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Molecular epidemiology of cryptosporidiosis in dogs and cats

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DESCRIPTION

Pets, especially cats and dogs, contribute significantly not only to develop their physical, social and emotional emotions, but also to facilitate recovery of some diseases. Cryptosporidiosis is a major cause of diarrhea and intestinal disease in humans and domestic animals. It has long been known to be the leading cause of watery diarrhea in pre-weaning calves and lambs, causing significant morbidity and mortality. Even subclinical infection in older animals has been associated with reduced growth rate, carcass weight and dressing efficiency. In zoos and domestic snakes, stomach infections with *Cryptosporidium serpentis* are chronic and often fatal. In birds, *C. baileyi* can cause respiratory and renal infections, resulting in high mortality. Recent human studies have implicated cryptosporidiosis as the second most important cause for moderate to severe diarrhea in young children in developing countries. Several *Cryptosporidium* species from mammals and birds, such as *C. parvum, C. meleagridis, C. canis, C. felis,* and *C. ubiquitum,* are important zoonotic pathogens, causing animal contactassociated or waterborne and foodborne cryptosporidiosis in humans (Wells 2009).

Cats are reservoirs for several zoonotic pathogens, including *Cryptosporidium* spp., Giardia duodenalis and Blastocystis sp. These parasites pose a significant, but often overlooked, threat to humans and animals. In addition, fetal Tritrichomonas has been described as living in the gastrointestinal tract of cats and can cause gastrointestinal symptoms. However, there are few data regarding the molecular epidemiology of these parasites in domestic cats in China (Amer 2010).

Puppies and cats in human cryptosporidiosis has been the point of interest of a good deal attention. Studies wherein genotyping of *Cryptospiridium oocysts* in feces of puppies and cats were a success and feature proven that maximum infections in those animals are as a result of host-particular *C. canis* and *C. felis,* respectively. Mosthuman instances of cryptosporidiosis are related to *C.hominis* and *C. parvum*; *C. canis* and *C. felis* are accountable for simplest a small range of instances. Thus, molecular epidemiologic research help the competition that the threat of zoonotic transmission of *Cryptosporidium* spp. from puppy cats and puppies is low. Veterinarians can tell their customers of this minimum threat, however although recommend them to decrease touch with puppy cat and canine feces (Walsh 2009).

The use of molecular tools has led to the identification of several *Cryptosporidium* spp. in dogs and cats. Among them, *Cryptosporidium canis* and *Cryptosporidium felis* are the predominant species causing cryptosporidiosis in dogs and cats. Several cases of *Cryptosporidium parvum* infection were also identified in both groups of animals. The determination of *C. canis, C. felis* and *C. parvum* in pets and owners showing the possibility of animal-to-human transmission of *Cryptosporidium* spp. between humans and animals. However, a small number of such concurrent infections have been reported. Therefore, cross transmission *Cryptosporidium* spp. between dogs or cats and people has long been a controversial issue. Recent development tools for *C. Canis* and *C. Felis* should be very useful in determining the zoonotic transmission of two *Cryptosporidium* spp. The data created using these tools have confirmed the appearance of zoonotic transmission of these two *Cryptosporidium* spp. Between their owners and pets, (Hijjawi 2022) but also shows the potential presence of hospital subgroups. Intensive use of this subheading tools in epidemiological studies on human cryptosporidiosis are needed to improve understanding of the importance of *Cryptosporidium* spp. Pet.

Dog and cat owners are often unaware of whether their pets contain microorganisms that can be transmitted to animals. Enteric cryptosporidiosis stands out among the zoonotic diseases that can be acquired by humans through

contact with these animals. The disease is a public health problem because its infectious form, *oocysts*, spreads easily in the environment, has multiple routes of transmission *via* the fecal-oral route, such as direct contact with humans. Infected with disease (human-to-human transmission) or animals (animal-to-human transmission), or indirectly from ingesting contaminated food (food transmission) and water (water transmission).

Molecular studies have shown that most infections in dogs and cats are caused by *C. canis* and *C. felis*, showing specificity for these hosts. However, *C. parvum* is not species-specific and has a wide range of hosts, including cattle, humans, and sometimes dogs and cats. *Cryptosporidium parvum* ranks as the second most commonly diagnosed *Cryptosporidium* species (after *C. hominis*) in humans, followed by *C. felis* and *C. canis*.

The molecular epidemiology of cryptosporidiosis in humans and animals is the most active *Cryptosporidium* research area in China. In these studies, taxonomic and genotyping tools were widely used to identify the source of infection and evaluate the interspecific transmission of *Cryptosporidium* spp. Chinese scientists, in collaboration with scientists from other countries, have played an important role in the development of several recent molecular epidemiological tools for *Cryptosporidium* spp. For example, PCRRFLP Small Subunit (SSU) rRNA gene analysis using SspI and MboII developed by Chinese scientists has become the most popular gene profiling tool for rapid differentiation of common *Cryptosporidium* species. (Abe 2003) Variable in ruminants (*C. parvum*, *C. oxen*, *C. ryanae* and *C. andersoni chez les bovins* and *C. small*, *C. ubiquitum* and *C. xiaoi* in sheep and goats). Several taxonomic tools targeting the 60 kDa glycoprotein (gp60) gene have been developed to assess the importance of animal-to-human infection with several emerging human pathogenic *Cryptosporidium* species such as *C. ubiquitum* and *Cryptosporidium* chipmunk genotype I.

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