

## A Novel FexA Variant from a Canine Staphylococcus pseudintermedius Isolate That Does Not Confer Florfenicol Resistance

Elena Gómez-Sanz, Kristina Kadlec, Andrea T. Feßler,  
Myriam Zarazaga, Carmen Torres and Stefan Schwarz  
*Antimicrob. Agents Chemother.* 2013, 57(11):5763. DOI:  
10.1128/AAC.00948-13.  
Published Ahead of Print 26 August 2013.

---

Updated information and services can be found at:  
<http://aac.asm.org/content/57/11/5763>

---

|                       |  |
|-----------------------|--|
|                       | <i>These include:</i>  |
| <b>REFERENCES</b>     | This article cites 21 articles, 15 of which can be accessed free at: <a href="http://aac.asm.org/content/57/11/5763#ref-list-1">http://aac.asm.org/content/57/11/5763#ref-list-1</a> |
| <b>CONTENT ALERTS</b> | Receive: RSS Feeds, eTOCs, free email alerts (when new articles cite this article), <a href="#">more»</a>  |

---

---

Information about commercial reprint orders: <http://journals.asm.org/site/misc/reprints.xhtml>  
To subscribe to to another ASM Journal go to: <http://journals.asm.org/site/subscriptions/>

---

# A Novel *FexA* Variant from a Canine *Staphylococcus pseudintermedius* Isolate That Does Not Confer Florfenicol Resistance

Elena Gómez-Sanz,<sup>a</sup> Kristina Kadlec,<sup>b</sup> Andrea T. Feßler,<sup>b</sup> Myriam Zarazaga,<sup>a</sup> Carmen Torres,<sup>a</sup> Stefan Schwarz<sup>b</sup>

Biochemistry and Molecular Biology, University of La Rioja, Logroño, Spain<sup>a</sup>; Institute of Farm Animal Genetics, Friedrich-Loeffler-Institut (FLI), Neustadt-Mariensee, Germany<sup>b</sup>

**Transposon Tn558 integrated in the chromosomal *radC* gene was detected for the first time in *Staphylococcus pseudintermedius*. It carried a novel *fexA* variant (*fexAv*) that confers only chloramphenicol resistance. The exporter *FexAv* exhibited two amino acid substitutions, Gly33Ala and Ala37Val, both of which seem to be important for substrate recognition. Site-directed mutagenesis that reverted the mutated base pairs to those present in the original *fexA* gene restored the chloramphenicol-plus-florfenicol resistance phenotype.**

In staphylococci, phenicol resistance is mediated either by the chloramphenicol acetyltransferase-encoding *cat* genes, which confer resistance to nonfluorinated phenicols (e.g., chloramphenicol), or either of the two genes *fexA* (coding for a phenicol-specific efflux pump) and *cfr* (coding for a rRNA methyltransferase), both of which mediate combined resistance to fluorinated phenicols (e.g., florfenicol) and nonfluorinated phenicols (1). Since the first description of the *fexA* gene in a bovine *Staphylococcus lentus* isolate (2), this gene has been detected—either as part of the small nonconjugative transposon Tn558 or in combination with the *cfr* gene in transposition-deficient Tn558 variants—in *S. aureus* and several coagulase-negative staphylococcal species from healthy and diseased cattle, swine, horses, or humans (3–9). The *fexA* gene has also been detected in a *Bacillus* isolate from swine feces and in environmental pollutants from swine feedlots in China (10, 11).

In a previous study that focused on the occurrence of methicillin-resistant coagulase-positive staphylococci in dogs in La Rioja, Spain, one methicillin-susceptible *S. pseudintermedius* isolate, named C2719, was identified (12). This isolate was recovered from a healthy dog admitted to a veterinary clinic for a routine checkup. No additional information on the living conditions of the dog and/or the possible contact with rural areas or livestock was recorded. Susceptibility testing by agar disk diffusion and/or broth microdilution (13) showed that isolate C2719 was resistant to penicillin (due to the *blaZ* gene) and to chloramphenicol (MIC 64 µg/ml) but exhibited a low MIC of 2 µg/ml for florfenicol. None of the three *cat* genes known to occur in staphylococci—*cat*<sub>PC194</sub>, *cat*<sub>PC221</sub>, and *cat*<sub>PC223</sub> (1)—was detected by PCR (14). The objective of this study was to identify the gene responsible for chloramphenicol resistance in this strain and to characterize its genetic environment.

