

## Antimicrobial Resistance in *Salmonella enterica* in Portugal: An Overview on Long-term Surveillance (2009-2017)

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**Background:** Antimicrobial resistance (AMR) is currently one of the greatest threats in Public Health. Research and monitoring of AMR supported by surveillance programs, are some of the strategic priorities aiming to control its spread. The National Reference Laboratory completed nine-years of surveying AMR in *Salmonella enterica* isolates from food-producing animals, animal feed and food products. An overview of the results obtained, regarding serotypes, phenotypic and genotypic-resistance profiles, is presented.

**Methods:** 2938 isolates of *Salmonella enterica* from different animal species and food products belonging to 106 different serotypes, were selected for MICs determination; results were assessed following EUCAST epidemiological-breakpoints. Resistance mechanisms associated to extended-spectrum  $\beta$ -lactamases (ESBL), plasmid-mediated AmpC- $\beta$ -lactamases (PMA $\beta$ ), plasmid-mediated colistin (PMCR) and plasmid-mediated quinolone (PMQR)-encoding genes, were investigated through multiplex PCR, followed by sequencing. For particular phenotypes whole-genome sequencing (WGS) was performed and analysed with adequate bioinformatic tools.

**Results:** Overall, the frequency of resistance towards ampicillin, tetracycline and sulfamethoxazole was particularly high in serotypes Typhimurium, Rissen and 4,[5],12:i:-, from swine and food. Reduced susceptibility to ciprofloxacin was high in poultry, particularly in serotypes Enteritidis, Mbandaka and Havana, unlike to 3<sup>rd</sup> generation cephalosporins, cephamycins and polymyxines, which was low and more common in serotypes to 4,[5],12:i:-, Havana and Enteritidis, respectively. A diversity of resistance determinants was detected, namely:  $\beta$ -lactamases [ESBL (*bla*<sub>TEM-1</sub>, *bla*<sub>TEM-52</sub>, *bla*<sub>SHV-12</sub>, *bla*<sub>CTX-M-1</sub>, *bla*<sub>CTX-M-14</sub>, *bla*<sub>CTX-M-15</sub>, *bla*<sub>CTX-M-32</sub>) and/or PMA $\beta$  (*bla*<sub>CMY-2</sub>)], PMCR (*mcr-1*) and PMQR (*qnrB*). WGS allowed the detection of an avian *S. Enteritidis* harbouring multiple efflux-pumps, pathogenicity factors, mobile genetic elements and heavy-metal-tolerance genes.

### Conclusion:

In summary, the results obtained indicate that animals and food are potential reservoirs for ESBL-/PMA $\beta$ -/PMCR-/PMQR-producing *S. enterica* isolates, reinforcing the importance of continuous monitoring of AMR mechanisms critically important for humans and animals. We also demonstrated the added value of WGS as a promising tool for surveillance programs in the veterinary field.

**Keywords:** Antimicrobial resistance; surveillance; *Salmonella enterica*; food-producing animals; molecular microbiology