



Complete Genome Sequences of Two Strains of *Streptococcus pyogenes* Belonging to an Emergent Clade of the Genotype emm89 in Brittany, France

Marie Devaere, Sarrah Boukthir, Séverine Moullec, Emeline Roux, Dominique Lavenier, Ahmad Faili, Samer Kayal

► To cite this version:

Marie Devaere, Sarrah Boukthir, Séverine Moullec, Emeline Roux, Dominique Lavenier, et al.. Complete Genome Sequences of Two Strains of *Streptococcus pyogenes* Belonging to an Emergent Clade of the Genotype emm89 in Brittany, France. *Microbiology Resource Announcements*, 2020, 9 (11), pp.e00129-20. 10.1128/MRA.00129-20 . hal-02532959

HAL Id: hal-02532959

<https://univ-rennes.hal.science/hal-02532959>

Submitted on 6 Apr 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License



Complete Genome Sequences of Two Strains of *Streptococcus pyogenes* Belonging to an Emergent Clade of the Genotype *emm89* in Brittany, France

Marie Devaere,^b Sarrah Boukthir,^{a,b} Séverine Moullec,^b Emeline Roux,^{c*} Dominique Lavenier,^c Ahmad Faili,^b  Samer Kayal^{a,b}

^aCHU Rennes—Service de Bactériologie et Hygiène Hospitalière, Rennes, France

^bINSERM CIC-1414, Rennes, France

^cINRIA/IRISA, GenScale Bioinformatics Team, Rennes, France

ABSTRACT The frequency of infections due to *Streptococcus pyogenes* M/*emm89* strains is increasing, presumably due to the emergence of a genetically distinct clone. We sequenced two *emm89* strains isolated in Brittany, France, in 2009 and 2010 from invasive and noninvasive infections, respectively. Both strains belong to a newly emerged *emm89* clade 3 clone.

Group A beta-hemolytic *Streptococcus pyogenes* (GAS) is a Gram-positive human pathogen associated with a variety of human diseases, with an estimated 517,000 deaths per year (1). For epidemiological surveying of GAS infections, the *emm* genotype is a worldwide accepted marker (2, 3). Within the genotype *emm89*, genome remodeling led to the emergence of a new clade variant designated clade 3, recognized to be frequently associated with invasive infections in Europe (4, 5). Whereas at the beginning of our epidemiological survey (2009), the proportion of *emm89* among all *emm* genotypes was less than 10%, it reached 29% in 2017 and represents the most dominant genotype in Brittany, France.

In order to decipher whether the genotype *emm89* belonging to clade 3 was already circulating in French Brittany as early as 2009, we sequenced the whole genomes of two strains isolated in the university hospital of Rennes from a case of noninvasive vaginitis (2009; 39.9-year-old female) and one of invasive facial dermo-hypodermatitis (2010; 2.6-year-old male), hereafter referred to as strains STAB09023 and STAB10048, respectively.

Strains were grown in Todd-Hewitt medium supplemented with 0.2% yeast (THY), and DNA was extracted as previously described (6). Libraries were prepared with the Nextera XT kit (Illumina, Inc., San Diego, CA) and subjected to paired-end sequencing (2 × 125 bp) on a HiSeq 2500 system (Illumina). The total read counts were 12,473,106 (STAB0902) and 13,677,462 (STAB10048), giving an average of 817-fold coverage for both strains. The quality of reads was assessed by FastQC (7).

Reads were assembled using CLC Genomics Workbench v. 6 software (Qiagen Bioinformatics, Aarhus, Denmark). Default parameters were used for all software. The resulting assembly consisted of 21 (STAB0902; *N*₅₀, 155,832 bp) and 22 (STAB1004; *N*₅₀, 162,752 bp) contigs, which were placed and oriented manually based on the *emm89* reference genome MGAS27061 (8). All the persistent gaps were filled by PCR, followed by Sanger sequencing of the amplified sequences, and the gapless genomes consisted of 1,741,934 bp (STAB0902) and 1,742,165 bp (STAB10048), with a G+C content of 38.5% for each of them. Annotations were performed by using the RAST server (9) and NCBI PGAP (http://ncbi.nlm.nih.gov/genome/annotation_prok), and prophages were examined using the PHAge search tool (PHAST) (10). For both genomes, we identified a total of 17,383 coding sequences (CDSs), 15 rRNAs, 57 tRNAs, 2 complete CRISPR

Citation Devaere M, Boukthir S, Moullec S, Roux E, Lavenier D, Faili A, Kayal S. 2020. Complete genome sequences of two strains of *Streptococcus pyogenes* belonging to an emergent clade of the genotype *emm89* in Brittany, France. Microbiol Resour Announc 9:e00129-20. <https://doi.org/10.1128/MRA.00129-20>.

Editor Steven R. Gill, University of Rochester School of Medicine and Dentistry

Copyright © 2020 Devaere et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Ahmad Faili, ahmad.faili@univ-rennes1.fr, or Samer Kayal, samer.kayal@univ-rennes1.fr.

