Fecal shedding of *Salmonella* by gilts before and after introduction to a swine breeding farm

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Summary

Fecal shedding of *Salmonella* serotypes was studied in two groups of gilts introduced to a swine breeding farm from a gilt-development farm. Fecal samples were collected from individually identified gilts (121 from group 1 and 81 from group 2) at the gilt farm before transport, and after arrival at the breeding farm (11 days post-arrival for group 1; 4 and 12 days post-arrival for group 2). In both groups of gilts, prevalence of fecal samples positive for *Salmonella* was lower (<4%) in samples collected at the gilt farm prior to transport than in samples collected after arrival at the breeding farm (>20%; $P < .001$). Changes in serotype profiles in the two groups suggested that both increased shedding by carrier animals after transport, and that new infections acquired after arrival contributed to the increase in prevalence. Regardless of mechanism, the marked increases observed indicate that high replacement rates and external sourcing of gilt replacements may contribute to the maintenance of *Salmonella* infections in some herds.

Keywords: swine, *Salmonella*, shedding, replacement gilts

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Epidemiologic studies of *Salmonella* in conventional farrow-to-finish farms concluded that sows and boars play an important role in maintaining *Salmonella* infection on farms.[1, 2] Monitoring suppliers of replacement breeding stock is a key component of national *Salmonella* control programs in both the Swedish and Danish swine industries.[3,4] This emphasis on replacement stock is founded on concerns that incoming pigs are a potentially important source of infection for breeding herds and, subsequently, growing pig populations. However, recent studies in systems with different stages of production raised on separate sites have provided evidence that infection of piglets occurring prior to weaning is a relatively minor source of *Salmonella* infections found in market-age hogs.[5–8] Although the role of breeding stock as a source of *Salmonella* infection in market hogs is unclear, *Salmonella* infection of breeding stock has direct implications for food safety, because culled sows provide a substantial component of the pork products available to consumers. The few reports of *Salmonella* infection of breeding swine in the United States[7,9,10] and the Netherlands[11] have indicated a relatively high prevalence (20%–84%) of infection.

Two features of contemporary swine farms in the United States are increasing sow inventory (herd size) and high replacement rates of sows. Annual sow replacement rates in confinement herds with stable female inventory are typically 45%–60%, with gilts often being the largest parity group.[12] Most large modern enterprises obtain replacement females from off-farm sources. The combination of large inventories and high rates of replacement with introduced gilts predisposes herds to rapid fluctuations in herd immunity to endemic infectious diseases, and provides a continual avenue for the introduction of new infectious agents. For these reasons, appropriate gilt pool management is considered a critical factor in achieving control of porcine reproductive and respiratory syndrome virus (PRRSV) in swine breeding herds,[13] and similarly may play a key role in the epidemiology of other infectious diseases of pigs. There appears to be no previously published studies investigating *Salmonella* infection in gilts introduced into breeding farms. As part of ongoing longitudinal studies of *Salmonella* in modern production systems in North Carolina, we observed patterns of fecal shedding of *Salmonella* by two cohorts of gilts introduced into a 1200-sow herd in 1996.

Materials and methods

Farms

The study was conducted on two farms. The gilt-development farm comprised 10 barns housing approximately 10,000 growing females that were supplied at approximately 23 kg (50 lb) liveweight by a breeding farm located in another state. The barns, built in 1994, had fully slotted concrete floors. Feed and water were supplied ad libitum. The farm was managed all-in–all-out (AIAO) by barn, and gilts were moved to breeding herds or slaughter at approximately 6 months of age. This herd was the only source of replacement females for the breeding herd studied, and also supplied other clients.

The breeding farm, established in 1981, was located approximately 110 miles from the gilt development farm and was part of a system described elsewhere (Figure 1).[7] At the time of the study, the farm was in the process of expanding from approximately 750 to 1500 sows. New farrowing and breeding accommodation was added in 1995, and as of April 1996 the herd comprised approximately 1200 breeding females. Sows in breeding and gestation barns were housed predominantly in individual crates on concrete floors slotted in the back half (some pens were used to house sows that had weaned their offspring and incoming gilts). Normally, incoming gilts were housed for 3–4 weeks in an

