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Gastroenteritis Caused by the Cryptosporidium Hedgehog Genotype in an Immunocompetent Man

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The Cryptosporidium hedgehog genotype, which has been reported previously in hedgehogs and horses, was identified as the cause of the diarrheal disease cryptosporidiosis in an immunocompetent man in the Czech Republic. This is the first report of human illness caused by the Cryptosporidium hedgehog genotype.

CASE REPORT

Diarrheal and nondiarrheal human stool samples from immunocompetent (n = 2,956) and immunodeficient patients (n = 561; HIV/AIDS and oncology patients) were obtained from public hospitals in the Czech Republic and Poland. In 2012, a 26-year-old man from an urban area who was HIV negative and had no history of immunodeficiency was admitted to a hospital in the Czech Republic with gastroenteritis. The patient had abdominal pain and produced a nonbloody stool sample with a soft consistency. The classification of the stool sample as soft was based on criteria described by Rossignol et al. (1). The individual was also examined for the presence of exogenous protozoan stages; helminth eggs; Shigella, Salmonella, Campylobacter, and Clostridium bacteria; amoebas; rotaviruses; and noroviruses. No other bacterial, viral, or parasitic pathogens were detected (data not shown). The stool sample was examined for the presence of Cryptosporidium oocysts by aniline-carbol-methyl violet staining and light microscopy at a magnification of ×1,000 (2), and the infection intensity was estimated by a method described previously (3). Cryptosporidium oocysts with typical staining characteristics were identified in fecal smears. The Cryptosporidium infection intensity was estimated to be 30,000 oocysts/g.

To identify the Cryptosporidium isolate to the species level, DNA was extracted and a nested PCR protocol was used to amplify partial sequences of the small-subunit (SSU) rRNA (4), Cryptosporidium 60-kDa glycoprotein (gp60) (5), and actin (6) genes. PCR amplicons were sequenced directly in both directions with an ABI 3130 sequence analyzer (Applied Biosystems, Foster City, CA). The identities of the sequences obtained were determined by a BLAST search (www.ncbi.nlm.nih.gov/blast). The relationships of the identified sequences to those from known species and genotypes were inferred from neighbor-joining phylogenies constructed with the software Treecon.

The SSU rRNA sequence was identical to a sequence from a Cryptosporidium hedgehog genotype isolated from horses in Algeria (accession no. KC305650) (Fig. 1). The actin sequence clustered with sequences previously obtained from European hedgehogs (accession no. GQ259142 and GQ214079), showing 99.6 to 99.8% similarity (Fig. 1). An established nomenclature (7) was used to describe the subtype families and subtypes of the gp60 gene sequences. The gp60 gene sequences clustered with the XIIIa subtype family originally reported from European hedgehogs (accession no. GQ259140, GQ214085, and GQ214081) and from a horse (KC305644) (Fig. 1). The gp60 subtype of the identified hedgehog genotype had 10 repeats of the sequence ACATCA immediately following 20 serine-coding TCA repeats. This subtype has not been detected previously in hedgehogs, horses, or other hosts. This study was approved by the ethics committee of the Institute of Parasitology, Biology Centre, Academy of Sciences of the Czech Republic, Ceske Budjovice, Czech Republic (protocol 1/2012).

Zoonotic pathogens are responsible for about 75% of the new diseases affecting humans (8). Cryptosporidium is a globally distributed protozoan parasite infecting humans, domestic animals, and many wild vertebrates (9). It is a significant cause of disease in developing and developed countries. In most cases, including those involving humans, Cryptosporidium causes an enteric infection leading to a gastrointestinal illness characterized by severe diarrhea (10). Although more than 90% of human infections are caused by two species, Cryptosporidium hominis and Cryptosporidium parvum, the increasing application of molecular diagnostic tools during the last decade has uncovered more than 17 other Cryptosporidium species and genotypes capable of infecting humans (11–16). Furthermore, infection by these atypical cryptosporidia can occur in immunocompetent hosts (17). In the present study, we report an unusual case of human cryptosporidiosis caused by the Cryptosporidium hedgehog genotype.

Gastroenteritis caused by the Cryptosporidium hedgehog genotype was detected in an immunocompetent 26-year-old man from the Czech Republic. The hedgehog genotype has previously been reported in hedgehogs and horses; however, it may not be pathogenic to these nonhuman hosts. Horses in Algeria showed no clinical signs of infection. Although a high prevalence of Cryptosporidium hedgehog genotype was observed in the stool samples from the Czech Republic, it was not detected in the stool samples from Poland. This finding may be related to differences in the specificity of the diagnostic methods used or to differences in the prevalence of the hedgehog genotype in the two countries. Further studies are needed to determine the prevalence of this genotype in other countries and to investigate its potential as a zoonotic pathogen.
ridium infection was reported in diarrheal hedgehogs in Germany, any association between diarrhea and the hedgehog genotype was unclear because of the frequent occurrence of coinfections with other parasite species (18). The patient in the present study did not report contact with hedgehogs or horses, and the source of infection is unknown. Nevertheless, the occurrence of this genotype in horses, hedgehogs, and humans indicates a broader host specificity than previously thought. Passive transport of oocysts through the digestive tract is unlikely considering the high infection intensity and manifestation of clinical disease. The infection intensity, disease symptoms, and stool consistency are similar to those described in a previous report of human cryptosporidiosis caused by *C. parvum* and *C. tyzzeri* (14). Moreover, identification of the infection in an immunocompetent patient underlines the zoonotic potential of this genotype, particularly among people who have contact with horses or hedgehogs. Although it is possible that the hedgehog genotype can be transmitted indirectly via food or water, there is no evidence to support these transmission routes. Generally, the importance of unusual genotypes in humans warrants further investigation.

**Nucleotide sequence accession numbers.** The actin, gp60, and SSU rRNA gene nucleotide sequences obtained in this study have been deposited in GenBank under accession numbers KF055452, KF055453, and KF055454, respectively.

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