
**Cryptosporidium felis Infection, Spain**

To the Editor: Coccidian protozoans that belong to the genus *Cryptosporidium* frequently cause gastrointestinal infection in humans and animals and are distributed worldwide. *Cryptosporidium hominis* and the cattle genotype of *C. parvum* are responsible for most human infections. However, other species and genotypes of *Cryptosporidium*, such as *C. felis*, *C. muris*, *C. meleagridis*, *C. canis*, *C. parvum* pig genotype, and *C. parvum* cervine genotype, have also been detected in stool samples of immunosuppressed and immunocompetent patients (1). Since 1999, when Pieniazek et al. described 3 cases of *C. felis* infection in HIV-positive patients (2), several studies have confirmed that this species can infect humans. Recently, Muthusamy et al. described *C. felis* infections in 5 HIV-positive persons in southern India (3). In this article, we describe our experience with an imported case of *C. felis* infection in Spain.

A pediatrician requested a parasitologic study for an immunocompetent, 4-year-old boy with diarrhea. The child came from an orphanage in Calcutta, India; he had arrived in Spain 10 days earlier after having been adopted by a Spanish family. Stool specimens were tested for a wide panel of enteric pathogens, including bacteria, viruses, and parasites. *Cryptosporidium* oocysts were detected by direct microscopic visualization of the samples, which had been concentrated by formalin—ethyl acetate sedimentation and stained with a modified Ziehl-Neelsen stain. Results were also positive for *Cryptosporidium* for samples tested by using an immunochromatographic (Crypto-Strip, Coris Bioconcept, Gembloux, Belgium) (4) and an immunofluorescent assay (Merifluor Cryptosporidium/Giardia, Meridian Diagnostics, Cincinnati, OH, USA).

DNA was extracted as described elsewhere (5), purified with polyvinyl-pyrolidone, and stored at –20°C in Tris-EDTA buffer. After DNA extraction, PCR–restriction fragment length polymorphism (RFLP) analysis was performed by using previously described protocols based on the small subunit (SSU) rRNA gene (6), with digestion of the amplicon by the restriction enzymes SspI for species diagnosis or VspI for *C. parvum* genotype identification. For DNA sequencing, PCR products of the 18S rRNA gene fragments were purified and used for direct sequencing in an ABI377 automated sequencer (Applied Biosystems, Foster City, CA, USA).

RFLP analysis showed a profile distinct from those of *C. hominis* and *C. parvum* cattle genotype and consistent with the published patterns for *Cryptosporidium felis*: 426 and 390 bp with SspI digestion; 476, 182, and 104 bp with VspI (6). The sequence of the PCR product was determined, and a comparison with all SSU rDNA *Cryptosporidium* sequences available in databanks showed 100% similarity with the homologous fragment of *C. felis* (GenBank accession no. AF112575).

To date, >30 cases of human infection by *C. felis* have been reported in the literature. Only 3 of them have occurred in immunocompetent patients: 2 in the United Kingdom (7) and 1 in Peru (8). To our knowledge, this is the first case of human *C. felis* infection diagnosed in Spain. The child had been in Spain for only 10 days, no pet animals lived in his new home, and he had not gone to kindergarten. Consequently, the infection was likely acquired in India.

The transmission route for the unusual *Cryptosporidium* species is unclear. In the study by Matos et al., only 1 of 4 immunocompromised patients with *C. felis* had been in close contact with a pet. However, recently, an outbreak of *C. felis* infection was described in a day camp in the United States (9), suggesting that this species may be transmitted by direct person-to-person contact or through contaminated food or water. In our case, the patient had traveled to India only 10 days before the onset of symptoms and had been in contact with sick children and uncooked food; the transmission route remains unclear.

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contact with cats at home (9). Unusual cryptosporidial infections are not restricted to immunocompromised hosts, and further investigation of the pathogenicity and epidemiology of these infections is necessary to establish their effect on public health and to identify risk factors for exposure and measures for prevention. The identification of species other than C. hominis and C. parvum that infect humans, and the transmission routes of such agents, has relevance for better understanding of the epidemiologic features of cryptosporidiosis.

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