

# Parasitology

<http://journals.cambridge.org/PAR>

Additional services for **Parasitology**:

Email alerts: [Click here](#)

Subscriptions: [Click here](#)

Commercial reprints: [Click here](#)

Terms of use : [Click here](#)



---

## ***Cryptosporidium* species in Australian wildlife and domestic animals**

UNA RYAN and MICHELLE POWER

Parasitology / Volume 139 / Issue 13 / November 2012, pp 1673 - 1688  
DOI: 10.1017/S0031182012001151, Published online: 20 August 2012

**Link to this article:** [http://journals.cambridge.org/abstract\\_S0031182012001151](http://journals.cambridge.org/abstract_S0031182012001151)

### **How to cite this article:**

UNA RYAN and MICHELLE POWER (2012). *Cryptosporidium* species in Australian wildlife and domestic animals. Parasitology, 139, pp 1673-1688 doi:10.1017/S0031182012001151

**Request Permissions :** [Click here](#)

## REVIEW ARTICLE

*Cryptosporidium* species in Australian wildlife and domestic animalsUNA RYAN<sup>1\*</sup> and MICHELLE POWER<sup>2</sup><sup>1</sup> *Division of Veterinary and Biomedical Sciences, Murdoch University, Murdoch, Western Australia, 6150*<sup>2</sup> *Department of Biological Sciences, Macquarie University, North Ryde, Sydney NSW 2109, Australia*

(Received 29 April 2012; revised 11 June 2012; accepted 13 June 2012; first published online 20 August 2012)

## SUMMARY

*Cryptosporidium* is an important enteric parasite that is transmitted via the fecal-oral route, water and food. Humans, wildlife and domestic livestock all potentially contribute *Cryptosporidium* to surface waters. Most species of *Cryptosporidium* are morphologically indistinguishable and can only be identified using molecular tools. Over 24 species have been identified and of these, 7 *Cryptosporidium* species/genotypes are responsible for most human cryptosporidiosis cases. In Australia, relatively few genotyping studies have been conducted. Six *Cryptosporidium* species (*C. hominis*, *C. parvum*, *C. meleagridis*, *C. fayeri*, *C. andersoni* and *C. bovis*) have been identified in humans in Australia. However, little is known about the contribution of animal hosts to human pathogenic strains of *Cryptosporidium* in drinking water catchments. In this review, we focus on the available genotyping data for native, feral and domestic animals inhabiting drinking water catchments in Australia to provide an improved understanding of the public health implications and to identify key research gaps.

Key words: *Cryptosporidium*, zoonotic, genotype, marsupials, sheep, cattle.

## INTRODUCTION

*Cryptosporidium* spp. are parasitic protists that infect a wide range of vertebrates including humans (Xiao and Ryan, 2004; Xiao, 2010). The parasite causes self-limiting diarrhoea in immunocompetent individuals but may be chronic and life threatening to those that are immunocompromised (Hunter *et al.* 2007). Humans can acquire *Cryptosporidium* infections through various transmission routes, such as direct contact with infected persons (person-to-person transmission) or animals (zoonotic transmission) and ingestion of contaminated food (foodborne transmission) or water (waterborne transmission) (Karanis *et al.* 2007; Xiao, 2010). Molecular data indicate that 7 *Cryptosporidium* species/genotypes are responsible for most human cryptosporidiosis cases, including *C. hominis*, *C. parvum*, *C. meleagridis*, *C. felis*, *C. canis*, *C. ubiquitum*, *C. cuniculus* (Xiao and Feng, 2008; Xiao, 2010; Chalmers *et al.* 2011) with *C. parvum* and *C. hominis* by far the most common species in humans worldwide (Xiao, 2010).

In Australia, 3 *Cryptosporidium* species (*C. hominis*, *C. parvum* and *C. meleagridis*) have been

identified in humans in Western Australia (WA), New South Wales (NSW), Victoria (VIC) and South Australia (SA), with *C. hominis* being the most frequently identified species of the 3 (Robertson *et al.* 2002; Chalmers *et al.* 2005; Jex *et al.* 2007; Ng *et al.* 2008; O'Brien *et al.* 2008, Jex *et al.* 2008; Alagappan *et al.* 2008; Waldron *et al.* 2009a,b; Ng *et al.* 2010a,b; 2012; Waldron and Power, 2011; Waldron *et al.* 2011a,b). Recently, *C. fayeri*, *C. andersoni* and *C. bovis* have been identified in individual human cases in NSW (Waldron *et al.* 2010, 2011a; Ng *et al.* 2012).

A major mode of transmission of *Cryptosporidium* is via contaminated drinking and recreational waters. The oocyst is the environmentally stable stage and is able to survive and penetrate routine wastewater treatment and is resistant to inactivation by commonly used drinking water disinfectants (Fayer *et al.* 2000). Of the waterborne protozoan parasitic outbreaks that have been reported worldwide between 2004 and 2010, *Cryptosporidium* was the aetiological agent in 60.3% (120) of the outbreaks (Baldursson and Karanis, 2011). Oocyst transport to surface water can occur by deposition of manure directly in the water or by wash off in surface runoff. Humans, wildlife and domestic livestock all potentially contribute *Cryptosporidium* to surface waters. A significant knowledge gap in assessing microbial risks to surface waters is the lack of genotyping data on the

\* Author for correspondence: Division of Health Sciences, School of Veterinary and Biomedical Sciences, Murdoch University, Murdoch, Perth WA 6150. Tel: +6189360 2482. Fax: +6189310 4144. E-mail: Una.Ryan@murdoch.edu.au

Table 1. Estimates of wildlife animal density for native vegetation land use areas

Animal	Country	Density (per km <sup>2</sup> )	Reference
Kangaroos	Australia	400–500	Fletcher (2007)
Kangaroos	Australia	~ 500	West (2008)
Kangaroos	Vic	178	Ramp (2002)
Pigs (feral)	WA	2	Dr Peter Adams, <i>personal communication</i>
Pigs (feral)	Qld	1–> 20	Dexter (1990)
Pigs (feral)	NSW	2	Saunders and Kay (1991)
Rodents	UK	Similar to human population	O'Keefe <i>et al.</i> (2003)
Rabbits	Australia	50–400	Williams <i>et al.</i> (1995)
Foxes	Australia	1–7·2	Saunders <i>et al.</i> (1995)
Dogs (feral)	Australia	0·25	Ferguson (2010)
Cats (feral)	Australia	1–57	Dickman (1996)

Table 2. Manure production rates for wildlife animals

Animal	Country	Kg manure/ animal <sup>-1</sup> /d <sup>-1</sup>	Reference
Kangaroos	Australia, Canberra	0·3	Dr Peter Adams, <i>personal communication</i>
Pigs (feral)	Western Australia	4–5	Dr Peter Adams, <i>personal communication</i>
Deer	USA	1–2	Anonymus (2003)
Rabbits	Netherlands	0·019	Medema (1999)
Dogs (feral)	Australia	0·003–0·014	Anonymus (2002)

contribution of animal hosts to human pathogenic strains of *Cryptosporidium* in drinking water catchments in Australia. Identification of the sources/carriers of human pathogenic strains is essential for accurate risk assessment and catchment management.

This review examines the current information from Australia on the prevalence and genotypes of *Cryptosporidium* identified in wildlife and domestic livestock to assist our understanding of the key host species contributing human pathogenic *Cryptosporidium* species to Australian water catchments.

#### SPECIES AND STRAINS OF *CRYPTOSPORIDIUM* INFECTING WILDLIFE

##### *Wildlife population density*

Animal density by area is an important determinant of pathogen loadings as higher animal density results in a larger volume of manure excreted per unit area. Thus there is an increase in pathogen source material that may be transported in runoff to surface waters and/or deposited directly to streams (Ferguson, 2010). It is difficult to quantify animal densities for wildlife, because animal movement is uncontrolled and because animal populations vary with season and environmental conditions, with many species being migratory but published values and estimates are summarized in Table 1.

##### *Volume of wildlife manure*

Manure excretion rates and volumes for wildlife are less well documented than for domestic animals. An estimate of the volume of manure produced by wildlife, however, is important to assess the impact of wildlife manure on catchments. Estimates of manure production rates for wildlife are shown in Table 2.

##### *Marsupials*

In Australia, marsupials are the dominant animals inhabiting many water catchment areas (Power, 2010) with densities >500 per square km sometimes recorded (West, 2008). Therefore, it is important to determine the potential role that marsupial species play in the dissemination of *Cryptosporidium* to drinking water sources and the associated human health risks associated with this. To date, *Cryptosporidium* has been identified in 15 Australian marsupial species and 7 of these host species belong to the family Macropodidae (kangaroos and wallabies) (Power, 2010; Yang *et al.* 2011; Dowle *et al.*, unpublished observations).

The prevalence of *Cryptosporidium* in marsupials varies, as does the oocyst shedding rate. In New South Wales (NSW), the prevalence of *Cryptosporidium* in fecal samples from eastern grey kangaroos (*Macropus giganteus*) was 6·3% (239/3,557) (Power

Table 3. *Cryptosporidium* species identified in marsupial hosts in Australia

Host species	<i>Cryptosporidium</i> species identified	Prevalence	Location	Reference
Red kangaroo ( <i>Macropus rufus</i> )	<i>C. fayeri</i>	N/A*	NSW	Morgan <i>et al.</i> (1997)
Koala ( <i>Phascolarctos cinereus</i> )	<i>C. fayeri</i>	N/A	NSW	Morgan <i>et al.</i> (1997)
Eastern grey kangaroos ( <i>Macropus giganteus</i> )	<i>C. fayeri</i> and <i>C. macropodum</i>	6.7%	NSW	Power <i>et al.</i> (2003, 2004, 2005)
Eastern grey kangaroos ( <i>Macropus giganteus</i> )	<i>C. macropodum</i> , <i>C. parvum</i> , <i>C. hominis</i>	16.9%	NSW	Ng <i>et al.</i> (2011a)
Yellow-footed rock wallaby ( <i>Petrogale xanthopus</i> ), Wallaby (no species identification)	<i>C. fayeri</i>	N/A	NSW	Power <i>et al.</i> (2009)
Swamp wallaby ( <i>Wallabia bicolor</i> )	<i>C. parvum</i>	5.9%	NSW	Ng <i>et al.</i> (2011a)
Western-barred bandicoot ( <i>Peremeles bougainville</i> )	<i>C. macropodum</i>	N.A	NSW	Ryan <i>et al.</i> , unpublished observations
Western grey kangaroos ( <i>Macropus fuliginosus</i> )	<i>C. fayeri</i>	N/A	WA	Weilinga <i>et al.</i> , unpublished observations
Bilby ( <i>Macrotis lagotis</i> )	<i>C. fayeri</i> , <i>C. macropodum</i> , kangaroo genotype I, <i>C. xiaoi</i>	9.3%	WA	McCarthy <i>et al.</i> (2008); Yang <i>et al.</i> (2011)
Long-nosed bandicoot ( <i>Perameles nasuta</i> )	<i>C. muris</i>	N/A	WA	Warren <i>et al.</i> (2003)
Southern Brown Bandicoot ( <i>Isodon obesulus</i> )	<i>C. parvum/hominis</i> like	9.3%	NSW	Dowle <i>et al.</i> , unpublished observations
Brush tail possum ( <i>Trichosurus vulpecula</i> )	<i>C. parvum/hominis</i> like	16.7%	NSW	Dowle <i>et al.</i> , unpublished observations
Brush tail possum ( <i>Trichosurus vulpecula</i> )	Brush tail possum genotype I, <i>C. parvum/hominis</i> -like.	11.3% (urban) 5.6% (wild)	NSW	Hill <i>et al.</i> (2008)

\* N/A, not attempted (in many cases only 1 sample was available).

*et al.* 2005). Oocyst shedding ranged from 20/g feces to  $2.0 \times 10^6$ /g feces (Power *et al.* 2005). Another study in NSW on common brushtail possums (*Trichosurus vulpecula*) reported that *Cryptosporidium* occurred with a higher prevalence in possums from urban habitats (11.3%) than in possums from woodland habitats (5.6%) (Hill *et al.* 2008). In Western Australia (WA), the prevalence of *Cryptosporidium* in wild western grey kangaroos (*Macropus fuliginosus*), was 9.3% (Yang *et al.* 2011). Prevalences can be seasonal with one study in NSW on eastern grey kangaroos reporting the highest rate was found in autumn (Power *et al.* 2004), while a study in WA on western grey kangaroos reported that the highest prevalence was detected in summer (Yang *et al.* 2011).

The main species identified in marsupials are *C. fayeri* and *C. macropodum* (previously marsupial genotype I and II) (Morgan *et al.* 1997; Power *et al.* 2004, 2005, 2009; McCarthy *et al.* 2008; Power and Ryan, 2008; Ryan *et al.* 2008; Power, 2010; Ng *et al.* 2011a). *Cryptosporidium fayeri* and *C. macropodum* have been reported in a red kangaroo (*Macropus rufus*), a koala (*Phascolarctos cinereus*), eastern grey kangaroos, (*M. giganteus*), western grey kangaroos (*M. fuliginosus*), a yellow-footed rock wallaby (*Petrogale xanthopus*), a swamp wallaby (*Wallabia bicolor*), a wallaby (no species identification) and a western-barred bandicoot (*Peremeles bougainville*) (Morgan *et al.* 1997; Power *et al.* 2004; 2009;

McCarthy *et al.* 2008; Ryan *et al.*, unpublished observations; Weilinga *et al.*, unpublished observations; Yang *et al.* 2011; Ng *et al.* 2011a) (Table 3). Neither of these species is associated with diarrhoea in their marsupial hosts (Power and Ryan, 2008; Ryan *et al.* 2008); however, *C. fayeri* has recently been identified in a 29-year-old woman in Sydney in 2009 (Waldron *et al.* 2010). The woman was immuno-competent but suffered prolonged gastrointestinal illness. The patient resided in a national forest on the east coast of New South Wales, Australia, an area where marsupials are abundant. She had frequent contact with partially domesticated marsupials (Waldron *et al.* 2010). Identification of *C. fayeri* in a human patient is a concern for water catchment authorities in the Sydney region. The main water supply for Sydney, Warragamba Dam, covers 9050 km<sup>2</sup> and is surrounded by national forest inhabited by diverse and abundant marsupials. The same *C. fayeri* subtype (IVaA9G4T1R1) was also identified in eastern grey kangaroos in Warragamba Dam (Power *et al.* 2009).

