

# Complete Genome Sequence of Noninvasive *Streptococcus pyogenes* M/*emm28* Strain STAB10015, Isolated from a Child with Perianal Dermatitis in French Brittany

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**We report here the complete genome sequence of a noninvasive strain of *Streptococcus pyogenes* M/*emm28*, isolated from perianal dermatitis in a child. The genome is composed of 1,950,454 bp, with a G+C content of 38.2%, and it has 1,925 identified coding sequences and harbors two intact prophages and a new integrating conjugative element (ICE).**

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*Streptococcus pyogenes*, or group A streptococcus (GAS), is a Gram-positive human-specific pathogen that causes a broad range of invasive and noninvasive diseases. Although the throat and skin are the primary ecological niches, the genotype M/*emm28* of GAS has been described as a disease specializing in perineal infections (1). Streptococcal perianal dermatitis (SPD) caused by GAS is a noninvasive infection that occurs mainly in children between 6 months and 5 years of age, affecting boys more often than girls (2). In an effort to gain new insights into invasive M/*emm28* GAS infections, we sequenced and annotated the whole genome of one strain, named STAB10015, isolated in 2010 from a child (a young boy) with SPD and compared it with that of the sequenced strain MGAS6180 isolated from a patient with puerperal sepsis (1).

The strain STAB10015 was 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 at the MGX facility of the CNRS in Montpellier, France. There is a total of 36,785,510 high-quality reads, giving an average of 1,933-fold coverage of the genome, which was assembled using the CLC Genomics Workbench version 6 software. The resulting assembly consisted of 56 contigs, which were oriented and connected with the module Microbial Genome Finishing Tools based on the MGAS6180 sequence. After reassembling, 11 gaps persisted, which were filled by PCR, followed by Sanger sequencing. Genome annotation was performed in parallel by using the RAST server (3) and NCBI PGAP ([http://ncbi.nlm.nih.gov/genome/annotation\\_prok](http://ncbi.nlm.nih.gov/genome/annotation_prok)). Prophages were identified using the PHAge Search Tool (PHAST) (4). Finally, strain STAB10015 was found to harbor a single circular genome of 1,950,454 bp, with a G+C content of 38.2%. We identified 1,925 coding sequences (CDSs), 65 tRNA genes, 18 rRNA genes, and two intact integrated

prophages. The multilocus sequence type (ST) (5) was determined to be ST52.

In comparison with MGAS6180, all known virulence factors (6, 7) (proteinases, gene regulators, and adhesion proteins) were also identified in STAB10015. It contains genes encoding the secreted superantigens SpeC, SpeG, SpeJ, SmeZ, and SpeK. Nonsynonymous single-nucleotide polymorphisms (SNPs) were present in several genes coding for proteases (*speB*), exoenzymes (*hylP*), immunoreactive antigens (*isp1*), and adhesion proteins (*sof*, *enn*, and *spr28* from the region-deleted 2 [RD2] region). Many genes encoding adhesins (*emm*, *mrp*-*emm*-like, *sclA*, *sclB*, and *sbfx*) or proteases (*scp*) presented significant deletions. We also identified a new integrating conjugative element (ICE) with a length of 54.2 kb, not encoding apparent virulence factors or antibiotic resistance genes, and it is inserted in the 3' end of the tRNA uracil-5-methyltransferase gene, described as a hot spot for ICE (8). Sequence comparisons indicated significant homology with other intestinal bacterial ICEs (*Streptococcus dysgalactiae* RE378 [9] and *Clostridium difficile* 630 [10]). These bacterial interactions might result in antibiotic resistance gene [*erm*(TR)-*tet*(O)] acquisition, as described for ICESp2905 in the IB21 GAS strain (11).

Before deciphering the bacterial phenotype and invasive potential, it is necessary to compare the STAB10015 sequence with that of strains isolated in the same geographical and temporal context.

**Nucleotide sequence accession numbers.** The complete genome sequence of *S. pyogenes* strain STAB10015 has been deposited in the NCBI under the accession no. [CP011068](https://ncbi.nlm.nih.gov/nucl/CP011068), part of BioProject PRJNA278400.

