



Complete Genome Sequences of Five *Salmonella enterica* Strains Used in Inoculation Cocktails in Low-Moisture Food Storage Studies

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ABSTRACT Survival kinetics of *Salmonella enterica* have been previously studied using an inoculum cocktail composed of different strains that have been associated with low-moisture foods. Here, we report the closed genome sequences of five strains of *Salmonella enterica* that are commonly used in these storage studies.

The incidence of salmonellosis associated with dry food products has been increasing in recent years. An aspect of public health concern is the ability of *Salmonella* spp. to survive on these foods (nuts, black pepper, and spices) in a low-moisture environment. Numerous studies on the survival of *Salmonella enterica* in dried foods have previously been published (1–3) using a cocktail of different strains. Here, we report the complete closed genome sequences of 5 strains commonly used in these studies, *S. enterica* serotype Anatum CFSAN076215 (strain 6802), isolated from peanuts; *S. enterica* serotype Enteritidis CFSAN076214 (strain ATCC BAA-1045), isolated from almonds; *S. enterica* serotype Oranienburg CFSAN076211 (strain 1839), isolated from pecans; *S. enterica* serotype Tennessee CFSAN076210 (strain K4643), isolated from peanut butter; and *S. enterica* serotype Mbandaka CFSAN076213 (strain 688538), isolated from tahini.

The isolates were cultured in Trypticase soy broth (Becton, Dickinson, Franklin Lakes, NJ, USA) overnight at 37°C. The genomic DNA was isolated using the DNeasy blood and tissue kit (Qiagen, Inc., Valencia, CA, USA). A single SMRTbell 20-kb library was prepared according to the 20-kb PacBio sample preparation protocol using the BluePippin size-selection system (Sage Science, Beverly, MA, USA). Each isolate was sequenced based on previously reported procedures on the PacBio RS II platform (Pacific Biosciences, Menlo Park, CA, USA) using a single small-molecule real-time (SMRT) cell (4). The sequencing statistics for each isolate can be found in Table 1. The genomes were *de novo* assembled using the Hierarchical Genome Assembly Process version 3.0 using default settings. The assembled sequences were annotated using the NCBI Prokaryotic Genomes Annotation Pipeline (PGAP) and have been deposited at DDBJ/EMBL/GenBank. The *S. Anatum* (CFSAN076215) chromosome size was 4,689,440 bp, with a G+C content of 52.1%, and the plasmid size was 104,123 bp, with 50.5% G+C content. The plasmid (pCFSAN076215) showed two toxin-antitoxin (TA) modules (*ccdA-ccdB* and *higA-2-higB-2*). The *ccdA-ccdB* TA module can lead to the formation of persister cells if induced by environmental stress. (5). The *S. Oranienburg* (CFSAN076211) genome size was 4,651,134 bp, with 52.1% G+C content. The *S. Tennessee* (CFSAN076210) chromosome size was 4,834,056 bp, with 52.2% G+C content, and the plasmid was 109,917 bp, with 50.7% G+C content. The plasmid (pCFSAN076210) has the oxidative stress gene *grxA*, which can be upregulated in response to preadaptation to cold stress and may

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TABLE 1 PacBio RS sequencing statistics

Isolate name	Coverage (×)	Total no. of reads	Avg read length (bp)	N ₅₀ read length (bp)
CFSAN076210	169	90,179	12,732	16,680
CFSAN076211	115	62,043	11,025	20,045
CFSAN076213	120	69,380	10,357	18,170
CFSAN076214	162	77,741	12,017	16,680
CFSAN076215	182	77,545	13,499	26,714

provide increased protection against hydrogen peroxide (6). The *S. Enteritidis* (CFSAN076214) chromosome size was 4,668,874 bp, with 52.0% G+C content; plasmid 1 was 59,261 bp, with 42.1% G+C content, and plasmid 2 was 56,636 bp, with 51.6% G+C content. Plasmid 1 (pCFSAN076214_1) has *vir* genes associated with the type IV secretion system. Plasmid 2 (pCFSAN076214_2) has virulence genes *spvA*, *spvB*, *spvC*, *spvD*, and *spvR*, which have been shown to express lethal disease in BALB/c mice (7). The *S. Mbandaka* (CFSAN076213) genome size was 4,709,669 bp, with 52.3% G+C content.

Data availability. The sequences have been deposited in GenBank under the following accession numbers (SRA accession numbers): [CP033338](#) and [CP033339](#) ([SRR8217764](#)) for *S. Anatum*, [CP033344](#) ([SRR8170031](#)) for *S. Oranienburg*, [CP033345](#) and [CP033346](#) ([SRR8170030](#)) for *S. Tennessee*, [CP033340](#), [CP033341](#), and [CP033342](#) ([SRR8170032](#)) for *S. Enteritidis*, and [CP033343](#) ([SRR8170034](#)) for *S. Mbandaka*.

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