Draft Genome Sequences of Ciprofloxacin-Resistant *Salmonella enterica* Strains with Multiple-Antibiotic Resistance, Isolated from Imported Foods

Ashraf A. Khan,a Bijay K. Khajanchi,a Sana A. Khan,a Christopher A. Elkins,b Steven L. Foleya
U.S. Food and Drug Administration, National Center for Toxicological Research, Jefferson, Arkansas, USAa; Division of Molecular Biology, Center for Food Safety and Applied Nutrition (CFSAN), U.S. Food and Drug Administration, Laurel, Maryland, USAb

**ABSTRACT** We report here the draft genome sequences of 15 ciprofloxacin-resistant *Salmonella enterica* strains with resistance to multiple other antibiotics, including aminoglycosides, β-lactams, sulfonamides, tetracycline, and trimethoprim, isolated from different imported foods. Three strains (NCTR75, NCTR281, and NCTR350) showed a high level of ciprofloxacin resistance compared to that of the other isolates. The whole-genome sequencing data provide a better understanding of the antibiotic resistance mechanisms and virulence properties of these isolates.

*Salmonella* spp. are recognized as major foodborne pathogens in humans worldwide (1, 2). In the United States, there are an estimated 800,000 to 4 million *Salmonella* infections annually (1, 2). Each year, these infections result in an estimated 160,000 physician visits, 15,000 hospitalizations, and 400 deaths (3, 4). Ninety-five percent of salmonellosis cases in the United States result from the ingestion of contaminated incompletely cooked foods, such as poultry, beef, eggs, milk, seafood, vegetables, and fruit (2, 5, 6). In the past decade, an increase in antimicrobial drug resistance, including resistance to nalidixic acid, among *Salmonella* spp. has been reported in many countries, particularly in Asia (7–9). Dissemination of antibiotic resistance among pathogenic bacteria has been a concern for public health because of the large quantity of antimicrobials that are used every day for various purposes, from treating bacterial infections in humans and farm animals to aquaculture and cleaning chicken houses. Overuse and/or misuse of antimicrobials facilitates the spread of antibiotic resistance determinants associated with mobile genetic elements. This leads to an increase in antibiotic-resistant populations, including those carrying mutations or deletions that can make bacteria antimicrobial resistant in the presence of selective pressure. The recent spread of a new metallo-β-lactamase gene, *bla*<sub>kem-1</sub>, from east Asian countries to Australia, the United States, and the United Kingdom warrants monitoring antibiotic resistance domestically, as well as internationally, to prevent further dissemination of resistance (10–12).

We sequenced 15 fluoroquinolone-resistant *Salmonella enterica* strains, isolated from a variety of processed or semiprocessed foods imported from different countries, including seafood and spices from Middle Eastern and east Asian countries (Table 1). In addition to fluoroquinolone resistance, these isolates were resistant to multiple antibiotics, including aminoglycosides, β-lactams, sulfonamides, tetracycline, and trimethoprim. Three isolates (NCTR75, NCTR281, and NCTR350) originating from Thailand and Egypt showed resistance to multiple antibiotics, including a high level of resistance to ciprofloxacin and other fluoroquinolones. The genome sequences of these isolates...
will be useful for further understanding the mechanisms of antibiotic resistance and virulence properties.

Genomic DNA was extracted from overnight cultures using the DNeasy blood and tissue kit (Qiagen, Valencia, CA). DNA libraries were constructed by using the Nextera XT library prep kit (Illumina, San Diego, CA, USA) and were then sequenced using a high-output version 2.0 flow cell on an Illumina NextSeq 500 platform. CLC Genomics Workbench version 8.5.1 (Qiagen, Germantown, MD) was used for the trimming and de novo assembly of the paired-end reads.

Rapid Annotations using Subsystems Technology (RAST) (13), the Pathosystems Resource Integration Center (PATRIC) (14), and the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP) (15) were employed to annotate the draft genomes of these strains (Table 1). The average G+C content of these strains is estimated to be approximately 52%, as examined by PATRIC. Table 1 shows the number of contigs, sequence assembly size, coding sequences, and functional coding sequences for the respective strains.

Accession number(s). The draft genome sequences for these 15 Salmonella enterica strains have been deposited at DDBJ/ENA/GenBank under the accession numbers listed in Table 1.

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