PCR analysis for the chloramphenicol/florfenicol resistance genes *fexA* and *cfr* (5) showed that, despite its low florfenicol MIC, strain C2719 harbored the *fexA* gene. PCR mapping and sequencing revealed that this *fexA* variant, named *fexAv*, exhibited 99.7% nucleotide sequence identity (99.2% identity and 99.6% similarity at the protein level) to the prototype *fexA* gene of *S. lentus* (GenBank accession no. AJ549214) (2). Moreover, the *fexAv* gene was found to be part of the Tn558 transposon (3, 15) (Fig. 1). Tn558 is a member of the Tn554 family (15). Transposons of this family exhibit several features that distinguish them from most other transposable elements: (i) their ends are asymmetric,

lacking either inverted or direct terminal repeats, (ii) they do not generate a duplication of the target sequence upon transposition, and (iii) they are extremely site specific, almost always inserting into the staphylococcal chromosome at the same location. This unique target site *att*, is located within the *radC* gene, which codes for a DNA repair protein (16–22). In addition to Tn558, first described in *S. lentus* (15), this group also includes at least another four members: Tn554 harboring the *erm(A)* gene for resistance to macrolides, lincosamides, and streptogramin B and the *spc* gene for spectinomycin resistance (19, 20); Tn5406 carrying the *vga(A)* gene for resistance to lincosamides, pleuromutilins, and streptogramin A (16); Tn559 harboring the *dfrK* gene for trimethoprim resistance (17); and Tn6133, which is composed of a Tn554-like element into which a segment with the novel gene *vga(E)* for resistance to lincosamides, pleuromutilins, and streptogramin A has been inserted (22). All these transposons have been found in *S. aureus*, with Tn559 and Tn6133 first detected in livestock-associated *S. aureus* of the lineage ST398.

The chromosomal/plasmid location of Tn558, as well as its specific integration site, was determined by plasmid preparation, specific PCRs, and sequencing (3, 23). As no plasmids were detected in *S. pseudintermedius* C2719, a chromosomal location of the *fexAv*-carrying transposon appeared to be likely. Primers *radC*<sub>SP-fw</sub> and *radC*<sub>SP-rv</sub> (Table 1) were designed to determine whether Tn558 was integrated within the chromosomal *radC* gene. The target recognition sequence, *att558*, was identified on the basis of the nucleotide similarity of (i) the 6-bp “core” sequence (*att*, 5'-GATGTA-3') of the *radC* gene of the original *S. lentus* isolate carrying Tn558 (accession no. AJ715531) (15) and that detected on the *radC* gene of *S. pseudintermedius* HKU10-03 and (ii) the sequences flanking this *att* site, which are also essential for transposition (19, 20).

An amplicon of 7,082 bp that comprised the complete Tn558

Received 3 May 2013 Returned for modification 16 June 2013

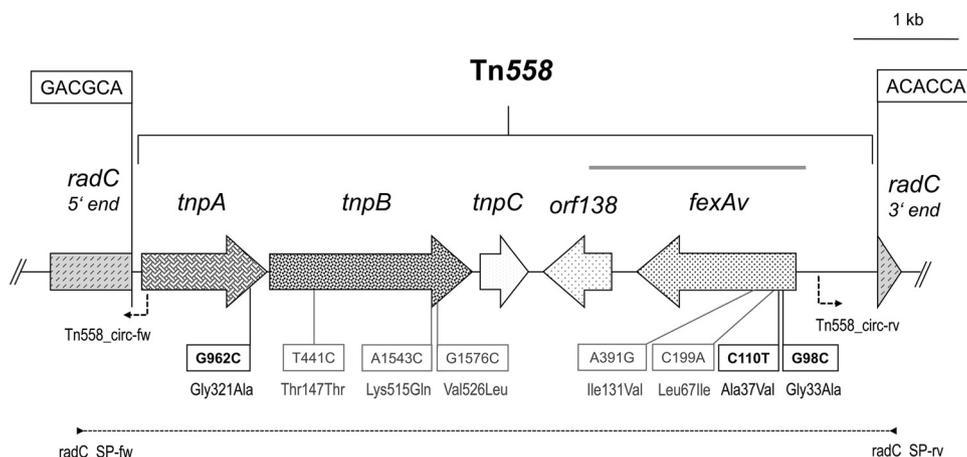
Accepted 21 August 2013

Published ahead of print 26 August 2013

Address correspondence to Carmen Torres, carmen.torres@unirioja.es.

