

Characterization of Tn5801.Sag, a Variant of *Staphylococcus aureus* Tn916 Family Transposon Tn5801 That Is Widespread in Clinical Isolates of *Streptococcus agalactiae*

Marina Mingoia,^a Eleonora Morici,^a Emily Tili,^a Eleonora Giovanetti,^b Maria Pia Montanari,^a Pietro E. Varaldo^a

Unit of Microbiology, Departments of Biomedical Sciences and Public Health^a and Life and Environmental Sciences,^b Polytechnic University of Marche, Ancona, Italy

Tn5801, originally detected in *Staphylococcus aureus* Mu50, is a Tn916 family element in which a unique *int* gene (*int*₅₈₀₁) replaces the *int* and *xis* genes in Tn916 (*int*₉₁₆ and *xis*₉₁₆). Among 62 *tet*(M)-positive tetracycline-resistant *Streptococcus agalactiae* isolates, 43 harbored Tn916, whereas 19 harbored a Tn5801-like element (Tn5801.Sag, ~20.6 kb). Tn5801.Sag was characterized (PCR mapping, partial sequencing, and chromosomal integration) and compared to other Tn5801-like elements. Similar to Tn5801 from *S. aureus* Mu50, tested in parallel, Tn5801.Sag was unable to undergo circularization and conjugal transfer.

Tn916 family elements (1, 2) are broad-host-range elements, widespread in Gram-positive bacteria, that mostly exhibit the distinctive properties of integrative and conjugative elements (ICEs) (3). Their open reading frames (ORFs) are organized into functional modules (conjugation, recombination, transcriptional regulation, and accessory functions): albeit with well-known variations (1, 2), the recombination module mostly consists of an integrase (*int*₉₁₆) gene and an excisionase (*xis*₉₁₆) gene, and the accessory gene is typically the tetracycline (TET) resistance determinant *tet*(M).

The best-known Tn916 family element from *Staphylococcus aureus* is Tn5801 (~25.8 kb) (2), which was detected in the genome of Mu50 (DDBJ accession no. BA000017) (4), a well-established methicillin-resistant and vancomycin-intermediate Japanese clinical isolate (5). Tn5801, regarded as one of the nine genomic islands in the Mu50 genome (6), shows a modular organization similar to that of Tn916 and has several similar ORFs. However, besides the presence of additional ORFs, whose functions are largely unknown, DNA identities are rather low except in the case of *tet*(M) (97.7%). In particular, the recombination module differs from that of Tn916, as it lacks the *xis* gene and shows very low DNA identity (38.6%) between *int*₅₈₀₁ and *int*₉₁₆. This organization closely resembles that found in CW459*tet*(M), a genetic element from *Clostridium perfringens* CW459 (GenBank accession no. AF329848) (7).

Tn5801-like transposons have been detected in other human isolates of *S. aureus* (8, 9); in one case the element, Tn6014 from *S. aureus* 1680, was able to transfer, at low frequency, to *S. aureus* recipients (8). Among streptococci, a Tn5801-like element has been described for *Streptococcus mitis* B6 (EMBL accession no. FN568063) (10).

In the present study, we showed that a Tn5801-like transposon, designated Tn5801.Sag, is found in about 30% of TET-resistant clinical isolates of *Streptococcus agalactiae*, a species in which TET resistance is around 90% worldwide. The genetic organization of Tn5801.Sag was determined and compared with that of other Tn5801-like elements, and the putative core site was identified. Similar to Tn5801 from *S. aureus* Mu50, which was tested in parallel in this study, Tn5801.Sag was unable to undergo circularization and conjugal transfer.

All PCR primers used are shown in Table 1.

