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GENOME ANNOUNCEMENT

Complete Genome Sequence of *Streptococcus pyogenes* M1 476, Isolated from a Patient with Streptococcal Toxic Shock Syndrome

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Here, we report the completely annotated genome sequence of *Streptococcus pyogenes* M1 476 isolated from a patient with streptococcal toxic shock syndrome (STSS) during pregnancy. The genome sequence will provide new insights into the mechanisms underlying STSS.

Group A streptococci (GAS) cause a wide variety of infectious diseases that range from relatively benign to life-threatening, including streptococcal toxic shock syndrome (STSS). GAS can be subtyped according to the genotype of *emm*, which encodes the M protein expressed on the bacterial cell surface. Particular *emm* types of GAS have been associated with certain diseases (2, 4). *emm1* GAS has been found predominantly in patients with STSS. *Streptococcus pyogenes* M1 GAS 476 was isolated from a patient with STSS during pregnancy in 1994 and showed the strongest virulence in a mouse STSS model (designated M1-d in reference 5).

Here, an 8-kb pair-end library of the *S. pyogenes* M1 476 genome was prepared and used for sequence analysis with a GS junior titanium sequencer (Roche). This generated 185,092 reads, covering 40,467,919 bp (22.2-fold coverage), which were assembled into contigs and scaffolds by using a GS De Novo Assembler 2.6 (Newbler; Roche). Gap filling among the contigs and scaffolds was then performed by conventional Sanger sequencing of the PCR fragments based on brute-force PCR. Finally, the 5,968,488 pair-end reads determined using a Genome Analyzer IIx (Illumina) were added to the draft genome sequence. Primary coding segment extraction was performed using MetaGeneAnnotator (6). Initial functional assignment and manual correction were carried out by *in silico* molecular cloning. Prophage regions and clustered regularly interspaced short palindromic repeats (CRISPRs) were identified by Prophage Finder (1) and CRISPRFinder (3), respectively. The *S. pyogenes* M1 GAS 476 genome consists of a single circular chromosome of 1,813,709 bp with an average GC content of 38.5%. The chromosome was shown to contain a total of 1,848 protein-coding genes, 57 tRNA genes for all amino acids, and 5 *rrn* operons. In addition, the chromosome harbors 5 prophage-like elements. The prophage regions contain genes corresponding to superantigen (two genes), streptodornase, and mitogenic factor. The chromosome also contains five putative CRISPRs.

Nucleotide sequence accession number. The nucleotide sequence of the chromosome of *S. pyogenes* M1 GAS 476 has been deposited in the DNA Database of Japan under accession no. AP012491.

ACKNOWLEDGMENTS

We thank M. Komiya and Y. Sakurai for excellent work in the genome analysis.

This study was supported by a Grant for International Health Research (GIHR) (23A301) from the Ministry of Health, Labor, and Welfare (MHLW). T.M.-A. was supported by a KAKENHI grant (24390109) from the Japanese Society for the Promotion of Science (JSPS).

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Received 12 July 2012 Accepted 17 July 2012

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doi:10.1128/JB.01265-12