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Invited review

The zoonotic transmission of *Giardia* and *Cryptosporidium*

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Abstract

The molecular characterisation of *Giardia* and *Cryptosporidium* has given rise to a more epidemiological meaningful and robust taxonomy. Importantly, molecular tools are now available for 'typing' isolates of the parasites directly from clinical and environmental samples. As a consequence, information on zoonotic potential has been obtained although the frequency of zoonotic transmission is still poorly understood. Analysis of outbreaks and case–control studies, especially when coupled with genotyping data, is slowly providing information on the public health significance of zoonotic transmission. Such studies support the hypothesis that *Cryptosporidium hominis* is spread only between humans but that the major reservoir for *Cryptosporidium parvum* is domestic livestock, predominantly cattle, and that direct contact with infected cattle is a major transmission pathway along with indirect transmission through drinking water. The situation is less clearcut for *Giardia duodenalis* but the evidence does not, in general, support zoonotic transmission as a major risk for human infections. However, for both parasites there is a need for molecular epidemiological studies to be undertaken in well-defined foci of transmission in order to fully determine the frequency and importance of zoonotic transmission.

Keywords: Giardia; Cryptosporidium; Epidemiology; Zoonoses; Zoonotic transmission

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1. Introduction

Giardia and *Cryptosporidium* are the most common enteric parasites of humans and domestic animals, and are being increasingly recognised as parasites of a diverse range of wildlife species (Fayer, 2004; Thompson, 2004; Thompson and Monis, 2004; Appelbee et al., 2005). Their clinical significance is largely restricted to humans and young livestock (Olson et al., 2004). *Giardia* is a common cause of diarrhoeal disease in humans, particularly among disadvantaged groups where chronic infections contribute to poor growth and other nutritional disorders particularly in children (Thompson and Monis, 2004). In young livestock, *Giardia* infections may adversely impact on production (Olson et al., 2004). The significance of *Cryptosporidium* was initially recognised to be one of an opportunistic pathogen in AIDS patients but the impact of such infections is now lessening, at least in developed countries, with the advent of retroviral therapies (Nannini and Okhuysen, 2002). Although *Cryptosporidium* infections are usually of short duration and self-limiting in individuals with an intact immune system the lack of effective anticryptosporidial drugs means the very young and elderly may be at risk of severe disease as a results of *Cryptosporidium* infection.

The life cycles of each parasite include asexual phases of proliferation on the mucosal surface, in addition to a sexual phase of reproduction in *Cryptosporidium* that also exhibits an unusual intracellular phase of development in its life cycle (reviewed in Thompson et al., in press). The infective stages of both parasites are encysted when released in the faeces and capable of prolonged survival in the environment. Re-infection is achieved when the cysts/oocysts are ingested which may be through direct host to host contact or via contaminated materials, water, food or arthropods.

The link between human and animal infections has been a question that has dominated much of the research effort on

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Giardia and *Cryptosporidium*. Since both organisms can be transmitted in water, the source of water contamination remains a critical issue for water authorities throughout the world (Fayer, 2004; Thompson, 2004). The role that animal infections may play in this regard remains controversial, particularly that of livestock and wildlife because of their potential role as zoonotic reservoirs of infection.

In order to better understand the zoonotic potential of *Giardia* and *Cryptosporidium* infections in wild and domestic animals, it has been important to determine whether humans and other animals are susceptible to infection with genetically identical forms of each parasite. The taxonomy of *Giardia* and *Cryptosporidium* has been extensively reviewed and will not be reviewed in detail here (Monis and Thompson, 2003; Thompson and Monis, 2004; Xiao et al., 2004; Caccio et al., 2005). However, elucidating a correct taxonomy for both *Giardia* and *Cryptosporidium* has provided the basis for better understanding the links between infections in humans and other animals. The issue has been difficult to resolve because of a paucity of morphological characters on which to discriminate species. In this respect, *Giardia* and *Cryptosporidium* share this problem with many other protozoa, and it is only recently with the advent of molecular typing tools that both the taxonomy and epidemiology of many protozoal infections are now being resolved.

Initially, species of *Giardia* and *Cryptosporidium* were described on the basis of host occurrence (Thompson et al., 1990; O'Donoghue, 1995). Subsequently, such an approach was criticised and the numbers of species was rationalised. Now, the picture is changing once again and many of the 'host based' species have been resurrected (Thompson and Monis, 1994; Xiao et al., 2004).

Table 1 lists currently recognised and recently proposed species of *Giardia* and *Cryptosporidium* and their host ranges, as well as a number of intraspecific variants, or genotypes, that have been characterised on the basis of their genetic distinctness, as well as other phenotypic characteristics including host origin. The taxonomic status of these latter forms remains to be resolved, and requires further studies in which both their geographic and host ranges are further investigated.

With both *Giardia* and *Cryptosporidium*, a large number of species and genotypes are now recognised that differ principally in their host range. Some species and genotypes appear to be restricted to particular species of hosts

Table 1
Species and genotypes of *Cryptosporidium* and *Giardia*

Cryptosporidium		Giardia	
Species	Major hosts	Species	Major hosts
C. muris	Rodents	G. duodenalis (=Assemblage A)	Humans and other primates, dogs, cats, livestock, rodents and other wild mammals
C. parvum	Cattle & other livestock, humans	Assemblage B[a]	Humans and other primates, dogs
C. melegridis	Birds	G. agilis	Amphibians
C. wrairi	Guinea pigs	G. muris	Rodents
C. felis	Cats	G. psittaci	Birds
C. serpentis	Reptiles	G. ardeae	Birds
C. baileyi	Poultry	Assemblage C[a]	Dogs
C. saurophilum	Lizards	Assemblage F[a]	Cats
C. galli		Assemblage E[a]	Cattle and other hoofed livestock
C. andersoni	Cattle	G. simondi (=Assemblage G)	Rats
C. canis	Dogs		
C. molnari	Fish		
C. hominis	Humans		
C. suis	Pigs		
Genotypes			
Ferret	Deer mice		
Mouse	Squirrel (×2)		
Skunk	Bear		
Marsupial (×4)	Goose (×2)		
Horse	Duck		
Rabbit	Bovine		
Monkey	Snake		
Pig (×2)	Tortoise		
Cervid (×2)	Lizard		
Fox	Woodcock		
Muskrat (×2)			

Details in Thompson and Monis (2004); Xiao et al. (2004).

[a] Recently proposed to be separate species: *G. enterica*, *G. canis*, *G. cati* and *G. bovis*. See Thompson and Monis (2004).