**Cryptosporidiosis was not tracked in Idaho until 1993. It was not tracked nationally until 1998.**

Methods

- We analyzed surveillance and laboratory records of cryptosporidiosis cases reported to Idaho Department of Health and Welfare during September 2012–August 2015. **

- Available stool specimens from cases with laboratory diagnosis were submitted by the Idaho Bureau of Laboratories to CDCs Cryptosporidium** not otherwise specified (NOS) laboratory.

- Molecular testing involved the following two techniques:

  1. Polymerase chain reaction-based restriction fragment length polymorphism (PCR-RFLP) (GP60 sequencing) (18S rRNA gene (18S rRNA)
  2. DNA sequencing of a portion of the 60-kb glycosomal protein (GP60)**

- We compared the characteristics of cryptosporidiosis cases with Idaho population (Table 1), and mapped their geographic distribution (Figure 2). We described molecular profiles of Cryptosporidium (Table 2), and examined characteristics of sporadic (not associated with an outbreak) cases by molecular profile (Table 3). **

- **Strengths**

  - Increased molecular surveillance has potential to disentangle transmission routes, and target prevention efforts.
  - The cryptosporidiosis molecular profile in Idaho might be dominated by C. parvum, but this needs to be confirmed with additional molecular testing of isolates.
  - A15G3R1 was the most common C. parvum subtype and was associated with the majority of the outbreaks. This subtype has been previously found in cattle and humans.

- **Weaknesses**

  - Small sample size
  - Concurrency, non-representative sample
  - State-wide surveillance and laboratory data are not available for specific geographic locations.


table 1. Characteristics of sporadic cryptosporidiosis cases with molecular testing results by Cryptosporidium species — Idaho, 2012–2015

<table>
<thead>
<tr>
<th>Species</th>
<th>Total (n = 24)</th>
<th>C. hominis (n = 6)</th>
<th>C. parvum (n = 18)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Patient</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Age ≤18 years</td>
<td>12 (46)</td>
<td>3 (50)</td>
<td>9 (45)</td>
</tr>
<tr>
<td>Hispanic</td>
<td>18 (75)</td>
<td>5 (83)</td>
<td>13 (72)</td>
</tr>
<tr>
<td>Exposure</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Child care association</td>
<td>3 (12)</td>
<td>2 (33)</td>
<td>1 (10)</td>
</tr>
<tr>
<td>Animal contact</td>
<td>17 (68)</td>
<td>4 (67)</td>
<td>13 (72)</td>
</tr>
<tr>
<td>Recreational water</td>
<td>9 (35)</td>
<td>2 (33)</td>
<td>7 (38)</td>
</tr>
<tr>
<td>Private well</td>
<td>7 (27)</td>
<td>1 (17)</td>
<td>6 (34)</td>
</tr>
</tbody>
</table>

**Strengths**

- State-wide surveillance and laboratory data
- Examined several epidemiologic characteristics
- Used validated laboratory methods for molecular testing

**Limitations**

- Convenience, non-representative sample
- Small sample size
- Cross-sectional design
- Did not examine molecular testing use in outbreak investigations

**Conclusions**

- Compared with Idaho population, cryptosporidiosis cases in Idaho were more likely to be in females and in children aged less than 18 years.
- The cryptosporidiosis molecular profile in Idaho might be dominated by C. parvum, but this needs to be confirmed with additional molecular testing of isolates.
- A15G3R1 was the most common C. parvum subtype and was associated with the majority of the outbreaks. This subtype has been previously found in cattle and humans.
- Increased molecular surveillance has potential to disentangle person-to-person, animal-to-person, waterborne, and foodborne Cryptosporidium transmission routes, and target prevention efforts. However, we could not confirm this in our study and this should be examined in future studies.

**Recommendations**

- Encourage stool sample submission to Idaho Bureau of Laboratories for Cryptosporidium testing.
- Consider allocating resources to perform molecular testing of Cryptosporidium isolates.