Real-time PCR detection and speciation of Cryptosporidium infection using Scorpion probes

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At least eight species of Cryptosporidium can cause human infection and disease. A real-time PCR (qPCR) assay based on the 18S rRNA gene and utilizing a Scorpion probe was developed to detect all human-pathogenic Cryptosporidium without the usual need for nested amplification. Sensitivity of detection in stool samples was highest using a glass bead-based DNA extraction method (under 103 oocysts per stool sample). The assay was validated against 123 human stool specimens from Bangladesh and Tanzania, exhibited a sensitivity and specificity of >91% versus microscopy, and detected an additional eight microscopy-negative infections. Cryptosporidium parvum-specific and Cryptosporidium meleagridis-specific Scorpion qPCR assays that provided 100% accurate speciation compared with Vsp I RFLP analysis and sequencing were developed subsequently. These Scorpion probe qPCR assays are simpler to perform than existing nested PCR and RFLP methods for diagnosis and epidemiological investigation of cryptosporidiosis.

INTRODUCTION

Since first appreciated as a protozoal pathogen in 1976, Cryptosporidium is now established as a major cause of diarrhoea in humans (Hlavsa et al., 2005). Cryptosporidium hominis and Cryptosporidium parvum are the major species that have emerged from human studies. However, the avian species Cryptosporidium meleagridis has been observed frequently, e.g. it was observed at a rate of 12% in a large study of Peruvian human immunodeficiency virus (HIV)-infected cryptosporidiosis patients (Cama et al., 2003). Several additional zoonotic species have been reported infrequently, including Cryptosporidium felis, Cryptosporidium canis, Cryptosporidium muris, Cryptosporidium suis and a cervine genotype (Cama et al., 2003; Gatei et al., 2003; Ong et al., 2002; Pedraza-Diaz et al., 2001; Xiao et al., 2001). Species data are important to aid outbreak investigation and provide information about Cryptosporidium transmission cycles, and may prove clinically relevant (Houpt et al., 2005; Hunter et al., 2004; Okhuysen et al., 1999).

We therefore sought to develop a Cryptosporidium assay that would be sensitive, provide species information and be simple to perform. The mainstay diagnostic modalities of microscopy or antigen detection do not discriminate species. Several PCR tests have been reported for Cryptosporidium; however, most require nested amplification if using faecal samples and an additional RFLP analysis step for speciation (Amar et al., 2004; Coupe et al., 2005; Gatei et al., 2003; Higgins et al., 2001). In this work, a real-time PCR (qPCR) assay is described that maintains reasonable sensitivity without nested amplification by targeting a relatively short fragment (108–125 bp) of the multicopy 18S rRNA gene. C. parvum- and C. meleagridis-specific qPCR assays were also developed; these assays were able to provide...
accurate species information on clinical samples from Bangladesh and Tanzania.

METHODS

Parasites and parasite DNA. C. parvum oocysts and C. hominis strain TU502 oocysts (kindly provided by Saul Tzipori, Tufts University School of Veterinary Medicine, Grafton, USA) were stored at 4 °C in PBS, sedimented and counted in a haemacytometer before spiking into 200 mg aliquots of parasite-free stool. DNA of C. meleagridis, C. felis and C. muris was obtained from stool specimens from patients from Moshi, Tanzania or Vellore, India (species identity was confirmed by sequencing the amplified 18S rRNA product).

Human faecal specimens. Stool specimens were obtained from individuals with and without diarrhoea at the International Centre for Diarrhoeal Diseases and Research, Dhaka, Bangladesh (n=70), and the Kilimanjaro Christian Medical Centre, Moshi, Tanzania (n=53). Informed consent was obtained from all participants and the human experimentation guidelines of the US Department of Health and Human Services, the University of Virginia, the Centre for Health and Population Research (Bangladesh) and the Kilimanjaro Christian Medical Centre Research Ethics Committee were followed. Specimens were tested for Cryptosporidium infection by microscopy after modified acid-fast stain. Available specimens with disparate microscopy/PCR results were tested by antigen detection via ELISA (Cryptosporidium II kit; Techlab) according to the manufacturer’s instructions.

