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Complete Genome Sequence of *bla*$_{CTX-M-27}$-Encoding *Escherichia coli* Strain H105 of Sequence Type 131 Lineage C1/H30R

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ABSTRACT *Escherichia coli* sequence type 131 (ST131) is the most frequent antimicrobial-resistant lineage of *E. coli*, propagating extended-spectrum β-lactamases (ESBL) worldwide. Recently, an alarming rate of increase in isolates of the sublineage C1/H30R-*bla*$_{CTX-M-27}$ of ST131 in geographically distant countries was reported. Here, we present the complete genome sequence of the ST131 sublineage C1/H30R *E. coli* isolate harboring *bla*$_{CTX-M-27}$ from Germany.

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We sequenced the *Escherichia coli* isolate H105, a sequence type 131 (ST131) C1/H30R extended-spectrum β-lactamase (ESBL)-producing isolate obtained in 2010 from a vaginal swab sample of an individual from Germany. The isolate harbors a *bla*$_{CTX-M-27}$ allele and represents an early isolate with this genotype combination in our collection. As reported in Japan (1) and in France (2), there is currently a strong surge in the number of ST131-C1/H30R-*bla*$_{CTX-M-27}$ isolates detected in Germany, particularly in the past 3 years, suggesting an ongoing shift in CTX-M alleles associated with ST131 infections.

For the whole-genome sequencing, genomic DNA was isolated using a PureLink genomic DNA kit (Invitrogen, Darmstadt, Germany) from an overnight culture grown at 37°C in LB medium. Short-read sequencing was performed on an Illumina MiSeq machine (Illumina, the Netherlands) using a Nextera XT library with MiSeq v3 (2 × 300 bp) reagent kit. Single-molecule real-time sequencing (SMRT) was conducted using the PacBio RSII system (Pacific Biosciences, USA).

De novo genome assembly of 59,447 PacBio reads with an average read length of 10,355 bp was performed using the "RS_HGAP_Assembly.3" included in the SMRT Portal version 2.3.0. Subsequently, Illumina short reads were mapped onto the assembled sequences in order to obtain a highly accurate genome with QV60 final quality. The chromosome was adjusted to *dnaA* as the first gene. Annotation was performed both using Prokka 1.10 (3) and the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html). Antimicrobial resistance genes and prophages were identified using Resfinder and PHAST, respectively (4, 5).

The assembly resulted in a closed, circular chromosomal contig of 4,978,342 bp and a plasmid of 134,499 bp, designated the plasmid pH 105. The chromosome of *E. coli* H105 exhibited a 50.7% G+C content, and harbored 4,635 open reading frames, 87 tRNAs, 15 rRNAs, and 6 intact prophage regions. *In silico* analysis revealed that *E. coli* H105 belongs to the sequence type ST131, serotype O25:H4, and phylogroup B2. The genome of H105 includes multiple chromosomally encoded virulence genes such as for

iron uptake (yersiniabactin, aerobactin, *sitABC*), serum resistance (*iss, traT*), autotransporter proteases (*sat, pic*), and the postsegregational killing system *ccdA/ccdB*.

The plasmid pH105 is a multireplicon plasmid, depicting IncFIA, FIB, and FII replicons with the pMLST type F1:A2:B20 (6). The ESBL gene $bla_{CTX\text{-}M\text{-}27}$ encoded on pH105 confers resistance to extended-spectrum β-lactams. In addition, pH105 also carries genes conferring resistance to aminoglycosides (*aadA5, strA, strB*), macrolides [*mph*(A)], tetracyclines [*tet*(B)], sulfonamide (*sul1, sul2*), and trimethoprim (*dfrA17*).

The sequence of H105 represents the first complete genome of the $bla_{CTX\text{-}M\text{-}27}$-encoding *E. coli* ST131 of the lineage C1/H30R. The high-quality genome of H105 will serve as a valuable resource for comparative studies on epidemiology of globally emerging ST131-C1/H30R-$bla_{CTX\text{-}M\text{-}27}$.

Accession number(s). The complete genome sequence of *E. coli* H105 has been deposited in GenBank under GenBank accession no. CP021454 (chromosome) and CP021871 (plasmid).

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