

A longitudinal study of the *Salmonella* status on Ontario swine farms within the time period 2001-2006

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Abstract

In order to describe the farm-level of *Salmonella* status, 113 Ontario swine farms were tested annually for *Salmonella* 1 to 5 times within the time period 2001-2006. During 422 visits, 6844 fecal samples were collected and cultured for *Salmonella*. *Salmonella* was recovered from 437 (6.4%) of the fecal samples and 69 (61%) of the farms had at least one positive sample over the entire period of the study. *Salmonella* was not recovered on 11 farms of the 54 farms visited five times, nor from 7 of the 17 farms visited four times. On 7 farms *Salmonella* was not recovered over the first 4 visits but were cultured on the fifth visit. The isolates belonged to 30 different serovars and serogroup B and C1 were the most common serogroups. *Salmonella* Typhimurium var. Copenhagen was the most common serovar followed by *S. Typhimurium*, rough *Salmonella* isolates (Rough-O), *S. Derby*, *S. Infantis*, *S. Brandenburg*, and *S. Mbandaka*. The most frequent phage type was DT104 (including DT104a and DT104b) followed by DT12, DT193, and U302. Significant trends were detected in apparent farm-level prevalence of *Salmonella* during 5 years of this study. Although the observed trends may be partly attributed to the different culturing methods, different types of samples, and sampling strategies used in each year, it may also denote the dynamics of *Salmonella* as a bacterial population on swine farms. These findings indicate that monitoring over time may be useful to detect changes in *Salmonella* on swine farms.

Introduction

Salmonella enterica subspecies *enterica* (*Salmonella*) are important foodborne pathogens associated with pork products (Berends et al., 1998; Borch et al., 1996; Mousing et al., 1997). Infection with non-typhoidal *Salmonella* is one of the most important causes of enteric illness in Canada, and in Ontario 23% of sporadic cases of reportable enteric diseases between 1997 and 2001 has been attributed to *Salmonella* spp (Lee et al. 2003). In order to limit and control *Salmonella* occurrence in swine herds, it may be useful to conduct epidemiological studies to determine the prevalence of *Salmonella* and provide knowledge on the distribution of *Salmonella* serovars on swine farms. The point estimates of *Salmonella* prevalence and serovars on the farms cannot represent the true *Salmonella* status in swine and it is very important to test swine farms for *Salmonella* over a period of time. The objective of this study was to describe the apparent farm-level prevalence of *Salmonella*, as well as the serovars, phage types, and serogroups during the years 2001-2006.

Material and methods

Sampling and Salmonella isolation: In total, 113 swine farms were tested annually for *Salmonella* 1 to 5 times within the time period 2001-2006 (2001: Year 1; 2002: Year 2; 2003: Year 3; 2004: Year 4; 2005-

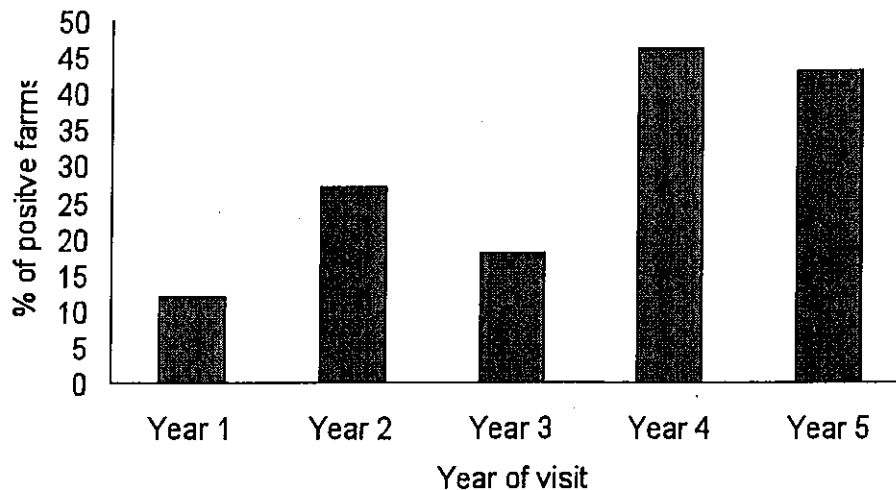
2006: Year 5) in which 9, 25, 8, 17, and 54 farms were visited one, two, three, four, and five times, respectively. On each farm, 1 grower-finisher barn was chosen and within the barn 5 pens with pigs close to market weight were selected for sampling. Fecal samples per-rectum were obtained from 2-3 pigs per pen and an additional pooled sample was collected from the fresh manure found on 5-8 spots on the floor of each of the 5 selected pens. In total 6844 fecal samples (4647 pig and 2197 pooled pen samples) were obtained on 113 farms during 422 visits over the entire study period. In Year 1 and 2, 1 g fecal sample and in the last three years of the study 25 g fecal sample was cultured for *Salmonella*. One to 5 colonies from each positive sample were submitted to the Reference Laboratory for Salmonellosis, Laboratory for Foodborne Zoonoses, Public Health Agency of Canada, Guelph for serotyping and phage typing.

