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

Marie Bugarel
*Texas Tech University*

Henk C. den Bakker
*Texas Tech University*

Kendra K. Nightingale
*Texas Tech University*

Dayna M. Brichta-Harhay
*USDA-ARS*

Thomas S. Edrington
*USDA-ARS*

*See next page for additional authors*

Follow this and additional works at: [http://digitalcommons.unl.edu/hruskareports](http://digitalcommons.unl.edu/hruskareports)


[http://digitalcommons.unl.edu/hruskareports/389](http://digitalcommons.unl.edu/hruskareports/389)
Two Draft Genome Sequences of a New Serovar of *Salmonella enterica*, Serovar Lubbock

Marie Bugarel, a Henk C. den Bakker, a Kendra K. Nightingale, a Dayna M. Brichta-Harhay, b Thomas S. Edrington, c Guy H. Loneragan a

International Center for Food Industry Excellence, Department of Animal and Food Sciences, Texas Tech University, Lubbock, Texas, USA; b U.S. Department of Agriculture, Agricultural Research Service, Southern Plains Agricultural Research Center, Food and Feed Safety Research Unit, College Station, Texas, USA; c U.S. Department of Agriculture, Agricultural Research Service, Roman L. Hruska U.S. Meat Animal Research Center, Clay Center, Nebraska, USA

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

A total of 4,712 (10TTU468) and 4,709 (11TTU1590) kbp and a median read depth of the assemblies of 85× was obtained for 10TTU468 and 11TTU1590, respectively. The total assembly size was 4.95 Mbp for both strains, with N₅₀ 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. AMRS0000000.1) and 2012K-0273 (GenBank accession no. ARTY0000000.1). 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_IDR1200012873-04, 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.

ACKNOWLEDGMENTS

This work was funded in part by the U.S. Department of Agriculture, National Institutes of Food and Agriculture’s National Integrated Food Safety Initiative award no. 2011-51110-31081 and by the Beef Checkoff Program.

We acknowledge the laboratory of Food Safety of the French Agency for Food, Environmental and Occupational Health and Safety (Maitons-Alfort, France) and the national reference laboratory for *Salmonella* at the Pasteur Institute (Paris, France) that performed the serological characterization of these strains, leading to the confirmation of the identification of the novel serovar Lubbock.

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

Received 16 February 2015 Accepted 3 March 2015 Published 16 April 2015


Address correspondence to Marie Bugarel, marie.bugarel@ttu.edu.
REFERENCES


