

Novel antimicrobial resistance genes among livestock-associated MRSA ST398 from swine and cattle

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Diversity of antimicrobial resistance pheno- and genotypes of methicillin-resistant *Staphylococcus aureus* ST398 from diseased swine

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Characterization of methicillin-resistant *Staphylococcus aureus* ST398 from cases of bovine mastitis

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Two studies on the analysis of LA-MRSA ST398 for virulence and resistance properties

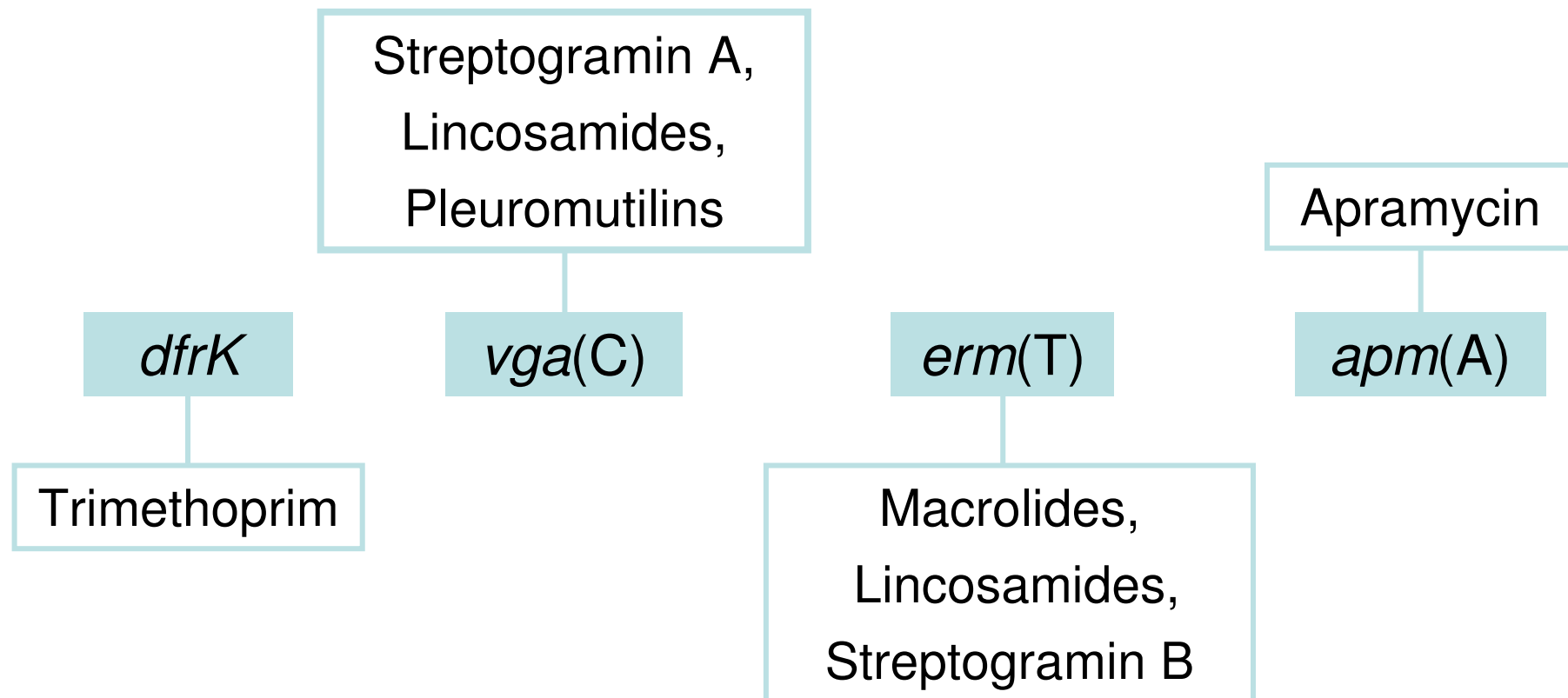


- little variation in virulence
- but considerable variation in antimicrobial resistance

Porcine MRSA ST398

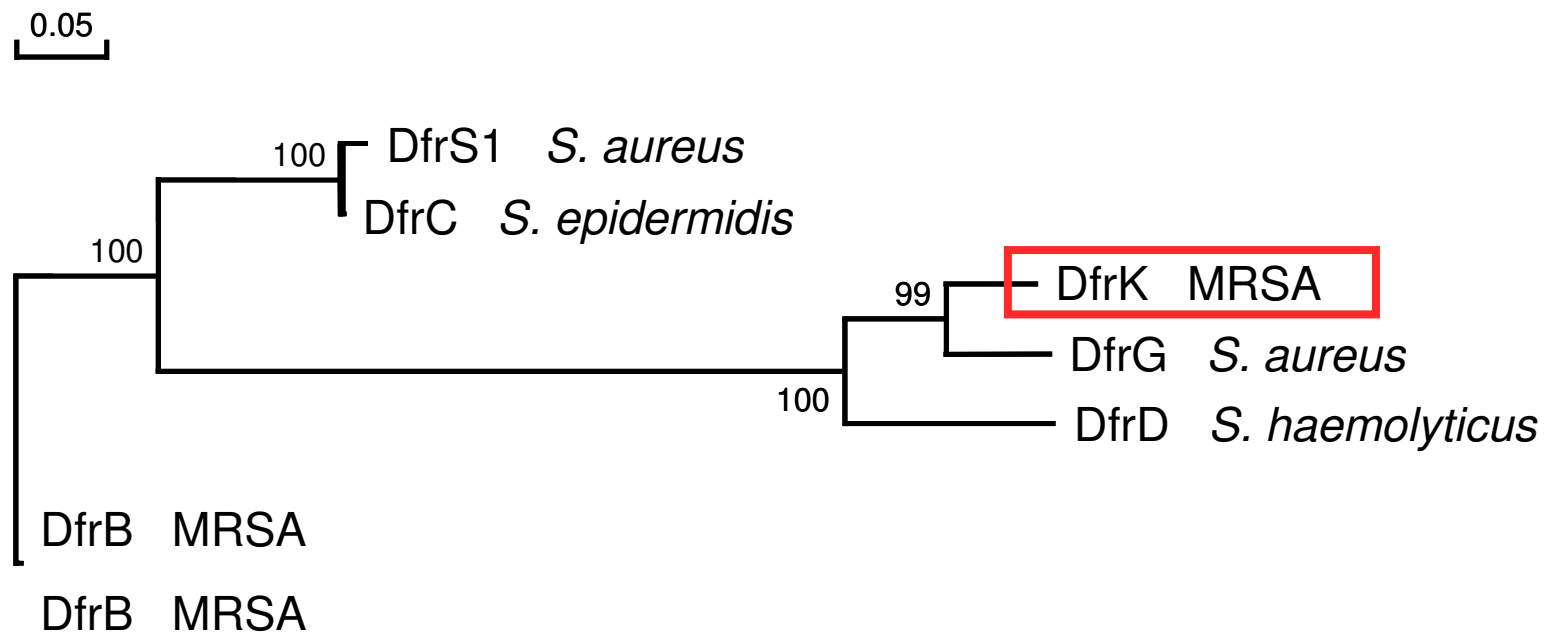
Resistance phenotype	N	Resistance to		
BLA, TET, CHL/FFC, MLS _B , TMP, GEN	1	6 classes of antimicrobial agents 9.3%		
BLA, TET, CHL, MLS _B , TMP, SXT	1			
BLA, TET, MLS _B , TMP, SPE, TIA	3			
BLA, TET, MLS _B , TMP, GEN	1	5 classes of antimicrobial agents 5.6%		
BLA, TET, MLS _B , TMP, ENR	1			
BLA, TET, MLS _B , TMP, TIA	1			
BLA, TET, CHL/FFC, TMP	1	4 classes of antimicrobial agents 29.6%		85.1%
BLA, TET, MLS _B , TMP	8			
BLA, TET, MLS _B , ENR	2			
BLA, TET, MLS _B , GEN	1			
BLA, TET, TMP, ENR	1			
BLA, TET, TMP, GEN	2			
BLA, TET, TMP, TIA	1			
BLA, TET, MLS _B	4	3 classes of antimicrobial agents 25.9 %	55.5%	
BLA, TET, TMP	7			
BLA, TET, GEN	1			
BLA, TET, SPE	1			
BLA, TET, TIA	1			
BLA, TET	16			

