a reemerging disease at the interface of domestic animals and  
723 wildlife. In: Childs JE, Mackenzie JS, Richt JA (eds) *Wildlife and Emerging Zoonotic Diseases: the*  
724 *Biology, Circumstances and Consequences of Cross-species Transmission*, 195-215. Springer Berlin  
725 Heidelberg, New York, USA.
- 726 Pech RP, Hone J (1988) A model of the dynamics and control of an outbreak of foot and mouth  
727 disease in feral pigs in Australia. *Journal of Applied Ecology* 25: 63-77.
- 728 Power AG, Mitchell CE (2004) Pathogen spillover in disease epidemics. *The American Naturalist* 164:  
729 S79-S89.
- 730 Presidente PJ (1978) Diseases and parasites of captive rusa and fallow deer in Victoria. *Australian*  
731 *Deer* 3: 23-38.
- 732 PricewaterhouseCoopers (2011) The Australian Beef Industry.  
733 <http://www.pwc.com.au/industry/agribusiness/assets/australian-beef-industry-nov11.pdf>
- 734 Pruvot M, Kutz S, Van Der Meer F, Musiani M, Barkema HW, Orsel K (2014) Pathogens at the  
735 livestock-wildlife interface in Western Alberta: does transmission route matter? *Veterinary Research*  
736 45: 1-12.
- 737 Radhakrishnan S, Gopalan AKK, Ravindran R, Rajagopal K, Sooryadas S, Promod K (2012) First record  
738 of *Chrysomya albiceps* Wiedemann, 1819 (Diptera: Calliphoridae) maggots from a sambar deer (*Rusa*  
739 *unicolor*) in Kerala, South India. *Journal of Parasitic Diseases* 36: 280-282.
- 740 Ramsey DS, O'Brien DJ, Cosgrove MK, Rudolph BA, Locher AB, Schmitt SM (2014) Forecasting  
741 eradication of bovine tuberculosis in Michigan white-tailed deer. *The Journal of Wildlife*  
742 *Management* 78: 240-254.
- 743 Rehbein S, Haupt W (1994) Possibilities of contagion of gastrointestinal and lung nematode  
744 infections of fallow deer for cattle, sheep and goats raised in the same fenced area as fallow  
745 deer. *Deutsche Tierärztliche Wochenschrift* 101: 456-460.

