



Resistance to colistin and production of extended-spectrum β -lactamases and/or AmpC enzymes in *Salmonella* isolates collected from healthy pigs in Northwest Spain in two periods: 2008–2009 and 201

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Resumen

Salmonellosis is a common subclinical infection in pigs and therefore apparently healthy animals may represent a reservoir of antibiotic-resistant *Salmonella* for humans. This study estimates and characterizes resistance to two classes of antimicrobials considered of the highest priority within the critically important antimicrobials for humans, i.e. colistin (CR) and 3rd generation cephalosporins (3GC), on a collection of *Salmonella* isolates from pigs from two periods: between 2008 and 09, when colistin was massively used; and in 2018, after three years under a National Plan against Antibiotic Resistance. Prevalence of CR was low (6 out of 625; 0.96%; 95%CI: 0.44–2.1) in 2008–09 and associated mostly to the *mcr-1* gene, which was detected in four *S. 4,5,12:i:-* isolates. Polymorphisms in the *pmrAB* genes were detected in a *S. 9,12:-:-* isolate. No CR was detected in 2018 out of 59 isolates tested. Among 270 *Salmonella* isolates considered for the assessment of resistance to 3GC in the 2008–2009 sampling, only one *Salmonella* Bredeney (0.37%; 95%CI: 0.07–2.1) showed resistance to 3GC, which was associated with the *bla*CMY-2 gene (AmpC producer). In 2018, six isolates out of 59 (10.2%; 95%CI: 4.7–20.5) showed resistance to 3GC, but only two different strains were identified (*S. 4,12:i:-* and *S. Rissen*), both confirmed as extended-spectrum β -lactamases (ESBL) producers. The *bla*CTX-M-3 and *bla*TEM-1b genes in *S. 4,12:i:-* and the *bla*TEM-1b gene in *S. Rissen* seemed to be associated with this resistance. Overall, the prevalence of CR in *Salmonella* appeared to be very low in 2008–2009 despite the considerable use of colistin in pigs at that time, and seemed to remain so in 2018. Resistance to 3GC was even lower in 2008–2009 but somewhat higher in 2018. Resistance was mostly coded by genes associated with mobile genetic elements. Most serotypes involved in these antimicrobial resistances displayed a multidrug resistance pattern and were considered zoonotic.

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