Spatial and Temporal Patterns of the Distribution of
Salmonella on Swine Farms in Illinois

Barber DA, Weigel RM, Isaacson RE, Bahnson PB, Jones CJ
University of Illinois, College of Veterinary Medicine, 2001 South Lincoln Avenue, Urbana, IL 61802, USA

Abstract

An ecological study was conducted to identify possible reservoirs of Salmonella. From March to November 1998 there were 4 visits to each of 6 selected swine farms in Illinois. Fecal samples were collected from swine in longitudinal and cross-sectional groups on each visit to each farm. Fecal samples were also collected from chickens, cattle, cats, dogs, rodents, and other wildlife. Overnight trapping and hand capture techniques were used to obtain samples from wildlife, cats, and arthropods. Environmental samples including feed, water, pen floor material, bootebris, and bird feces were collected. All samples were evaluated as Salmonella positive or negative by culture. A total of 3564 samples representing 40 sample types were collected and cultured. Of 2442 swine fecal samples, 935 were from longitudinal cohorts, and 1507 were from cross sectional groups. Non-swine fecal samples and environmental samples comprised the remaining 1123 samples. Salmonella was cultured from 157 samples in 19 different sample types. All positive samples are mapped with representation of location and time of collection on the farm.

Introduction

Food safety is an important issue in food animal production. The recent evolution of antibiotic resistant bacteria that infect food animals has made food safety a critical issue for human health. Salmonella bacteria, which are endemic in swine, have at least one antibiotic resistant strain, Salmonella typhimurium DT104.

The results of previous epidemiologic investigations suggest that reservoirs of Salmonella are widespread on swine farms, as well as persistent over time. (1, 2, 3, 4) However, there is a paucity of information on patterns of transmission of Salmonella on swine farms. The widespread distribution of Salmonella in time and space makes it more difficult to understand its transmission dynamics and, thus, creates obstacles in the development of effective intervention strategies. Since the farm is the initial source of infection for swine, prevention of infection at this stage of the food processing continuum could greatly enhance the safety of pork as food. Efforts by the United States Department of Agriculture and the Food and Drug Administration are targeted at improving pre-harvest food safety.

This study reported here examines the reservoirs of Salmonella on swine farms. Special attention is given to the distribution of Salmonella in time and space. The goal is to gain additional insight into the modes of transmission of Salmonella on swine farms.

Materials and Methods

This ecological study of Salmonella included 6 swine production facilities in Illinois. These farms were selected based on Salmonella isolations at slaughter identified in a risk factor study by Dammann D.J. et al. (5) Selected operations were all farrow to finish, ranging in size from 100 to 800 sows. A minimum herd size of 100 sows was established in order to ensure adequate numbers of available pigs at all cross-sectional stages at each visit.

Each farm was visited 4 times for sampling. Intervals between visits were 5 weeks for each farm except for a 10 week interval between visits 3 and 4. Each visit was completed in 2 days. On day 1 of the first visit to each farm, a map was made to indicate lots, buildings, rooms, pens, and layout of the operation facilities. Room length, width, and area were recorded. Each building, room, and pen was assigned an identifier to be used to maintain labelling continuity during sample collection on each visit. All collected samples were given an identifier and the location of origin was recorded on a map copy. Also on day 1 of the first visit to each farm, a cohort of 40 suckling pigs age 10 to 18 days was assembled. These cohort pigs were ear tagged and fecal samples were collected from them longitudinally on each visit throughout the study. These pigs were selected by a 2 stage process, systematic sampling of farrowing crates at uniform spatial intervals followed by random selection of pigs within the selected crates. These cohort pigs were sampled at 2, 7, 12, and 22 weeks of age. Fecal samples were collected from the sows in the farrowing crates with cohort pigs at the time of selection. Floor material was also collected from each crate containing cohort pigs. Cross-sectional sampling of swine on day 1 of the first visit to each farm included the sows in the cohort crates plus 20 other sows, 20 nursery (7 week), 20 grower (12 week), and 20 finisher (22 week) pigs. Cross sectional sampling on day 1 of visit 2 included 20 finisher pigs. Visit 3 to each farm included cross-sectional sampling of 40
suckling pigs and their sows, 20 other sows, 20 nursery, and 20 finisher pigs. Day 1 of trip 4 to each farm included cross-sectional sampling of 40 suckling pigs and their associated sows. Samples of floor material were collected for culture from each pen where swine were sampled. Feed samples were collected for each age class of swine from each room in which that age class was sampled. Water was collected from a source such as a spigot or faucet on each trip to each farm. Where water was available to swine in an open trough, water was collected from the trough. Observations during some initial visits prompted the addition of bird feces and boot swabs to the sample collection protocol for each site sampling visit. All samples were recorded on maps at the time of collection and given an identification code to facilitate spatial and temporal analysis. All samples were stored in coolers on ice for the return trip to the laboratory for 
Salmonella culturing procedures. After sampling of swine at each visit, live traps of 3 different sizes (mouse, rat, cat) were placed in the areas where swine were sampled. These traps were for collection of rodents, other wildlife, and cats that shared the same housing with the swine. Non-toxic roach traps were also placed in the same areas for collection of arthropods that occupied the swine areas. Strict biosecurity measures were observed in preparation for arrival and departure at all site visits.

