Salmonella serotypes in fourteen cohorts of Ontario pigs from birth to slaughter using whole genome sequencing data

Erika Myler[1,2], Vahab Farzan[1,2], Brandon N. Lillie[1]
Departments of Pathobiology[1] and Population Medicine[2], Ontario Veterinary College, University of Guelph



Background

- *Salmonella* is a major cause of foodborne illness, with 9% of outbreaks originating from pigs [1]
- *Salmonella* is prevalent on Ontario swine farms [2]
- Serotyping isolates from a longitudinal study would deepen our understanding of *Salmonella* shedding on farm
- Conventional serotyping is time-intensive
- Next-generation sequencing techniques allow for whole genome based serotyping of *Salmonella* isolates

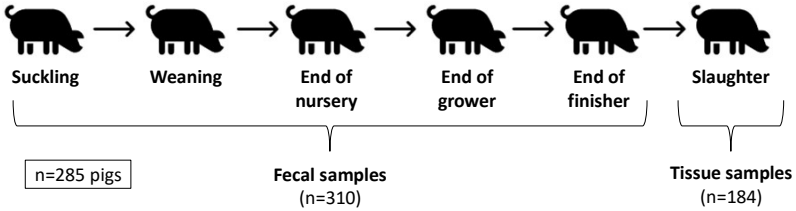
Objectives

1. Determine *Salmonella* serotypes shed at different stages of production using a whole genome sequencing approach
2. Identify serotypes shed on-farm and present in the tissues at slaughter and assess their association

Methods

- Selected 494 Salmonella isolates recovered from 832 pigs in 14 cohorts from eight farrowing sources in Ontario
- Extracted DNA using the DNeasy Blood & Tissue Kit (Qiagen)
- Serotyped isolates by whole genome sequencing (Illumina HiSeq) at the Animal and Plant Health Agency, UK
- Performed descriptive statistical analysis using Microsoft Excel

Longitudinal Study Design



Laboratory Methods



Results

Table 1. Serotype-level patterns of *Salmonella* infection in Ontario pigs (n=285) from birth to slaughter.

Serotype	No. positive samples (%)	No. positive farms	Presence across production stages: Suckling	Weaning	End of nursery	End of grower	End of finisher	Slaughter
Livingstone	98 (20)	3			■	■	■	■
Derby	87 (18)	5	■	■	■	■	■	■
Ohio	79 (16)	4		■	■		■	■
Infantis	68 (14)	5		■	■	■	■	■
Oranienburg	27 (5)	3						■
Typhimurium	29 (6)	3			■		■	■
Cerro	22 (4)	1		■	■	■	■	■
Mbandaka	19 (4)	1	■	■	■			
Worthington	18 (4)	1						■
Montevideo	13 (3)	1		■	■		■	
Senftenberg	13 (3)	3			■			
Bovismorbificans	9 (2)	1						■
Havana	4 (<1)	1		■		■		
Johannesburg	3 (<1)	1	■	■				
Orion	2 (<1)	1	■	■				
Brandenburg	1 (<1)	1					■	
Ouakam	1 (<1)	1					■	
Mono. Typhi.	1 (<1)	1						■

- Serotyped 494 *Salmonella* isolates representing 285 pigs using WGS data
- *S.* Livingstone, *S.* Derby, *S.* Ohio, and *S.* Infantis were the four most common serotypes and were each present at four to five time points
- *S.* Mbandaka, *S.* Johannesburg, and *S.* Orion were not present beyond end of nursery
- Several serotypes were shed on-farm but not recovered at slaughter, and vice versa
- Highest serotype diversity was found at the end of finisher and at slaughter

Conclusions

- **Eighteen serotypes** were identified from birth to slaughter, with differential patterns of shedding
- Ten serotypes were present in systemic tissues at slaughter, including *S.* Typhimurium – a leading cause of foodborne salmonellosis in Canada [3]
- *Salmonella* serotyping will help to develop effective on-farm control measures
- *Salmonella* shedding rate at different stages of production appeared to be serotype-dependent

Limitations & Next Steps

- Pigs were tested for *Salmonella* shedding 1-2 weeks before shipping to slaughterhouse
- Pigs were not tested for *Salmonella* shedding at lairage
- WGS data will be analyzed for the presence of antimicrobial resistance (AMR) and virulence genes

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ONTARIO PORK

References

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