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# Genome Sequence of the Clinical Isolate *Staphylococcus aureus* subsp. *aureus* Strain UAMS-1

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**We report here the draft genome sequence of *Staphylococcus aureus* subsp. *aureus* strain UAMS-1. UAMS-1 is a virulent oxacillin-susceptible clinical isolate. Its genome is composed of 2,763,963 bp and will be useful for further gene expression analysis using RNA sequencing (RNA-seq) technology.**

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*Staphylococcus aureus* is an opportunistic human bacterial pathogen responsible for nosocomial and community-associated infections. *S. aureus* subsp. *aureus* strain UAMS-1 was originally isolated from the bone of a patient suffering from osteomyelitis (1), and although it is a methicillin-susceptible *S. aureus* (MSSA) and oxacillin-susceptible *S. aureus* (OSSA) strain (2), UAMS-1 is generally considered to be most closely related to methicillin-resistant *S. aureus* strain MRSA252, whose genome was completed in 2004 (3, 4). While this strain is widely used by the community along with *S. aureus* strains RN1, Newman, COL, and USA300 (5), there are currently no genomic data available for UAMS-1. Here, we report the genome sequencing of strain UAMS-1, which is a prerequisite for sophisticated physiological or RNA-seq-based gene expression studies.

Genomic DNA was isolated from strain UAMS-1 grown in tryptic soy broth medium (5 ml) at 37°C using the Wizard genomic DNA purification kit (Promega), according to the manufacturer's recommendations for efficient lysis of *S. aureus*, washing it extensively with isopropanol and ethanol. Subsequently, the genomic DNA was precipitated with sodium acetate and washed twice with ethanol (70% [vol/vol]). DNA was sheared to yield ~600-bp fragments using an M220 focused ultrasonicator (Covaris). Unwanted small and large fragments were removed by size selection using AMPure XP beads (Beckman Coulter). The DNA library was prepared using the NEBNext Ultra DNA library prep kit for Illumina (NEB) and sequenced as paired-end reads using an Illumina MiSeq platform and the MiSeq reagent kit version 3 (600 cycles; Illumina, Inc.). The run generated 2,178,114 reads (630 Mb of sequence data) with 110× coverage.

The Illumina reads were trimmed using Trimmomatic (6), quality filtered using the Fastx-toolkit (http://hannonlab.cshl.edu/fastx_toolkit/), and then assembled using the SPAdes software (7, 8). GapFiller version 1.10 (9, 10) was used to improve the initial set of contigs, and the genome sequence of strain MRSA252 was used as the reference to order and orient the contigs. The draft genome sequence of *S. aureus* UAMS-1 yielded 2 scaffolds of 7 contigs containing 2,763,963 bp. The G+C content is 32.71%.

The genome of UAMS-1 was annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (11). The genome contains 2,808 genes, including 9 rRNAs (5S, 16S, and 23S), 60 tRNAs, and 86 pseudogenes. A total of 2,653 genes (94.5%) encode putative proteins that represent a coding capacity of 2,611,945 bp. Among these genes, 515 (19.41%) are annotated as encoding hypothetical proteins. Using the PHAge Search Tool (PHAST) (12) and CRISPRFinder (13), we detected one intact and complete *Staphylococcus* phage and five possible clustered regularly interspaced short palindromic repeats (CRISPRs), respectively. Finally, the average nucleotide identity between UAMS-1 and MRSA252 is 97.62%, suggesting that although they are considered to be closely related by the scientific community, there are potentially substantial differences between these two strains.

**Nucleotide sequence accession numbers.** The *S. aureus* subsp. *aureus* UAMS-1 genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. JTJK00000000. The version described in this paper is version JTJK01000000.

