



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

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**ABSTRACT** We report here the draft genome sequences of 15 ciprofloxacin-resistant *Salmonella enterica* strains with resistance to multiple other antibiotics, including aminoglycosides,  $\beta$ -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- $\beta$ -lactamase gene, *bla*<sub>NDM-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,  $\beta$ -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

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**TABLE 1** Summary of genome sequence analysis of *Salmonella enterica* strains isolated from different imported food sources

Strain	Serovar	Location/yr of isolation	Isolation source	No. of contigs	Assembly size (bp)	Total no. of CDSs <sup>a</sup>	No. of CDS genes	Accession no.
NCTR30	Schwarzengrund	Taiwan/2001	Tenderized squid roll	103	4,843,779	4902	4,721	NQYI00000000
NCTR75	Schwarzengrund	Thailand/2001	Dehydrated small chili without stem	204	4,805,014	4912	4,695	NQWP00000000
NCTR144	Aberdeen	Vietnam/2001	Frozen featherback fish meat	193	5,123,196	5364	5,100	NQWQ00000000
NCTR148	Kentucky	Pakistan/2001	Coriander and cumin mix	72	4,825,672	4850	4,673	NQWR00000000
NCTR177	Albany	Taiwan/2001	Frozen whole tilapia	89	4,849,875	4892	4,721	NQWS00000000
NCTR281	Kentucky	Egypt/2004	Okra	247	4,873,899	4933	4,734	NQWT00000000
NCTR341	Blockley	Egypt/2005	Basil	167	4,834,914	4882	4,730	NQWU00000000
NCTR350	Typhimurium	Egypt/2005	Ground cumin seeds	124	4,844,788	4891	4,697	NQWV00000000
NCTR361	Blockley	Egypt/2005	Extra-fancy basil	88	4,814,121	4841	4,695	NQW000000000
NCTR380	Enteritidis	Bangladesh/2005	Frozen raw headless shell shrimp	974	5,100,757	5791	5,319	NQWN00000000
NCTR409	Virchow	India/2005	Turmeric powder	378	4,787,146	5009	4,759	NQWM00000000
NCTR462	Anatum	Vietnam/2006	Food	228	4,911,797	5013	4,830	NQWL00000000
NCTR487	Schwarzengrund	Pakistan/2007	Barberry bark	162	4,653,404	4707	4,525	NQWK00000000
NCTR488	Hadar	Pakistan/2006	Barberry bark	141	4,724,356	4767	4,603	NQWJ00000000
NCTR730	Braenderup	Vietnam/2004	Frozen whole walking yellow fish	558	4,897,414	5159	4,913	NQWW00000000

<sup>a</sup>CDS, coding sequence.

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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