On day 2 of each visit to each farm, all traps were retrieved. Rodents were anesthetized, then euthanized for collection of intestines for culture. Collection was by aseptic surgical technique. Cats and non-rode species wildlife were sedated for collection of fecal samples. Insects were placed in porous plastic bags and placed in a sealed cooler with dry ice for CO₂ euthanasia and cold preservation. All fecal samples and intestine samples were placed in sterile containers and kept in coolers with ice until immediate return to the laboratory for 
Salmonella culture procedures. All samples collected in the study were recorded for their location and time of collection. All samples were cultured to determine a status of Salmonella positive or Salmonella negative. All positive samples from each trip to each farm were designated on a computer-generated map with a designation of sample type.

**Results**

A total of 3564 samples representing 40 sample types were collected and cultured to determine whether Salmonella was present or not. There were 2442 fecal samples from swine, 935 from pigs in the longitudinal cohorts, and 1507 in cross-sectional samples. There were 17 Salmonella positive samples in cohort samples (1.8%), with no cohort pig positive on more than one sample. However, when repeated samples are considered, 6.8% of the 250 cohort pigs were positive for Salmonella shedding over the course of the study. Only 2 of the 17 cohort pigs that were positive for Salmonella came from sows that also tested positive for Salmonella. The cross-sectional sample of 1200 swine from the same age classes produced an overall prevalence estimate of 2.6%. Culture results from the cross-sectional swine (Fig.1) resulted in an underestimation of the presence of Salmonella when compared to the results for the longitudinally sampled cohort group (Fig.2).

![Cross Sectional Results](image1)

**Fig. 1**

![Longitudinal Cohort Results](image2)

**Fig. 2**

SW = suckling swine; SN = Nursery swine; SG = Grower swine; SF = Finisher swine

Distinct farm-to-farm differences were detected in the overall prevalence of Salmonella in swine feces (Fig.3). One farm, designated with code RB, had an overall Salmonella prevalence of 6.1% in swine feces. The range on the other 5 operations in the study was 1.5% to 3.1% prevalence of Salmonella in swine feces. The RB farm also had markedly higher prevalence of Salmonella in floor samples (Fig.4) and in boot material (Fig.5) than did the other 5 farms.
There were 715 environmental samples, including boot material, floor material, water, feed, and bird feces. Non-swine vertebrate and invertebrate animals contributed 407 samples. *Salmonella* was present in samples from each of the 6 study farms and 23 of 24 sampling visits. *Salmonella* was present in 157 samples from 19 of the 40 sample types tested, including cats, mice, birds, arthropods, water, and feed, in addition to swine. All *Salmonella* positive samples were recorded on computer-drawn maps of the individual farms with designations of sample type and date of collection (presented as poster). These maps help in the visualization of the degree of spatial and temporal dispersion of *Salmonella* on the individual farms. Prevalence values were similar trip by trip on each farm. There is no apparent clustering of *Salmonella* in space or in time on any of the 6 operations in this study.

**Discussion**

Cross-sectional sampling of swine to determine *Salmonella* prevalence may lead to an underestimated perception of the presence of *Salmonella* in swine. This possibility is supported by the contrast that is observed in comparing the cross-sectional swine prevalence (2.58%) to the group followed longitudinally (6.8%).

Examination of the variation among farms in the distribution of *Salmonella* suggested one possible mechanism for transmission. The farm with the highest prevalence of infection of swine fecal samples also had the highest prevalence of floor and boot samples that were *Salmonella* positive. This suggests that pen floors are a primary source of new infection for swine, and human tracking may be a major mode of transmission of *Salmonella* between pens.

The occurrence of *Salmonella* infection in numerous reservoirs (swine, pen floors, cats, rodents, birds, arthropods, water, feed) indicates there are many possible sources for transmission to swine. The mapping of positive *Salmonella* samples on farms does not identify any spatial or temporal correlation of positive samples specifically implicating any biotic source as being more important than others in transmission. Patterns of transmission of *Salmonella* may have been obscured by the March through November sampling, which may miss periods of relatively low *Salmonella* population sizes, during which times persistent reservoirs of infection might be identified. Establishing transmission links between *Salmonella* from different reservoirs will require genetic analysis of isolates. Work is currently being done to examine the genetic relationship of the *Salmonella* isolates collected in this study.

Development of prudent science-based recommendations for on-farm control of *Salmonella* demands a solid knowledge of the spatial and temporal distribution of *Salmonella* and the relative importance of different sources of *Salmonella*. Some aspects of *Salmonella*

**References**


