



Complete Genome and Plasmid Sequences of *Staphylococcus aureus* EDCC 5055 (DSM 28763), Used To Study Implant-Associated Infections

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ABSTRACT *Staphylococcus aureus* EDCC 5055 (DSM 28763) is a human clinical wound isolate intensively used to study implant-associated infections in rabbit and rat infection models. Here, we report its complete genome sequence (2,794,437 bp) along with that of one plasmid (27,437 bp). This strain belongs to sequence type 8 and contains a *mecA* gene.

Staphylococci occur ubiquitously in nature and are colonizers of skin and mucous membranes of mammals and birds. *Staphylococcus aureus* is considered to be the most important human pathogen among the staphylococci. Approximately 30% of the human population carries this pathogen asymptotically in the anterior nares. However, *S. aureus* becomes an opportunistic pathogen when the host defense system is weakened, and it is considered a major nosocomial pathogen involved in soft skin infections, causing severe diseases comprising sepsis, endocarditis, toxic shock syndrome, and osteomyelitis (1). The clinical use of antibiotics for treatment of *S. aureus* infections has resulted in a rise in strains with antimicrobial resistance (2). *S. aureus* EDCC 5055 (Eugen Domann Culture Collection number 5055) deposited in German Collection of Microorganisms and Cell Cultures (DSM number 28763) was isolated from a human wound infection in 1995 and has been used as a model pathogen to study implant-associated infections (3–8). We determined the complete genome sequence of this strain using Illumina and PacBio sequencing platforms.

For whole-genome sequencing, genomic DNA was isolated from an overnight culture grown at 37°C in brain heart infusion (BHI) medium using the Qiagen Genomic-tip 100/G DNA extraction kit. Sequencing was performed with Illumina MiSeq (Illumina, The Netherlands) and PacBio RSII (Pacific Biosciences, USA) sequencers. For Illumina sequencing, a library was constructed using the Nextera XT sample prep kit. Paired-end sequencing yielded a total of 5,450,074 paired reads with a mean read length of 101 bp. P6-C4 chemistry was used for PacBio sequencing, which generated 150,292 prefiltered reads, with an average read length of 4,699 bp.

De novo genome assembly was carried out based on 48,617 postfiltered PacBio reads, with an average read length of 8,637 bp under the “RS_HGAP_Assembly.3” protocol included in SMRT Portal version 2.3.0. Finally, end trimming and circularization were performed. The chromosome was adjusted to *dnaA* as the first gene, and annotation was performed using Prokka 1.11 (9).

Received 15 December 2016 **Accepted** 23 December 2016 **Published** 23 February 2017

Citation Mannala GK, Hain T, Spröer C, Bunk B, Overmann J, Alt V, Domann E. 2017. Complete genome and plasmid sequences of *Staphylococcus aureus* EDCC 5055 (DSM 28763), used to study implant-associated infections. *Genome Announc* 5:e01698-16. <https://doi.org/10.1128/genomeA.01698-16>.

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The complete closed chromosome of *S. aureus* EDCC 5055 (DSM 28763) comprises 2,794,437 bp and has a G+C content of 32.84%, 2,549 coding sequences, 62 tRNAs, and 19 rRNAs. One intact prophage region was identified using PHAST. The strain also harbors a plasmid (termed pEDCC_5055) with a size of 27,437 bp.

In silico analysis revealed that the strain belongs to the sequence type 8 (ST8) and *spa* type 24 (t024). Its genome includes multiple chromosomal and plasmid-carried virulence genes (*sak*, *scn*, *splA*, *splB*, *splE*, *aur*, *lukD*, *lukE*, *hly*, *hlgA*, *hlgB*, and *hlgC*), enterotoxins (*ser*, *sej*, *sed*, and *sea*), and antimicrobial resistance genes (*spc*, *mecA*, *norA*, and *ermA*) (10–12). *S. aureus* EDCC 5055 (DSM 28763) appeared as a cryptic methicillin-resistant *S. aureus* (MRSA) strain (*mecA* gene present but not expressed), since the strain showed phenotypically no multiresistance at the beginning of isolation. Over the years of usage, the *mecA* gene became expressed and the MRSA phenotype became apparent (13). The high-quality closed genome sequence of *S. aureus* EDCC 5055 (DSM 28763) will provide the basis for future comparative genomics, for the understanding of the emergence of antimicrobial resistance, and in the study of host-pathogen interactions using transcriptomics.

Accession number(s). This whole-genome shotgun project has been deposited in the European Nucleotide Archive under the accession numbers [LT671859](#) (complete chromosome sequence) and [LT671860](#) (complete plasmid sequence). The versions described in this paper are the first versions.

ACKNOWLEDGMENTS

We thank Silke Zechel-Gran, Christina Gerstmann, Alexandra Amend, Nicole Hever, and Simone Severitt for excellent technical assistance.

This work was funded by two Research Grants of the University Medical Center Giessen and Marburg to E.D. and to V.A. The funders had no role in the study design, data collection and interpretation, or the decision to submit the work for publication.

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