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# Draft Genome Sequences of *Salmonella enterica* Isolates Containing Incompatibility Group I1 Plasmids from Swine, Poultry, and Human Sources

**Pravin R. Kaldhone,[a,b] Bijay K. Khajanchi,[a] Jing Han,[a] Rajesh Nayak,[a] Steven C. Ricke,[b] Steven L. Foley[a]**

U.S. Food and Drug Administration, National Center for Toxicological Research, Jefferson, Arkansas, USA[a]; Center for Food Safety, Department of Food Science, University of Arkansas, Fayetteville, Arkansas, USA[b]

**ABSTRACT** The draft genome sequences of eight *Salmonella enterica* isolates from various sources were evaluated for the influence of incompatibility group I1 (IncI1) plasmids on virulence. Strains SE142, SE143, SE144, and SE146 originated from swine, SE36N and SE89N from poultry-related sources, and SE991 and SE1148 from human patients.

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Address correspondence to Jing Han, jing.han1@fda.hhs.gov, or Steven L. Foley, steven.foley@fda.hhs.gov.

*Salmonella enterica* is one of the top five bacterial pathogens contributing to foodborne illnesses. *Salmonella* is also a leading foodborne pathogen associated with hospitalizations and deaths in the United States (1, 2). Food products originating from diverse sources like poultry, swine, and cattle are commonly associated with disease outbreaks caused by *Salmonella enterica* (2). Some serotypes of *Salmonella*, including Enteritidis, Typhimurium, and Heidelberg, are more prevalent as foodborne pathogens than other serotypes, such as Kentucky (3). Isolates containing certain mobile genetic elements, such as plasmids, have been associated with clinical manifestations of *Salmonella* infection (4). Plasmids encode genes responsible for antimicrobial resistance and virulence, which may have clinical significance associated with severe manifestations of diseases (5). Incompatibility group I1 (IncI1) plasmids have been reported to carry genes related to antimicrobial resistance and virulence (6).

Eight strains of *Salmonella enterica* containing IncI1 plasmids were sequenced (Table 1). Four of these strains were isolated from swine, two from poultry-related sources, and two from human patients. Previous studies showed that SE1148 and SE146 carried IncI1 plasmids and antimicrobial resistance genes (5). In addition to resistance genes, SE146 also contained an IncX4 plasmid which encodes a VirB/D4 type 4 secretion system that is likely involved in the increased virulence potential of this strain (7). Strains SE142, SE143, SE144, and SE146 were found to contain one or more plasmids and were resistant to commonly used antimicrobial agents (8). Overall analysis of the whole-genome sequences of these strains will improve our current understanding of the potential role of IncI1 plasmids in the pathogenicity of *Salmonella enterica* isolated from various foods and hosts.

To conduct the sequencing, total DNA was extracted using a DNeasy blood and tissue kit (Qiagen, Valencia, CA, USA). Nextera XT DNA sample kits (Illumina, San Diego, CA, USA) were used to construct a DNA library. Sequencing reactions were carried out at the DNA Sequencing Core at the University of Arkansas for Medical Sciences (UAMS) (Little Rock, AR, USA) and the Division of Microbiology, National Center for Toxicological Research (NCTR) (Jefferson, AR, USA) on an Illumina MiSeq instrument to generate 2 × 250 (UAMS) or 2 × 300 (NCTR) paired-end reads (9). Trimming and *de novo* assembly of the paired-end reads was performed using CLC

**TABLE 1** Summary of the genome sequence analysis of *Salmonella enterica* strains containing IncI1 plasmids

| Strain | Serovar | Source | Location, yr of isolation | No. of contigs | Assembly size (bp) | G+C content (%) | No. of CDS[a] | No. of functional proteins | Accession no. |
|---|---|---|---|---|---|---|---|---|---|
| SE142 | Heidelberg | Swine | Indiana, 2002 | 205 | 5,197,369 | 51.85 | 5,450 | 4,683 | NPFC00000000 |
| SE143 | Heidelberg | Swine | Minnesota, 2002 | 306 | 5,361,922 | 51.69 | 5,718 | 4,779 | NPEL00000000 |
| SE144 | Heidelberg | Swine | Minnesota, 2002 | 111 | 5,279,737 | 51.82 | 5,488 | 4,673 | NPEQ00000000 |
| SE146 | Heidelberg | Swine | Minnesota, 2002 | 221 | 5,356,597 | 51.59 | 5,704 | 4,801 | NPEM00000000 |
| SE36N | Typhimurium | Chicken | West Virginia, 2000 | 158 | 5,160,965 | 51.90 | 5,358 | 4,705 | NPER00000000 |
| SE89N | Kentucky | Poultry house water | West Virginia, 2000 | 120 | 5,146,652 | 51.69 | 5,799 | 4,811 | NPES00000000 |
| SE991 | Heidelberg | Human feces | Arkansas, 2009 | 98 | 5,053,493 | 51.82 | 5,161 | 4,493 | NPEP00000000 |
| SE1148 | Heidelberg | Human blood | Wisconsin, 2007 | 166 | 4,867,737 | 52.17 | 4,995 | 4,435 | NPEO00000000 |

[a]CDS, coding sequences.

Genomics Workbench versions 8.5.1 and 9 (Qiagen, Germantown, MD, USA). The Rapid Annotation using Subsystem Technology (RAST) server (10), the Pathosystems Resource Integration Center (PATRIC) (11), and the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP) (12) were employed to annotate the draft genomes of these strains (Table 1). The average G+C content of these strains is estimated to be 51.81%, as determined by PATRIC. Table 1 lists individual G+C content (%) and numbers of contigs, coding sequences, and functional proteins for respective strains.

**Accession number(s).** This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession numbers listed in Table 1.

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