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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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We report no financial conflicts of interest that arise because of material reported herein.

REFERENCES

1. **Grimont P, Weill F**. 2007. Antigenic formulae of the *Salmonella* serovars: WHO Collaborating Centre for reference and research on *Salmonella*. Institut Pasteur, Paris, France.
2. **Guibourdenche M, Roggentin P, Mikoleit M, Fields PI, Bockemühl J, Grimont PA, Weill F-X**. 2010. Supplement 2003–2007 (no. 47) to the White-Kauffmann-Le Minor scheme. Res Microbiol **161:**26–29. http://dx.doi.org/10.1016/j.resmic.2009.10.002.
3. **Gragg SE, Loneragan GH, Brashears MM, Arthur TM, Bosilevac JM, Kalchayanand N, Wang R, Schmidt JW, Brooks JC, Shackelford SD, Wheeler TL, Brown TR, Edrington TS, Brichta-Harhay DM**. 2013. Cross-sectional study examining *Salmonella enterica* carriage in subiliac lymph nodes of cull and feedlot cattle at harvest. Foodborne Pathog Dis **10:**368–374. http://dx.doi.org/10.1089/fpd.2012.1275.
4. **Gragg SE, Loneragan GH, Nightingale KK, Brichta-Harhay DM, Ruiz H, Elder JR, Garcia LG, Miller MF, Echeverry A, Ramírez Porras RG, Brashears MM**. 2013. Substantial within-animal diversity of *Salmonella* isolates from lymph nodes, feces, and hides of cattle at slaughter. Appl Environ Microbiol **79:**4744–4750. http://dx.doi.org/10.1128/AEM.01020-13.
5. **Den Bakker HC, Moreno Switt AI, Govoni G, Cummings CA, Ranieri ML, Degoricija L, Hoelzer K, Rodriguez-Rivera LD, Brown S, Bolchacova E, Furtado MR, Wiedmann M**. 2011. Genome sequencing reveals diversification of virulence factor content and possible host adaptation in distinct subpopulations of *Salmonella enterica*. BMC Genomics **12:**425. http://dx.doi.org/10.1186/1471-2164-12-425.
6. **Achtman M, Wain J, Weill F-X, Nair S, Zhou Z, Sangal V, Krauland MG, Hale JL, Harbottle H, Uesbeck A, Dougan G, Harrison LH, Brisse S**. 2012. Multilocus sequence typing as a replacement for serotyping in *Salmonella enterica*. PLoS Pathog **8:**e1002776. http://dx.doi.org/10.1371/journal.ppat.1002776.
7. **Tritt A, Eisen JA, Facciotti MT, Darling AE**. 2012. An integrated pipeline for *de novo* assembly of microbial genomes. PLoS One **7:**e42304. http://dx.doi.org/10.1371/journal.pone.0042304.
8. **Angiuoli SV, Gussman A, Klimke W, Cochrane G, Field D, Garrity G, Kodira CD, Kyrpides N, Madupu R, Markowitz V, Tatusova T, Thomson N, White O**. 2008. Toward an online repository of standard operating procedures (SOPs) for (meta)genomic annotation. Omics **12:**137–141. http://dx.doi.org/10.1089/omi.2008.0017.
9. **Zhou Y, Liang Y, Lynch KH, Dennis JJ, Wishart DS**. 2011. PHAST: a fast phage search tool. Nucleic Acids Res **39:**W347–W352. http://dx.doi.org/10.1093/nar/gkr485.
10. **Den Bakker HC, Allard MW, Bopp D, Brown EW, Fontana J, Iqbal Z, Kinney A, Limberger R, Musser KA, Shudt M, Strain E, Wiedmann M, Wolfgang WJ**. 2014. Rapid whole-genome sequencing for surveillance of *Salmonella enterica* serovar Enteritidis. Emerg Infect Dis **20:**1306–1314. http://dx.doi.org/10.3201/eid2008.131399.
11. **Gardner SN, Hall BG**. 2013. When whole-genome alignments just won't work: kSNP v2 software for alignment-free SNP discovery and phylogenetics of hundreds of microbial genomes. PLoS One **8:**e81760. http://dx.doi.org/10.1371/journal.pone.0081760.
12. **Timme RE, Pettengill JB, Allard MW, Strain E, Barrangou R, Wehnes C, Van Kessel JS, Karns JS, Musser SM, Brown EW**. 2013. Phylogenetic diversity of the enteric pathogen *Salmonella enterica* subsp. *enterica* inferred from genome-wide reference-free SNP characters. Genome Biol Evol **5:**2109–2123. http://dx.doi.org/10.1093/gbe/evt159.
13. **Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ**. 1990. Basic local alignment search tool. J Mol Biol **215:**403–410. http://dx.doi.org/10.1016/S0022-2836(05)80360-2.