Characterization of TET-resistant *S. agalactiae* isolates. Sixty-nine clinical isolates of *S. agalactiae*, recovered in laboratories of central Italy in 2010–2011 and confirmed as being Lancefield group B using Slidex Strepto Plus (bioMérieux, Marcy l'Étoile, France), were used. Of them, 64 (93%) were TET resistant (MICs, ≥8 μg/ml). PCR assays demonstrated that *tet*(M) and *tet*(O) were the sole *tet* genes in 58 and 2 isolates, respectively; 4 isolates carried both determinants. Among the 62 *tet*(M)-positive isolates, 43 yielded positive PCRs for *int*₉₁₆ and *xis*₉₁₆; the remaining 19 were negative for both genes as well as for three additional regions of the transposon. However, sequence analysis of the *tet*(M) amplicon, performed in 3/19 randomly selected isolates, showed 100% DNA identity to the corresponding *tet*(M) portion of Tn5801 from *S. aureus* Mu50 (4). This finding prompted us to look for *int*₅₈₀₁, the integrase gene of Tn5801, which was found in all 19 isolates. The latter fell into several serotypes and pulsotypes (data not shown), thus excluding that they represented a clonal population.

Characterization and comparative analysis of Tn5801 from *S. agalactiae* (Tn5801.Sag). The 19 *int*₅₈₀₁-positive isolates underwent PCR mapping using the primers and strategies summarized in Table 1 and Fig. 1A. All isolates yielded comparable results, with positive PCRs and amplicons of the expected sizes obtained with all but six of the relevant primer pairs. Specifically, negative reactions were obtained with those pairs in which at least one primer targeted one of the last three ORFs of Tn5801 from *S. aureus* Mu50 (*sav413*, *sav414*, and *sav415*), which thus appeared not to be found in Tn5801 from *S. agalactiae* (designated Tn5801.Sag).

One of the 19 isolates (strain 14774) was used in DNA sequencing experiments, performed as described elsewhere (16). Two amplicons, yielded by primer pairs 1812/400F [7,593 bp, encompassing the *tet*(M) gene and most *int*₅₈₀₁] and 408R/411F (3,814 bp), were sequenced (EMBL accession no. HF930766). The two se-

Received 16 March 2013 Returned for modification 11 May 2013

Accepted 23 June 2013

Published ahead of print 1 July 2013

Address correspondence to Pietro E. Varaldo, pe.varaldo@univpm.it.

Copyright © 2013, American Society for Microbiology. All Rights Reserved.

