Shiga toxin-producing *Escherichia coli* causes bloody diarrhea and hemolytic-uremic syndrome and serious outbreaks worldwide. Here, we report the draft genome sequence of *E. coli* NCCP15657 isolated from a patient. The genome has virulence genes, many in the locus of enterocyte effacement (LEE) island, encoding a metalloprotease, the Shiga toxin, and constituents of type III secretion.

The final assembly consists of 93 contigs of 5,015,691 bp (50.6% of G+C content). A total of 4,033 protein-coding sequences were assigned functions. The average nucleotide identity (ANI) value was calculated with Jspecies (10). The genome is most similar to that of *E. coli* N14639 (98.74 to 99.42%). The genome is most similar to that of the O123:H19 serotype. Interestingly, LEE is flanked by the selC RNA locus. This structure is similar to that of O157 unlike other non-O157 strains (9). The genome has virulence genes, many in the locus of enterocyte effacement (LEE) island, encoding a metalloprotease, the Shiga toxin, and constituents of type III secretion.

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Address correspondence to Jyhun F. Kim, jfk1@yonsei.ac.kr, or Seung-Hak Cho, skcho38@korea.kr.

B.K.K., G.C.S., and G.H.H. contributed equally to this work.

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