In addition to *C. fayeri* and *C. macropodum*, there have been several other host-adapted strains identified in Australian marsupials. Possum genotype I has been described in brush tail possums, a host species found in a range of habitats throughout Australia (Hill *et al.* 2008) and the novel kangaroo genotype I in western grey kangaroos (Yang *et al.* 2011). These *Cryptosporidium* genotypes were genetically distinct and the range of genetic similarities to all other

*Cryptosporidium* species at the 18S rRNA locus was 87.4–97.4% and at the actin locus it was 77.9–86.5%. This is within the range of the percentage similarities between currently accepted *Cryptosporidium* species at the 18S rRNA locus (89–99.8%) and the actin locus (76–98.7%) and is one of the criteria used to delimit species within the genus *Cryptosporidium* (Xiao and Ryan, 2004). Possum genotype 1 and kangaroo genotype I have not been reported in humans or other animals, and the zoonotic potential is unknown.

*Cryptosporidium* species typically found in non-marsupial mammalian hosts have also been reported in marsupial species. *Cryptosporidium muris*, commonly found in rodents, has been identified in bilbies (*Macrotis lagotis*) (Warren *et al.* 2003). In that report, oocyst morphology combined with molecular analyses confirmed the presence of *C. muris* in 11/28 (39.2%) bilbies housed at a captive breeding colony in WA (Warren *et al.* 2003). One mouse was trapped in the breeding enclosures and found to be positive for *C. muris*. It is likely that the bilbies acquired the infection from mice by fecal contamination of food and water. *Cryptosporidium xiaoi*, commonly found in sheep, has been identified in 6 wild western grey kangaroos in WA (Yang *et al.* 2011). The identification of *C. xiaoi* in the kangaroos suggests that they may have picked up the infection from grazing on sheep pastures. In a previous study on sheep, *C. fayeri* was identified in 4 sheep fecal samples (Ryan *et al.* 2005), indicating that grazing on contaminated pastures can result in transmission. Whether the kangaroos were actually infected or simply mechanically transmitting the organism remains to be determined.

There have also been reports of *C. parvum* and *C. hominis* in kangaroos (*M. giganteus*, a wallaby (no species identification), possums (*Trichosuris vulpecula*) and bandicoots (*Isoodon obesulus*) (Ng *et al.* 2011a; Hill *et al.* 2008; Dowle *et al.*, unpublished observations). These identifications were based on direct DNA extraction from feces and subsequent PCR screening. In all cases *Cryptosporidium* could only be amplified at the multi-copy 18S rDNA locus, other loci tested were single copy targets (Ng *et al.* 2011a; Hill *et al.* 2008; Dowle *et al.*, unpublished observations). The inability to amplify other loci may be due to low levels of *Cryptosporidium* present in the samples. Immunomagnetic separation coupled to cell sorting was used to determine oocyst numbers in *C. parvum* and *C. hominis* positive fecal samples in bandicoots and possums (Hill *et al.* 2008; Dowle *et al.*, unpublished observations). The authors reported that most samples contained less than 10 oocysts per gramme of feces. In those studies, the marsupial hosts were inhabiting areas associated with humans. It remains to be determined whether these marsupials were actually infected with *C. parvum* or *C. hominis* or whether they were simply passively transmitting the oocysts. Further studies are required

to clarify the potential role that marsupials play in contamination of the catchment with human-infectious oocysts.

#### *Feral and domestic pigs*

Pigs were introduced to Australia with the First Fleet in 1788 and today domestic pigs are agriculturally important, in addition to being pest species. Feral pig populations are now found within 40% of Australia's ecosystem (West, 2008) and represent a potential risk to drinking water supplies. It has been reported that Australia has the largest number of wild pigs in the world with an estimated 23 million feral pigs (Hampton *et al.* 2006). The high density of feral pigs, their foraging and wallowing behaviour of pigs, which can markedly increase the turbidity of water supplies and their ability to transmit and excrete a number of infectious waterborne organisms pathogenic to humans have made them a target for intense management for the protection of source (drinking) water supplies (Atwill *et al.* 1997; Hampton *et al.* 2006).

Little is known about the prevalence of *Cryptosporidium* in feral pigs. A study in California reported that 12 (5.4%) of 221 feral pigs were shedding *Cryptosporidium* oocysts (Atwill *et al.* 1997). The authors also reported that younger pigs (<or=8 months) and pigs from high-density populations (>2.0 feral pigs/km<sup>2</sup>) were significantly more likely to shed oocysts compared to older pigs (>8 months) and pigs from low-density populations (<or=1.9 feral pigs/km<sup>2</sup>) (Atwill *et al.* 1997). This trend makes reduction of feral pig abundance in high-density catchment areas even more important to reduce the risk of waterborne feral pig pathogens being introduced to reservoirs. In Spain, a prevalence of 7.6% was reported for wild boar and infections were significantly higher in juvenile male wild boars (22%) than in adult males (6%) (Castro-Hermida *et al.* 2011). The mean intensity of infection by *Cryptosporidium* was 5 to 200 oocysts per gramme of faeces (Castro-Hermida *et al.* 2011). A study in WA reported a prevalence of 0.3% (1/292) (Hampton *et al.* 2006). Genotyping attempts were unsuccessful. A more recent study of 237 wild pigs in WA, did not identify *Cryptosporidium* by PCR (Pallant *et al.*, unpublished observations).

Studies in Australia on domestic pigs have identified prevalence rates of 6–22.1% (Ryan *et al.* 2003, 2004; Johnson *et al.* 2008). The main *Cryptosporidium* species identified in pigs in Australia and worldwide are *C. suis* and pig genotype II, although *C. muris*, *C. tyzzeri* and *C. parvum* have also been reported (Ryan *et al.* 2003; Xiao *et al.* 2006; Zintel *et al.* 2007; Johnson *et al.* 2008; Kvac *et al.* 2009a; Jeníková *et al.* 2010; Jenkins *et al.* 2010; Sevá Ada *et al.* 2010; Xiao, 2010; Wang *et al.* 2010a;

Budu-Amoako *et al.* 2012; Chen *et al.* 2011; Farzan *et al.* 2011; Fiuza *et al.* 2011a; Yin *et al.* 2011). *Cryptosporidium suis* has been reported in humans (Xiao *et al.* 2002a; Xiao, 2010) and has frequently been recovered from water samples (Feng *et al.* 2011a). Pig genotype II has also been reported in an immunocompetent human (Kvác *et al.* 2009b).

*Cryptosporidium parvum* has been reported once in pigs from an indoor farm in Western Australia, in four 19-day-old pre-weaned piglets with diarrhoea (Morgan *et al.* 1999a). There have been 4 additional reports of *C. parvum* in pigs internationally; in asymptomatic sows from intensive commercial pig production units in Ireland (Zintel *et al.* 2007); in 2 piglets from Prince Edward Island, Canada (Budu-Amoako *et al.* 2012), in piglets in Ontario where it was the most prevalent species detected (55.4%) (Farzan *et al.* 2011) and in pig slurry lagoons in the US (Jenkins *et al.* 2010). This suggests that pigs may play an important role in the transmission of zoonotic *Cryptosporidium*. However, further research is required to understand the prevalence of *Cryptosporidium* species in feral pigs.

#### Deer

*Cryptosporidium* species have been found in various species of deer and the prevalence rates differed by study locations and animal species ranging from 0–100% (cf. Feng, 2010). *Cryptosporidium ubiquitum*, the deer genotype, *C. parvum* and a *C. hominis*-like genotype have been reported in wild deer (cf. Amer *et al.* 2009; Jellison *et al.* 2009; Feng, 2010).

Few studies have been conducted in wild deer in Australia (Cinque *et al.* 2008; Ng *et al.* 2011a). In a recent study in NSW, only 1 deer was positive out of 137 isolates screened (0.7%) (Ng *et al.* 2011a) and the target 18S rRNA sequence was identical to *Cryptosporidium* environmental sequence isolate 8059 (GenBank Accession no. AY737603) from water previously identified in New York storm water in the US (Jiang *et al.* 2005). The other study was conducted on Sambar deer (*Cervus unicolor*) from Melbourne catchments (Cinque *et al.* 2008). In that study, 16/32 pooled fecal samples were positive for *Cryptosporidium* and 7 of these were identified as *C. parvum* by sequence analysis of the 18S ribosomal RNA gene (Cinque *et al.* 2008). Analysis of a further 600 samples using PCR-based (single strand conformation polymorphism (SSCP) analysis and selective sequencing of the second internal transcribed spacer (ITS-2) as well as 18S rRNA and the glycoprotein 60 (*gp60*) gene did not identify *C. parvum* (Cinque *et al.* 2008). As both *C. parvum* and *C. ubiquitum* are infectious to humans, further research is required to understand the contribution of deer to catchment contamination with human-infectious species of *Cryptosporidium*.

#### Rodents

Mice are closely associated with human activity and are now distributed throughout the Australian continent, especially in agricultural and urban areas. The black rat (*Rattus rattus*), which originated in tropical mainland Asia and, later spreading to Europe and the rest of the world (Musser and Carleton, 1993), is now found throughout much of coastal Australia including urban and peri-urban habitats (West, 2008). Rodents, which are abundant and widespread, have been considered reservoirs of cryptosporidiosis in humans and farm animals (Lv *et al.* 2009). Nearly 40 rodent species belonging to 11 families (Sciuridae, Muridae, Cricetidae, Castoridae, Geomyidae, Hystricidae, Erethizontidae, Myocastoridae, Caviidae, Hydrochoeridae, and Chinchillidae) have been reported as hosts of *Cryptosporidium* spp. (cf. Lv *et al.* 2009; Feng, 2010). These include mice (*Mus musculus*, *M. spretus*, *Apodemus flavicollis*, *A. sylvaticus*, *A. speciosus*, *Peromyscus* sp.), rats (*Rattus norvegicus*, *R. rattus*), voles (*Clethrionomys glareolus*, *Clethrionomys gapperi*, *Microtus arvalis*, *M. agrestis*, *M. pennsylvanicus*, *Myodes gapperi*), muskrat (*Ondatra zibethicus*) and squirrels (*Spermophilus beecheyi*, *Sciurus carolinensis*, *Tamiasciurus hudsonicus*, *Sciurus vulgaris*) (Lv *et al.* 2009; Feng, 2010).

Prior to genotyping studies, it was thought that rodents were infected with *C. parvum* and *C. muris* (Feng, 2010). However, it is now believed that most infections in house mice are *C. tyzzeri* (formerly mouse genotype I), which differs significantly from *C. parvum* (Xiao *et al.* 2004; Ren *et al.* 2011). Thus, house mice are commonly infected with *C. muris* and *C. tyzzeri*, and occasionally with the mouse genotype II (Morgan *et al.* 1999c, 2000; Foo *et al.* 2007). Confirmed *C. parvum* infections have been reported in only a few rodents (Morgan *et al.* 1999c; Lv *et al.* 2009; Feng, 2010).

Several species/genotypes have been identified in rats including *C. tyzzeri* and 4 rat genotypes (I–IV) (Lv *et al.* 2009). Rat genotype 1 has previously been identified in a boa constrictor in the US (Xiao *et al.* 2004) and in wastewater in Shanghai (Feng *et al.* 2009) and the UK (Chalmers *et al.* 2010). Rat genotypes II and III have previously been described from brown rats (*Rattus norvegicus*) and Asian house rats (*Rattus tanezumi*) from China (Lv *et al.* 2009). Rat genotype IV (previously W19) has been identified in storm-water (Jiang *et al.* 2005; Lv *et al.* 2009). Despite the identification of *Cryptosporidium* rodent genotypes from stormwater and wastewater (Jiang *et al.* 2005; Feng *et al.* 2009; Lv *et al.* 2009; Chalmers *et al.* 2010), the contribution of rodents to contamination of drinking water supplies with *Cryptosporidium* is not well understood.

In Australia, *C. tyzzeri*, mouse genotype II and rat-like genotypes have been identified in mice

(Morgan *et al.* 1999b,c; Foo *et al.* 2007) and rat-like genotypes have been identified in black rats (Paparini *et al.* 2012). Recent evidence suggests that *C. tyzzeri*, however, could be a human pathogen, as subtype analysis at the hypervariable *gp60* locus identified a *C. tyzzeri* subtype in a symptomatic Kuwaiti child (Sulaiman *et al.* 2005; Feng *et al.* 2011b). Further studies are needed to determine the zoonotic potential of *C. tyzzeri*. This species was previously assumed to be *C. parvum* but subsequent re-analysis identified it as *C. tyzzeri* (Feng *et al.* 2011b). *Cryptosporidium parvum* has not been identified in Australian rodents but has been identified in mice in the UK (Morgan *et al.* 1999c). Limited studies of *Cryptosporidium* in rodents have been undertaken in Australia. Given the occurrence of zoonotic species in this host in other countries, it may represent an important reservoir for human infective species and requires further study.

