



# **2019 Conference of Research Workers in Animal Diseases**

## **Author Index & Presentation Abstracts**

**100th Conference of Research Workers in Animal Diseases**

**November 2-5, 2019**

**Chicago Marriott, Downtown Magnificent Mile  
Chicago, Illinois**

**265 - Phenotypic and genotypic characterization of *Salmonella enterica* serovar I 4,[5],12:i:- isolated from swine**

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Session: Salmonella - 2, Nov 5, 10:30 AM

**Objective**

The National Antimicrobial Resistance Monitoring System has reported a rise in multi-drug resistant (MDR) *Salmonella enterica* serovar I 4,[5],12:i:- in both humans and animals. *Salmonella* I 4,[5],12:i:- is antigenically similar to *Salmonella enterica* serovar Typhimurium yet lacks the phase 2 flagellar antigen. The overall objective of this study is to characterize and determine phenotypic and genotypic traits of *Salmonella* I 4,[5],12:i:- isolated from swine head trim and cheek meat collected from a pork processing plant in the United States.

**Methods**

Phenotypic antimicrobial susceptibility patterns were identified by broth microdilution on a Sensititre® system. Bacterial growth curves were determined using a BioScreen C under different concentrations of enrofloxacin, tetracycline, and ceftiofur, and growth curves were analyzed using a 4-parameter Gompertz-model in Stata® to evaluate bacterial fitness. Motility assays were used to assess swimming and swarming capabilities. Whole genome sequencing was performed on an Illumina MiSeq and Oxford Nanopore MinION. Resistance genes, plasmids, and point mutations were identified using the ResFinder, PlasmidFinder, and PointFinder databases on the Center for Genomic Epidemiology website. Whole-genome alignment was performed to detect differences in the phase 2 flagellar antigen region using Geneious Software.

**Results**

Phenotypic and genotypic analyses confirmed all 47 *Salmonella* I 4,[5],12:i:- isolates were MDR, 45 displaying the common ASSuT phenotype and 2 the SSuT phenotype, while 44 displayed the ASSuT genotype. Thirty-seven also harbored the plasmid-mediated quinolone resistance gene, *qnrB*. There was no fitness cost to *Salmonella* I 4,[5],12:i:- harboring the *qnrB*, *bla*CMY and *tet* genes. Further analyses of bacterial growth curves and motility assays, whole-genome alignment, and hybrid assembly between MinION and Illumina reads are ongoing.

**Conclusions**

This study is important to determining the characteristics of *Salmonella* I 4,[5],12:i:- that have led to an increased prevalence in swine for preventing salmonellosis linked to swine and pork products.

**266 - Brazilian *Salmonella* 4,[5],12:i:- carry multiple resistance genes: a potential threat to animal and public health**

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Session: Salmonella - 2, Nov 5, 10:45 AM

**Objective**

*Salmonella* 4,[5],12:i:-, a serologic variant of *S. enterica* Typhimurium, has emerged globally as a multiple-drug resistant serovar responsible for severe gastroenteritis in both humans and animals. The aim of this study was to compare four Brazilian *S.* 4,[5],12:i:- strains, being one isolated from a septicemic nursery pig (45584) representative of a clinical salmonellosis outbreak and other three subclinical *S.* 4,[5],12:i:- strains (C41, C74 and C78) from carcasses destined to packing.

**Methods**

Following whole genome sequencing, multilocus sequence typing was performed using MLST 2.0. Antimicrobial resistance genes were determined using ResFinder 3.1 and *Salmonella* pathogenicity islands (SPI) were identified using SPIFinder 1.0.

**Results**

All strains were shown to be ST-19 and shared resistance genes to aminoglycosides, sulphonamides and  $\beta$ -lactams. However, only 45584, C41 and C78 strains had resistance genes against phenicol (*floR* and *cmlA1*). Strains, C41 and C78 were presumptively resistant to colistin (*mcr-1*), C74 to quinolone (*QnrB19*), 45584 and C78 to trimethoprim (*dfrA1*), while only the C74 strain did not harbor resistance genes to tetracycline. C41 and C78 strains had more antimicrobial resistance genes (12 and 10 genes respectively) compared to 45584 (septicemic pig, seven genes). Eight SPI which contained genes associated with systemic infection, invasion and replication of intracellular bacteria in membrane-bound vacuoles and monocytes, as well as iron uptake were found in all strains.

**Conclusions**

The strains described here are likely resistant to multiple antibiotics, their association with SPI indicates their potential threat to animal and public health.