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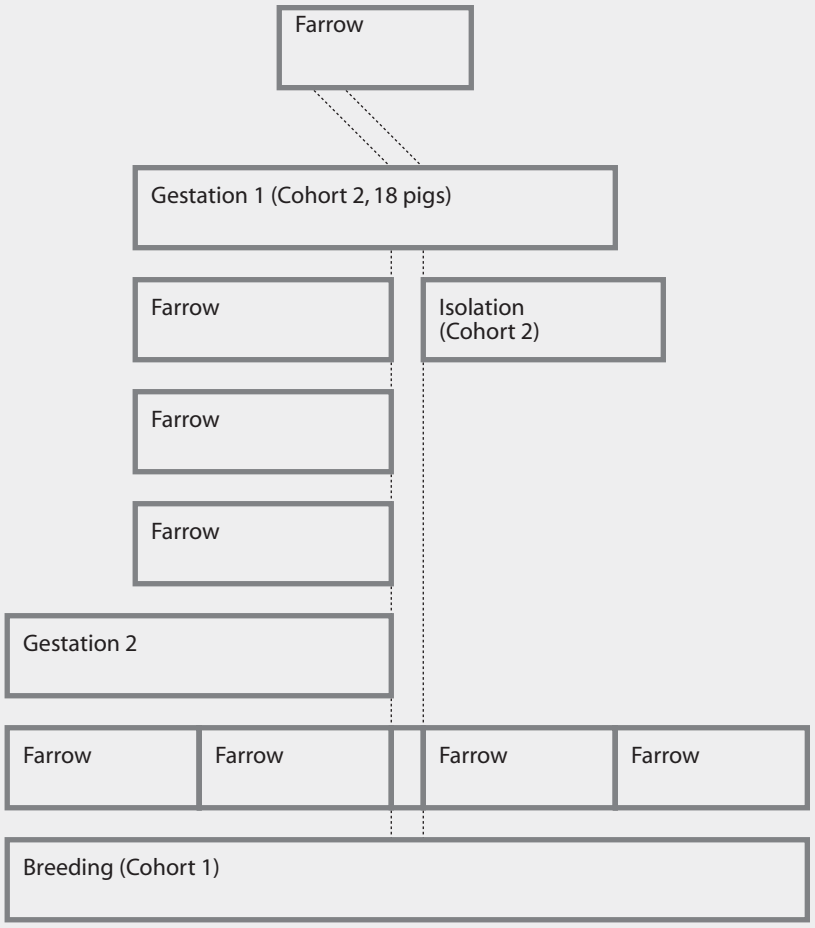
Figure 1: Schematic outline (not to scale) of buildings at the breeding farm indicating locations of gilts in cohorts 1 and 2



"isolation" room (Figure 1) with eight pens before being introduced into the herd. However, during the period of expansion, housing of incoming gilts varied according to availability of space. In the isolation room, two rows of four pens were separated by a central aisle. The pens had fully slotted concrete floors and open metal divisions.

Sampling

Cohort 1

The expansion of the herd provided an opportunity to identify a relatively large cohort of gilts as part of a long-term study. At the gilt farm on March 18, 1996, 121 gilts selected to be transported to the breeding farm were individually identified with ear tags, and rectal fecal samples were collected with a gloved hand (gloves changed between pigs). The gilts were housed in multiple pens (estimated 20 of 36 pens) in one barn, and were selected by the service person from the company purchasing the gilts. Fecal samples (>10 g) were placed into sterile plastic bags and transported to the laboratory to be processed on the same day. The gilts were transported to the breeding farm on March 21, 1996, and a second fecal sample from each study gilt was collected on April 1, 1996 (11 days after arrival). In the interim, the gilts had been housed in the new breeding building in individual gestation crates in the central rows of the barn (designed for holding mated females until heat checking after 21 days). Boars and older females were present in the peripheral rows of crates and pens (Lubbock system) in the same barn, and did not have direct physical contact with the introduced gilts. Also, the crates occupied by the cohort gilts had not been occupied previously nor did they share a common water trough with crates occupied by older stock.

Cohort 2

The second cohort of gilts was not part of the original long-term study design, but was sampled after results were obtained from Cohort 1 to evaluate whether the findings were repeatable. On April 29, 1996, a cohort of 81 pigs, selected by the company service person, was individually identified and sampled at the gilt-development farm. At the gilt-development farm, Cohort 2 gilts were housed in multiple pens in a different barn from Cohort 1. After transport to the breeding farm (May 2, 1996), 63 of the gilts were housed in eight pens in the isolation room (managed AIAO) used to house incoming stock. The remaining 18 gilts were housed in consecutive individual crates in an old gestation building (gestation 1) that also housed gestating sows (Figure 1). The crates containing these 18 gilts were in the middle of a row of crates sharing a common water trough, and the group of gilts was flanked by older sows on both sides. Fecal samples were collected from both groups of gilts 4 and 12 days after arrival.