* Present address: Emeline Roux, Calbinotox, Université de Lorraine, Nancy, France.

Received 10 February 2020

Accepted 19 February 2020

Published 12 March 2020

sequences, and 2 integrated prophages that vary in G+C content from 37.6 to 38.7%. In particular, we found a prophage element that carried the superantigen *SpeC* (*speC*) and the DNase (*spd1*) genes that, as previously described, were not found in strains outside the emergent clade 3 (4). The difference of 231 bp between our two strains is mainly located in noncoding regions and the polymorphic *scfB* gene. By comparison with the MGAS27061 genome, we identified in both strains the 27 single nucleotide polymorphisms (SNPs) described as shared by all the acapsular clade 3-associated strains of the genotype *emm89* (4).

Since 2009, the *emm89* genotype belonging to an emergent clade has been circulating in French Brittany. Herein, we have made available 2 complete sequences that could facilitate evolutionary studies of this highly invasive clone, which could provoke intrahospital epidemics and rapidly spread in the world (11).

Data availability. The complete genome sequences of these *S. pyogenes* strains have been deposited in NCBI GenBank and the raw data into the NCBI Sequence Read Archive (SRA). The genome versions described in this paper are the first versions. The BioProject, GenBank, and SRA accession numbers are [PRJNA524538](#), [CP036530](#), and [SRP237255](#) ([PRJNA524538](#)) for STAB09023 and [PRJNA524780](#), [CP036531](#), and [SRP237258](#) ([PRJNA524780](#)) for STAB10048, respectively.

ACKNOWLEDGMENT

This work was supported by the University of Rennes 1.

REFERENCES

1. Carapetis JR, Steer AC, Mulholland EK, Weber M. 2005. The global burden of group A streptococcal diseases. *Lancet Infect Dis* 5:685–694. [https://doi.org/10.1016/S1473-3099\(05\)70267-X](https://doi.org/10.1016/S1473-3099(05)70267-X).
2. Beall B, Facklam R, Thompson T. 1996. Sequencing *emm*-specific PCR products for routine and accurate typing of group A streptococci. *J Clin Microbiol* 34:953–958. <https://doi.org/10.1128/JCM.34.4.953-958.1996>.
3. Tartof SY, Reis JN, Andrade AN, Ramos RT, Reis MG, Riley LW. 2010. Factors associated with group A *Streptococcus emm* type diversification in a large urban setting in Brazil: a cross-sectional study. *BMC Infect Dis* 10:327. <https://doi.org/10.1186/1471-2334-10-327>.
4. Turner CE, Abbott J, Lamagni T, Holden MT, David S, Jones MD, Game L, Efstratiou A, Sriskandan S. 2015. Emergence of a new highly successful acapsular group A *Streptococcus* clade of genotype *emm89* in the United Kingdom. *mBio* 6:e00622. <https://doi.org/10.1128/mBio.00622-15>.
5. Zhu L, Olsen RJ, Nasser W, de la Riva Morales I, Musser JM. 2015. Trading capsule for increased cytotoxin production: contribution to virulence of a newly emerged clade of *emm89 Streptococcus pyogenes*. *mBio* 6:e01378-15. <https://doi.org/10.1128/mBio.01378-15>.
6. Soriano N, Vincent P, Moullec S, Meygret A, Lagente V, Kayal S, Faili A. 2014. Closed genome sequence of noninvasive *Streptococcus pyogenes* M/*emm3* strain STAB902. *Genome Announc* 2:e00792-14. <https://doi.org/10.1128/genomeA.00792-14>.
7. Andrews S. 2010. FastQC: a quality control tool for high throughput sequence data. <http://www.bioinformatics.babraham.ac.uk/projects/fastqc>.
8. Beres SB, Olsen RJ, Ojeda Saavedra M, Ure R, Reynolds A, Lindsay DSJ, Smith AJ, Musser JM. 2017. Genome sequence analysis of *emm89 Streptococcus pyogenes* strains causing infections in Scotland, 2010–2016. *J Med Microbiol* 66:1765–1773. <https://doi.org/10.1099/jmm.0.000622>.
9. 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. <https://doi.org/10.1186/1471-2164-9-75>.
10. Zhou Y, Liang Y, Lynch KH, Dennis JJ, Wishart DS. 2011. PHAST: a fast phage search tool. *Nucleic Acids Res* 39:W347–W352. <https://doi.org/10.1093/nar/gkr485>.
11. Plainvert C, Longo M, Seringe E, Saintpierre B, Sauvage E, Ma L, Beghain J, Dmytruk N, Collobert G, Hernandez E, Manuel C, Astagneau P, Glaser P, Arieu F, Poyart C, Fouet A. 2018. A clone of the emergent *Streptococcus pyogenes emm89* clade responsible for a large outbreak in a post-surgery oncology unit in France. *Med Microbiol Immunol* 207:287–296. <https://doi.org/10.1007/s00430-018-0546-1>.