

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

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**Tn5801**, originally detected in *Staphylococcus aureus* Mu50, is a Tn916 family element in which a unique *int* gene (*int*<sub>5801</sub>) replaces the *int* and *xis* genes in Tn916 (*int*<sub>916</sub> and *xis*<sub>916</sub>). 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*<sub>916</sub>) gene and an excisionase (*xis*<sub>916</sub>) 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*<sub>5801</sub> and *int*<sub>916</sub>. 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*<sub>916</sub> and *xis*<sub>916</sub>; 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*<sub>5801</sub>, 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*<sub>5801</sub>-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*<sub>5801</sub>] and 408R/411F (3,814 bp), were sequenced (EMBL accession no. HF930766). The two se-

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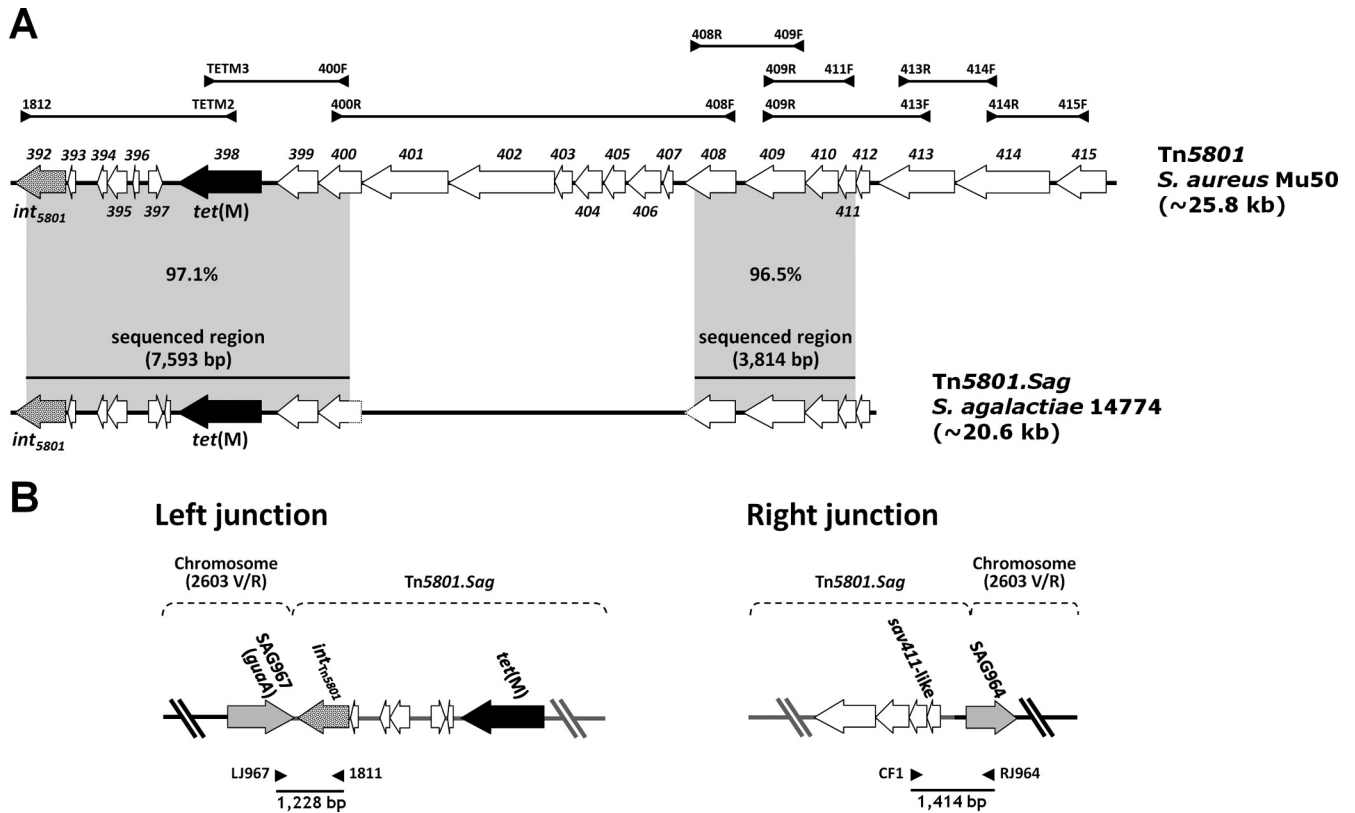
TABLE 1 Oligonucleotide primer pairs used