Bacteriologic culture

To detect *Salmonella* organisms, fecal samples (10 g per sample) were processed using conventional enrichment methods as described previously.[8]

Statistical analysis

McNemar's test for matched samples was used to compare the proportions of fecal samples with positive results at different samplings within cohorts. χ^2 analysis was used to compare the proportions of fecal samples with positive results for Cohorts 1 and 2 at the gilt development farm. Differences were considered significant at $P < .05$. All analyses were performed using a commercially available software package (Statistix 4.0, Analytical Software; Tallahassee, Florida).

Results

Neither the prevalence of positive cultures ($P = .88$) nor the serotype profiles of the two groups of gilts differed significantly before transport to the gilt development farm (Table 1). *Salmonella* serotypes Tennessee and Typhimurium var. Copenhagen were isolated from both cohorts, and one isolate of *Salmonella* serotype Mbandaka was obtained from Cohort 1 only. When Cohort 1 was sampled 11 days after arrival at the breeding farm, 57 of 121 (47%) fecal samples were positive for *Salmonella* (Table 1). Similarly, in Cohort 2, the prevalence of positive fecal samples was

Table 1: Prevalence and serotypes of *Salmonella* isolated from feces of gilts at the gilt-development farm and after arrival at the breeding farm

	n samples	n positive	Percent positive	Serotypes (n)
Cohort 1				
Gilt farm	121	4	3.3%	Tennessee(2), Typhimurium (var. Copenhagen)(1), Mbandaka(1)
11 day post-arrival	121	57	47%	Typhimurium (var. Copenhagen) (30), Worthington (10), Mbandaka (8), Heidelberg (8), 4:12b nonmotile (1)
Cohort 2				
Gilt farm	81	3	3.7%	Tennessee (1), Typhimurium var. copenhagen (2)
4 day post-arrival	81	16	20%	Typhimurium var. copenhagen (1), Heidelberg (9), Mbandaka (6)
12 day post-arrival	81	37	46%	Heidelberg (33), Mbandaka (4)

higher (P <.01) at day 4 (16 of 81; 20%) and day 12 (37 of 81; 46%) than in the samples collected at the gilt farm (Table 1).

At the breeding farm, five serotypes were isolated from Cohort 1 gilts, two of which (*Salmonella* Typhimurium var. Copenhagen, *Salmonella* Mbandaka) had been isolated previously at the gilt-development farm. Of the three serotypes isolated from Cohort 2 after arrival at the breeding farm (Table 1), *Salmonella* serotype Heidelberg was the predominant serotype at both the day-4 (9 of 16 isolates; 56%) and day-12 (33 of 37 isolates; 89%) samplings. *Salmonella* Tennessee, which was isolated from both cohorts at the gilt-development farm, was not isolated from either cohort at the breeding farm. Similarly, in Cohort 2, *Salmonella* Typhimurium var. Copenhagen was isolated from

- two pigs at the gilt-development farm,
- one of the same gilts 4 days after arrival, and
- none at 12 days after arrival (Table 1).

In Cohort 2, two of the 18 gilts housed adjacent to sows in the old gestation building were positive 4 days after arrival, and none of the 18 was positive 12 days after arrival. In contrast, of the 63 gilts housed in the isolation room at the breeding farm, 14 were positive after 4 days, and 37 were positive after 12 days. At day 12 after arrival, 30 of 32 pigs were positive on one side of the building compared with six of 33 pigs (P< .01) on the other side of the room, all of which were housed in one pen (Figure 2).

