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GENOME SEQUENCES

Draft Genome Sequence of a *Salmonella enterica* subsp. *enterica* Serotype Choleraesuis Strain Isolated from the Pulp of Muskmelons

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ABSTRACT *Salmonella enterica* subsp. *enterica* serotype Choleraesuis is a foodborne pathogen with zoonotic potential. We report the draft genome sequence and a closed plasmid sequence from a plant-internalized *S. Choleraesuis* strain that was isolated from the pulp of a Spanish Galia melon purchased from a German supermarket in 2015.

Salmonella enterica subsp. *enterica* serotype Choleraesuis bacteria are host adapted to pigs. However, human infections do occur and typically result in invasive disease (1). Transmission to humans might result from fecal contamination of plants that are grown close to the ground and consumed raw, such as salad, spinach, or melons (2–4). Several foodborne outbreaks caused by melons contaminated with *Salmonella* spp. have been reported (5, 6), and internalization into plants has been described for *Salmonella* spp. (7–9). This may offer the pathogen a growth advantage and therefore increase the risk to consumers. Strain 11-Galia-2015 was isolated from the pulp of a Galia melon (8) and serotyped at the German Federal Institute for Risk Assessment (BfR). Here, we present the draft whole-genome sequence of this strain.

Genomic DNA was extracted from a liquid culture grown in LB medium using the PureLink genomic DNA minikit (Themo Fisher Scientific, Germany). A sequencing library was created with the Nextera DNA Flex library prep kit (Illumina, USA) and sequenced using 2 × 201-bp format on a MiSeq benchtop sequencer with v3 600-cycle chemistry (Illumina), resulting in 1,585,934 total reads and 630-fold coverage. The generated paired-end reads (Q30 base fraction, 0.95) were trimmed and quality controlled using fastp v0.19.5 (10) with default parameters (except --length_required 15) and *de novo* assembled using Shovill v1.1.0 (10, 11) using SPAdes as the assembly method (with the options --noreadcorr --depth 100 and otherwise default parameters). The minimal contig size was set to 200 bp. Annotation of *S. Choleraesuis* with the antigenic profile 7:c:1,5 (SeqSero v1.2 Server [11]) was performed using PGAP (12). However, serological subtyping according to the White-Kauffmann-Le Minor scheme (13) resulted in the antigenic profile 6,7:−:1,5.

The assembled *S. Choleraesuis* genome sequence comprised 79 contigs with a total length of 4,723,419 bp, an N_{50} value of 216,747 bp, and 52.2% GC content. In total, 4,386 coding genes were predicted in the chromosome, including 23 rRNAs (5S, 16S, and 23S), 79 tRNAs, and 10 noncoding RNAs (ncRNAs).

In silico Multi-Locus Sequence Typing (MLST) v2.0 (14) (https://cge.cbs.dtu.dk/services/MLST/) identified this strain as sequence type 145, and cgMLSTFinder v1.1 (15) (https://cge.cbs.dtu.dk/services/cgMLSTFinder/) identified it as core genome sequence type (cgST) 168374.

PlasmidFinder (16) identified one complete circular multireplicon IncFIB(S)-FII(S)

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plasmid (p11-Galia-2015), with 49,465 bp and 52.2% GC content. ResFinder v4.1 (17, 18) found the aminoglycoside resistance gene *aac(6′)-Iaa* against amynoglycosides, not located on the plasmid.

A total of 111 virulence factors were identified using ABRicate v1.0.1 (https://github.com/tseemann/abricate) (with the parameters --minid 80 and --mincov 50). Among them, major virulence determinants belonging to *Salmonella* pathogenicity island 1 (SPI-1; e.g., *inv*, *sip*, *sptP*, *sopA*, and *sic*), SPI-2 (e.g., *ssa*, *ssc*, *sse*, *spiC*, *sifA*, *pipB*, and *sopD2*), and SPI-3 (*mgtCB* and *misL*) were found. Also, genes coding for virulence factors, such as *sodCI*, which protects against phagocytic superoxide during infection (19), Peyer's patch-specific virulence factors (*lpfA-E*), and the toxin-coding genes *spvB* or *mig-14*, responsible for resistance to antimicrobial peptides, were identified (20, 21).

Data availability. These sequences are available at GenBank (accession number JADWDF000000000 for the genome) and the SRA (accession number SRR13399484). The version described in this paper is the first version, JADWDF010000000.

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