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Review of of diseases and pathogens of invasive animals that may present food safety and human health risks

Chief Veterinary Officer's Unit

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SUMMARY

The following review was requested by PrimeSafe to support a submission to the Parliamentary Inquiry into the Control of Invasive Animals on Crown Land in 2016.

This document provides an overview of diseases and pathogens that may present a potential risk for food safety and human health when invasive animals are harvested in Australia. The review covers diseases and pathogens of both introduced species (pigs, goats, rabbits, hares, horses and deer) and native species (kangaroos and wallabies).

A range of bacterial, viral and parasitic pathogens were identified. Pathogens identified with serious zoonotic potential include *Coxiella burnetii* (causing Q fever), *Brucella suis* (causing brucellosis), *Leptospira* (causing leptospirosis), Murray Valley encephalitis virus and various gastrointestinal organisms such as *Salmonella* and *Campylobacter*. Many of these pathogens have broad host specificity.

As a result of the wide range of pathogens and disease conditions identified, the harvesting of invasive animals for human or pet consumption is likely to carry risks for food safety and human health unless mitigating procedures are adopted and implemented.

1. INTRODUCTION

Invasive animals have the potential to harbour or transmit many diseases that can seriously harm domesticated animals, native fauna or people.

An invasive animal species is a species occurring, as a result of human activities, beyond its accepted normal distribution and which threatens valued environmental, agricultural or other social resources by the damage it causes.

Invasive animals can carry the same diseases as domesticated animals and native fauna. As such, they are a potential source of infection for domesticated animals, negatively affecting disease control efforts and threatening Victoria's and Australia's trade reputation, as well as presenting risks to native fauna. The threat of invasive animals transmitting exotic animal disease following an incursion into Australia is also very real and requires constant vigilance.

The purpose of this document is to provide an overview of diseases and pathogens identified as a potential risk for food safety and human health when invasive animals are harvested in Australia. The review covers diseases and pathogens of both introduced invasive species (pigs, goats, rabbits, hares, horses and deer) and native invasive species (kangaroos and wallabies).

The review includes reports on the identification of disease (i.e. pathological condition), isolation of disease agents and evidence of exposure to pathogens (as demonstrated by the presence of antibodies i.e. seroconversion) in these hosts. It includes incidental findings from surveillance or research activities as well as available data on endemic diseases and outbreaks in populations. Overseas reports are also included to provide a better understanding of potential risks linked to handling and consumption of these species.

2. PATHOGENS AND DISEASES BY ANIMAL SPECIES

2.1. Pigs

Invasive pig populations became established in Australia soon after European settlement from pig stocks imported from Europe and Asia that were allowed to roam or escaped. The current invasive pig population of up to 23.5 million head is spread across approximately half of the Australian continent, from western Victoria, through New South Wales into Queensland and parts of South Australia, and across northern Australia. Isolated populations can also be found in Tasmania and a few offshore islands. As a result of wide habitat range, omnivorous diet and potential for rapid population growth in good seasons mean that few agricultural pursuits are unaffected by these pest animals.

Invasive pigs host a wide range of pathogens, some of these are specific to pigs, such as classical swine fever (exotic to Australia), and others can affect a wide range of species. Many of the pathogens are significant zoonoses, including leptospires, *Brucella suis*, mycobacteria, Ross River virus and Murray Valley encephalitis virus (Pavlov *et al.* 1992). Analyses of invasive pig populations have shown that pigs are likely to play a significant role in spreading endemic or exotic disease, particularly around major river catchments (Hampton *et al.* 2004; Cowled 2006, 2008a).

2.1.1. Bacteria

- **Leptospirosis** is considered the most common bacterial disease in invasive pigs (Choquenot *et al.* 1996). It is caused by *Leptospira interrogans* and results in infertility and birth disorders in pigs and other animals. The bacterium causes influenza-like disease in humans, also known as 'canecutter's disease'. Infections occur from contact with contaminated pig urine, and complications include jaundice and bleeding disorders. Leptospirosis is a significant cause of ill health in people, with high hospitalisation rates (46%) recorded in Australia (Smythe *et al.* 2000). At least 11 different *L. interrogans* serovars (a group of closely related microorganisms) have been found in invasive pigs in Australia (Pavlov and Edwards 1995, Heise-Pavlov and Heise -Pavlov 2003). Serovar Pomona is the most common in New South Wales, found in up to half the pigs that have been examined (Choquenot *et al.* 1996, Mason *et al.* 1998). This serovar is a threat to livestock and hunters and other outdoor recreational groups (Mason *et al.* 1998). A serovar Pomona infection leading to a 'bovine abortion storm' on a New South Wales property was attributed to invasive pigs (Animal Health Australia 2000). Another serovar, Hardjo, is more predominant in wildlife, but is also found in pigs (Mason *et al.* 1998). This serovar is the predominant serovar infecting people in temperate regions such in Victoria (Eymann *et al.* 2006).
- **Brucellosis**, caused by the bacterium *Brucella suis*, is considered endemic in invasive pigs in central Queensland and northern New South Wales (Mason and Fleming 1999), serving as a source of infection of domestic/commercial pigs and also cattle herds. Since successful eradication of *Brucella abortus* from

