



Draft Genome Sequences of 63 Swine-Associated Methicillin-Resistant *Staphylococcus aureus* Sequence Type 5 Isolates from the United States

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ABSTRACT Methicillin-resistant *Staphylococcus aureus* colonizes humans and other animals such as swine. Livestock-associated methicillin-resistant *Staphylococcus aureus* (LA-MRSA) sequence type 5 (ST5) isolates are a public concern due to their pathogenicity and ability to acquire mobile genetic elements. This report presents draft genome sequences for 63 LA-MRSA ST5 isolates in the United States.

Livestock-associated methicillin-resistant *Staphylococcus aureus* (LA-MRSA) was first isolated in association with the swine industry in 2004 (1). Healthy pigs were found to harbor LA-MRSA as a component of their normal microbiota, although there are reports of swine disease attributed to LA-MRSA (2–4). The most prevalent multilocus sequence type (ST) of LA-MRSA in swine varies based on geography, with ST398 and ST9 predominant in Europe and Asia, respectively (5, 6). In the United States, LA-MRSA isolates are more diverse, with ST398, ST9, and ST5 being found (7). Although ST398 and ST9 are considered to be livestock-adapted lineages, ST5 isolates comprise a widespread and highly pathogenic lineage (8). These characteristics have been attributed to the capacity of these isolates to acquire mobile genetic elements containing antimicrobial resistance genes or virulence factors (8). LA-MRSA ST5 isolates raise concerns due to their potential to cause disease and disseminate antimicrobial resistance elements, which can be further investigated through genome sequence analysis.

In this report, we present the draft genome sequences of 63 LA-MRSA ST5 isolates obtained during an Iowa State University study evaluating the presence and prevalence of LA-MRSA in the United States swine herd (7). Swabs were taken from healthy pigs and the environment of eight high-density livestock operations. All isolates and related information are listed in Table 1. Each isolate was grown in Trypticase soy broth (BD Biosciences, Sparks, MD) and total genomic DNA was extracted using the High Pure template preparation kit (Roche Applied Science, Indianapolis, IN).

Draft genome sequence data were produced using an Illumina MiSeq platform (Illumina, San Diego, CA). An indexed library was generated for each isolate using Nextera XT DNA sample preparation and index kits (Illumina). The isolates were then sequenced using a MiSeq v2 500-cycle reagent kit to generate 2 × 250-bp paired-end reads (Illumina).

Assemblies were generated using MIRA v.4.0.2 (<http://mira-assembler.sourceforge.net/docs/DefinitiveGuideToMIRA.html>). Average coverage for each isolate is listed in Table 1. Contigs were retained in the assembly if they were >1,500 bp in length and had a coverage of >66% of the average coverage for the genome. Repetitive elements identified by the assembly tool were required to be >2,000 bp for inclusion in the assembly.

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TABLE 1 LA-MRSA ST5 isolates

Isolate name	Isolate source	Farm no.	Avg coverage (%)	No. of contigs	GenBank accession no.
ISU 837	Environment	10	52.86	60	LKVQ00000000
ISU 839	Environment	10	40.15	138	LKVR00000000
ISU 842	Environment	10	77.53	115	LKVS00000000
ISU 871	Pig	24	62.61	137	LKVT00000000
ISU 872	Pig	24	64.16	107	LKVU00000000
ISU 873	Pig	24	57.95	110	LKVV00000000
ISU 874	Pig	24	58.50	175	LKVW00000000
ISU 875	Pig	24	50.01	107	LKVX00000000
ISU 876	Pig	24	35.52	198	LKVV00000000
ISU 877	Pig	24	25.39	168	LKVZ00000000
ISU 878	Pig	24	28.30	142	LKWA00000000
ISU 879	Pig	24	59.75	174	LKWB00000000
ISU 880	Pig	24	50.06	173	LKWC00000000
ISU 881	Pig	24	26.98	141	LKWD00000000
ISU 882	Pig	24	59.74	102	LKWE00000000
ISU 883	Environment	24	21.31	231	LKWF00000000
ISU 933	Pig	38	43.18	163	LKXB00000000
ISU 934	Pig	38	26.69	140	LKXC00000000
ISU 935	Pig	38	18.71	192	LKXD00000000
ISU 936	Pig	39	33.15	105	LKXE00000000
ISU 939	Pig	41	31.89	154	LKXF00000000
ISU 940	Environment	41	52.49	98	LKXG00000000
ISU 941	Pig	39	63.97	134	LKXH00000000
ISU 943	Environment	40	54.66	145	LKXI00000000
ISU 944	Environment	42	14.52	264	LKXJ00000000
ISU 946	Environment	41	36.83	80	LKXK00000000
ISU 947	Environment	42	39.23	164	LKXL00000000
ISU 948	Environment	42	18.98	172	LKXM00000000
ISU 949	Pig	42	52.56	126	LKXN00000000
ISU 951	Pig	42	35.47	131	LKXO00000000
ISU 952	Pig	42	34.31	153	LKXP00000000
ISU 953	Pig	42	27.51	115	LKXQ00000000
ISU 954	Pig	42	31.65	114	LKXR00000000
ISU 956	Pig	42	27.32	198	LKXS00000000
ISU 960	Environment	38	22.56	160	LKXT00000000
ISU 962	Environment	39	40.02	122	LKXV00000000
ISU 963	Environment	39	44.82	118	LKXW00000000
ISU 964	Environment	39	36.13	125	LKXX00000000
ISU 968	Pig	41	48.31	155	LKXY00000000
ISU 969	Pig	41	18.26	172	LKXZ00000000
ISU 970	Pig	41	30.09	91	LKYA00000000
ISU 971	Pig	39	21.67	187	LKYB00000000
ISU 972	Environment	42	17.93	91	LKYC00000000
ISU 973	Environment	42	52.18	200	LKYD00000000
ISU 976	Pig	39	16.94	261	LKYE00000000
ISU 978	Pig	39	53.16	188	LKYF00000000
ISU 979	Pig	41	51.52	176	LKYG00000000
ISU 980	Environment	41	68.97	126	LKYH00000000
ISU 981	Environment	39	78.78	142	LKYI00000000
ISU 982	Environment	42	46.30	272	LKYJ00000000
ISU 983	Environment	42	49.20	85	LKYK00000000
ISU 992	Pig	46	32.47	259	LKYL00000000
ISU 993	Environment	46	38.92	221	LKYM00000000
ISU 994	Environment	46	20.49	199	LKYN00000000
ISU 995	Environment	46	43.37	149	LKYO00000000
ISU 996	Environment	46	17.77	185	LKYP00000000
ISU 998	Environment	46	51.18	102	LKYQ00000000
ISU 1000	Pig	46	31.07	243	LKVI00000000
ISU 1001	Pig	46	22.23	157	LKVJ00000000
ISU 1002	Pig	46	29.08	157	LKVK00000000
ISU 1008	Pig	46	25.44	111	LKVN00000000
ISU 1009	Pig	46	55.49	69	LKVO00000000
ISU 1010	Pig	46	54.23	91	LKVP00000000

Accession number(s). The draft genome sequences generated in this study were deposited into DDBJ/ENA/GenBank with the accession numbers listed in Table 1.

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