AMERICAN SOCIETY FOR MICROBIOLOGY | genomeAnnouncements

Genome Sequences of *Salmonella enterica* subsp. *enterica* Serovar Lubbock Strains Isolated from Liver Abscesses of Feedlot Cattle

Raghavendra G. Amachawadi,[a] Milton Thomas,[b] Tiruvoor G. Nagaraja,[a] Joy Scaria[b]

Department of Diagnostic Medicine and Pathobiology, College of Veterinary Medicine, Kansas State University, Manhattan, Kansas, USA[a]; Department of Veterinary and Biomedical Sciences, South Dakota State University, Brookings, South Dakota, USA[b]

The genome sequencing of 13 *Salmonella enterica* subsp. *enterica* serovar Lubbock strains isolated from liver abscesses of feedlot cattle is reported here. The availability of these genomes will help to further understand the etiologic role of *Salmonella* strains in liver abscesses of cattle and will serve as references in microbial trace-back studies to improve food safety.

Received 8 March 2016 **Accepted** 11 March 2016 **Published** 5 May 2016

Citation Amachawadi RG, Thomas M, Nagaraja TG, Scaria J. 2016. Genome sequences of *Salmonella enterica* subsp. *enterica* serovar Lubbock strains isolated from liver abscesses of feedlot cattle. Genome Announc 4(3):e00319-16. doi:10.1128/genomeA.00319-16.

Address correspondence to Tiruvoor G. Nagaraja, tnagaraj@vet.k-state.edu, or Joy Scaria, joy.scaria@sdstate.edu.

Liver abscesses occur in feedlot cattle as a consequence of feeding them a high-grain diet (1). Cattle with severely abscessed livers have lower feed intake, reduced weight gain, and a decreased gain-to-feed ratio (2). The primary causative agent of liver abscess is *Fusobacterium necrophorum* (3). The ruminal acidosis resulting from the highly fermentable starch contained in the grains, and subsequent rumenitis, facilitate the migration of *F. necrophorum* from the rumen to the liver via portal circulation (1). Recently, for the first time, we reported the occurrence, along with *F. necrophorum*, of a novel *Salmonella* serotype, designated 6,7:g,m,s:e,n,z15, now named *Salmonella enterica* subsp. *enterica* serovar Lubbock (4), in liver abscesses of cattle (5). The newly reported serotype *S.* Lubbock is closely related to *S. enterica* subsp. *enterica* serovar Mbandaka and has been isolated from subiliac lymph nodes of healthy cattle (4). It is not known whether *S.* Lubbock is a causative agent of liver abscesses or is a secondary invader, via or lymph or blood, of an abscess initiated by *F. necrophorum*. In a recent study, we observed that *Salmonella* was prevalent in 20 to 25% of the abscesses cultured, and *S.* Lubbock was the predominant serotype. Here, we report the availability of draft genomes of 13 *S.* Lubbock strains isolated from liver abscesses.

S. Lubbock strains were isolated from liver abscesses of feedlot cattle, as per a previously described protocol (5). The serotypes of the isolates were determined at the National Veterinary Service Laboratory (NVSL), Ames, Iowa. Strains were grown in brain heart infusion broth for 12 h at 37°C. DNA from each strain was isolated from 1.0-ml cultures using the E.Z.N.A. bacterial DNA kit (Omega Bio-tek, Norcross, GA). According to the manufacturer's protocol, sequencing libraries were prepared using 1.0 ng of genomic DNA using the Nextera XT kit (Illumina, San Diego, CA). We used V2 paired-end chemistry (2 × 250 bp) to sequence the genomes on an Illumina MiSeq platform. *De novo* genome assembly was performed using SPAdes version 3.5.0 (6), available at http://bioinf.spbau.ru/spades. Genome annotation was performed using the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP) (7).