Australia in cattle, the most significant causal agent of brucellosis in humans is *B. suis* which can produce a serious and long lasting infection, resulting in fever, muscle and joint aches and abortion. It is strongly linked to workers associated with handling, hunting or butchering pigs (Choquenot *et al.* 1996, Mason and Fleming 1999). Human brucellosis cases are on the rise in Queensland (Robson *et al.* 1993), and a case also occurred in the Hunter Valley region of New South Wales (Communicable Diseases Bulletin 2006, 160); all these human cases were involved with killing invasive pigs. The threat to people is increasing with the growth of the lucrative pig hunting industry (Robson *et al.* 1993).

- **Q fever** is caused by *Coxiella burnetii* and can be transmitted from invasive pigs to other animal species and humans. Infection can occur through contact with blood, meat and urine through broken skin, intake of urine-contaminated food or water, and inhalation of infectious airborne organisms.
- ***Streptococcus suis*** is another bacterium causing occupational hazard for piggery workers, with recent cases reported in New South Wales (AB CRC newsletter 19 Dec 2008).
- ***Salmonella enterica* serotype Anatum and *S. enterica* serotype Typhimurium** were found in a third of 154 invasive pig carcasses processed for human consumption in Australia (Bersink *et al.* 1990). The prevalence of *Salmonella* in wild boar and invasive pig populations has been reported for a number of countries. In Switzerland, *Salmonella* were isolated from the tonsils of 12% (19/153) wild boar but not from the faeces of the same animals; eight *Salmonella* serovars were identified amongst the 19 isolates, the most common being Enteritidis, Stourbridge and Venezia (Wacheck *et al.* 2010). A small survey of the faeces of Swedish wild boar (n=66) was unable to detect *Salmonella* (Wahlstrom *et al.* 2003), whereas 22% (17/77) of wild boar in northern Portugal (Vieira-Pinto *et al.* 2011) and 5% (8/161) of invasive pigs in North Carolina, USA, were reported to be shedding *Salmonella* in faeces (Thakur *et al.* 2011). In Portugal, only *S. enterica* serovar Typhimurium and *S. enterica* serovar Rissen were detected in wild boar (Vieira-Pinto *et al.* 2011).
- Pathogenic ***Escherichia coli*** have been detected in the faeces of wild boar and invasive pigs in a number of countries. An outbreak of human *E. coli* O157:H7 in 2006 was linked to the consumption of bagged spinach and resulted in many deaths. The outbreak strain was isolated from cattle grazing nearby and from invasive pigs roaming in the vicinity of a spinach farm in California, USA, which was implicated in the spinach outbreak (Jay *et al.* 2007). In Spain, *E. coli* O157:H7 and non-O157 Shiga toxin-producing *E. coli* (STEC) were isolated from faeces of 3% (7/212) and 5% (11/212) respectively of wild boar killed during the hunting season of 2007-2008 (Sanchez *et al.* 2010) and STEC were isolated from 8% (22/262) of wild boar killed during the hunting season of 2009-2010 (Mora *et al.* 2012). *E. coli* were detected on 19% (42/217) of pig carcasses at the Queensland abattoir and the mean *E. coli* and bacterial count (aerobic plate count) was reported to be 1.9 and 4.7 log cfu/g, respectively. Five per cent and 1% of the pigs had an *E. coli* count greater than 2 and 3 log cfu/g respectively (Eglezos *et al.* 2008).
- Enteropathogenic ***Yersinia enterocolitica* and *Y. pseudotuberculosis*** in wild boars have been reported from Japan and Switzerland (Hayashidani *et al.* 2002; Fredriksson-Ahomaa *et al.* 2009; Fredriksson-Ahomaa *et al.* 2011).
- **Melioidosis**, caused by *Burkholderia pseudomallei*, was found in two thirds of invasive pigs tested in north Queensland (Pavlov and Edwards 1995). This disease appears more commonly during wetter weather in northern Australia (Animal Health Australia 2001).
- **Tuberculosis** caused by *Mycobacterium bovis* was rarely found in invasive pigs during the national bovine tuberculosis eradication campaign for cattle and buffalo in Australia, completed in 1997 (Choquenot *et al.* 1996). For example, *M. bovis* was identified in only 2 out of 790 invasive pigs examined in Northern Territory; this was a significant drop from prior to the commencement of the campaign in the early 1970s (McInerney *et al.* 1995).
- **Other bacteria** associated with invasive pigs include Spotted Fever Group rickettsia, found to be endemic in south west Western Australia (Li *et al.* 2007).

