

Isolation and Genomic Characterization of a Heat-Labile Enterotoxin 1-Producing *Escherichia fergusonii* Strain from a Human

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Abstract

*Escherichia fergusonii* strains have been isolated from patients with diarrhea, but their virulence determinant has not been well elucidated. Here, we report the first isolation of a heat-labile enterotoxin 1 (LT1)-producing *E. fergusonii* strain (strain 30038) from a patient in Japan. The complete genome sequence of strain 30038 was determined and subjected to comparative genomics and phylogenetic analyses with 195 publicly available genomes of *E. fergusonii*. In addition to strain 30038, the *elt1* gene was also identified in an *E. fergusonii* strain that is phylogenetically distinct and which was isolated from poultry in the United Kingdom. Fine genomic comparison revealed that these two strains share comparable *elt1*-bearing plasmids. However, an intriguing distinction arises in strain 30038, wherein the plasmid has integrated into the chromosome via a recombination process mediated by an insertion sequence. The production of active LT1 toxin by strain 30038 was verified through an *in vitro* assay using cultured cells. A large plasmid carrying 11 antimicrobial resistance genes was also identified in strain 30038. Our results indicate that extensive surveillance of *elt1*-positive *E. fergusonii* strains as diarrheagenic pathogens is needed.