### Rabbits

Rabbits (*Oryctolagus cuniculus*) were introduced in the mid- to late 1800s, are presently found in all states and territories throughout Australia and are one of the most widely distributed and abundant mammals in Australia. Rabbits presently inhabit an estimated 70% (i.e. 5.33 million square kilometres) of Australia and populations can reach 300–400 per square kilometre (Williams *et al.* 1995).

Our current knowledge and understanding of *Cryptosporidium* in rabbits is limited. In Australia, only 2 studies have been conducted. One study screened 176 fecal samples from rabbits from 4 locations northeast of Melbourne (< 90 km apart) in Victoria. The prevalence rate was 6.8% and all positives were identified as *C. cuniculus* (Nolan *et al.* 2010). Another screened 3 rabbits near the Denmark River in WA and found 1 positive, which was identified as *C. cuniculus* (Ferguson, 2010). The prevalence of *Cryptosporidium* in rabbits in other countries ranges from 0.9 to 42.9% (Robinson and Chalmers, 2010; Shi *et al.* 2010) and genotyping studies have all have identified that rabbits harbour *C. cuniculus* (previously the 'rabbit' genotype (cf. Robinson and Chalmers, 2010; Nolan *et al.* 2010; Ferguson, 2010; Shi *et al.* 2010).

*Cryptosporidium cuniculus* was initially thought to be host-specific until the recent discovery that *C. cuniculus* was linked to a human cryptosporidiosis outbreak in the UK (Chalmers *et al.* 2009), which has raised considerable awareness about the importance of investigating rabbits as a source of *Cryptosporidium* transmissible to humans. A recent study in the UK reported that *C. cuniculus* was the third most commonly identified *Cryptosporidium* species in patients with diarrhoea (Chalmers *et al.* 2011). *Cryptosporidium cuniculus* has a close genetic

relationship with *C. hominis* with limited differences at the 18S rRNA, *hsp70* and actin genes (0.51%, 0.25% and 0.12%, respectively) and only 0.27% of base pairs when combined multiple loci (4469 bp) were investigated (Robinson *et al.* 2010). *C. cuniculus* has also recently been identified in children in Nigeria (Molloy *et al.* 2010).

Rabbits are susceptible to experimental infection with *C. cuniculus*, *C. parvum* and *C. meleagridis* (Robinson and Chalmers, 2010). All these species are human pathogens and the role of rabbits as a potential source of zoonotic *Cryptosporidium* must be considered, although direct contact with rabbits or their feces has not been identified as a risk factor for human cryptosporidiosis (Robinson and Chalmers, 2010). However, our understanding of the potential risks from rabbits for human infection with *Cryptosporidium* is still at an early stage and its genetic similarity to *C. hominis* and the recent finding of the parasite in humans in the UK and children in Nigeria, indicate that rabbits can be a potential reservoir of zoonotic cryptosporidiosis. More systematic characterization of the parasite is needed to understand the taxonomic status of *C. cuniculus* and its public health significance.

### Foxes, wild dogs and feral cats

The wild dog population of Australia comprises all wild-living dogs and includes dingoes (*Canis lupus dingo*), feral dogs (*Canis lupus familiaris*) and their hybrids. They are distributed widely throughout the country and are pests in many agricultural areas. Wild dogs presently inhabit an estimated 82.8% (i.e. 6.3 million square kilometres) of Australia (West, 2008). Dingoes are thought to be descendants of East Asian dogs that were first introduced to Australia about 3500–4000 years ago (Corbett, 1995). Feral dogs are descendants of European domestic dogs that were introduced over the past 200 years.

The European red fox is one of the most widely spread feral animals in Australia and Australia's number one predator threatening the long-term survival of a many native wildlife species. The fox is found ranging from Australia's arid centre to the alps and coastal areas, and is also abundant in urban areas (West, 2008).

Domestic cats (*Felis catus*) were introduced to Australia either before or during European settlement and have been released deliberately in many areas to control rabbits, mice and rats (McLeod, 2004). Feral cat populations have now established in almost every significant habitat type throughout Australia, they also inhabit many of Australia's small islands. It is estimated that there are about 18 million feral cats (McLeod, 2004) and populations can reach as high as 57 cats per square kilometre (Dickman, 1996).

Table 4. Livestock numbers in Australia by State

(NSW, New South Wales; Vic, Victoria; Qld, Queensland; SA, South Australia; WA, Western Australia; Tas, Tasmania; NT, Northern Territory; ACT, Australian Capital Territory.)

Animal	Total no.	NSW	Vic	Qld	SA	WA	Tas	NT	ACT
Sheep and lambs	68085497	24366338	14377696	3622141	8989472	14691553	1991282	6	47010
Dairy cattle	2542363	348318	1588693	162200	138501	113023	1916221	1	5
Meat cattle	24007730	5107062	2079529	11193348	903861	2206183	445751	2065746	6250
Pigs	2289292	584614	509884	583144	381131	219393	11092	35	0

Recently published studies of *Cryptosporidium* infection in cats and dogs, worldwide, have reported prevalence rates in dogs ranging from 0.5% to 44.1% and in cats from 0% to 29.4% (cf. Lucio-Forster *et al.* 2010). In foxes, prevalence rates of 7.9–8.5% have been reported (Feng, 2010). Genotyping studies of *Cryptosporidium* oocysts in feces of dogs and cats, have demonstrated that most infections in these animals are caused by *C. canis* and *C. felis*, respectively. *Cryptosporidium felis* has a restricted host range and has been identified in cats, immunocompetent and immunocompromised humans and a cow (Bornay-Llinares *et al.* 1999; Lucio-Forster *et al.* 2010). Similarly, *C. canis* has been identified in dogs, foxes, wolves and immunocompetent and immunocompromised humans (Lucio-Forster *et al.* 2010). In children in developing countries, *C. felis* and *C. canis* are responsible for as much as 3.3% and 4.4% respectively of overall cryptosporidiosis cases (Lucio-Forster *et al.* 2010). *Cryptosporidium muris* and *C. parvum* have also occasionally been reported in dogs and cats (cf. Lucio-Forster *et al.* 2010). *Cryptosporidium muris* has a wide host range and has also been identified in a few humans in developing countries (Palmer *et al.* 2003; Gatei *et al.* 2006; Muthusamy *et al.* 2006). However, most human cases of cryptosporidiosis, worldwide, are associated with *C. hominis* and *C. parvum* (Xiao, 2010) and therefore *C. muris*, *C. canis* and *C. felis* are likely to be of low zoonotic risk to humans.

In Australia, a prevalence of 22.7% ( $n=44$ ) was reported for dingoes and wild dogs and genotyping identified *C. canis* and a *C. hominis*-like genotype (Ng *et al.* 2011a). In domestic dogs in Australia, only *C. canis* has been identified and *C. felis* and *C. muris* have been identified in domestic cats in Australia (Sargent *et al.* 1998; Morgan *et al.* 1998, 2000; Palmer *et al.* 2008; FitzGerald *et al.* 2011).

Of the few genotyping studies have been conducted in foxes, 3 species have been identified; the *Cryptosporidium* fox genotype, *C. canis* fox subtype (a variant of *C. canis*), and *C. canis* (Xiao *et al.* 2002b). In Australia, a prevalence of 10.5% ( $n=19$ ) was reported in foxes and *C. canis* and a *C. macropodum*-like genotype were identified (Ng *et al.* 2011a). Foxes, wild dogs and feral cats are unlikely to be a

major source of zoonotic *Cryptosporidium* in catchments but further research is required.

#### SPECIES AND STRAINS OF *CRYPTOSPORIDIUM* INFECTING DOMESTIC LIVESTOCK

Over the past 20 years, sheep and particularly pre-weaned cattle have been identified as being one of the main reservoir hosts for the zoonotic *C. parvum* (Davies *et al.* 2003, 2004, Ferguson *et al.* 2003; Fayer *et al.* 2006, 2007, 2008; Santin *et al.* 2004, 2008; Xiao and Feng, 2008; Xiao, 2010). However, studies worldwide suggest that cattle are infected with at least 5 *Cryptosporidium* parasites. In sheep a total of 8 species/genotypes of *Cryptosporidium* have been reported (Fayer *et al.* 2005, 2008; Xiao and Feng, 2008; Xiao, 2010).

Conclusive molecular evidence linking contamination of water supplies by sheep or cattle with outbreaks of cryptosporidiosis in human populations is scant; however, there have been several studies in which outbreaks of cryptosporidiosis have been strongly linked with sheep and cattle grazing near the implicated reservoir, catchment or river (Anonymus, 1999; Qamruddin *et al.* 1999; Yang *et al.* 2008; Ruecker *et al.* 2007). In addition, many studies have reported that *C. andersoni*, which is predominantly a parasite of adult cattle, *C. ubiquitum*, which is a common *Cryptosporidium* species in sheep and *C. parvum* are the dominant *Cryptosporidium* species detected in watersheds and raw and drinking water (Yang *et al.* 2008; Ruecker *et al.* 2007; Nichols *et al.* 2010; Smith and Nichols, 2010). In addition, the high density of cattle and sheep across Australia, which contribute a large volume of manure to catchments indicate that they are the main species that present a risk to public health in Australian catchments.

#### Population density of domestic livestock

An assessment of stock numbers within Australia was obtained from the Australian Bureau of Statistics Agricultural Commodities, Australia, 2009/2010 (Table 4). In 2009/2010, NSW had the highest



number of sheep (24.3 million), followed by WA (14.6 million) and Victoria (Vic) (14.3 million). Dairy cattle were reported at 2.5 million for 2009/2010, with Victoria continuing to dominate the dairy industry with 62% of Australia's total dairy herd at 1.5 million. Meat cattle were reported as 24 million in 2009/2010 with the highest number in Queensland (Qld) (11.1 million), followed by NSW (5.1 million), and WA (2.2 million). Pigs were reported as 2.2 million in 2009/2010, with the highest density in NSW at 0.58 million.

#### Volume of domestic livestock manure

Livestock excretion rates and volumes are reasonably well documented compared to those for wildlife. Estimates for manure production rates for domestic livestock were obtained from a 2003 revision of the Manure Production and Characteristics produced by the American Society of Agricultural Engineers (Anonymus, 2003). The data was combined from a wide base of published and unpublished information on livestock manure production and characterization (Anonymus, 2003). It has been estimated that a 400 kg adult beef cow will produce on average 23 kg of feces per day and a 400 kg dairy cow 34.4 kg of feces per day. A 45 kg adult sheep will produce on average 1.8 kg of feces per day and a 40 kg pig will produce on average 3.4 kg of feces per day (Anonymus, 2003).

#### Cattle

In cattle, cryptosporidiosis causes significant neonatal morbidity, resulting in weight loss and delayed growth, which leads to large economic losses (McDonald, 2000). Contamination of food or water by cattle manure has been identified as a cause of several foodborne and waterborne outbreaks of cryptosporidiosis (Glaberman *et al.* 2002; Blackburn *et al.* 2006). In case-control studies, contact with cattle was implicated as a risk factor for human cryptosporidiosis in the United States, United Kingdom, Ireland and Australia (Robertson *et al.* 2002; Goh *et al.* 2004; Hunter *et al.* 2004; Roy *et al.* 2004).

The environmental loading rate of *Cryptosporidium* in cattle has been estimated at between 3900 and  $1.7 \times 10^5$  oocysts  $\text{cow}^{-1} \text{day}^{-1}$  (Hoar *et al.* 2000; Atwill *et al.* 2003). In eastern Australian cattle feedlot manures, the occurrence of *Cryptosporidium* and other pathogens was quantified using quantitative PCR. High counts of *Cryptosporidium* ( $> 10^5 \text{g}^{-1}$ ) were sporadically identified in all manures (Klein *et al.* 2010). Cattle can therefore potentially contribute significantly to contamination of drinking water catchments with *Cryptosporidium*. It is essential, however, to determine the proportion of oocysts shed that are infectious to humans. Studies

worldwide suggest that cattle are infected with at least 5 *Cryptosporidium* parasites: *C. parvum*, *C. bovis*, *C. andersoni*, *C. ryanae* (previously called deer-like genotype) and *C. suis* (Santin *et al.* 2004; Fayer *et al.* 2006, 2007; Starkey *et al.* 2006; Coklin *et al.* 2007; Feng *et al.* 2007; Geurden *et al.* 2007; Langkjaer *et al.* 2007; Mendonça *et al.* 2007; Plutzer and Karanis, 2007; Halim *et al.* 2008; Nuchjangreed *et al.* 2008; Wielinga *et al.* 2008; Liu *et al.* 2009; Keshavarz *et al.* 2009; Santin *et al.* 2008, 2009; Xiao and Feng, 2008; Ondráčková *et al.* 2009; Paul *et al.* 2008, 2009; Amer *et al.* 2009, 2010; Ayinmode *et al.* 2010; Diaz *et al.* 2010; Silverlås *et al.* 2010; Fayer *et al.* 2010; Karanis *et al.* 2010; Khan *et al.* 2010; Xiao, 2010; Kváč *et al.* 2011; Maikai *et al.* 2011; Meireles *et al.* 2011; Muhid *et al.* 2011; Nazemalhosseini-Mojarad *et al.* 2011). Of these only *C. parvum* is a major human pathogen (Xiao, 2010).