2.1.2. Viruses

- **Arboviruses and parvoviruses** are reported in the literature (Pavlov *et al.* 1992, Caley 1993, Caley *et al.* 1994). Porcine parvovirus (PPV) antibodies were found in over half of 298 invasive pigs tested in the Douglas Daly district of Northern Territory, and PPV was concluded likely to be endemic in Australia (Caley 1993, Caley *et al.* 1994). This parvovirus is a common cause of reproductive failure in piggeries.
- **Menangle virus** is a highly infectious zoonotic pathogen. It was reported in pigs at a commercial piggery in the Northern Territory, although it was not detected in 190 invasive pigs tested by Kirkland *et al.* (2001). The disease causes reproductive disorders in pigs, and flu-like symptoms in people. Originating from bats, the virus is amplified in pigs, increasing the risk of transmission (similarly to Nipah virus in Malaysia, Hooper 2001). There has been only a single outbreak of Menangle disease in pigs in Australia, occurring in 1997.
- **Japanese encephalitis (JE) virus** is another virus that is amplified in pigs. Antibodies to JE virus were detected in sentinel pigs on Cape York Peninsula in 1998, and a fisherman in that area contracted an infection (Exotic Animal Diseases Bulletin 2003). These were the only known cases on the Australian mainland, until JE virus was again isolated from sentinel pigs in northern Cape York Peninsula in 2004, and invasive pigs in western Cape York showed serology (presence of antibodies) patterns consistent with exposure to the virus (Animal Health Australia 2006). There has been no evidence of transmission of JE virus since 2005.
- **Trubanaman virus** is another virus identified in invasive pigs by seroconversion (Johansen *et al.* 2005). This mosquito-borne virus was identified in 3.5% of invasive pigs tested in south-western Western Australia (Johansen *et al.* (2005). It is suspected of causing polyarthritic symptoms in people, similar to Gan Gan virus (Boughton *et al.* 1990).
- **Hepatitis E virus** was isolated from wild boars and caused human illness in Europe and North Asia, linked to consumption of wild boar meat. Several case reports linked to the consumption of raw liver or raw bile from wild boar in Japan and Korea without detection of virus in the boar meat (Matsuda *et al.* 2003; Kim *et al.* 2011b); in both cases genotype 4 Hepatitis E virus were recovered. Genotype 3 Hepatitis E virus RNA from a human case from Japan was found to have complete sequence homology over the entire ORF2 gene with Hepatitis E virus RNA isolated from wild boar meat that had been consumed by the case (Li *et al.* 2005). Furthermore, in Japan, genotype 3 Hepatitis E virus isolates from wild boar, deer and a human case that consumed the deer meat had near-complete sequence homology over the ORF1, ORF2 and ORF3 portion of the genome, demonstrating sylvatic transmission between wild game species in Japan (Takahashi *et al.* 2004). In this same survey, Hepatitis E virus RNA was isolated from three of seven wild boars (Takahashi *et al.* 2004). In Europe, Hepatitis E virus genotype 3 has been isolated from liver, bile and serum of wild boar in Germany and France (Kaci *et al.* 2008; Adlhoch *et al.* 2009; Kaba *et al.* 2010); however the literature search did not reveal human cases linked to the consumption of Hepatitis E virus contaminated wild boar in Europe.

2.1.3. Parasites

- Cysts of the tapeworm ***Echinococcus granulosus*** were found in 9% (Banks *et al.* 2006) and 31% (Lidetu and Hutchinson 2007) of invasive pigs studied in northern Queensland, and between 50 and 70% of these lung and liver cysts were viable. Viable cysts were also found in about half the pigs examined in the Kosciuszko region of New South Wales, although the viability of these cysts was lower (less than 22%; Jenkins and Morris 2003). These results show that invasive pigs can contribute a significant part in the sylvatic cycle of this parasite (Lidetu and Hutchinson 2007). *E. granulosus* was also found in invasive pigs in Western Australia, where they were involved in an unusual cycle involving kangaroos and domestic dogs (Thompson *et al.* 1988). Cysts of this parasite can occur in humans (and native wildlife, cattle, sheep and goats), often with serious consequences.
- **Other endoparasites**, such as stomach worm, lung worm and kidney worm, have also been found at high infection rates in invasive pigs in Australia (Pavlov and Edwards 1995, Heise-Pavlov and Heise-Pavlov 2003).
- **Spirometra tapeworms** that cause the zoonotic disease sparganosis, were found in high prevalence in pigs of northern Queensland (Pavlov *et al.* 1992). This parasite can also infect people who eat inadequately cooked pork.

