

Acquired quinolone resistance determinants among *Enterobacteriaceae* from Portuguese piggeries

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Background: Plasmid-mediated quinolone resistance (PMQR) genes are increasingly identified worldwide in *Enterobacteriaceae* of human and animal origin. They confer reduced susceptibility to quinolones that could facilitate the selection of mutants with high-level resistance.

Objectives: To evaluate the occurrence and diversity of genes coding for acquired resistance to quinolones among *Enterobacteriaceae* from Portuguese piggeries.

Methods: Forty-three samples (fresh/dry faeces, nasal/mucoid, drinking/waste water, feed, air, powder, surfaces, xerume) from 5 Portuguese piggeries located in different regions were analysed (2006-07). Samples were plated on MacConkey agar with/without antibiotics. Isolates were identified by API ID32GN and susceptibility testing was performed by CLSI disk diffusion method. *qnrA*, *qnrB*, *qnrS*, *qepA* and *aac-(6')-Ib-cr* genes were searched by PCR and further sequenced. Co-presence of *bla*ESBL genes was also evaluated (PCR, sequencing).

Results: We identified 173 *Enterobacteriaceae*, corresponding to different morphotypes/susceptibility patterns. A low rate of resistance to nalidixic acid (17%) and ciprofloxacin (2%) was observed. Occurrence of PMQR genes was found in 3% (5/173) of the isolates (4 piggeries, 3 regions). *qnrB* was the most frequent, being detected in four *Citrobacter freundii* isolates recovered from water, powder and swine feed of three piggeries (North, Centre and South of Portugal). *qnrS1* was found in one CTX-M-32-producing *E. coli* strain from feed. *qnrA*, *qepA* and *aac-(6')-Ib-cr* were absent.

Conclusions: Our results constitute the first description of *qnr* genes among *Enterobacteriaceae* from Portuguese swine or piggery environments, highlighting the piggeries as potential reservoirs of PMQR determinants. The role of *C. freundii* as relevant reservoir of *qnr* genes is also confirmed.