doi:10.1128/AAC.00521-13

TABLE 1 Oligonucleotide primer pairs used

Procedure and gene/amplicon	Primer designation	Sequence (5'–3')	Reference or source	Product size (bp)
Detection of TET resistance genes				
<i>tet</i> (M)	TETM3	ATGGAAGCCCAGAAAGGAT	11	740
	TETM2	GAACCTCGAACAAAGAGGAAAGC	11	
<i>tet</i> (O)	TETO1	AACTTAGGCATTCTGGCTCAC	11	519
	TETO2	TCCCCTGTCCATATCGTCA	11	
PCR evidence of Tn916				
<i>int</i> ₉₁₆	int-for	GCGTGATTGTATCTCACT	12	1,046
	int-rev	GACGCTCCTGTTGCTTCT	12	
<i>xis</i> ₉₁₆	xis-for	AAGCAGACTGAGATTCTTA	13	194
	xis-rev	GCGTCCAATGTATCTATAA	13	
<i>orf7-orf8</i> ^a	O15	GTACGTCCACCAATGTGG	14	902
	O16	GCACGCTTCCAGAAAGGAG	14	
<i>orf20-IR</i> _{18–19} ^a	J12	CCCATTGAAGACGCAGAAGT	15	801
	J11	AAAAATCCCTACCGCACT	15	
<i>orf24-orf20</i> ^a	TN6-rev	CCATCAAACATTCATTGAGC	15	3,358
	J13	GGTTTTGTGGTTAGTTTT	15	
PCR mapping of Tn5801.Sag ^b				
<i>int</i> ₅₈₀₁	1812	GTCCATACGTTCCCTAAAGTCGTC	8	726
	1811	CCGATATTGAGCCTATTGATGTG	8	
<i>sav400</i>	400R	TCGTATTTCAAGGCTTCGTC	This study	369
	400F	TACCGAAGAGTCCATCAAAC	This study	
<i>sav408</i>	408R	AATGTAGGGGCGACTTGATG	This study	1,005
	408F	ACTGGCTTATGGCGTTTCTC	This study	
<i>sav409</i>	409R	GCAGACAAACCAAGATAAGC	This study	940
	409F	GAGAGCGAATCAAAGCCAAC	This study	
<i>sav413</i>	413R	AACACCGTTGTCGTCTCCAC	This study	743
	413F	TTGCTAGTAATATAAGGGCGA	This study	
<i>sav414</i>	414R	ATTAGATACACAACATCCTCATC	This study	579
	414F	ACAGGCAATCCCATCAGAAC	This study	
<i>sav415</i>	415R	TAGATGAGGCTTGATACACC	This study	677
	415F	TTCTCGTAACGGCTCCTATG	This study	
<i>int</i> ₅₈₀₁ - <i>tet</i> (M)	1812	GTCCATACGTTCCCTAAAGTCGTC	8	4,971
	TETM2	GAACCTCGAACAAAGAGGAAAGC	11	
<i>tet</i> (M)- <i>sav400</i>	TETM3	ATGGAAGCCCAGAAAGGAT	11	3,362
	400F	TACCGAAGAGTCCATCAAAC	This study	
<i>sav400-sav408</i>	400R	TCGTATTTCAAGGCTTCGTC	This study	9,331
	408F	ACTGGCTTATGGCGTTTCTC	This study	
<i>sav408-sav409</i>	408R	AATGTAGGGGCGACTTGATG	This study	2,612
	409F	GAGAGCGAATCAAAGCCAAC	This study	
<i>sav409-sav411</i>	409R	GCAGACAAACCAAGATAAGC	This study	2,142
	411F	GAGATTAGCAGAAGGTATTGTG	This study	
<i>sav409-sav413</i>	409R	GCAGACAAACCAAGATAAGC	This study	3,874
	413F	TTGCTAGTAATATAAGGGCGA	This study	
<i>sav413-sav414</i>	413R	AACACCGTTGTCGTCTCCAC	This study	1,968
	414F	ACAGGCAATCCCATCAGAAC	This study	
<i>sav414-sav415</i>	414R	ATTAGATACACAACATCCTCATC	This study	3,295
	415F	TTCTCGTAACGGCTCCTATG	This study	
Tn5801.Sag chromosomal integration site ^c				
SAG967 (<i>guaA</i>)	LJ967	CGTGAAGAAATCGCTAAAG	This study	1,228
<i>int</i> ₅₈₀₁	1811	CCGATATTGAGCCTATTGATGTG	8	1,414
	CF1	TTCAAAGGAACAGAAGCGGG	This study	
SAG964	RJ964	GAAGTAGAAGAGGCCATAG	This study	
Search for circular form				
<i>int</i> ₅₈₀₁	1811	CCGATATTGAGCCTATTGATGTG	8	
	<i>sav411</i>	TTCAAAGGAACAGAAGCGGG	This study	

^a ORFs numbered according to the reported organization of Tn916 (GenBank accession no. U09422).

^b Tn5801 from the genome of *S. aureus* Mu50 (DDBJ accession no. BA000017; *sav* genes) was used as the reference sequence. In PCR assays, *S. aureus* Mu50 (ATCC 700699) was used as a positive control and *S. pneumoniae* BM4200 (Pasteur Institute Collection), harboring the Tn916-like transposon Tn1545 (1), was used as a negative control.

^c The genome of *S. agalactiae* strain 2603V/R (GenBank accession no. AE009948; SAG genes) was used as the reference sequence.