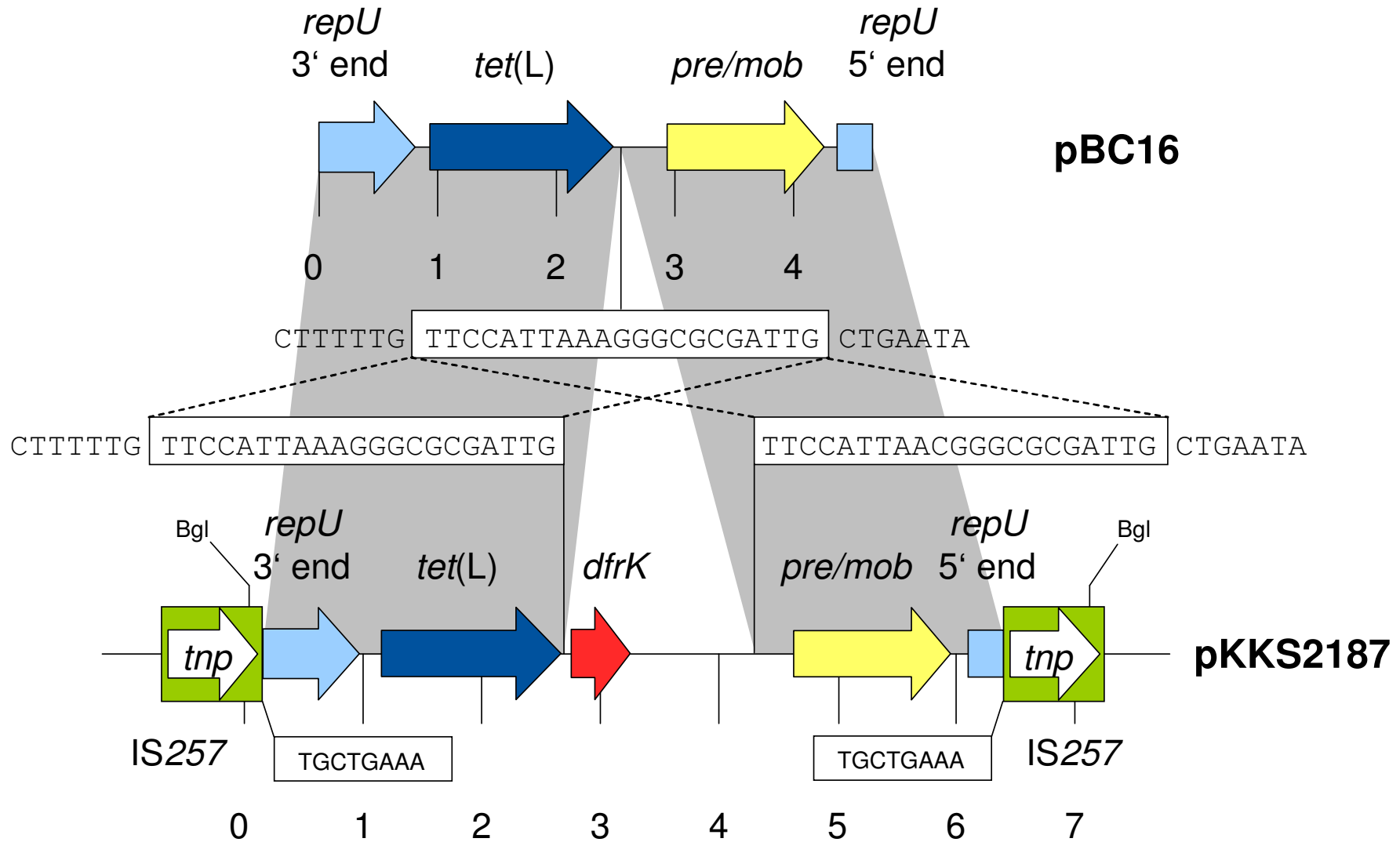
Novel resistance genes



Novel trimethoprim resistance gene *dfrK*

- *dfrK* has 86.2% nucleotide sequence identity to *dfrG*
- Protein DfrK has 87.9% amino acid identity to DfrG



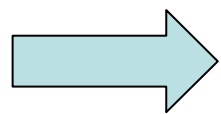


dfrK as part of a transposon

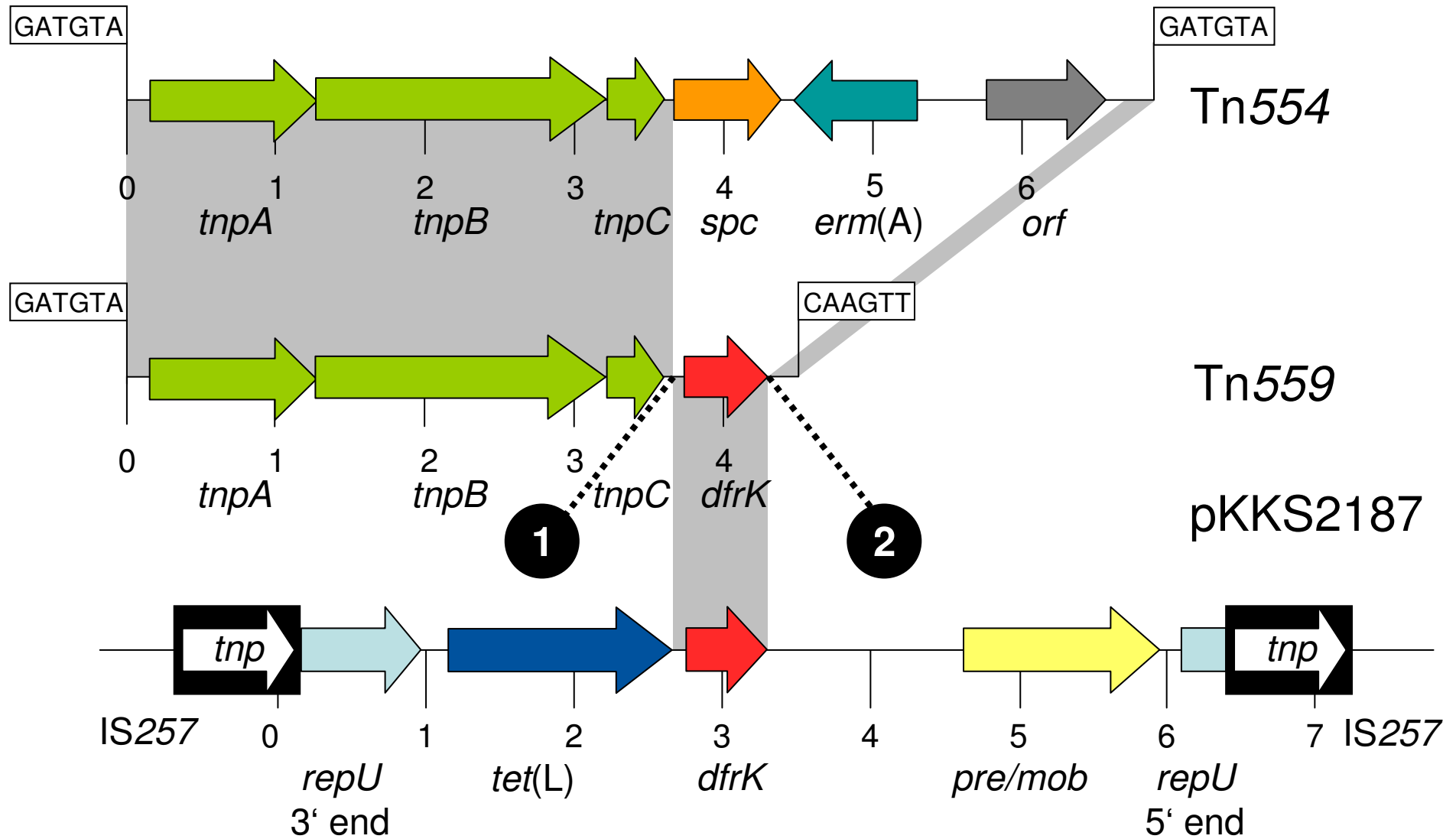
- present on structurally different plasmids in MRSA ST398
- usually linked to the tetracycline resistance gene *tet(L)*

