Shiga Toxin 2a in Escherichia albertii

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Escherichia albertii is an emerging human enteric pathogen (1). It belongs to the attaching and effacing group of bacteria, which also includes enteropathogenic and Shiga toxin-producing Escherichia coli (EPEC and STEC, respectively). Shiga toxin-producing E. albertii has been described, however, only in association with Shiga toxin (stx) subtype 2f (2). Sporadic infections as well as foodborne outbreaks caused by E. albertii have been reported, although rarely (3, 4). The prevalence, epidemiology, and clinical relevance of E. albertii are poorly understood, probably due to underestimation and misclassification of this pathogen (4). The phenotypic features distinguishing E. albertii from E. coli include a negative indole reaction and an inability to ferment lactose-, D-ribose, and D-xylene (1).

In Norway, all presumptive enteropathogenic E. coli strains isolated from humans are submitted to the National Reference Laboratory for Enteropathogenic Bacteria for biochemical verification and for classification into well-known pathotypes according to virulence genes present (L. T. Brandal, A. L. Wester, H. Lange, I. Løbersli, B. A. Lindstedt, L. Vold, and G. Kapperud, submitted for publication). For outbreak detection purposes, all E. coli isolates are investigated with a generic multilocus variable-number tandem-repeat analysis (MLVA) (5).

By these routine analyses, a nonmotile, β-D-glucuronidase-, lactose-, and xylose-negative isolate with eae and stx was identified. This isolate had an MLVA profile often seen in E. albertii (NA-NA-NA-NA-NA-5-X-X-X-NA, where NA designates a locus not present and X indicates different repeat numbers). A PCR specific for E. albertii was conducted (6), and 16S rRNA sequencing was performed (MicroSEC 500 16S RNA gene bacterial sequencing kit; Life Technologies), both of which confirmed the isolate as E. albertii. stx2 was subtyped and sequenced (7), and the expression of the stx2a gene was verified (ImmunoCard STAT!EHEC; Meridian Bioscience Europe). All E. albertii isolates identified from 2008 to 2014 (n = 39) were examined for the presence of stx2a (8) and the cytotoxid distending toxin B gene (cdtB) (9).

Interestingly, the E. albertii isolate identified in the present study carried stx2a, hitherto never reported in E. albertii. Additionally, we showed that stx2a was expressed. This indicates that E. albertii is able to transduce not only stx2a-carrying bacteriophages but also stx2a-carrying bacteriophages, STEC harboring eae and stx2a are considered highly virulent and have the ability to induce life-threatening hemolytic uremic syndrome (HUS) in infected patients (10). In contrast, STEC harboring stx2f are associated with milder symptoms (11) and have, to our knowledge, never previously been detected in HUS patients. The patient infected with stx2a-positive E. albertii was 48 years old, had bloody diarrhea, and was infected in Norway (Table 1). Domestically acquired E. albertii infection was commonly seen in patients included in the present study; however, the majority of the patients were young (≤5 years) and did not have bloody stools. In addition to carrying eae, all isolates harbored cdtB, a cyclomodulin and genotoxin gene also common in sorbitol-fermenting O157 STEC strains, bacteria leading to HUS in up to 50% of infected patients (12). stx2f was

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**TABLE 1** Characteristics of the stx2a-positive E. albertii isolate compared with E. albertii isolates received at the National Reference Laboratory for Enteropathogenic Bacteria from 2008 to 2014

<table>
<thead>
<tr>
<th>No. of patients/isolates (n = 39)</th>
<th>No. of patients</th>
<th>Age (yr)</th>
<th>No. with indicated clinical outcome</th>
<th>No. with a travel history</th>
<th>No. with virulence profile</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>No. of patients</td>
<td>≤5</td>
<td>&gt;5</td>
<td>D</td>
<td>BD</td>
</tr>
<tr>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>38</td>
<td>18</td>
<td>20</td>
<td>30</td>
<td>8</td>
<td>17</td>
</tr>
<tr>
<td>Total (% of total)</td>
<td>18</td>
<td>46</td>
<td>21</td>
<td>54</td>
<td>30</td>
</tr>
</tbody>
</table>

a F, females; M, males.

b D, diarrhea; BD, bloody diarrhea; Unkn, unknown (no information on clinical outcome was available).

c No, the patient was infected in Norway; Yes, the patient had been traveling abroad prior to the onset of infection; Unkn, unknown (no information on travel history was available).

d All E. albertii isolates were negative for ehxA, stx2, bfpA, LT1 gene, stla, stlb, sipA, and agrR (L. T. Brandal, A. L. Wester, H. Lange, I. Løbersli, B. A. Lindstedt, L. Vold, and G. Kapperud, submitted for publication) but positive for hypA and midA (/6). cdt-1 detects the cytotoxid distending toxin B (cdtB) subtypes II, III, and V, whereas cdt-2 detects the cdtB subtypes I and IV.
present in 10% (4/39) of the E. albertii isolates, a finding comparable with those of previous studies (4) (Table 1). Thus, E. albertii has the ability to carry virulence characteristics, including stx2a, that are associated with severe illness in infected patients. Therefore, an increased awareness of this underestimated and misidentified pathogen is important.

REFERENCES