Whole-Genome Sequence for Methicillin-Resistant Staphylococcus aureus Strain ATCC BAA-1680

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We report here the whole-genome sequence of the USA300 strain of methicillin-resistant Staphylococcus aureus (MRSA), designated ATCC BAA-1680, and commonly referred to as community-associated MRSA (CA-MRSA). This clinical MRSA isolate is commercially available from the American Type Culture Collection (ATCC) and is widely utilized as a control strain for research applications and clinical diagnosis. The isolate was propagated in ATCC medium 18, tryptic soy agar, and has been utilized as a model S. aureus strain in several studies, including MRSA genetic analysis after irradiation with 470-nm blue light.

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Methicillin-resistant Staphylococcus aureus (MRSA) is a Gram-positive bacterium responsible for a variety of clinical manifestations and increasing cases of community-acquired infections (1). MRSA infection accounts for 44% of all hospital-associated infections in the United States (2), and as many as 92% of persons hospitalized for MRSA have community-acquired (CA-MRSA), typically from the USA300 strain.

Whole-genome characterization has been performed for a number of MRSA clinical and reference S. aureus strains (3, 4). This is the first report of a whole-genome sequence for an American Type Culture Collection (ATCC) strain designated ATCC BAA-1680 (referred to here as reference strains 25b and 26b). Additionally, we report whole-genome sequences containing synonymous and non synonymous nucleotide mutations of four MRSA ATCC BAA-1680 isolates, 27b, 29b, 31b, and 33b, after exposure to blue light (at 470 nm) irradiation has on MRSA may be attributed to mutational changes identified by whole-genome analysis and may facilitate a better understanding of the antimicrobial effect of blue light, an alternative armamentarium for combating MRSA infections (6).

Nucleotide sequence accession numbers. The whole-genome sequences of MRSA ATCC BAA-1680 control strains 25b and 26b were deposited in the DDBJ/EMBL/GenBank databases under the accession numbers CP010299 and CP010298, respectively. The whole-genome sequences of four MRSA ATCC BAA-1680 blue light-treated strains were deposited in the DDBJ/EMBL/GenBank databases under the following accession numbers: CP010300 (strain 27b [at 3 J/cm²]), CP010295 (strain 29b [at 55 J/cm²]), CP010296 (strain 31b [at 110 J/cm²]), and CP010297 (strain 33b [at 110 J/cm²]).

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REFERENCES