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Draft Genome Sequence of *Streptococcus pyogenes* Strain 06BA18369, a Human Pathogen Associated with Skin and Soft Tissue Infections in Northern Canada

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We report the draft sequence of *Streptococcus pyogenes* 06BA18369 (*emm* type 41.2, sequence type 579 [ST579]), isolated from a skin and soft tissue infection (SSTI) mixed with *Staphylococcus aureus*. This genome provides insight into the genetic composition of *S. pyogenes* strains associated with mixed SSTIs.

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Streptococcus pyogenes can cause a variety of infections in humans that range from mild superficial infections to severe invasive disease. *S. pyogenes* isolates are uniformly susceptible to penicillin but have demonstrated resistance to other classes of antimicrobials, including macrolides, tetracyclines, and lincosamides (1–3). Epidemiological surveillance of *S. pyogenes* in Canada has identified *emm* type 1 as its leading cause of invasive infections (4). Recently, an epidemic of invasive *emm* type 59 infections has been described in Canada (4, 5). Concurrently, mixed skin and soft tissue infections (SSTI) associated with *S. pyogenes emm* type 41.2 and *Staphylococcus aureus spa* type t311 were found to be prevalent in a region of northern Canada that is endemic for community-associated methicillin-resistant *S. aureus* (CA-MRSA) (6, 7).

In this study, one mixed SSTI case was selected for further analysis, and *S. pyogenes* 06BA18369 (*emm* type 41.2; sequence type 579 [ST579]) was selected for genome sequencing. Whole-genome shotgun sequencing was performed with the 454 Life Sciences GS-FLX genome sequencer (Roche Applied Science, Laval, Quebec, Canada). The initial read assembly by Newbler v1.1.03.24 (Roche) generated 59 contigs of >500 bp. Gap closure was initiated by Sanger sequencing DNA inserts of clones isolated from a fosmid genomic DNA library. Sequence reads spanning the contig gaps were assembled using Gap4, provided in the Staden package (8). The final draft genome sequence consists of 47 contigs that includes a combined 1,813,404 bases with 38.4% G+C content. Contig sequences were analyzed for the presence of putative protein-coding sequences, tRNA genes, and rRNA regions with GeneMark (9), tRNAscan (10), and RNAmmer (11), respectively. GeneMark identified 1,840 putative coding sequences, while 30 tRNA genes and three rRNA regions were recognized.

Annotation of contig sequences indicated the presence of the *emm*-like genes *mrp* and *enn*. Phylogenetic analysis and genetic organization of the three *emm*-like gene sequences were consistent with the *emm* pattern D group, which includes strains associated with skin and soft tissue infections (12). Contig sequences were queried for prophage content using PHAST (13), revealing the presence of five regions consistent with a known prophage. These prophages are similar to those identified in other sequenced genomes with respect to integrase gene homology and virulence factor content. Four putative prophages harbor integrase-encoding genes, each showing 100% sequence identity with phage-1, phage-2, phage-3, and prophage-like element SpyCIM53 of *S. pyogenes* strain Alab49 (14), and carry the virulence factor genes *speL*, *speM*, *speC*, *mf2*, and *mf3*. The fifth prophage is similar to *S. pyogenes* strain MGAS315 phage 315.6 (15), based upon *int* sequence identity (100%) and the presence of the virulence factor gene *sdn*.

S. pyogenes 06BA18369 also carries a *cas*-CRISPR array that spans the gap between two contigs. As such, this array consists of at least seven spacers, all but one being homologous to known prophage sequences detected in either other *S. pyogenes* strains or *Streptococcus agalactiae* strains.

This draft genome sequence adds to the collection of genomes of *S. pyogenes* strains that originate from skin and soft tissue infections.

Nucleotide sequence accession numbers. This Whole-Genome Shotgun project has been deposited at GenBank under the accession no. APMZ00000000. The version described in this paper is the first version, accession no. APMZ01000000.

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