Discussion

Results from both cohorts show rapid changes in the prevalence of fecal shedding of *Salmonella* from the gilt-development farm to the post-arrival period at the breeding farm. Changes in apparent *Salmonella* status associated with transport have long been documented in pigs transported to slaughter,[14] as well as cattle[15] and poultry.[16]

Factors suggested to contribute to the 'transport-lairage' effect include:

- increased populations of *Salmonella* resulting from 'stress' of transport, including feed and water deprivation;[17,18] and
- cross-infection from other animals or contaminated vehicles or facilities.[5]

Examination of the serotypes isolated from the respective cohorts at the two farms may provide some insight into the origin of the infections found after arrival. In Cohort 1, 38 of the 57 isolates (67%) at the breeding farm were serotypes found in the same pigs at the gilt-development farm (*Salmonella* Typhimurium var. Copenhagen, *Salmonella* Mbandaka). This pattern is consistent with the hypothesis that transport of the gilts led to increased fecal shedding and/or transmission of serotypes originating at the gilt-development farm to other uninfected pigs in the cohort. In contrast, only one of 53 isolates (2%) from Cohort 2 at the breeding farm was a serotype isolated from the same pigs at the gilt farm. If one accepts that *Salmonella* Mbandaka (isolated at the gilt farm in Cohort 1) may also have originated from the gilt farm in Cohort 2, the proportion would be 11 of 53 isolates (21%). This pattern suggests the occurrence of new infections of the pigs after exposure during transport or after arrival at the breeding farm. It is relevant to recall that Cohort 1 gilts were housed in a new building in previously unoccupied crates with no direct contact with older pigs. Cohort 2 gilts were mostly (63 of 81) housed in the isolation room, which had previously housed many groups of pigs and consequently was more likely a contaminated facility. Although this room was managed AIAO, with cleaning and disinfection between groups, we have previously demonstrated residual *Salmonella* contamination of barns managed in this manner.[8] One cannot eliminate the possibility that sampling at the gilt farm failed to detect some serotypes in the pigs. However, the following observations point to the occurrence of new infection after leaving the gilt farm:

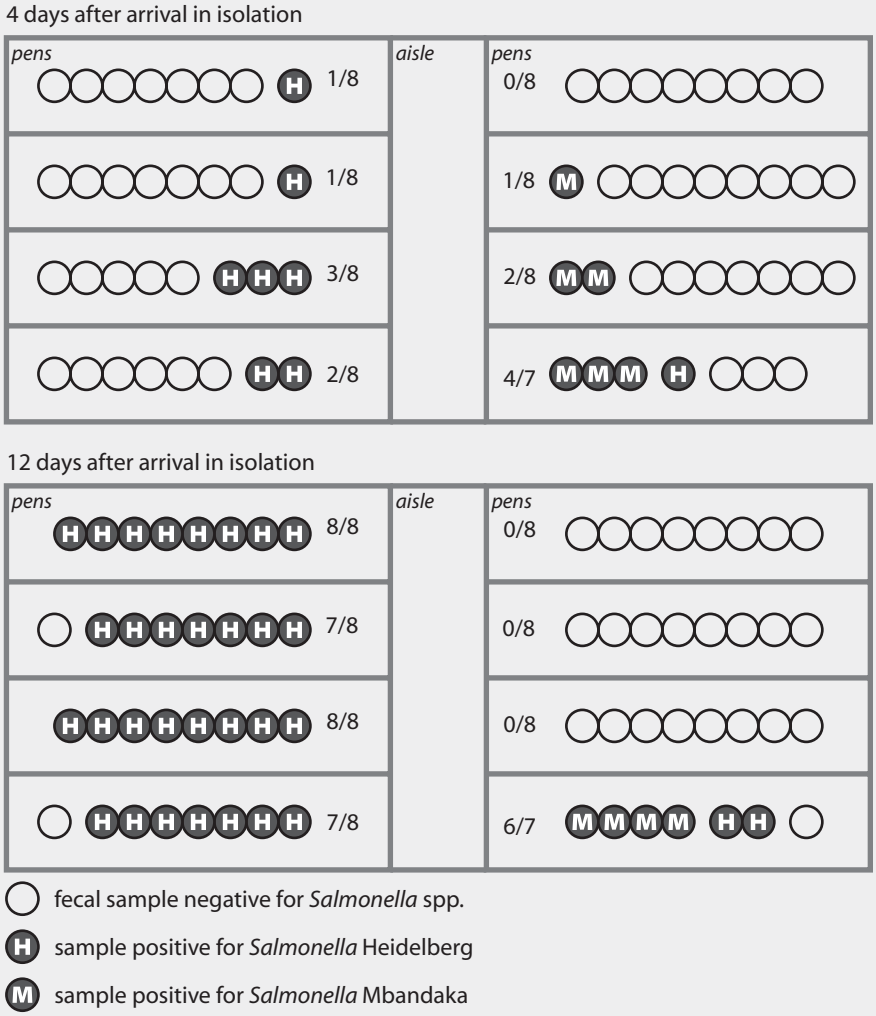
- Similar serotype profiles in both samplings at the gilt-development farm (*Salmonella* Tennessee and *Salmonella* Typhimurium var. Copenhagen) were detected in both groups, while *Salmonella* Heidelberg was found in neither.
- Increasing prevalence in Cohort 2 from day 4 to day 12 post-arrival, suggesting ongoing pig-to-pig transmission after arrival (Figure 2).
- Pigs shedding at the gilt-development farm in Cohort 2 were either culture negative or shedding *Salmonella* Heidelberg when sampled 12 days post arrival (Table 2).
- The absence of detectable fecal shedding in the 18 gilts housed in individual crates in the gestation accommodation (Cohort 2).

