Draft Genome Sequences of Four *Salmonella enterica* Strains Isolated from Turkey-Associated Sources

Bijay K. Khajanchi, Jing Han, Kuppan Gokulan, Shaohua Zhao, Allen Gies, Steven L. Foley

U.S. Food and Drug Administration, National Center for Toxological Research, Jefferson, Arkansas, USA; U.S. Food and Drug Administration, Center for Veterinary Medicine, Laurel, Maryland, USA; Department of Microbiology and Immunology, University of Arkansas for Medical Sciences, Little Rock, Arkansas, USA

We report the draft genomes of four *Salmonella enterica* isolates evaluated for the contribution of plasmids to virulence. Strains SE163A, SE696A, and SE710A carry plasmids demonstrated to facilitate plasmid-associated virulence, while SE819 is less virulent and has been used as a recipient for conjugation experiments to assess plasmid-encoded virulence mechanisms.

*Salmonella enterica* has been identified as the source of multiple outbreaks associated with meat and poultry products over the last few years in the United States and other countries (1). In the United States alone, it is estimated that more than 1 million *Salmonella* infections occur annually, resulting in nearly 20,000 hospitalizations and 400 deaths (2). Some *S. enterica* serovars cause more invasive infections than others; for example, a previous study demonstrated that the Heidelberg and Typhimurium strains were more invasive, responsible for 13% and 6% of infections, respectively, compared to the other serovars (3). Many *Salmonella* strains carry plasmids that harbor genes that contribute to increased virulence and antimicrobial resistance (4, 5). Previous studies in our laboratory characterized the impact of plasmids in *S. enterica* on antimicrobial resistance and virulence (4, 5).

We sequenced four *S. enterica* strains designated SE163A, SE696A, SE710A, and SE819, isolated from turkey-associated sources. SE163A and SE696A are virulent strains that possess plasmids including incompatibility group (Inc) FIB, IncA/C, and IncX4 (VirB/D4 type 4 secretion system–encoding plasmid) that carry virulence and/or antimicrobial resistance-associated genetic factors (5, 6). SE819 is a less virulent strain that lacks these virulence and antimicrobial resistance plasmids and has served as a recipient strain for studies evaluating the contribution of plasmids to antimicrobial resistance and virulence (4, 6, 7). Studies have demonstrated that genetic factors encoded by these transmissible SE163A- and SE696A-associated plasmids contribute to antibiotic resistance and the virulence in *Salmonella* species (6–8). SE710A also contains IncFIB, IncA/C, and IncX4 plasmids; however, contribution of these plasmids in virulence has not been examined for this isolate. Genome analysis of these particular *S. enterica* strains will be beneficial to our future understanding of the role of plasmid-encoded factors that contribute to virulence and antimicrobial resistance.

Genomic DNA was extracted using a DNeasy blood and tissue kit (Qiagen, Valencia, CA, USA) and sequenced by the DNA Sequencing Core Facility at the University of Arkansas for Medical Sciences (UAMS; Little Rock, AR, USA). The DNA library was constructed with a Nextera XT DNA sample prep kit according to the manufacturer's protocol (Illumina, San Diego, CA, USA), and sequencing was performed using the Illumina MiSeq with 2 × 250 paired-end reads. CLC Genomics Workbench version 8.5.1 (Qiagen, Germantown, MD, USA) was used for the trimming and *de novo* assembly of the paired-end reads.

Draft genomes of these four *S. enterica* strains were annotated using the Rapid Annotation using Subsystem Technology (RAST) server (9), the Pathosystems Resource Integration Center (PATRIC) (10), and the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (Table 1). The G+C content for these strains is identical, with an estimate of 52.1%. Annotation using PATRIC (10) revealed that strain SE163A contains 5,448 coding sequences, in which 4,637 encode functional proteins, while 811 encode hypothetical proteins. Strain SE696A contains 5,296 coding sequences, in which 4,584 encode functional proteins and 712 encode hypothetical proteins. Strain SE710A possesses 5,337 coding sequences, in which 4,626 proteins have functional assignments and 711 encode as hypothetical. Strain SE819 contains 5,103 cod-

| Strain | Location, yr | No. of contigs | Assembly size (bp) | G+C content (%) | No. of rRNAs | No. of tRNAs | Accession no. |
|--------|--------------|----------------|-------------------|----------------|--------------|--------------|---------------|
| SE163A | Ohio, 2002   | 257            | 5,202,941         | 52.1           | 7            | 74           | LSZJ00000000  |
| SE696A | Midwest United States, 2000 | 230 | 5,096,557 | 52.1 | 16 | 78 | LXHA00000000  |
| SE710A | North Dakota, 1992 | 318 | 5,100,225 | 52.1 | 8 | 78 | LXGZ00000000  |
| SE819  | Maryland, 2002 | 233 | 4,914,824 | 52.1 | 11 | 82 | LSZE00000000  |
ing regions, in which 4,450 encode functional proteins and 653 are assigned as hypothetical proteins.

