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:r5,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). We used V2 paired-end chemistry \((2 \times 250 \text{ bp})\) 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  | LSMA0000000000        | 4,973,701        | 52.1            | 128                 |
| LA-1-2013   | LSLN0000000000        | 4,955,079        | 52.1            | 100                 |
| LA-2-2013   | LSLO0000000000        | 4,959,869        | 52.1            | 108                 |
| LA-3-2013   | LSLP0000000000        | 4,988,702        | 52.1            | 174                 |
| LA-4-2013   | LSLQ0000000000        | 4,964,148        | 52.1            | 112                 |
| LA-5-2013   | LSLR0000000000        | 5,174,970        | 52.1            | 479                 |
| LA-5-2014   | LSLS0000000000        | 5,032,588        | 52.1            | 267                 |
| LA-6-2013   | LSLT0000000000        | 4,983,284        | 52.1            | 184                 |
| LA-7-2013   | LSLU0000000000        | 4,992,701        | 52.0            | 175                 |
| LA-7-2014   | LSLV0000000000        | 4,979,081        | 52.1            | 142                 |
| LA-8-2013   | LSLW0000000000        | 4,979,081        | 52.1            | 142                 |
| LA-8-2014   | LSLX0000000000        | 4,961,787        | 52.1            | 106                 |
| LA-9-2014   | LSLZ0000000000        | 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.

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