DNA extraction. All DNA was extracted from experimentally spiked and human faecal samples using the QIAamp DNA Stool Mini kit (Qiagen) according to the manufacturer’s instructions, except that the suspension was incubated in the kit’s stool lysis buffer at 95 °C and a 3 min incubation with InhibitEx tablets was performed. On experimentally spiked specimens, four methods of stool preparation prior to Qiagen DNA extraction were tested. For the glass bead method, 200 mg acid-washed glass beads (0.5 mm; Sigma) was added to 200 mg stool in Qiagen ASL buffer and the samples were vortexed for 2–5 min. For sonication, stool samples underwent two 1 min sonication bursts on ice water. For the freeze–thaw method, stool samples were subjected to one or six freeze–thaw cycles in liquid nitrogen and a 95 °C freeze–thaw method, stool samples were subjected to one or six freeze–thaw cycles in liquid nitrogen and a 95 °C and 3 min incubation with InhibitEx was performed. On experimentally spiked specimens, four methods of stool preparation prior to Qiagen DNA extraction were tested. For the glass bead method, 200 mg acid-washed glass beads (0.5 mm; Sigma) was added to 200 mg stool in Qiagen ASL buffer and the samples were vortexed for 2–5 min. For sonication, stool samples underwent two 1 min sonication bursts on ice water. For the freeze–thaw method, stool samples were subjected to one or six freeze–thaw cycles in liquid nitrogen and a 95 °C bath. For the proteinase K/SDS method, 200 µl of 200 µg proteinase K ml−1 in 0.2% SDS in water was added to the stool sample, which was then incubated at 55 °C for 1 h. For the Tanzanian clinical samples, stool samples received six freeze–thaw cycles prior to Qiagen DNA extraction. For the Bangladeshi clinical samples, 1 g stool sample was concentrated by ether-PBS sedimentation followed by sonication and six cycles of freeze–thaw prior to Qiagen DNA extraction.

Oligonucleotides. Sequences of the 18S rRNA gene of C. hominis (AF093491), C. parvum (AF164102), C. meleagridis (AF112574), C. canis (AB210854), C. felis (AF112575), C. muris (X64343) and C. suis (AF108861) were obtained from the NCBI database and aligned using CLUSTAL X v1.8 (http://www.ebi.ac.uk/clustalw/). Initially, a PCR assay was designed to amplify all human-pathogenic Cryptosporidium species (forward 5'-GGTTGTAATTTATAGATAAAGAC-3'), reverse 5'-AGGCAAATCCCTACCGTC-3' and internal probe 5'-GTGACATATCATTCAAGTTCTTGAC-3'). A C. parvum-specific assay was designed with a C. parvum/C. hominis-specific forward primer (5'-CTGACCTTTATGGAAAGGT-3'), a C. parvum-specific reverse primer (5'-CCGAAAATTTGACGTTATGTAC-3') and a C. meleagridis-specific internal probe (5'-GACCAAATATTTGACGTTAC-3'). A C. meleagridis-specific assay was designed with a C. meleagridis-specific forward primer (5'-GGCGAAACATTCATATTTGAGAA-3'), a C. meleagridis/C. canis-specific reverse primer (5'-GAACAAATATTTGACGTTAC-3') and a common Cryptosporidium probe (5'-GTTGGAATTTATAGATAAAG-3'). Primers and probes demonstrated no deleterious secondary structures or significant identity to non-Cryptosporidium sequences in a BLAST search (http://www.ncbi.nlm.nih.gov/blast/). Three Scorpion Uni-probes (Proligo) were generated: one with the pan-Cryptosporidium assay’s reverse primer linked to the probe; one with the C. parvum-specific assay’s reverse primer linked to the probe; and one with the C. meleagridis-specific assay’s forward primer linked to the probe. Scorpion Uni-probes incorporated a 5' reporter dye, a stem–loop sequence, a black-hole quencher and a hexethylene glycol reverse-extension blocker. Probe binding to the respective neosynthesized strands is indicated in Fig. 1.

PCR amplification, RFLP and sequencing. Amplification took place in a 25 µl volume containing 1 x PCR buffer (Qiagen), 8.0 mM total MgCl2 (including that contained in the PCR buffer), 0.5 mM of each deoxynucleoside triphosphate, 1.25 U Taq polymerase (HotStarTaq; Qiagen), 2.5 µg BSA, 7.5 pmol Scorpion probe, 30 pmol primer and 5 µl facely extracted DNA. Amplification was performed on an iCycler (Bio-Rad) under the following cycling conditions: 95 °C for 15 min; 40 cycles of 95 °C for 15 s, 51 °C for 15 s and 72 °C for 10 s; and then 75 °C for 10 min. RFLP analysis was performed by incubating 12 U Vsp1 (Promega) per 10 µl PCR product at 37 °C for 2 h. Digested products were fractionated on 2.0% agarose gel and visualized by ethidium bromide (2 µg ml−1). For sequencing, amplicons were purified using the QIAquick PCR Purification kit (Qiagen) and sequenced with the appropriate primers on an Applied Biosystems 377 Prism DNA Sequencer at the University of Virginia Biomolecular Research Facility.

Statistics. Proportions were compared by Fisher’s exact test. All P values were two-tailed.