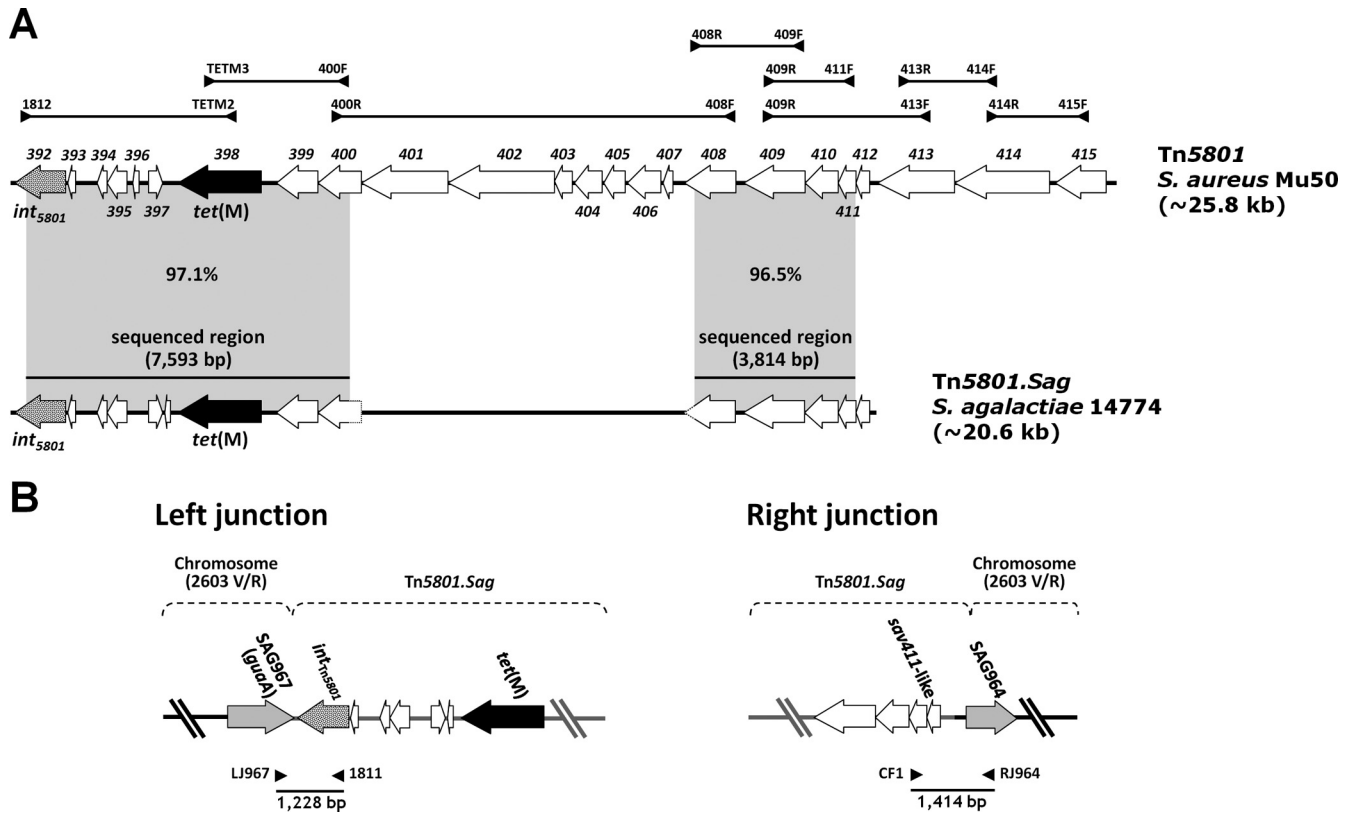


FIG 1 Schematic representation of Tn5801.Sag from *S. agalactiae* strain 14774 (A) and its chromosomal integration (left and right junctions) (B). (A) Tn5801.Sag was determined by PCR mapping and sequencing of two regions. The primers used are listed in Table 1. The mapping strategy is outlined in the upper portion (the amplicons used to detect individual ORFs, i.e., obtained by pairing two primers internal to the same ORF, are not shown). The two regions sequenced initially (7,593 bp, left, and 3,814 bp, right) are indicated by horizontal bars. Tn5801.Sag is compared to Tn5801 from *S. aureus* Mu50, where ORFs are numbered *sav*₃₉₂ to *sav*₄₁₅ according to the original designations (DDBJ accession no. BA000017); percent DNA identities are reported in gray areas between sequenced regions. *tet*(M) and *int*₅₈₀₁ are represented as black and spotted arrows, respectively. (B) Tn5801.Sag was integrated at the 3' end of the *guaA* gene. This gene, detected in all *S. agalactiae* genomes sequenced to date, corresponds to ORF967 from *S. agalactiae* 2603V/R (GenBank accession no. AE009948), from which chromosomal ORF designations derive. The amplicons obtained by pairing primers LJ967/1811 (left junction) and CF1/RJ964 (right junction), whose sequencing extended the two portions of Tn5801.Sag sequenced initially, are shown as bars. *tet*(M) and *int*₅₈₀₁ are represented as black and spotted arrows, respectively, and other Tn5801.Sag ORFs as white arrows; chromosomal ORFs are depicted as gray arrows.

