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Draft Genome Sequence of an *Escherichia coli* O157:H43 Strain Isolated from Cattle

Domonkos Sváb,[a] Balázs Horváth,[b] Attila Szűcs,[b] Gergely Maróti,[b] István Tóth[a]

Institute for Veterinary Medical Research, Centre for Agricultural Research, Hungarian Academy of Sciences, Budapest, Hungary[a]; Biological Research Centre, Institute of Biochemistry, Hungarian Academy of Sciences, Szeged, Hungary[b]

Here we report the draft genome sequence of an *Escherichia coli* O157:H43 strain, designated T22, with an atypical virulence gene profile and isolated from healthy cattle. T22 produces cytolethal distending toxin V (CDT-V) and belongs to phylogenetic group B1 and sequence type 155 (ST155).

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Address correspondence to István Tóth, tothi@vmri.hu.

Enterohemorrhagic *Escherichia coli* (EHEC) strain O157:H7 has become a significant food-borne pathogen since its discovery (1). Additionally, strains of the serotype O157:NM (nonmotile) caused severe outbreaks in Europe (2). Typical EHEC O157 strains produce Shiga toxin (Stx) and carry the locus of enterocyte effacement (LEE) pathogenicity island encoding the adhesin intimin (3). Due to their clinical and epidemiological significance, the whole genomes of several outbreak strains have been fully sequenced (4, 5, 6). However, there are fewer data available on Stx-negative O157 strains and O157 strains that express flagellar antigens other than H7.

Recently, we identified atypical *E. coli* O157:H43 strains from healthy cattle that harbor neither *stx* nor *eae* virulence genes but that produce cytolethal distending toxin V (CDT-V), carry the genes encoding long polar fimbriae (*lpf2*), and belong to phylogenetic group B1 (7, 8).

The present study announces the first assembled draft genome of an *E. coli* O157:H43 strain. Chromosomal and plasmid DNA of an overnight culture of strain T22 of *E. coli* O157:H43 was isolated by GenElute bacterial genomic DNA kit (Sigma-Aldrich) and alkaline lysis, respectively. The chromosome and the plasmid DNA was sequenced and assembled using the combination of three next-generation sequencing (NGS) approaches (high-quality trimmed reads generated on the Life Technologies SOLiD V4 and Ion Torrent PGM as well as Roche's 454 Titanium). Altogether, 6,994,992 SOLiD mate-paired reads of 50 plus 50 bp were combined with 233,333 Ion Torrent reads (mean read length, 161.1) and 73,764 reads from 454 Titanium (mean read length, 619). Trimming and assembly were performed manually using CLC Genomics Workbench 6.0 (9). The draft genome of T22 consists of a circular 4,959,535-bp chromosome and a plasmid with a length of 80,112 bp. The bacterial chromosome was assembled into 64 contigs containing 5,587 predicted genes (open reading frames [ORFs]) coding for 5,511 proteins, 17 rRNAs, and 59 tRNAs, while the plasmid was covered by 8 contigs harboring 90 genes (89 coding sequences [CDS] and 1 tRNA). Annotation was added by NCBI Prokaryotic Genomes Automatic Annotation Pipeline, which utilizes GeneMark, Glimmer, and tRNAscan-SE searches. The G+C content of the genome is 50.8%. None of the key virulence genes (10) of enterohemorrhagic (*stx, eae*), enteropathogenic (*eae, bfp*), enterotoxigenic (*lt, st*), enteroinvasive (*ihaH*), or enteroaggregative (*aggR*) *E. coli* strains were observed in the T22 genome. All the known integration sites of Stx phages (5, 10, 11) and LEE pathogenicity islands (12) were intact in the T22 chromosome. Multilocus sequence typing (MLST) analysis (13) based on the nucleotide sequences of seven housekeeping genes revealed that T22 belongs to the group sequence type 155 (ST155). These data could provide useful information for better understanding the evolution of *E. coli* O157.

Nucleotide sequence accession numbers. This Whole-Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. AHZD00000000. The version described in this paper is the second version, accession no. AHZD02000000.

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