There also appear to be geographical differences in the age-related prevalence of different *Cryptosporidium* species in cattle (Table 5). Few longitudinal studies have been conducted but a study in the US reported that the highest prevalence of infection occurs in calves <8 weeks of age (45.8%), followed by post-weaned calves (3–12 months of age) (18.5%) and heifers (12–24 months of age) (2.2%) (Santin *et al.* 2008). Other studies have reported prevalences as high as (75.9%) in 11 to 22-day-old calves, which subsequently decreased (Coklin *et al.* 2010). In parts of the US, Belgium, Ireland, Germany, Malaysia, the UK and Sweden, it has been reported that the zoonotic *C. parvum* is responsible for the majority of *Cryptosporidium* infections in pre-weaned calves and only a small percentage of *Cryptosporidium* infections in post-weaned calves and heifers (Santin *et al.* 2004, 2008; Brook *et al.* 2009; Coklin *et al.* 2007; Geurden *et al.* 2007; Thompson *et al.* 2007; Xiao *et al.* 2007; Broglia *et al.* 2008; Halim *et al.* 2008; Paul *et al.* 2008; Fayer *et al.* 2010; Silverlås *et al.* 2010). Post-weaned calves were mostly infected with *C. bovis*, *C. andersoni* and *C. ryanae* (Fayer *et al.* 2010). Other studies in China, India, Georgia, Nigeria and western North Dakota however, have reported that *C. bovis* was the most common species found in pre-weaned calves (Feng *et al.* 2007; Feltus *et al.* 2008; Maikai *et al.* 2011). A recent study in Nigeria reported that there were no significant differences ( $P > 0.05$ ) in *Cryptosporidium* infection rates by sex, herd location, management system, breed of calves, or fecal consistency but that calves 180 days or younger had a higher infection rate of *Cryptosporidium* than older calves ( $P = 0.034$ ) and that younger calves also had higher occurrence of *C. bovis* and *C. ryanae* ( $P = 0.022$ ) (Maikai *et al.* 2011).

In Australia, the prevalence of *Cryptosporidium* in cattle ranges from 2 to 58.8% (Becher *et al.* 2004; Nolan *et al.* 2009; Ng *et al.* 2011b; Izzo *et al.* 2011). The most recent study reported that the total prevalence of *Cryptosporidium* in calves from

Table 5. Prevalence and species of *Cryptosporidium* identified in pre- and post-weaned cattle in Australia

Country	Age Preweaned/ postweaned	Prevalence	No genotyped	<i>Cryptosporidium</i> species					Reference
				<i>C. parvum</i>	<i>C. bovis</i>	<i>C. ryanae</i>	<i>C. andersoni</i>	Others	
Australia – WA	0–12 weeks	48.3% (36/54)	6	100% (6)	0	0	0	0	Becher <i>et al.</i> (2004)
Australia – Vic	Preweaned	46.3% (124/268)	124	100%	0	0	0	0	Nolan <i>et al.</i> (2009)
Australia – WA	Postweaned	15% (17/111)	4	0	100% (4/4)	0	0	0	Ferguson (2010)
Australia – WA	Preweaned	47% (9/19)	4	0	75% (3/4)	0	0	<i>C. ubiquitum</i> 25% (1/4)	Ferguson (2010)
Australia – WA and NSW	Preweaned	22.5% (82/364)	71	38% (27/71)	39.5% (28/71)	21% (15/71)	0	1.5% (1/71)	Ng <i>et al.</i> (2011b)
Australia – NSW	Preweaned	73.5% (144/196)	142	60% (85/142)	20.4% (29/142)	9.8% (14/142)	0	9.8%* (14/142)	Ng <i>et al.</i> (2012)

\* Mixed *C. parvum/bovis/ryanae* infections.

84 dairy and dairy beef properties across Australia was 58.5% (Izzo *et al.* 2011) (Table 6). In Victoria, the prevalence of *Cryptosporidium* in fecal samples from 268 individual calves on pasture-based dairy farms in three regions (Northern Victoria, South Gippsland and Western District) was 46.3% (124/268) (Nolan *et al.* 2009). The detection tool employed, however, (PCR analysis of the *gp60* locus) was specific to *C. parvum/C. hominis* and therefore only *C. parvum* was detected in all samples typed (Nolan *et al.* 2009). *Cryptosporidium andersoni* is usually only found in older cattle and is morphologically distinct (7.4 × 5.5 μm) from the intestinal species, which includes *C. parvum* (5.0 × 4.5 μm) (Ralston *et al.* 2010). The prevalence of *C. andersoni* in fecal samples from 10 groups of feedlot beef cattle in Western Australia ranging in age from 11 to 36 months, ranged from 0% to 26% (Ralston *et al.* 2010). *Cryptosporidium andersoni* is commonly detected in water samples in the US and UK but is not considered a human pathogen (Xiao and Feng, 2008; Xiao, 2010; Wang *et al.* 2011).

A recent study screened a total of 364 fecal specimens from randomly selected pre-weaned calves, aged up to 4 months, from 5 different farms in the south of Western Australia and 1 farm from New South Wales (Ng *et al.* 2011b). There were substantial differences in prevalence between the farms with the highest prevalence in a WA farm (37.5%). The overall prevalence was 22.3% (81/364) (Ng *et al.* 2011b). *Cryptosporidium bovis* was the most common species detected (39.5%) followed by *C. parvum* (38%) and *C. ryanae* (21%) (Ng *et al.* 2011b).

In NSW, a preliminary study in 2006 that examined the species/genotypes and subgenotypes of *Cryptosporidium* in 7 human and 15 cattle cases of sporadic cryptosporidiosis in rural western NSW, reported that 4 of the 6 *C. parvum* subtypes found in humans were also found in the cattle, indicating that zoonotic transmission may be an important contributor to sporadic human cases of cryptosporidiosis in rural NSW (Ng *et al.* 2008). A more extensive study conducted in 2009, screened 196 fecal samples from diarrhoeic (scouring) calves on 20 farms and 63 fecal samples from humans on 14 of these farms (Ng *et al.* 2012). The overall prevalence of *Cryptosporidium* in cattle and humans by PCR and sequence analysis of the 18S rRNA was 73.5% (144/196) and 23.8% (15/63) respectively. Three species were identified in cattle; *C. parvum*, *C. bovis* and *C. ryanae*, and from humans, *C. parvum* and *C. bovis* (Ng *et al.* 2012). This is only the second report of *C. bovis* in humans. The previous report *C. bovis* was in a dairy farm worker in India, where the infection was asymptomatic (Khan *et al.* 2010). Subtype analysis at the *gp60* locus identified the same *C. parvum* subtype in the calves in some of the humans, suggesting that zoonotic transmission may have occurred but more

Table 6. Prevalence and species of *Cryptosporidium* identified in pre- and post-weaned sheep in Australia

Country	Age Pre-weaned/ post-weaned	Prevalence	No genotyped	<i>Cryptosporidium</i> species				Reference
				<i>C. parvum</i>	<i>C. ubiquitum</i>	<i>C. xiaoi</i>	Others	
Australia-WA	Post-weaned	26.2% (131/500)	60	0	55% (33/60)	23.3% (14/60)	Pig genotype II (6.6%), <i>C. fayeri</i> (6.6%), <i>C. suis</i> (3.3%), <i>C. andersoni</i> (1.6%), <i>C. hominis</i> (1.6%), unknown genotype (1.6%)	Ryan <i>et al.</i> (2005)
Australia-WA	Pre-weaned	24.5% (117/477)	66	4.5% (3/66)	15.1% (10/66)	79% (52/66)	90.1% (60/66) (Mixed <i>C. parvum</i> / <i>C. xiaoi</i> ).	Yang <i>et al.</i> (2009)
Australia-WA	Post-weaned	17% (12/70)	7	14.3% (1/7)	28.5% (2/7)	57% (4/7)	1.5% (2/134) Sheep 0 <i>C. andersoni</i>	Ferguson (2010)
Australia-WA	Pre-weaned	~ 29%	134	3% (4/134)	16.4% (22/134)	61% (82/134)	10.4% (14/134) mixed	Sweeny <i>et al.</i> (2011a)
Australia-WA	Post-weaned	~ 35%	251	7.5% (19/253)	3.2% (8/253)	80.3% (203/253)	1.6% (4/253) Sheep I 1.6% (4/253) <i>C. andersoni</i> 6% (15/253) mixed	Sweeny <i>et al.</i> (2011b)

\* Combined data from several samplings and farms.

studies involving extensive sampling of both calves and farm workers are needed for a better understanding of the sources of *Cryptosporidium* infections in humans from rural areas of Australia.

*Sheep*

In sheep, cryptosporidiosis presents as a mild to severe yellowish liquid diarrhoea with a strong odour, loss of weight, depression, abdominal pain, and death usually involving animals up to 1 month of age and is associated with reduced lamb carcass productivity (cf. Fiuza *et al.* 2011b; Sweeny *et al.* 2011a). *Cryptosporidium* has been reported in sheep worldwide, with prevalences ranging from 2.6 to 82% for *Cryptosporidium* (cf. Ryan *et al.* 2005; Yang *et al.* 2009, Wang *et al.* 2010b; Sweeny *et al.* 2011b). In Australia, reported prevalences for ewes in Western Australia ranged from 6.3–8.3% (Sweeny *et al.* 2011b) and for lambs from 9.3–56.3% on different properties (Ryan *et al.* 2005; Yang *et al.* 2009; Sweeny *et al.* 2011a, b).

A total of 9 species/genotypes of *Cryptosporidium* have been reported in sheep and lambs in Australia; *C. parvum*, *C. hominis*, *C. xiaoi*, *C. bovis*, *C. ubiquitum*, sheep genotype I, *C. andersoni*, pig genotype II, *C. fayeri* and *C. suis* and sheep genotype I (Ryan *et al.* 2005; Giles *et al.* 2009; Yang *et al.* 2009; Robertson, 2009; Sweeny *et al.* 2011a, b), with *C. xiaoi* and *C. ubiquitum* most common although Yang *et al.* (2009) found high proportions of *C. parvum* isolates in pre-weaned sheep in Western Australia when a *C. parvum*-specific PCR was used. In that study, using both 18S and a *C. parvum*-specific PCR for *Cryptosporidium* produced very different results. At the 18S locus, *C. bovis* was the most common species identified (95% of positives) in the pre-weaned lambs and *C. parvum* was only identified in two samples (0.4%) (Yang *et al.* 2009). However, using a *C. parvum*-specific PCR and additional 53 *C. parvum*-positives were identified (mostly mixed *C. bovis*/*C. parvum* infections). Quantitative PCR revealed that *C. parvum* was present in low numbers compared to *C. bovis* and it is likely that the 18S PCR preferentially amplified the more abundant template. It may be that the use of *C. parvum*-specific primers is necessary to determine the true prevalence of *C. parvum*. In a previous study on post-weaned sheep (Ryan *et al.* 2005), *C. parvum* was not detected; however, *C. parvum*-specific primers were not used and it is possible that *C. parvum* was present in those animals.

*Cryptosporidium ubiquitum* (previously known as the cervine genotype) has been identified in humans worldwide (Ong *et al.* 2002; cf. Xiao, 2010) but has not been detected in any human cryptosporidiosis cases in Australia to date. Quantification analysis using quantitative PCR (qPCR) and microscopy

indicated that oocyst output in sheep feces varies widely and ranges from  $\sim 1$  to  $10^6$  oocysts per gramme (Yang *et al.* 2009; Ryan *et al.*, unpublished observations). Because sheep can harbour *C. parvum*, they should be considered a potential source of infection of *Cryptosporidium* either by direct transmission or by contamination of the environment.

As with cattle, there appears to be both geographical and age-related differences in the prevalence of zoonotic and non-zoonotic genotypes in sheep based on recent molecular characterization studies worldwide (Santin *et al.* 2007; Geurden *et al.* 2008; Quilez *et al.* 2008; Mueller-Doblies *et al.* 2008; Paoletti *et al.* 2009; Diaz *et al.* 2010; Robertson *et al.* 2010; Wang *et al.* 2010; Fiuza *et al.* 2011b; Shen *et al.* 2011). A recent longitudinal study of *Cryptosporidium* in meat lamb farms in southern Western Australia reported that *Cryptosporidium* prevalences at individual samplings ranged between 18.5 and 42.6% in lambs and were <10% in the ewes. *Cryptosporidium xiaoi* was the most prevalent species detected at all 5 samplings and was also isolated from lamb dam water on 1 farm. *Cryptosporidium ubiquitum* was most commonly detected in younger lambs and *Cryptosporidium parvum* was detected in lambs at all 5 samplings, typically in older lambs and as part of a mixed species infection with *C. xiaoi*. The novel sheep genotype I, was identified in 6 *Cryptosporidium* isolates from 1 farm. The longitudinal study revealed that sampling a random selection of animals from a flock/herd on 1 occasion (point prevalence), underestimates the overall prevalence of these parasites in the flock/herd across an extended time-period (Sweeny *et al.* 2011b).

#### CONCLUSIONS AND PERSPECTIVES

Wildlife host-adapted species of *Cryptosporidium* are likely to have evolved in close association with marsupials. Confirmation of human-infectious species in these animals is rare, with detection of such isolates based on sequence data from direct fecal DNA extraction. There is a need to confirm whether molecular detection of zoonotic *Cryptosporidium* species is associated with actual infections. Additionally the presence of an atypical species in one or two individual marsupial hosts does not indicate that the parasite will be successful in all marsupials. The low abundance detected in individuals and low prevalence of human-infectious species in marsupial host groups, suggests that even if marsupial hosts are infected, it may not be a very successful host parasite interaction. However, marsupial hosts should still be monitored given the risk of emergence and the public health implications.

Non-marsupial hosts in Australia fall into 2 categories. (1) Those that have been introduced and become feral (cats, deer, dingos, foxes, pigs, rabbits, rodents, etc.) and (2) those that have become domesticated (sheep, cattle and pigs). Many of these

hosts represent important agricultural resources. Although there have been limited studies in Australia, deer, rabbits and rodents appear to be potential reservoirs of human infectious species and more systematic studies of the prevalence, oocyst numbers and species infecting these hosts are essential to understand the public health significance.