sequenced regions of Tn5801.Sag displayed 97.1% [*tet*(M), 100%] and 96.5% DNA identities with the corresponding regions of Tn5801 from *S. aureus* Mu50 (Fig. 1A) and 96.9% [*tet*(M), 99.5%] and 96.5% with those of *S. mitis* B6; the former sequence displayed 96.1% identity [*tet*(M), 100%] with the corresponding region (the only one that has been sequenced; GenBank accession no. EU918655) of Tn6014 from *S. aureus* 1680. Greater identities [99.9% and 100%; *tet*(M), 100%] were recorded with the corresponding regions of *E. faecalis* 62, for which a “Tn916 element” (not identified as Tn5801-like) was reported (17) in the sequenced genome (GenBank accession no. CP002491). The latter element (~20.6 kb) was very similar to Tn5801.Sag (~20.6 kb based on sequencing and PCR mapping data) also as to ORF organization: in particular, the two elements share the lack of the last three ORFs of Tn5801 from *S. aureus* Mu50 (*sav*₄₁₃, *sav*₄₁₄, and *sav*₄₁₅), located after the conjugation module and not present in Tn916. It is worth noting that the last ORF (*sav*₄₁₅, a transposase gene) is also missing in the Tn5801-like element from *S. mitis* B6, in which *sav*₄₁₃ and *sav*₄₁₄ are present.

Chromosomal integration of Tn5801.Sag and identification of the putative core site. The early study of CW459*tet*(M) (7) and

later studies of genetic elements related to Tn5801 (10, 18, 19) concur in describing an integration site just downstream of *guaA*, a chromosomal gene encoding a GMP synthase that is consistently found adjacent to *int*₅₈₀₁ in the sequenced genomes containing a Tn5801 element. Using strategies refined in previous studies (16, 20–22), this site was thus explored in the 19 *S. agalactiae* isolates harboring Tn5801.Sag. The genome of *S. agalactiae* strain 2603V/R (GenBank accession no. AE009948) (23) was used as the reference sequence. As illustrated in Fig. 1B, pairing of primers LJ967/1811 (left junction) gave an ~1.2-kb amplicon from all 19 *S. agalactiae* isolates; by pairing primers CF1/RJ964 (right junction), an ~1.4-kb amplicon was obtained from all but one isolate, which yielded an ~1-kb-larger amplicon; this was subsequently shown to reflect the presence of SAG965 and SAG966, encoding insertion sequences in the *S. agalactiae* 2603V/R genome that were not found in the other 18 isolates. By analyzing and comparing the two amplicon sequences from strain 14774, it was possible to determine the chromosomal junctions of Tn5801.Sag. The putative core site was an almost completely overlapping 11-bp sequence identified on the left (GAGTGGG AGTA) and right (GAGTGGGAATA) ends of the transposon; the

latter sequence was identical to that found in both Tn5801 junctions of *S. aureus* Mu50.

Transferability studies. Three isolates, including strain 14774, were used as donors in conjugal transfer experiments, performed as described elsewhere (24). No transconjugants were obtained with any of the three recipients used: *S. agalactiae* 1357RF (25), *S. pyogenes* 12RF (24), and *S. aureus* RN4220RF (26), used in the sole successful conjugative transfer of a Tn5801 element (Tn6014) reported so far (8). Similar negative results were obtained using *S. aureus* Mu50 (ATCC 700699) as the donor.

The apparent nontransferability of Tn5801.Sag and of Tn5801 from *S. aureus* Mu50 was consistent with the absence, in both cases, of an intermediate circular form, as resulting from the negative PCR obtained using the outward-directed primer pair 1811/CF1.

