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Oxazolidinones: mechanisms of resistance and mobile genetic elements involved

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The oxazolidinones (linezolid and tedizolid) are last-resort antimicrobial agents used for the treatment of severe infections in humans caused by MDR Gram-positive bacteria. They bind to the peptidyl transferase centre of the bacterial ribosome inhibiting protein synthesis. Even if the majority of Gram-positive bacteria remain susceptible to oxazolidinones, resistant isolates have been reported worldwide. Apart from mutations, affecting mostly the 23S rDNA genes and selected ribosomal proteins, acquisition of resistance genes (*cfr* and *cfr*-like, *optrA* and *poxA*), often associated with mobile genetic elements [such as non-conjugative and conjugative plasmids, transposons, integrative and conjugative elements (ICEs), prophages and translocatable units], plays a critical role in oxazolidinone resistance. In this review, we briefly summarize the current knowledge on oxazolidinone resistance mechanisms and provide an overview on the diversity of the mobile genetic elements carrying oxazolidinone resistance genes in Gram-positive and Gram-negative bacteria.

Background

Oxazolidinones are a synthetic class of antimicrobials developed over the past 30 years by numerous pharmaceutical companies.¹ Linezolid is the first member of the oxazolidinones introduced into clinical use in the early new century to treat serious infections by Gram-positive organisms, including MRSA, VRE, MDR pneumococci and MDR mycobacteria.² Clinical success of linezolid has driven considerable interest in developing new oxazolidinone molecules. Tedizolid is a second generation oxazolidinone designed to provide enhanced activity against Gram-positive pathogens that carry *cfr* genes³ and approved for the treatment of acute bacterial skin and soft tissue infections in 2014.^{4,5} Gram-negative pathogens are intrinsically resistant to oxazolidinones due to efflux pumps that force linezolid out of the cell faster than it can accumulate.^{6,7} Currently, therapeutic recommendations for oxazolidinones include severe infections caused by the aforementioned pathogens, such as community-acquired and nosocomial pneumonia, bloodstream infections and skin and soft tissue infections involving MDR isolates, or in case of therapeutic failure. Despite the synthetic nature of oxazolidinones, linezolid resistance appeared shortly after its introduction,⁸ representing a significant risk to public health and, therefore, attracting considerable attention.

This review presents the current knowledge about the mechanisms involved in oxazolidinone resistance, the resistance

genes and the relevant mobile genetic elements (MGEs) responsible for their spread,^{9–15} thereby providing an update on the latest findings on this topic.

Mode of action and mechanisms of resistance

Oxazolidinones inhibit both bacterial and archaeal protein synthesis by binding to the 50S ribosomal subunit; this mechanism of action differs from that of other protein synthesis inhibitors as it occurs at a very early stage. Oxazolidinones interact with the A-site pocket at the peptidyl transferase centre (PTC) by interfering with the binding and/or positioning of the amino acyl moiety of the incoming aminoacyl tRNA. As a result, these antibiotics prevent the formation of the ribosomal-fMet-tRNA initiation complex,^{16,17} the translocation of peptidyl-tRNA from A site to P site and thereby the mRNA translation.¹⁸ X-ray crystallography studies identified several conserved ribonucleotides that interact with oxazolidinones. The binding of linezolid stabilizes a distinct conformation of the universally conserved 23S rRNA nucleotide U2585 (*Escherichia coli* numbering) and induces a non-productive conformation of the PTC.¹⁶ The PTC binding site for tedizolid is similar to the binding site for linezolid, although the D-ring of tedizolid may involve additional sites on the ribosome and is likely responsible for the better activity versus linezolid.¹⁹ Several studies have in fact demonstrated that tedizolid is at

least 4-fold more active than linezolid against key Gram-positive pathogens.²⁰⁻²³

Linezolid resistance was first reported in enterococci in 2001,²⁴ then in *Staphylococcus aureus*²⁵ and later also in CoNS²⁶ and in *Streptococcus pneumoniae*.²⁷ Two programmes monitoring infections due to linezolid-resistant isolates are currently being conducted: LEADER (Linezolid Experience and Accurate Determination of Resistance) which gathers data in the USA and ZAAPS (Zyvox Annual Appraisal of Potency and Spectrum Program), operating worldwide. Although resistance to linezolid remains uncommon (>99% of Gram-positive pathogens are still susceptible),²⁸ different antimicrobial surveillance studies demonstrated that the number of linezolid-resistant isolates has increased during recent years.^{28,29}

Currently, several mechanisms of resistance, or reduced susceptibility, to oxazolidinones have been identified. They can be summarized as follows: (i) ribosomal mutations in 23S rRNA and/or in L3 and/or L4 ribosomal proteins; (ii) loss of the *rlmN* gene activity; (iii) active efflux; and (iv) transferable mechanisms including the Cfr and Cfr-like methyltransferases and the ABC-F proteins OptrA, PoxA and PoxA2.

23S rRNA mutations

The linezolid binding site at the PTC is composed entirely of 23S rRNA and the binding pocket is lined with the universally conserved nucleotides which interact directly with the drug.^{10,16} Several mutations of the 23S rRNA conferring oxazolidinone resistance have been described (induced *in vitro* and identified in resistant clinical isolates) that involve both nucleotides that directly interact with linezolid, such as G2061, C2452, A2503, U2504 and G2505, and nucleotides located more distally, such as A2062, G2447, A2453, C2499, U2500 and G2576.¹⁰ The G2576U mutation, which is the most widespread in linezolid-resistant isolates, has been identified in both staphylococci and enterococci.¹⁰ Reviews by Stefani *et al.*,⁹ Long and Vester¹⁰ and Mendes *et al.*¹² summarized the 23S rRNA mutations responsible for linezolid resistance. Studies carried out on *Mycobacterium smegmatis* have also shown that double mutations in 23S rRNA had remarkable synergistic effects on resistance leading to a 4–32-fold increase in linezolid MICs when compared with the single mutations.³⁰ Several authors reported that the MICs of linezolid for resistant *Enterococcus faecalis* and *S. aureus* isolates are related to the number of rDNA gene copies harbouring the G2576T mutation.^{31,32}

However, these 23S rRNA alterations cause a considerable bacterial fitness cost, mainly when several alleles are mutated. Indeed, isolates containing alterations in 23S rRNA reverted to a WT genotype and phenotype once selective pressure was removed. In some cases the reversion was not complete and single alleles might remain mutated, providing a rapid selection of resistance phenotypes when selective pressure returned.³³ Cross-resistance between PTC-targeting antibiotics resulting from 23S rRNA mutations is not uncommon, for example, the G2576U mutation also confers resistance to chloramphenicol.³⁰ Interestingly, also a deletion of one 23S rDNA (*rrl*) copy can contribute to the development of linezolid resistance in *Staphylococcus capitis* and *Staphylococcus warneri*.^{34,35}

Amino acid exchanges in the ribosomal proteins L3, L4 and L22

Other linezolid resistance mechanisms involve mutations in the genes coding for the ribosomal proteins L3, L4 and L22. Although these proteins are not part of the PTC, mutations in the respective genes that result in changes of amino acids that are located close to the PTC likely impact their conformation and stability.³⁶ Locke *et al.*³⁶ investigated the potential of MSSA and MRSA isolates to develop resistance to linezolid and tedizolid, obtaining several mutations both in 23S rRNA and in the genes for the L3 and L4 ribosomal proteins. However, they found that only the 23S rRNA mutations resulted in high resistance to oxazolidinones.³⁶

Amino acid substitutions in L3 and L4 able to cause reduced susceptibility to linezolid have been reported in several isolates either alone or in association with other resistance mechanisms.¹⁰ Reviews by Stefani *et al.*,⁹ Long and Vester¹⁰ and Mendes *et al.*¹² summarized the linezolid resistance-mediating amino acid alterations in the ribosomal proteins. The majority of the amino acid exchanges are found in the L3 protein (encoded by the *rplC* gene) due to the close proximity of this protein to the PTC and F147L and/or A157R alterations appear to be the most widespread and associated with linezolid resistance.¹⁰ Furthermore, a study suggested that amino acid exchanges in L3 could have a compensatory effect in terms of fitness in isolates that also have mutations in the 23S rRNA (for example G2576U).³⁷ In addition, a region of the L4 ribosomal protein (encoded by the *rplD* gene) is located close to the PTC and several studies indicated a higher frequency of insertions and deletions related to linezolid resistance in this region.^{10,12} Wolter *et al.*²⁷ demonstrated that deletions in the *rplD* gene resulting in amino acid substitutions in the L4 protein (65WR66 and 68KG69) are responsible for a 4-fold increase in the linezolid MIC value. Moreover, the K86Q substitution found in *S. aureus*, plays a role in linezolid resistance.³⁶ Overall, data demonstrating the association of amino acid alterations in the L3 and L4 proteins with increased levels of linezolid resistance in staphylococci are rare;³⁸ only Locke *et al.*³⁶ by analysing laboratory-derived resistant isolates, have confirmed a correlation for selected mutations.

Mutations were also detected in the *rplV* gene which encodes the L22 protein. Little is known about the effects of these mutations and the resulting amino acid substitutions on linezolid resistance, although it is assumed that they play a role due to their close proximity to the linezolid binding site.^{10,39,40}

Non-ribosomal linezolid resistance mechanisms

A decade ago, Gao *et al.*⁴¹ described in a clinical MRSA isolate a mutation in the *rlmN* gene (encoding a RNA methyltransferase) that was thought to decrease the susceptibility to the linezolid. However, it was reported that a mutant lacking RlmN activity out-competed those with active RlmN under selective pressure imposed by linezolid,⁴² suggesting that loss of RlmN activity decreases susceptibility to linezolid.

Another reported non-ribosomal linezolid resistance mechanism is related to mutations increasing expression of ABC

transporter genes in *S. pneumoniae*.^{37,43} In *S. aureus*, a major facilitator-superfamily-type multidrug efflux pump, encoded by the *lmrS* gene, was found to be able to extrude linezolid.⁴⁴

Very recently, a novel mutation (A1345G) in the *rpoB* gene encoding the β subunit of bacterial RNA polymerase, has been implicated in resistance to tedizolid in MRSA after *in vitro* serial passages.⁴⁵

Acquisition of transferable linezolid resistance genes and MGEs involved

The *cfr* gene

The onset of a new non-mutational and transmissible mechanism of linezolid resistance raised great concern within the scientific community about the future clinical efficacy of oxazolidinones. The *cfr* gene (chloramphenicol and florfenicol resistance) was firstly described in a bovine *Staphylococcus sciuri* (recently reclassified as *Mammaliococcus sciuri*) isolate.⁴⁶

The multiresistance *cfr* gene encodes an rRNA methyltransferase that adds a methyl group at the C-8 position of 23S rRNA nucleotide A2503.⁴⁷ The methylation confers combined resistance to five different classes of antimicrobial agents that bind at overlapping non-identical sites at the PTC.⁴⁸ The resulting phenotype is called PhLOPS_A, for resistance to phenicols, lincosamides, oxazolidinones, pleuromutilins and streptogramin A antibiotics. The gene *cfr* also confers significant increases in the MICs of selected 16-membered ring macrolides, such as josamycin and spiramycin, but not to tylosin.⁴⁹ Notably, the *cfr*-mediated methylation of A2503 of 23S rRNA does not interfere with the binding of tedizolid to the PTC—because of structural differences in A-ring C5 substituents between the two drugs—and therefore, does not confer resistance to tedizolid.³

A great potential for dissemination is underlined by the common location of *cfr* on MGEs, typically non-conjugative and conjugative plasmids, which are important vehicles for its spread not only among bacteria of the same species, but also among those of different species and genera.^{11,15} In addition, the transduction mechanism can be considered an alternative pathway for transmission of the *cfr* gene between staphylococcal isolates.⁵⁰ The *cfr* spreading may also be promoted by other factors: (i) the presence of ISs next to the gene which can form so-called translocatable units;^{15,51,52} (ii) the low fitness cost associated to its acquisition;⁵³ and (iii) the co-selection and persistence in the absence of a direct selective pressure (i.e. PhLOPS_A agents) due to other antimicrobial resistance genes located on the same MGE.¹⁵

Several studies have confirmed this wide dissemination reporting on the occurrence of the *cfr* gene in a large number of Gram-positive genera (*Staphylococcus*, *Enterococcus*, *Bacillus*, *Macroccoccus*, *Jeotgalicoccus* and *Streptococcus*) and even in Gram-negative genera (*Proteus*, *Escherichia*, *Morganella*, *Pasteurella*, *Providencia*, *Vibrio* and *Leclercia*).