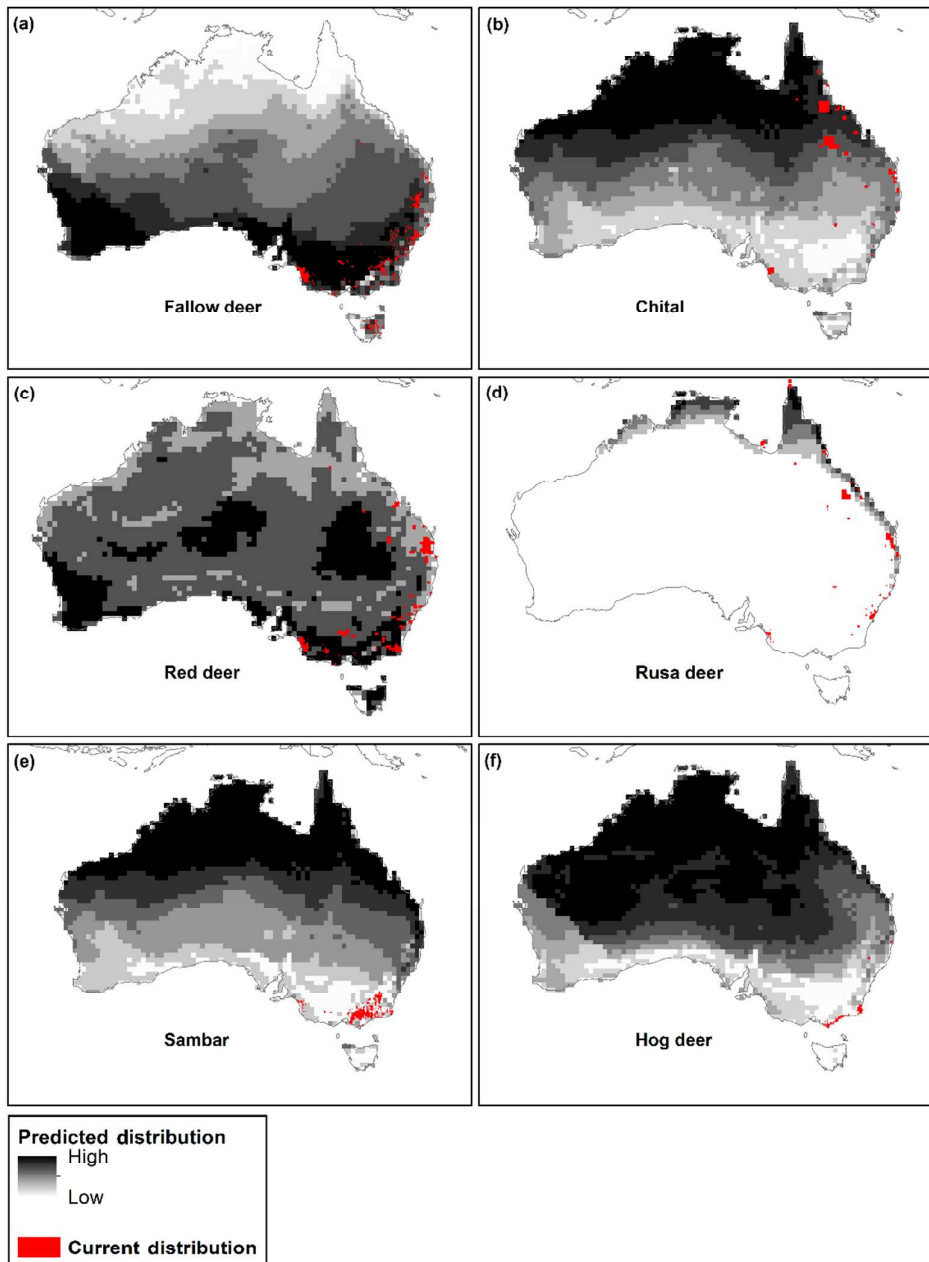
- 746 Reid HW, Buxton D. (1984) Malignant catarrhal fever of deer. *Proceedings of the Royal Society of*  
747 *Edinburgh. Section B. Biological Sciences* 82: 261-273.
- 748 Reid HW, Buxton D, Corrigall W, Hunter AR, McMartin DA, Rushton R (1979) An outbreak of  
749 malignant catarrhal fever in red deer (*Cervus elephus*). *The Veterinary Record* 104: 120-123.
- 750 Reid SA (2002) *Trypanosoma evansi* control and containment in Australasia. *Trends in*  
751 *Parasitology* 18: 219-224.
- 752 Reid SA, Husein A, Hutchinson GW, Copeman DB (1999) A possible role for rusa deer (*Cervus*  
753 *timorensis rusa*) and wild pigs in spread of *Trypanosoma evansi* from Indonesia to Papua New  
754 Guinea. *Memorias do Instituto Oswaldo Cruz* 94: 195-197.
- 755 Rhyan JC, Spraker TR (2010) Emergence of diseases from wildlife reservoirs. *Veterinary Pathology*  
756 *Online* 47: 34-39.
- 757 Rivière J, Strat Y Le, Dufour B, Hendriks P (2015) Sensitivity of bovine tuberculosis surveillance in  
758 wildlife in France: a scenario tree approach. *PLoS ONE*, 10: 1–18.
- 759 Robinson RC, Phillips PH, Stevens G, Storm PA (1989) An outbreak of *Mycobacterium bovis* infection  
760 in fallow deer (*Dama dama*). *Australian Veterinary Journal* 66: 195-197.
- 761 Ryan TJ, Livingstone PG, Ramsey DSL, De Lisle GW, Nugent G, Collins DM, Buddle BM (2006)  
762 Advances in understanding disease epidemiology and implications for control and eradication of  
763 tuberculosis in livestock: the experience from New Zealand. *Veterinary Microbiology* 112: 211-219.
- 764 Ryan U, Power M (2012) *Cryptosporidium* species in Australian wildlife and domestic animals.  
765 *Parasitology* 139: 1673-1688.
- 766 Sah P, Mann J, Bansal S (2018) Disease implications of animal social network structure: a synthesis  
767 across social systems. *Journal of Animal Ecology*. 87: 1-13.
- 768 Salinas J, Caro MR, Vicente J, Cuello F, Reyes-Garcia AR, Buendía AJ, Rodolakis A, Gortázar C (2009)  
769 High prevalence of antibodies against Chlamydiaceae and *Chlamydophila abortus* in wild ungulates  
770 using two “in house” blocking-ELISA tests. *Veterinary Microbiology* 135: 46-53.
- 771 Samuel WM, Pybus MJ, Kocan AA (eds; 2001) *Parasitic Diseases of Wild Mammals*. Iowa State  
772 University Press, Ames, Iowa, USA.
- 773 Sanchez S, Hofacre CL, Lee MD, Maurer JJ, Doyle MP (2002) Animal sources of salmonellosis in  
774 humans. *Journal of the American Veterinary Medical Association* 221: 492-497.