Conclusions. Among the so-called Tn916-like elements (1, 2), major differences are found in the recombination module, where the prevailing two-gene organization (*int*₉₁₆ and *xis*₉₁₆) typical of Tn916 may be replaced by a single gene. This is the case of *tndX* in Tn5397 from *Clostridium difficile* (7), a gene that in streptococci is commonly found in *S. pyogenes* in ICESp1116 (22); of *int*₄₅₉ in CW459tet(M) from *C. perfringens* (7); and of *int*₅₈₀₁ (identical to *int*₄₅₉) in Tn5801 from *S. aureus* (4). Now, the finding that in no less than 30% of TET-resistant clinical isolates of *S. agalactiae*—a species for which TET resistance rates are around 90%—resistance was mediated by the *tet*(M) gene carried by a Tn5801-like transposon (Tn5801.Sag) is a major result of this study. Accordingly, a sizable proportion (about 50/250) of *S. agalactiae* scaffolds and contigs currently found in GenBank harbors Tn5801.Sag. The frequent occurrence of Tn5801.Sag in *S. agalactiae* strengthens the notion of a composite organization of the chromosome of this species (27–29).

Subsequent to the original detection of Tn5801 in *S. aureus* Mu50, Tn5801-like transposons were detected in other human *S. aureus* isolates; one such transposon (Tn6014) was shown to be able to transfer to an *S. aureus* recipient (8). Conversely, Tn5801.Sag is apparently unable to transfer, like Tn5801 from *S. aureus* Mu50, whose actual transferability had not been tested before the present study.

As to the genetic organization of Tn5801.Sag, differences from other Tn5801-like transposons mainly involved the right terminus of the element, with the last three ORFs of Tn5801 from *S. aureus* Mu50 (*sav*₄₁₃, *sav*₄₁₄, and *sav*₄₁₅, not present in Tn916) missing in Tn5801.Sag, while only the last one (*sav*₄₁₅) is missing in Tn5801-like from *S. mitis* B6. In contrast, the left termini are very similar in all Tn5801-like transposons, and the adjacent chromosomal gene is unvaryingly *guaA*. Therefore, while Tn916 preferentially integrates into A-T-rich targets in a broad range of hosts (2), *int*₅₈₀₁ and related genes appear to code for integrases leading to site-specific recombination at the 3' end of *guaA*.

Nucleotide sequence accession number. Two new nucleotide sequences reported in this work have been deposited in the EMBL database under accession no. HF930766.

ACKNOWLEDGMENTS

We are grateful to Andrea Brenciani and Claudio Palmieri for helpful discussions.

This work was partly supported by the Italian Ministry of Education, University and Research.

