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Two Draft Genome Sequences of a New Serovar of *Salmonella enterica*, Serovar Lubbock

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***Salmonella enterica* is principally a foodborne pathogen that shows considerable serovar diversity. In this report, we present two draft genome sequences of *Salmonella enterica* subsp. *enterica* serovar Lubbock, a novel serovar.**

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Salmonella enterica is a foodborne pathogen, showing considerable antigenic diversity with more than 2,500 serovars characterized to date (1, 2). This bacterium inhabits and colonizes a large variety of hosts and environments. Recent studies (3, 4) have highlighted the presence of *Salmonella* in bovine peripheral lymph nodes, which may be incorporated with meat to produce ground beef and therefore become a source of food contamination. We isolated atypical strains initially identified as serovar Montevideo. However, molecular interrogation of targeted genetic clades (5) revealed an atypical profile for *Salmonella enterica* serovar Montevideo. Further serological characterization of these isolates provided the antigenic formula of *S.* I. 6,7:g,m,s:e,n,z_{15}, representing a novel serovar that has been designated Lubbock. The strains sequenced in this announcement are 10TTU468 and 11TTU1590; both were isolated from subiliac lymph nodes from cattle at a commercial abattoir. Initial subtyping using multilocus sequence typing (6) or CRISPR locus content characterization showed subtypes previously associated with *Salmonella enterica* serovar Mbandaka.

Paired-end 151-bp reads were generated using an Illumina MiSeq platform. Reads were *de novo* assembled using the a5-pipeline version 20141120 (7), resulting in 38 and 36 contigs for 10TTU468 and 11TTU1590, respectively. The total assembly size was 4.95 Mbp for both strains, with N_{50} values of 263 kbp and 264 kbp and a median read depth of the assemblies of 85× and 74× for 10TTU468 and 11TTU1590, respectively. The draft genomes were annotated using the NCBI Prokaryotic Genome Automated Annotation Pipeline (8). Prophages were identified using PHAST (9). High-quality single nucleotide polymorphisms (hqSNPs) were called using software and parameters described previously by Den Bakker et al. (10), using the concatenated genome sequence of 10TTU468 as a reference, with rRNA and prophage regions excluded.

A total of 4,712 (10TTU468) and 4,709 (11TTU1590) protein-coding sequences were annotated in each genome. No plasmid-associated sequences were found, and both genome sequences contain seven intact prophages and five incomplete prophage regions. A kSNP-based (11) phylogenetic comparison using a representative variety of *S. enterica* serovars (12) and additional serovar Mbandaka isolates showed that both strains are closely related to *S. enterica* serovar Mbandaka 2009k-0807 (GenBank accession no. AMRS00000000.1) and 2012K-0273 (GenBank accession no. ARYT00000000.1). Further hqSNP-based comparison of the two isolates with 128 *S.* Mbandaka isolates publicly available from the NCBI Sequence Read Archive (SRA) (February 2015) showed that 10TTU468 and 11TTU1590 differ by 187 shared hqSNPs from the most closely related *S. enterica* serovar Mbandaka strain (NY_IDR1200021873-04, SRA accession no. SRX426108). Fifty-two hqSNPs mapped to a 4.5-kbp region containing the *fliC* gene. The high SNP density suggests homologous recombination within this region, and a BLASTn (13) search of the *fliC* sequences of Lubbock strains shows that this gene has a 100% identity to *fliC* in *S. enterica* serovar Montevideo strain 507440-20.

Nucleotide sequence accession numbers. These whole-genome shotgun projects have been deposited in DDBJ/EMBL/GenBank under the accession numbers JXYU00000000 (10TTU468) and JXYV00000000 (11TTU1590). The versions described in this paper are JXYU01000000 and JXYV01000000.

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