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Complete Genome Sequence of Livestock-Associated Methicillin-Resistant *Staphylococcus aureus* Sequence Type 398 Isolated from Swine in the United States

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ABSTRACT Methicillin-resistant *Staphylococcus aureus* (MRSA) colonizes and causes disease in many animal species. Livestock-associated MRSA (LA-MRSA) isolates are represented by isolates of the sequence type 398 (ST398). These isolates are considered to be livestock adapted. This report provides the complete genome sequence of one swine-associated LA-MRSA ST398 isolate from the United States.

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Methicillin-resistant *Staphylococcus aureus* (MRSA) has been found as a commensal of humans and other mammals. It can cause disease in animals, including mastitis in cattle, exudative dermatitis in swine, and mild skin infections to severe invasive disease in humans (1–3). MRSA isolates are classified as hospital-acquired MRSA (HA-MRSA), community-acquired MRSA (CA-MRSA), and livestock-associated MRSA (LA-MRSA) based on epidemiological characteristics. The prototypical LA-MRSA isolate was characterized by multilocus sequence typing (MLST) and defined as sequence type 398 (ST398). The identification and prevalence of this strain in livestock species indicate that livestock are potentially the largest reservoir for MRSA outside the hospital setting. This lineage has been identified in a variety of livestock species and is considered to be adapted to colonization of nonhuman mammals (4, 5), although colonization and infection have been noted in humans (6, 7).

We generated whole-genome sequence data for one LA-MRSA ST398 isolate (ISU926) obtained from Iowa State University (8). This isolate was acquired by nasal swab from a healthy pig. The isolate was grown in Trypticase soy broth (BD Biosciences, Sparks, MD), and genomic DNA was extracted using a High Pure PCR template preparation kit (Roche Applied Science, Indianapolis, IN).

Whole-genome sequence data were derived using PacBio and Illumina MiSeq technologies. The PacBio library was generated from high-quality genomic DNA using the PacBio 10-kb insert library preparation protocol found online (http://www.pacb.com/wp-content/uploads/2015/09/Procedure-Checklist-10-kb-Template-Preparation-and-Sequencing.pdf). The library was sequenced using a single single-molecule real-time (SMRT) cell on a PacBio RSII platform. MiSeq indexed libraries were generated using the Nextera XT DNA sample preparation and index kits (Illumina, San Diego, CA). Samples were pooled and sequenced on the Illumina MiSeq platform (Illumina, San Diego, CA) using a MiSeq v2 500-cycle reagent kit, resulting in 2- × 250-bp paired-end reads.

Whole-genome sequence data were assembled using PacBio smrtanalysis v. 2.3.0 and CANU v. 1.3 software. Average coverage for the PacBio data from ISU926 was 394×.

The assembled PacBio data were then trimmed of overlapping sequences and oriented with *dnaA* as the start of the genome. Genome polishing and error correction were completed using the Broad Institute's Pilon v. 1.18 and Illumina data with an average coverage of 37×.

Accession number(s). The whole-genome sequence for ISU926 was deposited in DDBJ/ENA/GenBank with the accession number CP017091.

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