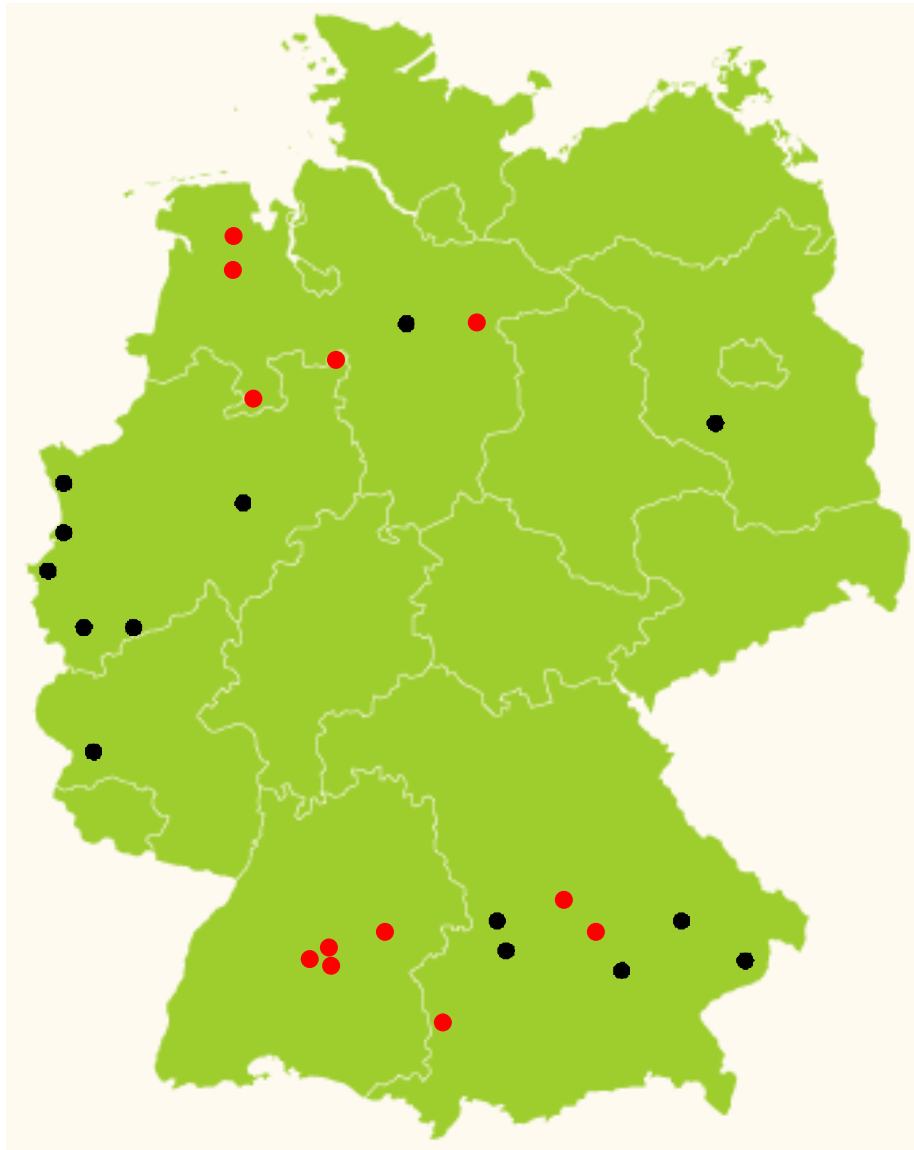
However,

- during screening of staphylococci of the BfT-GermVet study, a **porcine MSSA ST398 strain** was detected, in which
 - *dfrK* was **not** located on a plasmid
 - *dfrK* was **not** linked to *tet(L)*



cloning of the *dfrK* gene region from the chromosome and subsequent sequence analysis





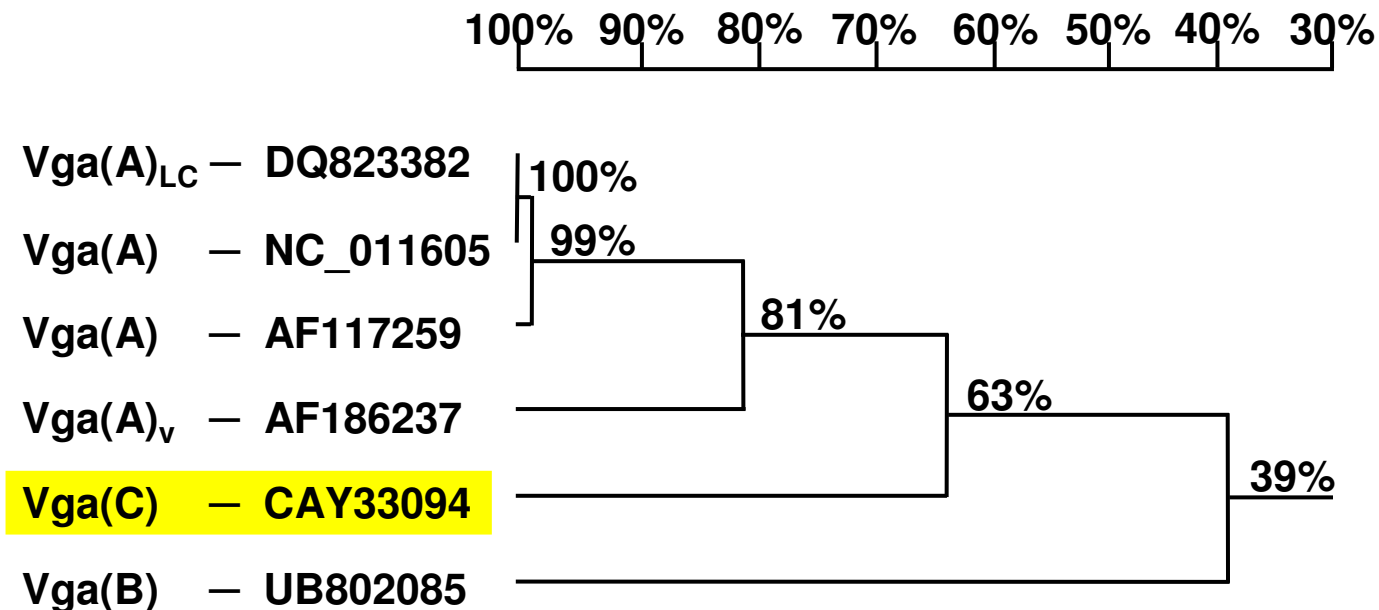
Distribution of the *dfcK* gene among 54 porcine and 25 bovine MRSA ST398 isolates from Germany

