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LETTER TO THE EDITOR

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-sorbitol, and D-xylose (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_2 was identified. This isolate had an MLVA profile often seen in *E. albertii* (NA-NA-NA-NA-NA-NA-5-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 rRNA gene bacterial sequencing kit; Life Technologies), both of which confirmed the isolate as *E. albertii*. stx_2 was subtyped and sequenced (7), and the expression of the stx_{2a} 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 stx_{2f} (8) and the cytolethal distending toxin B gene (*cdtB*) (9).

Interestingly, the *E. albertii* isolate identified in the present study carried stx_{2a}, hitherto never reported in *E. albertii*. Additionally, we showed that stx_{2a} was expressed. This indicates that *E. albertii* is able to transduce not only stx_{2f}-carrying bacteriophages but also stx_{2a}-carrying bacteriophages. STEC harboring *eae* and stx_{2a} are considered highly virulent and have the ability to induce life-threatening hemolytic uremic syndrome (HUS) in infected patients (10). In contrast, STEC harboring stx_{2f} are associated with milder symptoms (11) and have, to our knowledge, never previously been detected in HUS patients. The patient infected with stx_{2a}-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). stx_{2f} was

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TABLE 1 Characteristics of the stx_{2a}-positive *E. albertii* isolate compared with *E. albertii* isolates received at the National Reference Laboratory for Enteropathogenic Bacteria from 2008 to 2014

No. of patients/ isolates ($n = 39$)	No. of[a]:		Age (yr)		No. with indicated clinical outcome[b]			No. with a travel history[c]			No. with virulence profile[d]				
	F	M	≤5	>5	D	BD	Unkn	No	Yes	Unkn	*eae*	stx_{2a}	stx_{2f}	*cdt-1*	*cdt-2*
1		1		1		1		1			1	1		1	
38	18	20	30	8	17	3	18	17	5	16	38		4	38	4
Total (% of total)	18 (46)	21 (54)	30 (77)	9 (23)	17 (44)	4 (10)	18 (46)	18 (46)	5 (5.1)	16 (41)	39 (100)	1 (2.6)	4 (10)	39 (100)	4 (10.3)

[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*, stx_1, *bfpB*, LT1 gene, *stIa*, *stIb*, *ipaH*, and *aggR* (L. T. Brandal, A. L. Wester, H. Lange, I. Løbersli, B. A. Lindstedt, L. Vold, and G. Kapperud, submitted for publication) but positive for *lysP* and *mdh* (6). *cdt-1* detects the cytolethal 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 stx_{2a}, that are associated with severe illness in infected patients. Therefore, an increased awareness of this underestimated and misidentified pathogen is important.

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