Molecular Characterization of *Giardia duodenalis* and *Cryptosporidium parvum* in Fecal Samples of Individuals in Mongolia

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Abstract. The *Giardia* and *Cryptosporidium* species are widespread and frequent diarrhea-related parasites affecting humans and other mammalian species. The prevalence of these parasites in Mongolia is currently unknown. Therefore, we performed molecular analyses of *G. duodenalis* and *C. parvum* in stool samples from 138 patients hospitalized with diarrhea in Mongolia using nested polymerase chain reaction (PCR). A total of 5 (3.62%) and 7 (5.07%) fecal samples were positive for *G. duodenalis* and *C. parvum*, respectively. *Giardia duodenalis* and *C. parvum* infections were prevalent in children < 9 years of age. The assemblage-specific fragment patterns for the β-giardin gene of *G. duodenalis* revealed that all five samples testing positive belonged to Assemblage A by the PCR-restriction fragment polymorphism method. For sequencing and phylogenetic analysis of the 18S rDNA and HSP70 genes of all seven patients testing positive the genes were further identified to be of the *C. parvum* bovine genotype. This study is the first to report the prevalence of *G. duodenalis* and *C. parvum* and its molecular characterization of fecal samples from individuals with diarrhea in Mongolia.

INTRODUCTION

*Giardia* and *Cryptosporidium*, genera of common protozoan parasites that infect domestic and wild animals and humans, generally cause diarrhea.1–3 The *Giardia* genus is composed of intestinal flagellates that infect a wide range of vertebrate hosts. The *Giardia* genus currently comprises six species that are distinguished on the basis of the morphology and ultrastructure of their trophozoites.4,5 *Giardia duodenalis*, *Giardia intestinalis*, and *Giardia lamblia* should be considered as a species complex, with little variation in morphology among them. Recently, genetic analyses using polymerase chain reaction (PCR) characterized isolates of *Giardia* directly from feces, allowing the identification of a comprehensive range of genotypes from humans and animals.6–8 The species *G. duodenalis* has assigned even assemblages from A to H. Assemblage A and B have been identified to infect humans and other mammalian hosts.9,10 Although “Assemblage C” infects only dogs, Assemblage F infects only cats, and Assemblage D infects both dogs and cats.11 Assemblage E infects cattle, sheep, and goats, and Assemblage G infects rats. Recently, Assemblage H infecting marine vertebrates has been reported.12 Regarding the *Cryptosporidium* species, 22 valid species have been identified on the basis of differences in oocyst morphology, the site of infection, vertebrate clade specificity, and genetic differences.1 In the *Cryptosporidium* species, *Cryptosporidium parvum* and *Cryptosporidium hominis* are known to infect cattle, humans, and other mammals.

The *Giardia* and *Cryptosporidium* are shed in feces as oocysts and cysts and can be directly transmitted by the fecal–oral route by contaminated water or food, especially raw vegetables.13 Clinical giardiasis and cryptosporidiosis accompanied by diarrhea are major public health concerns in developing nations.14,15 Approximately 200 million people currently have symptomatic giardiasis in Asia, Africa, and Latin America, and ~500,000 new cases are reported each year16; alternatively, 300,000 persons in the United States are expected to be infected with *Cryptosporidium* species annually.17 In addition, the occurrence of *Giardia* and *Cryptosporidium* species has been reported in Russia and China.18,19 Therefore, individuals in Mongolia may be considered to have a naturally high risk of contact with zoonotic parasites. However, no studies to date have examined specific *G. duodenalis* and *C. parvum* infections among individuals who have diarrhea in Mongolia. The aim of this study was to perform molecular detection and phylogenetic characterization of *G. duodenalis* and *C. parvum* from diarrheal fecal samples of individuals in Mongolia.

MATERIALS AND METHODS

**Fecal sample collection and DNA isolation.** A total of 138 stool samples from 138 patients admitted to the intestinal ward of the National Center for Communicable Diseases located in Mongolia who had diarrhea were collected and transported to the Laboratory of Parasitology for diagnosis of parasitic diseases. Each fresh stool sample (5 g) was suspended in 15 mL of phosphate buffered saline and filtered using four layers of gauze to remove coarse material. The filtrate was then centrifuged at 3,000 rpm for 10 min. The supernatant was eliminated, and the sediment was mixed with 5 mL of phosphate buffered saline. The pellet underwent repeated boiling (100°C) and deep freezing (−70°C) 10 times to break the thick wall of the *Cryptosporidium* and *Giardia* cyst. Total genomic DNA was isolated from the pellet using DNAzol (MRC, Cincinnati, OH) and stored at −20°C until use.