- *dfcK* (n = 14) in MRSA ST398 from pigs
- *dfcK* (n = 12) in MRSA ST398 from dairy cattle

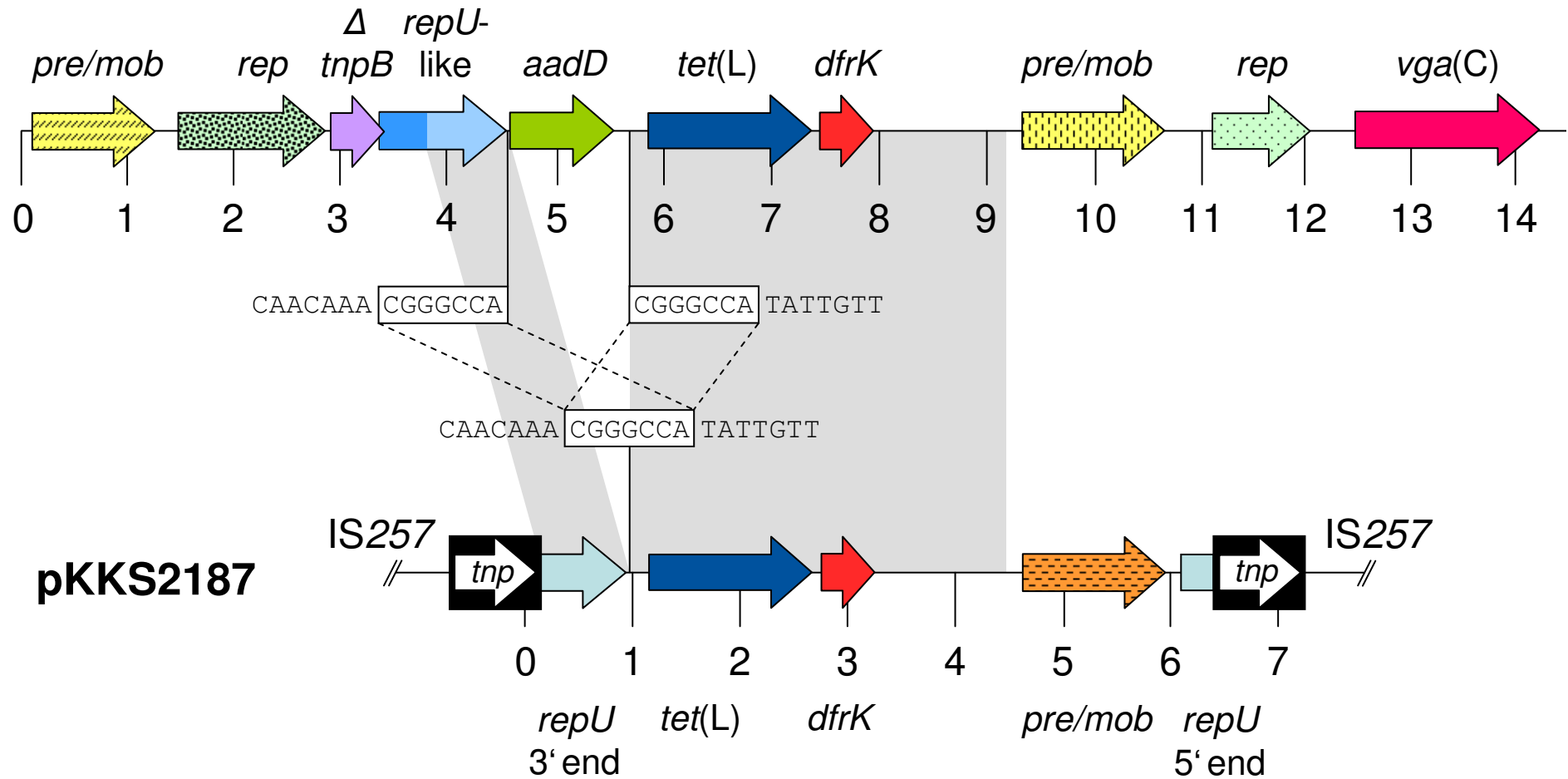
(28 porcine and 14 bovine isolates were trimethoprim-resistant)

Novel resistance gene *vga(C)*

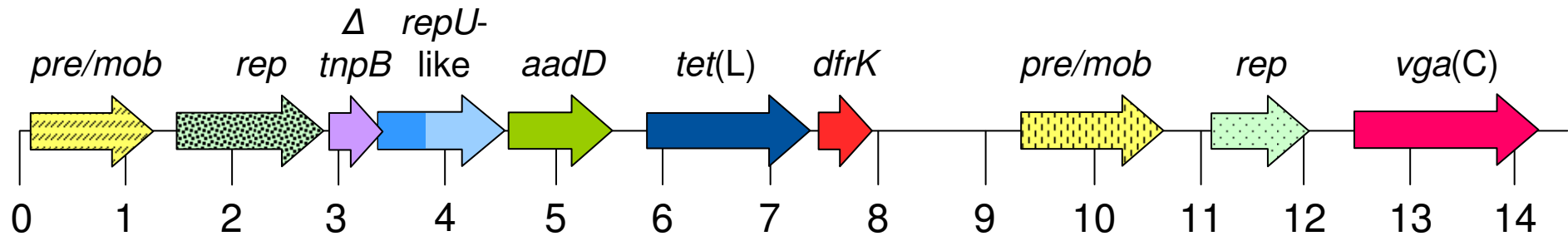
- streptogramin A antibiotics: virginiamycin M1
- lincosamides: lincomycin, pirlimycin, clindamycin
- pleuromutilins: tiamulin, valnemulin