Cattle and sheep are present in high numbers across Australia, contribute a large volume of manure to catchments and can shed oocysts in high concentrations. It has been reported that manure from cattle and sheep are the second-most significant source of pathogens that cause waterborne disease (Hrudey and Hrudey, 2004). Preliminary evidence suggests that pre-weaned lambs and cattle in Australia may be an important source of *C. parvum*, which is of concern for public health. Larger numbers of both pre-weaned and post-weaned sheep and cattle from different geographical areas within Australia need to be screened at different times of the year at multiple loci and the numbers of oocysts quantified to confirm this.

The 2011 Australian Drinking Water Guidelines recommend managing water quality risks at source, within the catchment. Therefore management practices, particularly of cattle and sheep (including vegetation management of riparian zones) play a major role in reducing the risk of water contamination with *Cryptosporidium*. This can be achieved by compulsory land acquisition by government and drinking water companies, but this is an expensive option that is not widely practiced. It is more usually achieved by restricting stock access to riparian areas. In areas where permanent fencing is not an option, minimizing infection (and *Cryptosporidium* shedding) rates in stock – especially calves and lambs, by implementing good animal health practices such as excluding calves from pastures grazed by infected cows, is important.

Australia has a unique ecosystem with wildlife species specific to the continent. The introduction of non-marsupial animals and their parasites has resulted in complex and often devastating effects on the endemic fauna. It is therefore important to understand these intricate associations between wildlife, domestic animals and humans in the Australian context to enable management of the zoonotic risk of *Cryptosporidium*.

#### REFERENCES

- Alagappan, A., Tujula, N.A., Power, M., Ferguson, C.M., Bergquist, P.L. and Ferrari, B.C. (2008). Development of fluorescent in situ hybridization for *Cryptosporidium* detection reveals zoonotic and anthroponotic transmission of sporadic cryptosporidiosis in Sydney. *Journal of Microbiological Methods* **75**, 535–539.
- Amer, S., Harfoush, M. and He, H. (2010). Molecular and phylogenetic analyses of *Cryptosporidium* spp. from dairy cattle in Egypt. *Journal of the Egyptian Society for Parasitology* **40**, 349–366.

- Amer, S., Honma, H., Ikarashi, M., Oishi, R., Endo, M., Otawa, K., Nakai, Y. (2009). The first detection of *Cryptosporidium* deer-like genotype in cattle in Japan. *Parasitology Research* **104**, 745–752.
- Anonymous (1999). Communicable Disease Report Weekly. *Outbreak of cryptosporidiosis in north west England*. ([http://www.hpa.org.uk/cdr/archives/back\\_issues.htm](http://www.hpa.org.uk/cdr/archives/back_issues.htm)) **20**, 175–178.
- Anonymous (2002). Australian Water Technologies. Pilot study investigation of potential sources of pathogens in Sydney's water supply catchments. Sydney, Sydney Catchment Authority: 68.
- Anonymous. (2003). Manure Production and Characteristics. American Society of Agricultural Engineers ASAE D384-1 FEB03. <http://www.manuremanagement.cornell.edu/Docs/ASAStandard.pdf>.
- Atwill, E. R., Hoar, B., das Graças Cabral Pereira, M., Tate, K. W., Rulofson, F. and Nader, G. L. (2003). Improved quantitative estimates of low environmental loading and sporadic periparturient shedding of *Cryptosporidium parvum* in adult beef cattle. *Applied and Environmental Microbiology* **69**, 4604–4610.
- Atwill, E. R., Sweitzer, R. A., Pereira, M. G., Gardner, I. A., Van Vuren, D. and Boyce, W. M. (1997). Prevalence of and associated risk factors for shedding *Cryptosporidium parvum* oocysts and *Giardia* cysts within feral pig populations in California. *Applied and Environmental Microbiology* **63**, 3946–3949.
- Ayinmode, A. B., Olakunle, F. B. and Xiao, L. (2010). Molecular characterization of *Cryptosporidium* spp. in native calves in Nigeria. *Parasitology Research* **107**, 1019–1021.
- Baldursson, S. and Karanis, P. (2011). Waterborne transmission of protozoan parasites: review of worldwide outbreaks – an update 2004–2010. *Water Research* **45**, 6603–6614.
- Becher, K. A., Robertson, I. D., Fraser, D. M., Palmer, D. G. and Thompson, R. C. (2004). Molecular epidemiology of *Giardia* and *Cryptosporidium* infections in dairy calves originating from three sources in Western Australia. *Veterinary Parasitology* **123**, 1–9.
- Blackburn, B. G., Mazurek, J. M., Hlavsa, M., Park, J., Tillapaw, M., Parrish, M., Salehi, E., Franks, W., Koch, E., Smith, F., Xiao, L., Arrowood, M., Hill, V., da Silva, A., Johnston, S. and Jones, J. L. (2006). Cryptosporidiosis associated with ozonated apple cider. *Emerging Infectious Disease* **12**, 684–686.
- Bornay-Llinares, F. J., da Silva, A. J., Mourna, I. N., Myjap, P., Pietkiewicz, H., Kruminis-Lozowska, W., Graczak, T. K. and Pieniazek, N. J. (1999). Identification of *Cryptosporidium felis* in a cow by morphologic and molecular methods. *Applied and Environmental Microbiology* **65**, 1455–1458.
- Brogli, A., Reckinger, S., Cacciò, S. M. and Nöckler, K. (2008). Distribution of *Cryptosporidium parvum* subtypes in calves in Germany. *Veterinary Parasitology* **154**, 8–13.
- Brook, E. J., Anthony Hart, C., French, N. P. and Christley, R. M. (2009). Molecular epidemiology of *Cryptosporidium* subtypes in cattle in England. *Veterinary Journal* **179**, 378–382.
- Budu-Amoako, E., Greenwood, S. J., Dixon, B. R., Barkema, H. W., Hurnik, D., Estey, C. and McClure, J. T. (2012). Occurrence of *Giardia* and *Cryptosporidium* in pigs on Prince Edward Island, Canada. *Veterinary Parasitology* **184**, 18–24.
- Castro-Hermida, J. A., García-Precedo, I., González-Warleta, M. and Mezo, M. (2011). Prevalence of *Cryptosporidium* and *Giardia* in roe deer (*Capreolus capreolus*) and wild boars (*Sus scrofa*) in Galicia (NW, Spain). *Veterinary Parasitology* **179**, 216–219.
- Cinque, K., Stevens, M. A., Haydon, S. R., Jex, A. R., Gasser, R. B. and Campbell, B. E. (2008). Investigating public health impacts of deer in a protected drinking water supply watershed. *Water Science and Technology* **58**, 127–132.
- Chalmers, R. M., Elwin, K., Hadfield, S. J. and Robinson, G. (2011). Sporadic human cryptosporidiosis caused by *Cryptosporidium cuniculus*, United Kingdom, 2007–2008. *Emerging Infectious Diseases* **17**, 536–538.
- Chalmers, R. M., Ferguson, C., Cacciò, S., Gasser, R. B., Abs EL-Osta, Y. G., Heijnen, L., Xiao, L., Elwin, K., Hadfield, S., Sinclair, M. and Stevens, M. (2005). Direct comparison of selected methods for genetic categorisation of *Cryptosporidium parvum* and *Cryptosporidium hominis* species. *International Journal for Parasitology* **35**, 397–410.
- Chalmers, R. M., Robinson, G., Elwin, K., Hadfield, S. J., Thomas, E., Watkins, J., Casemore, D., Kay, D. (2010). Detection of *Cryptosporidium* species and sources of contamination with *Cryptosporidium hominis* during a waterborne outbreak in north west Wales. *Journal of Water Health* **8**, 311–325.
- Chalmers, R. M., Robinson, G., Elwin, K., Hadfield, S. J., Xiao, L., Ryan, U., Modha, D. and Mallaghan, C. (2009). *Cryptosporidium* sp. rabbit genotype, a newly identified human pathogen. *Emerging Infectious Diseases* **15**, 829–830.
- Chen, Z., Mi, R., Yu, H., Shi, Y., Huang, Y., Chen, Y., Zhou, P., Cai, Y. and Lin, J. (2011). Prevalence of *Cryptosporidium* spp. in pigs in Shanghai, China. *Veterinary Parasitology* **181**, 113–119.
- Coklin, T., Farber, J. M., Parrington, L. J., Coklin, Z., Ross, W. H. and Dixon, B. R. (2010). Temporal changes in the prevalence and shedding patterns of *Giardia duodenalis* cysts and *Cryptosporidium* spp. oocysts in a herd of dairy calves in Ontario. *Canadian Veterinary Journal* **51**, 841–846.
- Coklin, T., Farber, J., Parrington, L. and Dixon, B. (2007). Prevalence and molecular characterization of *Giardia duodenalis* and *Cryptosporidium* spp. in dairy cattle in Ontario, Canada. *Veterinary Parasitology* **150**, 297–305.
- Corbett, L. K. (1995). *The Dingo in Australia and Asia*. University of NSW Press, Sydney, Australia.
- Davies, C. M., Ferguson, C. M., Kaucner, C., Krogh, M., Altavilla, N., Deere, D. A. and Ashbolt, N. J. (2004). Dispersion and Transport of *Cryptosporidium* Oocysts from Fecal Pats under Simulated Rainfall Events. *Applied and Environmental Microbiology* **70**, 1151–1159.
- Davies, C. M., Kaucner, C., Deere, D. and Ashbolt, N. J. (2003). Recovery and enumeration of *Cryptosporidium parvum* from animal fecal matrices. *Applied and Environmental Microbiology* **69**, 2842–2847.
- Dexter, N. (1990). *Population Density and Management of Feral Pigs at Aurukun, North Queensland*. Bureau of Rural Resources, Report R/11/90, Canberra, Australia.
- Diaz, P., Quílez, J., Chalmers, R. M., Panadero, R., López, C., Sánchez-Acedo, C., Morrondo, P. and Diez-Baños, P. (2010). Genotype and subtype analysis of *Cryptosporidium* isolates from calves and lambs in Galicia (NW Spain). *Parasitology* **137**, 1187–1193.
- Dickman, C. R. (1996). *Overview of the Impacts of Feral Cats on Australian Native Fauna*. Report to the Australian Nature Conservation Agency, Canberra, Australia.
- Farzan, A., Parrington, L., Coklin, T., Cook, A., Pintar, K., Pollari, F., Friendship, R., Farber, J. and Dixon, B. (2011). Detection and characterization of *Giardia duodenalis* and *Cryptosporidium* spp. on swine farms in Ontario, Canada. *Foodborne Pathogenic Diseases* **8**, 1207–1213.
- Fayer, R., Morgan, U. and Upton, S. J. (2000). Epidemiology of *Cryptosporidium*: transmission, detection and identification. *International Journal for Parasitology* **30**, 1305–1322.
- Fayer, R., Santín, M. and Dargatz, D. (2010). Species of *Cryptosporidium* detected in weaned cattle on cow-calf operations in the United States. *Veterinary Parasitology* **170**, 187–192.
- Fayer, R., Santín, M. and Trout, J. M. (2007). Prevalence of *Cryptosporidium* species and genotypes in mature dairy cattle on farms in eastern United States compared with younger cattle from the same locations. *Veterinary Parasitology* **145**, 260–266.
- Fayer, R., Santín, M. and Trout, J. M. (2008). *Cryptosporidium ryanae* n. sp. (Apicomplexa: Cryptosporidiidae) in cattle (*Bos taurus*). *Veterinary Parasitology* **156**, 191–198.
- Fayer, R., Santín, M., Trout, J. M. and Greiner, E. (2006). Prevalence of species and genotypes of *Cryptosporidium* found in 1–2-year-old dairy cattle in the eastern United States. *Veterinary Parasitology* **135**, 105–112.
- Fayer, R., Santín, M. and Xiao, L. (2005). *Cryptosporidium bovis* n. sp. (Apicomplexa: Cryptosporidiidae) in cattle (*Bos Taurus*). *Journal of Parasitology* **91**, 624–629.
- Feltus, D. C., Giddings, C. W., Khaitsa, M. L. and McEvoy, J. M. (2008). High prevalence of *Cryptosporidium bovis* and the deer-like genotype in calves compared to mature cows in beef cow-calf operations. *Veterinary Parasitology* **151**, 191–195.
- Feng, Y. (2010). *Cryptosporidium* in wild placental mammals. *Experimental Parasitology* **124**, 128–137.
- Feng, Y., Lal, A. A., Li, N. and Xiao, L. (2011b). Subtypes of *Cryptosporidium* spp. in mice and other small mammals. *Experimental Parasitology* **127**, 238–242.
- Feng, Y., Li, N., Duan, L. and Xiao, L. (2009). *Cryptosporidium* genotype and subtype distribution in raw wastewater in Shanghai, China: evidence for possible unique *Cryptosporidium hominis* transmission. *Journal of Clinical Microbiology* **47**, 153–157.
- Feng, Y., Ortega, Y., He, G., Das, P., Xu, M., Zhang, X., Fayer, R., Gatei, W., Cama, V. and Xiao, L. (2007). Wide geographic distribution of *Cryptosporidium bovis* and the deer-like genotype in bovines. *Veterinary Parasitology* **144**, 1–9.
- Feng, Y., Zhao, X., Chen, J., Jin, W., Zhou, X., Li, N., Wang, L. and Xiao, L. (2011a). Occurrence, source, and human infection potential of *Cryptosporidium* and *Giardia* spp. in source and tap water in Shanghai, China. *Applied and Environmental Microbiology* **77**, 3609–3616.
- Ferguson, C. M., de Roda Husman, A. M., Altavilla, N., Deere, D. and Ashbolt, N. J. (2003). Fate and transport of surface water pathogens in watersheds. *Critical Reviews in Environmental Science Technology* **33**, 299–361.

