only risk factor identified among the persons reported here was older age. Unlike persons in other reports, persons in our report were all men, and 2 reported GI symptoms. The mechanism for UTI in these cases is unclear but could have included ascending and hematogenous spread.

We calculated incubation periods for GI symptoms for 6 persons as the time between onset of GI symptoms and the May 14 wedding (5 persons) or last travel date (1 person). The incubation period was 5–7 days (average 5.5 days). The incubation period for UTI, which could be calculated for 2 persons, was an average of 25.5 days. Long incubation periods for *Salmonella* spp. infections have been reported (6–9); reasons include exposure to a low dose of bacteria, specific populations (e.g., young children, child day care attendees), and method of food preparation (6–9). The age of persons in our investigation did not affect the length of the incubation period. The amount of food eaten was not collected during the interview; however, most persons in our investigation reported eating a wide variety of foods, and 1 reported eating small portions. All food was prepared during the week before the wedding and served cold. This length of time and the potential for temperature abuse could have increased the infectious dose and decreased the incubation period (6). In addition, the 1 person with travel-related infection was not exposed to these food items. We found no literature on the incubation period for *S. enterica* ser. Agbeni. The reason for the long incubation period in this investigation is unclear and could be due to host-specific factors, the implicated serotype, or the food source.

The 3-day time frame for exposures was not sufficient to identify appropriate exposures. Expanding the period for collecting exposure information about *Salmonella* spp. infections and the reporting and investigation of persons with *Salmonella* spp. identified in urine to public health authorities might be needed to help identify and solve outbreaks.

**Acknowledgments**

We thank representatives from the public health authorities for their follow-up of case-patients and the clinical microbiology laboratories in British Columbia responsible for diagnosis of enteric infections.

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DOI: http://dx.doi.org/10.3201/eid1809.120008

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**Entamoeba bangladeshi nov. sp., Bangladesh**

To the Editor: Diarrheal diseases have a major effect on global health, particularly the health of malnourished children (1). The enteric parasites *Entamoeba histolytica* and *E. moshkovskii* are potential causes of diarrheal disease in children (2). For the past 20 years, we have been studying *Entamoeba* infections in children from the urban slum of Mirpur in Dhaka, Bangladesh (3).

*E. histolytica* infections can be detected through fecal microscopy, culture, PCR, and antigen detection. Microscopy and culture have limited specificity because several species of *Entamoeba*, which vary in their pathogenic potential, have morphologically similar cysts and trophozoites (4). In 2010–2011,
Fecal samples (129) and cultures derived from fecal material (20) were tested by PCR. Forty-four fecal samples were positive for *E. histolytica*, 42 for *E. dispar*, and 7 for *E. moshkovskii*. PCR results for 48 samples were negative for all 3 parasites (mixed infections account for the total being >129); 5 cultures also were negative for all 3 parasites. ENTAGEN-F and ENTAGEN-R primers, which exhibit a broad specificity for the small subunit ribosomal RNA (SSU rRNA) gene sequences of *Entamoeba*, were used in PCR to amplify DNA fragments from 43 of the samples that were negative by PCR for the 3 *Entamoeba* species; amplification conditions were adapted from Stensvold et al. (10). The amplified DNA was separated by electrophoresis by using a 2% agarose gel. Bands of the size predicted for the *Entamoeba* spp. SSU rRNA gene amplicon were detected in 15 samples (online Technical Appendix Table, wwwnc.cdc.gov/EID/pdfs/12-0122-Techapp.pdf). The PCR products were extracted by using the QIAquick Gel Extraction Kit (QIAGEN) and cloned by using the Zero Blunt TOPO Cloning Kit (Invitrogen, Carlsbad, CA, USA). The sequenced clones from 2 different isolates, 1 diarrheal and 1 surveillance specimen, were completely novel when compared with the SSU rRNA gene sequences from other organisms and did not match any previously sequenced *Entamoeba* species. These isolates represent a new species of *Entamoeba* (GenBank accession nos. JQ412861 and JQ412862), here named *E. bangladeshi* (online Technical Appendix). We examined the phylogenetic relationship between *E. bangladeshi* and other *Entamoeba* parasites by using maximum-likelihood analysis as implemented in MEGA 5 (online Technical Appendix Figure, panel A). *E. bangladeshi*, although distinct, clearly grouped with the clade of *Entamoeba* infecting humans, including *E. histolytica*. *E. bangladeshi*, however, appeared more distantly related than the noninvasive *E. dispar*, but closer than *E. moshkovskii*, to *E. histolytica*.

To further characterize *E. bangladeshi*, we established it in xenic culture, and it displayed the ability to grow at 37°C and 25°C, a characteristic shared with *E. moshkovskii* and *E. eucudariensis* but that distinguishes it from *E. histolytica* and *E. dispar*. Cultured trophozoites were evaluated through light and transmission electron microscopy (online Technical Appendix Figure, panel B). By light microscopy, we detected no apparent differences between *E. bangladeshi* and *E. histolytica*. The physical resemblance between *E. histolytica* and *E. bangladeshi* is notable because direct microscopic examination of fecal samples is still used as a diagnostic tool in areas to which these species are endemic to detect *E. histolytica* parasites.