- 775 Scagliarini A, Vaccari F, Turrini F, Bianchi A, Cordioli P, Lavazza, A (2011) Parapoxvirus infections of  
776 red deer, Italy. *Emerging Infectious Diseases* 17: 684-688.
- 777 Schmitt SM, Fitzgerald SD, Cooley TM, Bruning-Fann CS, Sullivan L, Berry D et al. (1997) Bovine  
778 tuberculosis in free-ranging white-tailed deer from Michigan. *Journal of Wildlife Diseases* 33: 749–  
779 758.
- 780 Semiadi G, Muir PD, Barry TN (1994) General biology of sambar deer (*Cervus unicolor*) in  
781 captivity. *New Zealand Journal of Agricultural Research* 37: 79-85.
- 782 Siembieda JL, Kock RA, McCracken TA, Newman SH (2011) The role of wildlife in transboundary  
783 animal diseases. *Animal Health Research Reviews* 12: 95-111.
- 784 Simpson V (2002) Wild animals as reservoirs of infectious diseases in the UK. *The Veterinary Journal*  
785 163: 128–146.
- 786 Skuce PJ, Zadoks RN (2013) Liver fluke—a growing threat to UK livestock production. *Cattle*  
787 *Practice* 21: 138-149.
- 788 Spradbery P, Tozer RS (2013) Trapping Old World screw-worm fly, *Chrysomya bezziana* Villeneuve  
789 (Diptera: Calliphoridae), in Papua New Guinea including the coastal border with Torres Strait.  
790 *Australian Journal of Entomology* 52: 164-167.
- 791 St George TD (1988) Bovine ephemeral fever: a review. *Tropical Animal Health and Production* 20:  
792 194-202.
- 793 Streicker DG, Turmelle AS, Vonhof MJ, Kuzmin IV, McCracken GF, Rupprecht CE (2010) Host  
794 phylogeny constrains cross-species emergence and establishment of rabies virus in bats. *Science*  
795 329: 676-679.
- 796 Sutmoller P, Barteling SS, Olascoaga RC, Sumption KJ (2003) Control and eradication of foot-and-  
797 mouth disease. *Virus Research* 91: 101-144.
- 798 Tapia-Escárate D, Pomroy WE, Scott I, Wilson PR, Lopez-Villalobos N (2015) Establishment rate of  
799 sheep gastrointestinal nematodes in farmed red deer (*Cervus elaphus*). *Veterinary Parasitology* 209:  
800 138-141.
- 801 Taylor MA, Coop RL, Wall RL (2007) *Veterinary Parasitology*. Blackwell Publishing, Ames, Iowa, USA.
- 802 Tomkins NW, Jonsson NN, Young MP, Gordon AN, McColl KA (1997) An outbreak of malignant  
803 catarrhal fever in young rusa deer (*Cervus timorensis*). *Australian Veterinary Journal* 75: 722-723.