- Ferguson, C. (2010). *Quantifying Infectious Pathogen Sources in WA Drinking Water Catchments*. Report by ASL Water services group.
- Fiuza, V.R., Cosendey, R.I., Frazão-Teixeira, E., Santin, M., Fayer, R. and de Oliveira, F.C. (2011b). Molecular characterization of *Cryptosporidium* in Brazilian sheep. *Veterinary Parasitology* **175**, 360–362.
- Fiuza, V.R., Gallo, S.S., Frazão-Teixeira, E., Santin, M., Fayer, R. and Oliveira, F.C. (2011a). *Cryptosporidium* pig genotype II diagnosed in pigs from the state of Rio De Janeiro, Brazil. *Journal of Parasitology* **97**, 146–147.
- FitzGerald, L., Bennett, M., Ng, J., Nicholls, P., James, F., Elliot, A., Slaven, M. and Ryan, U. (2011). Morphological and molecular characterisation of a mixed *Cryptosporidium muris*/*Cryptosporidium felis* infection in a cat. *Veterinary Parasitology* **175**, 160–164.
- Fletcher, D. (2007). Managing Eastern Grey Kangaroos *Macropus giganteus* in the Australian Capital Territory: reducing the overabundance – of opinion. In *Pest or Guest: the Zoology of Overabundance* (ed. Lunney, D., Hutchins, P., Eby, P. and Burgin, S.). Royal Zoological Society of NSW, Sydney, Australia.
- Foo, C., Farrell, J., Boxell, A., Robertson, I. and Ryan, U.M. (2007). Novel *Cryptosporidium* genotype in wild Australian mice (*Mus domesticus*). *Applied and Environmental Microbiology* **73**, 7693–7696.
- Gatei, W., Wamae, C.N., Mbae, C., Waruru, A., Mulinge, E., Waithera, T., Gatika, S.M., Kamwari, S.K., Revathi, G. and Hart, C.A. (2006). Cryptosporidiosis: prevalence, genotype analysis, and symptoms associated with infections in children in Kenya. *American Journal of Tropical Medicine and Hygiene* **75**, 78–82.
- Geurden, T., Berkvens, D., Martens, C., Casaert, S., Vercruyse, J. and Claerebout, E. (2007). Molecular epidemiology with subtype analysis of *Cryptosporidium* in calves in Belgium. *Parasitology* **134**, 1981–1987.
- Geurden, T., Thomas, P., Casaert, S., Vercruyse, J. and Claerebout, E. (2008). Prevalence and molecular characterisation of *Cryptosporidium* and *Giardia* in lambs and goat kids in Belgium. *Veterinary Parasitology* **155**, 142–145.
- Glaberman, S., Moore, J.E., Lowery, C.J., Chalmers, R.M., Sulaiman, I., Elwin, K., Rooney, P.J., Millar, B.C., Dooley, J.S., Lal, A.A. and Xiao, L. (2002). Three drinking water associated cryptosporidiosis outbreaks, Northern Ireland, *Emerging Infectious Disease* **8**, 631–633.
- Giles, M., Chalmers, R., Pritchard, G., Elwin, K., Mueller-Doblies, D. and Clifton-Hadley, F. (2009). *Cryptosporidium hominis* in a goat and a sheep in the UK. *Veterinary Record* **164**, 24–25.
- Goh, S., Reacher, M., Casemore, D.P., Verlander, N.Q., Chalmers, R., Knowles, M., Williams, J., Osborn, K. and Richard, S. (2004). Sporadic cryptosporidiosis, North Cumbria, England, 1996–2000. *Emerging Infectious Disease* **10**, 1007–1015.
- Halim, N.A., Plutzer, J., Bakheit, M.A. and Karanis, P. (2008). First report of *Cryptosporidium* deer-like genotype in Malaysian cattle. *Veterinary Parasitology* **152**, 325–329.
- Hampton, J., Spencer, P.B.S., Elliot, A.D. and Thompson, R.C.A. (2006). Prevalence of zoonotic pathogens from feral pigs in major public drinking water catchments in Western Australia. *EcoHealth* **3**, 103–108.
- Hill, N.J., Deane, E.M. and Power, M.L. (2008). Prevalence and genetic characterization of *Cryptosporidium* isolates from common brushtail possums (*Trichosurus vulpecula*) adapted to urban settings. *Applied and Environmental Microbiology* **74**, 5549–5555.
- Hoar, B., Atwill, T.B. and Farver, E.R. (2000). Estimating maximum possible environmental loading amounts of *Cryptosporidium parvum* attributable to adult beef cattle. *Quantitative Microbiology* **2**, 21–36.
- Hrudey, S.E. and Hrudey, E.J. (2004). *Safe Drinking Water. Lessons From Recent Outbreaks in Affluent Nations*. International Water Association Publishing. <http://www.ourwater.vic.gov.au/monitoring/river-health/isc>
- Hunter, P.R., Hadfield, S.J., Wilkinson, D., Lake, I.R., Harrison, F.C. and Chalmers, R.M. (2007). Subtypes of *Cryptosporidium parvum* in humans and disease risk. *Emerging Infectious Disease* **13**, 82–88.
- Hunter, P.R., Hughes, S., Woodhouse, S., Syed, Q., Verlander, N.Q., Chalmers, R.M., Morgan, K., Nichols, G., Beeching, N. and Osborn, K. (2004). Sporadic cryptosporidiosis case-control study with genotyping. *Emerging Infectious Diseases* **10**, 1241–1249.
- Izzo, M.M., Kirkland, P.D., Mohler, V.L., Perkins, N.R., Gunn, A.A. and House, J.K. (2011). Prevalence of major enteric pathogens in Australian dairy calves with diarrhoea. *Australian Veterinary Journal* **89**, 167–173.
- Jellison, K.L., Lynch, A.E. and Ziemann, J.M. (2009). Source tracking identifies deer and geese as vectors of human-infectious *Cryptosporidium* genotypes in an urban/suburban watershed. *Environmental Science Technology* **43**, 4267–4272.
- Jeníková, M., Němejc, K., Sak, B., Květoňová, D. and Kváč, M. (2010). New view on the age-specificity of pig *Cryptosporidium* by species-specific primers for distinguishing *Cryptosporidium suis* and *Cryptosporidium* pig genotype II. *Veterinary Parasitology* **176**, 120–125.
- Jenkins, M.B., Liotta, J.L., Lucio-Forster, A. and Bowman, D.D. (2010). Concentrations, viability, and distribution of *Cryptosporidium* genotypes in lagoons of swine facilities in the Southern Piedmont and in coastal plain watersheds of Georgia. *Applied and Environmental Microbiology* **76**, 5757–5763.
- Jex, A.R., Pangasa, A., Campbell, B.E., Whipp, M., Hogg, G., Sinclair, M.I., Stevens, M. and Gasser, R.B. (2008). Classification of *Cryptosporidium* species from patients with sporadic cryptosporidiosis by use of sequence-based multilocus analysis following mutation scanning. *Journal of Clinical Microbiology* **46**, 2252–2262.
- Jex, A.R., Whipp, M., Campbell, B.E., Caccio, S.M., Stevens, M., Hogg, G. and Gasser, R.B. (2007). A practical and cost-effective mutation scanning based approach for investigating genetic variation in *Cryptosporidium*. *Electrophoresis* **28**, 3875–3883.
- Jiang, J., Alderisio, K.A. and Xiao, L. (2005). Distribution of *Cryptosporidium* genotypes in storm event water samples from three watersheds in New York. *Applied and Environmental Microbiology* **71**, 4446–4454.
- Johnson, J., Buddle, R., Reid, S., Armson, A. and Ryan, U.M. (2008). Prevalence of *Cryptosporidium* genotypes in pre and post-weaned pigs in Australia. *Experimental Parasitology* **119**, 418–421.
- Karanis, P., Eiji, T., Palomino, L., Boonrod, K., Plutzer, J., Ongerth, J. and Igarashi, I. (2010). First description of *Cryptosporidium bovis* in Japan and diagnosis and genotyping of *Cryptosporidium* spp. in diarrheic pre-weaned calves in Hokkaido. *Veterinary Parasitology* **169**, 387–390.
- Karanis, P., Kourenti, C. and Smith, H. (2007). Waterborne transmission of protozoan parasites: a worldwide review of outbreaks and lessons learnt. *Journal of Water Health* **5**, 1–38.
- Keshavarz, A., Haghighi, A., Athari, A., Kazemi, B., Abadi, A. and Mojarad, E.N. (2009). Prevalence and molecular characterization of bovine *Cryptosporidium* in Qazvin province, Iran. *Veterinary Parasitology* **160**, 316–318.
- Khan, S.M., Debnath, C., Pramanik, A.K., Xiao, L., Nozaki, T. and Ganguly, S. (2010). Molecular characterization and assessment of zoonotic transmission of *Cryptosporidium* from dairy cattle in West Bengal, India. *Veterinary Parasitology* **171**, 41–47.
- Klein, M., Brown, L., Tucker, R.W., Ashbolt, N.J., Stuetz, R.M. and Roser, D.J. (2010). Diversity and abundance of zoonotic pathogens and indicators in manures of feedlot cattle in Australia. *Applied and Environmental Microbiology* **76**, 6947–6950.
- Kváč, M., Hanzlíková, D., Sak, B. and Kvetonová, D. (2009a). Prevalence and age-related infection of *Cryptosporidium suis*, *C. muris* and *Cryptosporidium* pig genotype II in pigs on a farm complex in the Czech Republic. *Veterinary Parasitology* **160**, 319–322.
- Kváč, M., Hromadová, N., Květoňová, D., Rost, M. and Sak, B. (2011). Molecular characterization of *Cryptosporidium* spp. in pre-weaned dairy calves in the Czech Republic: absence of *C. ryanae* and management-associated distribution of *C. andersoni*, *C. bovis* and *C. parvum* subtypes. *Veterinary Parasitology* **177**, 378–382.
- Kváč, M., Kvetonová, D., Sak, B. and Ditrich, O. (2009b). *Cryptosporidium* pig genotype II in immunocompetent man. *Emerging Infectious Diseases* **15**, 982–983.
- Langkjaer, R.B., Enemark, Vigre, H.L. and Maddox-Hyttel, C. (2007). Molecular and phylogenetic characterization of *Cryptosporidium* and *Giardia* from pigs and cattle in Denmark. *Parasitology Today* **134**, 339–350.
- Liu, A., Wang, R., Li, Y., Zhang, L., Shu, J., Zhang, W., Feng, Y., Xiao, L. and Ling, H. (2009). Prevalence and distribution of *Cryptosporidium* spp. in dairy cattle in Heilongjiang Province, China. *Parasitology Research* **105**, 797–802.
- Lucio-Forster, A., Griffiths, J.K., Cama, V.A., Xiao, L. and Bowman, D.D. (2010). Minimal zoonotic risk of cryptosporidiosis from pet dogs and cats. *Trends in Parasitology* **26**, 174–179.
- Lv, C., Zhang, L., Wang, R., Jian, F., Zhang, S., Ning, C., Wang, H., Feng, C., Wang, X., Ren, X., Qi, M. and Xiao, L. (2009). *Cryptosporidium* spp. in wild, laboratory, and pet rodents in China: prevalence and molecular characterization. *Applied and Environmental Microbiology* **75**, 7692–7699.
- Maikai, B.V., Umoh, J.U., Kwaga, J.K., Lawal, I.A., Maikai, V.A., Cama, V. and Xiao, L. (2011). Molecular characterization of *Cryptosporidium* spp. in native breeds of cattle in Kaduna State, Nigeria. *Veterinary Parasitology* **178**, 241–245.
- McCarthy, S., Ng, J., Gordon, C., Miller, R., Wyber, A. and Ryan, U.M. (2008). Prevalence of *Cryptosporidium* and *Giardia* species in