RESULTS AND DISCUSSION

Selection of oligonucleotides

The multicopy 18S rRNA gene was chosen for amplification given the desire to optimize detection sensitivity and based on findings by others that this gene could be successfully amplified from all human-pathogenic Cryptosporidium species (Jiang & Xiao, 2003). 18S rRNA sequences from the eight Cryptosporidium species that have been reported thus far to cause disease in humans were downloaded from GenBank. Primers and probes were designed to detect all Cryptosporidium species that spanned the widely used Vsp1 C. hominis restriction site (Fig. 1, pan-Cryptosporidium assay). A C. hominis-specific Scorpion assay was developed, but exhibited suboptimal performance (see below). Therefore, C. parvum- and C. meleagridis-specific reactions were designed that maximized primer and probe polymorphisms against the other species (Fig. 1, right-hand column).

Sensitivity of the Cryptosporidium Scorpion probe qPCR assays

The sensitivity of the pan-Cryptosporidium assay was determined on parasite-free stool spiked with known quantities of purified C. parvum or C. hominis oocysts. Four methods of initial stool preparation were tested including glass bead homogenization, sonication, freeze–thaw cycles and treatment with proteinase K with SDS. DNA
Fig. 1. Primer and Scorpion probe sequences for pan-Cryptosporidium, C. parvum-specific and C. meleagridis-specific qPCR. 18S rRNA sequences for C. hominis, C. parvum, C. meleagridis, C. canis, C. felis, C. muris and C. suis were obtained from GenBank (nt 172–322 of AF093491, AF164102, AF112574 and AB210854, nt 173–333 of AF112575, nt 150–302 of X64343 and nt 172–325 of AF108861 are shown for the seven Cryptosporidium species, respectively) and aligned using CLUSTAL software. Primers (boxed) and probes (bold) were designed to detect all Cryptosporidium species, C. parvum or C. meleagridis. Sequence mismatches of primers or probes against other species are highlighted and shown in the column on the right. Probes were linked to forward or reverse primers via Scorpion Uni-probes as indicated. Separation of fluorophore (HEX, FAM or TEX) from the black-hole quencher (BHQ) during PCR synthesis is shown below sequences. HEG, Hexethylene glycol reverse-extension blocker. The Vsp1 restriction site, AT ↓ TAAT (underlined in the uppermost C. hominis sequence), is exclusive to C. hominis.
The lowest cycle threshold (CT) was consistently observed for stool samples using the cecal QIAamp DNA Stool Mini kit and subjected to qPCR. DNA was then purified from all preparations using the commercial QIAamp DNA Stool Mini kit. DNA was extracted with the QIAamp DNA Stool Mini kit, which then stored at -70 °C. DNA was then extracted via a freeze–thaw/Qiagen method (note that sufficient quantities of DNA were not available for subsequent PCR amplification). The qPCR assay exhibited a sensitivity of 92% (95% confidence interval of 78–98%) and a specificity of 91% (95% confidence interval of 83–96%) versus microscopy. Specifically, of 36 microscopy-positive specimens, 33 were qPCR-positive; of 87 microscopy-negative specimens, 79 were qPCR-negative. For specimens with inconsistent qPCR/microscopy results, available samples were retested by Cryptosporidium ELISA; results showed that all three microscopy-positive/qPCR-negative specimens were antigen-negative and six of the eight microscopy-negative/qPCR-positive specimens were antigen-positive. Overall, therefore, the qPCR sensitivity appeared to exceed that of microscopic analysis and that reported for traditional PCR assays for Cryptosporidium (Kostrzynska et al., 1999), perhaps due to the short (~125 bp) target sequence, which increases PCR efficiency. Sensitivity of PCR in faecal specimens has historically been a limitation for Cryptosporidium such that nested amplification has frequently been used (Bialek et al., 2002; Morgan et al., 1998). Whereas the sensitivity of the present assay would be predicted to improve with nested amplification, we do not recommend this because of the risks of contamination and increased reagent cost of nested PCR, but rather favour future use of the glass bead method for DNA extraction (Fig. 2).