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## REFERENCES

- Green NM, Zhang S, Porcella SF, Nagiec MJ, Barbian KD, Beres SB, LeFebvre RB, Musser JM. 2005. Genome sequence of a serotype M28 strain of group A streptococcus: potential new insights into puerperal sepsis and bacterial disease specificity. *J Infect Dis* 192:760–770. <http://dx.doi.org/10.1086/430618>.
- Amren DP, Anderson AS, Wannamaker LW. 1966. Perianal cellulitis associated with group A streptococci. *Am J Dis Child* 112:546–552. <http://dx.doi.org/10.1001/archpedi.1966.02090150090007>.
- Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 9:75. <http://dx.doi.org/10.1186/1471-2164-9-75>.
- Zhou Y, Liang Y, Lynch KH, Dennis JJ, Wishart DS. 2011. PHAST: a fast phage search tool. *Nucleic Acids Res* 39:W347–W352. <http://dx.doi.org/10.1093/nar/gkr485>.
- Enright MC, Spratt BG, Kalia A, Cross JH, Bessen DE. 2001. Multilocus sequence typing of *Streptococcus pyogenes* and the relationships between *emm* type and clone. *Infect Immun* 69:2416–2427. <http://dx.doi.org/10.1128/IAI.69.4.2416-2427.2001>.
- Chen L, Yang J, Yu J, Yao Z, Sun L, Shen Y, Jin Q. 2005. VFDB: a reference database for bacterial virulence factors. *Nucleic Acids Res* 33:D325–D328. <http://dx.doi.org/10.1093/nar/gki008>.
- Nakagawa I, Kurokawa K, Yamashita A, Nakata M, Tomiyasu Y, Okahashi N, Kawabata S, Yamazaki K, Shiba T, Yasunaga T, Hayashi H, Hattori M, Hamada S. 2003. Genome sequence of an M3 strain of *Streptococcus pyogenes* reveals a large-scale genomic rearrangement in invasive strains and new insights into phage evolution. *Genome Res* 13:1042–1055. <http://dx.doi.org/10.1101/gr.1096703>.
- Brenciani A, Tiberi E, Bacciaglia A, Petrelli D, Valardo PE, Giovanetti E. 2011. Two distinct genetic elements are responsible for *erm*(TR)-mediated erythromycin resistance in tetracycline-susceptible and tetracycline-resistant strains of *Streptococcus pyogenes*. *Antimicrob Agents Chemother* 55:2106–2112. <http://dx.doi.org/10.1128/AAC.01378-10>.
- Okumura K, Shimomura Y, Murayama SY, Yagi J, Ubukata K, Kirikae T, Miyoshi-Akiyama T. 2012. Evolutionary paths of streptococcal and staphylococcal superantigens. *BMC Genomics* 13:404. <http://dx.doi.org/10.1186/1471-2164-13-404>.
- Sebahia M, Wren BW, Mullany P, Fairweather NF, Minton N, Stabler R, Thomson NR, Roberts AP, Cerdeño-Tárraga AM, Wang H, Holden MT, Wright A, Churcher C, Quail MA, Baker S, Bason N, Brooks K, Chillingworth T, Cronin A, Davis P, Dowd L, Fraser A, Feltwell T, Hance Z, Holroyd S, Jagels K, Moule S, Mungall K, Price C, Rabinowitsch E, Sharp S, Simmonds M, Stevens K, Unwin L, Whithead S, Dupuy B, Dougan G, Barrell B, Parkhill J. 2006. The multidrug-resistant human pathogen *Clostridium difficile* has a highly mobile, mosaic genome. *Nat Genet* 38:779–786. <http://dx.doi.org/10.1038/ng1830>.
- Giovanetti E, Brenciani A, Tiberi E, Bacciaglia A, Valardo PE. 2012. ICE $Sp2905$ , the *erm*(TR)-*tet*(O) element of *Streptococcus pyogenes*, is formed by two independent integrative and conjugative elements. *Antimicrob Agents Chemother* 56:591–594. <http://dx.doi.org/10.1128/AAC.05352-11>.