Draft Genome Sequences of Nine Livestock-Associated Methicillin-Resistant Staphylococcus aureus Sequence Type 5 Isolates Obtained from Humans after Short-Term Swine Contact

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ABSTRACT Livestock-associated methicillin-resistant Staphylococcus aureus (LA-MRSA) sequence type 5 (ST5) has raised concerns surrounding the potential for these isolates to colonize or cause disease in humans with swine contact. Here, we report draft genome sequences for nine LA-MRSA ST5 isolates obtained from humans after short-term swine contact.

Methicillin-resistant Staphylococcus aureus (MRSA) was first isolated in 1961. Isolates have since been categorized based on epidemiological characteristics into hospital acquired (HA-MRSA), community acquired (CA-MRSA), and livestock associated (LA-MRSA). Humans can be colonized by all categories of MRSA isolates; however, LA-MRSA isolates have been considered less pathogenic and livestock adapted compared to HA- and CA-MRSA isolates (1, 2). The predominant multilocus sequence type (ST) found in European swine is ST398, while Asian swine harbor ST9 (3, 4). In the United States, swine carry a more diverse population of isolates, including ST398, ST9, and ST5 isolates (5). LA-MRSA ST5 isolates are concerning due to the widespread and pathogenic nature of MRSA ST5 isolates in the hospital and community settings (6). This has been attributed to the ability of this lineage to acquire mobile genetic elements encoding virulence factors and antimicrobial resistance genes (6), which are found rarely in LA-MRSA ST398 and ST9 isolates. Genome sequence data can be used to further evaluate the capacity of LA-MRSA ST5 isolates to colonize and cause disease in humans.

Here, we report the draft genome sequences of nine LA-MRSA ST5 isolates obtained from humans after short-term contact with swine (ISU 886, ISU 887, ISU 888, ISU 889, ISU 928, ISU 930, ISU 1004, and ISU 1007). Each isolate was obtained by Iowa State University from nasal swabs taken from veterinary students after visiting high-density swine operations (5). To obtain genomic DNA, isolates were grown in Trypticase soy broth (BD Biosciences, Sparks, MD, USA), and total genomic DNA was extracted utilizing the High Pure PCR Template preparation kit (Roche Applied Science, Indianapolis, IN, USA).

The Illumina MiSeq platform (Illumina, San Diego, CA, USA) was employed to generate draft genome data. Indexed libraries were produced using the Nextera XT DNA sample preparation and index kits (Illumina), pooled, and sequenced using the MiSeq V2 500-cycle reagent kit (Illumina) to generate 2 × 250-bp paired-end reads. The data were then assembled using MIRA version 4.0.2 software (http://mira-assembler.sourceforge.net/docs/DefinitiveGuideToMIRA.html). This resulted in average coverages
for each isolate as follows: ISU 886 (82.26×), ISU 887 (41.07×), ISU 888 (42.62×), ISU 889 (39.08×), ISU 928 (29.49×), ISU 930 (37.43×), ISU 931 (36.54×), ISU 1004 (31.37×), and ISU 1007 (54.60×). For inclusion in the assembly, contigs were filtered allowing only those with a length greater than 1,500 bp and coverage greater than two-thirds the average coverage of the genome. When potentially repetitive elements were identified, the contig was required to be greater than 2,000 bp for inclusion in the assembly.

Accession number(s). The draft genome sequences produced in this study were deposited in DDBJ/ENA/GenBank with the following accession numbers: ISU 886, LKWG00000000; ISU 887, LKWH00000000; ISU 888, LKWI00000000; ISU 889, LKWJ00000000; ISU 928, LKWY00000000; ISU 930, LKWZ00000000; ISU 931, LKXA00000000; ISU 1004, LKVL00000000; and ISU 1007, LKVM00000000.

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