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PROKARYOTES

Draft Genome Sequences of *Salmonella enterica* Serovar Enteritidis and Kentucky Isolates from Retail Poultry Sources

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ABSTRACT The draft genome sequences of four *Salmonella enterica* serovar Enteritidis and Kentucky isolates were evaluated for biofilm formation and antibiotic resistance. The *Salmonella* serovar Kentucky strains CFS84 and CFS85 and *Salmonella* serovar Enteritidis strains CFS86 and CFS87 were isolated from retail poultry sources in Arkansas.

Salmonella enterica remains one of the most common foodborne pathogens causing illnesses leading to numerous hospitalizations and causing millions of dollars in health care costs and productivity losses (1, 2). Within the food industry, *Salmonella* spp. have been shown to possess the ability to form biofilms on processing equipment (3, 4). This ability can confer resistance to disinfection and allow bacteria to persist over time and serve as a reservoir for future contamination (5). *Salmonella enterica* serovar Enteritidis is one of the primary serovars associated with human illnesses in the United States and is often associated with the consumption of contaminated poultry products (6). *S. enterica* serovar Kentucky has been identified as one of the more commonly isolated serovars from poultry production and often possesses a multidrug resistance phenotype (6). Although *S.* Kentucky has been affiliated with fewer hospitalizations than other *Salmonella* serovars, it has demonstrated the ability to obtain and spread plasmids that contribute to increased virulence and colonization in poultry (7). These abilities could become problematic if the strains are allowed to persist in processing and storage environments.

Four strains of *S. enterica* isolated from retail poultry carcasses from Arkansas were sequenced (Table 1) (8). Of these, two (CFS84 and CFS85) belonged to serovar Kentucky and two to serovar Enteritidis (CFS86 and CFS87). Phenotypic testing of the *S.* Enteritidis strains showed wild-type morphologies and biofilm growth, while the *S.* Kentucky strains exhibited morphologies and growth associated with increased extracellular matrix component production (our unpublished data). All strains were previously found to exhibit resistance to multiple antimicrobial agents, with each strain showing resistance to sulfisoxazole and novobiocin. Strain CFS84 demonstrated additional resistance to neomycin, and CFS86 encoded resistance to ampicillin and nalidixic acid as well. Both *S.* Kentucky strains were detected to carry plasmids identified as incompatibility type I1 (IncI1), while both *S.* Enteritidis strains carried IncFIIA plasmids (8). Analysis of the genome sequences may be useful in identifying mitigation strategies to control *Salmonella* spp. found in retail environments.

To carry out whole-genome sequencing, total bacterial DNA was extracted using a DNeasy blood and tissue kit (Qiagen, Valencia, CA, USA). DNA libraries were constructed using the Nextera XT DNA sample kits (Illumina, San Diego, CA, USA). Sequencing reactions were carried out on an Illumina MiSeq instrument to generate 2 × 300 paired-end reads (9). Trimming and *de novo* assembly were performed using CLC Genomics Workbench version 9 (Qiagen, Germantown, MD, USA). Annotation of the

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TABLE 1 Summary of the genome sequence analyses of *Salmonella enterica* strains from poultry in Arkansas

Strain	Serovar	No. of contigs	Assembly size (bp)	G+C content (%)	No. of CDSs[a]	No. of functional proteins	GenBank accession no.
CFS84	Kentucky	232	4,935,761	51.99	5,081	4,293	PHUN00000000
CFS85	Kentucky	151	4,908,583	51.98	4,987	4,230	PHUO00000000
CFS86	Enteritidis	128	4,665,166	52.13	4,724	4,159	PHUP00000000
CFS87	Enteritidis	95	4,656,278	52.14	4,705	4,136	PIJU00000000

[a]CDSs, coding sequences.

draft genomes was done using Rapid Annotations using Subsystems Technology (RAST) (10), Pathosystems Resource Integration Center (PATRIC) (11), and the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP) (12) (Table 1). Table 1 lists the numbers of contigs, predicted coding sequences, and functional proteins, as well as the G+C content for each of the sequenced 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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