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Whole-Genome Sequence of Staphylococcus aureus S54F9 Isolated from a Chronic Disseminated Porcine Lung Abscess and Used in Human Infection Models

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We obtained a draft genome sequence of Staphylococcus aureus strain S54F9, which was isolated from a chronic disseminated porcine lung abscess and used in porcine infection models. Genes coding for a number of toxins, including enterotoxins and superantigens, were demonstrated in this strain.

Staphylococcus aureus strain S54F9 was isolated in 2005 from a chronic embolic porcine lung abscess and has been applied in a number of porcine models of human infections, including hematogenous osteomyelitis (1–4), sepsis (5, 6), pyemia (7), endocarditis (8), and encephalitis (9). The strain was found to be useful in these types of porcine model infections, and information on relevant doses for inducing various degrees of sepsis has been obtained (5). In a comparative study, the strain was found to have a higher virulence in pigs than that of two human S. aureus strains, NCTC8325-4 and UAMS-1 (3).

The genome was sequenced with MiSeq (Illumina, San Diego, CA) using the paired-end method. The genome was assembled by CLC Genomics Workbench 7.0 (CLC bio, Qiagen, Hilden, Germany), with a quality trim level of 0.01, resulting in 3,688,424 reads with an average length of 248 nucleotides (nt), which assembled into 51 contigs >1,000 nt and resulted in a total genomic length of 2,775,659 nt. The G+C content was 32.8%. The genome has been annotated by the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP).

Based on an analysis of the genome sequence, the strain was found to belong to spa type t1333 and multilocus sequence type (MLST) ST433, confirming the results of previous typing (10). The strain was found to have a higher virulence in pigs than that of two human S. aureus strains, NCTC8325-4 and UAMS-1 (3).

The genome has been deposited at DDBJ/EMBL/GenBank under the accession no. LMIPHO000000. The first version is described here. The BioSample and BioProject numbers are SAMN04002937 and PRJNA293432, respectively.

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REFERENCES