Staphylococcus spp

The *cfr* gene, mainly found in staphylococcal isolates from animal origin, shows a great variability in its genetic contexts.¹⁵ The gene is often flanked by IS elements: so far four different IS elements have been identified to bracket the *cfr* gene including IS256, IS21-558, IS431 and ISEnf4.¹⁵ These elements can mediate the

recombination/transposition events responsible for the *cfr* spread in staphylococci.^{11,15} Stability tests confirmed that these *cfr*-containing regions could be looped out via IS-mediated recombination.^{11,15,54} Initially identified in a bovine *S. sciuri*,⁴⁶ *cfr* was first described in 2005 in a clinical MRSA from sputum in Colombia.⁵⁵ The *cfr* gene and/or ribosomal mutations have also been reported in clinical staphylococcal isolates associated to hospital outbreaks.⁵⁶⁻⁶⁰ These first reports were followed by several other studies showing the occurrence of the *cfr* gene in staphylococci isolated from both human and animal specimens (Table 1).

After the characterization of plasmid pSCFS1 from *S. sciuri* on which *cfr* was first detected,⁶¹ the gene has been identified on a variety of other plasmids, but rarely in the chromosomal DNA. Interestingly, a truncated chromosomal *cfr* gene was detected in a livestock-associated MRSA (ST398) of porcine origin; the isolate was linezolid-susceptible owing to a frameshift mutation in the gene.⁶²

Moreover, a non-truncated *cfr* gene was detected in MRSA-CC398 (where CC stands for clonal complex) isolates of pig origin,⁶³ as well as in MRSA-CC398 implicated in pig farmer colonization.⁶⁴ The *cfr* gene was also detected in *Staphylococcus equorum* and *Staphylococcus arlettae* from air sample of a swine farm with intensive-production.⁶⁵ To date, a plethora of different *cfr*-carrying plasmids have been reported in *Staphylococcus* spp., differing substantially in size and other features, such as backbone, cargo genes, transposase genes etc. (Table 1). A review by Schwarz *et al.*¹⁵ showed and summarized the *cfr* genetic backbones in staphylococci.

Enterococcus spp

The first *cfr*-carrying plasmid (named pEF-01) in enterococci was identified in 2010 in an *E. faecalis* isolate of animal origin in China; the Cfr protein diverged from the WT of *S. sciuri* only by two amino acids.⁹⁴ The *cfr*-containing segment of pEF-01 is characterized by the presence of three copies of IS1216 which probably play a key role in the gene dissemination by recombination processes into different plasmids and chromosomes, mainly of enterococci.^{11,15} Enterococcal plasmids responsible for the spread of the *cfr* gene, as well as of other antimicrobial resistance genes, are typically mosaic structures which probably result from plasmid recombination and co-integration events involving replicative transposition of IS1216.⁹⁴⁻⁹⁷

Diaz *et al.*⁹⁸ first reported the characterization of a transferable *cfr*-carrying plasmid from a human isolate of *E. faecalis*. Later studies have identified several *cfr*-harbouring plasmids showing different features in enterococci of both animal and human origin (Table 1). A review by Schwarz *et al.*¹⁵ showed and summarized the *cfr* genetic backbones in enterococci. However, to date the contribution of the *cfr* gene to linezolid resistance in *Enterococcus* spp. is still debated. It has been shown in single isolates that, probably due to yet unknown isolate-specific reasons, the Cfr protein failed to mediate linezolid resistance and a full PhLOPS_A resistance phenotype in enterococci.^{29,100,109}

Other Gram-positive bacteria

The *cfr* gene has been also found in other Gram-positive bacteria i.e.: *Bacillus* spp., *Streptococcus suis*, *Macroccoccus caseolyticus* and *Jeotgalicoccus pinnipedialis*, all of animal origin.

Table 1. *cfr*-carrying genetic elements currently known

Bacterial species	Origin (Country)	Genetic element (kb)	Accession numbers	References
<i>Staphylococcus</i> spp.				
<i>S. aureus</i>	Pig (Germany)	pSCFS3 (~35.7)	AM086211 (partial sequence)	66
<i>S. aureus</i> 004-737X	Human (USA)	p004-737X (~55)	EU598691 (partial sequence)	67
<i>S. aureus</i> M05/0060	Human (Ireland)	pSCFS7 (~45)	FR675942 (partial sequence)	68
<i>S. aureus</i> CM05	Human (Colombia)	Chromosomal pSM19035-like (15.7)	JN849634	69
<i>S. aureus</i> 69371	Human (Spain)	pERGB (15.2)	JN970906	70
<i>S. aureus</i> SA16	Cow milk (China)	pMSA16 (7.0)	JQ246438	71
<i>S. aureus</i> 004-737X	Human (USA)	pSA737 (39.2)	KC206006	56
<i>S. aureus</i> 1128105	Human (USA)	p1128105 (~37.0)	KJ866414 (partial sequence)	72
<i>S. aureus</i> 417	Human (China)	pLRS417 (39.5)	KJ922127	73
<i>S. aureus</i> 048-45547X	Human (Brazil)	p45547X (~48.5)	KJ192337 (partial sequence)	74
<i>S. aureus</i> 1518F	Pig (China)	Chromosomal SCCmec IVb (26.7)	KP777553	75
<i>S. aureus</i> M12/0145	Human (Ireland)	pSAM12-0145 (41.5)	KU521355	40
<i>S. aureus</i> M13/0401	Human (Ireland)	pSAM13-0401 (27.5)	KU510528	40
<i>S. aureus</i> AQUC 09-15	Human (Italy)	Tn6349 (48.3)	MH746818.1	76
<i>S. aureus</i> GDC6P096P	Pig (China)	Unnamed plasmid 1 (37.5)	CP065195	77
<i>S. aureus</i> X2063	Pig (Spain)	pSCFS7 (~55)	FR675942 (partial sequence)	63
<i>S. aureus</i> X1761	Human (Spain)	pSCFS3 (~35.7)	AM086211 (partial sequence)	64
<i>S. aureus</i> GDY8P96A	Pig (China)	pY96A (39.2)	CP065516	15
<i>S. aureus</i> SR153	Human (China)	pSR01 (39.5)	CP048644	15
<i>S. aureus</i> CFSAN064038	Human (Denmark)	pGMI17-006 (45.8)	CP028164	15
<i>S. aureus</i> 2868B2	Food (China)	p2868B2 (39.1)	CP060142	78
<i>S. aureus</i> SA12	Pig (Korea)	pSA12 (38.1)	CP049977	79
<i>S. epidermidis</i> 426-3147L	Human (USA)	p7LC (~30.5)	JX910899 (partial sequence)	80
<i>S. epidermidis</i> 1243-07	Human (USA)	pSEPI8573 (39.3)	KC222021	56
<i>S. epidermidis</i> 12-00322	Human (Germany)	p12-00322 (36.7)	KM521836	38
<i>S. epidermidis</i> 12-00323	Human (Germany)	p12-02300 (38.8)	KM521837	38
<i>S. epidermidis</i> SP1	Human (Italy)	pSP01 (76.9)	KR230047	81
<i>S. epidermidis</i> M13/0451	Human (Ireland)	pSAM13-0451 (8.5)	KY579373	82
<i>S. epidermidis</i>	Human (France)	p-cfr-PBR-B (40.1)	PRJEB22222	59
<i>S. epidermidis</i> MB151	Human (USA)	pMB151a (49.0)	PRJNA434275	83
<i>S. epidermidis</i> 14-01514	Human (Germany)	p14-01514 (39.2)	KX520649	58
<i>S. sciuri</i>	Cattle (Germany)	pSCFS1 (17.1)	NC_005076	61
<i>S. sciuri</i> GN5-1	Pig (China)	pSS-04 (~40)	KF129410 (partial sequence)	52
<i>S. sciuri</i> W28-3	Pig (China)	pWo28-3 (60.5)	KT601170	84
<i>S. sciuri</i> Wo35-20	Pig (China)	pWo35-20 (NA)	KX982166 (partial sequence)	85
<i>S. sciuri</i> Wo28-1	Pig (China)	pWo28-1 (60.5)	KX982171	85
<i>S. sciuri</i> Wo27-9	Pig (China)	pWo27-9 (55.7)	KX982169	85
<i>S. sciuri</i> Wo33-7	Pig (China)	Chromosomal fragment (20.3)	KX982173	85
<i>S. sciuri</i> W33-13	Pig (China)	Chromosomal fragment (25)	KX982174	85
<i>S. sciuri</i> Wo48-2	Pig (China)	pWo48-2 (NA)	KX982175 (partial sequence)	85
<i>S. sciuri</i> Wo19-3	Pig (China)	pWo19-3 (NA)	KX982172 (partial sequence)	85
<i>S. sciuri</i> GDK8D55P	Duck (China)	pK8D55P-cfr (12.7)	CP065963	15
<i>S. sciuri</i> GDH8C110P	Animal feed (China)	pH8C110P-cfr (24.1)	CP065796	15
<i>S. sciuri</i> GDK8D6P	Duck (China)	pk8D6P-cfr (53.7)	CP065793	15
<i>S. lentus</i> LQQ47	Chicken (China)	pJP1-like (~40)	KF129408 (partial sequence)	52
<i>S. lentus</i> LQQ24-1	Chicken (China)	Chromosomal fragment (6.8)	KF029594	52
<i>S. lentus</i> LQW5	Chicken (China)	Chromosomal fragment (7.4)	KF129407	52
<i>S. lentus</i> LQQ9	Chicken (China)	Chromosomal fragment (8.6)	KF049005	52
<i>S. lentus</i> H29	Chicken (China)	Chromosomal DNA	CP059679	86
<i>S. lentus</i> H29	Chicken (China)	pH29-46 (46.1)	CP059680	86
<i>S. cohnii</i> 2-8	Pig (China)	pSS-01 (15.7)	JF834909	87
<i>S. cohnii</i> SS-03	Pig (China)	pSS-03 (7.0)	JQ219851	87

Continued

Table 1. Continued

Bacterial species	Origin (Country)	Genetic element (kb)	Accession numbers	References
<i>S. cohnii</i> SA17 1206047024	Human (China)	pHK01 (NA)	KC820816 (partial sequence)	88
<i>S. saprophyticus</i> DV3	Pig (China)	pSS-02 (~35.4)	JF834910 (partial sequence)	87
<i>S. saprophyticus</i> GDY8P168P	Pig (China)	pY8P168P-cfr (41.5)	CP065798	15
<i>S. delphini</i> 2794-1	Food (China)	Chromosomal fragment (20.3)	CP063367	89
<i>S. delphini</i> 245-1	Food (China)	Chromosomal fragment (20.3)	CP063368	89
<i>S. warneri</i>	Pig (Denmark)	pSCFS6 (~43.0)	AM408573 (partial sequence)	51
<i>S. capitis</i> MHZ	Human (China)	pMHZ (~54.7)	JX232067 (partial sequence)	90
<i>S. equorum</i> TLD18	Raw chicken (China)	pHNTLD18 (NA)	KF751702 (partial sequence)	91
<i>S. equorum</i> X109	Air (Spain)	pSP01-like (34.1)	MN6420001	65
<i>S. rostri</i> GT5	Duck (China)	pJP2 (~50)	KC989517 (partial sequence)	52
<i>S. simulans</i> DKCR35	Human (China)	pHNCR35 (9.8)	KF861983	92
<i>S. arlettae</i> SA-01	Chicken (China)	pSA-01 (63.5)	KX274135	93
<i>S. arlettae</i> X114	Air (Spain)	pSP01-like (30.1)	MN637835	65
<i>S. xylosus</i> 378	Pig (China)	pSX01 (39.9)	KP890694	15
<i>Enterococcus</i> spp.				
<i>E. faecalis</i> 603-50427X	Human (Thailand)	pHOU-cfr (~97)	JQ660368 (partial sequence)	98
<i>E. faecalis</i> EF-01	Cattle (China)	pEF-01 (32.3)	NC_014508	94
<i>E. faecalis</i> W9-2	Sewage (China)	pW9-2 (~55)	JQ911741 (partial sequence)	99
<i>E. faecalis</i> CPPF5	Pig (China)	pCPPF5 (12.2)	KC954773	100
<i>E. faecalis</i> S251	Pig (Italy)	Unnamed plasmid (~97)	MT723957 (partial sequence)	101
<i>E. faecalis</i> L9	Pig (Brazil)	pL9-A (7.7)	CP041775	102
<i>E. faecalis</i> EF02	Human (China)	pEF-L18/cfr (11.8)	MT874923	103
<i>E. faecalis</i> FC	Cattle (China)	Plasmid unnamed5 (11.9)	CP028840	15
<i>E. faecalis</i> 5ZG10E	Unknown (China)	pE30 (12.2)	KT717888	15
<i>E. faecalis</i>	Pig (China)	p4 (95.6)	MH830362	15
<i>E. faecium</i> F120805	Human (Ireland)	pF120805 (72.9)	KY579372	82
<i>E. faecium</i> E35048	Human (Italy)	pE35048-oc (41.8)	MF580438	104
<i>E. faecium</i> FSIS1608820	Cow (USA)	pFSIS1608820 (28.2)	CP028728	105
<i>E. thailandicus</i> W3	Sewage (China)	pW3 (~75)	JQ911739 (partial sequence)	99
<i>E. thailandicus</i> 3-38	Pig (China)	p3-38 (~72)	JQ911740 (partial sequence)	99
<i>E. gallinarum</i> 325	Pig (Italy)	Chromosomal fragment (9.5)	MT723959	101
<i>E. gallinarum</i> FS4	Pig (Italy)	pEgFS4-1 (34.6)	MZ291452	106
<i>E. hirae</i> Fas4-2	Pig (China)	pfas4-2 (85.6)	MK798156	107
<i>E. casseliflavus</i> DY31	Pig (China)	pDY31-cfr (12.3)	MW207672	108
Other Gram-positive bacteria				
<i>Bacillus</i> sp. BS-01	Pig (China)	pBS-01 (16.5)	GU591497	110
<i>Bacillus</i> sp. BS-02	Pig (China)	pBS-02 (16.5)	HQ128580	111
<i>Bacillus</i> sp. BS-03	Pig (China)	pBS-03 (7.4)	JQ394981	112
<i>M. caseolyticus</i> 207	Pig (China)	pJP1 (~53)	JQ320084 (partial sequence)	115
<i>J. pinnipedialis</i> 102	Pig (China)	pJP1 (~53)	JQ320084 (partial sequence)	115
<i>S. suis</i> S10	Pig (China)	pStrcfr (~100)	KC844836 (partial sequence)	113
<i>S. suis</i> SFJ44	Pig (China)	Genomic island (57.5)	CP031970	114
Gram-negative bacteria				
<i>E. coli</i> LYP-C-BCTb11	Pig (China)	pEC-01 (~110)	JN982327 (partial sequence)	116
<i>E. coli</i> SCEC2	Pig (China)	pSCEC2 (135.6)	KF152885	117
<i>E. coli</i> 8ZG6D	Pig (China)	pSD11 (37.6)	KM212169	118
<i>E. coli</i> GXEC6	Pig (China)	pGXEC6 (38.4)	KM580533	119
<i>E. coli</i> GXEC3	Pig (China)	pGXEC3 (41.6)	KM580532	119
<i>E. coli</i> FS-01	Pig (China)	pFSEC-01 (33.8)	KR779901	120
<i>E. coli</i> FS-02	Pig (China)	Chromosomal fragment (18.4)	KR779900	120
<i>E. coli</i> EP28	Pig (China)	pHNEP28 (108.8)	KT845955	121
<i>E. coli</i> SH21G	Pig (China)	pEC295cfr (67)	KY865320	122
<i>E. coli</i> LN310P	Pig (China)	pEC12 (70.1)	MG677985	122