- ***Trichinella* spp.** are endemic in the wild boar populations of Europe. Consumption of affected meat can cause serious illness including death in humans. Significant numbers of people have been affected in incidents in France and Canada. Surveys of wild boar reported in the international literature identified at least three species: *T. spiralis*, *T. britovi* and *T. pseudospiralis* (Nockler *et al.* 2006; Hurnikova and Dubinsky 2009; Garcia-Sanchez *et al.* 2009; Meriardi *et al.* 2011). *T. pseudospiralis* has been isolated from wild boar in the USA (Gamble *et al.* 2005); *T. spiralis* from wild boar in Argentina (Cohen *et al.* 2010). A small survey in Canada was unable to detect larvae in wild boar by either artificial digestion of muscle tissue or by serology (Gajadhar *et al.* 1997). *T. papuae* larvae were isolated from one of 12 invasive pigs sampled on two islands in the Torres Strait; in the same study, muscle samples were collected from 438 invasive pigs on the Cape York Peninsula and no larvae were detected (Cuttell *et al.* 2012).
- **Toxoplasmosis** occurs in invasive pigs, with the national serological prevalence for *Toxoplasma gondii* estimated at 9% (Animal Health Australia 1998) Surveys for the detection of antibodies to *T. gondii* in wild boar have been reported from Japan, USA, France, Czech Republic, the Netherlands, Switzerland and Slovakia. Like that seen for deer, prevalence of *T. gondii* antibody detection in European and North American wild boar populations was high, ranging from 6.7% in Switzerland and 8% in the Slovakia to 18% in France, 26% in Czech Republic, 24% in the Netherlands and 28% on North Carolina, whilst on Corsica, seroprevalence was reported as 0.6% in the summer of 2006-2007 and 0.3% in the summer of 2007-2008 (Bartova *et al.* 2006; Antolova *et al.* 2007; Richomme *et al.* 2009; Richomme *et al.* 2010; Sandfoss *et al.* 2011; Opsteegh *et al.* 2011; Berger-Schoch *et al.* 2011). Two studies from Japan have reported seroprevalence of 6% and 1% (Shiibashi *et al.* 2004; Matsumoto *et al.* 2011). In France, *T. gondii* cysts were isolated by mouse bioassay from 48% (21/44) of seropositive wild boar and only genotype II isolates were identified (Richomme *et al.* 2009).
- ***Giardia*, *Cryptosporidium*, *Balantidium* and *Entamoeba*** were detected in faeces from invasive pigs caught in metropolitan drinking water catchment areas in Western Australia (Hampton *et al.* 2006). The pigs not only aid in transmission of diseases directly through faecal contamination of water, but water turbidity from pig wallowing may also protect waterborne pathogens from chemical disinfection treatment (Hampton *et al.* 2006).

2.2. Rabbits and hares

Rabbits were first introduced to Australia with the first fleet in 1788 but numbers remained relatively contained until the European rabbit was introduced into Victoria in 1859, resulting in an explosive increase in the population. Rabbits have been harvested from the wild in large numbers since the mid-1800s, however due to the pest status of wild rabbits, commercial farming was prohibited throughout Australia until 1987.

The majority of pathogens of rabbits and hares only present a disease threat to domestic or commercially bred rabbits, although some zoonoses have been identified

2.2.1. Bacteria

- **Zoonotic faecal coliforms** have been isolated from rabbits in water quality studies near Sydney (Ferguson 2005, Cox *et al.* 2005). Two international studies provide data on the prevalence of pathogenic bacteria in wild rabbit populations of Europe. In the United Kingdom, 8% (8/97) of wild rabbits on six properties sharing grazing land with cattle in summer had *E. coli* O157 isolated from faecal samples. In the same region, no rabbits (0/32) were found to be shedding *E. coli* O157 in winter. Of the 97 samples collected in summer, 21% (20/97) of rabbits were shedding non-O157 verocytotoxigenic *E. coli* (Scaife *et al.* 2006). Two European studies also report on carcass quality of rabbits at slaughter or rabbit meat at retail. A survey of 51 farmed rabbit carcasses and retail meat samples collected in Spain found no evidence of *Salmonella* or pathogenic *E. coli* contamination (Rodriguez-Calleja *et al.* 2006). Four samples were positive for *E. coli* but none were O157 and all were negative for stx1/stx2 genes.
- ***Salmonella*** in faeces of 48% (38/80) of wild rabbits were found in a study in northern Portugal; the serovars detected were *Salmonella enterica* serovar Rissen (11), *S. enterica* serovar Enteritidis (10), *S. enterica* serovar Havana (9), *S. enterica* serovar Typhimurium (6) and *S. enterica* serovar Derby (2) (Vieira-Pinto *et al.* 2011).

- ***Staphylococcus aureus*** was isolated from 53% (27/51) of samples, 23 samples were negative for the genes encoding enterotoxin A, B, C, D and E; two samples each were PCR positive for enterotoxin B and C genes, *seb* and *sec* (Rodriguez-Calleja *et al.* 2006). *S. aureus* was detected on 30% (151/500) of carcasses and staphylococcal enterotoxin genes were detected in 102 (20%) of the *S. aureus* isolates; in the same study, **Enterobacteriaceae** were detected on 24% (118/500) of carcasses and total viable counts (TVC) from carcasses ranged from 2 - 5 log CFU/cm² and the daily mean TVC ranged from 3 - 4 log CFU/cm² (Kohler *et al.* 2008).

2.2.2. Viruses

- The Myxoma virus responsible for myxomatosis, and rabbit calicivirus (RCV) that causes rabbit haemorrhagic disease, were introduced to Australia for the purpose of biological control and are now considered endemic (Williams *et al.* 1994). Recently a benign endemic strain of RCV ('RCV-A1') was identified, possibly conferring immunity to the introduced strain, compromising its effectiveness (Strive *et al.* 2009).
- **Trubanaman virus**, suspected of causing polyarthritic symptoms in people (Boughton *et al.* 1990), has been identified in rabbits in Australia, at 0.8% and 2.4% prevalence respectively (Johansen *et al.* 2005).

