

# Fecal shedding of *Salmonella* by a cohort of finishing pigs in North Carolina

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## Summary

This longitudinal case study investigated patterns of *Salmonella* shedding in a cohort of 41 finishing pigs in a finishing barn managed all-in–all-out. Drag swab samples of the finishing barn floor were collected 1 day before placement of pigs (day 0). Individual fecal samples, pooled pen fecal samples, and feed samples were collected on study days 2, 37, and 78. All samples were cultured for *Salmonella* using selective enrichment. Serotypes isolated were *Salmonella* serotype Derby, *Salmonella* serotype Typhimurium (Copenhagen), *Salmonella* serotype Heidelberg, *Salmonella* serotype Typhimurium, and *Salmonella* serotype Mbandaka. *Salmonella* Mbandaka and *Salmonella* Typhimurium (Copenhagen) were isolated from floor swabs prior to pig placement. The serotype profiles determined in both individual pig samples and pooled pen fecal samples were similar and changed markedly from day 2 postplacement, when *Salmonella* Derby comprised 63% of isolates from pigs, to day 78 post placement, when *Salmonella* Typhimurium comprised 87% of isolates from pigs. The *Salmonella* status of finishing pigs is dynamic and our observations support previous studies that indicate that infection during the finishing phase may be the major source of *Salmonella* found in market-age hogs.

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The importance of clinical salmonellosis of pigs (most often caused by *Salmonella* serotype Choleraesuis or *Salmonella* serotype Typhimurium),<sup>1</sup> is now overshadowed by the perceived risks to food safety associated with asymptomatic *Salmonella* infections of pigs. Improved control of *Salmonella* and other human foodborne pathogens in food animal populations has become a common call from consumers, government, and industry groups in many countries. A report of the World Health Organization in 1988 advocated “improving production systems” as a necessary step toward reducing *Salmonella* infection in food animal populations.<sup>2</sup> Over the last 15 years, there have been radical changes in systems used to produce pigs in the United States, including the wide adoption of multisite production, segregated early weaning, and all-in–all-out (AIAO)

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management of growing pigs, together with marked increases in herd sizes (Centers for Epidemiology and Animal Health, Fort Collins, Colorado. USDA:APHIS:VS. October, 1995. Item #N186.995).<sup>3</sup> The veterinary profession has advocated these approaches because they are associated with improved production performance and better control of infectious diseases.<sup>3</sup> However, AIAO management has also been recommended specifically for its potential to control *Salmonella* infections in swine.<sup>1,4</sup>

Data regarding the prevalence of human foodborne pathogens in modern production systems in the United States are limited, although in initial studies we found antibodies to *Trichinella spiralis* and *Toxoplasma gondii* occurred at very low prevalence in modern production systems in North Carolina.<sup>5</sup> In contrast, we found a higher proportion of finishing barns positive for *Salmonella* in herds using AIAO finishing in multisite production systems than in farrow-to-finish herds with continuous-flow finishing.<sup>6</sup> Subsequently, in a cross-sectional sampling of one multisite system in North Carolina we found that the predominant *Salmonella* serotypes in pigs at finishing farms were distinct from those isolated from the breeding herds and the nursery in the same system.<sup>7</sup> Our observation was consistent with results from Dutch and Danish work suggesting that upstream infection (i.e., pigs being infected before arriving at finishing farms) is a relatively unimportant source of *Salmonella* infection of finished hogs.<sup>1,4</sup> This issue has considerable importance for developing interventions aimed to reduce the risk of *Salmonella* infection in market hogs raised in multisite systems. However, the different serotype patterns of *Salmonella* we found in finishing pigs compared with breeding and nursery pigs could be explained just as plausibly by changes in serotype patterns in ‘upstream’ herds over time. To address this concern, we undertook a longitudinal study to describe temporal patterns of *Salmonella* shedding by a cohort of finishing pigs within the same production system.

## Materials and methods

The particular farm site was chosen because *Salmonella* prevalence data were available from previous studies.<sup>6,7</sup> Fecal samples (January 1995)<sup>6</sup> were taken from 88 pigs previously housed in the barn that housed the cohort sampled in the present study. We isolated *Salmonella* Typhimurium, *Salmonella* Typhimurium (Copenhagen), *Salmonella* Muenster, *Salmonella* Mbandaka, and *Salmonella* Worthington from those samples.

