

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

Erika Myler^{1,2}, Vahab Farzan^{1,2}, Brandon N. Lillie¹

Departments of Pathobiology¹ and Population Medicine², Ontario Veterinary College, University of Guelph

Salmonella is a major cause of foodborne illness and is prevalent in swine. Infected pigs are often asymptomatic, intermittent shedders and pose a risk to food safety via the contamination of carcasses at the time of slaughter. This study investigated the presence of *Salmonella* serotypes on commercial swine farms in Ontario from birth to slaughter. Fourteen groups of pigs from eight different farrowing sources were selected and fecal samples were collected at suckling, weaning, at the end of nursery, grower, and finisher. At slaughter, the palatine tonsils and submandibular lymph nodes were collected from a subset of pigs. All samples were cultured for *Salmonella* and isolates were serotyped using whole genome sequencing data. In total, 494 isolates were recovered from 285 pigs and 18 serotypes were identified. The top four serotypes across all production stages were *S. Livingstone*, *S. Derby*, *S. Ohio*, and *S. Infantis*. Farms exhibited a high degree of variation with regards to serotype presence, abundance, and diversity, as well as serotype-specific infection patterns over the course of production. Reinfection with a different serotype occurred in 18 % of pigs included in the study, which highlights the importance of effective on-farm control measures to reduce shedding and transmission. The serotypes shed on-farm differed from those recovered from the tonsils and lymph nodes at slaughter. At slaughter, the most common serotypes were *S. Derby*, *S. Infantis*, and *S. Oranienburg*. In pigs that were shedding at the end of finisher (n=115), the serotype recovered at the end of finisher did not match the serotype recovered at slaughter in 94 % of pigs (n=108). Overall, these findings shed light on the complexity of *Salmonella* infection on commercial swine farms and suggest that universal on-farm control measures may be less effective than anticipated due to high inter-farm variability.

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