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

doi:10.1128/AAC.00948-13



**FIG 1** Schematic presentation of the Tn558 structure carrying the *fexA<sub>v</sub>* gene detected in this study as well as its integration region (within the *radC* gene) in the chromosomal DNA of *S. pseudintermedius* C2719 (EMBL accession no. [HF679552](#)). The arrows indicate the extents and directions of transcription of chloramphenicol resistance (*fexA<sub>v</sub>*) and transposase (*tnpA*, *tnpB*, *tnpC*) genes as well as reading frame *orf138*. The 6-bp core nucleotide sequences at the transposon junctions are shown within boxes. The positions of primers used to amplify the region between the *radC* gene extremes are indicated as arrowheads, with a dashed line showing the extension length. The primers employed to detect circular intermediates, as well as the direction of amplification, are also shown. The gray bar over the *fexA<sub>v</sub>* gene indicates the region that has been used for cloning and mutagenesis experiments. A size scale in kilobases (kb) is displayed in the upper right-hand corner of the figure.

(6,645 bp) and part of the *radC* gene (437 bp) was obtained (Fig. 1). Complete analysis of the sequence of this transposon revealed 99.7% nucleotide identity to that of *S. lentus* (GenBank accession no. [AJ715531](#)). Sequence analysis identified three semiconserved amino acid substitutions in two reading frames: (i) Gly321Ala in the transposase protein TnpA (nucleotide G962C in the transposase gene *tnpA*) and (ii) Gly33Ala and Ala37Val in the FexAv protein (nucleotides G98C and C110T, respectively, within the *fexA<sub>v</sub>* gene) (Fig. 1). Four additional conserved amino acid substitutions were observed in Tn558: (i) Lys515Gln and Val526Leu in the TnpB transposase (nucleotides A1543C and G1576C, respectively) and (ii) Leu67Ile and Ile131Val within the FexAv protein (nucleotides C199A and A391G, respectively). No circular intermediates of Tn558, which are indicative for the mobility of the transposon, were detected by specific PCR (Fig. 1) (3) either when the bacteria were grown under normal growth conditions

(13) or after growth under stress conditions (overnight cultures were exposed to ultraviolet light for 10 min or to a heat shock of 60°C for 2 h; growth of bacteria under conditions of anaerobiosis or at 45°C). Whether the observed amino acid changes in TnpA and/or TnpB or other factors account for the lack of mobility of Tn558 under the tested conditions remains to be determined.

To confirm that the *fexA<sub>v</sub>* gene is in fact responsible for chloramphenicol but not for florfenicol resistance, a PCR assay using primers *entire\_fexA-1* and *entire\_fexA-2* (Table 1) that amplified the complete *fexA<sub>v</sub>* gene (1,428 bp), including 201 bp and 452 bp of its upstream and downstream region, respectively, was conducted. This 2,081-bp amplicon was first cloned into the pCR 2.1-TOPO vector and transformed into the recipient *Escherichia coli* TOP10 strain using a TOPO TA cloning kit (Invitrogen, Groningen, The Netherlands). Subsequent transformation into *E. coli* HB101 was conducted to test the functionality of the *fexA<sub>v</sub>* gene in

**TABLE 1** Primers used to detect the chromosomal integration site of the *fexA*-carrying Tn558 of *S. pseudintermedius* isolate C2719, those to amplify the complete *fexA* gene, and those to perform the site-directed-mutagenesis