## Facilities

The finishing farm chosen was one of four finishing sites in a multisite production system that has been described elsewhere.<sup>7</sup> At this finishing site, approximately 4000 pigs were housed in six barns with 32 pens per barn (two rows of 16 pens with a central aisle) and about 20 pigs per pen. The pigs were housed on fully slotted concrete floors with feed and water supplied ad libitum. The pits under the floors were flushed with recycled lagoon water. Individual barns at the finishing site were filled consecutively from a nursery room at weekly intervals, such that the age of the pigs at the finishing sites typically ranged over 6 weeks. Therefore, the finishing site was managed AIAO by barn, with common lagoons and labor. In the present study, samples were taken only from the barn housing the study cohort (“cohort barn”) and from three other randomly selected barns on this site.

## Sampling

The time frame for sample collection was as follows:

- 5/30/96: As part of a preceding study,<sup>7</sup> 32 pigs from the nursery room from which the cohort group originated were sampled. Another 64 individual pig fecal samples and 11 pooled pen fecal samples were collected from other rooms at the nursery on that day.
- 6/17/96 (day 0): One day before the cohort was moved into the cohort barn (day 0), we conducted cross-sectional sampling of pigs remaining in the three other barns at the finishing site.<sup>7</sup> On day 0 of the study, the cohort barn had been emptied, cleaned, and disinfected, and was due to receive pigs from the nursery the following day. Samples (n = 26) from the surface of the pen floors in the cohort barn were collected using drag swabs moistened with buffered peptone water.<sup>8</sup> Mouse traps were placed along the walls inside the pens.
- 6/18/96 (day 1): the cohort barn was filled with 10-week-old pigs, all from one room in the nursery.
- 6/19/96 (day 2):
  - Fecal samples (approximately 10–15 g) were collected from 41 individually selected and ear-tagged pigs in the cohort barn. Pigs in every fourth pen were sampled (total of eight pens), starting from the third pen on the north side of the barn. Within the eight selected pens, five pigs were chosen by convenience without formal random sampling (in one pen, an additional pig was mistakenly sampled and tagged).
  - Pooled fecal samples (pooling four to six samples, each about 3–8 g, yielding approximately 25 g of feces per pen) were collected from 31 of 32 pens (one pen was left empty as a sick pen and never sampled).
  - Feed samples were collected from the top of the feeders where pigs did not have direct access.
  - Mousetraps were removed from the pens.
- 7/25/96 (day 37) and 9/4/96 (day 78): Sampling of individually identified pigs, pooled feces from pens, and feed was repeated in the cohort barn.

## Bacteriologic culture

To detect *Salmonella* organisms, fecal and feed samples were diluted 1:9 by weight with 2% buffered peptone water (BPW) solution and

incubated overnight at 37°C. Drag swabs were similarly incubated after approximately 60 mL of BPW was added. A 0.1-mL aliquot of all diluted samples was transferred to 9.9 mL of Rappaport-Vassiliadis (RV) broth (Difco, Detroit, Michigan) and incubated in a water bath at 42°C for 24 hours.

For all samples, a loopful of incubated RV broth was streaked on xylose-lysine-tergitol 4 agar (Difco) and modified brilliant green agar (Oxoid, Basingstoke, Hampshire, England) plates, which were incubated overnight at 37°C. Colonies suspected of being *Salmonella* spp. were transferred to triple-sugar-iron and urea agars. Isolates presumptively identified as *Salmonella* spp. were forwarded to the National Veterinary Services Laboratory (Ames, Iowa) for serotyping.

## Results

### Data obtained prior to cohort placement

None of 32 individual samples collected in the nursery from the piglets destined for the cohort barn were positive for *Salmonella*. However, six of 64 (9%) individual samples, and three of 11 (27%) pooled fecal samples from other rooms at the nursery site were positive for *Salmonella*. *Salmonella* Derby was found in three of the six rooms sampled. *Salmonella* Mbandaka was the other serotype isolated (Table 1).

On day 0 of the study, seven of 26 (27%) drag swabs of the floors in the cohort barn were positive for *Salmonella*. *Salmonella* Mbandaka (six isolates) and *Salmonella* Typhimurium (Copenhagen) (one isolate) were the serotypes identified (Table 1). A variety of *Salmonella* serotypes were also identified in the other barns sampled at the finishing site on day 0 (Table 1).

