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High-Quality Draft Genome Sequences for Four Drug-Resistant or Outbreak-Associated *Shigella sonnei* Strains Generated with PacBio Sequencing and Whole-Genome Maps

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ABSTRACT Drug-resistant *Shigella sonnei* poses a clinical and public health challenge. We report here the high-quality draft whole-genome sequences of four outbreak-associated *S. sonnei* isolates; three were resistant to two or more antibiotics, and one was resistant to streptomycin only.

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Drug-resistant *Shigella* causes 27,000 infections per year in the United States (1). Symptoms of *Shigella* infection can include mild to severe diarrhea and bloody diarrhea, and in some individuals, infection can progress to serious complications, including reactive arthritis. Outbreaks of drug-resistant *Shigella sonnei* are increasingly occurring in the United States (2–4).

We report here four high-quality draft whole-genome sequence assemblies generated by PacBio sequencing and verified using the strain's whole-genome map (WGM). The sequenced strains were isolated between 2014 and 2015 and are from separate outbreaks in different states.

Shigella genomic DNA was extracted according to the manufacturer's protocol (Archive Pure; 5 Prime, Gaithersburg, MD). The DNA was sheared to 20-kb fragments using needle shearing and were size selected utilizing BluePippin. DNA fragments were used to generate large SMRTbell libraries using the standard library protocols of the Pacific Biosciences DNA template preparation kit (Menlo Park, CA). One single-molecule real-time (SMRT) cell was used to sequence each isolate. Finished libraries were bound to proprietary P6v2 polymerase and sequenced on a PacBio RSII sequencer using C4 chemistry for 360-min movies. Sequence reads were filtered and assembled *de novo* utilizing the PacBio Hierarchical Genome Assembly Process version 3 (5). WGMs were generated according to the OpGen protocol. The sequence order in the resulting PacBio assemblies was verified using restriction enzymes NcoI and AflII and WGMs.

The accession numbers and assembly metrics for each draft genome sequence are listed in Table 1. A single chromosomal contig was generated for each isolate of 51.0% G+C content and 78 to 158× coverage, and was determined to be circular, with overlapping ends that were subsequently trimmed from one end. The plasmid contigs associated with these isolates had 23 to 79× coverage, did not have overlapping ends, and were not closed. These sequences were annotated with the NCBI Prokaryotic Genome Annotation Pipeline (6).

Antimicrobial susceptibility testing was performed by broth microdilution (Sensititre, Cleveland, OH) and used to determine the MICs for 14 antimicrobial agents: ampicillin, amoxicillin-clavulanic acid, azithromycin, cefoxitin, ceftriaxone, chloram-

TABLE 1 Accession numbers and assembly metrics of the four annotated *Shigella* draft whole-genome sequences

Shigella isolate	NCBI accession no.	Genome size (bp)	Associated plasmid size(s) (bp)	Phenotypic resistance or Azm non-wild type[a]
2015AM-1099	CP021144	4,935,567	None	S Su T Cot
2015C-3566	CP022457, CP022458	4,893,408	55,820	S
2015C-3794	CP022455, CP022456	4,818,812	87,791	A Cx Cip Nal S Su T Cot
2015C-3807	CP022459–CP022461	4,794,648	67,988, 66,524	A Azm S Su T Cot

[a]Phenotypic resistance codes: S, streptomycin; Su, sulfisoxazole; T, tetracycline; Cot, trimethoprim-sulfamethoxazole; A, ampicillin; Cx, ceftriaxone; Cip, ciprofloxacin; Nal, nalidixic acid; Azm, azithromycin.

phenicol, ciprofloxacin, gentamicin, meropenem, nalidixic acid, streptomycin, sulfisoxazole, tetracycline, and trimethoprim-sulfamethoxazole (7). Resistance was defined by the Clinical and Laboratory Standards Institute (CLSI) interpretive standards, when available (8). For streptomycin, where no CLSI interpretive criteria for human isolates exist, resistance was defined as ≥64 mg/liter.

Accession number(s). The annotated whole-genome *S. sonnei* sequences have been deposited in DDBJ/ENA/GenBank under the accession numbers CP022455 to CP022461 and CP021144 (see Table 1). The version described in this paper is the first version.

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The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention. The use of trade names is for identification only and does not imply endorsement by the Centers for Disease Control and Prevention or by the U.S. Department of Health and Human Services.

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