- 804 Tweddle NE, Livingstone P (1994) Bovine tuberculosis control and eradication programs in Australia  
805 and New Zealand. *Veterinary Microbiology* 40: 23–39.
- 806 Walker JG, Morgan ER (2014) Generalists at the interface: nematode transmission between wild and  
807 domestic ungulates. *International Journal for Parasitology: Parasites and Wildlife* 3: 242-250.
- 808 Weaver GV, Domenech J, Thiermann AR, Karesh WB (2013) Foot and mouth disease: a look from the  
809 wild side. *Journal of Wildlife Diseases* 49: 759-785.
- 810 Welch MC, Kwan PW, Sajeev ASM (2014) Applying GIS and high performance agent-based simulation  
811 for managing an Old World screwworm fly invasion of Australia. *Acta Tropica* 138: S82-S93.
- 812 Woolhouse ME, Taylor LH, Haydon DT (2001) Population biology of multihost pathogens. *Science*  
813 292: 1109-1112.

**Figure 1.**

Current (red; West 2011) and potential distribution (greyscale) of the six deer species established in the wild in Australia (republished from Davis *et al.* 2016). The potential distributions were estimated using the Climatch algorithm (Invasive Animals CRC 2011).



**Table 2.** Pathogens and parasites of concern for both deer and livestock species in Australia, and their likely transmission routes. Vertical transmission takes place from mother to offspring

\* Infected under experimental transmission only

# combined due to similar epidemiology and clinical signs

| Pathogen                                | Disease                             | Host deer species                     | Host domestic species                    | Transmission route  | Present in Australia? | References  |
|---|-------------------------------------|---------------------------------------|--|---|-----------------------|---|
| <b>Bacterial</b>                        |                                     |                                       |  |   |                       |   |
| <i>Mycobacterium bovis</i>              | Tuberculosis                        | Red deer, fallow deer, chital         | Cattle, sheep, goats, pigs, deer, horses | Respiratory, faecal-oral, urinary-oral, contact with infected skin/wounds | No                    | Coleman & Cooke 2001<br>Simpson 2002<br>Böhm et al. 2007<br>Siembieda et al. 2011<br>De Lisle et al. 2001 |
| <i>Mycobacterium avium</i> spp. complex | Johne's disease<br>Paratuberculosis | Red deer, fallow deer, chital, sambar | Cattle, sheep, goats, pigs, deer         | Faecal-oral, vertical   | Yes                   | Mackintosh et al. 2004<br>Simpson 2002<br>Böhm et al. 2007<br>Siembieda et al. 2011<br>Coelho et al. 2013 |
| <i>Leptospira</i> spp.                  | Leptospirosis                       | Red deer, fallow deer                 | Cattle, sheep, goats, pigs, deer, horses | Urinary-oral, ingestion (e.g. water)                                      | Yes                   | Mackintosh et al. 2002<br>Böhm et al. 2007<br>Siembieda et al. 2011<br>Miller et al. 2013<br>Ellis 2015   |
| <i>Salmonella</i> spp.                  | Salmonella                          | Red deer                              | Cattle, sheep, goats, pigs, deer, horses | Faecal-oral, ingestion  | Yes                   | Mackintosh et al. 2002<br>Sanchez et al. 2002<br>Böhm et al. 2007   |
| <i>Brucella</i> spp.                    | Brucellosis                         | Red deer                              | Cattle, sheep, goats, pigs, deer, horses | Reproductive-oral   | Yes                   | Corbel 1997<br>Böhm et al. 2007<br>Conner et al. 2008   |
| <i>Bacillus anthracis</i>               | Anthrax                             | Red deer, fallow deer                 | Cattle, sheep, goats, horses             | Ingestion (e.g. soil, water)  | Yes                   | Mackintosh et al. 2002<br>Siembieda et al. 2011   |
| <i>Yersinia</i> spp.                    | Yersiniosis                         | Red deer, fallow deer, chital         | Cattle, sheep, goats, pigs, deer, horses | Faecal-oral, ingestion  | Yes                   | Mackintosh et al. 2002<br>Jerrett et al. 1990<br>Böhm et al. 2007<br>Mair 1973                            |
| <i>Chlamydia</i> spp.                   | Chlamydiosis                        | Red deer, fallow deer                 | Cattle, sheep, goats, pigs               | Faecal-oral, urinary-oral   | Yes                   | Mohamad & Rodolakis 2010<br>Salinas et al. 2009   |