The marked differences, in both time and space, observed in detectable fecal shedding of *Salmonella* by pigs in this isolation room (Figure 2) underscores the dynamic nature of *Salmonella* infection in swine populations. In previous studies we have commonly found clustering of pigs shedding *Salmonella* in certain pens within barns, including clustering of serotypes by pen.[19,20] While seven pigs on each side of the barn were shedding *Salmonella* 4 days after arrival, it appears that on one side extensive pig-to-pig transmission occurred, such that 30 of 32 pigs (94%) yielded positive fecal samples by day 12 after arrival. In

Table 2: *Salmonella* isolated from individual pigs in Cohort 2 before and after introduction to the breeding farm

Ear tag	Gilt farm	4 days post-arrival	12 days post-arrival
143			Heidelberg
145		Heidelberg	
147			Heidelberg
149	Typhimurium (Copenhagen)	Typhimurium (Copenhagen)	
154			Heidelberg
155			Heidelberg
156			Heidelberg
158			Heidelberg
159			Heidelberg
160		Heidelberg	Heidelberg
161			Heidelberg
164			Heidelberg
169		Mbandaka	
181			Heidelberg
184			Heidelberg
185	Tennessee		Heidelberg
187		Mbandaka	
188			Heidelberg
189			Heidelberg
190		Heidelberg	
191			Heidelberg
195		Heidelberg	Heidelberg
196		Mbandaka	
197	Typhimurium (Copenhagen)		Heidelberg
198			Heidelberg
199			Heidelberg
201			Heidelberg
202			Heidelberg
204		Heidelberg	Heidelberg
206		Mbandaka	Heidelberg
207			Heidelberg
209			Heidelberg
213		Heidelberg	Heidelberg
215		Heidelberg	Heidelberg
217			Mbandaka
218		Mbandaka	Heidelberg
219		Heidelberg	Heidelberg
220		Mbandaka	Mbandaka
221			Mbandaka
222		Heidelberg	Heidelberg
223			Heidelberg
224			Mbandaka
226			Heidelberg

Figure 2: Proportion of *Salmonella*-positive fecal samples and serotypes isolated from gilts of Cohort 2 housed in pens in the isolation room 4 and 12 days after arrival



contrast, on the other side of the barn only six of 31 pigs were positive on day 12, suggesting negligible transmission among pigs despite essentially identical conditions. One possible explanation for these differences would be the chance occurrence of individual pigs shedding large numbers of *Salmonella,* resulting in a high probability of infection and shedding by pigs in direct contact with them.

Regardless of whether the increased shedding of *Salmonella* after arrival was primarily attributable to activation of latent infections of carrier animals or the acquisition of new infections by gilts after leaving the gilt farm, the practical consequence is that a high prevalence of fecal shedding by introduced gilts is likely to make a significant contribution to contamination of the farm environment. It remains to be seen whether the dramatic changes in detectable fecal shedding by introduced gilts in this study represent a common scenario or an atypical result. It is likely that both mechanisms (activation of latent infections and acquisition of new infections) occur in pigs moved from farm to slaughter, or between farms within production systems. The magnitude of these events and their contribution to the 'big picture' of *Salmonella* transmission in swine may be highly variable. However our data in these gilts, and in a previous study of a cohort of finishing pigs,[8] suggest that movement of animals among farms may be an important component of the epidemiology of *Salmonella*.

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