| Primer name       | Primer sequence (5'→3') <sup>a</sup>   | Amplicon size (bp)      | PCR conditions  | Polymerase             |
|-------------------|--|-------------------------|---|------------------------|
| radC_SP-fw        | GTTTGTTCGGAATAGGGCGTA  | 437 <sup>b</sup> /7,082 | 1 min at 94°C; 30 cycles of 10 s at 98°C, 15 min at 68°C and 10 min at 72°C                   | La <i>Taq</i> (TaKaRa) |
| radC_SP-rv        | ACGATTCTTCCCAATCACA  |                         |   |                        |
| entire_fexA-1     | GATCCGTAAGCCCATCCATA   | 2,081                   | 3 min at 94°C; 30 cycles of 30 s at 94°C, 45 s at 55°C, and 2 min at 72°C; 5 min at 72°C      | BioTaq (Bioline)       |
| entire_fexA-2     | AGGCACCGGTTGTAAACTG  |                         |   |                        |
| fexA_33-inv1      | ATCTGTA <sup>u</sup> CTTGTAG <sup>u</sup> TGCAATTACGGTTG                               | 6,012 <sup>c</sup>      | 3 min at 98°C; 20 cycles of 1 min at 98°C, 1 min at 55°C, and 2.5 min at 72°C; 10 min at 72°C | Phusion (Finnzymes)    |
| fexA_33-inv2      | CAACCGTAATTGCAC <sup>u</sup> CTACAAGTACAGAT  |                         |   |                        |
| fexA_37-inv1      | TAGCTGCAATTACGG <sup>u</sup> CTGATTTAGTCAATCC  |                         |   |                        |
| fexA_37-inv2      | GGGATTGACTAAATCAG <sup>u</sup> CCGTAATTGCAGCTA   |                         |   |                        |
| fexA_33 + 37-inv1 | CTATCTGTA <sup>u</sup> CTTGTAG <sup>u</sup> TGCAATTACGG <sup>u</sup> CTGATTTAGTCAATCCC |                         |   |                        |
| fexA_33 + 37-inv2 | GGGATTGACTAAATCAG <sup>u</sup> CCGTAATTGCAC <sup>u</sup> CTACAAGTACAGATAG              |                         |   |                        |

<sup>a</sup> Nucleotides in bold type and underlined are those modified by the site-directed-mutagenesis PCR.

<sup>b</sup> Amplicon size obtained when an intact copy of the *radC* gene was present.

<sup>c</sup> Size of the complete recombinant and mutated plasmid, composed of the PCR 2.1-TOPO vector (3,931 bp) and the insertion obtained with the *entire\_fexA-1* and *entire\_fexA-2* primers (2,081 bp).

a phenicol-susceptible *E. coli* host (chloramphenicol MIC, 2 µg/ml; florfenicol MIC, 4 µg/ml). *E. coli* HB101 carrying the recombinant vector exhibited a 16-fold increase in the chloramphenicol MIC (32 µg/ml), while the florfenicol MIC value remained unchanged.

In a study on the FloR chloramphenicol/florfenicol efflux protein, Braibant et al. (24) determined by site-directed mutagenesis (SDM) that the Asp23 residue seems to participate directly in the affinity pocket involved in phenicol-derivative recognition. When Asp23 was mutated to Glu23, the corresponding FloR protein still conferred chloramphenicol resistance but lost its ability to export florfenicol. A model ([http://www.ch.embnet.org/software/TMPRED\\_form.html](http://www.ch.embnet.org/software/TMPRED_form.html)) of the transmembrane segments (TMS) of the 12-TMS FloR protein and the 14-TMS FexA protein predicted that the Asp23 residue in FloR and the Gly33/Ala37 residues in the prototype FexA protein are all located in transmembrane segment 1 and hence may have similar functions. Based on these data, SDM was conducted on the *fexA*<sub>v</sub> nucleotide substitutions G98C and C110T separately and on G98C and C110T in combination to revert them to those of the *fexA* prototype from *S. lentus*. For this, inverse PCR assays with specific “mutagenesis primers” were performed (Table 1). A plasmid preparation (Qiagen Plasmid MidiKit; Qiagen, Hilden, Germany) of the aforementioned recombinant pCR 2.1-TOPO vector served as the template for SDM. After SDM, digestion of the obtained SDM products with the DpnI restriction enzyme (Fermentas, St. Leon-Rot, Germany) was performed to eliminate the original methylated template plasmid DNA. An aliquot from the SDM approach was then transferred by electrotransformation into *E. coli* HB101. Correctly mutated recombinant vectors (TOPO/*fexA*<sub>v</sub><sup>C98G</sup>, TOPO/*fexA*<sub>v</sub><sup>T110C</sup>, and TOPO/*fexA*<sub>v</sub><sup>C98G+T110C</sup>) were confirmed by PCR of the complete *fexA* gene and sequence analysis of the amplicon (Table 1). Macrodilution assays for chloramphenicol and florfenicol (13) showed a florfenicol MIC of 16 µg/ml for the *E. coli* HB101 transformants carrying TOPO/*fexA*<sub>v</sub><sup>C98G+T110C</sup> that was 4-fold higher than that seen with the recipient strain alone (MIC 4 µg/ml) and clones carrying each of the reverted positions separately, while the chloramphenicol MIC remained unchanged in all mutants (MIC, 32 µg/ml). This increase in the florfenicol MIC was similar to that described for *E. coli* JM109 carrying the cloned *fexA* gene from *S. lentus* (2) and confirms that reversion of the naturally mutated positions restores the florfenicol resistance phenotype. It should be noted that the observed MIC changes might differ, at least slightly, in different bacterial hosts, such as in Gram-positive bacteria.