2.2.3. Parasites

- ***Cryptosporidium* and *Eimeria* protozoa** have been observed in rabbits (Cox *et al.* 2005).
- **Helminth parasites**, including liver fluke caused by *Fasciola hepatica*, dog tapeworms (*Taenia pisiformis* and *T. serialis*) and gastrointestinal worms (*Graphidium strigosum* and *Trichostrongylus retortaeformis*) are carried by rabbits (Williams *et al.* 1994).
- ***Toxoplasma gondii*** was identified in a survey of 1,697 wild rabbits from 24 sites in Victoria from 1971 to 1980 (Cox *et al.* 1981). The survey found high titre antibodies to *T. gondii* in rabbits sampled from five sites, Dartmouth (1%), Seaspray (3%), Dreeite (6%), Mud Island (13%) and the land filtration area of the Werribee sewage treatment plant (26%), and rabbits with low titre antibodies to *T. gondii* were detected in all locations. No records of toxoplasmosis in Australian farmed rabbits were identified.

2.3. Goats

Invasive goats are prone to a number of diseases currently in Australia, including Q fever, tetanus, leptospirosis, *Brucella melitensis* infection, hydatids, pulpy kidney, blackleg, and various parasitic worms (Biosecurity Queensland 2007).

2.3.1. Bacteria

- **Q fever** is considered to be widespread in invasive goat populations in Australia. For example, a seroprevalence of 52% was reported in one study (Parkes *et al.* 1996). Although usually non-pathogenic in goats, Q fever can cause pneumonia, hepatitis and death in humans, and is considered the most infectious disease in the world, with people becoming infected from a single cell (Maurin and Raoult 1999, OIE 2006). An outbreak of Q fever was reported in Victorian abattoir staff involved in the slaughter of invasive goats (Buckley 1980). Another case occurred in Waikerie in South Australia, where a cluster of Q fever cases, including one death, were thought to be linked to inhalation of contaminated dust from the local abattoir, affecting townsfolk not involved in meat preparation (Pedler 2007, ABC News 10/9/2007).
- **Melioidosis**, caused by the bacterium *Burkholderia pseudomallei*, is considered to be endemic in tropical Australia, with sheep and goats particularly susceptible (Choya *et al.* 2000).
- ***Corynebacterium ovis*** infection can result in caseous lymphadenitis (i.e. abscesses in the lymph nodes) (Batey *et al.* 1985, Parkes *et al.* 1996). Reported cases in humans are uncommon.
- Other non-specific bacteria, namely **faecal coliforms**, have been identified from invasive goats in studies of possible sources of water supply contamination (Ferguson 2005).
- An infection of ***Mycobacterium bovis*** in a domestic goat in Australia has been described (Cousins *et al.* 1993).

- No specific reports of **Johne's disease** (paratuberculosis) in invasive goats were found. Some authors have suggested an association between Johne's disease and human Crohn's disease, but causality has not been demonstrated.
- Parkes *et al.* (1996) comment that other important diseases of livestock, such as yersiniosis, leptospirosis and mycobacterial diseases are apparently rare in invasive goats.

2.3.2. Viruses

- **Caprine arthritis/encephalitis (CAE) virus** infection has been found in invasive goats in South Australia (Surman *et al.* 1987). A retroviral infection of goats, incidence of CAE is low and sporadic. It can lead to chronic disease of the joints and, on rare occasions, encephalitis in goat kids.

2.3.3. Parasites

- Invasive goats have been found to carry 22 nematode, two cestode, two trematode, four arthropod, and three protozoan parasites (Parkes *et al.* 1996 and references therein). Many of these can infect farmed sheep and all can infect farmed goats. The most common health problem causing death in invasive goats in the Northern Territory is reportedly nematodes (Rural ABC May 2008). A link has been suggested between invasive goats and the occurrence of hydatid tapeworms in cattle in the Kimberley region of Western Australia, where populations were previously uninfected (Lymbery *et al.* 1995).
- **Enteric coccidiosis**, an economically important parasitic disease particularly of neonatal domestic goats, has been found in invasive goats (Main and Creeper 1998). Coccidiosis of Brunner's (duodenal) glands in invasive goats that died during overseas transport to the Middle East was described by Main and Creeper (1998). The researchers concluded the condition was likely caused by the protozoan parasite *Eimeria* spp., and that stress associated with transport contributed to severe coccidiosis and death (Main and Creeper 1998).

2.4. Deer

A comprehensive search of the literature found no published articles describing the prevalence or level of contamination of microbiological hazards of deer or deer products, either farmed or wild, in Australia. International literature identified a number of foodborne pathogens and provided some information on foodborne illness associations.