| 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              | GAACTCGAACAAGAGGAAAGC    | 11                   |                   |
| <i>tet</i> (O)                                       | TETO1              | AACTTAGGCATTCTGGCTCAC    | 11                   | 519               |
|  | TETO2              | TCCCCTGTCCATATCGTCA      | 11                   |                   |
| PCR evidence of Tn916                                |                    |                          |                      |                   |
| <i>int</i> <sub>916</sub>                            | int-for            | GCGTGATTGTATCTCACT       | 12                   | 1,046             |
|  | int-rev            | GACGCTCCTGTTGCTTCT       | 12                   |                   |
| <i>xis</i> <sub>916</sub>                            | xis-for            | AAGCAGACTGAGATTCCCTA     | 13                   | 194               |
|  | xis-rev            | GCGTCCAATGTATCTATAA      | 13                   |                   |
| <i>orf7-orf8</i> <sup>a</sup>                        | O15                | GTACGTCCACCAATGTGG       | 14                   | 902               |
|  | O16                | GCACGCTTCCACGAAAGGAG     | 14                   |                   |
| <i>orf20-IR</i> <sub>18–19</sub> <sup>a</sup>        | J12                | CCCATTGAAGACGCAGAAGT     | 15                   | 801               |
|  | J11                | AAAAATCCCTACCGCACT       | 15                   |                   |
| <i>orf24-orf20</i> <sup>a</sup>                      | TN6-rev            | CCATCAAACATTCATTCAGC     | 15                   | 3,358             |
|  | J13                | GGTTTTGTGGTTAGTTTT       | 15                   |                   |
| PCR mapping of Tn5801.Sag <sup>b</sup>               |                    |                          |                      |                   |
| <i>int</i> <sub>5801</sub>                           | 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> <sub>5801</sub> - <i>tet</i> (M)          | 1812               | GTCCATACGTTCCCTAAAGTCGTC | 8                    | 4,971             |
|  | TETM2              | GAACTCGAACAAGAGGAAAGC    | 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 <sup>c</sup> |                    |                          |                      |                   |
| SAG967 ( <i>guaA</i> )                               | LJ967              | CGTGAAGAAATCGCTAAAG      | This study           | 1,228             |
| <i>int</i> <sub>5801</sub>                           | 1811               | CCGATATTGAGCCTATTGATGTG  | 8                    | 1,414             |
|  | CF1                | TTCAAAGGAACAGAAGCGGG     | This study           |                   |
| SAG964   | RJ964              | GAAGTAGAAGAGGCCATAG      | This study           |                   |
| Search for circular form                             |                    |                          |                      |                   |
| <i>int</i> <sub>5801</sub>                           | 1811               | CCGATATTGAGCCTATTGATGTG  | 8                    |                   |
|  | <i>sav411</i>      | CF1                      | TTCAAAGGAACAGAAGCGGG |                   |

<sup>a</sup> ORFs numbered according to the reported organization of Tn916 (GenBank accession no. U09422).

<sup>b</sup> 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.

<sup>c</sup> 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*<sub>5801</sub> 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 L1967/1811 (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*<sub>5801</sub> are represented as black and spotted arrows, respectively, and other Tn5801.Sag ORFs as gray 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*<sub>5801</sub> 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 L1967/1811 (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*<sub>916</sub> and *xis*<sub>916</sub>) 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*<sub>459</sub> in CW459tet(M) from *C. perfringens* (7); and of *int*<sub>5801</sub> (identical to *int*<sub>459</sub>) 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*<sub>413</sub>, *sav*<sub>414</sub>, and *sav*<sub>415</sub>, not present in Tn916) missing in Tn5801.Sag, while only the last one (*sav*<sub>415</sub>) 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*<sub>5801</sub> 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.

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