AMERICAN SOCIETY FOR MICROBIOLOGY | genomeAnnouncements™

PROKARYOTES

Complete Genome Sequence of a Livestock-Associated Methicillin-Resistant *Staphylococcus aureus* Sequence Type 5 Isolate from the United States

Samantha J. Hau,[a] Darrell O. Bayles,[b] David P. Alt,[b] Timothy S. Frana,[a] Tracy L. Nicholson[b]

Department of Veterinary Diagnostic and Production Animal Medicine, College of Veterinary Medicine, Iowa State University, Ames, Iowa, USA[a]; National Animal Disease Center, Agriculture Research Service, USDA, Ames, Iowa, USA[b]

ABSTRACT Livestock-associated methicillin-resistant *Staphylococcus aureus* (LA-MRSA) may be the largest MRSA reservoir outside the hospital setting. One concern with LA-MRSA is the acquisition of novel mobile genetic elements by these isolates. Here, we report the complete genome sequence of a swine LA-MRSA sequence type 5 isolate from the United States.

Received 26 June 2017 **Accepted** 27 June 2017 **Published** 10 August 2017

Citation Hau SJ, Bayles DO, Alt DP, Frana TS, Nicholson TL. 2017. Complete genome sequence of a livestock-associated methicillin-resistant *Staphylococcus aureus* sequence type 5 isolate from the United States. Genome Announc 5:e00791-17. https://doi.org/10.1128/genomeA.00791-17.

Address correspondence to Tracy L. Nicholson, tracy.nicholson@ars.usda.gov.

Methicillin-resistant *Staphylococcus aureus* (MRSA) has circulated primarily in hospitals since the 1960s (1). More recently, MRSA has been isolated outside the hospital setting (community-acquired MRSA) and from livestock (livestock-associated MRSA [LA-MRSA]) (2, 3). Outside of the United States, LA-MRSA isolates are primarily sequence type 398 (ST398) and ST9 in Europe and Asia, respectively (4, 5). LA-MRSA in the United States also contains MRSA ST5 isolates (6). These isolates have raised concerns because, unlike ST398 and ST9, which are considered livestock adapted, ST5 isolates are a widespread and successful hospital-acquired MRSA (HA-MRSA) lineage (2). The pathogenicity of ST5 isolates is thought to be associated with the capacity and ease with which they acquire mobile genetic elements (7).

Here, we report the generation of whole-genome sequence data for one swine-associated LA-MRSA ST5 isolate (ISU935) obtained from a study conducted at Iowa State University (6). ISU935 was isolated from a healthy pig in a high-density swine operation. The isolate was grown in Trypticase soy broth (BD Biosciences, Sparks, MD), and the High Pure template preparation kit (Roche Applied Science, Indianapolis, IN) was used to extract total genomic DNA from the sample.

Both PacBio and Illumina MiSeq platforms were used to generate whole-genome sequence data. The PacBio library was prepared utilizing 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 with a PacBio RSII platform on a single-molecule real-time (SMRT) cell. A MiSeq indexed library was created using the Nextera XT DNA sample preparation and index kits (Illumina, San Diego, CA). The library was sequenced with a MiSeq v2 500-cycle reagent kit, generating 2- × 250-bp paired-end reads on the Illumina MiSeq platform (Illumina, San Diego, CA).

PacBio SmrtAnalysis v. 2.3.0 and CANU v. 1.3 software were used to generate the whole-genome assembly. ISU935 had an average PacBio coverage of 449×. After assembly, the PacBio data were trimmed to remove overlapping sequences and oriented with *dnaA* as the start of the genome. The Broad Institute's Pilon v. 1.18 was used to polish and error correct the ISU935 genome using Illumina data with an average coverage of 18×.

Accession number(s). The whole-genome sequence for ISU935 was deposited in DDBJ/ENA/GenBank with the accession number CP017090.

ACKNOWLEDGMENTS

We thank Yale University for its assistance in producing the PacBio sequence data.

Funding for this research was provided by the USDA Agricultural Research Service and the National Pork Board. S.J.H. is supported by the Veterinary Diagnostic Laboratory at Iowa State University. Funding sources did not impact study design, data collection, data analysis, decisions on publication, or preparation of the manuscript.

Mention of trade names or commercial products in this article is solely for the purpose of providing specific information and does not imply recommendation or endorsement by the U.S. Department of Agriculture.

REFERENCES

1. Jevons M. 1961. "Celbenin"-resistant staphylococci. BMJ 1:124–125.
2. Bal AM, Coombs GW, Holden MT, Lindsay JA, Nimmo GR, Tattevin P, Skov RL. 2016. Genomic insights into the emergence and spread of international clones of healthcare-, community- and livestock-associated methicillin-resistant *Staphylococcus aureus*: blurring of the traditional definitions. J Glob Antimicrob Resist 6:95–101. https://doi.org/10.1016/j.jgar.2016.04.004.
3. Voss A, Loeffen F, Bakker J, Klaassen C, Wulf M. 2005. Methicillin-resistant *Staphylococcus aureus* in pig farming. Emerg Infect Dis 11:1965–1966. https://doi.org/10.3201/eid1112.050428.
4. Wagenaar JA, Yue H, Pritchard J, Broekhuizen-Stins M, Huijsdens X, Mevius DJ, Bosch T, Van Duijkeren E. 2009. Unexpected sequence types in livestock associated methicillin-resistant *Staphylococcus aureus* (MRSA): MRSA ST9 and a single locus variant of ST9 in pig farming in China. Vet Microbiol 139:405–409. https://doi.org/10.1016/j.vetmic.2009.06.014.
5. Anonymous. 2009. Scientific opinion of the Panel on Biological Hazards on a request from the European Commission on Assessment of the Public Health significance of meticillin resistant *Staphylococcus aureus* (MRSA) in animals and foods. EFSA J 993:1–73.
6. Frana TS, Beahm AR, Hanson BM, Kinyon JM, Layman LL, Karriker LA, Ramirez A, Smith TC. 2013. Isolation and characterization of methicillin-resistant *Staphylococcus aureus* from pork farms and visiting veterinary students. PLoS One 8:e53738. https://doi.org/10.1371/journal.pone.0053738.
7. Monecke S, Coombs G, Shore AC, Coleman DC, Akpaka P, Borg M, Chow H, Ip M, Jatzwauk L, Jonas D, Kadlec K, Kearns A, Laurent F, O'Brien FG, Pearson J, Ruppelt A, Schwarz S, Scicluna E, Slickers P, Tan HL, Weber S, Ehricht R. 2011. A field guide to pandemic, epidemic and sporadic clones of methicillin-resistant *Staphylococcus aureus*. PLoS One 6:e17936. https://doi.org/10.1371/journal.pone.0017936.