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GENOME SEQUENCES

Draft Genome Sequence of a Uropathogenic *Escherichia coli* Sequence Type 44 Strain Carrying Multiple Antimicrobial Resistance Genes

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ABSTRACT *Escherichia coli* is a reservoir of antimicrobial resistance genes (ARGs). Here, we report the draft genome sequence of an *E. coli* strain (31HGR-CBG) that was isolated from a urine sample in Tamaulipas, Mexico. 31HGR-CBG harbors multiple ARGs, including $bla_{CTX\text{-}M\text{-}15}$ and class 1 integron. This strain also carries multiple virulence genes.

Antimicrobial-resistant *Escherichia coli* represents a threat to public health (1). Strains of extraintestinal pathogenic *E. coli* (ExPEC) are genetically diverse and complex (2). ExPEC acts as an opportunistic pathogen, mainly causing urinary tract infections (UTIs) (3). In Mexico, UTIs are a public health problem and represent the third leading cause of morbidity (4, 5).

The 31HGR-CBG strain was isolated in 2018 from a urine sample from a second-level hospital in Reynosa, Tamaulipas, Mexico, from specimens obtained for routine testing of nosocomial pathogens; therefore, neither institutional review board (IRB) approval nor informed consent was required. 31HGR-CBG was grown on Trypticase soy agar and CHROMagar Orientation medium and incubated overnight at 37°C. Standard biochemical tests were also performed.

Genomic DNA was isolated from an overnight culture grown in LB broth (Condalab, Madrid, Spain) at 37°C. DNA was extracted using the Wizard genomic DNA purification kit (Promega, USA). DNA quantification was performed with the Qubit double-stranded DNA (dsDNA) HS assay kit in the Qubit 3.0 fluorometer (Thermo Fisher Scientific, USA). Libraries were constructed with the Nextera Flex library preparation kit and were sequenced using the MiniSeq sequencing system (150-bp paired-end reads). A total of 10,918,316 raw reads were generated. FastQC v0.11.3 (https://www.bioinformatics.babraham.ac.uk/projects/fastqc) and Trim Galore! v0.6.6 (https://www.bioinformatics.babraham.ac.uk/projects/trim_galore) were used to evaluate quality and to trim the raw reads, respectively. Assembly was performed using SPAdes v3.15.2 (6) (with options --isolate and –k 21,31,41,51,61,71,81,91). The quality of the assemblies was assessed with QUAST v5.0.2 (https://github.com/ablab/quast). Contigs smaller than 900 bp were removed. Bacterial identification was confirmed by a BLASTN search (http://blast.ncbi.nlm.nih.gov) against the NCBI database and ribosomal multilocus sequence typing (rMLST) (7).

Automatic annotation was performed by the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v5.2. Multilocus sequence typing (MLST) was executed with PubMLST v1 (8). Serotype, plasmid replicons, antimicrobial resistance genes (ARGs), and virulence genes were analyzed using SerotypeFinder v2.0 (9), PlasmidFinder v2.1 (10), ResFinder v3.0 (11), and VirulenceFinder v2.0 (12), respectively, available from the Center for Genomic Epidemiology (http://genomicepidemiology.org). ARGs were also predicted with the CARD v3.1.4 database

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using RGI v5.2.0 (13). Phages were determined by PHASTER (14). Default parameters were used for all software unless otherwise specified.

The genome was 4,981,584 bp in size and was assembled into 141 contigs, with an N_{50} value of 91,860 bp, a GC content of 50.82%, and genome coverage of 220×. Annotation identified 4,939 genes, 4,850 coding sequences, and two CRISPR arrays. 31HGR-CBG belongs to sequence type 44 (ST44) and serotype 0101:H4.

Multiple ARGs were identified, including genes conferring resistance to aminoglycosides [*aadA5*, *aph(6)-Id*, *aac(6′)-Ib-cr*, and *aph(3″)-Ib*], extended-spectrum β-lactams ($bla_{CTX-M-15}$ and bla_{OXA-1}), phenicol (*catB3*), macrolides [*mph*(A)], sulfonamides (*sul1* and *sul2*), tetracycline [*tet*(B)], trimethoprim (*dfrA17*), and quaternary ammonium compounds (*qacEΔ1*). In addition, plasmid replicons IncFIA, IncFIB, and IncFII were detected.

Chromosomal mutations in *gyrA*, *parC*, and *parE* were found, indicating fluoroquinolone resistance. Virulence-associated genes and four intact prophages were identified.

Data availability. This draft genome has been deposited in GenBank under the accession number JAKJKJ000000000. The reads were deposited in the Sequence Read Archive (SRA) under the accession number SRR15258840.