Continued

Table 1. Continued

Bacterial species	Origin (Country)	Genetic element (kb)	Accession numbers	References
<i>E. coli</i> GDE6P124	Pig (China)	pHNEP124 (60.4)	MT667260	123
<i>E. coli</i> GDE6P129	Pig (China)	pHNEP129 (35.3)	MT667261	123
<i>E. coli</i> LHM10-1	Pig (China)	Plasmid unnamed4 (28.5)	CP037908	15
<i>E. coli</i> SY3018	Pig (China)	pEC14cfr (37.6)	KY865319	15
<i>E. coli</i> FT130	Bird (China)	pFT130-1 (52)	CP040091	15
<i>E. coli</i> FP671	Pig (China)	pHNFP671 (82.8)	KP324830	15
<i>E. coli</i> EP28	Livestock (China)	pHNEP28_cfr (108.8)	KT845955	15
<i>P. vulgaris</i> PV-01	Pig (China)	Chromosomal fragment (11.2)	JF969273	124
<i>P. vulgaris</i> PvSC3	Pig (China)	pPvSC3 (284.5)	CP034667	125
<i>P. vulgaris</i> BC22	Pig (China)	ICEPvuChnBC22 (148.7)	MH160822	126
<i>P. vulgaris</i> ZN3	Pig (China)	pZN3-cfr-121 kb (121.2)	CP047346	15
<i>P. mirabilis</i> BCP11	Pig (China)	ICEPmiChnBCP11 (139.3)	MG773277	127
<i>P. mirabilis</i> STP3	Pig (China)	ICEPmiChnSTP3 (118.9)	MT449450	128
<i>P. mirabilis</i> SCBX1.1	Pig (China)	plas1.1.1 (12.7)	CP047113	15
<i>P. mirabilis</i> YPM35	Duck (China)	pJPM35-2 (35.2)	CP053900	15
<i>P. cibarius</i> G32	Goose (China)	pG32-51 (51.6)	CP053373	129
<i>P. cibarius</i> G11	Goose (China)	pG11-51 (152.8)	CP047288	130
<i>P. cibarius</i> ZF1	Pig (China)	pZF1-cfr (59.1)	CP047341	15
<i>P. cibarius</i> ZF2	Pig (China)	pZF2-cfr (59.1)	CP045009	15
<i>P. multocida</i> FJ6671	Duck (China)	cfr plasmid (~40)	MK240189 (partial sequence)	131
<i>P. multocida</i> FJ6683	Duck (China)	cfr plasmid (~40)	MK240188 (partial sequence)	131
<i>M. morgani</i> BCM24	Pig (China)	Tn6451 (116.1)	MG832661	132
<i>P. rettgeri</i> YPR25	Duck (China)	pYPR25-2 (35.2)	CP060728	15
<i>V. diabolicus</i> NV27	<i>Mactra veneriformis</i> (China)	pNV27-cfr-208K (208)	CP085846	133
<i>L. adecarboxylata</i>	Pig feed (China)	pYUSHP29-3 (56.3)	NZ_CP087283	134

NA, not available.

In the genus *Bacillus*, three types of *cfr*-carrying plasmids have been described in isolates from swine faeces: (i) pBS-01 [also harbouring a complete copy of the *erm*(B)-carrying transposon Tn917];¹¹⁰ (ii) pBS-02 (exhibiting a genetic background similar to that of pBS-01 but lacking of Tn917);¹¹¹ and (iii) pBS-03 (also co-carrying the streptomycin resistance gene *aadY*) (Table 1).¹¹²

In *S. suis*, the *cfr* gene was detected in the Tn6644 transposon⁷⁶ located on the ~100 kb non-conjugative plasmid pStrcfr and on an antibiotic-resistance-associated genomic island (Table 1).^{113,114}

In *M. caseolyticus*, the *cfr* gene was found on a plasmid highly related to pSS-03—widespread in porcine staphylococci—and on the pJP1 plasmid. In this latter plasmid, also detected in *J. pinnipedialis*, the *cfr* genetic context was very similar to the one of the staphylococcal plasmid pSCFS3 (Table 1).¹¹⁵

Gram-negative bacteria

Although the *cfr* gene is widespread in Gram-positive bacteria, it has also been identified in isolates, always of animal origin, belonging to different Gram-negative genera (*Escherichia*, *Proteus*, *Morganella*, *Pasteurella*, *Providencia*, *Vibrio* and *Leclercia*). The gene was located in the chromosomal DNA, or on plasmids, but also on integrative and conjugative elements (ICEs) (Table 1). A review by Schwarz et al.¹⁵ showed the structural

comparison of *cfr*-carrying plasmids detected in *E. coli* and in *Proteus* spp.

The first report of the *cfr* gene in a naturally occurring Gram-negative bacterium was from Wang et al.,¹²⁴ who found that a *cfr*-carrying segment with homology to a staphylococcal plasmid was found to be inserted into the chromosomal DNA of a florfenicol-resistant *Proteus vulgaris* isolate from swine. In this bacterial genus, *cfr* was also found on ICEs belonging to the family SXT/R391 in both *Proteus mirabilis* and *P. vulgaris*^{126–128} and on conjugative MDR plasmids in *P. vulgaris* and *Proteus cibarius* (Table 1).^{125,129,130}

The *cfr* gene was also detected in several *E. coli* isolates located on MDR conjugative plasmids exhibiting different backbones and sizes,^{116–122,135} in *Morganella morganii* on a novel MDR Tn6451 transposon derived from Tn7,¹³² and in *Pasteurella multocida* isolates from sick ducks on two conjugative plasmids in China.¹³¹ Several *cfr*-carrying plasmids have also been identified in some *Providencia rettgeri* isolates from duck and poultry samples,^{15,136} in a *Vibrio diabolicus* from a clamshell of *Mactra veneriformis*¹³³ and in *Leclercia adecarboxylata* from pig feed.¹³⁴ Interestingly, IncP and IncX4 plasmids co-harboured the *mcr*-1 (responsible to colistin resistance) and *cfr* genes were detected in *E. coli* of swine origin in China.¹²³

Most of the *cfr* genetic contexts were flanked by two IS26 elements (IS26-*cfr*-IS26) with the same orientation; these ISs might

have a key role in the spread of the *cfr* gene among Gram-negative bacteria.¹⁵

cfr-like genes

The cfr(B) gene

Many years after the characterization of the *cfr* gene, a *cfr*-like determinant has been identified in seven linezolid-resistant human clinical isolates of *Clostridioides difficile* (formerly known as *Clostridium difficile* or *Peptoclostridium difficile*). Sequence analysis revealed that the clostridial Cfr showed an amino acid identity of 75.1% compared with the WT protein of *S. sciuri* (Table 2).¹³⁷ A following study named this novel resistance determinant *cfr*(B) and clarified that also this gene conferred a PhLOPS_A phenotype.¹³⁸ The *cfr*(B) gene was not only detected in clinical *C. difficile* isolates,^{137,139,140} but also in *E. faecalis*¹⁴¹ and *Enterococcus faecium*^{138,142,143} isolates from human specimens. The comparison between the Cfr(B) proteins found in *C. difficile*, *E. faecalis* and *E. faecium*, revealed an amino acid identity ranging from 99.7% to 100%.¹⁵

The *cfr*(B) gene was located both on the Tn6218 transposon (or its variants)—a non-conjugative chromosomal transposon belonging to the Tn916 family^{15,142,144}—and on a not further characterized genetic element highly similar to a chromosomal fragment of *Faecalibacterium prausnitzii* L2/6.¹⁴⁰ The *cfr*(B) gene was also detected on mega plasmids larger than 200 kb in *E. faecium* isolates of human origin.^{15,142} All *cfr*(B) genetic elements known to date are shown in Table 3.

The cfr(C) gene

In 2017, Tang *et al.*¹⁴⁵ identified and characterized a novel *cfr* variant emerged in the foodborne pathogen *Campylobacter* in five different US states. The protein exhibited a high similarity with enzymes of the S-adenosylmethionine superfamily and showed an amino acid identity of 55.4% and 52.2% with the Cfr of *S. sciuri* and with Cfr(B) of *E. faecium*, respectively (Table 2).¹⁴⁵ In addition, this novel *cfr*-like gene, named *cfr*(C), was able to confer a PhLOPS_A resistance phenotype.

The *cfr*(C) gene was located on the conjugative plasmid pTx40 (48 kb) associated with the *tet*(O) and *aphA*-3 genes responsible for tetracycline and aminoglycoside resistance, respectively.^{145,146} Other studies carried out in China identified *cfr*(C) variants in *Campylobacter coli* isolates of porcine and chicken origin (Table 4).^{147,148} Some of these genes, apparently dormant, failed to elevate MICs of phenicols for *C. coli*; however, when cloned and expressed in *Campylobacter jejuni*, they appeared to be fully functional. These *cfr*(C) variants were located on novel MDR genomic islands containing multiple antimicrobial resistance genes of Gram-positive origin or on five different chromosomal regions.^{147,148}

The *cfr*(C) gene was also detected in Gram-positive—*C. difficile* and *Clostridium bolteae*—species and identified in three ICE-type organizations: ICE_{DA275}, ICE_{F548} and ICE_{90B3}.¹⁴⁹ In two *C. difficile* isolates from Greek hospitals, *cfr*(C) was located on a small pCd13-Lar plasmid,¹³⁹ while in *C. difficile* clinical isolates from Honduras and Costa Rica, it was detected on the ICE F548-like element.¹⁴⁰ Very recently, a chromosomal *cfr*(C) was also found in an isolate of *Clostridium perfringens* of cattle origin in China.¹⁵⁰

Table 2. Percentage amino acid identities between the *cfr* variants

	<i>cfr</i>	<i>cfr</i> (B)	<i>cfr</i> (C)	<i>cfr</i> (D)	<i>cfr</i> (E)
<i>cfr</i>	100	75.14	55.39	65.29	52.37
<i>cfr</i> (B)	75.14	100	52.17	64.08	54.73
<i>cfr</i> (C)	55.39	52.17	100	49.13	57.77
<i>cfr</i> (D)	65.29	64.08	49.13	100	52.07
<i>cfr</i> (E)	52.37	54.73	57.77	52.07	100

All *cfr*(C)-carrying genetic elements known to date are indicated in Table 3 and the review by Schwarz *et al.*¹⁵ showed the structural comparison of *cfr*(C)-carrying plasmids in *C. coli*.