| Pathogen                   | Disease   | Host deer species                       | Host domestic species                            | Transmission route                                     | Present in Australia? | References   |
|----------------------------|---|---|--|--|-----------------------|--|
| <b>Viral</b>               |   |   |  |  |                       |  |
| <i>Aphthae epizooticae</i> | Foot-and-mouth disease                                | Red deer, fallow deer, sambar           | Cattle, sheep, goats, pigs, deer                 | Respiratory, faecal-oral, urinary-oral                 | No                    | Haigh et al. 2002<br>Simpson 2002<br>Sutmoller et al. 2003<br>Böhm et al. 2007                   |
| <i>Flavivirus</i>          | Louping ill   | Red deer                                | Sheep, cattle (occasionally), pigs, horses, deer | Vector –borne (tick)                                   | No                    | Simpson 2002<br>Callan & Van Metre 2004<br>Böhm et al. 2007                                      |
| <i>Orbivirus</i>           | Epizootic haemorrhagic disease, bluetongue            | Red deer, fallow deer                   | Cattle, sheep, deer                              | Vector –borne (midge)                                  | Yes                   | Haigh et al. 2002<br>Maclachlan et al. 2015a<br>Maclachlan et al. 2015b                          |
| <i>Ephemerovirus</i>       | Bovine ephemeral fever                                | Red deer                                | Cattle   | Vector –borne (unknown)                                | Yes                   | St George 1988<br>Nandi & Negi 1999<br>Haigh et al. 2002   |
| <i>Pestivirus</i>          | Bovine viral diarrhoea disease                        | Red deer, fallow deer                   | Cattle, sheep, goats, deer                       | Faecal-oral, urinary-oral, reproductive-oral, vertical | Yes                   | Haigh et al. 2002<br>Simpson 2002<br>Böhm et al. 2007  |
| <i>Parapoxvirus</i>        | Parapoxvirus  | Red deer                                | Cattle, sheep, goats, deer                       | Contact with infected skin/wounds                      | Yes                   | Horner et al. 1987<br>Haigh et al. 2002<br>Scagliarini et al. 2011                               |
| <i>Gammaherpesvirus</i>    | Malignant catarrhal fever                             | Red deer, fallow deer, sambar, hog deer | Cattle, sheep, pigs, deer                        | Respiratory, vertical, wind-borne                      | Yes                   | Heuschele et al. 1984<br>Mackintosh 1992<br>Haigh et al. 2002                                    |
| <i>Alphaherpesvirus</i>    | Infectious bovine rhinotracheitis, cervid herpesvirus | Red deer, fallow deer                   | Cattle, deer                                     | Respiratory, vertical                                  | Yes                   | Nettleton et al. 1988<br>Engels & Ackermann 1996<br>Haigh et al. 2002<br>Callan & Van Metre 2004 |
| <b>Prion diseases</b>      |   |   |  |  |                       |  |
|                            | Chronic wasting disease                               | Fallow deer*, red deer                  | NA   | Respiratory, faecal-oral, urinary-oral,                | No                    | Williams et al. 2002<br>Williams 2005<br>Hartley et al. 2013                                     |