### Data obtained after cohort placement

No rodents were trapped in the barn.

On day 2, four of 32 (13%) feed samples were positive (*Salmonella* Heidelberg). All subsequent feed samples were culture negative (Table 2).

On all three sampling days (days 2, 37, and 78) during finishing, *Salmonella* were detected in both individual and pooled pen fecal samples (Table 2). Serotype profiles obtained from individual animal samples and pooled pen samples generally corresponded closely. Notably, *Salmonella* Derby was the predominant serotype in fecal samples (individual and pooled) 24 hours after placement (20 of 34 isolates; 59%) and *Salmonella* Typhimurium, which was not found in the day 2 samples, was the predominant serotype (28 of 34 isolates; 82%) in the day 78 sampling.

## Discussion

Two observations in this study are notable. First, there was a marked disparity between the prevalence of *Salmonella* observed in the cohort while it was in the nursery (0%) and that observed 24 hours after the cohort arrived at the finishing site 18 days later (46% of individual pigs). Possible explanations, which are not mutually exclusive, include:

- infection spread through the cohort group after sampling at the

**Table 1***Salmonella* organisms isolated at the nursery and finishing sites before placement of the cohort pigs

Date	Sampling location	Sampling method	Number of samples	Number positive (%)	<i>Salmonella</i> serotypes (n)
1/4/95	Cohort barn	individual 25g fecal samples	88	25 (28%)	Typhimurium (12), Typhimurium (Copenhagen) (7), Muenster(4), Mbandaka (1), Worthington (1)
5/30/96	Cohort nursery room	individual 10g fecal samples	32	0	—
5/30/96	Other nursery rooms	individual 10g fecal samples	64	6 (19%)	Derby (5), Mbandaka (1)
5/30/96	Other nursery rooms	pooled 25g fecal samples	11	3 (27%)	Derby (3)
6/17/96 (Study day 0)	Cohort barn	floor swab samples	26	7 (27%)	Mbandaka (6), Typhimurium (Copenhagen) (1)
6/17/96 (Study day 0)	Other barns at finishing site	individual 10g fecal samples	96	12 (12.5%)	Typhimurium (1), Typhimurium (Copenhagen) (7), Derby (1), multiple serotypes (3)

**Table 2***Salmonella* organisms isolated from fecal samples of individual pigs, pooled pen fecal samples and feed samples in cohort barn

Sampling method	Sample date (study day)	Number of samples	Number positive (%)	<i>Salmonella</i> serotypes (n)
individual 10g fecal samples	6/19/96 (2)	41	19 (46%)	Derby (12), Mbandaka (4), Typhimurium (Copenhagen) (2), Heidelberg (1)
	7/25/96 (37)	41	8 (20%)	Derby (4), Typhimurium (Copenhagen)(4)
	9/4/96 (78)	32	16 (50%)	Typhimurium (14), Derby (2)
pooled 25g fecal samples	6/19/96 (2)	31	15 (48%)	Derby (8), Mbandaka (6), Heidelberg (1)
	7/25/96 (37)	31	18 (58%)	Derby (8),Typhimurium (5), Typhimurium (Copenhagen)(2), Mbandaka(1)
	9/4/96 (78)	31	18 (58%)	Typhimurium (14), Typhimurium (Copenhagen)(2), Derby (2)
10g feed samples from cohort barn	6/19/96 (2)	31	4 (13%)	Heidelberg (4)
	7/25/96 (37)	31	0	—
	9/4/96 (78)	31	0	—

nursery and prior to transport to the finisher;

- increased prevalence of fecal shedding resulted from handling and transport, leading to increased pig-to-pig transmission during and after transport; and/or
- infection of the group occurred from a contaminated transport vehicle or after arrival at the finishing site.