- animals in irrigation catchments in the southwest of Australia. *Experimental Parasitology* **118**, 596–599.
- McDonald, V.** (2000). Host cell-mediated responses to infection with *Cryptosporidium*. *Parasite Immunology* **22**, 597–604.
- McLeod, R.** (2004). *Counting the Cost: Impact of Invasive Animals in Australia 2004*. Cooperative Research Centre for Pest Animal Control, Canberra, Australia.
- Medema, G. J.** (1999). *Cryptosporidium and Giardia*: new challenges to the water industry. Ph.D. thesis. University of Utrecht, The Netherlands. ISBN 90-393-2120-5.
- Meireles, M. V., de Oliveira, F. P., Teixeira, W. F., Coelho, W. M. and Mendes, L. C.** (2011). Molecular characterization of *Cryptosporidium* spp. in dairy calves from the state of São Paulo, Brazil. *Parasitology Research* **109**, 949–951.
- Mendonça, C., Almeida, A., Castro, A., de Lurdes Delgado, M., Soares, S., da Costa, J.M. and Canada, N.** (2007). Molecular characterization of *Cryptosporidium* and *Giardia* isolates from cattle from Portugal. *Veterinary Parasitology* **147**, 47–50.
- Molloy, S. F., Smith, H. V., Kirwan, P., Nichols, R. A., Asaolu, S. O., Connelly, L. and Holland, C. V.** (2010). Identification of a high diversity of *Cryptosporidium* species genotypes and subtypes in a pediatric population in Nigeria. *American Journal of Tropical Medicine and Hygiene* **82**, 608–613.
- Morgan, U. M., Buddle, J. R., Armson, A., Elliot, A. and Thompson, R. C.** (1999a). Molecular and biological characterisation of *Cryptosporidium* in pigs. *Australian Veterinary Journal* **77**, 44–47.
- Morgan, U. M., Constantine, C. C., Forbes, D. A. and Thompson, R. C.** (1997). Differentiation between human and animal isolates of *Cryptosporidium parvum* using rDNA sequencing and direct PCR analysis. *Journal of Parasitology* **83**, 825–830.
- Morgan, U. M., Deplazes, P., Forbes, D. A., Spano, F., Hertzberg, H., Sargent, K. D., Elliot, A. and Thompson, R. C.** (1999). Sequence and PCR-RFLP analysis of the internal transcribed spacers of the rDNA repeat unit in isolates of *Cryptosporidium* from different hosts. *Parasitology* **118**, 49–58.
- Morgan, U. M., Sargent, K. D., Elliot, A. and R. C. A. Thompson.** (1998). *Cryptosporidium* in cats—additional evidence for *C. felis*. *The Veterinary Journal* **15**, 159–161.
- Morgan, U. M., Sturdee, A. P., Singleton, G., Gomez, M. S., Gracenea, M., Torres, J., Hamilton, S. G., Woodside, D. P. and Thompson, R. C.** (1999c). The *Cryptosporidium* “mouse” genotype is conserved across geographic areas. *Journal of Clinical Microbiology* **37**, 1302–1305.
- Morgan, U. M., Xiao, L., Monis, P., Fall, A., Irwin, P. J., Fayer, R., Denholm, K., Limor, J., Lal, A. and Thompson, R. C. A.** (2000). *Cryptosporidium* in domestic dogs—the ‘dog’ genotype. *Applied and Environmental Microbiology* **66**, 2220–2223.
- Morgan, U., Xiao, L., Sulaiman, I., Weber, R., Lal, A. A., Thompson, R. C. and Deplazes, P.** (1999b). Which genotypes/species of *Cryptosporidium* are humans susceptible to? *Journal of Eukaryotic Microbiology* **46**, 42S–43S.
- Mueller-Doblies, D., Giles, M., Elwin, K., Smith, R. P., Clifton-Hadley, F. A. and Chalmers, R. M.** (2008). Distribution of *Cryptosporidium* species in sheep in the UK. *Veterinary Parasitology* **154**, 214–219.
- Muhid, A., Robertson, I., Ng, J. and Ryan, U.** (2011). Prevalence of and management factors contributing to *Cryptosporidium* sp. infection in pre-weaned and post-weaned calves in Johor, Malaysia. *Experimental Parasitology* **127**, 534–538.
- Musser, G. G. and Carleton, M. D.** (1993). Family Muridae. In *Mammal Species of the World: A Taxonomic and Geographic Reference* (ed. Wilson, D. E., Reeder, D. M.), pp. 501–770. Smithsonian Institution, Washington DC, USA.
- Muthusamy, D., Rao, S. S., Ramani, S., Monica, B., Banerjee, I., Abraham, O. C., Mathai, D. C., Primrose, B., Muliylil, J., Wanke, C. A., Ward, H. D. and Kang, G.** (2006). Multilocus genotyping of *Cryptosporidium* sp. isolates from human immunodeficiency virus-infected individuals in South India. *Journal of Clinical Microbiology* **44**, 632–634.
- Nazemalhosseini-Mojarad, E., Haghghi, A., Taghipour, N., Keshavarz, A., Mohebi, S. R., Zali, M. R. and Xiao, L.** (2011). Subtype analysis of *Cryptosporidium parvum* and *Cryptosporidium hominis* isolates from humans and cattle in Iran. *Veterinary Parasitology* **179**, 250–252.
- Ng, J., Eastwood, K., Durrheim, D., Massey, P., Walker, B., Armson, A. and Ryan, U.** (2008). Evidence supporting zoonotic transmission of *Cryptosporidium* in rural New South Wales. *Experimental Parasitology* **119**, 192–195.
- Ng, J., Eastwood, K., Walker, B., Durrheim, D. N., Massey, P., Porigneaux, P., Kenp, R., McKinnon, B., Laurie, K., Miller, D., Bramley, E. and Ryan, U.** (2012). Evidence of *Cryptosporidium* transmission between cattle and humans in northern New South Wales. *Experimental Parasitology* **130**, 437–441.
- Ng, J., MacKenzie, B. and Ryan, U.** (2010a). Longitudinal multi-locus molecular characterization of sporadic Australian human clinical cases of cryptosporidiosis from 2005–2008. *Experimental Parasitology* **125**, 348–356.
- Ng, J. S., Pingault, N., Gibbs, R., Koehler, A. and Ryan, U.** (2010b). Molecular characterisation of *Cryptosporidium* outbreaks in Western and South Australia. *Experimental Parasitology* **125**, 325–328.
- Ng, J., Yang, R., McCarthy, S., Gordon, C., Hijjawi, N. and Ryan, U.** (2011b). Molecular characterization of *Cryptosporidium* and *Giardia* in pre-weaned calves in Western Australia and New South Wales. *Veterinary Parasitology* **176**, 145–150.
- Ng, J., Yang, R., Whiffin, V., Cox, P. and Ryan, U.** (2011a). Identification of zoonotic *Cryptosporidium* and *Giardia* genotypes infecting animals in Sydney’s water catchments. *Experimental Parasitology* **128**, 138–144.
- Nichols, R. A., Connelly, L., Sullivan, C. B. and Smith, H. V.** (2010). Identification of *Cryptosporidium* species and genotypes in Scottish raw and drinking waters during a one-year monitoring period. *Applied and Environmental Microbiology* **76**, 5977–5986.
- Nolan, M. J., Jex, A. R., Haydon, S. R., Stevens, M. A. and Gasser, R. B.** (2010). Molecular detection of *Cryptosporidium cuniculus* in rabbits in Australia. *Infection Genetics and Evolution* **10**, 1179–1187.
- Nolan, M. J., Jex, A. R., Mansell, P. D., Browning, G. F. and Gasser, R. B.** (2009). Genetic characterization of *Cryptosporidium parvum* from calves by mutation scanning and targeted sequencing-zoonotic implications. *Electrophoresis* **30**, 2640–2647.
- Nuchjangreed, C., Boonrod, K., Ongerth, J. and Karanis, P.** (2008). Prevalence and molecular characterization of human and bovine *Cryptosporidium* isolates in Thailand. *Parasitology Research* **103**, 1347–1353.
- O’Brien, E., McInnes, L. and Ryan, U.** (2008). *Cryptosporidium gp60* genotypes from humans and domesticated animals in Australia, North America and Europe. *Experimental Parasitology* **118**, 118–121.
- O’Keefe, B., D’Arcy, B. J., Davidson, J., Barbarito, B. and Clelland, B.** (2003). Urban diffuse sources of faecal indicators. *Seventh International Water Association Conference Diffuse Pollution and Basin Management, Dublin, Ireland, International Water Association*.
- Ondrácková, Z., Kvác, M., Sak, B., Kvetonová, D. and Rost, M.** (2009). Prevalence and molecular characterization of *Cryptosporidium* spp. in dairy cattle in South Bohemia, the Czech Republic. *Veterinary Parasitology* **165**, 141–144.
- Ong, C. S., Eisler, D. L., Alikhani, A., Fung, V. W., Tomblin, J., Bowie, W. R. and Isaac-Renton, J. L.** (2002). Novel *Cryptosporidium* genotypes in sporadic cryptosporidiosis cases: first report of human infections with a cervine genotype. *Emerging Infectious Diseases* **8**, 263–268.
- Palmer, C. S., Traub, R. J., Robertson, I. D., Devlin, G., Rees, R. and Thompson, R. C.** (2008). Determining the zoonotic significance of *Giardia* and *Cryptosporidium* in Australian dogs and cats. *Veterinary Parasitology* **154**, 142–147.
- Paoletti, B., Giangaspero, A., Gatti, A., Iorio, R., Cembalo, D., Milillo, P. and Traversa, D.** (2009). Immunoenzymatic analysis and genetic detection of *Cryptosporidium parvum* in lambs from Italy. *Experimental Parasitology* **122**, 349–352.
- Paparini, A., Jackson, B., Ward, S., Young, S. and Ryan, U. M.** (2012). *Cryptosporidium* genotypes detected in wild black rats (*Rattus rattus*) from northern Australia. *Experimental Parasitology* (in the Press.)
- Paul, S., Chandra, D., Ray, D. D., Tewari, A. K., Rao, J. R., Banerjee, P. S., Baidya, S. and Raina, O. K.** (2008). Prevalence and molecular characterization of bovine *Cryptosporidium* isolates in India. *Veterinary Parasitology* **153**, 143–146.
- Paul, S., Chandra, D., Tewari, A. K., Banerjee, P. S., Ray, D. D., Raina, O. K. and Rao, J. R.** (2009). Prevalence of *Cryptosporidium andersoni*: A molecular epidemiological survey among cattle in India. *Veterinary Parasitology* **161**, 31–35.
- Power, M. L.** (2010). Biology of *Cryptosporidium* from marsupial hosts. *Experimental Parasitology* **124**, 40–44.
- Power, M. L., Cheung-Kwok-Sang, C., Slade, M. and Williamson, S.** (2009). *Cryptosporidium fayeri*: diversity within the *gp60* locus of isolates from different marsupial hosts. *Experimental Parasitology* **121**, 219–223.
- Power, M. L. and Ryan, U. M.** (2008). A new species of *Cryptosporidium* (Apicomplexa: Cryptosporidiidae) from eastern grey kangaroos (*Macropus giganteus*). *Journal of Parasitology* **94**, 1114–1117.
- Power, M. L., Sangster, N. C., Slade, M. B. and Veal, D. A.** (2005). Patterns of *Cryptosporidium* oocyst shedding by eastern grey kangaroos inhabiting an Australian watershed. *Applied and Environmental Microbiology* **71**, 6159–6164.
- Power, M. L., Shanker, S. R., Sangster, N. C. and Veal, D. A.** (2003). Evaluation of a combined immunomagnetic separation/flow