**PCR and characterization of *G. duodenalis* by PCR-restriction fragment length polymorphism (RFLP)** assay. The amplification of the β-giardin gene was performed using a nested PCR protocol. In the primary PCR reaction, a 753 basepair (bp) fragment was amplified using Accure PCR Master Mix (Bioneer, Daejeon, Korea) containing 1 μM of...
Detection of *Giardia duodenalis* and *Cryptosporidium parvum* infections using polymerase chain reaction analysis in human fecal samples from Mongolia, by age and sex

| Variables     | No. of sample | Positive no. of *G. duodenalis* (%) | Positive no. of *C. parvum* (%) |
|---------------|---------------|-------------------------------------|---------------------------------|
| Age (year)    |               |                                     |                                 |
| < 4           | 65            | 4 (6.15)                            | 3 (4.62)                        |
| 5–9           | 17            | –                                   | 3 (17.65)                       |
| 10–14         | 3             | –                                   | –                               |
| 15–19         | 7             | –                                   | –                               |
| 20–29         | 19            | 1 (5.26)                            | –                               |
| 30–39         | 15            | –                                   | 1 (6.67)                        |
| 40–49         | 4             | –                                   | –                               |
| 50–59         | 7             | –                                   | –                               |
| 60+           | 1             | –                                   | –                               |
| Sex           |               |                                     |                                 |
| Female        | 64            | 1 (1.56)                            | 2 (3.13)                        |
| Male          | 74            | 4 (5.41)                            | 5 (6.76)                        |
| Total         | 138           | 5 (3.62)                            | 7 (5.07)                        |

| Variables     | No. of sample | Positive no. of *G. duodenalis* (%) | Positive no. of *C. parvum* (%) |
|---------------|---------------|-------------------------------------|---------------------------------|
| Positive no. of *G. duodenalis* (%) | 4 (6.15) | 3 (4.62) | 3 (17.65) | 1 (5.26) | 1 (6.67) | 1 (3.13) | 5 (6.76) | 7 (5.07) |

The 138 patients comprised 85 children and 53 adults, respectively.

Phylogenetic analysis of the 18S rDNA and HSP70 genes of *C. parvum*. The PCR products were analyzed by electrophoresis, purified using an agarose gel DNA purification kit (Qiagen), and sequenced with an ABI PRISM 3730xl Analyzer (Applied Biosystems, Foster City, CA). A search of highly similar 18S rDNA gene fragment sequences was performed using nucleotide BLAST (National Center for Biotechnology Information, Bethesda, MD) to confirm the genotype. *Cryptosporidium* 18S rDNA sequences were obtained from GenBank. Sequence alignment was performed using CLUSTAL W (Multiple sequence alignment computer program, Histon, Cambridgeshire, UK). Phylogenetic trees were constructed using the neighbor-joining method with maximum composite likelihood distance correction in the Molecular Evolutionary Genetics Analysis (MEGA) program, with robustness of groupings assessed using 1,000 bootstrap replicates of the data.

RESULTS

Prevalence of *G. duodenalis* and *C. parvum* in human fecal samples in Mongolia. The 138 patients comprised 85 children and 53 adults, respectively.
1–15 years of age (mean age, 3.6 years) and 53 adults 16–74 years of age (mean age, 32.5 years). Of the 138 patients included, 5 (3.62%) and 7 (5.07%) tested positive for *G. duodenalis* and *C. parvum*, respectively. Four of the 5 patients with a *G. duodenalis* infection were <4 years of age, and 3 of the 7 patients with a *C. parvum* infection were <4 years of age and 3 patients were 5–9 years of age except 1 patient. Our results showed that the positive rate of *G. duodenalis* and *C. parvum* in children was higher than that in adults (Table 1).

**Identification of *G. duodenalis* assemblages by PCR-RFLP.** The five samples with *G. duodenalis* were confirmed by β-giardin gene amplification by nested PCR (Figure 1A). After digestion by *Hae* III, the assemblage-specific patterns were obtained, showing patterns of 201, 150, 110, and 50 bp (Figure 1B). All five samples with *G. duodenalis* belonged to Assemblage A.

**Identification and phylogenetic analysis of *C. parvum*.** A total of seven fecal samples (sample numbers Mongol-H05, H07, H08, H16, H28, H32, and H39) tested positive for the 18S rDNA and HSP70 genes of *C. parvum* in the nested PCR. A sequence analysis of these seven samples suggested the presence of *C. parvum* in all patients, with homologies from 97% to 99% (Table 2). Phylogenetic analysis showed that the 18S rDNA gene fragments were of the *C. parvum* bovine genotype in all patients except Mongol-H32 (Figure 2A). An analysis of the HSP70 gene showed similar results (all patients except Mongol-H39) (Figure 2B).