The fact that *Salmonella* Derby (the predominant serotype found at the nursery) was also the predominant serotype found 24 hours after the cohort was placed at the finishing site favors the first two explanations. Although not found in the 32 pigs from the cohort room sampled at the nursery, *Salmonella* Derby was the predominant serotype in other rooms at the nursery site. However, *Salmonella* Derby had also been isolated from one of the other barns at the finishing site the day

before placement. We cannot rule out the possibility that widespread infection of the group with *Salmonella* Derby may have occurred late in the nursery phase. However, the phenomenon of increased detection of *Salmonella* after transport of pigs is well documented,<sup>9,10</sup> although the mechanisms involved are not understood. We have observed comparable increases in prevalence (<5% before transport to approximately 50% post-transport) of detectable fecal shedding of *Salmonella* in two groups of gilts after arrival at a breeding farm (Davies PR, et al. *Proceedings*, NPPC Pork Quality & Safety Summit, Des Moines IA, 1998, 41–46). Multisite production systems inherently involve transport of pigs among sites. It is feasible that effects of transport on fecal shedding of *Salmonella* by pigs, resulting in an elevated risk of pig-to-pig transmission, may be a crucial component of the

epidemiology of *Salmonella* infection in multisite systems.

The second notable feature of this study was the pronounced shift in serotype profile, from *Salmonella* Derby to *Salmonella* Typhimurium, observed during the finishing phase. *Salmonella* Typhimurium and *Salmonella* Typhimurium (Copenhagen) were the predominant serotypes found in previous samplings of the finishing site (Table 1). However, neither of these serotypes was detected in sampling of the nursery and breeding farms in this system during May and June 1996.<sup>6</sup> It appears that infection earlier in life with *Salmonella* Derby was succeeded by infection with *Salmonella* Typhimurium during the finishing phase, such that the latter serotype predominated in pigs approaching market age. Evidence for this changing pattern was consistent for both individual pig fecal samples and pooled pen samples. This suggests that both sampling approaches (individual pig and pooled pen samples) provided reasonable point estimates of the predominant serotypes in the barn.

The presence of multiple serotypes of *Salmonella* appears to be common in finishing pig populations in the United States (Bush E. *Proc Livestock Cons Inst*, Kansas City, MO, 1996, 207–208),<sup>6</sup> which probably reflects multiple sources of infection. Our observations support that residual floor contamination (*Salmonella* Mbandaka, *Salmonella* Typhimurium [Copenhagen]) and feed (*Salmonella* Heidelberg) were potential sources of infection for this group during the finishing phase. Given the modest intensity of sampling of the floors and feed, it is highly probable that other serotypes were present but not detected in these sources. *Salmonella* Typhimurium, isolated from one of the other barns at the site on day 0, emerged as the dominant serotype as the pigs approached market age. However, we wish to emphasize that failure to detect *Salmonella* Derby in most pigs in the final sampling does not indicate that the previously infected pigs did not continue to harbor the organism. Studies of *Salmonella* infections of pigs indicate that fecal shedding declines over time,<sup>1,11</sup> and animals harboring *Salmonella* may often yield negative results on fecal culture. Individual pigs often harbor more than one *Salmonella* serotype simultaneously.<sup>9,12,13</sup> In addition, serotype profiles of market-age hogs are likely to be biased towards the serotypes that have most recently infected the animals. Thus, although studies based on fecal sampling of hogs on farms may well point to a relatively minor role of upstream infection as a determinant of *Salmonella* infection of market age hogs (i.e., biased towards detecting more recent infections), infection occurring early in the life of pigs may still represent a significant risk to food safety (as the gastrointestinal tracts of previously infected, fecal-negative pigs often will constitute a contamination hazard after transport and lairage).

Dutch and Danish studies conducted predominantly in two-site (farrow-to-feeder/finishing) systems have indicated that upstream infection (pigs infected before arriving at finishing farms) may be a

relatively unimportant source of *Salmonella* infection of finished hogs.<sup>1,4</sup> Our cross-sectional study<sup>7</sup> and this longitudinal study of this multisite system in North Carolina are consistent with the European results. If upstream infection is truly of minor importance, it implies that control measures instituted in the finisher phase of multisite systems should have the greatest impact in reducing the risk of carcass contamination with *Salmonella* at slaughter. Further longitudinal studies are required to define the complex epidemiology of *Salmonella* infection in multisite systems, and to determine appropriate interventions for reducing the risk of transmission.

## Implications

- Point prevalence estimates of *Salmonella* shedding and serotypes may vary markedly during the finishing phase.
- *Salmonella* infection of growing pigs during the finishing phase is more relevant to food safety than infection at the breeding and nursery sites.
- There is a need for more intensive longitudinal studies of *Salmonella* in multisite systems, including investigating the role of transporting pigs among sites.

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