



The closed chromosomes of these STEC strains varied in size from 5.2 to 5.5 Mb, with an average G+C content of 50.7%, similar to those results found in other STEC strains (7). These STEC strains belonged to three sequence types (ST), and all carried one exceptionally large >200-kb virulence plasmid (8) (Table 1). Although these strains were isolated from foods and belong to serogroups that are rarely implicated in human disease (1), *in silico* analysis identified the enterotoxin-encoding genes *stx1* and *stx2*, both associated with the development of diarrhea (9). Furthermore, two strains carried the highly HUS-associated *stx2a* variant, one carried *stx1a*, and one carried *stx2g*; the role of *stx2g* in human pathogenicity remains to be elucidated (10). Additionally, these STEC strains carry genes encoding K88 fimbriae, long polar fimbriae (Lpf), the Iha adhesin, and/or the metalloprotease StcE (Table 1), which presumably enable these STEC strains to colonize the human gut (11–13). Moreover, all carry the glutamate decarboxylase gene *gad*, enabling these organisms to survive gastric acidity (14).

Trace-back analysis is crucial during investigations of foodborne illness outbreaks. The data provided can aid in future efforts to identify the source of infection when matching clinical, food, and environmental isolates. The availability of complete genome sequences will further contribute to the ongoing investigation of genetic differences among various pathogenic *E. coli* strains.

**Accession number(s).** The closed and annotated chromosome and plasmid sequences were deposited in GenBank and are listed in Table 1.

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