**Comparison of Cryptosporidium Scorpion probe qPCR with microscopy on clinical specimens**

The pan-Cryptosporidium assay was validated on 123 banked stool DNA samples obtained during case-control studies in Bangladesh (n = 70) and Tanzania (n = 53) during the preceding 3 years. Sixty-three patients had diarrhoea (≥3 loose or watery stools over the previous 24 h), 60 did not and all 53 Tanzanian patients were HIV-infected. Fresh specimens were tested by microscopy after acid-fast staining and then stored at −70 °C. DNA was then extracted via a freeze–thaw/Qiagen method (note that sufficient quantities of DNA were not available for re-extraction via the more sensitive glass bead method). The qPCR assay exhibited a sensitivity of 92% (95% confidence interval of 78–98%) and a specificity of 91% (95% confidence interval of 83–96%) versus microscopy. Specifically, of 36 microscopy-positive/qPCR-negative specimens, 33 were qPCR-positive; of 87 microscopy-negative specimens, 79 were qPCR-negative. For specimens with inconsistent qPCR/microscopy results, available samples were retested by Cryptosporidium ELISA; results showed that all three microscopy-positive/qPCR-negative specimens were antigen-negative and six of the eight microscopy-negative/qPCR-positive specimens were antigen-positive. Overall, therefore, the qPCR sensitivity appeared to exceed that of microscopic analysis and that reported for traditional PCR assays for Cryptosporidium (Kostrzynska et al., 1999), perhaps due to the short (~125 bp) target sequence, which increases PCR efficiency. Sensitivity of PCR in faecal specimens has historically been a limitation for Cryptosporidium such that nested amplification has frequently been used (Bialek et al., 2002; Morgan et al., 1998). Whereas the sensitivity of the present assay would be predicted to improve with nested amplification, we do not recommend this because of the risks of contamination and increased reagent cost of nested PCR, but rather favour future use of the glass bead method for DNA extraction (Fig. 2).
Speciation using Scorpion probes

The accuracy of the C. parvum and C. meleagridis assays for species identification compared with VspI RFLP digestion analysis was examined. First, each of the 82 pan-Cryptosporidium qPCR-negative specimens was tested by the C. parvum- and C. meleagridis-specific qPCR assays and no false positives were observed (Table 1). Upon testing each of the 41 pan-Cryptosporidium qPCR-positive specimens with the specific qPCR assays, 26 specimens were C. parvum qPCR-negative/C. meleagridis qPCR-negative, 12 were C. parvum qPCR-positive/C. meleagridis qPCR-negative, two were C. parvum qPCR-positive/C. meleagridis qPCR-positive and one was C. parvum qPCR-negative/C. meleagridis qPCR-positive. Each amplicon from the pan-Cryptosporidium qPCR, C. parvum-specific qPCR and C. meleagridis-specific qPCR assays (total = 58) was then analysed by VspI RFLP digestion to confirm species identity and identify C. hominis infections (the only species with the internal VspI site; Fig. 1). This analysis revealed no VspI digestion of any C. parvum-specific or C. meleagridis-specific qPCR product. Furthermore, for the two C. parvum qPCR-positive/C. meleagridis qPCR-positive specimens, both the C. parvum qPCR and C. meleagridis qPCR products were sequenced and the presence of both species was confirmed. Finally, two of the 26 pan-Cryptosporidium qPCR-positive/C. parvum qPCR-negative/C. meleagridis qPCR-negative specimens that were not digested with VspI were sequenced and were found to be C. felis infections (the first C. felis infections reported from Bangladesh). Overall, therefore, the C. parvum- and C. meleagridis-specific qPCR assays were 100% accurate compared with VspI RFLP and sequencing analysis. By combining pan-Cryptosporidium and C. parvum-specific results, C. hominis infection could be reasonably inferred from a pan-Cryptosporidium qPCR-positive/C. parvum qPCR-negative result (24 of 27 such samples were confirmed as C. hominis by RFLP analysis).

Interestingly, six of 14 C. parvum infections were mixed infections compared with only four of 28 C. hominis infections (P=0.06). Mixed C. hominis/C. parvum infections have been clearly documented in up to 4–12% of cases in diverse regions including the United States, Uganda and

Table 1. Speciation using C. parvum- and C. meleagridis-specific qPCR assays

<table>
<thead>
<tr>
<th>Pan-Cryptosporidium qPCR result</th>
<th>C. parvum qPCR result</th>
<th>C. meleagridis qPCR result</th>
<th>RFLP and/or sequencing result</th>
</tr>
</thead>
<tbody>
<tr>
<td>−</td>
<td>82</td>
<td>−</td>
<td>Not applicable</td>
</tr>
<tr>
<td>+</td>
<td>26</td>
<td>−</td>
<td>C. hominis (24), C. felis (2)*</td>
</tr>
<tr>
<td>+</td>
<td>12</td>
<td>+</td>
<td>C. parvum (12)†</td>
</tr>
<tr>
<td>+</td>
<td>2</td>
<td>+</td>
<td>Mixed C. parvum/C. meleagridis (2)*</td>
</tr>
<tr>
<td>+</td>
<td>1</td>
<td>−</td>
<td>C. meleagridis (1)</td>
</tr>
</tbody>
</table>

The presence of C. felis and mixed C. parvum/C. meleagridis infection was confirmed by sequencing.

†Four of these 12 C. parvum infections were found to be mixed C. parvum/C. hominis infections, as shown by VspI digestion of the pan-Cryptosporidium qPCR amplicon without VspI digestion of the C. parvum-specific qPCR amplicon.
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