The cfr(D) gene

The *cfr*(D) variant was first documented in France in a clinical *E. faecium* isolate¹⁵¹ and shortly thereafter in an *E. faecium* isolated in a blood culture from an Australian patient in 2020.¹⁵² The *cfr*(D) gene encoded a 357 amino acid protein, which shared 65.3%, 64.1% and 49.1% amino acid identity with Cfr, Cfr(B) and Cfr(C), respectively (Table 2).

In *E. faecium* clinical isolates, *cfr*(D) was initially reported to be located on plasmids of different sizes (ranging from 11 to >100 kb). In these plasmids, the gene was flanked by IS1216 located in the same orientation and associated with a complete, truncated or even missing *guaA* gene (encoding a glutamine-hydrolysing GMP synthase).^{15,153,154} When expressed in *E. faecium* and *E. faecalis*, *cfr*(D) did not confer any resistance, whereas it was responsible for an expected PhLOPS_A resistance phenotype in *E. coli*, suggesting that enterococci could constitute an unknown reservoir of *cfr*(D).¹⁵³ Some studies reported the occurrence of *cfr*(D)-carrying *E. faecalis* isolates in Spanish, Chinese and Scottish hospitals,^{155–157} in enterococcal isolates from swine and manure in Italy,^{101,158} and from food-producing animals in Korea.¹⁵⁹ The *cfr*(D) gene was also detected in *Streptococcus parasuis* and in *Vagococcus lutrae* isolates of swine origin in China.^{160,161} All *cfr*(D) genetic elements known to date are indicated in Table 3.

The cfr(E) gene

The so far latest *cfr* variant, termed *cfr*(E), was recently discovered in a linezolid-resistant *C. difficile* clinical isolate collected in Mexico. Cfr(E) shares only 52.1%–57.8% amino acid identity with Cfr, Cfr(B), Cfr(C) and Cfr(D) proteins (Table 2). The putative new *cfr*-like gene was part of a not further described genetic element that shows partial hits to genomic sequences of various intestinal Firmicutes.^{15,140}

The optrA gene

The *optrA* gene (oxazolidinone phenicol transferable resistance) was initially identified in the linezolid-resistant *E. faecalis* E349 recovered from a Chinese patient in 2015. In this isolate, which lacked the *cfr*/*cfr*-like genes and ribosomal mutations, the *optrA* gene was located on a conjugative plasmid (pE349, 36331 bp in size) that also carried the phenicol exporter gene *fexA*.¹⁶² The *optrA* gene encodes an ABC-F protein resulting in resistance

Table 3. *cfr*-like-carrying genetic elements currently known

Bacterial species	Origin (Country)	Genetic element (kb)	Accession numbers	References
<i>cfr</i> (B)				
<i>C. difficile</i> Ox2167	Human (UK)	Tn6218 (8.7)	HG002396	144
<i>C. difficile</i> Ox3196	Human (UK)	Tn6218 (11.3)	HG002389	144
<i>C. difficile</i> PUC51	Human (Chile)	Unknown genetic element (NA)	CAADRH000000000	140
<i>C. difficile</i> PUC347	Human (Chile)	Unknown genetic element (NA)	CAADRI000000000	140
<i>E. faecium</i> 448-18961R	Human (USA)	Tn6218 (8.4)	KR610408	138
<i>E. faecium</i> UW11590	Human (Germany)	Tn6218 (~10.2)	SRP078305	142
<i>E. faecium</i> UW11733	Human (Germany)	Tn6218 (~9.7)	SRP078305	142
<i>E. faecium</i> UW11858	Human (Germany)	ΔTn6218 (~4.1)	SRP078305	142
<i>E. faecium</i> UW12712	Human (Germany)	ΔTn6218 on plasmid (~300)	SRP078305	142
<i>E. faecium</i> UW10882	Human (Germany)	Tn6218 on plasmid (~200)	SRP078305	142
<i>E. faecium</i> E7948	Human (Netherlands)	plasmid 2 (293.8)	LR135358	15
<i>E. faecium</i> 687669, 687671	Human (Panama)	Tn6218-like (8.4)	KR610408	29
<i>E. faecalis</i> KUB3006	Human (Japan)	Tn6218 (11.3)	AP018538	141
<i>cfr</i> (C)				
<i>C. coli</i> Tx40	Cattle (USA)	pTx40 (48)	KX686749	145
<i>C. coli</i> SHP40	Pig (China)	Genomic island (20)	MF037584	147
<i>C. coli</i> SHP63	Pig (China)	Genomic island (17.7)	MF037585	147
<i>C. coli</i> SHP35	Pig (China)	Genomic island (12.7)	MF037586 (partial sequence)	147
<i>C. coli</i> CVM N61925F	Cattle (USA)	pN61925F (48)	MK541989	146
<i>C. coli</i> CVM N61740F	Cattle (USA)	pN61740F (48)	MK541988	146
<i>C. coli</i> CVM N46788F	Cattle (USA)	pN46788F (50.4)	MK541987	146
<i>C. coli</i> JZ_1_79	Pig (China)	pJZ_1_79 (62.4)	CP047213	148
<i>C. coli</i> SH89	Pig (China)	pSH89 (57.3)	CP047217	148
<i>C. coli</i> JP10	Pig (China)	Chromosomal fragment (19.5)	MT107515	148
<i>C. coli</i> SH96	Pig (China)	Chromosomal fragment (19.6)	MT107516	148
<i>C. coli</i> JZ_1_74	Pig (China)	Chromosomal fragment (9)	MT107517	148
<i>C. coli</i> JZ_1_53	Pig (China)	Chromosomal fragment (9.4)	MT107518	148
<i>C. coli</i> JZ_2_24	Pig (China)	Chromosomal fragment (10.8)	MT107519	148
<i>C. difficile</i> DA00275	Human (USA)	ICE _{DA275} (NA)	NA	149
<i>C. difficile</i> F548	Human (USA)	ICE _{F548} (NA)	NA	149
<i>C. difficile</i> Cd-13Lar	Human (Greece)	pCd13-Lar (6.9)	MH229772	139
<i>C. difficile</i> HON10	Human (Honduras)	F548-like ICE (NA)	NA	140
<i>C. difficile</i> LIBA5707	Human (Costa Rica)	F548-like ICE (NA)	NA	140
<i>C. bolteae</i> 90B3	Human (France)	ICE _{90B3} (24)	NA	149
<i>C. perfringens</i> 19TSBNCP	Cattle (China)	Chromosomal fragment (15.9)	CP073070	150
<i>cfr</i> (D)				
<i>E. faecium</i> 15-307-1	Human (France)	p15-307-1_02 (103)	CP044318	153
<i>E. faecium</i> E8014	Human (Netherlands)	Plasmid 4 (11.4)	LR135354	153
<i>E. faecium</i> M17/0314	Human (Ireland)	pM17/0314 (103.6)	MN831413	154
<i>E. faecium</i> BP5067	Human (India)	pBP5067_P1 (122.1)	CP059807	15
<i>E. faecium</i> BA17124	Human (India)	pBA17124_P1 (130.5)	CP059785	15
<i>E. faecalis</i> EF36	Food (Korea)	pEFS36_2 (35.8)	NZ_CP085293	159
<i>E. faecalis</i> EF108	Food (Korea)	pEFS108_1 (97.5)	NZ_CP085295	159
<i>E. faecalis</i> V386	Manure (Italy)	pV386 (33.4)	MZ603802	158
<i>S. parasuis</i> H35	Pig (China)	pH35-cfrD (7.5)	CP076722	160
<i>V. lutrae</i> BN31	Pig (China)	pBN31-cfrD (33.5)	CP081834	161
<i>E. faecalis</i> BX8117	Human (Scotland)	pBX8117-2 (NA)	PRJEB36950	157

NA, not available

to oxazolidinones (linezolid and tedizolid) and phenicols (chloramphenicol and florfenicol).¹⁶² Some recent reports showed that OptrA, as well as other ABC-F proteins, is able to confer

antimicrobial resistance through a ribosomal protection mechanism.^{163,164} Unlike other ABC transporters using an active efflux.¹⁶⁵

Table 4. General features of *cfr*(C)-positive *C. coli* and *C. difficile* isolates

Cfr(C) amino acid sequence			Isolates				MIC (mg/L)		
Variant	Amino acid substitution(s)	<i>cfr</i> (C) gene location	Species	Year of isolation	Source	ST	LZD	FFC	References
WT	—	P	<i>C. coli</i>	2017	a	ST1068	128	32	142
K	E94 <u>K</u>	C	<i>C. difficile</i> DA00154	2010	h	NA	NA	NA	146
KV	T225 <u>K</u> , I318 <u>V</u>	C	<i>C. coli</i> SHP35	2015	a	ST7426	16	1	144
KV	T225 <u>K</u> , I318 <u>V</u>	C	<i>C. coli</i> SHP37	2015	a	ST7426	16	2	144
RV	K178 <u>R</u> , I318 <u>V</u>	C	<i>C. coli</i> SHP40	2015	a	ST828	32	4	144
SMQKRV ^a	R15 <u>S</u> , I134 <u>M</u> , K178 <u>Q</u> , T225 <u>K</u> , P298 <u>R</u> , I318 <u>V</u>	C	<i>C. coli</i> SHP63	2015	a	ST854	16	2	144
	ΔF247–S379	C	<i>C. coli</i> JP10	2018–19	a	ST854	8	1	145
RQ	K178 <u>R</u> , R240 <u>Q</u>	C	<i>C. coli</i> JZ_1_53	2018–19	a	ST5947	8	2	145
RQ	K178 <u>R</u> , R240 <u>Q</u>	C	<i>C. coli</i> JZ_1_74	2018–19	a	ST5947	128	32	145
ARV	E94 <u>A</u> , K178 <u>R</u> , I318 <u>V</u>	P	<i>C. coli</i> JZ_1_79	2018–19	a	ST1058	128	32	145
AR	E94 <u>A</u> , K178 <u>R</u>	C	<i>C. coli</i> JZ_2_24	2018–19	a	ST828	128	32	145
RQ	K178 <u>R</u> , R240 <u>Q</u>	P	<i>C. coli</i> SH89	2018–19	a	ST828	128	64	145
ARV	E94 <u>A</u> , K178 <u>R</u> , I318 <u>V</u>	C	<i>C. coli</i> SH96	2018–19	a	ST1450	128	64	145

P, plasmid; C, chromosome; a, animal origin; h, human origin; LZD, linezolid; FFC, florfenicol; NA, not available.

^aSince this Cfr(C) protein variant is largely truncated it could be not functional.

Although the *optrA* gene was first detected in a human *Enterococcus*, its wide occurrence in bacteria from several sources, including animals, food of animal origin, vegetable products (even fresh flowers) and natural habitats, has been reported worldwide.^{15,101,166–173} Overall, *optrA* has proven to be widespread especially in enterococci of animal origin which, therefore, represent an important reservoir for the dissemination of this resistance gene.¹⁷⁴ Though the 23S rRNA alterations remained the main oxazolidinone resistance mechanism in enterococci, a recent analysis on a global collection of enterococcal clinical isolates showed that *optrA* prevailed in *E. faecalis* species.²⁹

A distinctive feature of *optrA* is its nucleotide variability consequently reflected in its amino acid sequence. Shortly after identification of the gene, two studies on the prevalence of the *optrA* gene in enterococci of clinical and animal origin in China displayed the presence of several gene variants compared with the WT.^{175,176} All the allelic variants showed amino acid substitutions whose impact on the phenotype of resistance was not to date clarified. Very recently, Schwarz *et al.*¹⁵ proposed that the WT OptrA and some protein variants (D, EDP, KD, KLDP, RD, RDK and RDKP) are commonly found in linezolid-resistant isolates, while other variants (DDTD, EYDM, EYDDK, EYNDM and KDTP) are commonly identified in linezolid-susceptible ones. From the comparison of all the OptrA variants known so far, it was found that the Italian variant (OptrA_{E35048}) is much more dissimilar from the WT and from other variants showing a limited number of amino acid substitutions. Morroni *et al.*¹⁷⁷ and Schwarz *et al.*¹⁵ listed the OptrA protein variants.

