



Complete Genome Sequence of a *Salmonella enterica* subsp. *enterica* Serovar Tennessee Strain from Tahini

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ABSTRACT *Salmonella* sp. infections are associated with contaminated low-moisture foods (with high fat content) with increasing frequency. Here, we report the complete genome sequence of *Salmonella enterica* subsp. *enterica* serovar Tennessee, which was isolated from tahini (a paste made from ground sesame seeds) purchased at a local retailer in Berlin, Germany.

Recent transnational outbreaks of various *Salmonella* serovars associated with tahini sesame paste highlight the issue of *Salmonella* contamination of processed sesame food (1, 2). In a study analyzing nine different tahini products purchased in Berlin, Germany, we found one that was positive for *Salmonella*, and we isolated (3) *Salmonella enterica* subsp. *enterica* Tennessee. Briefly, 25 g of tahini was mixed with 225 mL buffered peptone water and incubated for 19 h at 37°C. On modified semisolid Rappaport-Vassiliadis (MSRV) agar, 100 μ l was incubated for 24 h at 41.5°C. Cell material from MSRV agar was plated on xylose-lysine-desoxycholate (XLD) agar and incubated for 22 h at 37°C. Black colonies were confirmed as *Salmonella* spp. using matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) (Bruker Daltonics). Serological typing was performed according to the White-Kaufmann-Le Minor scheme using standard reagents (Sifin Diagnostics GmbH, Berlin, Germany) (4).

For isolation of genomic DNA (gDNA) used for both short-read Illumina sequencing and long-read Oxford Nanopore Technologies (ONT) sequencing, one single colony was enriched in lysogeny broth for 18 h at 37 \pm 1°C. The PureLink gDNA minikit (Invitrogen, Carlsbad, CA, USA) was used for gDNA isolation.

The library for short-read sequencing was prepared using the DNA preparation (M) tagmentation kit (Illumina, San Diego, CA, USA). The library was sequenced on the Illumina NextSeq benchtop sequencer using the NextSeq 500/550 midoutput kit v2.5 (300 cycles; Illumina) in 2 \times 149-bp cycles. The short-read sequence data were trimmed using fastp v0.19.5 (5). Trimming resulted in 1,666,364 high-quality reads (82.8% [quality scores of \geq Q30]).

The library for the MinION platform (ONT, Oxford, UK) was prepared using the rapid barcoding kit SQK-RBK004 (ONT). The DNA isolation and sequencing kits were used according to the instructions of the manufacturer.

The MinION library was sequenced for 24 h on an ONT MinION Mk1C device (MinKNOW v20.03.5, including Guppy base caller v3.4.8) using a Flongle adapter and a FLO-FLG001 Flongle flow cell. The reads obtained were trimmed using Porechop v0.2.3 (<https://github.com/rwick/Porechop>), filtered using NanoFilt v2.7.1, and quality checked using NanoStat v1.4.0 (6). Trimming and filtering resulted in 30,938 reads, with a read N_{50} value of 10,167 bp and 71.6% of bases reaching quality scores above 10.

To assemble and circularize the genome sequence, short- and long-read data sets were subjected to the hybrid assembler Unicycler v0.4.8 including Pilon v1.23 (7–9).

Editor Vincent Bruno, University of Maryland School of Medicine

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The authors declare no conflict of interest.

Received 28 April 2022

Accepted 14 July 2022

Published 27 July 2022

TABLE 1 Summary of determined genetic features of *S. Tennessee* strain 21-SA00318-0