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REFERENCES

1. Shin SW, Shin K, Jung M, Belaynehe M, Yoo S. 2015. Prevalence of antimicrobial resistance and transfer of tetracycline resistance genes in *Escherichia coli* isolates from beef cattle. Appl Environ Microbiol 81:5560–5566. https://doi.org/10.1128/AEM.01511-15.
2. Sarowska J, Futoma-Koloch B, Jama-Kmiecik A, Frej-Madrzak M, Ksiazczyk M, Bugla-Ploskonska G, Choroszy-Krol I. 2019. Virulence factors, prevalence, and potential transmission of extraintestinal pathogenic *Escherichia coli* isolated from different sources: recent reports. Gut Pathog 11:10. https://doi.org/10.1186/s13099-019-0290-0.
3. Massella E, Giacometti F, Bonilauri P, Reid CJ, Djordjevic SP, Merialdi G, Bacci C, Fiorentini L, Massi P, Bardasi L, Rubini S, Savini F, Serraino A, Piva S. 2021. Antimicrobial resistance profile and ExPEC virulence potential in commensal *Escherichia coli* of multiple sources. Antibiotics 10:351. https://doi.org/10.3390/antibiotics10040351.
4. Garza-Montúfar ME, Treviño-Valdez PD, De la Garza-Salinas LH. 2018. Resistencia bacteriana y comorbilidades presentes en pacientes urológicos ambulatorios con urocultivos positivos. Rev Med Inst Mex Seguro Soc 56:347–353.
5. Ramírez-Castillo FY, Moreno-Flores AC, Avelar-González FJ, Márquez-Díaz F, Harel J, Guerrero-Barrera AL. 2018. An evaluation of multidrug-resistant *Escherichia coli* isolates in urinary tract infections from Aguascalientes, Mexico: cross-sectional study. Ann Clin Microbiol Antimicrob 17:34. https://doi.org/10.1186/s12941-018-0286-5.
6. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol 19:455–477. https://doi.org/10.1089/cmb.2012.0021.
7. Jolley KA, Bliss CM, Bennett JS, Bratcher HB, Brehony C, Colles FM, Wimalarathna H, Harrison OB, Sheppard SK, Cody AJ, Maiden MCJ. 2012. Ribosomal multilocus sequence typing: universal characterization of bacteria from domain to strain. Microbiology (Reading) 158:1005–1015. https://doi.org/10.1099/mic.0.055459-0.
8. Jolley KA, Bray JE, Maiden MCJ. 2018. Open-access bacterial population genomics: BIGSdb software, the PubMLST.org website and their applications. Wellcome Open Res 3:124. https://doi.org/10.12688/wellcomeopenres.14826.1.
9. Joensen KG, Tetzschner AM, Iguchi A, Aarestrup FM, Scheutz F. 2015. Rapid and easy in silico serotyping of *Escherichia coli* using whole genome sequencing (WGS) data. J Clin Microbiol 53:2410–2426. https://doi.org/10.1128/JCM.00008-15.
10. Carattoli A, Zankari E, García-Fernández A, Larsen MV, Lund O, Villa L, Aarestrup FM, Hasman H. 2014. *In silico* detection and typing of plasmids using PlasmidFinder and plasmid multilocus sequence typing. Antimicrob Agents Chemother 58:3895–3903. https://doi.org/10.1128/AAC.02412-14.
11. Zankari E, Hasman H, Cosentino S, Vestergaard M, Rasmussen S, Lund O, Aarestrup FM, Larsen MV. 2012. Identification of acquired antimicrobial resistance genes. J Antimicrob Chemother 67:2640–2644. https://doi.org/10.1093/jac/dks261.
12. Joensen KG, Scheutz F, Lund O, Hasman H, Kaas RS, Nielsen EM, Aarestrup FM. 2014. Real-time whole-genome sequencing for routine typing, surveillance, and outbreak detection of verotoxigenic *Escherichia coli*. J Clin Microbiol 52:1501–1510. https://doi.org/10.1128/JCM.03617-13.
13. Alcock BP, Raphenya AR, Lau TTY, Tsang KK, Bouchard M, Edalatmand A, Huynh W, Nguyen A-LV, Cheng AA, Liu S, Min SY, Miroshnichenko A, Tran H-K, Werfalli RE, Nasir JA, Oloni M, Speicher DJ, Florescu A, Singh B, Faltyn M, Hernandez-Koutoucheva A, Sharma AN, Bordeleau E, Pawlowski AC, Zubyk HL, Dooley D, Griffiths E, Maguire F, Winsor GL, Beiko RG, Brinkman FSL, Hsiao WWL, Domselaar GV, McArthur AG. 2020. CARD 2020: antibiotic resistome surveillance with the Comprehensive Antibiotic Resistance Database. Nucleic Acids Res 48:D517–D525. https://doi.org/10.1093/nar/gkz935.
14. Arndt D, Grant J, Marcu A, Sajed T, Pon A, Liang Y, Wishart DS. 2016. PHASTER: a better, faster version of the PHAST phage search tool. Nucleic Acids Res 44:W16–W21. https://doi.org/10.1093/nar/gkw387.