To date, a plethora of *optrA*-carrying genetic environments into the chromosomal DNA and on different plasmids, prophages

and transposons have been reported (Table 5). The review by Schwarz *et al.*¹⁵ showed the structural comparison of *optrA*-carrying plasmids in enterococci. In these platforms, the gene is often associated with *fexA*, responsible for phenicol resistance, and other resistance genes, suggesting that *optrA* may persist and spread also thanks to the selective pressure imposed by the use of antimicrobial agents other than phenicols and oxazolidinones.^{15,212} Sex pheromone-responsive *optrA*-carrying plasmids have been found in *E. faecalis* isolates pointing out the huge flexibility of the *optrA* genetic background within the enterococcal population.^{186,188} Notably, the *optrA* genetic contexts are often flanked by IS elements (mainly IS1216) in the same or opposite orientation, which could be able to form minicircles (also known as translocatable units), thereby promoting the *optrA* mobility.^{15,178} Besides IS1216, *optrA* was also associated with ISEfa15 in a novel composite transposon Tn6628 and with ISChh1-like in a porcine *C. coli* isolate from China.^{104,209}

The spread of the *optrA* gene, besides to *Enterococcus* spp., also in other bacterial genera from several sources is a matter of great concern. The gene was in fact detected in other Gram-positive bacteria, such as *S. aureus*,^{198,213} *S. sciuri* and *Staphylococcus simulans*,^{84,85,169,196,197} *Streptococcus agalactiae*, *S. suis*, *S. parasuis* and *Streptococcus gallolyticus*,^{28,114,160,179,199–201,214} *Aerococcus viridans*,²⁰⁷ *Lactococcus garvieae*,²⁰³ *Listeria monocytogenes*,¹⁵ *Listeria innocua*,²⁰⁴ *V. lutrae*¹⁶¹ and *C. perfringens*,^{205,206} and even in Gram-negative isolates, such as *C. coli* and *C. jejuni*^{208–211} and *Fusobacterium* spp. and *Salmonella* spp.¹⁵ In the most bacterial genera, the *optrA* genetic contexts are located on conjugative plasmids or, less frequently, on chromosomal transposons, such as Tn6647, Tn6823, Tn6261, Tn7363 and Tn6993.^{157,161,185,197,198} In

Table 5. *optrA*-carrying genetic elements currently known

Strain	Origin	Genetic element (kb)	Accession numbers	References
<i>Enterococcus</i> spp.				
<i>E. faecalis</i> E349	Human (China)	pE349 (36.3)	KP399637	162
<i>E. faecalis</i> 10-2-2	Pig (China)	p10-2-2 (~60)	KT862775	178
<i>E. faecalis</i> E121	Human (China)	pE121 (~80)	KT862776	178
<i>E. faecalis</i> E419	Human (China)	pE419 (~80)	KT862777	178
<i>E. faecalis</i> FX13	Pig (China)	pFX13 (~34)	KT862778	178
<i>E. faecalis</i> SF35	Chicken (China)	pSF35 (~65)	KT862779	178
<i>E. faecalis</i> XY17	Pig (China)	pXY17 (~30)	KT862780	178
<i>E. faecalis</i> E016	Human (China)	Chromosomal fragment (29.1)	KT862781	178
<i>E. faecalis</i> E079	Human (China)	Chromosomal fragment (14.2)	KT862782	178
<i>E. faecalis</i> E147	Human (China)	Chromosomal fragment (6.0)	KT862783	178
<i>E. faecalis</i> G20	Pig (Tibet)	Chromosomal fragment (17.5)	KT862784	178
<i>E. faecalis</i> LY4	Chicken (China)	Chromosomal fragment (13.1)	KT862785	178
<i>E. faecalis</i> 599	Human (USA)	NA	ALZ101000000	179
<i>E. faecalis</i> E1379A	Water (Tunisia)	pAF379 (45.6)	NHNF00000000	167
<i>E. faecalis</i> 6742	Human (Poland)	p6742_1 (36.3)	KY513280	180
<i>E. faecalis</i> UW13078	Human (Germany)	NA	SRP128637	181
<i>E. faecalis</i> UW14261	Human (Germany)	pE349-like (40.0)	SRP128637	181
<i>E. faecalis</i> UW15200	Human (Germany)	Unnamed plasmid (~75)	SRP128637	181
<i>E. faecalis</i> UW15335	Human (Germany)	Unnamed plasmid (~75)	SRP128637	181
<i>E. faecalis</i> UW15420	Human (Germany)	Unnamed plasmid (~80)	SRP128637	181
<i>E. faecalis</i> UW15589	Human (Germany)	Unnamed plasmid (~100)	SRP128637	181
<i>E. faecalis</i> UW15602	Human (Germany)	Unnamed plasmid (~75)	SRP128637	181
<i>E. faecalis</i> UW15712	Human (Germany)	Unnamed plasmid (~70)	SRP128637	181
<i>E. faecalis</i> KUB3006	Human (Japan)	pKUB3006-4 (36.3)	AP018542	141
<i>E. faecalis</i> KUB3007	Human (Japan)	pKUB3007-4 (36.3)	AP018547	141
<i>E. faecalis</i> N60443F	Cattle (USA)	pN60443F-2 (41.6)	CP028725	105
<i>E. faecalis</i> N48037F	Pig (USA)	pN48037F-3 (40.3)	CP028723	105
<i>E. faecalis</i> 29462	Human (China)	p29462 (21.6)	MH225419	182
<i>E. faecalis</i> 1203_10W003	Human (China)	p1203_10W003 (9.1)	MH225415	182
<i>E. faecalis</i> 1207_26W003	Human (China)	p1207_26W003 (8.1)	MH225416	182
<i>E. faecalis</i> WHXH	Human (China)	pWHXH (6.7)	MH225422	182
<i>E. faecalis</i> TZ2	Human (China)	Chromosomal fragment (75.1)	MH225421	182
<i>E. faecium</i> 19506	Human (China)	Chromosomal fragment (22.7)	MH225417	182
<i>E. faecalis</i> E035	Pig (China)	pE035 (121.5)	MK140641	183
<i>E. faecalis</i> C25	Pig (China)	Chromosomal fragment (16.6)	MK251150	184
		pC25-1 (45.6)	CP030043	
<i>E. faecalis</i> C54	Pig (China)	pC54 (64.5)	CP030046	184
<i>E. faecalis</i> E1731	Pig (China)	Tn6674 (12.9)	MK737778	185
<i>E. faecalis</i> E211	Pig (China)	pE211 (77.5)	MK425644	186
<i>E. faecalis</i> E508	Pig (China)	pE508 (84.5)	MK425645	186
<i>E. faecalis</i> 190AC	Dog (China)	Unnamed plasmid (~60)	VWNX00000000	169
<i>E. faecalis</i> 3-8	Beef (China)	Unnamed plasmid (~60)	VWNN00000000	169
<i>E. faecalis</i> 82AC	Dog (China)	Unnamed plasmid (~100)	VWNU00000000	169
<i>E. faecalis</i> 114AC	Dog (China)	Unnamed plasmid (~100)	VRVK00000000	169
<i>E. faecalis</i> 8-2	Caraway seed (China)	Unnamed plasmid (~60)	VWOG00000000	169
<i>E. faecalis</i> 75AC	Dog (China)	Unnamed plasmid (~90)	VWNJ00000000	169
<i>E. faecalis</i> 131AC	Dog (China)	Unnamed plasmid (~60)	VRVN00000000	169
<i>E. faecalis</i> 109AC	Dog (China)	Chromosomal DNA	VWNK00000000	169
<i>E. faecalis</i> 11-7	Egg (China)	Chromosomal DNA	VWNO00000000	169
<i>E. faecalis</i> 52AC	Dog (China)	Chromosomal DNA	VWNR00000000	169
<i>E. faecalis</i> 121NS	Dog (China)	Chromosomal DNA	VWNW00000000	169
<i>E. faecalis</i> L9	Pig (Brazil)	pL9 (58.6)	CP041776	102

Continued

Table 5. Continued

Strain	Origin	Genetic element (kb)	Accession numbers	References
<i>E. faecalis</i> EF02	Human (China)	pEF-L13/optrA (8.3)	MT874924	103
<i>E. faecalis</i> M17/0149	Human (Ireland)	pM17/0149 (36.3)	MN831410	154
<i>E. faecium</i> strain M17/0314	Human (Ireland)	pM17/0314 (103.6)	MN831413	154
<i>E. faecalis</i> M17/0240	Human (Ireland)	plasmid optrA_I (10.5)	MN831414 (partial)	154
<i>E. faecalis</i> M18/0173	Human (Ireland)	plasmid optrA_II (9.7)	MN831415 (partial)	154
<i>E. faecalis</i> M18/0906	Human (Ireland)	plasmid optrA_IV (11.7)	MN831417 (partial)	154
<i>E. faecalis</i> M18/0497	Human (Ireland)	plasmid optrA_VI (12.6)	MN831419 (partial)	154
<i>E. faecalis</i> S7316	Human (Japan)	pS7316optrA (68.4)	LC499744	187
<i>E. faecalis</i> X526	Human (Spain)	Unknown genetic element (11.2)	MN731743 (partial)	155
<i>E. faecalis</i> C9952	Human (Spain)	Unknown genetic element (12.7)	MN731744 (partial)	155
<i>E. faecalis</i> C9901	Human (Spain)	Unnamed plasmid (21.5)	MN848142 (partial)	155
<i>E. faecalis</i> P10748	Human (China)	pEF10748 (53.2)	MK993385	188
<i>E. faecalis</i> F106	Water (Switzerland)	Chromosomal DNA	JAGMTZ00000000	172
<i>E. faecalis</i> F143	Water (Switzerland)	Chromosomal DNA	JAGMTY00000000	172
<i>E. faecalis</i> F162_1	Water (Switzerland)	plasmid (53)	JAMTX00000000	172
<i>E. faecalis</i> EN3	Water (Italy)	pEfs-EN3 (16.5)	MT683614	171
<i>E. faecalis</i> ES-1	Pig (China)	Chromosomal DNA	PRJNA609523	189
<i>E. faecalis</i> EFs17-1	Animal (South Korea)	pEFs17-1 (36.3)	MT223178	15
<i>E. faecalis</i>	Pig (China)	p1 (74.5)	MH830363	15
<i>E. faecalis</i> EF123	Chicken (China)	pEF123 (79.7)	KX579977	15
<i>E. faecalis</i> L15	Pig (Brazil)	pL15 (82.9)	CP042214	15
<i>E. faecalis</i> L8	Pig (Brazil)	pL8-A (91.5)	CP042217	15
<i>E. faecalis</i> E211	Pig (China)	pE211-2 (87.8)	MK784777	15
<i>E. faecalis</i> AR-0780	Human (USA)	Tn6674 (12.9)	PRJNA523425	190
<i>E. faecalis</i> WE0851	Human (Scotland)	pWE0851-1 (59.7)	PRJEB36950	157
<i>E. faecalis</i> WE0254	Human (Scotland)	pWE0254-1 (80.5)	PRJEB36950	157
<i>E. faecalis</i> WE0438	Human (Scotland)	pWE0438 (61.3)	PRJEB36950	157
<i>E. faecalis</i> TM6294	Human (Scotland)	pTM6294-2 (52.8)	PRJEB36950	157
<i>E. faecalis</i> BX5936	Human (Scotland)	pBX5936-1 (68.6)	PRJEB36950	157
<i>E. faecalis</i> BX8117	Human (Scotland)	pBX8117-2 (41.8)	PRJEB36950	157
<i>E. faecalis</i> EFS17	Pig (South Korea)	Chromosomal DNA	NZ_CP085289	159
<i>E. faecalis</i> EFS108	Pig (South Korea)	Chromosomal DNA	NZ_CP085294	159
<i>E. faecalis</i> SY-1	Goat (China)	pSY-1-optrA (36.0)	CP078016	191
<i>E. faecium</i> C1904	Human (USA)	NA	AMBD01000000	179
<i>E. faecium</i> F120805	Human (Ireland)	pF120805 (72.9)	KY579372	82
<i>E. faecium</i> UW7931	Human (Germany)	Unnamed plasmid (~105)	SRP128637	181
<i>E. faecium</i> UW9805	Human (Germany)	Unnamed plasmid (~100)	SRP128637	181
<i>E. faecium</i> UW10156	Human (Germany)	Unnamed plasmid (~80)	SRP128637	181
<i>E. faecium</i> UW10862	Human (Germany)	Unnamed plasmid (~245)	SRP128637	181
<i>E. faecium</i> UW12119	Human (Germany)	Unnamed plasmid (~245)	SRP128637	181
<i>E. faecium</i> UW12227	Human (Germany)	Unnamed plasmid (~130)	SRP128637	181
<i>E. faecium</i> UW15425	Human (Germany)	Unnamed plasmid (~75)	SRP128637	181
<i>E. faecium</i> E35048	Human (Italy)	pE35048-oc (41.8)	MF580438	104
<i>E. faecium</i> FSIS1608820	Cattle (USA)	pFSIS1608820 (28.2)	CP028728	105
<i>E. faecium</i> GJA5	Pig (China)	Chromosomal fragment (16.1)	MK251151	184
<i>E. faecium</i> SC1	Pig (China)	Chromosomal fragment (26.0)	MK251152	184
<i>E. faecium</i> SC18	Pig (China)	Chromosomal fragment (26.7)	MK251153	184
<i>E. faecium</i> YG1	Pig (China)	Chromosomal fragment (26.7)	MK251154	184
<i>E. faecium</i> 15-307-1	Human (France)	p15-307-1_02 (103)	CP044318	153
<i>E. faecium</i> M17/0314	Human (Ireland)	plasmid optrA_III (8.0)	MN831416 (partial)	154
<i>E. faecium</i> M16/0594	Human (Ireland)	Chromosomal fragment (10.7)	MN831418	154
<i>E. faecium</i> O_03	Human (Ireland)	pEfmO_03 (58.6)	MT261365	192
<i>E. faecium</i> VB3025	Human (India)	Chromosomal DNA,	CP040236	193