2.4.1. Bacteria

- Isolation of **Salmonella** from the faeces of farmed and wild deer, including white-tailed deer, roe deer, red deer, fallow deer and reindeer, has been reported from the USA, Sweden, Finland and Norway. No *Salmonella* were detected in the faeces of 2,243 semi-domesticated deer from eight herds in northern Finland and Norway (Kemper *et al.* 2006), 484 harvested wild deer in Norway (Lillehaug *et al.* 2005), nor in the faeces of 200 wild roe deer in Sweden (Wahlstrom *et al.* 2003). In the USA, no *Salmonella* was detected in the faeces of white-tailed deer collected from 30 farms in Ohio (French *et al.* 2010). *Salmonella enterica* serovars Litchfield, Dessau, Infantis and Enteritidis were isolated from the faeces of 500 free-ranging white-tailed deer harvested by hunters in Nebraska, with an overall prevalence of 1% (Renter *et al.* 2006). Two out of 26 (7.7%) wild white-tailed deer that were simultaneously grazing the same rangeland as cattle and sheep at a university farm in Texas had *Salmonella* cultured from rumen contents (Branham *et al.* 2005).
- Pathogenic **Escherichia coli** in the faeces of farmed and wild deer, including white-tailed deer, roe deer, red deer, fallow deer and reindeer, has been reported from Germany, USA, Sweden, Finland, Norway, Spain and Belgium. In Belgium, STEC or enteropathogenic *E. coli* were present in 15% (20/133) of roe and red deer and 12% (16/133) were positive for one or both the stx1 or stx2 gene; no pathogenic isolates belonging to serogroups O157, O26, O111, O103 or O145 were detected. In Spain, STEC O157:H7 was isolated from 1.5% (3/206) of wild red deer and no STEC O157 isolates were recovered from wild roe deer (0/20) or fallow deer (0/6) (Garcia-Sanchez *et al.* 2007). In contrast non-STEC O157 were detected in 25% (51/206) of red deer, 5% (1/20) of roe deer and 33% (2/6) of fallow deer (Sanchez *et al.* 2009). Lillehaug *et al.* (2005) were unable to detect STEC in the faeces of 206 Norwegian roe deer and 1.5% (2/135) of red deer were stx gene-positive. In northern Finland and Norway, *E. coli* was isolated from the faeces of 95% (2,123/2,243) of semi-domesticated reindeer; no pathogenic strains were detected after screening by PCR for stx1, stx2, eae and hlyEHEC virulence genes (Kemper *et al.* 2006). Wahlstrom *et al.* (2003) were unable to detect STEC O157

from the faeces of 285 wild and farmed roe, red and fallow deer in Sweden and STEC O157:H7 was cultured from the faeces of 0.25% (4/1,608) wild deer in Nebraska, USA (Renter *et al.* 2001). In the USA state of Louisiana, 0.3% (1/338) and 1.8% (1/55) of wild and farmed white-tailed deer, respectively, had STEC O157 cultured from faecal samples (Dunn *et al.* 2004) and in Ohio, 3.3% (1/30) of deer farms had STEC O157 detected in deer faeces (French *et al.* 2010). In a recent German study of wild red and roe deer, 72% (43/60) of deer excreted stx gene-positive faeces and STEC was isolated from 42% (25/60) of deer irrespective of the serogroup (Eggert *et al.* 2012). The review identified two studies that assessed STEC contamination of raw or processed venison. In Belgium, 46% (52/113) of wild venison samples were stx gene-positive by PCR and 16% (19/119) were culture positive; no isolates were STEC O157 (Pierard *et al.* 1997). In Spain, 46% (22/48) of frozen venison and 5% (2/37) of venison ready-to-eat meat products were stx-gene positive by PCR, for the same products 8% (4/48) and 3% (1/37), respectively, were culture positive and all were non-STE C O157 (Diaz-Sanchez *et al.* 2012).

- ***Campylobacter jejuni*** was isolated from the faeces of 0 - 3% of various deer species in Sweden and Norway (Wahlstrom *et al.* 2003; Lillehaug *et al.* 2005). Although *C. hyointestinalis* was isolated from the faeces of 0.04% (1/2243) reindeer in northern Finland and Norway, no *C. jejuni* was detected in this study (Kemper *et al.* 2006).
- ***Yersinia spp.*** was isolated by Kemper *et al.* (2006) from the faeces of 5% (108/2243) of reindeer in northern Finland and Norway and of these isolates, 28 were identified as *Y. enterocolitica*. In the USA, 30.3% of deer farms in Ohio (9/30) had deer infected with *Y. enterocolitica* (French *et al.* 2010).
- ***Listeria monocytogenes*** has been isolated from farmed deer in the USA. One out of thirty (3.3%) deer farms in Ohio isolated *L. monocytogenes* from faecal samples (French *et al.* 2010).
- ***Clostridium perfringens*** was isolated in Norway from faecal samples from 166 semi-domesticated reindeer; 59% (98/166) were culture positive and all carried the gene for α -toxin (Aschfalk *et al.* 2002). In the USA state of Ohio, 37% (11/30) of deer farms were positive for *C. difficile*, 7 of these farms yielded isolates with a toxigenic gene profile and 4 farms yielded isolates with the human epidemic ribotype 078 strain (French *et al.* 2010).

