



Draft Genome Sequences of 14 Livestock-Associated Methicillin-Resistant *Staphylococcus aureus* Sequence Type 398 Isolates from Swine Farms in 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) is a bacterium carried by or obtained from swine and other livestock. The initial and predominant swine-associated LA-MRSA sequence type (ST) identified is ST398. Here, we present 14 draft genome sequences from LA-MRSA ST398 isolates found in the United States.

The isolation of livestock-associated methicillin-resistant *Staphylococcus aureus* (LA-MRSA) from swine in 2004 raised public health concerns that swine may serve as the largest reservoir of MRSA outside the hospital setting. Initial surveillance in Europe revealed that the primary multilocus sequence type (ST) of European swine-associated LA-MRSA was ST398 (1), which has also been identified in North American swine (2–4). While ST398 is generally considered a livestock-adapted lineage (5, 6), there have been reports of colonization and infection of humans with LA-MRSA ST398 isolates (7, 8). To address the concerns surrounding LA-MRSA ST398, genetic studies have evaluated isolate relatedness and found that LA-MRSA ST398 is likely derived from a methicillin-sensitive ST398 lineage from humans (9). Detection of genetic changes and potential for human outbreaks with LA-MRSA ST398 isolates relies on continuing evaluation of genomic data from LA-MRSA field isolates.

Here, we provide draft genome sequences for 14 LA-MRSA ST398 isolates from a study conducted by Iowa State University that examined U.S. swine farms for the presence and prevalence of LA-MRSA (4). Isolates were obtained by swabbing the nares of healthy pigs or the environment within three high-density livestock operations. Farm and source information for each isolate is shown in Table 1. The isolates were grown in Trypticase soy broth (BD Biosciences, Sparks, MD, USA) and the High Pure template preparation kit (Roche Applied Science, Indianapolis, IN, USA) was used to extract total genomic DNA.

The Illumina MiSeq platform (Illumina, San Diego, CA, USA) was used to generate draft genomic sequence data. Indexed libraries were generated using the Nextera XT DNA sample preparation and index kit (Illumina). Libraries were pooled and run on an Illumina MiSeq instrument with the MiSeq V2 500-cycle reagent kit (Illumina), generating 2 × 250-bp paired-end reads.

The sequence data were assembled using MIRA version 4.0.2 (<http://mira-assembler.sourceforge.net/docs/DefinitiveGuideToMIRA.html>). The average coverage obtained for each isolate can be found in Table 1. To be retained in the assembly, contigs were required to be >1,500 bp in length and have a coverage of >66% of the average

Received 30 August 2017 Accepted 1 September 2017 Published 2 November 2017

Citation Hau SJ, Bayles DO, Alt DP, Frana TS, Nicholson TL. 2017. Draft genome sequences of 14 livestock-associated methicillin-resistant *Staphylococcus aureus* sequence type 398 isolates from swine farms in the United States. *Genome Announc* 5:e01082-17. <https://doi.org/10.1128/genomeA.01082-17>.

This is a work of the U.S. Government and is not subject to copyright protection in the United States. Foreign copyrights may apply.

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

TABLE 1 Isolate information and genome assembly characteristics

Isolate name	Isolate source	Farm no.	Avg coverage (x)	No. of contigs	GenBank accession no.
ISU 909	Environment	35	53.51	113	LKWK00000000
ISU 912	Pig	37	22.28	157	LKWL00000000
ISU 913	Environment	37	48.98	131	LKWM00000000
ISU 914	Environment	37	66.90	91	LKWN00000000
ISU 915	Pig	36	69.78	131	LKWO00000000
ISU 916	Pig	36	19.05	180	LKWP00000000
ISU 917	Pig	36	55.79	118	LKWQ00000000
ISU 918	Pig	36	34.41	113	LKWR00000000
ISU 919	Environment	36	21.71	140	LKWS00000000
ISU 920	Environment	36	55.34	177	LKWT00000000
ISU 922	Pig	36	36.63	105	LKWU00000000
ISU 924	Pig	36	41.26	71	LKWV00000000
ISU 925	Pig	36	37.02	116	LKWW00000000
ISU 927	Environment	35	38.79	109	LKWX00000000

coverage for the genome. The assembly tool identified repetitive elements that were required to be >2,000 bp to remain in the assembly.

Accession number(s). The assembled draft genome sequences generated in this study can be found in DDBJ/ENA/GenBank with the accession numbers listed in Table 1.

ACKNOWLEDGMENTS

This research was supported by the USDA Agricultural Research Service and the National Pork Board.

There was no influence on study design or execution from funding sources. The products and trade names provided here were given for specificity and clarity. They do not imply recommendation by the USDA.

REFERENCES

1. Andreoletti O, Budka H, Buncic S, Colin P, Collins JD, De Koeijer A, Griffin J, Halvelaar A, Hope J, Klein G, Kruse H, Magnino S, Martinez Lopez A, McLauchlin J, Nguyen-The C, Noeckler K, Noerrung B, Prieto Maradona M, Roberts T, Vagsholm I, Vanopdenbosch E. 2009. Scientific opinion of the panel on biological hazards on a request from the European Commission on assessment of the public health significance of methicillin resistant *Staphylococcus aureus* (MRSA) in animals and foods. EFSA J 993:1–73.
2. Smith TC, Male MJ, Harper AL, Kroeger JS, Tinkler GP, Moritz ED, Capuano AW, Herwaldt LA, Diekema DJ. 2009. Methicillin-resistant *Staphylococcus aureus* (MRSA) strain ST398 is present in midwestern U.S. swine and swine workers. PLoS One 4:e4258. <https://doi.org/10.1371/journal.pone.0004258>.
3. Weese JS, Avery BP, Reid-Smith RJ. 2010. Detection and quantification of methicillin-resistant *Staphylococcus aureus* (MRSA) clones in retail meat products. Lett Appl Microbiol 51:338–342. <https://doi.org/10.1111/j.1472-765X.2010.02901.x>.
4. 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>.
5. Bal AM, Coombs GW, Holden MTG, 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>.
6. Aires-de-Sousa M. 2017. Methicillin-resistant *Staphylococcus aureus* among animals: current overview. Clin Microbiol Infect 23:373–380. <https://doi.org/10.1016/j.cmi.2016.11.002>.
7. Krziwanek K, Metz-Gercek S, Mittermayer H. 2009. Methicillin-resistant *Staphylococcus aureus* ST398 from human patients, upper Austria. Emerg Infect Dis 15:766–769. <https://doi.org/10.3201/eid1505.080326>.
8. Golding GR, Bryden L, Levett PN, McDonald RR, Wong A, Wylie J, Graham MR, Tyler S, Van Domselaar G, Simor AE, Gravel D, Mulvey MR. 2010. Livestock-associated methicillin-resistant *Staphylococcus aureus* sequence type 398 in humans, Canada. Emerg Infect Dis 16:587–594. <https://doi.org/10.3201/eid1604.091435>.
9. Price LB, Stegger M, Hasman H, Aziz M, Larsen J, Andersen PS, Pearson T, Waters AE, Foster JT, Schupp J, Gillece J, Driebe E, Liu CM, Springer B, Zdovc I, Battisti A, Franco A, Zmudzki J, Schwarz S, Butaye P, Jouy E, Pomba C, Porrero MC, Ruimy R, Smith TC, Robinson DA, Weese JS, Arriola CS, Yu F, Laurent F, Keim P, Skov R, Aarestrup FM. 2012. *Staphylococcus aureus* CC398: host adaptation and emergence of methicillin resistance in livestock. mBio 3:e00305-11. <https://doi.org/10.1128/mBio.00305-11>.