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Table 5. Continued

Strain	Origin	Genetic element (kb)	Accession numbers	References
<i>E. faecium</i> VB3240	Human (India)	pV3240_2 (142.8)	CP040238	193
<i>E. faecium</i> AVS0243	Water (Switzerland)	Chromosomal DNA	CP040369	193
<i>E. faecium</i> F39	Water (Switzerland)	pAVS02435_2 (36.4)	CP072896	172
<i>E. faecium</i> F88	Water (Switzerland)	Chromosomal DNA	CP072881	172
<i>E. faecium</i> DY28	Pig (China)	pF88_1 (246.3)	CP072879	172
<i>E. faecium</i> DY32	Pig (China)	pDY28-optrA (54.9)	PRJNA673930	108
<i>E. faecium</i> VB976	Pig (China)	pDY32 (175.5)	PRJNA673930	108
<i>E. faecium</i> BP5067	Human (India)	pVB976_p2 (123.6)	CP072588	194
<i>E. faecium</i> BA17124	Human (India)	pBP5067_P1 (122.1)	CP059807	194
<i>E. casseliflavus</i> 10-1	Human (India)	pBA17124_P1 (130.5)	CP059785	194
<i>E. casseliflavus</i> DY31	Beef (China)	Chromosomal DNA	VWOB00000000	169
<i>E. gallinarum</i> EG81	Pig (China)	pDY31 (75.6)	PRJNA673930	108
		Chromosomal Tn554-like (NA)	CP050816	195
		pEG81-1 (51.6)	CP050817	
<i>E. gallinarum</i> FS4	Pig (Italy)	pEgFS4-1 (34.6)	MZ291452	106
<i>E. hirae</i> F104	Water (Switzerland)	pF104_2 (56.9)	CP072892	172
<i>E. hirae</i> F105	Water (Switzerland)	Unnamed plasmid (36)	JAGMUA00000000	172
<i>E. raffinosus</i> F162_2	Water (Switzerland)	Chromosomal DNA	CP072888	172
<i>Staphylococcus</i> spp.				
<i>S. sciuri</i> S25-1	Pig (China)	Chromosomal fragment (23.9)	KX447566	196
<i>S. sciuri</i> MS58	Pig (China)	Chromosomal fragment (28.8)	KX447567	196
<i>S. sciuri</i> S13-1	Pig (China)	Chromosomal fragment (3.4)	KX447568	196
<i>S. sciuri</i> S031-25	Pig (China)	Chromosomal fragment (24.0)	KX447569	196
<i>S. sciuri</i> S032-3	Pig (China)	Chromosomal fragment (21.5)	KX447570	196
<i>S. sciuri</i> MS11-3	Pig (China)	Chromosomal fragment (28.2)	KX447571	196
<i>S. sciuri</i> S49-1	Pig (China)	Chromosomal fragment (21.8)	KX447572	196
<i>S. sciuri</i> W028-3	Pig (China)	pWo28-3 (60.5)	KT601170	84
<i>S. sciuri</i> Wo35-20	Pig (China)	pWo35-20, partial (31.3)	KX982166	85
<i>S. sciuri</i> Wo28-1	Pig (China)	pWo28-1 (60.5)	KX982171	85
<i>S. sciuri</i> Wo27-9	Pig (China)	pWo27-9 (55.7)	KX982169	85
<i>S. sciuri</i> Wo33-7	Pig (China)	Chromosomal fragment (20.3)	KX982173	85
<i>S. sciuri</i> Wo33-13	Pig (China)	Chromosomal fragment (25.0)	KX982174	85
<i>S. sciuri</i> W72	Pig (China)	Chromosomal fragment (29.1)	KX982167	85
<i>S. sciuri</i> Wo19-3	Pig (China)	Chromosomal fragment (12.3)	KY056650	85
<i>S. sciuri</i> Wo35-29	Pig (China)	Chromosomal fragment (14.6)	KX982168	85
<i>S. sciuri</i> BY05	Pig (China)	Chromosomal fragment (22.7)	MF805731	197
<i>S. sciuri</i> G07	Dog (China)	Chromosomal fragment (17.5)	MF805732	197
<i>S. sciuri</i> 53NC	Dog (China)	Chromosomal DNA	VWOD00000000	169
<i>S. aureus</i> SA01	Chicken (China)	Tn6823 (16.3)	CP053075	198
<i>S. simulans</i> IY19	Pig (China)	Chromosomal fragment (18.8)	MF805730	197
<i>Streptococcus</i> spp.				
<i>S. suis</i> YS21	Pig (China)	Chromosomal DNA	ALMH01000001	179
<i>S. suis</i> YS35	Pig (China)	Chromosomal DNA	ALMN01000021	179
<i>S. suis</i> YS39	Pig (China)	Chromosomal DNA	ALMO01000001	179
<i>S. suis</i> YS49	Pig (China)	Chromosomal DNA	ALMT01000101	179
<i>S. suis</i> YS50	Pig (China)	Chromosomal DNA	ALMV01000119	179
<i>S. suis</i> YS57	Pig (China)	Chromosomal DNA	ALMZ01000078	179
<i>S. suis</i> YSJ17	Pig (China)	φSsuYSJ17-3 (56.7)	CP032064	199
<i>S. suis</i> SFJ44	Pig (China)	Genomic island (43.8)	CP031970	114
<i>S. suis</i> SC181	Pig (China)	φSC181 (54.8)	MK359990	200
<i>S. suis</i> SC216	Pig (China)	ICESsuSC216 (53.0)	MK359991	200
<i>S. suis</i> SC317	Pig (China)	ICESsuSC317 (103.3)	MK359989	200
<i>S. suis</i> CQ2B66	Pig (China)	Chromosomal DNA	PRJNA623715	201

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Table 5. Continued

Strain	Origin	Genetic element (kb)	Accession numbers	References
<i>S. suis</i> BJCY50	Pig (China)	Chromosomal DNA	PRJNA623715	201
<i>S. suis</i> F5-1HN	Pig (China)	Chromosomal DNA	PRJNA623715	201
<i>S. suis</i> BJCY29	Pig (China)	Chromosomal DNA	PRJNA623715	201
<i>S. suis</i> BJAY75	Pig (China)	Chromosomal DNA	PRJNA623715	201
<i>S. suis</i> BS11F	Pig (China)	Chromosomal DNA	PRJNA623715	201
<i>S. suis</i> SC3B24	Pig (China)	Chromosomal DNA	PRJNA623715	201
<i>S. suis</i> CQ2B20R	Pig (China)	Chromosomal DNA	PRJNA623715	201
<i>S. suis</i> HNAY30	Pig (China)	Chromosomal DNA	PRJNA623715	201
<i>S. suis</i> HNBY23	Pig (China)	Chromosomal DNA	PRJNA623715	201
<i>S. suis</i> HNAY3	Pig (China)	Unnamed plasmid (~40)	PRJNA623715	201
<i>S. suis</i> 1112S	Pig (China)	ICESsu1112S (74.3)	MW790610	202
<i>S. parasuis</i> H35	Pig (China)	Chromosomal DNA	CP076721	160
Other Gram-positive bacteria				
<i>L. garvieae</i> LG592	Human (China)	pLG592-optrA (42.0)	MW310586	203
<i>L. garvieae</i> LG606	Human (China)	pLG606-optrA (69.6)	MW310587	203
<i>L. garvieae</i> LG728	Human (China)	pLG728-optrA (77.6)	MW310588	203
<i>L. garvieae</i> LG791	Human (China)	pLG791-optrA (76.8)	MW310589	203
<i>L. garvieae</i> LG1074	Human (China)	pLG1074-optrA (85.8)	MW310590	203
<i>L. garvieae</i> LG1267	Human (China)	pLG1267-optrA (71.8)	MW310591	203
<i>L. innocua</i> LI42	Food (China)	Chromosomal DNA	SAMN18079989	204
<i>L. innocua</i> LI47	Food (China)	Chromosomal DNA	SAMN18080006	204
<i>L. innocua</i> LI203	Food (China)	Chromosomal DNA	SAMN18080009	204
<i>C. perfringens</i> 2C45	Chicken (China)	p2C45 (148.6)	NZ_JAAQTM010000004	205
<i>C. perfringens</i> QHY-2	Sheep (China)	Unknown	PRJNA735902	206
<i>A. viridans</i> 1417-4A	Pig (Italy)	pAv-optrA (37.8)	MW364930	207
<i>V. lutrae</i> BN31	Pig (China)	Tn7363 (12.3)	CP081833	161
Gram-negative bacteria				
<i>C. coli</i> 1712SZ1KX20C	Chicken (China)	Genomic island (14.6)	PRJNA613634	208
<i>C. coli</i> 18QD2YX29C	Duck (China)	Genomic island (18)	PRJNA613634	208
<i>C. coli</i> JZ_1_15	Pig (China)	Chromosomal fragment (6.8)	CP047214	209
<i>C. coli</i> JZ_1_95	Pig (China)	Chromosomal fragment (6.8)	CP047197	209
<i>C. coli</i> SH52	Pig (China)	Chromosomal fragment (6.8)	MT780491	209
<i>C. coli</i> SH_72	Pig (China)	Chromosomal fragment (6.8)	MT780492	209
<i>C. coli</i> SH_22	Pig (China)	Chromosomal fragment (10.3)	MT780493	209
<i>C. coli</i> CC19CH075	Chicken (China)	Genomic island (18.5)	CP068581	210
<i>C. coli</i> CC19DZ036	Duck (China)	Genomic island (11.2)	CP068565	210
<i>C. jejuni</i> 542-1C	Pigeon meat (China)	Genomic island (21.3)	NA	211
<i>C. jejuni</i> CC19PF065	Pig (China)	Genomic island (18.2)	CP068567	210
<i>C. jejuni</i> ZS007	Duck meat (China)	Genomic island (22.7)	CP048771	210

NA, not available.

streptococci, *optrA* is instead carried by ICEs, prophages or pathogenicity islands,^{114,179,199,200} though very recently, the first non-conjugative *optrA*-carrying plasmid was reported in a porcine *S. suis* isolate from China.²⁰¹ Of particular concern is the co-occurrence of *vanA* (associated with Tn1546 variants) and *optrA* (located on a Tn554-related transposon) in linear plasmids that seem to have become increasingly important in the dissemination of Tn1546 among *E. faecium* isolates.¹⁹⁴ Interestingly, a study demonstrated that the acquisition of an *optrA*-harbouring plasmid by *E. faecalis* did not affect the growth rates of the transconjugant compared with the recipient. Therefore, as assumed for the *cfr*-carrying plasmids, a low fitness cost could promote the spread

and the maintenance of the *optrA* gene within the bacterial population.¹⁸⁰

The *poxA* gene

In 2018, Antonelli *et al.* described a novel transferable oxazolidinone resistance gene, named *poxA* (phenicols, **ox**azolidinones and **t**etracyclines resistance), in a linezolid-resistant *cfr*-positive MRSA from a cystic fibrosis patient.^{215,216} The *poxA* gene encodes a ribosomal protection protein of the ARE ABC-F family (lineage F of the ABC superfamily proteins associated with antibiotic resistance),¹⁶³ which is distantly related to *OptrA* and able to

confer reduced susceptibility to phenicols, oxazolidinones and tetracyclines.²¹⁶ Very recently, Crowe-McAuliffe *et al.*¹⁶⁴ demonstrated that perturbation of the P-site tRNA by the PoxTA protein modifies the conformation of the attached nascent chain, thereby reducing the affinity of the antimicrobial agents to their binding site and leading to phenicol and oxazolidinone resistance. Furthermore, the same authors found no evidence for PoxTA conferring resistance to tetracycline, suggesting to reassigning the letters from the PoxTA acronym from **p**henicol-**o**xazolidinone **t**etracycline **A** to **p**henicol-**o**xazolidinone **t**ransmissible **A**, analogous to OptrA.¹⁶⁴