**DISCUSSION**

*Giardia* and *Cryptosporidium* are significant worldwide causes of diarrhea and nutritional disorders in humans. In Asia, among patients with diarrhea in a study from the Philippines, the prevalence rates for *Giardia* and *Cryptosporidium* species were 2.0% and 1.9%, respectively;28 furthermore, the prevalence rates from a study in Malaysia were 0.7% for *Giardia* species and 0.3% for *Cryptosporidium* species.29 In our study, the percentage of patients with diarrhea infected with *G. duodenalis* and *C. parvum* in Mongolia was higher than the above rates from the Philippines and Malaysia. Most outbreaks of human giardiasis in developing countries have mainly been detected in children <2 years of age.30 Furthermore, it has been reported that cryptosporidiosis generally affects children <4 years of age.31 In our data, children were more frequently infected than adults, and it is a finding similar to the findings from studies in other countries. In previous reports, the reasons for high prevalence of giardiasis and cryptosporidiosis in young children may be caused by the lack of immunity, and because they are easily exposed to contaminated water through playing water games.31 In addition, Faubert reported that numerous factors contributed to infection with *Giardia* species, including the number of cysts ingested, the age of the host, the virulence of the *Giardia* strain, and the situation of the immune system at the time of infection.32 Interestingly, in the current study, there was only one case of an adult infected with *G. duodenalis*, whereas the rest were all children. The reason for the high prevalence in children was unclear because we did not acquire any information on the patients except that they had diarrhea. Almost all of the infected children were living in Gers or houses equipped with indoor latrines and without tap water located in a steppe. The poor hygiene conditions of a
steppe, such as the low quality of water, poor cleanliness of containers for transporting water, and poor hand washing facilities, should be considered as contributing factors to infection with various pathogens, and these may be critical causes of infections. Further surveys for the detection of pathogens and the transmission through contamination of waters in poor environmental conditions should be performed. Additionally, in 3 of the 5 cases of C. parvum, Shigella flexneri (N = 2) and Salmonella enteritidis (N = 1), and in 2 of the 7 cases of G. duodenalis, S. flexneri were also detected (data not shown). These findings indicate that we detected the existence of mixed infections, both bacterial and parasitic, in patients with diarrhea in Mongolia. To understand the epidemiologic characteristics of the infections and to implement control measures, it is important to determine whether G. duodenalis and C. parvum can infect humans through a zoonotic route. Therefore, further epidemiologic studies examining the risk factors of infection among these protozoa in individuals with diarrhea should be carried out in the near future for improving public health.

Recently, molecular epidemiologic studies with Giardia DNA directly extracted from feces have been performed to amplify techniques, and several PCR assays have been developed. In this study, we successfully performed a molecular analysis of the β-giardin gene and pattern analysis using a PCR-RFLP assay with Hae III on Giardia DNA from fecal samples. An investigation of human isolates from stool samples in diverse geographic areas established that only G. duodenalis Assemblages A and B are related to almost all human infections. For example, the occurrence of Assemblage A and B of G. duodenalis have been reported in Thailand, China, and the Philippines. In this study population, only Assemblage A was identified, and this result is similar to the previous studies from Korea, Japan, Egypt, and Brazil.

Cryptosporidium species are classified on the basis of different oocyst morphology, sites of infection, vertebrate class, and genetic differences; such classifications of Cryptosporidium species include C. parvum, (a parasite of humans, cattle, and other mammals), C. hominis (a parasite of humans), and Cryptosporidium felis (a parasite of cats). Particularly, Morgan and others reported that the C. parvum bovine genotype and C. hominis are responsible for the majority of human infections. Our results showed that the Cryptosporidium DNA isolated from diarrheal fecal samples belonged to the bovine genotype using phylogenetic analysis. Our results are meaningful because they reveal that zoonotic parasitic infection cycles from cattle to humans may be possible in Mongolia.

In this study, G. duodenalis and C. parvum genes from human diarrheal fecal samples in patients from Mongolia were identified by molecular analysis. In particular, G. duodenalis was classified as a zoonotic pathogen belonging to Assemblage A, and the C. parvum bovine genotype was discovered through phylogenetic analysis. From our results, we assume that C. parvum can possibly emerge important human pathogens with contact between humans and animals in Mongolia. Further epidemiological studies subject to humans and animals in different areas and/or a big population in Mongolia are needed to better characterize the transmission of Giardiasis and Cryptosporidiosis in humans. To our knowledge, this is the first study to report the prevalence and genetic identification of G. duodenalis and C. parvum, and it may contribute to the understanding of the epidemiologic characteristics and improve the preventive control of both parasites in Mongolia.

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