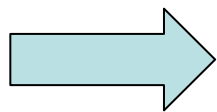
pKKS825



Plasmid pKKS825

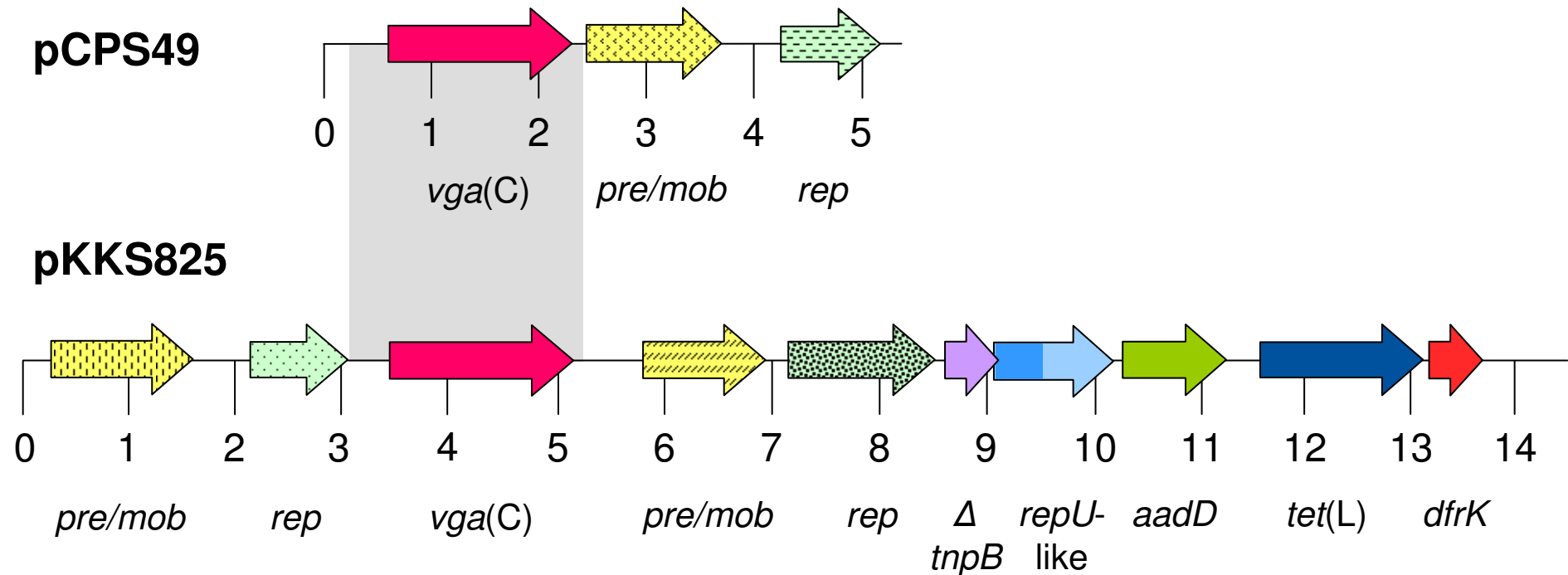


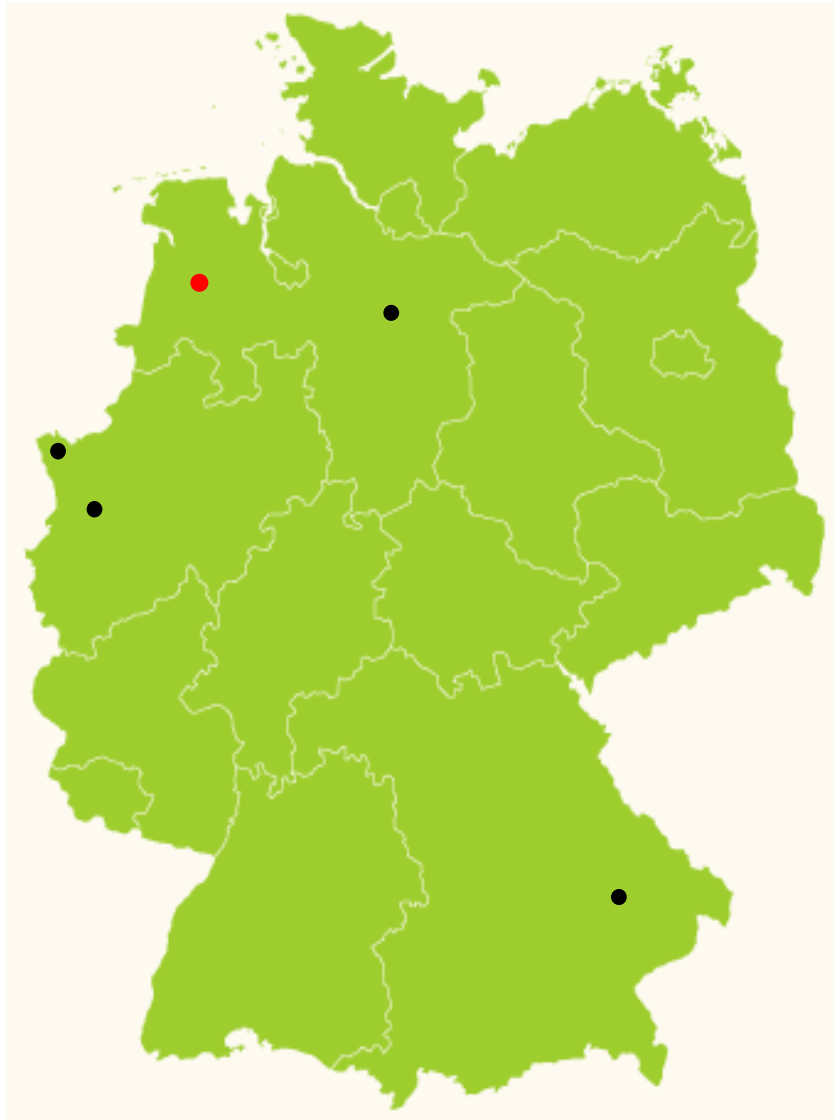
- mediates resistance to tetracycline, trimethoprim, kanamycin/neomycin, streptogramin A antibiotics, lincosamides, and pleuromutilins
- carries three different *rep* genes for potential replication in different bacterial hosts
- carries two different *pre/mob* genes for plasmid mobilization and plasmid recombination