The *poxTA* gene, flanked by two IS1216 elements, was found to be associated with a 48 kb Tn6349 composite transposon, inserted into a ϕ N315-like prophage found in the chromosome of MRSA AUC-0915. Tn6349, bounded by two IS1216 elements, carried two transposons: the *poxTA*- and *flexB*-containing Tn6657 and the *cfr*-carrying Tn6644.⁷⁶ Schwarz *et al.* suggested that Tn6349 may not be considered a true composite transposon—since this transposon was bounded by IS1216 (members of the IS26 family) orientated in the same direction—thus, it should be termed as pseudo-compound transposon.^{15,217}

In enterococci, a plasmid carrying *poxTA* was first detected in Italy from a porcine *E. faecium* isolate; the gene was able to confer linezolid resistance also in the absence of other known oxazolidinone resistance mechanisms.²¹⁸ Later, the *poxTA* gene was also detected in enterococci from humans,^{15,154,219–222} from animals,^{15,101,107,108,183,184,221,223,224} from food-producing animals^{15,225–228} and from environmental sources.^{15,171,172,229} Latest surveillances on the prevalence of the *poxTA* gene among clinical, animal or environmental linezolid-resistant enterococci collected in several countries reported that this resistance gene is the most prevalent oxazolidinone resistance mechanism in *E. faecium* independently from the presence of *optrA* gene and 23S rRNA alterations.^{15,97,108,221,222,225,226}

Unlike the OptrA and Cfr(C) proteins, the amino acid sequence of PoxTA is essentially conserved, only five amino acid substitutions have been identified: R256H and I219L in *E. faecium* isolates^{226,229} and E14K, E140K, F141L in a *Lactobacillus salivarius* strain.²³⁰ Very recently, a new gene variant, named *poxTA2*, was found in *E. faecalis* and *Enterococcus casseliflavus* isolates of pig origin and in a human *Enterococcus gallinarum* isolate.^{158,231,232} Unlike *poxTA*, *poxTA2* was not truncated by an IS1216 insertion at the 3' end, thus eight new amino acid (TPEEQKY) replaced the six amino acid (GSVAKF) of WT protein. Baccani *et al.*²³² confirmed that *poxTA2* was functional in conferring protection against linezolid in the enterococcal background and hypothesized that this variant could be considered as a presumed *poxTA* ancestor. Another considerable difference between the *optrA* and *poxTA* genes concerns their diffusion: *optrA* is widespread in Gram-positive and even in Gram-negative bacteria, while to date *poxTA* was only identified in *Enterococcus* spp. except the first detection in an MRSA,²¹³ in *Staphylococcus haemolyticus* and *Staphylococcus saprophyticus* isolates²³³ and very recently in a *L. salivarius* strain.²³⁰ Interestingly, *L. salivarius* harboured two *poxTA* copies: one located on a non-conjugative MDR plasmid and another chromosomal copy, which was truncated by the insertion of an IS_{Lasa1} element into the 3'-end of *poxTA*.²³⁰ Some *poxTA* genetic contexts have been characterized, they were mainly found on different plasmids that seem to play a

key role in the spread of this oxazolidinone resistance gene among enterococci (Table 6). The *poxTA* genetic contexts, often bracketed by IS1216-like elements in the same or in opposite orientation, were mobilizable as translocatable units.^{15,234,221} On the other hand, Shan *et al.*²³⁴ have suggested that IS1216E-mediated transposition and translocation processes can promote the spread of *poxTA* gene and ensure its persistence within the enterococcal population. The same authors also showed how mobilizable *poxTA*-carrying plasmids could transfer with the help of a conjugative plasmid by homologous recombination in *E. faecalis* and by replicative transposition in *Enterococcus lactis*.⁹⁶ Very recently, Xu *et al.*⁹⁷ observed that, during the conjugation process, *poxTA* plasmids can undergo recombination phenomena leading to the formation of mosaic structures that differ in size and organization from those of the parental isolates. The review by Schwarz *et al.*¹⁵ showed the structural comparison of *poxTA*-carrying plasmids in enterococci.

Occurrence of multiple oxazolidinone resistance genes

The presence of two or more oxazolidinone resistance genes may account for higher oxazolidinone MICs both when genes are located on the same genetic element or co-harboured in the same bacterial host but on different genetic backgrounds. Immediately after the discovery of the *optrA* gene, two isolates carrying simultaneously *cfr* and *optrA*, the only characterized oxazolidinone resistance genes at that time, were identified.¹⁰⁹ Since then, a number of publications described the presence of two oxazolidinone resistance determinants on the same genetic element (Table 7). The co-location occurred both in plasmids and chromosomal elements and so far, has been reported in *Mammaliococcus*, *Staphylococcus* and *Enterococcus* both of human and animal origin. The most common co-localization involved *cfr* and *optrA* or *cfr*(D) and *optrA* (Table 7).

Along with the co-locations, several publications described the presence of two or more oxazolidinone resistance genes (even a double copy of the same gene) in a single isolate but carried by diverse genetic elements (Table 8). In these cases, the combinations involved all genes other than *cfr*(E) and *poxTA2*. Such co-occurrences were reported in *Enterococcus*, *Clostridium*, *Streptococcus*, *Vagococcus* and *Lactobacillus* and mainly involved *cfr* and *optrA* or *optrA* and *poxTA* (Table 8). Interestingly, the *cfr*(D) gene is always associated with other oxazolidinone resistance genes: co-localized with *optrA* or *poxTA2* on enterococcal plasmids,^{15,153,154,158,159} or co-harboured with a chromosomal *optrA*.^{160,161} Worthy of note is the occurrence of the *cfr*, *optrA* and *poxTA* genes in two non-conjugative plasmids of an *E. gallinarum* isolate in Italy,¹⁰⁶ in three distinct plasmids of several sizes found in *E. casseliflavus* in China¹⁰⁸ and in an *E. faecalis* isolate in Belgium,²²⁸ all of swine origin.

Moreover, various genetic lineages or CCs of *S. aureus*, *E. faecalis* and *E. faecium* isolates carrying *cfr*, *optrA* and *poxTA* genes have been detected during the past two decades all over the world. Due to the mobile character of these genes, their frequent association with MGEs and the observation that these MGEs can be exchanged across strain, species and genus boundaries, the oxazolidinone resistance genes are not found preferentially in a

Table 6. *poxA/poxA2*-carrying genetic elements currently known

Strain	Origin	Genetic element (kb)	Accession numbers	References
<i>Enterococcus</i> spp.				
<i>E. faecium</i> 25	Pig (China)	pC25-1 (67.6)	MH784601	223
<i>E. faecium</i> 27	Pig (China)	pC27-2 (62.3)	MH784602	223
<i>E. faecium</i> GZ8	Pig (China)	pGZ8 (36.9)	CP038162	226
<i>E. faecium</i> HB2-2	Chicken (China)	pHB2-2 (32.1)	CP038165	226
<i>E. faecium</i> SC3-1	Chicken (China)	pSC3-1 (36.8)	CP038167	226
<i>E. faecium</i> SCBC1	Pig (China)	pSCBC1 (41)	CP038169	226
<i>E. faecium</i> SDGJP3	Pig (China)	pSDGJP3 (51.6)	CP038171	226
<i>E. faecium</i> YN2-1	Pig (China)	pYN2-1 (41.3)	CP038173	226
<i>E. faecium</i> SDGJQ5	Chicken (China)	pSDGJQ5 (30.4)	CP038175	226
<i>E. faecium</i> HN11	Pig (China)	pHN11 (69.7)	CP038176	226
<i>E. faecium</i> M16/0594	Human (Ireland)	pM16/0594 (21.8)	MN831411	154
<i>E. faecium</i> E1077	Pig (China)	pE1077-23 (23.7)	MT074684	234
<i>E. faecium</i> T-E1077-31	Pig (China)	pT-E1077-31 (31.7)	MT074685	234
<i>E. faecium</i> F88	Surface water (Switzerland)	pF88_2 (41)	CP072880	172
<i>E. faecium</i> 18-465	Human (France)	p18-465_1 (24.3)	CP065753	222
<i>E. faecium</i> 18-276	Human (France)	p18-276_3 (35.6)	CP065757	222
<i>E. faecium</i> 18-042	Human (France)	p18-042_1 (9.4)	CP066216	222
<i>E. faecium</i> 17-318	Human (France)	p17-318_2 (38.4)	CP065772	222
<i>E. faecium</i> 16-164	Human (France)	p16-164 (27.2)	CP065776	222
<i>E. faecium</i> 16-021	Human (France)	p16-021_2 (38.7)	CP065779	222
<i>E. faecium</i> EF-3	Marine sediment (Italy)	pEfm-EF3 (27.7)	MT683615	171
<i>E. faecium</i> DY40	Pig (China)	pDY40-poxA (21.2)	MW207677	108
<i>E. faecium</i> DY32	Pig (China)	pDY32-poxA (27.3)	MW207676	108
<i>E. faecium</i> DY28	Pig (China)	pDY28-poxA (43.3)	MW207671	108
<i>E. faecium</i> DY18	Pig (China)	pDY18-poxA (34.9)	MW207668	108
<i>E. faecium</i> F179	Surface water (Switzerland)	pF179_3 (26.6)	CP072887	172
<i>E. faecium</i> F88	Surface water (Switzerland)	pF88_2 (41)	CP072880	172
<i>E. faecium</i> E843xGE-1-TC1	Pig (China)	pE843-TC-200 (200.5)	CP081503	96
<i>E. faecium</i> fac90	Pig (China)	pFac90-54 (54.3)	CP068246	97
<i>E. faecalis</i> E076	Pig (China)	pE076 (19.8)	MK140642	183
<i>E. faecalis</i> E035	Pig (China)	pE035 (121.5)	MK140641	183
<i>E. faecalis</i> C10	Pig (China)	pC10 (37.9)	MK861852	224
<i>E. faecalis</i> M18/0011	Human (Ireland)	pM18/0011 (18.2)	MN831412	154
<i>E. faecalis</i> V386	Manure (Italy)	pV386 (33.4)	MZ603802	158
<i>E. faecalis</i> 18-243	Human (France)	p18-243_2 (51.9)	CP065786	222
<i>E. faecalis</i> EF36	Food (South Korea)	pEFS36_2 (35.8)	NZ_CP085293	159
<i>E. faecalis</i> EF108	Pig (South Korea)	pEFS108_1 (97.5)	NZ_CP085295	159
<i>E. faecalis</i> E006	Pig (China)	pE006-19 (19.8)	CP082233	96
<i>E. faecalis</i> E006xJH2-2-TC1	Pig (China)	pE006-TC-121 (121.5)	CP081506	96
<i>E. faecalis</i> T90-3	Pig (China)	pT90-3 (71.1)	CP069131	97
<i>E. faecalis</i> T90-5	Pig (China)	pT90-5 (101.7)	CP069130	97
<i>E. faecalis</i> T90-6	Pig (China)	pT90-6 (149.5)	CP069129	97
<i>E. hirae</i> HDC14-2	Pig (China)	pHDC14-2.27K (27.3)	CP042294	15
<i>E. hirae</i> HDC14-2	Pig (China)	pHDC14-2.133K (133.3)	CP042290	15
<i>E. hirae</i> CQP3-9	Pig (China)	pCQP3-9_2 (33.1)	CP037957	184
<i>E. hirae</i> Fas4	Pig (China)	pFas4-1 (57.2)	MK798157	107
<i>E. hirae</i> GE-2	Marine sediment (Italy)	pEh-GE2 (24.8)	MT683616	171
<i>E. hirae</i> DY27	Pig (China)	pDY27-poxA (53.5)	MW207669	108
<i>E. hirae</i> DY13	Pig (China)	pDY13-poxA (25.2)	MW207667	108
<i>E. gallinarum</i> Eg-IV02	Human (Bolivia)	pIB-BOL (13.7)	MZ171245	232
<i>E. gallinarum</i> FS4	Pig (Italy)	pEgFS4-2 (38.3)	MZ291453	106
<i>E. casseliflavus</i> DY31	Pig (China)	pDY31-poxA (16.5)	MW207674	108

Continued

Table 6. Continued

Strain	Origin	Genetic element (kb)	Accession numbers	References
<i>E. lactis</i> E843	Pig (China)	pE843-27 (27.8)	CP082268	96
<i>Staphylococcus</i> spp.				
<i>S. aureus</i> AOUC 09-15	Human (Italy)	Tn6349 (48.3)	MH746818.1	76
<i>S. haemolyticus</i> GDY8P80P	Pig (China)	pY80 (55.7)	CP063444	233
<i>Lactobacillus</i> spp.				
<i>L. salivarius</i> BNS11	Pig (China)	Chromosomal fragment (10.9) pBNS11-37 kb (37.2)	CP089850 CP089852	230

Table 7. General features of strains containing co-located oxazolidinone resistance genes