| Pathogen                        | Disease      | Host deer species                       | Host domestic species            | Transmission route              | Present in Australia? | References   |
|---------------------------------|--------------|---|----------------------------------|---------------------------------|-----------------------|--|
|                                 |              |   |                                  | contact with infected material  |                       |  |
| <b>Parasites - Nematodes</b>    |              |   |                                  |                                 |                       |  |
| <i>Ostertagia</i> spp.          |              | Red deer, fallow deer                   | Cattle, sheep, goats, deer.      | Faecal-oral                     | Yes                   | Presidente 1978<br>Bisset 1980<br>Barth & Matzke 1984<br>Taylor et al. 2007          |
| <i>Haemonchus</i> spp.          |              | Red deer, fallow deer, hog deer         | Cattle, sheep, goats, deer       | Faecal-oral                     | Yes                   | McKenzie 1985<br>Ferté et al. 2000<br>Taylor et al. 2007<br>Chintoan-Uta et al. 2014 |
| <i>Spiculopteragia</i> spp.     |              | Red deer, fallow deer, sambar           | Cattle, sheep, goats, deer       | Faecal-oral                     | Yes                   | Andrews 1973<br>Rehbein & Haupt 1994   |
| <i>Cooperia</i> spp.            |              | Red deer, fallow deer, sambar           | Cattle, sheep, goats, deer       | Faecal-oral                     | Yes                   | Taylor et al. 2007<br>Tapia-Escárate et al. 2015                                     |
| <i>Dictyocaulus</i> spp.        |              | Red deer, fallow deer, sambar           | Cattle, deer                     | Faecal-oral                     | Yes                   | Simpson 2002<br>Johnson et al. 2003<br>Taylor et al. 2007                            |
| <i>Oesophagostomum</i> spp.     |              | Red deer, fallow deer, sambar           | Cattle, sheep, goats, pigs, deer | Faecal-oral                     | Yes                   | Andrews 1973<br>Taylor et al. 2007<br>Tapia-Escárate et al. 2015                     |
| <i>Trichostrongylus</i> spp.    |              | Red deer, fallow deer, sambar, hog deer | Cattle, sheep, goats, pigs, deer | Faecal-oral                     | Yes                   | Taylor et al. 2007<br>Tapia-Escárate et al. 2015                                     |
| <i>Elaphostrongylus cervi</i>   |              | Red deer                                | Sheep, goats, deer               | Intermediate host (gastropod)   | No                    | Handeland et al. 2000<br>Böhm et al. 2006<br>Taylor et al. 2007                      |
| <b>Parasites - Trematodes</b>   |              |   |                                  |                                 |                       |  |
| <i>Fasciola</i> spp.            | Liver flukes | Red deer, fallow deer, sambar           | Cattle, sheep, deer              | Intermediate host (gastropod)   | Yes                   | Samuel et al. 2001<br>Taylor et al. 2007<br>Malcicka 2015                            |
| <i>Dicrocoelium dendriticum</i> | Lancet fluke | Red deer, fallow deer                   | Sheep, deer                      | Intermediate hosts (gastropods) | No                    | Samuel et al. 2001   |

| Pathogen   | Disease                         | Host deer species             | Host domestic species                    | Transmission route<br>and ants) | Present in Australia? | References                                  |
|--|---------------------------------|-------------------------------|--|---------------------------------|-----------------------|---|
| <i>Paramphistomes</i>                                | Rumen flukes                    | Red deer, fallow deer         | Cattle, sheep, deer                      | Intermediate host (gastropod)   | Yes                   | Skuce & Zadoks 2013<br>O'Toole et al. 2014  |
| <b>Parasites - Cestodes</b>                          |                                 |                               |  |                                 |                       |   |
| <i>Taenia hydatigena</i>                             |                                 | Red deer, fallow deer, sambar | Cattle, sheep, goats, deer               | Faecal-oral                     | Yes                   | Samuel et al. 2001<br>Taylor et al. 2007    |
| <i>Echinococcus granulosus</i>                       |                                 | Red deer, fallow deer         | Sheep                                    | Faecal-oral                     | Yes                   | Jenkins 2005<br>Taylor et al. 2007          |
| <b>Parasites - Protozoa</b>                          |                                 |                               |  |                                 |                       |   |
| <i>Giardia</i> spp. and <i>Cryptosporidium</i> spp.# | Giardiasis<br>Cryptosporidiosis | Red deer, sambar              | Cattle, sheep, goats, pigs, deer, horses | Faecal-oral                     | Yes                   | Samuel et al. 2001<br>Ryan & Power 2012     |
| <i>Neospora caninum</i>                              | Neosporosis                     | Red deer, fallow deer         | Cattle, sheep, goats, pigs, deer, horses | Faecal-oral, vertical           | Yes                   | Donahoe et al. 2015<br>Dubey 1999           |
| <i>Trypanosoma evansi</i>                            | Surra                           | Sambar, hog deer              | Cattle, sheep, goats, pigs, deer         | Vector –borne (tabanid flies)   | No                    | Reid 2002<br>Desquesnes et al. 2013         |
| <i>Sarcocystis</i> spp.                              |                                 | Red deer                      | Cattle, sheep, goats, pigs, deer         | Faecal-oral                     | Yes                   | Levine & Tadros 1980<br>Kutkienė 2003       |
| <i>Eimeria</i> spp.                                  |                                 | Red deer, fallow deer         | Cattle, sheep, goats, pigs, deer         | Faecal-oral                     | Yes                   | Dauguschies & Najdrowski 2005               |
| <b>Parasites - Ectoparasites</b>                     |                                 |                               |  |                                 |                       |   |
| <i>Rhipicephalus microplus</i>                       | Cattle tick infestation         | Red deer                      | Cattle                                   | Direct                          | Yes                   | George 1990<br>Barré et al. 2002            |
| <i>Chrysomya bezziana</i>                            | Screw-worm fly infestation      | Fallow deer, sambar           | Cattle, sheep, goats, pigs, deer         | Direct                          | No                    | Spradbery & Tozer 2013<br>Welch et al. 2014 |

