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Full-Length Genome Sequence of Type M/*emm83* Group A *Streptococcus pyogenes* Strain STAB1101, Isolated from Clustered Cases in Brittany

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Here, we announce the complete annotated genome sequence of a *Streptococcus pyogenes* M/*emm83* strain, STAB1101, isolated from clustered cases in homeless persons in Brittany (France). The genome is composed of 1,709,790 bp, with a G+C content of 38.4% and 1,550 identified coding sequences (CDS), and it harbors a Tn*916*-like transposon.

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Streptococcus pyogenes, or group A *Streptococcus* (GAS), is an important Gram-positive human pathogen that causes a wide variety of infectious diseases ranging from noninvasive to life-threatening in severity (1). GAS strains are currently typed by sequencing the 5′ hypervariable region of the *emm* gene, which encodes the M protein (2). Studies of large numbers of GAS isolates worldwide have shown that only a few genotypes account for the most invasive infections (3). The *emm* genotypes that cause rare disease are mainly described during epidemics (4–7). We recently described the clonal spread of GAS M/*emm44* and sequenced a virulent strain (STAB901) isolated in 2009 (7, 8). Subsequent to the extinction of M/*emm44* GAS at the end of 2010 (our unpublished data), we observed clustered cases of infections due to M/*emm83*. This is a rare genotype that has been reported in injecting drug users (IDUs) in the United Kingdom (9). We recorded 7 new cases of infections during the summer of 2011, from which 5 patients lived in the same town, and 4 had poor living conditions (homeless and/or IDUs).

In order to understand bacterial epidemics and to add new information to the emerging field of molecular pathogenomics, we sequenced and annotated the whole genome of an M/*emm83* group A *Streptococcus* invasive strain (necrotizing fasciitis) isolated in Brittany, named STAB1101.

The STAB1101 strain grown in Todd-Hewitt medium supplemented with 0.2% yeast extract (THY) and DNA for sequencing was extracted and purified using the phenol-chloroform technique. Genomic DNA was sequenced using HiSeq 2000 technology (Illumina, Inc., San Diego, CA), and the paired-end library was built using the Montpellier GenomiX (MGX) facility of the CNRS in Montpellier, France. There were a total of 37,090,274 high-quality reads giving an average of 2,390-fold coverage of the genome, which was assembled *de novo* using the CLC Genomics Workbench version 6 software.

The resulting assembly consisted of 104 contigs, which were oriented and connected with the module Microbial Genome Finishing Tools. After reassembling, 9 gaps persisted. The gaps were filled by PCR, followed by Sanger sequencing. Genome annotation was performed in parallel using the RAST server (10) and NCBI-PGAP (http://ncbi.nlm.nih.gov/genome/annotation_prok). Prophages were identified using the PHAge Search Tool (PHAST) (11). Finally, strain STAB1101 was found to harbor a single circular genome of 1,709,790 bp, with a G+C content of 38.4%. We identified 1,550 coding sequences (CDSs), 67 tRNA genes, 18 rRNA genes, and one incomplete prophage (33 Kb, 44 CDSs, and a G+C content of 35.24%). The superantigen genes identified were *speG*, *speL*, *speM*, and *smeZ*. In addition, and as found within the chromosome of the GAS strain STAB901, the genome analysis of strain STAB1101 showed the presence of a Tn*916*-like transposon that has a close similarity to Tn*6253* (8) but does not harbor a group II intron. Its insertion site is located in a noncoding sequence between inosine 5-monophosphate and a sugar transporter.

This complete genome of a GAS strain isolated from clustered cases brings the opportunity to study its clonal origin and rate of genome diversification over the short epidemic period.

Nucleotide sequence accession number. The complete whole-genome sequence of *S. pyogenes* strain STAB1101 has been deposited in the NCBI under the accession no. CP007240.1. The version described in this paper is the first version.

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