AMERICAN SOCIETY FOR MICROBIOLOGY | genomeAnnouncements™

PROKARYOTES

Draft Genome Sequence of *Escherichia coli* KL53

Katarina Soltys,[a] Silvia Vavrova,[a] Jaroslav Budis,[b] Lenka Palkova,[c] Gabriel Minarik,[d] Jozef Grones[a]

[a]Faculty of Natural Sciences, Department of Molecular Biology in Bratislava, Comenius University in Bratislava, Bratislava, Slovakia

[b]Faculty of Mathematics, Physics and Informatics in Bratislava, Department of Computer Science Bratislava, Comenius University in Bratislava, Bratislava, Slovakia

[c]Faculty of Medicine, Institute of Molecular Biomedicine, Comenius University in Bratislava, Bratislava, Slovakia

[d]Geneton Ltd., Bratislava, Slovakia

ABSTRACT Here, we report the draft genome sequence of a clinical isolate of the uropathogenic strain *Escherichia coli* KL53. A total of 5,083,632 bp was *de novo* assembled into 170 contigs containing 89 RNAs and 5,034 protein-coding genes. Remarkable is the presence of the tellurite resistance (*ter*) operon on a plasmid.

The genus *Escherichia* belongs to the family of *Enterobacteriaceae*, and due to the cooccurrence of antibiotic and heavy metal resistance genes, these organisms can, through plasmid carryover, evolve multidrug and multimetal resistance, including tellurium resistance. Tellurite oxyanions are highly toxic for most forms of life, even at micromolar levels. A group of pathogens, including foodborne pathogen *Escherichia coli* O157:H7, *Klebsiella pneumoniae* (1), *Bacillus subtilis*, *Staphylococcus aureus*, *Yersinia pestis* (2), *Vibrio cholerae*, and *Shigella* spp., possess tellurite resistance genes; *E. coli* KL53 has this cluster on a plasmid (3).

We report here the draft genome sequence of a uropathogenic isolate of *E. coli* strain KL53 serotype O18:H14 recovered from the hospital environment of the Department of Urology of University Hospital in Bratislava, Slovakia. The strain was found to grow at a high concentration of tellurite under laboratory conditions. The complete genome was sequenced by next-generation sequencing. The sequencing libraries were prepared using the Tn-based library preparation chemistry Nextera XT (Illumina, Inc., San Diego, CA, USA), according to the manufacturer's instructions. One nanogram of total DNA was fragmented and amplified. Purified fragments were quantified fluorometrically with a Qubit fluorimeter (Thermo Fisher Scientific, Waltham, MA, USA). The quality was assessed using a high-sensitivity (HS) DNA chip (Agilent Technologies, Waldbronn, Germany). Paired-end sequencing was performed using an Illumina MiSeq platform (Illumina, Inc.). The sequence quality was checked with the bioinformatics tool FastQC. For the *de novo* assembly, SPAdes version 3.10.1 was used. Gene identification and annotation were provided by the NCBI Prokaryotic Genome Annotation Pipeline (https://www.ncbi.nlm.nih.gov/genome/annotation_prok/), with the best-placed reference set and GeneMarkS+ version 4.2.

The total sequence length was 5,083,632 bp. *De novo* assembly of the *E. coli* KL53 genome resulted in a set of 170 contigs with GC content of 50.77%. The total DNA contains 5,418 genes, of which 5,034 genes were protein-coding and 89 were RNA genes (14 rRNA, 66 tRNA, and 9 noncoding RNA [ncRNA]). The presence of 3 plasmid incompatibility group-determining sequences was detected [IncI1, 100% identity; IncHI2, 100% identity; IncFIB(K), 98.93% identity] by PlasmidFinder (https://cge.cbs.dtu.dk/services/PlasmidFinder/). An exact match of IncI1 plasmid genes *repI1-ardA-trbA-sogS-pilL* with database alleles 1-4-17-1-3 was determined using pMLST (http://pubmlst.org/plasmid/).

Received 22 February 2018 **Accepted** 9 March 2018 **Published** 29 March 2018

Citation Soltys K, Vavrova S, Budis J, Palkova L, Minarik G, Grones J. 2018. Draft genome sequence of *Escherichia coli* KL53. Genome Announc 6:e00220-18. https://doi.org/10.1128/genomeA.00220-18.

Address correspondence to Katarina Soltys, katarina.soltys@uniba.sk.

The KL53 strain includes multiple heavy metal resistance genes for zinc (*znuC*, *znuB*, *zupT*, and *zntB*), copper (*copA* to *copD*), a cation efflux system for silver and other heavy metals (*cusA*, *cusC*, and *cusF*), arsenic (*arsCBR*), and a tellurium resistance system (*terZABCDEF* and *terWY1XY2Y3*), part of which was determined to be localized on a plasmid by transconjugation (GenBank accession no. AJ888883) (4).

Multidrug resistance genes include multidrug efflux resistance-nodulation-division (RND) transporter MexE, which is involved in resistance to a number of compounds, including lipophilic antibiotics, multidrug and toxic compound extrusion (MATE) family efflux transporter DinF, Bcr/CflA (bicyclomycin resistance protein), and the BlaEC family class C β-lactamase providing multiresistance to β-lactam antibiotics.

Furthermore, genes for the resistance to bacitracin, UV resistance, and resistance to N4 and lambda phages were detected in annotated draft genome sequence of *E. coli* KL53.

Accession number(s). This whole-genome shotgun project has been deposited in GenBank under the accession no. NXEL00000000. This version of the project (01) has the accession no. NXEL01000000 and consists of sequences NXEL01000001 to NXEL01000170.

ACKNOWLEDGMENTS

This publication is a result of the implementation of the project REVOGENE (grant ITMS 26240220067), which is supported by the Research & Development Operational Programme funded by the ERDF, and of the project implementation of Comenius University Science Park-2 phase (grant ITMS 2014+313021D075), which is supported by the Research & Innovation Operational Programme funded by the ERDF.

REFERENCES

1. Chen YT, Chang HY, Lai YC, Pan CC, Tsai SF, Peng HL. 2004. Sequencing and analysis of the large virulence plasmid pLVPK of *Klebsiella pneumoniae* CG43. Gene 337:189–198. https://doi.org/10.1016/j.gene.2004.05.008.
2. Ponnusamy D, Clinkenbeard KD. 2015. Role of tellurite resistance operon in filamentous growth of *Yersinia pestis* in macrophages. PLoS One 10:e0141984. https://doi.org/10.1371/journal.pone.0141984.
3. Burian J, Tu N, Kl'učár L, Guller L, Lloyd-Jones G, Stuchlík S, Fejdi P, Siekel P, Turna J. 1998. *In vivo* and *in vitro* cloning and phenotype characterization of tellurite resistance determinant conferred by plasmid pTE53 of a clinical isolate of *Escherichia coli*. Folia Microbiol 43:589–599. https://doi.org/10.1007/BF02816374.
4. Kormutakova R, Klucar L, Turna J. 2000. DNA sequence analysis of the tellurite-resistance determinant from clinical strain of *Escherichia coli* and identification of essential genes. Biometals 13:135–139. https://doi.org/10.1023/A:1009272122989.