**Table 3.** Qualitative assessment of disease risk for deer and livestock in Australia. The pathogens and parasites are listed in Table 2, the method for the overall assessment is explained in Table 1. ‘Susceptible’ refers to the degree to which there is certainty that the six deer species considered are susceptible to the pathogen. ‘Infected’ refers to the likelihood of these deer species acquiring the infection given that they are exposed to the pathogen (based on whether the pathogen is present or has a likely risk of being introduced into Australia, the geographical distribution of the pathogen and its route of transmission). Risks are tabulated for the likelihood that, once present in deer populations in Australia, this pathogen will infect livestock, and conversely, the likelihood of deer being infected if the pathogen is present in livestock. ‘Impact’ refers to the potential additional economic impact that a disease would have on Australian livestock farming, should deer become an additional route of transmission.

| Pathogen                                | Disease                             | Susceptible | Infected | Infecting livestock | Being infected by livestock | Impact | Overall assessment |
|---|-------------------------------------|-------------|----------|---------------------|-----------------------------|--------|--------------------|
| <b>Bacterial</b>                        |                                     |             |          |                     |                             |        |                    |
| <i>Mycobacterium bovis</i>              | Tuberculosis                        | High        | Medium   | Medium              | Low                         | High   | High               |
| <i>Mycobacterium avium</i> spp. complex | Johne’s disease<br>Paratuberculosis | High        | High     | Medium              | Low                         | Low    | Medium             |
| <i>Leptospira</i> spp.                  | Leptospirosis                       | High        | High     | Low                 | Medium                      | Low    | Medium             |
| <i>Salmonella</i> spp.                  | Salmonella                          | Medium      | High     | Low                 | Medium                      | Low    | Low                |
| <i>Brucella</i> spp.                    | Brucellosis                         | Medium      | High     | Low                 | Medium                      | Low    | Low                |
| <i>Bacillus anthracis</i>               | Anthrax                             | High        | Medium   | Low                 | Low                         | Medium | Medium             |
| <i>Yersinia</i> spp.                    | Yersiniosis                         | Medium      | High     | Low                 | Low                         | Low    | Low                |
| <i>Chlamydia</i> spp.                   | Chlamydia                           | Medium      | High     | Low                 | Medium                      | Medium | Medium             |
| <b>Viral</b>                            |                                     |             |          |                     |                             |        |                    |
| <i>Aphthae epizooticae</i>              | Foot-and-mouth disease              | High        | High     | Medium              | Medium                      | High   | High               |
| <i>Flavivirus</i>                       | Louping ill                         | Low         | Low      | Low                 | Low                         | Low    | Low                |
| <i>Orbivirus</i>                        | Epizootic haemorrhagic              | High        | Medium   | Low                 | Low                         | Medium | Medium             |

