Full Sequencing and Genomic Analysis of Three emm75 Group A Streptococcus Strains Recovered in the Course of an Epidemiological Shift in French Brittany

Aude Rochefort, Sarrah Boukthir, Séverine Moullec, Alexandra Meygret, Yahia Adnani, Dominique Lavenier, Ahmad Faili, Samer Kayal

To cite this version:
Aude Rochefort, Sarrah Boukthir, Séverine Moullec, Alexandra Meygret, Yahia Adnani, et al.. Full Sequencing and Genomic Analysis of Three emm75 Group A Streptococcus Strains Recovered in the Course of an Epidemiological Shift in French Brittany. Genome Announcements, American Society for Microbiology, 2017, 5 (39), pp.e00957. 10.1128/genomeA.00957-17. hal-01617890

HAL Id: hal-01617890
https://hal-univ-rennes1.archives-ouvertes.fr/hal-01617890
Submitted on 17 Oct 2017

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.
Full Sequencing and Genomic Analysis of Three emm75 Group A Streptococcus Strains Recovered in the Course of an Epidemiological Shift in French Brittany

Aude Rochefort,a Sarrah Boukthir,a,b Séverine Moullec,a Alexandra Meygret,b*, Yahia Adnani,a Dominique Lavenier,c Ahmad Faili,a Samer Kayala,b

CIC-1414 INSERM, Université Rennes 1, Faculté de Médecine, Team GeRMO, Rennes, France; CHU Rennes Service de Bactériologie et Hygiène Hospitalière, Rennes, France; INRIA/IRISA/GenScale, Team Bioinformatique, Campus de Beaulieu, Rennes, France

ABSTRACT While the incidence and invasiveness of type emm75 group A Streptococcus (GAS) infections increased in French Brittany during 2013, we sequenced and analyzed the genomes of three independent strains isolated in 2009, 2012, and 2014, respectively. In this short-term evolution, genomic analysis evidenced mainly the integration of new phages encoding virulence factors.

The group A Streptococcus (GAS) or Streptococcus pyogenes is a Gram-positive human pathogen associated with a broad spectrum of diseases ranging from mild to life-threatening infections (1). The epidemiology varies over time and geographic regions, possibly reflecting the emergence of new virulent clones (2–4). By conducting a systematic survey based on emm typing of all GAS isolates in French Brittany, we observed in 2013 a shift in the epidemiological behavior of type emm75 GAS infections. During 3 years (2009 to 2012), only 4 infections were recorded, whereas from 2013 to 2014, we documented 27 infections. The multilocus sequence type (5) was determined for all the strains as sequence type 150 (ST150). Anticipating a genetic heterogeneity, we then sequenced the whole genome of three independent emm75 strains, here named STAB090229, STAB120304, and STAB14018, isolated from patients with puerperal sepsis (2009), oropharyngeal carriage (2012), and an unexplained bacteremia (2014), respectively.

Whole-genome sequencing was performed with HiSeq 2000 technology (Illumina, Inc., San Diego, CA), and the paired-end libraries were built using the MGX facility of the CNRS in Montpellier, France. For each strain (STAB090229, STAB120304, and STAB14018), a total of 15,201,760, 11,304,212, and 14,127,274 high-quality reads, giving average coverages of 1,253-, 1,068-, and 927-fold, respectively, were assembled using CLC Genomics Workbench v.6 software. The resulting assembly consisted of 25, 25, and 30 contigs oriented on the basis of available sequences of GAS, and 21, 23, and 25 persisting gaps, respectively, were filled as previously described (6, 7). Genome annotations were performed in parallel by using the Rapid Annotations using Subsystems Technology (RAST) server (8) and NCBI-PGAAP (http://ncbi.nlm.nih.govgenome/annotation_prok). Prophages were identified using the PHAge Search Tool (PHAST) (9).

For each of the three genomes of the sizes 1,846,347, 1,890,354, and 1,890,465 bp, we identified 1,810, 1,868, and 1,804 coding sequences (CDSs), 57, 67, and 67 tRNA genes, and 15, 18, and 18 rRNA genes, respectively. Overall, the main identified genomic differences were focused in 5 intact integrated prophages ($\Phi$STAB75.1 to $\Phi$STAB75.5) that varied in G+C percentages from 38.3% to 39.3% and are inserted in intergenic and noncoding regions of the sequenced genomes. The strains STAB090229 integrates 3 prophages ($\Phi$STAB75.1 to $\Phi$STAB75.3), and both strains STAB120304 and

Received 5 August 2017 Accepted 8 August 2017 Published 28 September 2017

STAB14018 integrates 4 prophages (ϕSTAB75.1, ϕSTAB75.2, ϕSTAB75.4, and ϕSTAB75.5). The sizes and the genes encoding virulence factors vary for each identified prophage as follows: ϕSTAB75.1 (41.3 kb; streptodorase sdn), ϕSTAB75.2 (45.0 kb; SpeL and SpeM exotoxins), ϕSTAB75.3 (55.4 kb; lack of known virulence factors), ϕSTAB75.4 (40.3 kb; SpeC exotoxin), and ϕSTAB75.5 (57.0 kb; SpeK exotoxin). Otherwise, the chromosomal genes encoding SpeG, SmeZ, and NAD glycohydrolase exotoxins and SpeB cysteine protease are found in all sequenced strains.

Until 2013, infections caused by emm75 GAS were uncommon in French Brittany. The genetic changes (10), and the acquisition of new virulence factors identified in recovered strains within the same population, demonstrate mechanisms that might explain the short-term shift in epidemiological behavior of type emm75 GAS in French Brittany.

Accession number(s). The complete whole-genome sequence for each GAS emm75 strain is available in GenBank under the accession numbers CP020027 (STAB090229), CP020082 (STAB120304), and CP014542 (STAB14018).

ACKNOWLEDGMENTS
This work was supported by the University of Rennes 1. We acknowledge Pascal Vincent (retired) for his helpful input in this work.

REFERENCES