Feature ^a	Result(s)	Tool(s), database(s), and options ^b
Serovar	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Tennessee	Sistr_cmd v1.1.1 (20)
MLST	ST319	MLST v2.19.0, PubMLST database (18, 19)
Chromosome size (bp)	4,825,110	
Plasmid type	ColRNAI_1 plasmid	ABRicate v1.0.1, Center for Genomic Epidemiology database, PlasmidFinder, Platon v1.4.0 (mode: accuracy, -verbose) (14–16)
Plasmid size (bp)	3,967	
Virulence determinants		SPIFinder v2.0, ABRicate v1.0.1, VFDB (minicov/minid: 80) (16, 17, 21)
No. of SPIs	7 (SPI-1 to SPI-5, SPI-8, and SPI-9)	
No. of virulence genes	102	
Virulence genes located on SPIs ^c	SPI-1: <i>invH</i> , <i>invFGEABCIJ</i> , <i>spaOPQRS</i> , <i>sicA</i> , <i>sipBCDA</i> , <i>sicP</i> , <i>sptP</i> , <i>prgHIJK</i> , <i>orgABC</i> , and <i>avrA</i> ; SPI-2: <i>ssaUTSRQPONVMLK</i> , <i>ssaJIHG</i> , <i>sseGF</i> , <i>sscB</i> , <i>sseEDC</i> , <i>sscA</i> , <i>sseBA</i> , and <i>ssaEDCB</i> ; SPI-3: <i>mgtCB</i> and <i>misL</i> ; SPI-5: <i>sopB</i> and <i>pipB</i>	
Other virulence genes	Genes associated with, e.g., adhesion (e.g., <i>fim</i> and <i>lpf</i>), curli (<i>csg</i>), effectors (e.g., <i>sif</i> , <i>slrP</i> , <i>sop</i> , <i>sse</i> , and <i>ste</i>), iron transport (<i>ent</i> and <i>fep</i>), and resistance (<i>mig-14</i>)	
Antibiotic resistance factors	<i>mdsAB</i>	NCBI AMRFinderPlus v3.10.1 (-nucleotide -O Salmonella -ident_min -1 coverage_min 0.5) (12, 13)
Stress resistance factors	<i>golST</i>	NCBI AMRFinderPlus v3.10.1 (-nucleotide -O Salmonella -ident_min -1 coverage_min 0.5) (12, 13)

^a The virulence and resistance genes listed here were located on the chromosome. MLST, multilocus sequence typing.

^b Default parameters were used for all tools unless otherwise specified.

^c Contribution was confirmed by visualization of the chromosome annotation in Geneious Prime v2020.2.2 (22).

The assembly resulted in a circular bacterial chromosome (start gene, *dnaA*) and a circular ColRNAI_1 plasmid sequence (Table 1). The overall G+C content of the genome sequence was 52.2%. For annotation, NCBI PGAP v6.0 was used (10).

For further analysis of the genome sequence, the BakCharak pipeline v2.1.0 was used (11). The pipeline includes modules (tools, databases, and options) (Table 1) for identifying antimicrobial resistance genes, plasmids, and virulence factors and for predicting sequence types (STs) and serotypes (12–20). For screening of *Salmonella* pathogenicity islands (SPIs), SPIFinder2.0 was used (21, 22). Default parameters were used for all tools unless otherwise specified.

Data availability. Sequencing raw reads were deposited in the NCBI Sequence Read Archive (SRA) (accession numbers [SRR17858527](https://www.ncbi.nlm.nih.gov/sra/SRR17858527) [ONT data] and [SRR17858528](https://www.ncbi.nlm.nih.gov/sra/SRR17858528) [Illumina data]). The complete genome sequence of 21-SA00318-0 is available at NCBI (GenBank accession numbers [CP091878](https://www.ncbi.nlm.nih.gov/genbank/CP091878) [chromosome], [CP091879](https://www.ncbi.nlm.nih.gov/genbank/CP091879) [plasmid], and [GCF_022162985.1](https://www.ncbi.nlm.nih.gov/genbank/GCF_022162985.1) [latest]). All data are encompassed under BioProject accession number [PRJNA802760](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA802760).

ACKNOWLEDGMENTS

This work was supported by the German Federal Institute for Risk Assessment (BfR) (research project number 42-LOM). O.S. was a recipient of a study scholarship of the Rosa-Luxemburg-Stiftung.

We gratefully thank Angelina Bloch and Katharina Thomas for excellent technical support.

We declare no conflicts of interest.

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