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

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Abstract

The aim of this study was to assess the occurrence of Cryptosporidium in domestic animals in rural properties surrounding rain forest fragments within the municipality of Teodoro Sampaio, southeastern Brazil. Conventional sucrose flotation method followed by molecular characterization of the parasites by sequencing PCR products amplified from SSU rRNA gene were used. Stool samples were collected from domestic animals raised as pets and livestock in all rural properties surrounding three forest fragments. Samples from cattle (197), equine (63), pigs (25), sheep (11), and dogs (28) were collected from 98 rural properties. The frequency of occurrence of Cryptosporidium within each animal species was 3.0% (6/197) among cattle and 10.7% (3/28) among dogs. Cryptosporidium was not detected in stool samples from equine, sheep, and pigs. All sequences obtained from the six samples of calves showed molecular identity with Cryptosporidium andersoni while all sequences from dog samples were similar to C. canis. The frequency of occurrence of Cryptosporidium in these domestic animal species was low. The absence of C. parvum in the present study suggests that the zoonotic cycle of cryptosporidiosis may not be relevant in the region studied. The presence of Cryptosporidium species seldom described in humans may be, otherwise, important for the wild fauna as these animals are a source of infection and dissemination of this protozoan to other animal species. The impact and magnitude of infection by C. andersoni in wild ruminants and C. canis in wild canids have to be assessed in future studies to better understand the actual importance of these species in this region.

Keywords: Cryptosporidiosis, molecular characterization, SSU rRNA, Atlantic Dry Forest, domestic animals.

Resumo

O objetivo deste estudo foi avaliar a ocorrência de Cryptosporidium, em animais domésticos de propriedades rurais ao redor de fragmentos de mata Atlântica de interior no município de Teodoro Sampaio, por exame convencional de flutuação em solução de sacarose, seguido de caracterização molecular dos parasitas através do sequenciamento dos produtos amplificados na PCR do gene SSU rRNA. Foram coletadas amostras de fezes de animais domésticos criados para subsistência e estimação nas propriedades rurais do entorno de três fragmentos florestais. Amostras de bovinos (197), equinos (63), suínos (25), ovinos (11) e cães (28) foram coletadas de 98 propriedades rurais. A ocorrência de Cryptosporidium para a espécie bovina foi de 3,0% (6/197); para os cães, de 10,7% (3/28); e para os demais animais os resultados foram negativos. Todas as sequências obtidas das seis amostras de bovinos apresentaram identidade molecular com Cryptosporidium andersoni, enquanto as sequências oriundas de amostras de fezes de cães revelaram-se similares.
surrounding MDSP and from two smaller forest fragments

Material and Methods

In June 2007, stool samples were collected from domestic animals raised as pets and for subsistence at all rural properties surrounding MDSP and from two smaller forest fragments (Figure 1). A total of 98 rural properties were sampled. All the animals sampled were mixed breed.

Cattle samples were collected from 79 properties, equine from 46, pigs from 20, sheep from nine, and dogs from 21. Only fresh samples were collected directly from the ground, fixed in 2.0% potassium dichromate and stored at 5.0 °C for up to three weeks. The samples were collected with the help of the owners, providing that same animal was not sampled twice. They were sent to the laboratory immediately after collection in plastic bags under refrigeration.

Altogether, samples were collected from 197 bovine (118 less than 3 months old), 63 equine (5 less than 3 months old), 25 pigs (2 less than 3 months old), 11 sheep (1 less than 3 months old), and 28 dogs (1 less than 3 months old).

Stool samples were examined for oocysts of Cryptosporidium spp., by a conventional sucrose flotation method. Floated material was transferred to a slide and examined by light microscopy. When 4-8 µm sized oocysts were observed, the slide was washed and DNA was extracted from the material as previously described (THOMAZ et al., 2007).

To amplify fragments of the SSU rRNA gene, a nested-PCR was used (THOMAZ et al., 2007). The nested-PCR products were sequenced using secondary PCR primers and Big Dye chemistry (Applied Biosystems, Foster City, California). Sequencing products were analyzed on an ABI377 automated sequencer. Both strands of each nested-PCR products were sequenced at least twice to increase the confidence of sequencing. The sequences were assembled and the contig formed with the phred-base-calling and the phrap-assembly tool available in the suite Codoncode aligner v.1.5.2. (Codoncode Corp. Dedham, MA, USA). SSU rRNA sequences of Cryptosporidium spp. were aligned and the resulting alignment matrix was used as input to Molecular Evolutionary Genetics Analysis (MEGA) software version 4 (TAMURA et al., 2007). Phylogeny was reconstructed with distance matrix method using the maximum composite likelihood.

Results

The occurrence of Cryptosporidium was detected in eight of the 98 properties (8.2%). In six of them, the parasites were found only in feces of young calves less than 3 months old and in two properties the parasites were found only in feces from dogs. In one of the properties an adult dog was eliminating the parasite while in the other property the parasite was found in stool samples from a puppy and an adult dog.
The frequency of occurrence of *Cryptosporidium* within each animal species was 3.0% (6/197) among cattle and 10.7% (3/28) among dogs. *Cryptosporidium* was not detected in stool samples from equine, ovine, and pigs.

