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GENOME SEQUENCES

Complete Genome Sequences of Four *Salmonella enterica* Strains (Including Those of Serotypes Montevideo, Mbandaka, and Lubbock) Isolated from Peripheral Lymph Nodes of Healthy Cattle

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ABSTRACT *Salmonella enterica* serotype Lubbock emerged most likely from a *Salmonella enterica* serotype Mbandaka ancestor that acquired by recombination the *fliC* operon from *Salmonella enterica* serotype Montevideo. Here, we report the complete genome sequence of two *S.* Lubbock, one *S.* Montevideo, and one *S.* Mbandaka strain isolated from bovine lymph nodes.

Salmonella enterica serotype Lubbock (6,7:g,m,s:e,n,z_{15}) has been isolated from peripheral lymph nodes (PLNs) of healthy cattle and bovine liver abscesses (1, 2). This novel antigenic formula was first defined by agglutination and confirmed genetically. This novel serotype most likely emerged from a recombination event transferring the *fliC* operon of *Salmonella enterica* serotype Montevideo into a *Salmonella enterica* serotype Mbandaka ancestor (3). At least two recombination events occurred, given that two *S.* Lubbock lineages represented by the distinct isolates 10TTU468x and 11TTU1590 were recovered from PLNs of healthy cattle. The closed genome sequences are presented here together with the closed genome sequences of one *S.* Mbandaka strain (11TTU1615b) and one *S.* Montevideo strain (11TTUC-046) also isolated from PLNs (4, 5). Whole-genome sequencing of these four strains was performed to inform possible genomic evolutionary events leading to the emergence of the novel mosaic *S.* Lubbock serotype. Genomic DNA was extracted from a single-colony overnight culture at 37°C in tryptic soy broth using Qiagen Genomic-tip 100/G columns and blood and cell culture DNA midi kits (Qiagen, Valencia, CA), following the manufacturer's recommendations. Long-read sequencing was performed by single-molecule real-time technology, using C4/P6 (chemistry/polymerase) on an RS II instrument (Pacific Biosciences, Menlo Park, CA). Raw data were assembled using SMRT Analysis software version 2.3.0 (Pacific Biosciences) and polished with MiSeq-generated paired-end Illumina reads using Pilon version 1.18 (6).

Primary analysis revealed that none of the four strains carried a plasmid and that chromosome size and GC content varied slightly (average coverage, 68×) (Table 1) (6). Default parameters were used for all analyses. Serotypes were confirmed using the SeqSero pipeline (7). The presence of antimicrobial resistance genes was queried using CARD (minimum identity and query coverage minimum, 95%), highlighting the presence of the same single cryptic resistance gene against aminoglycosides [*aac(6′)-Iaa*] in each strain (8, 9). Furthermore, all four genomes contain genes encoding transporters noted for their involvement in resistance phenotypes to various antimicrobials. The presence of virulence genes and *Salmonella* pathogenicity islands (SPI) was investi-

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TABLE 1 Characteristics of the four *S. enterica* strain genomes

Characteristic	Value for strain			
	10TTU468x	11TTU1590	11TTU1615b	11TTUC-046
GC content (%)	52.11	52.11	52.11	52.35
PacBio reads				
No. of reads	96,785	347,976	243,332	274,427
Avg read length (bp)	7,166	10,035	9,873	9,254
Total bases sequenced (bp)	693,598,459	3,491,953,649	2,402,449,873	2,539,597,496
Assembly size (bp)	4,985,863	4,985,874	4,985,867	4,588,222
Illumina reads				
No. of reads	2,838,092	2,567,890	1,040,576	2,341,584
Avg read length (bp)	144	141	222	142
No. of contigs	176	167	201	115
Assembly size (bp)	4,946,889	4,944,961	5,035,112	4,556,712

gated (SPIFinder, version 1.0; https://cge.cbs.dtu.dk/services/SPIFinder/) and revealed the presence of C63PI (iron transport in SPI-1), SPI-2, and SPI-4 in each strain. While only the *S.* Montevideo isolate carried SPI-3, SPI-13, and SPI-14, the *S.* Lubbock and *S.* Mbandaka isolates harbored more virulence-associated genes (242 and 245 genes, respectively) than did the *S.* Montevideo isolate (227 genes) (10). This difference may be explained by mobile genetic elements. The *S.* Lubbock and *S.* Mbandaka strains possessed a larger number of mobile elements (87, 88, and 88 for 10TTU468x, 11TTU1590, and 11TTU1615b, respectively) than did the *S.* Montevideo isolate (22 genes) (RASTk; http://rast.nmpdr.org/). These data support the hypothesis that *S.* Mbandaka is likely a progenitor of *S.* Lubbock that arose from the acquisition of $fliC_{g,m,s}$ in a recombination event with *S.* Montevideo.

Data availability. Whole-genome sequences have been deposited in DDBJ/ENA/GenBank under the accession and BioProject numbers CP032814 and PRJNA494676 (10TTU468x), CP032817 and PRJNA494681 (11TTU1590), CP032815 and PRJNA494678 (11TTU1615b), and CP032816 and PRJNA494679 (11TTUC-046), respectively. Whole-genome shotgun projects have been deposited in DDBJ/ENA/GenBank under the accession and BioProject numbers JXYU00000000 and PRJNA274416 (10TTU468x), JXYV00000000 and PRJNA274419 (11TTU1590), QYWD00000000 and PRJNA491195 (SRA number SRX5075396) (11TTU1615b), and QYWT00000000 and PRJNA491195 (SRA number SRX5075395) (11TTUC-046), respectively.

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