REFERENCES

- Roberts AP, Mullany P. 2009. A modular master on the move: the Tn916 family of mobile genetic elements. *Trends Microbiol.* 17:251–258.
- Roberts AP, Mullany P. 2011. Tn916-like genetic elements: a diverse group of modular mobile elements conferring antibiotic resistance. *FEMS Microbiol. Rev.* 35:856–871.
- Wozniak RA, Waldor MK. 2010. Integrative and conjugative elements: mosaic mobile genetic elements enabling dynamic lateral gene flow. *Nat. Rev. Microbiol.* 8:552–563.
- Kuroda M, Ohta T, Uchiyama I, Baba T, Yuzawa H, Kobayashi I, Cui L, Oguchi A, Aoki K, Nagai Y, Lian JQ, Ito T, Kanamori M, Matsumaru H, Maruyama A, Murakami H, Hosoyama A, Mizutani-Ui Y, Takahashi NK, Sawano T, Inoue R, Kaito C, Sekimizu K, Hirakawa H, Kuhara S, Goto S, Yabuzaki J, Kanehisa M, Yamashita A, Oshima K, Furuya K, Yoshino C, Shiba T, Hattori M, Ogasawara N, Hayashi H, Hiramatsu K. 2001. Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*. *Lancet* 357:1225–1240.
- Hiramatsu K. 2001. Vancomycin-resistant *Staphylococcus aureus*: a new model of antibiotic resistance. *Lancet Infect. Dis.* 1:147–155.
- Gill SR, Fouts DE, Archer GL, Mongodin EF, Deboy RT, Ravel J, Paulsen IT, Kolonay JF, Brinkac L, Beanan M, Dodson RJ, Daugherty SC, Madupu R, Angiuoli SV, Durkin AS, Haft DH, Vamathevan J, Khouri H, Utterback T, Lee C, Dimitrov G, Jiang L, Qin H, Weidman J, Tran K, Kang K, Hance IR, Nelson KE, Fraser CM. 2005. Insights on evolution of virulence and resistance from the complete genome analysis of an early methicillin-resistant *Staphylococcus aureus* strain and a biofilm-producing methicillin-resistant *Staphylococcus epidermidis* strain. *J. Bacteriol.* 187:2426–2438.
- Roberts AP, Johanesen PA, Lyras D, Mullany P, Rood JI. 2001. Comparison of Tn5397 from *Clostridium difficile*, Tn916 from *Enterococcus faecalis* and the CW459tet(M) element from *Clostridium perfringens* shows that they have similar conjugation regions but different insertion and excision modules. *Microbiology* 147:1243–1251.
- de Vries LE, Christensen H, Skov RL, Aarestrup FM, Agerso Y. 2009. Diversity of the tetracycline resistance gene *tet*(M) and identification of Tn916- and Tn5801-like (Tn6014) transposons in *Staphylococcus aureus* from humans and animals. *J. Antimicrob. Chemother.* 64:490–500.
- Li H, Zhao C, Chen H, Zhang F, He W, Wang X, Wang Q, Yang R, Zhou D, Wang H. 2013. Identification of gene clusters associated with host adaptation and antibiotic resistance in Chinese *Staphylococcus aureus* isolates by microarray-based comparative genomics. *PLoS One* 8:e53341. doi:10.1371/journal.pone.0053341.
- Denapaite D, Brückner R, Nuhn M, Reichmann P, Henrich B, Maurer P, Schähle Y, Selbmann P, Zimmermann W, Wambutt R, Hakenbeck R. 2010. The genome of *Streptococcus mitis* B6—what is a commensal? *PLoS One* 5:e9426. doi:10.1371/journal.pone.0009426.
- Olsvik B, Olsen I, Tenover FC. 1995. Detection of *tet*(M) and *tet*(O) using the polymerase chain reaction in bacteria isolated from patients with periodontal disease. *Oral Microbiol. Immunol.* 10:87–92.
- Doherty N, Trzcinski K, Pickerill P, Zawadzki P, Dowson CG. 2000. Genetic diversity of the *tet*(M) gene in tetracycline-resistant clonal lineages of *Streptococcus pneumoniae*. *Antimicrob. Agents Chemother.* 44:2979–2984.
- Amezaga MR, Carter PE, Cash P, McKenzie H. 2002. Molecular epidemiology of erythromycin resistance in *Streptococcus pneumoniae* isolates from blood and noninvasive sites. *J. Clin. Microbiol.* 40:3313–3318.
- Poyart C, Quesne G, Acar P, Berche P, Trieu-Cuot P. 2000. Characterization of the Tn916-like transposon Tn3872 in a strain of *Abiotrophia defectiva* (*Streptococcus defectivus*) causing sequential episodes of endocarditis in a child. *Antimicrob. Agents Chemother.* 44:790–793.
- Cochetti I, Tili E, Vecchi M, Manzin A, Mingoia M, Varaldo PE, Montanari MP. 2007. New Tn916-related elements causing *erm*(B)-mediated erythromycin resistance in tetracycline-susceptible pneumococci. *J. Antimicrob. Chemother.* 60:127–131.
- Brenciani A, Tiberi E, Bacciaglia A, Petrelli D, Varaldo 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.
- Brede DA, Snipen LG, Ussery DW, Nederbragt AJ, Nes IF. 2011. Complete genome sequence of the commensal *Enterococcus faecalis* 62, isolated from a healthy Norwegian infant. *J. Bacteriol.* 193:2377–2378.