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## REFERENCES

1. **Gillaspy AF, Hickmon SG, Skinner RA, Thomas JR, Nelson CL, Smeltzer MS.** 1995. Role of the accessory gene regulator (*agr*) in pathogenesis of staphylococcal osteomyelitis. Infect Immun **63**:3373–3380.
2. **Cassat JE, Dunman PM, McAleese F, Murphy E, Projan SJ, Smeltzer MS.** 2005. Comparative genomics of *Staphylococcus aureus* musculoskeletal isolates. J Bacteriol **187**:576–592. http://dx.doi.org/10.1128/JB.187.2.576-592.2005.
3. **Holden MT, Feil EJ, Lindsay JA, Peacock SJ, Day NP, Enright MC, Foster TJ, Moore CE, Hurst L, Atkin R, Barron A, Bason N, Bentley SD, Chillingworth C, Chillingworth T, Churcher C, Clark L, Corton C, Cronin A, Doggett J, Dowd L, Feltwell T, Hance Z, Harris B, Hauser H, Holroyd S, Jagels K, James KD, Lennard N, Line A, Mayes R, Moule S, Mungall K, Ormond D, Quail MA, Rabbinowitsch E, Rutherford K, Sanders M, Sharp S, Simmonds M, Stevens K, Whitehead S, Barrell BG, Spratt BG, Parkhill J.** 2004. Complete genomes of two clinical *Staphylo-*

*coccus aureus* strains: evidence for the rapid evolution of virulence and drug resistance. Proc Natl Acad Sci U S A **101:**9786–9791. http://dx.doi.org/10.1073/pnas.0402521101.

4. **Olson PD, Kuechenmeister LJ, Anderson KL, Daily S, Beenken KE, Roux CM, Reniere ML, Lewis TL, Weiss WJ, Pulse M, Nguyen P, Simecka JW, Morrison JM, Sayood K, Asojo OA, Smeltzer MS, Skaar EP, Dunman PM.** 2011. Small molecule inhibitors of *Staphylococcus aureus* RnpA alter cellular mRNA turnover, exhibit antimicrobial activity, and attenuate pathogenesis. PLoS Pathog. **7:**e1001287. http://dx.doi.org/10.1371/journal.ppat.1001287.
5. **Herbert S, Ziebandt AK, Ohlsen K, Schäfer T, Hecker M, Albrecht D, Novick R, Götz F.** 2010. Repair of global regulators in *Staphylococcus aureus* 8325 and comparative analysis with other clinical isolates. Infect Immun **78:**2877–2889. http://dx.doi.org/10.1128/IAI.00088-10.
6. **Lohse M, Bolger AM, Nagel A, Fernie AR, Lunn JE, Stitt M, Usadel B.** 2012. RobiNA: a user-friendly, integrated software solution for RNA-seq-based transcriptomics. Nucleic Acids Res **40:**W622–W627. http://dx.doi.org/10.1093/nar/gks540.
7. **Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA.** 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol **19:**455–477. http://dx.doi.org/10.1089/cmb.2012.0021.
8. **Nurk S, Bankevich A, Antipov D, Gurevich AA, Korobeynikov A, Lapidus A, Prjibelski AD, Pyshkin A, Sirotkin A, Sirotkin Y, Stepanauskas R, Clingenpeel SR, Woyke T, McLean JS, Lasken R, Tesler G, Alekseyev MA, Pevzner PA.** 2013. Assembling single-cell genomes and mini-metagenomes from chimeric MDA products. J Comput Biol **20:**714–737. http://dx.doi.org/10.1089/cmb.2013.0084.
9. **Nadalin F, Vezzi F, Policriti A.** 2012. GapFiller: a *de novo* assembly approach to fill the gap within paired reads. BMC Bioinformatics **13**(Suppl 14):S8. http://dx.doi.org/10.1186/1471-2105-13-S14-S8.
10. **Boetzer M, Pirovano W.** 2012. Toward almost closed genomes with GapFiller. Genome Biol **13:**R56. http://dx.doi.org/10.1186/gb-2012-13-6-r56.
11. **Angiuoli SV, Gussman A, Klimke W, Cochrane G, Field D, Garrity G, Kodira CD, Kyrpides N, Madupu R, Markowitz V, Tatusova T, Thomson N, White O.** 2008. Toward an online repository of standard operating procedures (SOPs) for (meta)genomic annotation. Omics **12:**137–141. http://dx.doi.org/10.1089/omi.2008.0017.
12. **Zhou Y, Liang Y, Lynch KH, Dennis JJ, Wishart DS.** 2011. PHAST: a fast phage search tool. Nucleic Acids Res **39:**W347–W352. http://dx.doi.org/10.1093/nar/gkr485.
13. **Grissa I, Vergnaud G, Pourcel C.** 2007. CRISPRFinder: a Web tool to identify clustered regularly interspaced short palindromic repeats. Nucleic Acids Res **35:**W52–W57. http://dx.doi.org/10.1093/nar/gkm360.