3rd ASM Conference on AMR in Zoonotic Bacteria and Foodborne Pathogens

Aix-en-Provence, France

26 to 29 June 2012

Accessing the molecular basis of transferable quinolone resistance in *Escherichia coli* and *Salmonella* spp from food-producing animals and products

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Background: *Salmonella* and *Escherichia coli* resistant to quinolones frequently arise in animals, being easily transferred to humans through the food chain, which can ultimately lead to the development of untreatable infectious diseases. The aim of the present study was to investigate the presence of PMQR determinants among *Salmonella* spp and *E. coli* from food-producing animals and derivative food products.

Methods: *Salmonella* spp (n=183) and *E. coli* (n=182) isolates were collected from food-producing animals (n=274) and derivative food products (n=91). Antimicrobial susceptibility testing was performed by standard disk diffusion method, according to the CA-SFM veterinary guidelines. PCR and sequencing were used to detect PMQR- (*qnrA*, *qnrB*, *qnrC*, *qnrD*, *qnrS*, *aac(6')-Ib-cr*, and *qepA*) and β-lactamase-encoding genes (bla_{TEM}, bla_{SHV}, bla_{OXA} and *ampC*) and to examine the QRDR of *gyrA*, *gyrB*, *parC* and *parE* genes in PMQR positive isolates. Plasmid characterization was accessed by conjugation followed by replicon-typing. Genetic relatedness of PMQR positive *E. coli* was examined by MLST and *Salmonella* isolates were serotyped according to the Kauffmann-White scheme. Mobile genetic elements were also investigated through PCR mapping assays.

Results: Overall, 4.7% (17/365) harbored Qnr-encoding genes from *qrnB* and *qnrS* families, specifically *qnrB2* (n=3), *qrnB19* (n=3), and *qnrS1* (n=11). All but one isolate presented at least one mutation in QRDR region of genes *gyrA*, *parC* or *parE* genes. 35.3% of Qnr-producing isolates presented resistance to β-lactam antibiotics that were justified by the presence of β-lactamases from TEM (TEM-1, n=10; and TEM-135, n=1) and SHV (SHV-108, n=1) families in QnrB19- and QnrS1-harbouring isolates. All but one Qnr-producing isolates were positively typed by replicon-typing, varying among IncN (n=2), IncFIB (n=11), IncFIC (n=3), IncI1 (n=2), IncHI2 (n=5), IncY (n=1) and IncL/M (n=3) and were, mostly, genetic unrelated. Qnr genes were detected nearby several mobile elements like IS*Ecl2*, IS*26* and ISCR*1*.

Conclusions: This study illustrated the existence of Qnr-producing *E. coli* and *Salmonella* from food-producing animals, associated to specific mobile elements that can mediate their transference between species and among distinct settings. Epidemiology of PMQR mechanisms and the dissemination of plasmids carrying Qnr-encoding genes in veterinary isolates can compromise the efficacy of fluroquinolone treatments in both animals and humans.