Co-located oxazolidinone resistance genes	Species/isolate	Source (country)	Localization/genetic element (kb)	Accession numbers	References
<i>cfr</i> , <i>optrA</i>	<i>S. sciuri</i> W28-3	Pig (China)	pWo28-3 (60.5)	KT601170	84
	<i>S. sciuri</i> W35-20	Pig (China)	pWo35-20 (NA)	KX982166 (partial sequence)	85
	<i>S. sciuri</i> W28-1	Pig (China)	pWo28-1 (60.5)	KX982171	85
	<i>S. sciuri</i> W27-9	Pig (China)	pWo27-9 (55.7)	KX982169	85
	<i>S. sciuri</i> Wo33-7	Pig (China)	Chromosomal fragment (20.3)	KX982173	85
	<i>S. sciuri</i> W33-13	Pig (China)	Chromosomal fragment (25)	KX982174	85
	<i>E. faecium</i> F120805	Human (Ireland)	pF120805 (72.9)	KY579372	82
	<i>E. faecium</i> E35048	Human (Italy)	pE35048-oc (41.8)	MF580438	104
	<i>E. faecium</i> FSIS1608820	Cow (USA)	pFSIS1608820 (28.2)	CP028728	105
	<i>E. faecalis</i> S251	Pig (Italy)	Unnamed plasmid (~97)	MT723957 (partial sequence)	101
	<i>E. avium</i> S252	Pig (Italy)	Chromosomal fragment (16.4)	MT723957 (partial sequence)	101
	<i>E. gallinarum</i> FS4	Pig (Italy)	pEgFS4-1 (34.6)	MZ291452	106
<i>cfr</i> , <i>poxxA</i>	<i>S. aureus</i> AOUC 09-15	Human (Italy)	Tn6349 (48.3)	MH746818.1	76
<i>cfr(D)</i> , <i>optrA</i>	<i>E. faecium</i> 15-307-1	Human (France)	p15-307-1_02 (103)	CP044318	153
	<i>E. faecium</i> E8014	Human (Netherlands)	Plasmid 4 (11.4)	LR135354	153
	<i>E. faecium</i> M17/0314	Human (Ireland)	pM17/0314 (103.6)	MN831413	154
	<i>E. faecium</i> BP5067	Human (India)	pBP5067_P1 (122.1)	CP059807	15
	<i>E. faecium</i> BA17124	Human (India)	pBA17124_P1 (130.5)	CP059785	15
<i>cfr(D)</i> , <i>poxxA2</i>	<i>E. faecalis</i> BX8117	Human (Scotland)	pBX8117-2 (NA)	PRJEB36950	157
	<i>E. faecalis</i> EFS0019	Pig (South Korea)	node #26 (31.8)	QUSQ000000000	231
	<i>E. faecalis</i> EF36	Food (South Korea)	pEFS36_2 (35.8)	NZ_CP085293	159
	<i>E. faecalis</i> EF108	Food (South Korea)	pEFS108_1 (97.5)	NZ_CP085295	159
	<i>E. faecalis</i> V386	Manure (Italy)	pV386 (33.4)	MZ603802	158
<i>optrA</i> , <i>poxxA</i>	<i>E. faecalis</i> E035	Pig (China)	pE035 (121.5)	MK140641	183
	<i>E. faecalis</i> S157	Pig (Italy)	Unnamed plasmid (~97)	MT723951 (partial sequence) MH746818 ^a	101

NA, not available.

^aAccession number of the *poxxA* genetic context of *S. aureus* AOUC 09-15 identical to the *poxxA* genetic background of *E. faecium* S157.

Table 8. General features of strains containing co-occurring oxazolidinone resistance genes

Species/isolate	Source (country)	Oxazolidinone resistance genes	Localization/genetic element (kb)	Accession numbers	References
<i>E. faecalis</i> 599799	Human (Thailand)	<i>cfr</i>	Chromosomal fragment (5.8)	JX910899 ^a	29
		<i>optrA</i>	Unnamed plasmid (NA)	MF443373 (partial sequence)	
<i>E. faecalis</i> EF02	Human (China)	<i>cfr</i>	pEF-L18/ <i>cfr</i> (11.8)	MT874923	103
		<i>optrA</i>	pEF-L13/ <i>optrA</i> (8.3)	MT874924	
<i>E. faecalis</i> L9	Pig (Brazil)	<i>cfr</i>	pL9-A (7.7)	CP041775	102
		<i>optrA</i>	pL9 (57.5)	CP041776	
<i>E. gallinarum</i> 325	Pig (Italy)	<i>cfr</i>	Chromosomal fragment (9.5)	MT723959	101
		<i>optrA</i>	Chromosomal fragment (11.7)	MT723960	
<i>E. hirae</i> fas4	Pig (China)	<i>cfr</i>	pfas4-2 (85.6)	MK798156	107
		<i>poxA</i>	pfas4-1 (57.2)	MK798157	
<i>E. gallinarum</i> FS4	Pig (Italy)	<i>cfr</i> , <i>poxA</i>	pEgFS4-1 (34.6)	MZ291452	106
		<i>poxA</i>	pEgFS4-2 (38.3)	MZ291453	
<i>E. casseliflavus</i> DY31	Pig (China)	<i>cfr</i>	pDY31- <i>cfr</i> (12.3)	MW207672	108
		<i>optrA</i>	pDY31- <i>optrA</i> (75.5)	MW207673	
		<i>poxA</i>	pDY31- <i>poxA</i> (16.5)	MW207674	
<i>E. faecalis</i> 687669, 687671	Human (Panama)	<i>cfr</i> (B)	Tn6218-like (8.4)	KR610408 ^b	29
		<i>optrA</i>	Unnamed plasmid (NA)	MF443374 (partial sequence)	
<i>E. faecalis</i> KUB3006	Human (Japan)	<i>cfr</i> (B)	Tn6218-like (9.7)	AP018538	141
		<i>optrA</i>	pKUB3006-4 (36.3)	AP018542	
<i>C. perfringens</i> 19TSBNCP	Cattle (China)	<i>cfr</i> (C)	Chromosomal fragment (15.9)	CP073070	150
		<i>optrA</i>	Plasmid unnamed1 (63.8)	CP073071	
<i>E. faecalis</i> EF108	Food (South Korea)	<i>cfr</i> (D), <i>poxA2</i>	pEFS108_1 (97.5)	NZ_CP085295	159
		<i>optrA</i>	Chromosomal fragment (NA)	SUB10526593	
<i>E. faecalis</i> X528	Human (Spain)	<i>cfr</i> (D)	Unknown genetic element (NA)	LR135354 ^c	155
		<i>optrA</i>	Unknown genetic element (NA)	NA	
<i>S. parasuis</i> H35	Pig (China)	<i>cfr</i> (D)	pH35- <i>cfr</i> D (7.5)	CP076722	160
		<i>optrA</i>	Chromosomal fragment (10.4)	CP076721	
<i>V. lutrae</i> BN31	Pig (China)	<i>cfr</i> (D)	pBN31- <i>cfr</i> D (33.4)	CP081834	161
		<i>optrA</i>	Chromosomal Tn7363 (13.6)	CP081833	
<i>E. faecium</i> M16/0594	Human (Ireland)	<i>optrA</i>	Chromosomal fragment (10.7)	MN831418	154
		<i>poxA</i>	pM16/0594 (21.8)	NZ_MN831411	
<i>E. faecium</i> C10004	Air (Spain)	<i>optrA</i>	Unknown genetic element (NA)	NA	229
		<i>poxA</i>	Unknown genetic element (NA)	NA	
<i>E. faecium</i> C10009	Air (Spain)	<i>optrA</i>	Unknown genetic element (NA)	NA	229
		<i>poxA</i>	Unnamed plasmid (NA)	MN661250 (partial sequence)	
<i>E. faecium</i> F88		<i>optrA</i>	pF88_1 (246.3)	CP072879	172

Continued

Table 8. Continued

Species/isolate	Source (country)	Oxazolidinone resistance genes	Localization/genetic element (kb)	Accession numbers	References
	Surface water (Switzerland)	<i>poxtA</i>	pF88_2 (41)	CP072880	
<i>E. faecium</i> DY28	Pig (China)	<i>optrA</i>	pDY28- <i>optrA</i> (55)	MW207670	108
		<i>poxtA</i>	pDY28- <i>poxtA</i> (43.3)	MW207671	
<i>E. casseliflavus</i> DY32	Pig (China)	<i>optrA</i>	pDY32- <i>optrA</i> (175.5)	MW207675	108
		<i>poxtA</i>	pDY32- <i>poxtA</i> (27.3)	MW207676	
<i>E. gallinarum</i> EG81	Pig (China)	<i>optrA</i>	Chromosomal Tn554-like (NA)	CP050816	195
		<i>optrA</i>	pEG81-1 (51.6)	CP050817	
<i>E. faecalis</i> C25	Pig (China)	<i>optrA</i>	Chromosomal fragment (16.6)	MK251150	184
		<i>optrA</i>	pC25-1 (45.6)	CP030043	
<i>E. faecium</i> VB3025	Human (India)	<i>optrA</i>	Chromosomal DNA	CP040236	193
		<i>optrA</i>	pV3240_2 (142.8)	CP040238	
<i>E. hirae</i> HDC14-2	Pig (China)	<i>poxtA</i>	pHDC14-2.27K (27.3)	CP042294	15
		<i>poxtA</i>	pHDC14-2.133K (133.3)	CP042290	
<i>L. salivarius</i> BNS11	Pig (China)	Δ <i>poxtA</i>	Chromosomal fragment (10.9)	CP089850	230
		<i>poxtA</i>	pBNS11-37 kb (37.2)	CP089852	

NA, not available.
^aAccession number of the *cfr* genetic context of *S. epidermidis* 426-3147L identical to the *cfr* genetic background of *E. faecalis* 599799.
^bAccession number of the *cfr*(B) genetic context of *E. faecium* 448-18961R 98% identical to the *cfr*(B) genetic background of *E. faecalis* 687669 and 687671 isolates.
^cAccession number of the *cfr*(D)-plasmid 4 of *E. faecium* E8014 100% identical to the *cfr*(D) genetic background of *E. faecalis* X528.

specific lineage of the aforementioned Gram-positive pathogens. The apparently disproportionately frequent occurrence of the gene *cfr* in the livestock-associated MRSA CC398 from livestock in Europe and North America is likely due to the fact that isolates of this CC are widespread among pigs, cattle and poultry and have—in contrast to isolates of other *S. aureus* CCs—been preferentially investigated for their antimicrobial resistance genes. The same is true for the *S. aureus* CC9 in Asian countries.

Concluding remarks

This review summarizes the current knowledge concerning the mechanisms of oxazolidinone resistance (ribosomal mutations and acquired resistance genes) and highlights the wide flexibility of all the genetic elements carrying the oxazolidinone resistance genes known to date. In particular, acquired resistance genes associated with MGEs, including plasmids, transposons, ICEs, prophages, genomic islands and ISs, pose a particular threat of dissemination of this type of resistance.¹⁵ Our knowledge of the MGEs carrying oxazolidinone resistance genes points to the existence of a significant reservoir of such elements, especially among bacterial isolates from farm animals which in turn could easily end up in the food chain and thereby posing huge risks to public health.

Florfenicol, exclusively approved for use in veterinary medicine, is a broad-spectrum antimicrobial agent extensively used in livestock to prevent or to cure bacterial infections, but also as

growth promoter in some countries.¹⁵ It has a considerable impact on the dissemination of florfenicol resistance genes, including those also encoding resistance to oxazolidinones, despite the latter have not been approved for veterinary use.¹⁵ Furthermore, it should be noted that *cfr*, *optrA* and *poxtA* are often co-localized on the same genetic element with genes that confer resistance to non-PhLOPS_A antimicrobial agents, biocides and heavy metals.¹⁵ Overall, both a direct and indirect selective pressure could play an important role in the selection, persistence and spread of the mobile oxazolidinone resistance genes in the bacterial population in human and veterinary settings.¹⁵ The most efficient way of limiting the spread of these multiresistance genes is to reduce the selective pressure for acquired resistance determinants and other co-located resistance genes. This can only be achieved by the prudent use of phenicols, lincosamides and pleuromutilins, and also macrolides, tetracyclines and aminoglycosides, in animal production and veterinary medicine and of oxazolidinones in human medicine.^{11,15} The knowledge of the genetic backgrounds of *cfr/cfr-like*-, *optrA*- and *poxtA*-mediated resistance—as summarized in this review—is essential for the understanding of the emergence and the spread of the mobile oxazolidinone resistance genes in several countries and in Gram-positive and Gram-negative bacteria.^{11,15}

Further efforts, with consideration of the ‘One Health’ approach, are crucial to preserve the activity of oxazolidinones in clinical settings. An ongoing surveillance of the oxazolidinone-resistant isolates and distribution of *cfr* and its

variants, as well as *optrA* and *poxTA*, among Gram-positive and Gram-negative bacteria, is pivotal to limit their spread in environmental, animal and human settings.

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Transparency declarations

None to declare.

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