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Topic Area: Bacterial Disease

Title: Multiple-drug resistant *Salmonella enterica* serovar Typhimurium monophasic variant (4,[5],12:i:-) isolated from swine of Santa Catarina state - Brazil

Author(s): Mariana Meneguzzi, Department of Veterinary Population Medicine, University of Minnesota; Caroline Pissetti, Federal University of Santa Catarina - Campus Curitibanos, Brazil.; Raquel Rebelatto, Embrapa Swine and Poultry, Brazil; Matheus de Oliveira Costa, Department of Veterinary Population Medicine, University of Minnesota; Jalusa Deon Kich, Embrapa Swine and Poultry, Brazil

Santa Catarina (SC) raises approximately 30% of all pigs produced in Brazil, and is responsible for 50% of total pork exports. In recent years, *Salmonella* 4,[5],12:i:- which is considered to be a serologic variant of *S. enterica* serovar Typhimurium, has emerged as an important cause of salmonellosis in pigs. Between 2012 and 2016, 62.85% (22/35) of *Salmonella* strains submitted to an animal diagnostic center were identified as *S.* 4,[5],12:i:-. Although this data represents laboratory occurrence and not prevalence, it raises an alert due to its clinical relevance. Here we objective to characterize the strain and its in-farm epidemiology. The twenty-two *S.* 4,[5],12:i:- strains were categorized according to clinical presentation: enteric (isolated from intestinal samples) or septicaemic (isolated from internal organs). One strain (recovered from a septicaemic nursery pig) was submitted for whole genome sequencing (WGS), sequence-typed (ST) and analyzed for the presence of antibiotic resistance traits. Out of the 22 isolates, one was isolated from a suckling pig and was classified as enteric. Eleven isolates were recovered from nursery pigs, being nine enteric and two septicaemic presentations. Ten were isolated from grower/finishers pigs, whereas 8 were classified as enteric and 2 as septicaemic. WGS identified the *S.* 4,[5],12:i:- strain as ST-19, which was previously associated with serovar Typhimurium isolated from swine. The sequenced strain is predicted to be resistant to multiple drugs (MDR), as acquired resistance genes against aminoglycosides (*aac(6')*-*laa*, *aadA1*, *aac(3)*-*lia*), to beta lactam (*bla*TEM-*IB*), to fluoroquinolone (*qnrE1*), to phenicol (*floR*), to sulphonamide (*sul1*), to tetracycline (*tetA*), and to trimethoprim (*drfA1*). Furthermore, the antibiotic resistance plasmids *IncHI2*-type (predominant in antibiotic resistant *Salmonella*), *IncFIA*-type, *IncH12A*-type and *pO111*-type (associated with other Enterobacteriaceae genera) were also detected. Finally, chromosomal point mutations to nalidixic acid and ciprofloxacin (*gyrA* gene and point mutation p.S83Y) were also identified, typically related to *Salmonella* isolated from swine. These findings suggest that *S.* 4,[5],12:i:- is an emerging threat to commercial farms in SC. Its presumptive resistance to multiple antibiotics may have major public health implications. Further analyses will be carried out to compare *S.* 4,[5],12:i:- strains from outbreaks occurred in Brazil and other countries, to derive directions in regard to pathogen control and disease eradication.