Complete Genome Sequence of *Staphylococcus aureus* MCRF184, a Necrotizing Fasciitis-Causing Methicillin-Sensitive Sequence Type 45 *Staphylococcus* Strain

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We report here the complete genome sequence of a highly virulent methicillin-sensitive *Staphylococcus aureus* strain, MCRF184, belonging to sequence type 45. This staphylococcal strain was isolated from a surgical biopsy specimen from a patient with necrotizing fasciitis.

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*S*taphylococcus aureus is a remarkable pathogen with emerging virulence. It is an uncommon cause of necrotizing fasciitis (1). However, the virulence associated with certain *S. aureus* strains and their increased ability to cause necrotizing fasciitis compared to others is not understood. To gain a better understanding of the overall pathogenesis and identify novel targets for new chemotherapeutic agents, researchers have been sequencing particularly virulent strains of *S. aureus* (2). In this paper, we report the complete annotated genome sequence obtained for *S. aureus* MCRF184, a strain isolated from the wounds of a 72-year-old diabetic male who suffered an above-the-knee amputation on his left leg due to necrotizing fasciitis (3).

The MCRF184 genome was sequenced by both a shotgun (single-end) and paired-end library approach. The shotgun and paired-end libraries were prepared and sequenced by using the GS TLX Titanium and GS FLX standard kits and protocols (Roche), respectively. The average read lengths for the shotgun and paired-end libraries were 171 bp and 300 bp, respectively. The 454 data were assembled using the gsAssembler program (version 2.0; Roche), which produced an overall depth of coverage between 25 and 30× for a 2.66-Mbp genome (70 to 84 Mbp of input sequence).

Overall, the assembly generated 233 large (≥500 bp) contigs spanning a total length of 2.66 Mbp. The paired-end information was then used to arrange 49 contigs into 19 scaffolds (total length of scaffolds, 2.66 Mbp). The two largest scaffolds, at 1.32 Mbp and 1.03 Mbp, account for 88% of this length. Further, they were assembled into 15 single contig scaffolds and 4 multicontig scaffolds (incorporating 33 contigs) representing the entire genome. The 33 contig sequences from MCRF184 were reordered in progressive-Mauve (4) using reference strain *S. aureus* MRSA252 (accession no. BX571856). Transfer RNAs and ribosomal RNAs were predicted by using Rfam (5). Putative open reading frames (ORFs) of the MCRF184 genome were predicted by Glimmer (6) and from a progressiveMauve (4) alignment using reference strain *S. aureus*

MRSA252 (accession no. BX571856). The final assembly and annotation were done in Geneious version 9.1.2 (7).

The MCRF184 genome contains 2,664,662 bp, with a G+C content of 32.9%. The genome contains 2,569 open reading frames, including 59 tRNA genes, 1 transfer-messenger RNA (tm-RNA), and 16 rRNAs.

The initial characterization of the genome using multilocus sequence typing (MLST) analysis (8) revealed *S. aureus* MCRF184 to be a member of sequence type 45 (ST45), a USA600 strain, and it lacked the staphylococcal chromosomal cassette, confirming its methicillin-susceptible phenotype.

Nucleotide sequence accession numbers. The complete genome sequence of *S. aureus* MCRF184 has been deposited at DDBJ/EMBL/GenBank under the accession no. CP014791. The version described in this paper is version CP014791.1. *S. aureus* MRCF184 belongs to BioProject no. PRJNA39571 and BioSample no. SAMN02953006.

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