well equipped for horizontal gene transfer and maintenance in different hosts

vga(C) on a small plasmid from porcine MRSA ST398





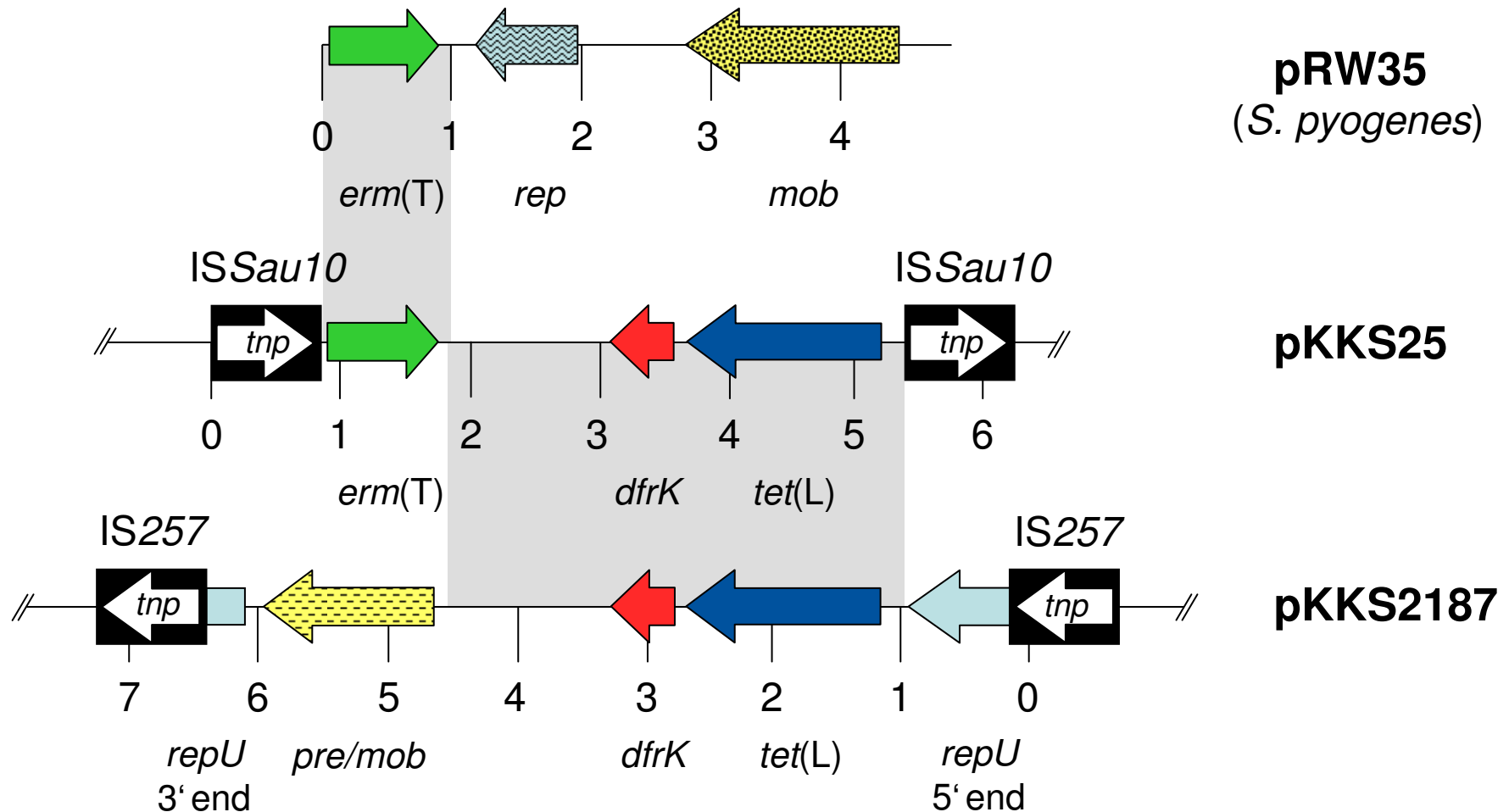
Geographical distribution of the gene *vga(C)* among 54 porcine and 25 bovine MRSA ST398 isolates from Germany

- *vga(C)* (n = 4) in MRSA ST398 from pigs
- *vga(C)* (n = 1) in MRSA ST398 from dairy cattle

MLS_B resistance gene *erm*(T)

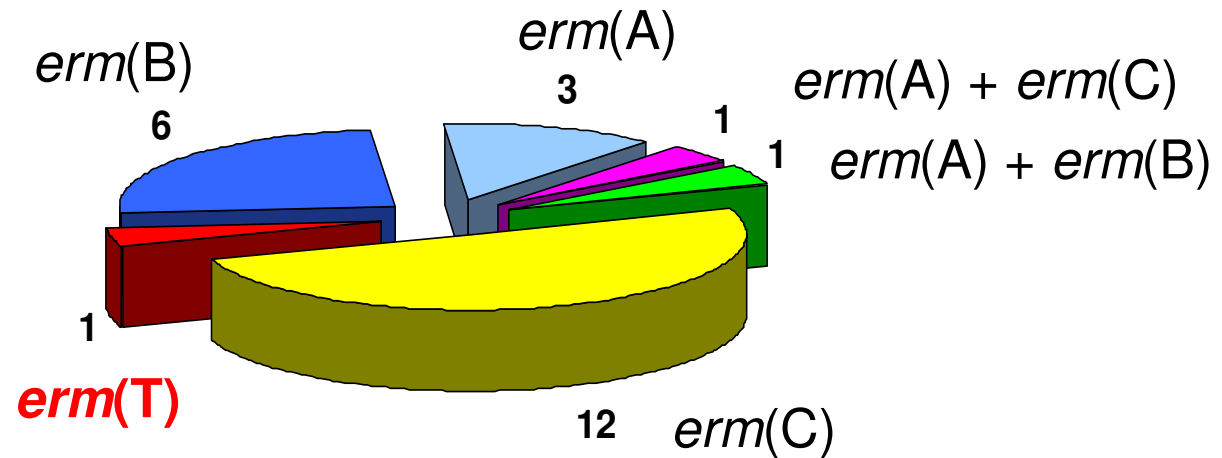
- *erm*(T) described in *Streptococcus pyogenes*, *Streptococcus pasteurianus*, *Lactobacillus reuteri*, *Lactobacillus* spp. and *Enterococcus faecium*
- commonly located on small plasmids which do **NOT** replicate in *Staphylococcus*
- first described in *Staphylococcus* in 2010

