**Genome Sequence of the Hemolytic-Uremic Syndrome-Causing Strain* Escherichia coli *NCCP15647**

Haeyoung Jeong, a,b,c Fumei Zhao, b,c Davaaajargal Igori, b,c Kyung-Hwan Oh, d Seon-Young Kim, a,f Sung Gyun Kang, b,h Byung Kwon Kim, a Soon-Kyeong Kwon, a,b Choong Hoon Lee, a Ju Yeon Song, a Dong Su Yu, a Mi-Sun Park, d Seung-Hak Cho, d and Jihyun F. Kim, b,h

Enterohemorrhagic *Escherichia coli* (EHEC) causes a disease involving diarrhea, hemorrhagic colitis, and hemolytic-uremic syndrome (HUS). Here we present the draft genome sequence of NCCP15647, an EHEC isolate from an HUS patient. Its genome exhibits features of EHEC, such as genes for verotoxins, a type III secretion system, and prophages.

Infection by enterohemorrhagic *Escherichia coli* (EHEC) that produces Shiga toxin or verotoxin can cause severe watery or bloody diarrhea and can be fatal for children and the elderly (12, 17). Although *E. coli* O157:H7 is the main EHEC serotype (10, 14), non-O157 EHEC strains such as O111, O103, O145, and O26 have been isolated in 2003 from a Korean male patient who suffered from hemolytic-uremic syndrome.

The genome contains two genes for verotoxins I and II. Contrary to the common integration of the locus of enteroocyte effacement (LEE) pathogenicity island harboring a type III secretion system (TTSS) and *cag* genes at the *sbeC* site in other typical EHEC strains, such as O157:H7, the TTSS from NCCP15647 was found at another site without *cag* and was not associated with prophages. We could also identify several prophage-related gene clusters and at least three putative plasmid contigs harboring genes for replication, one of them also having a colicin gene. Genome sequence analysis can rapidly reveal the genetic makeup of the causative agents of a serious infection, which can help source tracking of infection and proper treatment.

**Nucleotide sequence accession number.** The draft sequence determined in this study has been deposited in GenBank under the accession no. AJMB00000000. The sequence and annotation are also available from the Genome Encyclopedia of Microbes (GEM) site at [http://www.gem.re.kr/](http://www.gem.re.kr/).

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

H.J., F.Z., and D.I. contributed equally to this article.

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