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GENOME SEQUENCES

Draft Genome Sequence of an *Escherichia coli* Sequence Type 155 Strain Isolated from Sewage in Kerala, India

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ABSTRACT We report the draft genome sequence of *Escherichia coli* ASBT-1, a representative of *E. coli* sequence type 155 (ST155), obtained from India. Considering the known wide variety of pathogenic and antibiotic resistance potentials, this strain should be of great interest for detailed comparative genomic analysis.

Escherichia coli sequence type 155 (ST155) represents important strains responsible for zoonotic transmission of extended-spectrum β-lactamase genes to humans (1–8). We announce an assembled draft genome of an *E. coli* ST155 strain obtained from wastewater in Kerala, India, and explore the diversity of different antibiotic resistance profiles in the region.

The organism was isolated from sewage in eosin-methylene blue agar, biochemically characterized as *E. coli*, and confirmed by 16S rRNA gene ribotyping (9). Genomic DNA was extracted using the phenol-chloroform method (10). The paired-end sequencing library was prepared using the TruSeq Nano DNA library prep kit. The Illumina HiSeq platform was used for sequencing the paired-end library, with a read length of 2 × 150 bp and coverage of 850×. Both quantity and quality checks of the amplified library were performed in a Bioanalyzer 2100 (Agilent Technologies) using a high-sensitivity DNA chip per the manufacturer's instructions. The reads generated were filtered using Trimmomatic (v0.30) with a quality value (QV) of >20, and adapters were also removed. Subsequently, the high-quality (4.15 Gb) data were used for assembly. *De novo* assembly of paired-end reads was performed using Velvet v1.2.10. The total number of reads was 28,029,838. The details of the assembled genome are listed in Table 1. An NCBI genome annotation tool was used to annotate the genome and detected a total of 4,393 protein-coding genes with an average size of 945 bp. This genome was found to harbor 75 tRNA and 8 rRNA genes, as predicted by tRNAscan-SE v2.0 (11) and DFAST v1.0.1 (12), respectively. A total of 5 intact prophage regions were identified using the

TABLE 1 Summary of the genome sequence of strain ASBT-1

Assembly or annotation element	Data
Genome size (bp)	4,696,000
No. of contigs	54
No. of scaffolds	50
Scaffold N_{50} (bp)	383,050
Avg scaffold length (bp)	93,920
GC content (%)	50.81
No. of protein-coding genes	4,393
Coding ratio (%)	88.1
Avg protein length (amino acids)	313.9
No. of tRNAs	75
No. of rRNAs	8
No. of CRISPRs	2
No. of intact prophage regions	5

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PHAST tool (13) (last accessed date, 18 September 2018). Two CRISPR-Cas sequences were detected, one by CRISPRFinder (14) (last accessed date, 18 September 2018) and one by Prokka v1.12 (15), respectively. Altogether, as an Indian representative of an *E. coli* ST155 clone, ASBT-1 warrants additional in-depth research on its genomic features, pathotype, and antibiotic resistance profile.

Data availability. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number RWJY00000000 (BioProject number PRJNA509104). The version described in this paper is RWJY01000000, with SRA accession number SRR8480428.

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We declare no conflicts of interest.