**Nucleotide sequence accession number.** The 7,698-bp nucleotide sequence enclosing the complete Tn558 and the *radC* gene of *S. pseudintermedius* strain C2719 has been deposited on the EMBL database under accession number [HF679552](https://www.ebi.ac.uk/EMBL/nuclseq/EMBL/entry/NA01679552).

(Part of these data was presented at the 2nd Conference on Methicillin-resistant Staphylococci in Animals [ASM-ESCMID], Washington, DC, 8 to 11 September 2011, and at the 15th International Symposium on Staphylococci and Staphylococcal Infections [ISSSI], Lyon, France, 26 to 30 August 2012.)

## ACKNOWLEDGMENTS

The work conducted at the University of La Rioja was financially supported by Project SAF2012-35474 from the Ministerio de Economía y Competitividad of Spain and FEDER. The work conducted at the Friedrich-Loeffler-Institut was financially supported by the German Federal Ministry of Education and Research (BMBF) through the German

Aerospace Center (DLR), grant number 01KI1014D (MedVet-Staph). E.G.-S. is supported by a fellowship from the Gobierno de La Rioja of Spain.

We thank Kerstin Meyer for excellent technical assistance.

## REFERENCES

- Schwarz S, Kehrenberg C, Doublet B, Cloeckert A. 2004. Molecular basis of bacterial resistance to chloramphenicol and florfenicol. *FEMS Microbiol. Rev.* 28:519–542.
- Kehrenberg C, Schwarz S. 2004. *fexA*, a novel *Staphylococcus lentus* gene encoding resistance to florfenicol and chloramphenicol. *Antimicrob. Agents Chemother.* 48:615–618.
- Kehrenberg C, Schwarz S. 2006. Distribution of florfenicol resistance genes *fexA* and *cfr* among chloramphenicol-resistant *Staphylococcus* isolates. *Antimicrob. Agents Chemother.* 50:1156–1163.
- Kadlec K, Ehrlich R, Monecke S, Steinacker U, Kaspar H, Mankertz J, Schwarz S. 2009. Diversity of antimicrobial resistance pheno- and genotypes of methicillin-resistant *Staphylococcus aureus* ST398 from diseased swine. *J. Antimicrob. Chemother.* 64:1156–1164.
- Shore AC, Brennan OM, Ehrlich R, Monecke S, Schwarz S, Slickers P, Coleman DC. 2010. Identification and characterization of the multidrug resistance gene *cfr* in a Pantone-Valentine leukocidin-positive sequence type 8 methicillin-resistant *Staphylococcus aureus* IVa (USA300) isolate. *Antimicrob. Agents Chemother.* 54:4978–4984.
- Feßler A, Scott C, Kadlec K, Ehrlich R, Monecke S, Schwarz S. 2010. Characterization of methicillin-resistant *Staphylococcus aureus* ST398 from cases of bovine mastitis. *J. Antimicrob. Chemother.* 65:619–625.
- Argudín MA, Tenhagen BA, Fetsch A, Sachsenröder J, Käsbohrer A, Schroeter A, Hammerl JA, Hertwig S, Helmuth R, Bräunig J, Mendoza MC, Appel B, Rodicio MR, Guerra B. 2011. Virulence and resistance determinants of German *Staphylococcus aureus* ST398 isolates from non-human sources. *Appl. Environ. Microbiol.* 77:3052–3060.
- Wang Y, Zhang W, Wang J, Wu C, Shen Z, Fu X, Yan Y, Zhang Q, Schwarz S, Shen J. 2012. Distribution of the multidrug resistance gene *cfr* in *Staphylococcus* species isolates from swine farms in China. *Antimicrob. Agents Chemother.* 56:1485–1490.
- Lozano C, Ruiz-García M, Gómez-Sanz E, López-García P, Royo-García G, Zarazaga M, Torres C. 2012. Characterization of a *cfr*-positive methicillin-resistant *Staphylococcus epidermidis* strain of the lineage ST22 implicated in a life-threatening human infection. *Diagn. Microbiol. Infect. Dis.* 73:380–382.
