

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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Efforts 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) iden-

tified 59 tRNA genes, while RNAmmer (11) identified 6 rRNA regions.

This draft genome contains the genomic islands ν Sa α and ν Sa β , with the latter carrying the cytotoxin genes *lukD* and *lukE*, as well as enterotoxin genes *seg*, *sen*, *sei*, *sem*, and *seo*, and the truncated genes ψ ent1 and ψ ent2. 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 PFAST (12) as belonging to the bacteriophage families ϕ Sa1, ϕ Sa3, ϕ Sa6, and ϕ Sa7 (13). ϕ Sa3 harbors the staphylokinase and staphylococcal complement inhibitor-encoding genes *sak* and *scin*, respectively.

S. aureus 06BA18369 contains a staphylococcal cassette chromosome (SCC) element with a type 1 *ccr* gene complex, but it lacks a *mec* complex (14). This SCC (SCC₁₈₃₆₉) 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, SCC₁₈₃₆₉ 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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REFERENCES

1. Simor A, Boyd D, Louie L, McGeer A, Mulvey M, Willey B, Canadian Hospital Epidemiology Committee and the Canadian Nosocomial Infection Surveillance Program. 1999. Characterization and proposed nomenclature of epidemic strains of MRSA in Canada. *Can. J. Infect. Dis.* 10:333–336.
2. Simor AE, Ofner-Agostini M, Bryce E, McGeer A, Paton S, Mulvey MR, Canadian Hospital Epidemiology Committee and Canadian Nosocomial Infection Surveillance Program, Health Canada. 2002. Laboratory characterization of methicillin-resistant *Staphylococcus aureus* in Canadian hospitals: results of 5 years of national surveillance, 1995–1999. *J. Infect. Dis.* 186:652–660.
3. Mulvey MR, MacDougall L, Cholin B, Horsman G, Fidyk M, Woods S, Saskatchewan CA-MRSA Study Group. 2005. Community-associated methicillin-resistant *Staphylococcus aureus*, Canada. *Emerg. Infect. Dis.* 11:844–850.
4. Gilbert M, MacDonald J, Gregson D, Siushansian J, Zhang K, Elsayed S, Laupland K, Louie T, Hope K, Mulvey M, Gillespie J, Nielsen D, Wheeler V, Louie M, Honish A, Keays G, Conly J. 2006. Outbreak in Alberta of community-acquired (USA300) methicillin-resistant *Staphylococcus aureus* in people with a history of drug use, homelessness or incarceration. *CMAJ* 175:149–154.
5. Nichol KA, Adam HJ, Hussain Z, Mulvey MR, McCracken M, Mataseje LF, Thompson K, Kost S, Lagacé-Wiens PR, Hoban DJ, Zhanel GG, Canadian Antimicrobial Resistance Alliance (CARA). 2011. Comparison of community-associated and health care-associated methicillin-resistant *Staphylococcus aureus* in Canada: results of the CANWARD 2007–2009 study. *Diagn. Microbiol. Infect. Dis.* 69:320–325.
6. Golding GR, Levett PN, McDonald RR, Irvine J, Quinn B, Nsungu M, Woods S, Khan M, Ofner-Agostini M, Mulvey MR, Northern Antibiotic Resistance Partnership. 2011. High rates of *Staphylococcus aureus* USA400 infection, northern Canada. *Emerg. Infect. Dis.* 17:722–725.
7. McDonald RR, Golding GR, Levett PN, Yost CK, Irvine J, Horsman GB, Mulvey MR, the Northern Antibiotic Resistance Partnership. 2008. Characterization of *Streptococcus pyogenes* and *Staphylococcus aureus* isolates associated with mixed skin and soft tissue infections in northern Saskatchewan. *Can. J. Infect. Dis. Med. Microbiol.* 19:77–142.
8. Bonfield JK, Smith KF, Staden R. 1995. A new DNA sequence assembly program. *Nucleic Acids Res.* 23:4992–4999.
9. Besemer J, Borodovsky M. 2005. GeneMark: web software for gene finding in prokaryotes, eukaryotes and viruses. *Nucleic Acids Res.* 33:W451–W454.
10. Schattner P, Brooks AN, Lowe TM. 2005. The tRNAscan-SE, snoscan and snoGPS web servers for the detection of tRNAs and snoRNAs. *Nucleic Acids Res.* 33:W686–W689.
11. Lagesen K, Hallin P, Rødland EA, Staerfeldt HH, Rognes T, Ussery DW. 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. *Nucleic Acids Res.* 35:3100–3108.
12. Zhou Y, Liang Y, Lynch KH, Dennis JJ, Wishart DS. 2011. PHAST: a fast phage search tool. *Nucleic Acids Res.* 39:W347–W352.
13. Lindsay JA, Holden MT. 2004. *Staphylococcus aureus*: superbug, super genome? *Trends Microbiol.* 12:378–385.
14. International Working Group on the Classification of Staphylococcal Cassette Chromosome Elements (IWG-SCC). 2009. Classification of staphylococcal cassette chromosome *mec* (SCC*mec*): guidelines for reporting novel SCC*mec* elements. *Antimicrob. Agents Chemother.* 53:4961–4967.
15. 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, Rabinowitsch 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 *Staphylococcus aureus* strains: evidence for the rapid evolution of virulence and drug resistance. *Proc. Natl. Acad. Sci. U. S. A.* 101:9786–9791.
16. Katayama Y, Takeuchi F, Ito T, Ma XX, Ui-Mizutani Y, Kobayashi I, Hiramatsu K. 2003. Identification in methicillin-susceptible *Staphylococcus hominis* of an active primordial mobile genetic element for the staphylococcal cassette chromosome *mec* of methicillin-resistant *Staphylococcus aureus*. *J. Bacteriol.* 185:2711–2722.
17. Mongkolrattanothai K, Boyle S, Murphy TV, Daum RS. 2004. Novel non-*mecA*-containing staphylococcal chromosomal cassette composite island containing *pbp4* and *tagF* genes in a commensal staphylococcal species: a possible reservoir for antibiotic resistance islands in *Staphylococcus aureus*. *Antimicrob. Agents Chemother.* 48:1823–1836.