Data analysis: The Chi-squared Test for Trend in Proportions (Cochran-Armitage Test) (Argesti, 2002) was applied to detect annual changes at the isolate and farm level. In addition, a Generalized Linear Latent and Mixed Models (GLLAMM) with farm as a random effect was used in order to take the correlation between repeated measurements on each farm into account (Dohoo et al., 2003).

Results

Salmonella was recovered from 437 (6.4%) of the fecal samples; it was cultured from 1.2%, 3.9%, 2.8%, 13.7%, and 18.6% of the samples collected in Year 1, Year 2, Year 3, Year 4, and Year 5, respectively. *Salmonella* was cultured from at least 1 sample collected on 69 (61%) farms over the entire period of the study. The farm-level prevalence of *Salmonella* increased significantly over time ($P < 0.001$); however, no significant difference was observed in farm-level prevalence between Year 4 and Year 5 (Figure 1). *Salmonella* were not recovered on 11 farms of the 54 farms that were visited 5 times, nor from 7 of the 17 farms visited 4 times. On 7 farms *Salmonella* were not recovered during the first 4 visits but were finally cultured on the fifth visit.

Figure 1: Apparent prevalence of *Salmonella* on 113 Ontario swine farms, 2001-2006



Salmonella isolates belonged to 30 different serovars. *S. Typhimurium* var. Copenhagen was found on 27% of the farms followed by *S. Typhimurium* (18%), rough *Salmonella* isolates (Rough-O) (11%), *S. Derby* (11%), *S. Infantis* (11%), *S. Brandenburg* (9%), and *S. Mbandaka* (6%). The prevalence of the serovars changed over the five visits ($P < 0.05$). A significant change was observed for the prevalence of serogroup B and C1 ($P < 0.05$). The most frequent phage type was DT104 (including DT104a and DT104b) seen on 28% of the 113 farms. There was a significant change in the prevalence of DT104 over the 5 years ($P < 0.05$).

Discussion

Significant trends were detected in apparent farm-level prevalence of *Salmonella* during 5 years of this study. These trends may denote the dynamics of *Salmonella* as a bacterial population on swine farms. However, they need to be interpreted with caution since the weight of the fecal sample, different media, incubation temperature, and selective enrichment was used in each year and it might influence the probability of isolating *Salmonella* (Funk et al., 2000; Davies et al., 2000; Champagne et al., 2005). Although no individual pig samples were collected in Year 5, there was only 3% decrease in this year compared to 2004. Thus, if the objective is to determine the farm-level prevalence, it may not be necessary to test individual pigs. The fact that *Salmonella* was recovered on 69 (61%) of farms at least in one visit and that *S. Typhimurium* including var Copenhagen was the most frequent serovar in the current study needs to be considered as a serious issue when implementing a preventive program. Knowing the predominant serovars present in the Ontario pig population is important in considering a control strategy. For example if vaccination was to be chosen as a method to reduce *Salmonella* prevalence it may be important to know what antigens would need to be present in the vaccine to provide protection. The longitudinal approach used in the current study could also provide a deeper insight into serogroups distributed on Ontario swine farms which might be used to revise serological tests such as ELISA for application in the Ontario swine industry. Possibly the most important aspect of this study is that by providing a picture of *Salmonella* serovars distributed on Ontario swine farms, this information may be used to study the extent of the relationship between human salmonellosis and pork consumption.

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