REFERENCES

1. Ben Sallem R, Ben Slama K, Rojo-Bezares B, Porres-Osante N, Jouini A, Klibi N, Boudabous A, Sáenz Y, Torres C. 2014. IncI1 plasmids carrying $bla_{CTX-M-1}$ or bla_{CMY-2} genes in Escherichia coli from healthy humans and animals in Tunisia. Microb Drug Resist 20:495–500. https://doi.org/10.1089/mdr.2013.0224.
2. Wang J, Stephan R, Power K, Yan Q, Hächler H, Fanning S. 2014. Nucleotide sequences of 16 transmissible plasmids identified in nine multidrug-resistant Escherichia coli isolates expressing an ESBL phenotype isolated from food-producing animals and healthy humans. J Antimicrob Chemother 69:2658–2668. https://doi.org/10.1093/jac/dku206.
3. Leverstein-van Hall MA, Dierikx CM, Cohen Stuart J, Voets GM, van den Munckhof MP, van Essen-Zandbergen A, Platteel T, Fluit AC, van de Sande-Bruinsma N, Scharinga J, Bonten MJM, Mevius DJ, National ESBL Surveillance Group. 2011. Dutch patients, retail chicken meat and poultry share the same ESBL genes, plasmids and strains. Clin Microbiol Infect 17:873–880. https://doi.org/10.1111/j.1469-0691.2011.03497.x.
4. Castellanos LR, Donado-Godoy P, León M, Clavijo V, Arevalo A, Bernal JF, Timmerman AJ, Mevius DJ, Wagenaar JA, Hordijk J. 2017. High heterogeneity of Escherichia coli sequence types harbouring ESBL/AmpC genes on IncI1 plasmids in the Colombian poultry chain. PLoS One 12:e0170777. https://doi.org/10.1371/journal.pone.0170777.
5. Matamoros S, van Hattem JM, Arcilla MS, Willemse N, Melles DC, Penders J, Vinh TN, Thi Hoa N, COMBAT Consortium, de Jong MD, Schultsz C. 2017. Global phylogenetic analysis of Escherichia coli and plasmids carrying the mcr-1 gene indicates bacterial diversity but plasmid restriction. Sci Rep 7:15364. https://doi.org/10.1038/s41598-017-15539-7.
6. Grall N, Barraud O, Wieder I, Hua A, Perrier M, Babosan A, Gaschet M, Clermont O, Denamur E, Catzeflis F, Decré D, Ploy M-C, Andremont A. 2015. Lack of dissemination of acquired resistance to β-lactams in small wild mammals around an isolated village in the Amazonian forest. Environ Microbiol Rep 7:698–708. https://doi.org/10.1111/1758-2229.12289.
7. Skurnik D, Clermont O, Guillard T, Launay A, Danilchanka O, Pons S, Diancourt L, Lebreton F, Kadlec K, Roux D, Jiang D, Dion S, Aschard H, Denamur M, Cywes-Bentley C, Schwarz S, Tenaillon O, Andremont A, Picard B, Mekalanos J, Brisse S, Denamur E. 2016. Emergence of antimicrobial-resistant Escherichia coli of animal origin spreading in humans. Mol Biol Evol 33:898–914. https://doi.org/10.1093/molbev/msv280.
8. Gomi R, Matsuda T, Matsumura Y, Yamamoto M, Tanaka M, Ichiyama S, Yoneda M. 2017. Whole-genome analysis of antimicrobial-resistant and extraintestinal pathogenic Escherichia coli in river water. Appl Environ Microbiol 83:e02703-16. https://doi.org/10.1128/AEM.02703-16.
9. Marín M, Garcia-Lechuz JM, Alonso P, Villanueva M, Alcalá L, Gimeno M, Cercenado E, Sánchez-Somolinos M, Radice C, Bouza E. 2012. Role of universal 16S rRNA gene PCR and sequencing in diagnosis of prosthetic joint infection. J Clin Microbiol 50:583–589. https://doi.org/10.1128/JCM.00170-11.
10. Park D. 2007. Genomic DNA isolation from different biological materials. Methods Mol Biol 353:3–13. https://doi.org/10.1385/1-59745-229-7:3.
11. Lowe TM, Chan PP. 2016. tRNAscan-SE On-line: integrating search and context for analysis of transfer RNA genes. Nucleic Acids Res 44:W54–W57. https://doi.org/10.1093/nar/gkw413.
12. Tanizawa Y, Fujisawa T, Nakamura Y. 2018. DFAST: a flexible prokaryotic genome annotation pipeline for faster genome publication. Bioinforma 34:1037–1039. https://doi.org/10.1093/bioinformatics/btx713.
13. Zhou Y, Liang Y, Lynch KH, Dennis JJ, Wishart DS. 2011. PHAST: a fast phage search tool. Nucleic Acids Res 39:W347–W352. https://doi.org/10.1093/nar/gkr485.
14. Grissa I, Vergnaud G, Pourcel C. 2007. CRISPRFinder: a Web tool to identify clustered regularly interspaced short palindromic repeats. Nucleic Acids Res 35:W52–W57. https://doi.org/10.1093/nar/gkm360.
15. Seemann T. 2014. Prokka: rapid prokaryotic genome annotation. Bioinformatics 30:2068–2069. https://doi.org/10.1093/bioinformatics/btu153.