Draft Genome Sequence of Methicillin-Susceptible Staphylococcus aureus Strain 06BA18369, a Pathogen Associated with Skin and Soft Tissue Infections in Northern Saskatchewan, Canada

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Here, we announce the draft sequence of a representative methicillin-susceptible Staphylococcus aureus (MSSA) isolate (06BA18369) whose strain type (spa type t311) was commonly isolated from skin and soft tissue coinfections with Streptococcus pyogenes. This strain sequence provides insight into a highly successful community-associated MSSA strain type.

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E fforts to elucidate the molecular epidemiology of Staphylococcus aureus in Canada have been largely focused on methicillin-resistant S. aureus (MRSA) infections acquired in health care settings and the emergence of MRSA that is associated with at-risk community populations (1–5). However, strains of methicillin-susceptible S. aureus (MSSA) isolated from community-acquired infections are seldom the subject of surveillance for antimicrobial susceptibility and strain typing. In northern Saskatchewan communities, MSSA was found to cause a high rate of skin and soft tissue infections (SSTI), in addition to those caused by community-acquired MRSA (CA-MRSA) USA400 strains (6). While MSSA isolates exhibited a greater genetic diversity than the collection of MRSA isolates, many of these MSSA isolates were coisolated with Streptococcus pyogenes in SSTI; MSSA spa type t311 and S. pyogenes emm type 41.2 made up the most commonly encountered pair of bacterial subtypes (7).

S. aureus 06BA18369 (spa type t311, sequence type 5 [ST5]) was isolated from an SSTI specimen, which also harbors S. pyogenes 06BA18369 (emm type 41.2, ST579), and was chosen for further genomic investigation.

Genome sequence data from S. aureus 06BA18369 were generated by the 454 Life Sciences GS-FLX genome sequencer (Roche Applied Science, Laval, Quebec, Canada) and consist of 262,689 reads with an average read length of 246 bases. Pyrosequencing reads were assembled with Newbler v1.1.03.24 (Roche) to generate 79 contigs of >500 bp. A fosmid genomic DNA library was screened to identify cloned fragments that were useful for gap closure. Direct sequencing reads of cloned fragments spanning gaps were assembled with existing contigs using Gap4 of the Staden package (8), and resulted in 59 contigs totaling 2,865,757 bases, with a G+C content of 32.7%.

Initial sequence analysis using GeneMark (9) revealed the presence of 2,793 putative protein-coding genes. tRNAscan (10) identified 59 tRNA genes, while RNAmmer (11) identified 6 rRNA genes.

This draft genome contains the genomic islands rSaα and rSaβ, with the latter carrying the cytotoxin genes lukD and lukE, as well as enterotoxin genes seg, sen, sef, sdu, and soo, and the truncated genes ets1 and ets2. In addition, S. aureus pathogenicity island 2 (SaPI2) is present, harboring the superantigen-encoding genes sec, sel, and tst. Four putative prophage sequences were identified using PHAST (12) as belonging to the bacteriophage families φSa1, φSa3, φSa6, and φSa7 (13). φSa3 harbors the staphylococcal cassette chromosome (SCC) element with a type 1 ccr gene complex, but it lacks a mec complex (14). This SCC (SCC476) is approximately 18.5 kb in size and contains 16 open reading frames (ORFs). BLASTn searches of ORFs returned sequences homologous to the SCC regions originating from S. aureus strain MSSA476 (15). Staphylococcus hominis GIFU12263 (16), and Staphylococcus epidermidis isolates ATCC 12228 (17) and VCU120. Most notably, SCC476 harbors an ORF with 100% nucleotide identity to the putative fusidic acid resistance gene far1 harbored by SCC476 of S. aureus MSSA476 (15).

Further work is required to ascertain the prevalence of MSSA harboring SCC in individuals in northern Saskatchewan communities.

Nucleotide sequence accession numbers. This Whole-Genome Shotgun project has been deposited at GenBank under the accession no. ARXY00000000. The version described in this paper is the first version, accession no. ARXY01000000.

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