The genome characteristics of the 13 *S.* Lubbock strains are summarized in Table 1. The serotypes of the 13 strains were confirmed using SeqSero (8). Genome size and G+C content

TABLE 1 Characteristics of 13 *S.* Lubbock strains isolated from liver abscesses of cattle

Strain name	GenBank accession no.	Genome size (bp)	G+C content (%)	Total no. of contigs
LA-10-2013	LSMA00000000	4,973,701	52.1	128
LA-1-2013	LSLN00000000	4,955,079	52.1	100
LA-2-2013	LSLO00000000	4,959,869	52.1	108
LA-3-2013	LSLP00000000	4,988,702	52.1	174
LA-4-2013	LSLQ00000000	4,964,148	52.1	112
LA-5-2013	LSLR00000000	5,174,970	52.1	479
LA-5-2014	LSLS00000000	5,032,588	52.1	267
LA-6-2013	LSLT00000000	4,983,284	52.1	184
LA-7-2013	LSLU00000000	4,992,701	52.0	175
LA-7-2014	LSLV00000000	4,979,081	52.1	142
LA-8-2013	LSLW00000000	4,979,081	52.1	142
LA-8-2014	LSLX00000000	4,961,787	52.1	106
LA-9-2014	LSLZ00000000	4,870,086	52.1	159

were estimated for all contigs of each strain. Among the 13 strains, the median values for genome size and G+C content were 4.97 Mb and 52.1%, respectively (Table 1), and were similar to those of previously published *S. enterica* genomes.

The availability of the genomes of 13 *S.* Lubbock strains is the first report of this serotype isolated from liver abscesses of cattle. The availability of these genomes will help to further understand the etiologic role of *Salmonella* strains in liver abscesses in cattle and will serve as references in microbial trace-back studies to improve food safety.

Nucleotide sequence accession numbers. The sequences have been deposited as whole-genome shotgun projects at GenBank under the accession numbers listed in Table 1.

ACKNOWLEDGMENTS

This work was supported in part by grants from SD BIC and FDA CFSAN awarded to J.S. and Elanco Animal Health, Greenfield, IN to T.G.N.

We acknowledge use of the High-Performance Computing (HPC) cluster managed by the University Networking and Research (UNRC) group at South Dakota State University.

The funding agencies had no role in the study design, data collection and interpretation, or the decision to submit the work for publication.

FUNDING INFORMATION

This work, including the efforts of Joy Scaria, was funded by South Dakota Beef Industry Council. This work, including the efforts of Joy Scaria, was funded by FDA CFSAN. This work, including the efforts of T. G. Nagaraja, was funded by Elanco Animal Health, Greenfield, IN.

REFERENCES

1. **Nagaraja TG, Chengappa MM**. 1998. Liver abscesses in feedlot cattle: a review. J Anim Sci **76:**287–298.
2. **Brink DR, Lowry SR, Stock RA, Parrott JC**. 1990. Severity of liver abscesses and efficiency of feed utilization of feedlot cattle. J Anim Sci **68:** 1201–1207.
3. **Scanlan CM, Hathcock TL**. 1983. Bovine rumenitis—liver abscess complex: a bacteriological review. Cornell Vet **73:**288–297.
4. **Bugarel M, den Bakker HC, Nightingale KK, Brichta-Harhay DM, Edrington TS, Loneragan GH**. 2015. Two draft genome sequences of a new serovar of *Salmonella enterica,* serovar Lubbock. Genome Announc **3**(2): e00215-15. http://dx.doi.org/10.1128/genomeA.00215-15.
5. **Amachawadi RG, Nagaraja TG**. 2015. First report of anaerobic isolation of *Salmonella enterica* from liver abscesses of feedlot cattle. J Clin Microbiol **53:**3100–3101. http://dx.doi.org/10.1128/JCM.01111-15.
6. **Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA**. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol **19:**455–477. http://dx.doi.org/10.1089/cmb.2012.0021.
7. **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.
8. **Zhang S, Yin Y, Jones MB, Zhang Z, Deatherage KBL, Dinsmore BA, Fitzgerald C, Fields PI, Deng X**. 2015. *Salmonella* serotype determination utilizing high-throughput genome sequencing data. J Clin Microbiol **53:** 1685–1692. http://dx.doi.org/10.1128/JCM.00323-15.