2.4.2. Viruses

- **Hepatitis E virus (HEV)** infections have been traced to venison. Human case isolates had identical nucleotide sequence homology with HEV isolated from frozen venison kept by one of the case patients; family members who did not consume the venison remained uninfected (Tei *et al.* 2003).

2.4.3. Parasites

- ***Toxoplasma gondi*** antibodies were detected in surveys conducted for a variety of wild and farmed deer species, including sika, white-tailed, black-tailed, mule, red, roe and reindeer, in Japan, Brazil, USA, France, Spain, Belgium, Czech Republic, Finland and Sweden (Lindsay *et al.* 1991; Chomel *et al.* 1994; Vanek *et al.* 1996; Ferreira *et al.* 1997; Dubey *et al.* 2004; Vikoren *et al.* 2004; Lindsay *et al.* 2005; Omata *et al.* 2005; Gauss *et al.* 2006; Bartova *et al.* 2007; Gamarra *et al.* 2008; Dubey *et al.* 2008; Dubey *et al.* 2009; Jokelainen *et al.* 2010; Panadero *et al.* 2010; Aubert *et al.* 2010; Malmsten *et al.* 2011; De Craeye *et al.* 2011; Matsumoto *et al.* 2011). The surveys indicate that toxoplasmosis is highly prevalent and widely distributed in the USA, Europe and Brazil, with very low prevalence observed in the two surveys of sika deer in Japan. Unlike cattle and buffalo, deer are not resistant to *T. gondii* infection and several studies have successfully demonstrated viability of *T. gondii* tissue cysts by feeding heart muscle from seropositive animals to mice. In one study in the USA, *T. gondii* was isolated from the hearts of 61% (21/34) of seropositive white-tailed deer (Dubey *et al.* 2004) and in another study, isolates were obtained from 21% (4/19) of seropositive white-tailed deer (Lindsay *et al.* 1991). In France, *T. gondii* cysts were isolated from 36% (12/33) of seropositive roe deer and 25% (1/4) of red deer (Aubert *et al.* 2010). Genotype II *T. gondii* has been isolated from deer in the USA and France (Dubey *et al.* 2004; Aubert *et al.* 2010).

2.4.4. Other agents

- Chronic wasting disease (CWD) is a fatal transmissible spongiform encephalopathy (TSE) disease. It is currently known to infect farmed and free-ranging deer, elk, and moose in North America and Scandinavia, and has not been detected to date in Australia. No treatment is known and the disease is typically fatal. The TSE group of diseases includes bovine spongiform encephalopathy (BSE) in cattle, scrapie in sheep and goats, and Creutzfeldt-Jacob disease (CJD) in humans. There is no evidence currently that CWD is zoonotic.

2.5. Kangaroo and wallaby

2.5.1. Bacteria

- A study by Rupan *et al.* (2012) demonstrated that kangaroos are a potential carrier of pathogenic *Escherichia coli*, but the public health importance of kangaroos with respect to the transmission of pathogenic *E. coli* to humans could not be determined. No outbreaks or cases of salmonellosis or pathogenic *E. coli* infection have been associated with the consumption of kangaroo meat. A survey of Australian marsupials in south east Queensland found 8.6% (13/151) of wild eastern grey kangaroos were infected with *E. coli* that were stx gene-positive by PCR; none of the detected isolates had an O serotype that was typically associated with human STEC (Rupan *et al.* 2012). Several studies have assessed the microbiological quality of kangaroo carcasses at processing plants and kangaroo meat at retail premises, two in Queensland and two in South Australia.
- A survey in Queensland detected *Salmonella* in 25 g meat samples in 0.84% (7/836) of kangaroo carcasses sampled from February 2003 to February 2006; *Salmonella* was only detected on carcasses sampled in January and February. *E. coli* and aerobic bacteria were detected on 13.9% (116/836) and 68.7% (574/836) of carcasses, respectively. The mean bacterial count for *E. coli* and aerobic bacteria was 0.7 and 2.8 log cfu/g, respectively (Eglezos *et al.* 2007). In comparison, a smaller study reported in 1991 found 11% (9/81) of processed kangaroo carcasses were contaminated with *Salmonella* and 49% (40/81) were contaminated with coliforms with a mean count of 3.54 log coliforms/g and the mean total count of 5.2 log/g of muscle (Bensink *et al.* 1991). In South Australia, a small survey of kangaroo meat purchased from retail outlets in Adelaide in 2002 found 31% (11/35) of steaks and 49% (17/35) of mince samples were contaminated with *Salmonella*. *Campylobacter* spp. was not isolated from kangaroo samples collected in this retail survey (Delroy *et al.* 2008). A survey of five processing plants in 2002 and 2004 in South Australia detected *Salmonella* on 1% (4/385) of carcasses. Eighteen per cent (9/50) of minced kangaroo meat samples in 2002 were found to be contaminated with *Salmonella*. Six of the contaminated minced meat samples came from a single processor. Seventy per cent (70/120) of minced meat samples collected in 2002 were contaminated with *E. coli* with a mean count of 2.1 log cfu/g (Holds *et al.* 2008). It is not possible to make comparisons between the different studies due to the different sampling strategies and testing protocols used
- *Salmonella* was detected in faecal samples of commercially harvested western grey kangaroos from ten locations in Western Australia was 3.6% (23/645), ranging from 0% to 9.8%. *Salmonella* was only detected in kangaroos from six locations and prevalence was significantly associated with increased rainfall in the 30 days prior to sample collection (Potter *et al.* 2011). The authors of this study did not report multivariable analysis and it was therefore not clear if the significant geographical differences in prevalence were due to variable rainfall patterns between the collection sites. All isolates were *Salmonella enterica* and the most frequently isolated serovar was Muenchen (12/23), followed by Kiambu (6/23). Other serovars detected were Lindern, Champaign, Saintpaul, II 42:g,t:-, and Rubislaw (Potter *et al.* 2011).