MLS_B resistance gene *erm(T)*

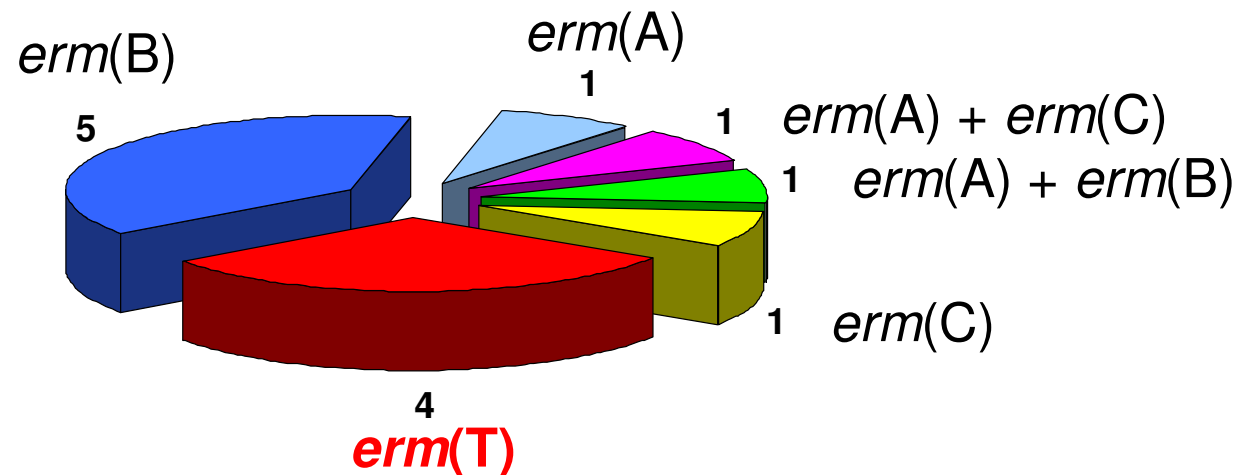


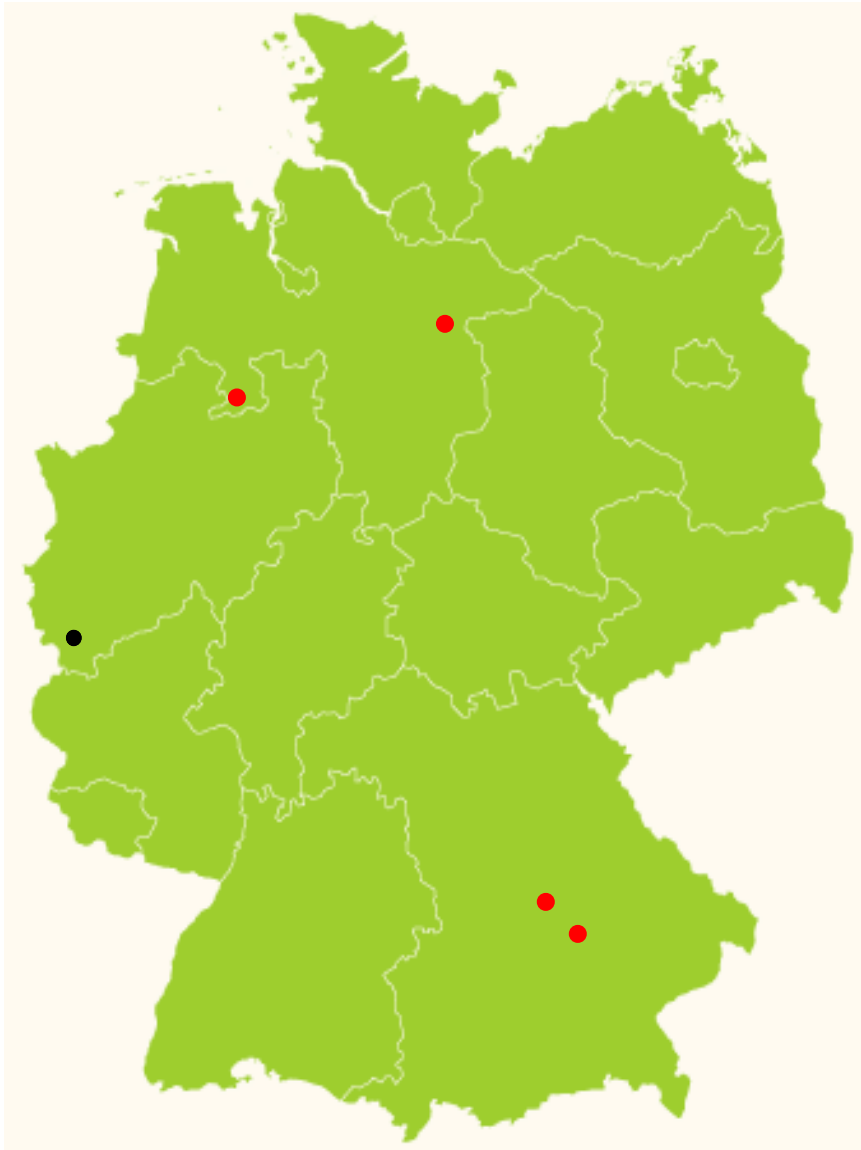
Macrolide / lincosamide resistance of

porcine
MRSA
ST398



bovine
MRSA
ST398



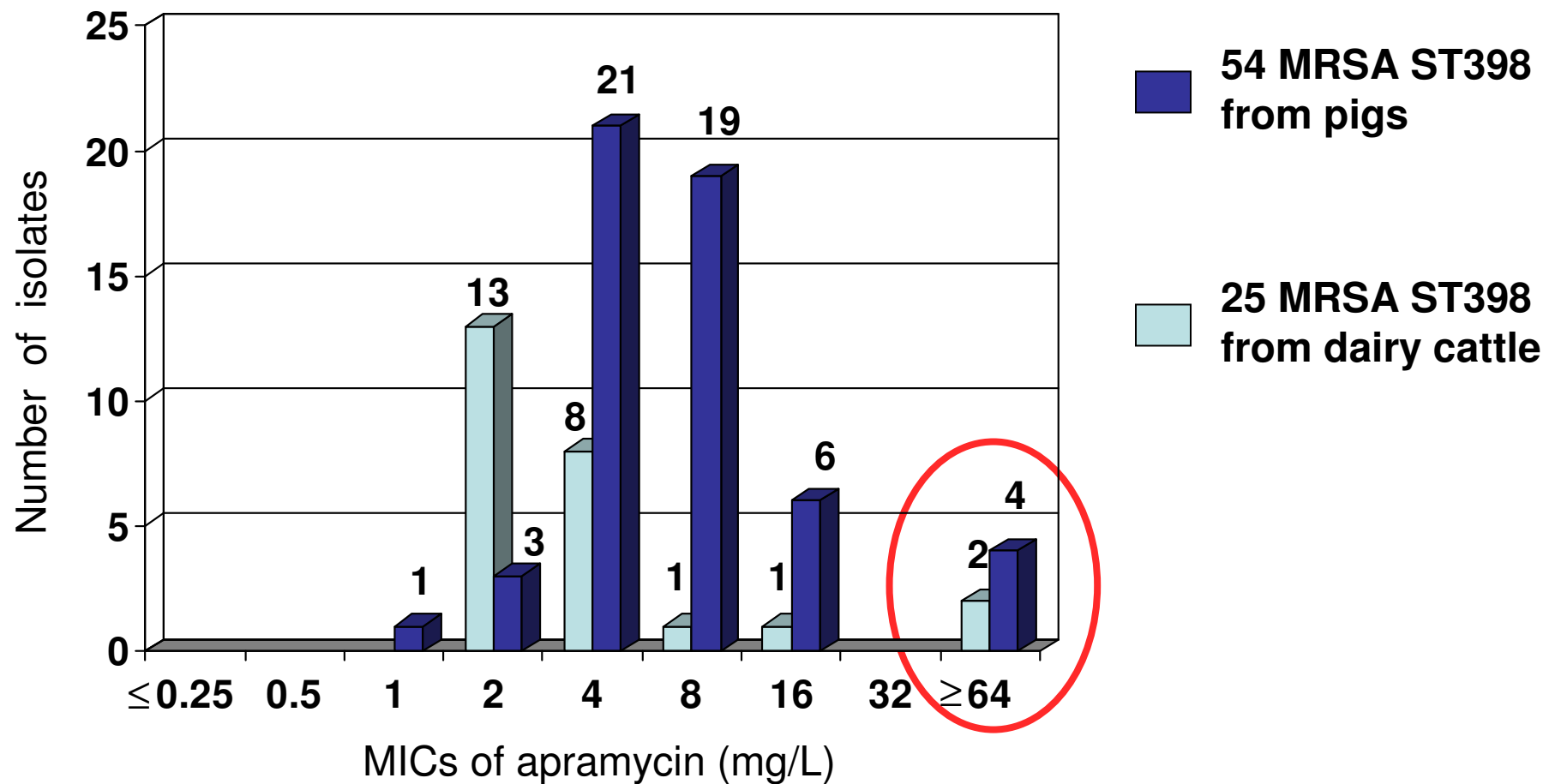


Geographical distribution of the gene *erm*(T) among 54 porcine and 25 bovine MRSA ST398 isolates from Germany