- cytometry technique for epidemiological investigations of *Cryptosporidium* in domestic and Australian native animals. *Veterinary Parasitology* **112**, 21–31.
- Power, M. L., Slade, M. B., Sangster, N. C. and Veal, D. A.** (2004). Genetic characterisation of *Cryptosporidium* from a wild population of eastern grey kangaroos *Macropus giganteus* inhabiting a water catchment. *Infection Genetics and Evolution* **4**, 59–67.
- Plutzer, J. and Karanis, P.** (2007). Genotype and subtype analyses of *Cryptosporidium* isolates from cattle in Hungary. *Veterinary Parasitology* **146**, 357–362.
- Qamruddin, A. O., Keaney, M. G., McCann, R. and Chadwick, P. R.** (2002). Increased stool sampling during a waterborne outbreak of cryptosporidiosis does not increase the detection of other faecal pathogens. *Journal of Clinical Pathology* **55**, 274–274.
- Quilez, J., Torres, E., Chalmers, R. M., Hadfield, S. J., Del Cacho, E. and Sánchez-Acedo, C.** (2008). *Cryptosporidium* genotypes and subtypes in lambs and goat kids in Spain. *Applied and Environmental Microbiology* **74**, 6026–6031.
- Ralston, B., Thompson, R. C., Pethick, D., McAllister, T. A. and Olson, M. E.** (2010). *Cryptosporidium andersoni* in Western Australian feedlot cattle. *Australian Veterinary Journal* **88**, 458–460.
- Ramp, D. C. G.** (2002). Density dependence in foraging habitat preference of eastern grey kangaroos. *Oikos* **98**, 393–402.
- Ren, X., Zhao, J., Zhang, L., Ning, C., Jian, F., Wang, R., Lv, C., Wang, Q., Arrowood, M. J. and Xiao, L.** (2011). *Cryptosporidium tyzzeri* n. sp. (Apicomplexa: Cryptosporidiidae) in domestic mice (*Mus musculus*). *Experimental Parasitology* **130**, 274–281.
- Robertson, B., Sinclair, M. I., Forbes, A. B., Veitch, M., Cunliffe, D., Willis, J. and Fairley, C. K.** (2002). Case-control studies of sporadic cryptosporidiosis in Melbourne and Adelaide, Australia. *Epidemiology and Infection* **128**, 419–431.
- Robertson, L. J.** (2009). *Giardia* and *Cryptosporidium* infections in sheep and goats: a review of the potential for transmission to humans via environmental contamination. *Epidemiology and Infection* **137**, 913–921.
- Robertson, L. J., Gjerde, B. K. and Furuseth Hansen, E.** (2010). The zoonotic potential of *Giardia* and *Cryptosporidium* in Norwegian sheep: a longitudinal investigation of 6 flocks of lambs. *Veterinary Parasitology* **171**, 140–145.
- Robinson, G. and Chalmers, R. M.** (2010). *The European rabbit (Oryctolagus cuniculus)*, a source of zoonotic cryptosporidiosis. *Zoonoses Public Health* **57**, e1–13.
- Robinson, G., Wright, S., Elwin, K., Hadfield, S. J., Katzer, F., Bartley, P. M., Hunter, P. R., Nath, M., Innes, E. A. and Chalmers, R. M.** (2010). Re-description of *Cryptosporidium cuniculus* Inman and Takeuchi, 1979 (Apicomplexa: Cryptosporidiidae): morphology, biology and phylogeny. *International Journal for Parasitology* **40**, 1539–1548.
- Roy, S. L., DeLong, S. M., Stenzel, S. A., Shiferaw, B., Roberts, J. M., Khalakdina, A., Marcus, R., Segler, S. D., Shah, D., Thomas, S., Vugia, D. J., Zansky, S. M., Dietz, V. and Beach, M. J.** (2004). Risk factors for sporadic cryptosporidiosis among immunocompetent persons in the United States from 1999 to 2001. *Journal of Clinical Microbiology* **42**, 2944–2951.
- Ruecker, N. J., Braithwaite, S. L., Topp, E., Edge, T., Lapen, D. R., Wilkes, G., Robertson, W., Medeiros, D., Sensen, C. W. and Neumann, N. F.** (2007). Tracking host sources of *Cryptosporidium* spp. in raw water for improved health risk assessment. *Applied and Environmental Microbiology* **73**, 3945–3957.
- Ryan, U. M., Bath, C., Robertson, I., Read, C., Elliot, A., McInnes, L., Traub, R. and Besier, B.** (2005). Sheep may not be an important zoonotic reservoir for *Cryptosporidium* and *Giardia* parasites. *Applied and Environmental Microbiology* **71**, 4992–4997.
- Ryan, U. M., Monis, P., Enemark, H. L., Sulaiman, I., Samarasinghe, B., Read, C., Buddle, R., Robertson, I., Zhou, L., Thompson, R. C. and Xiao, L.** (2004). *Cryptosporidium suis* n. sp. (Apicomplexa: Cryptosporidiidae) in pigs (*Sus scrofa*). *Journal of Parasitology* **90**, 769–773.
- Ryan, U. M., Power, M. and Xiao, L.** (2008). *Cryptosporidium fayeri* n. sp. (Apicomplexa: Cryptosporidiidae) from the Red Kangaroo (*Macropus rufus*). *Journal of Eukaryotic Microbiology* **55**, 22–26.
- Ryan, U. M., Samarasinghe, B., Read, C., Buddle, J. R., Robertson, I. D. and Thompson, R. C.** (2003). Identification of a novel *Cryptosporidium* genotype in pigs. *Applied and Environmental Microbiology* **69**, 3970–3974.
- Santín, M., Trout, J. M. and Fayer, R.** (2007). Prevalence and molecular characterization of *Cryptosporidium* and *Giardia* species and genotypes in sheep in Maryland. *Veterinary Parasitology* **146**, 17–24.
- Santín, M., Trout, J. M. and Fayer, R.** (2008). A longitudinal study of cryptosporidiosis in dairy cattle from birth to 2 years of age. *Veterinary Parasitology* **155**, 15–23.
- Santín, M., Trout, J. M. and Fayer, R.** (2009). A longitudinal study of *Giardia duodenalis* genotypes in dairy cows from birth to 2 years of age. *Veterinary Parasitology* **162**, 40–45.
- Santín, M., Trout, J. M., Xiao, L., Zhou, L., Greiner, E. and Fayer, R.** (2004). Prevalence and age-related variation of *Cryptosporidium* species and genotypes in dairy calves. *Veterinary Parasitology* **122**, 103–117.
- Sargent, K. D., Morgan, U. M., Elliot, A. and R. C. A. Thompson.** (1998). Morphological and Genetic characterisation of *Cryptosporidium* oocysts from domestic cats. *Veterinary Parasitology* **77**, 221–227.
- Saunders, G. and Kay, B.** (1991). Movements of feral pigs (*Sus scrofa*) at Sunny Corner, New South Wales. *Wildlife Research* **18**, 49–61.
- Saunders, G., Coman, B., Kinnear, J. and Braysher, M.** (1995). Managing Vertebrate Pests: Foxes. Australian Government Publishing Service, Canberra.
- Sevá Ada, P., Funada, M. R., Souza Sde, O., Nava, A., Richtzenhain, L. J. and Soares, R. M.** (2010). Occurrence and molecular characterization of *Cryptosporidium* spp. isolated from domestic animals in a rural area surrounding Atlantic dry forest fragments in Teodoro Sampaio municipality, State of São Paulo, Brazil. *Revista Brasileira de Parasitologia Veterinária* **19**, 249–253.
- Shen, Y., Yin, J., Yuan, Z., Lu, W., Xu, Y., Xiao, L. and Cao, J.** (2011). The identification of the *Cryptosporidium ubiquitum* in pre-weaned Ovines from Aba Tibetan and Qiang autonomous prefecture in China. *Biomedical and Environmental Sciences* **24**, 315–320.
- Shi, K., Jian, F., Lv, C., Ning, C., Zhang, L., Ren, X., Dearen, T. K., Li, N., Qi, M. and Xiao, L.** (2010). Prevalence, genetic characteristics, and zoonotic potential of *Cryptosporidium* species causing infections in farm rabbits in China. *Journal of Clinical Microbiology* **48**, 3263–3266.
- Silverlås, C., Näslund, K., Björkman, C. and Mattsson, J. G.** (2010). Molecular characterisation of *Cryptosporidium* isolates from Swedish dairy cattle in relation to age, diarrhoea and region. *Veterinary Parasitology* **169**, 289–295.
- Smith, H. V. and Nichols, R. A.** (2010). *Cryptosporidium*: detection in water and food. *Experimental Parasitology* **124**, 61–79.
- Starkey, S. R., Zeigler, P. E., Wade, S. E., Schaaf, S. L. and Mohammed, H. O.** (2006). Factors associated with shedding of *Cryptosporidium parvum* versus *Cryptosporidium bovis* among dairy cattle in New York State. *Journal of the American Veterinary Medical Association* **229**, 1623–1626.
- Sulaiman, I. M., Hira, P. R., Zhou, L., Al-Ali, F. M., Al-Shelahi, F. A., Shweiki, H. M., Iqbal, J., Khalid, N. and Xiao, L.** (2005). Unique endemicity of cryptosporidiosis in children in Kuwait. *Journal of Clinical Microbiology* **43**, 2805–2809.
- Sweeny, J. P., Ryan, U. M., Robertson, I. D. and Jacobson, C.** (2011a). *Cryptosporidium* and *Giardia* associated with reduced lamb carcass productivity. *Veterinary Parasitology* **182**, 127–139.
- Sweeny, J. P., Ryan, U. M., Robertson, I. D., Yang, R., Bell, K. and Jacobson, C.** (2011b). Longitudinal investigation of protozoan parasites in meat lamb farms in southern Western Australia. *Preventative Veterinary Medicine* **101**, 192–203.
- Thompson, H. P., Dooley, J. S., Kenny, J., McCoy, M., Lowery, C. J., Moore, J. E. and Xiao, L.** (2007). Genotypes and subtypes of *Cryptosporidium* spp. in neonatal calves in Northern Ireland. *Parasitology Research* **100**, 619–624.
- Waldron, L. S., Cheung-Kwok-Sang, C. and Power, M. L.** (2010). Wildlife-associated *Cryptosporidium fayeri* in human, Australia. *Emerging Infectious Disease* **16**, 2006–2007.
- Waldron, L. S., Dimeski, B., Beggs, P. J., Ferrari, B. C. and Power, M. L.** (2011a). Molecular epidemiology, spatiotemporal analysis, and ecology of sporadic human cryptosporidiosis in Australia. *Applied and Environmental Microbiology* **77**, 7757–7765.
- Waldron, L. S., Ferrari, B. C., Cheung-Kwok-Sang, C., Beggs, P. J., Stephens, N. and Power, M. L.** (2011b). Molecular epidemiology and spatial distribution of a waterborne cryptosporidiosis outbreak in Australia. *Applied and Environmental Microbiology* **77**, 7766–7771.
- Waldron, L. S., Ferrari, B. C., Gillings, M. R. and Power, M. L.** (2009a). Terminal restriction fragment length polymorphism for identification of *Cryptosporidium* species in human feces. *Applied and Environmental Microbiology* **75**, 108–112.
- Waldron, L. S., Ferrari, B. C. and Power, M. L.** (2009b). Glycoprotein 60 diversity in *C. hominis* and *C. parvum* causing human cryptosporidiosis in NSW, Australia. *Experimental Parasitology* **122**, 124–127.
- Waldron, L. S. and Power, M. L.** (2011). Fluorescence analysis detects *gp60* subtype diversity in *Cryptosporidium* infections. *Infection Genetics and Evolution* **11**, 1388–1395.



- Wang, R., Qiu, S., Jian, F., Zhang, S., Shen, Y., Zhang, L., Ning, C., Cao, J., Qi, M. and Xiao, L. (2010a). Prevalence and molecular identification of *Cryptosporidium* spp. in pigs in Henan, China. *Parasitology Research* **107**, 1489–1494.
- Wang, Y., Feng, Y., Cui, B., Jian, F., Ning, C., Wang, R., Zhang, L. and Xiao, L. (2010b). Cervine genotype is the major *Cryptosporidium* genotype in sheep in China. *Parasitology Research* **106**, 341–347.
- Wang, R., Ma, G., Zhao, J., Lu, Q., Wang, H., Zhang, L., Jian, F., Ning, C. and Xiao, L. (2011). *Cryptosporidium andersoni* is the predominant species in post-weaned and adult dairy cattle in China. *Parasitology International* **60**, 1–4.
- Warren, K. S., Swan, R. A., Morgan-Ryan, U. M., Friend, J. A. and Elliot, A. (2003). *Cryptosporidium muris* infection in bilbies (*Macrotis lagotis*). *Australian Veterinary Journal* **81**, 739–741.
- West, W. (2008). *Assessing Invasive Animals in Australia 2008*. Invasive Animals Cooperative Research Centre. National Land & Water Resources Audit. ISBN 978 0 642 37150 8.
- Wielinga, P. R., de Vries, A., van der Goot, T. H., Mank, T., Mars, M. H., Kortbeek, L. M. and van der Giessen, J. W. (2008). Molecular epidemiology of *Cryptosporidium* in humans and cattle in The Netherlands. *International Journal for Parasitology* **38**, 809–817.
- Williams, C. K., Parer, I., Coman, B. J., Burley, J. and Braysher, M. (1995). *Managing Vertebrate Pests: Rabbits*. Bureau of Resource Sciences/CSIRO Division of Wildlife and Ecology, Australian Government Publishing Service, Canberra, Australia.
- Xiao, L. (2010). Molecular epidemiology of cryptosporidiosis: an update. *Experimental Parasitology* **124**, 80–89.
- Xiao, L., Bern, C., Arrowood, M., Sulaiman, I., Zhou, L., Kawai, V., Vivar, A., Lal, A. A. and Gilman, R. H. (2002a). Identification of the *Cryptosporidium* pig genotype in a human patient. *Journal of Infectious Diseases* **185**, 1846–1848.
- Xiao, L. and Feng, Y. (2008). Zoonotic cryptosporidiosis. *FEMS Immunology and Medical Microbiology* **52**, 309–323.
- Xiao, L., Moore, J. E., Ukoh, U., Gatei, W., Lowery, C. J., Murphy, T. M., Dooley, J. S., Millar, B. C., Rooney, P. J. and Rao, J. R. (2006). Prevalence and identity of *Cryptosporidium* spp. in pig slurry. *Applied and Environmental Microbiology* **72**, 4461–4463.
- Xiao, L. and Ryan, U. M. (2004). Cryptosporidiosis: an update in molecular epidemiology. *Current Opinion in Infectious Diseases* **17**, 483–490.
- Xiao, L., Ryan, U. M., Graczyk, T. K., Limor, J., Li, L., Kombert, M., Junge, R., Sulaiman, I. M., Zhou, L., Arrowood, M. J., Koudela, B., Modry, D. and Lal, A. A. (2004). Genetic diversity of *Cryptosporidium* spp. in captive reptiles. *Applied and Environmental Microbiology* **70**, 891–899.
- Xiao, L., Sulaiman, I. M., Ryan, U. M., Zhou, L., Atwill, E. R., Tischler, M. L., Zhang, X., Fayer, R. and Lal, A. A. (2002b). Host adaptation and host-parasite co-evolution in *Cryptosporidium*: implications for taxonomy and public health. *International Journal of Parasitology* **32**, 1773–1785.
- Xiao, L., Zhou, L., Santin, M., Yang, W. and Fayer, R. (2007). Distribution of *Cryptosporidium parvum* subtypes in calves in eastern United States. *Parasitology Research* **100**, 701–706.
- Yang, W., Chen, P., Villegas, E. N., Landy, R. B., Kanetsky, C., Cama, V., Dearen, T., Schultz, C. L., Orndorff, K. G., Prelewicz, G. J., Brown, M. H., Young, K. R. and Xiao, L. (2008). *Cryptosporidium* source tracking in the Potomac River watershed. *Applied and Environmental Microbiology* **74**, 6495–6504.
- Yang, R., Fenwick, S., Potter, A., Ng, J. and Ryan, U. (2011). Identification of novel *Cryptosporidium* genotypes in kangaroos from Western Australia. *Veterinary Parasitology* **179**, 22–27.
- Yang, R., Jacobson, C., Gordon, C. and Ryan, U. (2009). Prevalence and molecular characterisation of *Cryptosporidium* and *Giardia* species in pre-weaned sheep in Australia. *Veterinary Parasitology* **161**, 19–24.
- Yin, J., Shen, Y., Yuan, Z., Lu, W., Xu, Y. and Cao, J. (2011). Prevalence of the *Cryptosporidium* pig genotype II in pigs from the Yangtze River Delta, China. *PLoS One* **6**, e20738.
- Zintl, A., Neville, D., Maguire, D., Fanning, S., Mulcahy, G., Smith, H. V. and De Waal, T. (2007). Prevalence of *Cryptosporidium* species in intensively farmed pigs in Ireland. *Parasitology* **134**, 1575–1582.