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# Complete Genome Sequence of the Quality Control Strain *Staphylococcus aureus* subsp. *aureus* ATCC 25923

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***Staphylococcus aureus* subsp. *aureus* ATCC 25923 is commonly used as a control strain for susceptibility testing to antibiotics and as a quality control strain for commercial products. We present the completed genome sequence for the strain, consisting of the chromosome and a 27.5-kb plasmid.**

**Received** 18 September 2014 **Accepted** 28 September 2014 **Published** 6 November 2014

**Citation** Treangen TJ, Maybank RA, Enke S, Friss MB, Diviak LF, Karaolis DKR, Koren S, Ondov B, Phillippy AM, Bergman NH, Rosovitz MJ. 2014. Complete genome sequence of the quality control strain *Staphylococcus aureus* subsp. *aureus* ATCC 25923. Genome Announc. 2(6):e01110-14. doi:10.1128/genomeA.01110-14.

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*Staphylococcus aureus* is an opportunistic pathogen that can cause food poisoning, as well as a variety of infections (1). *Staphylococcus aureus* subsp. *aureus* ATCC 25923 is a clinical isolate with the designation Seattle 1945 that is used as a standard laboratory testing control strain. It is sensitive to a variety of antibiotics, including methicillin. The isolate contains a staphylococcal cassette chromosome–like (SCC-like) element that lacks both recombinases and *mecA* (2, 3). We report the complete genome of the isolate, comprising a 2,778,854-bp chromosome and a 27,491-bp plasmid, pS1945.

Genomic DNA was prepared from an isolate purchased through Remel Inc. (Lenexa, KS) under license with American Type Culture Collection (ATCC), and a 10-kb insert library was sequenced on the Pacific Biosciences RSII system. *De novo* assembly with Celera Assembler version 8.1 (4) and polishing with Quiver version 0.8 (5) resulted in a single contig each for the chromosome and plasmid. The average coverage for the chromosomal contig was 408×, and average coverage for the plasmid contig was 593×.

To our knowledge, this is the first report of a native plasmid in the ATCC 25923 (Seattle 1945) strain. The plasmid was nearly identical to plasmid SAP019A from the *S. aureus* strain NRS104 (GenBank accession GQ900385), containing two small insertions relative to SAP019A.

**Nucleotide sequence accession numbers.** The complete genome sequences of the chromosome and plasmid have been deposited in DDBJ/ENA/GenBank under the accession numbers CP009361 and CP009362, respectively.

## ACKNOWLEDGMENTS

This work was funded under agreement no. HSHQDC-07-C-00020 awarded by the Department of Homeland Security Science and Technology Directorate (DHS/S&T) for the management and operation of the National Biodefense Analysis and Countermeasures Center (NBACC), a Federally Funded Research and Development Center.

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## REFERENCES

1. **David MZ, Daum RS.** 2010. Community-associated methicillin-resistant *Staphylococcus aureus*: epidemiology and clinical consequences of an emerging epidemic. Clin. Microbiol. Rev. **23:**616–687. http://dx.doi.org/10.1128/CMR.00081-09.
2. **Ito T, Katayama Y, Asada K, Mori N, Tsutsumimoto K, Tiensasitorn C, Hiramatsu K.** 2001. Structural comparison of three types of staphylococcal cassette chromosome *mec* integrated in the chromosome in methicillin-resistant *Staphylococcus aureus*. Antimicrob. Agents Chemother. **45:**1323–1336. http://dx.doi.org/10.1128/AAC.45.5.1323-1336.2001.
3. **Jansen WT, Beitsma MM, Koeman CJ, van Wamel WJ, Verhoef J, Fluit AC.** 2006. Novel mobile variants of staphylococcal cassette chromosome *mec* in *Staphylococcus aureus*. Antimicrob. Agents Chemother. **50:**2072–2078. http://dx.doi.org/10.1128/AAC.01539-05.
4. **Koren S, Harhay GP, Smith TP, Bono JL, Harhay DM, McVey SD, Radune D, Bergman NH, Phillippy AM.** 2013. Reducing assembly complexity of microbial genomes with single-molecule sequencing. Genome Biol. **14:**R101. http://dx.doi.org/10.1186/gb-2013-14-9-r101.
5. **Chin CS, Alexander DH, Marks P, Klammer AA, Drake J, Heiner C, Clum A, Copeland A, Huddleston J, Eichler EE, Turner SW, Korlach J.** 2013. Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data. Nat. Methods **10:**563–569. http://dx.doi.org/10.1038/nmeth.2474.