18. Boyd DA, Cabral T, Van Caesele P, Wylie J, Mulvey MR. 2002. Molecular characterization of the *vanE* gene cluster in vancomycin-resistant *Enterococcus faecalis* N00-410 isolated in Canada. *Antimicrob. Agents Chemother.* 46:1977–1979.
19. Smyth DS, Robinson DA. 2009. Integrative and sequence characteristics of a novel genetic element, ICE6013, in *Staphylococcus aureus*. *J. Bacteriol.* 191:5964–5975.
20. Brenciani A, Bacciaglia A, Vignaroli C, Pugnali A, Varaldo PE, Giovanetti E. 2010. Characterization of Φ m46.1, the main *Streptococcus pyogenes* element carrying *mef(A)* and *tet(O)* genes. *Antimicrob. Agents Chemother.* 54:221–229.
21. Giovanetti E, Brenciani A, Tiberi E, Bacciaglia A, Varaldo PE. 2012. ICESp2905, the *erm(TR)-tet(O)* element of *Streptococcus pyogenes*, is formed by two independent integrative and conjugative elements. *Antimicrob. Agents Chemother.* 56:591–594.
22. Brenciani A, Tiberi E, Morici E, Oryasin E, Giovanetti E, Varaldo PE. 2012. ICESp1116, the genetic element responsible for *erm(B)*-mediated, inducible resistance to erythromycin in *Streptococcus pyogenes*. *Antimicrob. Agents Chemother.* 56:6425–6429.
23. Tettelin H, Masignani V, Cieslewicz MJ, Eisen JA, Peterson S, Wessels MR, Paulsen IT, Nelson KE, Margarit I, Read TD, Madoff LC, Wolf AM, Beanan MJ, Brinkac LM, Daugherty SC, DeBoy RT, Durkin AS, Kolonay JF, Madupu R, Lewis MR, Radune D, Fedorova NB, Scanlan D, Khouri H, Mulligan S, Carty HA, Cline RT, Van Aken SE, Gill J, Scarselli M, Mora M, Iacobini ET, Brettoni C, Galli G, Mariani M, Vegni F, Maione D, Rinaudo D, Rappuoli R, Telford JL, Kasper DL, Grandi G, Fraser CM. 2002. Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V *Streptococcus agalactiae*. *Proc. Natl. Acad. Sci. U. S. A.* 99:12391–12396.
24. Giovanetti E, Magi G, Brenciani A, Spinaci C, Lupidi R, Facinelli B, Varaldo PE. 2002. Conjugative transfer of the *erm(A)* gene from erythromycin-resistant *Streptococcus pyogenes* to macrolide-susceptible *S. pyogenes*, *Enterococcus faecalis*, and *Listeria innocua*. *J. Antimicrob. Chemother.* 50:249–252.
25. Palmieri C, Magi G, Mingoia M, Bagnarelli P, Ripa S, Varaldo PE, Facinelli B. 2012. Characterization of a *Streptococcus suis tet(O/W/32/O)*-carrying element transferable to major streptococcal pathogens. *Antimicrob. Agents Chemother.* 56:4697–4702.
26. Kreiswirth BN, Lofdahl S, Betley MJ, O'Reilly M, Schlievert PM, Bergdoll MS, Novick RP. 1983. The toxic shock syndrome exotoxin structural gene is not detectably transmitted by a prophage. *Nature* 305:709–712.
27. Tettelin H, Masignani V, Cieslewicz MJ, Donati C, Medini D, Ward NL, Angiuoli SV, Crabtree J, Jones AL, Durkin AS, Deboy RT, Davidsen TM, Mora M, Scarselli M, Margarit y Ros I, Peterson JD, Hauser CR, Sundaram JP, Nelson WC, Madupu R, Brinkac LM, Dodson RJ, Rosovitz MJ, Sullivan SA, Daugherty SC, Haft DH, Selengut J, Gwinn ML, Zhou L, Zafar N, Khouri H, Radune D, Dimitrov G, Watkins K, O'Connor KJ, Smith S, Utterback TR, White O, Rubens CE, Grandi G, Madoff LC, Kasper DL, Telford JL, Wessels MR, Rappuoli R, Fraser CM. 2005. Genome analysis of multiple pathogenic isolates of *Streptococcus agalactiae*: implications for the microbial “pan-genome.” *Proc. Natl. Acad. Sci. U. S. A.* 102:13950–13955.
28. Brochet M, Rusniok C, Couv E, Dramsi Poyart C, Trieu-Cuot P, Kunst F, Glaser P. 2008. Shaping a bacterial genome by large chromosomal replacements, the evolutionary history of *Streptococcus agalactiae*. *Proc. Natl. Acad. Sci. U. S. A.* 105:15961–15966.
29. Brochet M, Couv E, Glaser P, Guédon G, Payot S. 2008. Integrative conjugative elements and related elements are major contributors to the genome diversity of *Streptococcus agalactiae*. *J. Bacteriol.* 190:6913–6917.