TITLE: FIRST REPORT OF THE MULTI-RESISTANCE GENE CLUSTER lsa(E)/spw/aadE/lnu(B) IN BRAZIL

AUTHORS: CALUMBY, R.J.N.¹; DAS VIRGENS, S.B.¹; GOMES, D.C.S.¹; SILVA SOBRINHO, L.A.R.¹; SANTOS, L.P.R.¹; MEDEIROS, K.J.G.¹; FILSNER, P.²; MORENO, A.M.²; GRILLO, L.A.M.¹; ALMEIDA, L.M.¹

Institution: ¹UNIVERSIDADE FEDERAL DE ALAGOAS (UFAL), CAMPUS A.C SIMÕES (AV. LOURIVAL MELO MOTA, S/N TABULEIRO DO MARTINS, MACEIÓ, AL, BRASIL) E ²UNIVERSIDADE DE SÃO PAULO (USP), CIDADE UNIVERSITÁRIA (AV. PROFESSOR LINEU PRESTES, 580, SÃO PAULO, SP, BRASIL).

ABSTRACT:

Enterococci are gut commensal bacteria from human and animal species which can readily acquire and share resistances with other pathogens. Recently, it has been suggested that the new multi-resistance gene cluster comprised of the ABC transporter gene *lsa*(E) (pleuromutilin/lincosamide/streptogramin A resistance), and the *spw* (spectinomycin), *aadE* (streptomycin) and *lnu*(B) (lincosamides) genes may have evolved in enterococci. In this study, we detected the plasmid-borne lsa(E)/spw/aadE/lnu(B) cluster in eight Enterococcus faecalis (ST591, ST710, ST711) isolated from healthy nursery pigs from unrelated piggeries located in different Brazilian states (DP, PR, SP). We were able to spot that the genetic environment containing the lsa(E)/spw/aadE/lnu(B) gene cluster in these porcine E. faecalis strains showed high similarity to the sequences identified in other bacteria in Europe and Asia. Minimum inhibitory concentrations (MIC) were determined by broth microdilution testing (CLSI). Genomic DNA of the *E. faecalis* strains was sequenced (Illumina Miseg), assembled (CLC Genomics Workbench 8.0.3) and annotated (Rapid Annotation Server/ RAST). All E. faecalis strains exhibited elevated MICs for tiamulin, quinupristin/dalfopristin, streptomycin, and lincomycin. A lsa(E)/spw/ aadE/lnu(B)-carrying segment of 18.325 bp was detected in all ST591, ST710, ST711 E. faecalis tested. Upstream of the multi-resistance gene cluster, a 7.088 bp DNA sequence containing the macrolide/lincosamide/streptogramin B resistance gene erm(B), and the aminoglycoside resistance genes aac(6')-aph(2"), aadE, and aph(3')-III was detected. Distal to the resistance gene cluster, a disrupted recombinase gene repUS12 was observed. Two insertion sequences of the IS1380 and ISL3 families were detected downstream of repUS12, which are most likely to be involved in interplasmid recombinaion events. Besides lsa(E)/spw/aadE/lnu(B), all E. faecalis strains also carried the oxazolidinone phenicol-transferable resistance gene optrA, and two of them co-carried the multiresistance gene cfr as well. The use of antibiotics in swine is a common practice in Brazilian farms and it is contributing to the spread of resistances among Gram-positive pathogens.

Keywords: Enterococcus faecalis, multi-resistance, food-producing animals.

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