2.5.2. Parasites

- No confirmed cases of **toxoplasmosis** in humans have been linked to the consumption of kangaroo or wallaby meat. A presumptive outbreak of toxoplasmosis in humans was linked to consuming kangaroo meat in 1994 (Robson *et al.* 1995), however the study was unable to confirm kangaroo meat as a source of the outbreak. A serological survey of western grey kangaroos culled from seven sites around Perth found 15.5% (34/219) positive for *Toxoplasma gondii* antibodies; *T. gondii* DNA was detected by PCR from brain, tongue and heart muscle samples collected from nine seropositive kangaroos, and DNA was not detected in the tissue samples of nine seronegative kangaroos (Parameswaran *et al.* 2009). A relatively small study of the genotypes circulating in Australian marsupials found kangaroos were infected predominantly with atypical

strains and a small number were infected with archetypal genotypes I and II strains, with all isolates being avirulent in mice. One atypical isolate from a Tasmanian wallaby caused neurologic disease in mice (Parameswaran *et al.* 2010).

- ***Cryptosporidium*** - oocysts in faecal samples from a population of wild eastern grey kangaroos inhabiting a protected watershed in Sydney, Australia. Over a 2-year period, *Cryptosporidium* oocysts were detected in 239 of the 3,557 (6.7%) eastern grey kangaroo faecal samples tested by using a combined immunomagnetic separation and flow cytometric technique. The prevalence of *Cryptosporidium* in this host population was estimated to range from 0.32% to 28.5%, with peaks occurring during the autumn months. Oocyst shedding intensity ranged from below 20 oocysts/g faeces to 2.0×10^6 oocysts/g faeces, and shedding did not appear to be associated with diarrhea. Although morphologically similar to the human-infective *Cryptosporidium hominis* and the *Cryptosporidium parvum* “bovine” genotype oocysts, the oocysts isolated from kangaroo faecal samples were identified as the *Cryptosporidium* “marsupial” genotype I or “marsupial” genotype II. Kangaroos are the predominant large mammal inhabiting Australian watersheds and are potentially a significant source of *Cryptosporidium* contamination of drinking water reservoirs. However, this host population was predominantly shedding the marsupial-derived genotypes, which to date have been identified only in marsupial host species.

2.6. Horses

Domestic horses arrived in Australia with the First Fleet in 1788. The first record of escape or release was in 1804. Feral horses were first recognised as ‘pests’ in the 1860s. Currently, there may be more than 400 000 feral horses in Australia.

Meat of invasive and domestic horses is sold as pet food and exported to Europe for human consumption. A comprehensive search of the literature found no published articles describing the prevalence or level of contamination of microbiological hazards on carcasses or on final processed products in Australia. International literature provides data on a number of foodborne pathogens and some information on foodborne illness associations. A French study by Pomares *et al.* (2011) describes three human cases of *Toxoplasma gondii* infection, linked to the consumption of undercooked imported horse meat from the USA and Canada.

3. CONCLUSION

This report has demonstrated a range of pathogenic bacteria, viruses, parasitic helminths and protozoa that are carried by invasive species in Australia. As a result of these pathogens and the diseases they cause, the harvesting of invasive animals for human or pet consumption is likely to carry risks of food safety and human health unless mitigating procedures are adopted and implemented.

In addition to potential threats to food safety and human health, these pathogens and diseases present risks to wildlife and domestic animals. According to Gortazar *et al.* (2007), one area that causes concern to authorities is that diseases largely under control in domestic populations may still exist as a reservoir in invasive and wildlife species.

This review provides evidence of the potential for transmission of pathogens from invasive populations in high-risk areas (e.g. in close proximity to livestock, or in coexistence in high densities with wildlife species), or where other environmental conditions become favourable (e.g. from a change in climate, land use and cultural behaviour).

Further research is required to improve our understanding and knowledge of the diseases circulating in invasive species in Victoria, the risks posed to food safety and human health, and mitigating procedures or steps required to reduce these risks.

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