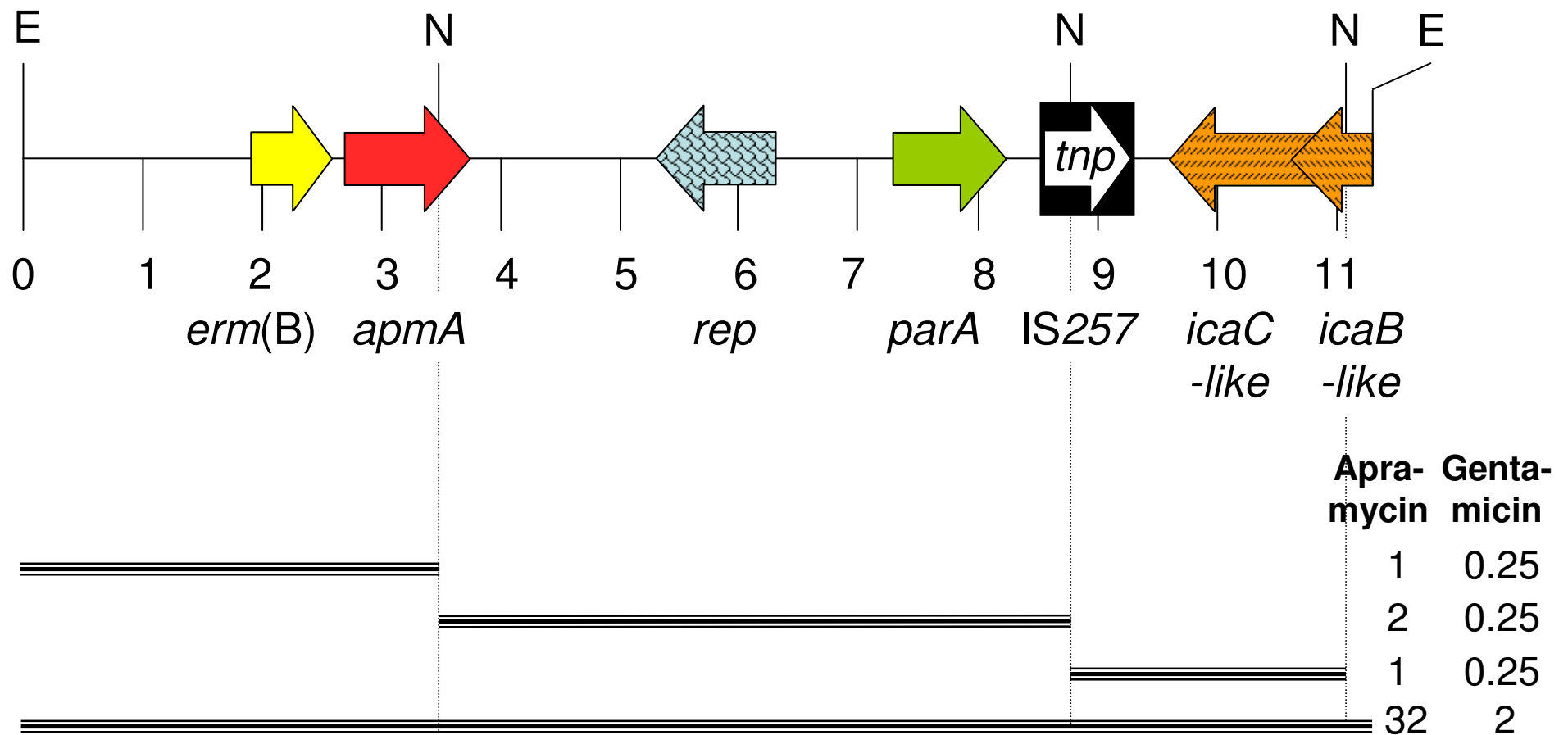
- *erm*(T) (n = 1) in MRSA ST398 from pigs
- *erm*(T) (n = 4) in MRSA ST398 from dairy cattle

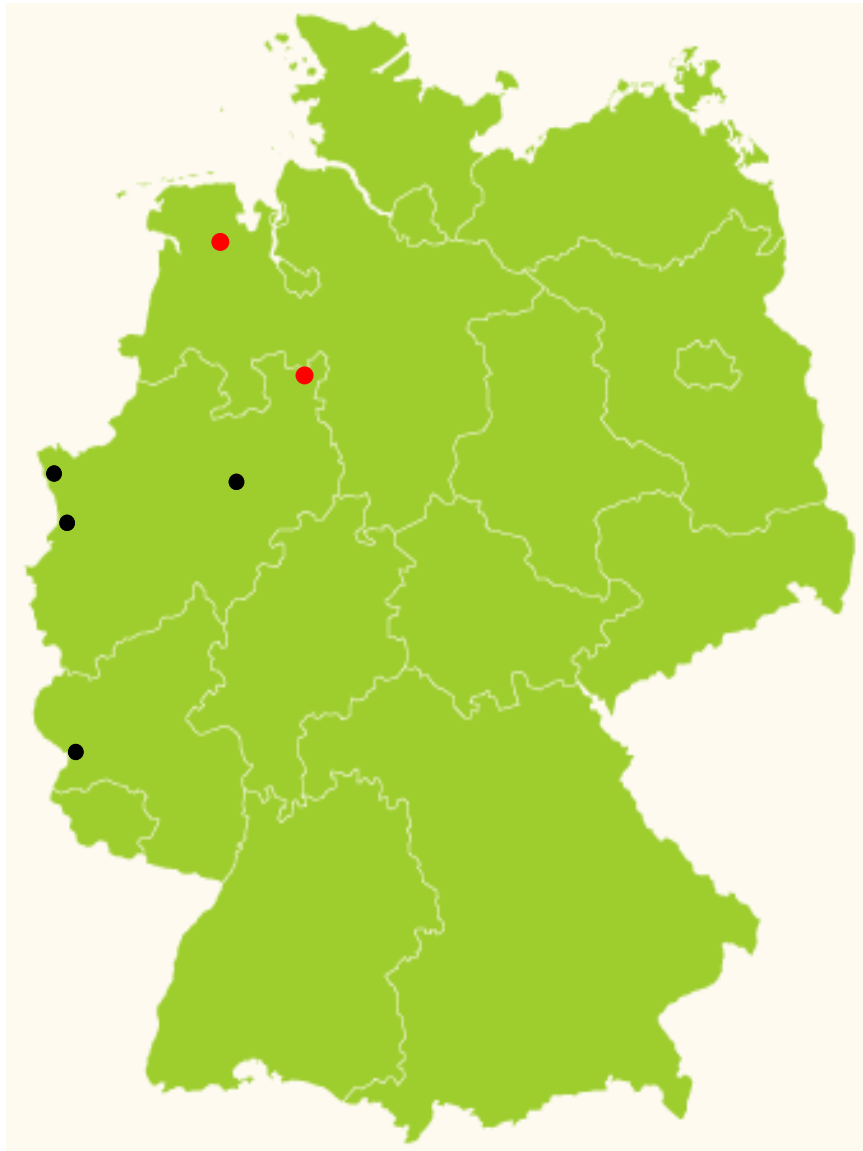
(24 porcine and 13 bovine isolates
were ML-resistant)

Distribution of apramycin MICs



Novel apramycin resistance gene *apmA*





Geographical distribution of the gene *apm(A)* among 54 porcine and 25 bovine MRSA ST398 isolates from Germany

- *apm(A)* (n = 4) in MRSA ST398 from pigs
- *apm(A)* (n = 2) in MRSA ST398 from dairy cattle

Conclusions

- MRSA ST398 can acquire resistance genes from other bacteria
- plasmids play an important role in these acquisition processes
- multiresistance plasmids enable the co-selection and persistence of resistance genes — even in the absence of a direct selective pressure

Perspective

- detailed analysis of (multi)resistance plasmids in MRSA ST398 will be performed in the MedVetStaph project
- MedVetStaph is a BMBF-funded joint project of human and veterinary medicine (<http://medvetstaph.net>)