Table. Oligonucleotide primers used for screening and sequencing of *Entamoeba bangladeshi* nov. sp., Bangladesh*

<table>
<thead>
<tr>
<th>Target organism</th>
<th>Primer name</th>
<th>Primer sequence, 5’ → 3’</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Broad specificity</td>
<td>Entagen-F</td>
<td>ACT TCA GGG GGA GTA TGG TCA C</td>
<td>(6)</td>
</tr>
<tr>
<td><em>Entamoeba</em> sp.</td>
<td>Entagen-R</td>
<td>CAA GAT GTC TAA GGG CAT CAC AG</td>
<td>(6)</td>
</tr>
<tr>
<td><em>E. histolytica</em></td>
<td>Eh-F</td>
<td>AAC AGT AAI AGT TTC TTT GGT TAG TAA AA</td>
<td>(8)</td>
</tr>
<tr>
<td></td>
<td>Eh-R</td>
<td>CTT AGA ATG TCA TTT TCT CTC AAT TCA T</td>
<td>(8)</td>
</tr>
<tr>
<td></td>
<td>Eh-YYT Probe</td>
<td>YYT-ATT AGT ACA AAA TGG CCA ATT CAT TCA-Dark Quencher</td>
<td>(8)</td>
</tr>
<tr>
<td><em>E. moshkovskii</em></td>
<td>Em-1</td>
<td>CTC TTC AGC GGG AGT GCG</td>
<td>(7)</td>
</tr>
<tr>
<td></td>
<td>Em-2</td>
<td>TCG TTA GGT TCA TTA CCT</td>
<td>(7)</td>
</tr>
<tr>
<td></td>
<td>nEm-1</td>
<td>GAA TAA GGA TGG TAT GAC</td>
<td>(7)</td>
</tr>
<tr>
<td></td>
<td>nEm-2</td>
<td>AAG TGG AGT TAA CCA CCT</td>
<td>(7)</td>
</tr>
<tr>
<td><em>E. dispar</em></td>
<td>E-1</td>
<td>TTT GTA TTA GTA CAA A</td>
<td>(9)</td>
</tr>
<tr>
<td></td>
<td>E-2</td>
<td>GTA [A/G]TA TG TTA TAC T</td>
<td>(9)</td>
</tr>
<tr>
<td></td>
<td>Ed-1</td>
<td>AGT GGC CAA TTT ATG TAA GT</td>
<td>(9)</td>
</tr>
<tr>
<td></td>
<td>Ed-2</td>
<td>TTT AGA AAC AAT GCT TCT T</td>
<td>(9)</td>
</tr>
</tbody>
</table>

*Boldface indicates the probe fluorophore and quencher.*
Our findings add to the diversity of *Entamoeba* species found in humans. The incidence and effect of infection in infants by the newly recognized species *E. bangladeshii* await future epidemiologic studies.

**Acknowledgments**

We thank B. Mann for careful reading of this manuscript.

This investigation was supported by grant R01AI043596 from the National Institute of Allergy and Infectious Diseases to W.A.P.

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DOI: http://dx.doi.org/10.3201/eid1809.120122

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**Autochthonous Leishmania siamensis in Horse, Florida, USA**

To the Editor: *Leishmania siamensis*, a recently described species, was identified as the cause of autochthonous visceral leishmaniasis in 2 men in southern Thailand (1,2). Cutaneous leishmaniasis has been reported in horses in Europe and South America. Lesions in horses are solitary or multiple nodules that are often ulcerated and most commonly occur on the head, pinnae, legs, and neck. Other clinical signs are usually absent. In South America, biochemical characterization has identified *L. braziliensis* in horses (3). Leishmaniasis has been reported in horses in Puerto Rico (4), and equine leishmaniasis has been described, but no reports have been published, in the United States. *L. infantum* has been reported in equine cutaneous leishmaniasis in Europe (5). A report from central Europe recently identified an organism with 98% nucleotide identity over the ITS (internal transcribed spacer) 1 region to *L. siamensis* as the cause of cutaneous leishmaniasis in 4 horses (6). *L. siamensis* was also identified in a case of cutaneous bovine leishmaniasis in Switzerland (7).

In August 2011, a 10-year-old, 505-kg Morgan horse mare in Florida, USA, with no history of travel outside the eastern United States was evaluated at the University of Florida for an ulcerated mass in the left pinna. When, 6 months earlier, the owner had noticed the mass, it was ≈1 cm in diameter, firm, raised, and covered with hair. Three months later, the ear was unchanged, and the mare was successfully impregnated. Over the subsequent 2 months, the mass began to grow and ulcerate. At that time, veterinary consultation was obtained and a biopsy performed. Histologic