All the sequences from calves showed molecular identity with *C. andersoni* while all sequences from dogs were revealed a similarity to *C. canis* (Figure 2). The SSU rRNA nucleotide sequences of five isolates of cattle revealed 100% identity with homologous sequences of *C. andersoni* (identical to sequence AF093496). The nucleotide sequence of the remaining isolates of cattle was also 100% similar to AF093496 except for a thymidine insertion. The SSU rRNA nucleotide sequences of all the isolates of dogs revealed 100% identity with homologous sequences of *C. canis* (identical to sequence AB210854). The sequences were deposited in Genbank under the accession numbers GU365874 – GU365876.

**Discussion**

The frequency of occurrence of *Cryptosporidium* among domestic animals raised in rural properties surrounding the forests in Pontal do Paranaíba was low. In ruminants, cattle in particular, the occurrences of the low specific *C. parvum*, and the host-adapted species *C. andersoni* and *C. bovis* have been reported. *Cryptosporidium andersoni* is considered of low pathogenicity (ANDERSON, 1991) and rarely pose risk of infection to humans (LEONI et al., 2006). In dogs, two species of *Cryptosporidium* can be found, *C. parvum* and *C. canis*. (FAYER et al., 2001) Within the genus *Cryptosporidium*, five species, *C. hominis*, *C. parvum*, *C. meleagridis*, *C. felis* and *C. canis* may infect immunocompetent and immunocompromised humans. Among them, the latter one is the rarest in humans (XIAO; FENG, 2008). The results of the present study showed that the zoonotic cycle of cryptosporidiosis appears to be of less relevance in the region studied.

The frequency of bovines positive for the presence of *Cryptosporidium* was equivalent to 3.0%, a low frequency compared to those reported in other studies. Thomaz et al. (2007) found 17.1% (21/123) of positive samples of *Cryptosporidium* spp. in calves from dairy farms in the State of São Paulo (THOMAZ et al., 2007). Huber et al. (2005) found 10 positive samples (5.6%) in dairy cattle in the State of Rio de Janeiro, while Langoni et al. (2004) found 21.2% of *Cryptosporidium* positivity in 203 fecal samples of calves from several farms in the State of São Paulo. The exclusive occurrence of *C. andersoni* in bovines in this study is a result which is markedly different from those reported elsewhere in which *C. parvum* predominates. Thomaz et al. (2007) found 88.9% of *C. parvum* and 11.1% of *C. bovis* in cattle, whereas Huber et al. (2005) found *C. parvum* only. In other regions of the...
World, C. parvum and C. andersoni were the two most common genotypes in bovines (XIAO; HERD, 1994; WADE et al., 2000; HUETINK et al., 2001; ENEMARK et al., 2002; PENG et al., 2003). In Maryland, United States, C. parvum accounted for 97% of infections in pre-weaned calves but only 4 and 0% of infections in post-weaned calves and heifers, respectively (SANTÍN et al., 2008).

Cryptosporidium infection in pigs, sheep and goats can be zoonotic as these hosts are susceptible to C. parvum infection. The fact that C. parvum was not found in these animals may indicate that the role of this species in the epidemiological cycle of cryptosporidiosis is of less zoonotic importance in the region studied. Cryptosporidium is recognized as one of the main causes of diarrhea in lambs (de GRAAF et al., 1999), causing high morbidity and mortality and major economic losses (CASEMORE et al., 1997). In pigs and equines Cryptosporidium appear to be of less zoonotic importance, although diarrhea in post-weaning piglets and reduction in growth rate, food absorption and weight loss in equine have already been described (MUSIC et al., 2003; GRINBERG et al., 2003).

The proportion of positive samples among dogs was 10.7% (3/28 animals), a frequency similar to that reported by Thomaz et al. (2007) who found 12.5% (15/120) of positivity in dogs from an urban area and also found C. canis only. Other studies in urban areas in Brazil also revealed low frequency of Cryptosporidium in dogs. Gennari et al. (1999) have found 2.8% of 353 animals shedding Cryptosporidium. Funada et al. (2007) found 2.4% of positivity for Cryptosporidium in 1,755 samples of dogs, collected between January 2000 and December 2004. In Londrina, Paraná State, Brazil, 2.2% of samples of dogs were positive to Cryptosporidium sp. (NAVARRO et al., 1997) and in the city of Rio de Janeiro, Rio de Janeiro State, Brazil, the positivity in dogs was 2.4% (HUBER et al., 2005). However, it is worth mentioning that none of the aforementioned studies included molecular identification of the parasite.

Although the results of our study potentially indicate a low frequency of occurrence of Cryptosporidium in domestic animals, three points should be highlighted. First, the samples from animals other than bovines were predominantly from adults, which can explain the low frequency of Cryptosporidium. It is well known that oocyst shedding is more common in younger animals (THOMPSON et al., 2005). Second, sample collection was performed during the dry season (from April to September) which may lead to an underestimation of the frequency of infection because of lower transmission of the parasites during this period. It is noteworthy that oocyst dispersion and transmission are greatly favored in wet environment during the rainy season. Third, the presence of Cryptosporidium of less relevance in terms of zoonotic

Figure 2. Phylogenetic relationships among Cryptosporidium spp. isolates inferred from the alignment of the SSU-rRNA sequences and distance analysis. The tree is unrooted. The numbers indicate the number of times that the branches are supported after 1,000 bootstrap replicates. Taxons identified in this study: C. andersoni 36, C. andersoni 65B and C. canis 40.
transmission may be, otherwise, important for the wild fauna as these animals can be considered a source of Cryptosporidium infection. The impact and magnitude of infection by C. andersoni in wild ruminants and by C. canis in wild canids need to be assessed in future studies to better understand the actual importance of this genus of parasite for the wild fauna living in the MDSP and other rain forest fragments.

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References