- Dai L, Wu CM, Wang MG, Wang Y, Wang Y, Huang SY, Xia LN, Li BB, Shen JZ. 2010. First report of the multidrug resistance gene *cfr* and the phenicol resistance gene *fexA* in a *Bacillus* strain from swine feces. *Antimicrob. Agents Chemother.* 54:3953–3955.
- Li J, Shao B, Shen J, Wang S, Wu Y. 2013. Occurrence of chloramphenicol-resistance genes as environmental pollutants from swine feedlots. *Environ. Sci. Technol.* 47:2892–2897.
- Gómez-Sanz E, Torres C, Lozano C, Sáenz Y, Zarazaga M. 2011. Detection and characterization of methicillin-resistant *Staphylococcus pseudintermedius* in healthy dogs in La Rioja, Spain. *Comp. Immunol. Microbiol. Infect. Dis.* 34:447–453.
- Clinical and Laboratory Standards Institute. 2013. Performance standards for antimicrobial susceptibility testing; Twenty-third informational supplement. CLSI Document M100-S23. Clinical and Laboratory Standards Institute, Wayne, PA.
- Schnellmann C, Gerber V, Rossano A, Jaquier V, Panchaud Y, Doherr MG, Thomann A, Straub R, Perreten V. 2006. Presence of new *mecA* and *mph(C)* variants conferring antibiotic resistance in *Staphylococcus* spp. isolated from the skin of horses before and after clinic admission. *J. Clin. Microbiol.* 44:4444–4454.
- Kehrenberg C, Schwarz S. 2005. Florfenicol-chloramphenicol exporter gene *fexA* is part of the novel transposon Tn558. *Antimicrob. Agents Chemother.* 49:813–815.
- Haroche J, Allignet J, El Solh N. 2002. Tn5406, a new staphylococcal transposon conferring resistance to streptogramin and related compounds including dalfopristin. *Antimicrob. Agents Chemother.* 46:2337–2343.
- Kadlec K, Schwarz S. 2010. Identification of the novel *dfrK*-carrying transposon Tn559 in a porcine methicillin-susceptible *Staphylococcus aureus* ST398 strain. *Antimicrob. Agents Chemother.* 54:3475–3477.
- López M, Kadlec K, Schwarz S, Torres C. 2012. First detection of the

- staphylococcal trimethoprim resistance gene *dfrK* and the *dfrK*-carrying transposon Tn559 in enterococci. *Microb. Drug Resist.* **18**:13–18.
19. **Murphy E.** 1989. Transposable elements in gram-positive bacteria, p 269–288. *In* Berg DE, Howe MM (ed), *Mobile DNA*. ASM Press, Washington, DC.
  20. **Murphy E.** 1990. Properties of the site-specific transposable element Tn554, p 123–135. *In* Novick RP (ed), *Molecular biology of the staphylococci*. VCH Publishers, New York, NY.
  21. **Schwarz S, Feßler AT, Hauschild T, Kehrenberg C, Kadlec K.** 2011. Plasmid-mediated resistance to protein biosynthesis inhibitors in staphylococci. *Ann. N. Y. Acad. Sci.* **1241**:82–103.
  22. **Schwendener S, Perreten V.** 2011. New transposon Tn6133 in methicillin-resistant *Staphylococcus aureus* ST398 contains *vga(E)*, a novel streptogramin A, pleuromutilin, and lincosamide resistance gene. *Antimicrob. Agents Chemother.* **55**:4900–4904.
  23. **Kehrenberg C, Aarestrup FM, Schwarz S.** 2007. IS21-558 insertion sequences are involved in the mobility of the multiresistance gene *cfr*. *Antimicrob. Agents Chemother.* **51**:483–487.
  24. **Braibant M, Chevalier J, Chaslus-Dancla E, Pagès JM, Cloeckaert A.** 2005. Structural and functional study of the phenicol-specific efflux pump FloR belonging to the major facilitator superfamily. *Antimicrob. Agents Chemother.* **49**:2965–2971.