Draft Genome Sequences of Seven Extended-Spectrum β-Lactamase-Producing *Escherichia coli* Strains Isolated from New Zealand Waterways

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**ABSTRACT** Draft genomes of seven extended-spectrum β-lactamase (ESBL)-producing *Escherichia coli* strains recovered from New Zealand waterways are described. The mean genome size was 5.1 Mb, with 4,724 coding sequences. All genomes contained the ESBL gene *bla*CTX-M, and one carried a plasmid-mediated AmpC gene, *bla*CMY-2. A multidrug-resistant genotype was detected in three isolates.

Extended-spectrum β-lactamase (ESBL)-producing *Escherichia coli* strains are commonly associated with multidrug-resistant urinary tract infections (1, 2). An important pathway for the spread of antimicrobial-resistant bacteria is person-to-person transmission (3), but other transmission pathways, including contaminated waterways, may also be relevant (4–6).

Mixed cellulose ester filters (0.45 μm; Millipore, Germany) from 100-ml samples of water from two storm water drains (Meola Reef Park and Northboro Reserve, Auckland, New Zealand) and one stream (Momutu Stream, Auckland, New Zealand) were enriched in 10 ml of buffered peptone water (BD Difco, Becton, Dickinson, Heidelberg, Germany) and subcultured on MacConkey agar (BD Difco; supplied by Fort Richard Laboratories, Auckland, New Zealand) or ChromESBL (CHROMagar, Paris, France; supplied by Fort Richard Laboratories), and single colonies were purified on Columbia horse blood agar (Fort Richard Laboratories). DNA extractions were performed using the QIAamp DNA minikit (Qiagen, Hilden, Germany); each isolate was cultured on Columbia horse blood agar overnight at 35°C, and approximately three colonies were resuspended in 180 μl ATL buffer according to the manufacturer’s instructions.

Libraries were prepared using the Nextera XT DNA library preparation kit (Illumina, San Diego, CA) and submitted to Otago Genomics Ltd. (University of Otago, Dunedin, New Zealand) for sequencing using the Illumina HiSeq platform with 2 × 125-bp paired-end reads. The read quality was assessed using FastQC (v.0.11.9). The reads were processed using the default settings in the Nullarbor pipeline (v. 2.0.20181010) ([https://github.com/tseemann/nullarbor](https://github.com/tseemann/nullarbor)), in which trimming was carried out using Trimmomatic (v.0.39), assembly was carried out using SKESA (v.2.3.0), and annotation was carried out using Prokka (v.1.13.3) (7–9). Sequencing, assembly, and genome statistics are presented in Table 1.

The mean genome size was 5.1 Mb, with an average GC content of 50.6% and 4,724 coding sequences (CDSs). Antimicrobial resistance (AMR) genes were identified using ResFinder (v.3.1) (10). The seven isolates all contained the ESBL gene *bla*CTX-M, and one isolate also carried a plasmid-mediated AmpC gene, *bla*CMY-2. A multidrug-resistant genotype (AMR genes associated with three or more classes of antibiotics) was detected in the three strains isolated from the Momutu Stream. This study reinforces the need to take a holistic “One Health” approach to understanding the sources and transmission pathways for the community spread of antimicrobial-resistant bacteria.


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\(^a\) ND, not detected.
Data availability. The draft genome assemblies have been deposited in GenBank, and their accession numbers are detailed in Table 1.

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We declare no conflicts of interest.

REFERENCES


