



# 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  $\beta$ -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  $2 \times 150$  bp and coverage of  $850\times$ . 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

**Citation** Salim A, Babu P, Mohan K, Moorthy M, Raj D, Kallampillil Thirumeni S, Suresh S, Madhavan A, Nair BG, Chattopadhyay S, Pal S. 2019. Draft genome sequence of an *Escherichia coli* sequence type 155 strain isolated from sewage in Kerala, India. Microbiol Resour Announc 8:e01707-18. <https://doi.org/10.1128/MRA.01707-18>.

**Editor** David Rasko, University of Maryland School of Medicine

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**Received** 18 January 2019

**Accepted** 4 June 2019

**Published** 3 July 2019

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](https://doi.org/10.1093/bioinformatics/btu153) (BioProject number [PRJNA509104](https://doi.org/10.1093/bioinformatics/btu153)). The version described in this paper is RWJY01000000, with SRA accession number [SRR8480428](https://doi.org/10.1093/bioinformatics/btu153).

## ACKNOWLEDGMENTS

This work was supported by the Reinvent the Toilet Challenge (RTTC) award (2014) funded by the Bill & Melinda Gates Foundation–BIRAC (Government of India) (grant number BIRAC/GCI/0067/02/13-RTTC OPP1107707) and School of Biotechnology, Amrita Vishwa Vidyapeetham, Kerala, India. We acknowledge the University Grant Commission (UGC) and Council of Industrial and Scientific Research (CSIR), New Delhi, India, for providing fellowships for the authors.

We declare no conflicts of interest.

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