| Pathogen                     | Disease   | Susceptible | Infected | Infecting livestock | Being infected by livestock | Impact | Overall assessment |
|------------------------------|---|-------------|----------|---------------------|-----------------------------|--------|--------------------|
|                              | disease, bluetongue                                   |             |          |                     |                             |        |                    |
| <i>Ephemerovirus</i>         | Bovine ephemeral fever                                | High        | Medium   | Low                 | Low                         | Low    | Low                |
| <i>Pestivirus</i>            | Bovine viral diarrhoea disease                        | High        | High     | Medium              | Medium                      | Low    | Medium             |
| <i>Parapoxvirus</i>          | Parapoxvirus  | High        | Medium   | Low                 | Low                         | Low    | Low                |
| <i>Gammaherpesvirus</i>      | Malignant catarrhal fever                             | High        | Medium   | Low                 | Medium                      | High   | High               |
| <i>Alphaherpesvirus</i>      | Infectious bovine rhinotracheitis, cervid herpesvirus | High        | High     | Low                 | Low                         | Low    | Low                |
| <b>Prion diseases</b>        |   |             |          |                     |                             |        |                    |
|                              | Chronic wasting disease                               | High        | High     | Low                 | Low                         | Low    | Low                |
| <b>Parasites - Nematodes</b> |   |             |          |                     |                             |        |                    |
|                              | <i>Ostertagia</i> spp.                                | High        | High     | Low                 | Medium                      | Low    | Medium             |
|                              | <i>Haemonchus</i> spp.                                | High        | High     | Low                 | Medium                      | Low    | Medium             |
|                              | <i>Spiculoptera</i> spp.                              | High        | High     | Low                 | Low                         | Low    | Low                |
|                              | <i>Cooperia</i> spp.                                  | High        | High     | Low                 | Low                         | Low    | Low                |
|                              | <i>Dictyocaulus</i> spp.                              | High        | High     | Medium              | Low                         | Low    | Medium             |
|                              | <i>Oesophagostomum</i> spp.                           | High        | High     | Low                 | Low                         | Low    | Low                |
|                              | <i>Trichostrongylus</i> spp.                          | High        | High     | Low                 | Low                         | Low    | Low                |

| Pathogen  | Disease                         | Susceptible | Infected | Infecting livestock | Being infected by livestock | Impact | Overall assessment |
|---|---------------------------------|-------------|----------|---------------------|-----------------------------|--------|--------------------|
| <i>Elaphostrongylus cervi</i>                       |                                 | High        | Medium   | Low                 | Low                         | Low    | Low                |
| <b>Parasites - Trematodes</b>                       |                                 |             |          |                     |                             |        |                    |
| <i>Fasciola</i> spp.                                | Liver flukes                    | High        | High     | Medium              | Medium                      | Low    | Medium             |
| <i>Dicrocoelium dendriticum</i>                     | Lancet fluke                    | High        | Medium   | Low                 | Low                         | Low    | Low                |
| <i>Paramphistomes</i>                               | Rumen flukes                    | High        | High     | Low                 | Low                         | Low    | Low                |
| <b>Parasites - Cestodes</b>                         |                                 |             |          |                     |                             |        |                    |
| <i>Taenia hydatigena</i>                            |                                 | High        | High     | Low                 | Low                         | Low    | Low                |
| <i>Echinococcus granulosus</i>                      |                                 | High        | High     | Low                 | Low                         | Low    | Low                |
| <b>Parasites - Protozoa</b>                         |                                 |             |          |                     |                             |        |                    |
| <i>Giardia</i> spp. and <i>Cryptosporidium</i> spp. | Giardiasis<br>Cryptosporidiosis | High        | High     | Low                 | Medium                      | Low    | Medium             |
| <i>Neospora caninum</i>                             | Neosporosis                     | High        | High     | Low                 | Low                         | Low    | Low                |
| <i>Trypanosoma evansi</i>                           | Surra                           | High        | Medium   | High                | Medium                      | High   | High               |
| <i>Sarcocystis</i> spp.                             |                                 | High        | Medium   | Low                 | Low                         | Low    | Low                |
| <i>Eimeria</i> spp.                                 |                                 | Low         | Medium   | Low                 | Low                         | Low    | Low                |
| <b>Parasites - Ectoparasites</b>                    |                                 |             |          |                     |                             |        |                    |
| <i>Rhipicephalus microplus</i>                      | Cattle tick infestation         | Low         | Medium   | Low                 | Low                         | Low    | Low                |
| <i>Chrysomya</i>                                    | Screw-worm fly                  | High        | High     | High                | High                        | Medium | High               |

---

| <b>Pathogen</b> | <b>Disease</b> | <b>Susceptible</b> | <b>Infected</b> | <b>Infecting livestock</b> | <b>Being infected by livestock</b> | <b>Impact</b> | <b>Overall assessment</b> |
|-----------------|----------------|--------------------|-----------------|----------------------------|------------------------------------|---------------|---------------------------|
| <i>bezziana</i> | infestation    |                    |                 |                            |                                    |               |                           |

---