**Accession number(s).** The genome sequences of SE163A, SE696A, SE710A, and SE819 were deposited in GenBank under the accession numbers shown in Table 1.

**ACKNOWLEDGMENTS**

The research project and B.K.K. are supported by the FDA Commissioner’s Fellowship Program. The Sequencing Facility is supported in part by grants from NIH to UAMS’s Translational Research Institute (UL1TR000039) and the Center for Microbial Pathogenesis and Host Inflammatory Responses (P20GM103625). The opinions expressed in this manuscript are solely the responsibility of the authors and do not necessarily represent the official views and policy of the U.S. Food and Drug Administration or National Institutes of Health. Reference to any commercial materials, equipment, or process does not in any way constitute approval, endorsement, or recommendation by the Food and Drug Administration.

**FUNDING INFORMATION**

This work, including the efforts of Steven L. Foley, Bijay K. Khajanchi, Jing Han, Kuppan Gokulan, Shaohua Zhao, and Allen Gies, was funded by HHS | U.S. Food and Drug Administration (FDA) (E0759601).

**REFERENCES**

1. Folster JP, Pecic G, Rickert R, Taylor J, Zhao S, Fedorka-Cray PJ, Whichard J, McDermott P. 2012. Characterization of multidrug-resistant *Salmonella enterica* serovar Heidelberg from a ground turkey-associated outbreak in the United States in 2011. Antimicrob Agents Chemother 56:3465–3466. http://dx.doi.org/10.1128/AAC.00201-12.

2. Scallan E, Hoekstra RM, Angulo FJ, Tauxe RV, Widdowson MA, Roy SL, Jones JL, Griffin PM. 2011. Foodborne illness acquired in the United States—major pathogens. Emerg Infect Dis 17:7–15. http://dx.doi.org/10.3201/eid1701.P11101.

3. Jones TF, Ingram LA, Geslak PR, Vugia DJ, Tobin-D’Angelo M, Hurd S, Medus C, Cronquist A, Angulo FJ. 2008. Salmonellosis outcomes differ substantially by serotype. J Infect Dis 198:109–114. http://dx.doi.org/10.1086/588823.

4. Han J, Lynne AM, David DE, Tang H, Xu J, Nayak R, Kaldhone P, Logue CM, Foley SL. 2012. DNA sequence analysis of plasmids from multidrug resistant *Salmonella enterica* serotype Heidelberg isolates. PLoS One 7:e51160. http://dx.doi.org/10.1371/journal.pone.0051160.

5. Han J, Gokulan K, Barnette D, Khare S, Rooney AW, Deck J, Nayak R, Stefanova R, Hart ME, Foley SL. 2013. Evaluation of virulence and antimicrobial resistance in *Salmonella enterica* serovar Enteritidis isolates from humans and chicken- and egg-associated sources. Foodborne Pathog Dis 10:1008–1015. http://dx.doi.org/10.1089/fpd.2013.1518.

6. Gokulan K, Khare S, Rooney AW, Han J, Lynne AM, Foley SL. 2013. Impact of plasmids, including those encoding VirB/D4 type IV secretion systems, on *Salmonella enterica* serovar Heidelberg virulence in macrophages and epithelial cells. PLoS One 8:e77866. http://dx.doi.org/10.1371/journal.pone.0077866.

7. Kaldhone P, Nayak R, Lynne AM, David DE, McDermott PF, Logue CM, Foley SL. 2008. Characterization of *Salmonella enterica* serovar Heidelberg from turkey-associated sources. Appl Environ Microbiol 74:5038–5046. http://dx.doi.org/10.1128/AEM.00409-08.

8. Johnson TJ, Thorsness JL, Anderson CP, Lynne AM, Foley SL, Han J, Fricke WF, McDermott PF, White DG, Khatri M, Stall AL, Flores C, Singer RS. 2010. Horizontal gene transfer of a CoV plasmid has resulted in a dominant avian clonal type of *Salmonella enterica* serovar Kentucky. PLoS One 5:e15524. http://dx.doi.org/10.1371/journal.pone.0015524.

9. Aziz RK, Bartels D, Best AA, Dejongh M, Disz T, Edwards RA, Formisano K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil JK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, von Stein V, Wilke A, Zagnitko O. 2008. The RAST server: rapid annotations using subsystems technology. BMC Genomics 9:75. http://dx.doi.org/10.1186/1471-2164-9-75.

10. Wattam AR, Abraham D, Dalay O, Disz TL, Driscoll T, Gabbard JL, Gillespie JG, Gough R, Hix D, Kenyon R, Machi D, Mao C, Nordberg EK, Olson R, Overbeek R, Pusch GD, Shukla M, Schulman J, Stevens RL, Sullivan DE, Vonstein V, Warren A, Will R, Wilson MJ, Yoo HS, Zhang C, Zhang Y, Sobral BW. 2014. PATRIC, the bacterial bioinformatics database and analysis resource. Nucleic Acids Res 42:D581–D591. http://dx.doi.org/10.1093/nar/gkt1099.