Sub-Iliac Lymph Nodes at Slaughter Lack Ability to Predict Salmonella enterica Prevalence for Swine Farms

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Sub-Iliac Lymph Nodes at Slaughter Lack Ability to Predict \textit{Salmonella enterica} Prevalence for Swine Farms

Bing Wang,\textsuperscript{1} Irene V. Wesley,\textsuperscript{2} James D. McKean,\textsuperscript{1} and Annette M. O'Connor\textsuperscript{1}

Abstract

The aim of this study was to assess the value of deep systemic sub-iliac lymph nodes collected at slaughter as predictors of \textit{Salmonella} prevalence in live hogs. An observational study was conducted on 24 farms from September 2006 to February 2009. At least one cohort of market-weight pigs was visited for each farm. Within each cohort, 30 farm fecal samples on farm and 30 sub-iliac lymph nodes from matched pigs at slaughter were collected. Samples were cultured for \textit{Salmonella enterica} and serotyped by conventional methods. Overall, 3.4\% (51 of 1490) of farm feces and 0.06\% (1 of 1739) of sub-iliac lymph nodes were \textit{Salmonella} positive; 71.4\% (15 of 21) of farms had at least one positive fecal sample, and 4.2\% (1 of 24) had at least one positive sub-iliac lymph node. The median within-farm prevalence of \textit{Salmonella} in farm fecal samples was 1.7\%, ranging from 0\% to 38.3\%; for sub-iliac lymph nodes the median was 0\%, ranging from 0\% to 1.1\%. The median within-cohort prevalence in farm fecal samples was 0\%, ranging from 0\% to 43.3\%; for sub-iliac lymph nodes the median was 0\%, ranging from 0\% to 4\%. The predominant serotype detected was Derby, followed by Anatum and Typhimurium (Copenhagen). \textit{Salmonella} Braenderup was recovered from the sub-iliac lymph node. The low detection rate of \textit{Salmonella} in sub-iliac lymph nodes (0.06\%) limits its usefulness as a dependable predictor of \textit{Salmonella} contamination originating on farm (3.4\%).

Introduction

\textit{Salmonella enterica} are major human foodborne pathogens causing gastroenteritis (Tokumaru et al., 1990), resulting in an estimated 1.4 million cases and 500 deaths annually in the United States (Mead et al., 1999). In several foodborne disease outbreak investigations, pork has been identified as a source for human salmonellosis (Molbak and Hald, 1997; Delpech et al., 1998; Pontello et al., 1998; Murase et al., 2000). In Europe, \textit{Salmonella enterica} is a frequently reported pathogen correlated with pork consumption (Fosse et al., 2008). The most efficient interventions to reduce foodborne diseases likely occur postharvest, including carcass-processing practices and proper food storage, handling, and preparation. However, responsibility for a wholesome product extends beyond retailers and packers to pork producers. Key to applying preharvest interventions at the farm level to reduce \textit{Salmonella enterica} is rapid and accurate identification methods for candidate farms suitable for interventions.

Serological testing of diaphragm muscle meat juice samples for antibodies to \textit{Salmonella} has been used by several countries to identify farms likely to have a high prevalence of \textit{Salmonella}, and therefore candidates for preharvest interventions (Mousing et al., 1997; Osterkorn et al., 2001; Quirke et al., 2001). The U.S. pork industry has not adopted the on-farm \textit{Salmonella} control programs employed by European programs. Diaphragm muscle meat juice samples have a significant advantage over other approaches, as samples can be collected at harvest (Nielsen et al., 1998). Such a sampling method simplifies logistics and reduces costs, as many swine production sites are processed at a single abattoir daily. Despite adoption by several countries, this approach is limited by the prevalence of \textit{Salmonella} antibodies in the tissues of the diaphragm and may be an imperfect monitor of \textit{Salmonella} prevalence beyond the carcass such as the farm level. This disconnect arises because antibodies persist long after infection has been cleared by the host (Nielsen et al., 1995; Casey et al., 2004). The gut-associated lymph nodes can also be readily collected at slaughter, but these tissues are poor predictors of on-farm \textit{Salmonella} status. The association is confounded by transient \textit{Salmonella} introduced into the gut from the lairage environment immediately before harvest (Hurd et al., 2001, 2002; Larsen et al., 2003).

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Prior studies have shown that the proportion of farms with a high *Salmonella* prevalence in the United States is low (O’Connor et al., 2006; McKeen and O’Connor, 2009); therefore, a strongly correlated screening test collected at slaughter must also have low prevalence. Limited small studies with relatively large variation in prevalence suggested that nongut-associated lymph nodes may be a candidate tissue for evaluation: 0% in 300 superficial cervical lymph nodes (Bahnson et al., 2006b); 0.4% (1 of 272); and 2% (4 of 181) in ventral thoracic lymph nodes and sub-iliac lymph nodes (Hurd et al., 2001; Larsen et al., 2003). On the basis of these data, sub-iliac lymph nodes were selected as the tissue for evaluation as a screening tool as these tissues are rarely positive and easy to collect.

The objective of this study was to evaluate the predictive value of deep systemic sub-iliac lymph nodes, tissues that are easily collected at harvest either during carcass processing or in the postharvest cooler. It was hypothesized that if there was a strong association between presence of *Salmonella* in sub-iliac lymph nodes and the prevalence of pigs shedding *Salmonella* in the feces, then deep systemic sub-iliac lymph nodes could serve as a readily accessible tissue for identifying farms with a high prevalence of *Salmonella*. Easier identification of farms with a high prevalence of *Salmonella* would facilitate research and screening programs. Therefore, this tissue could be an alternative to the current screening tool for *Salmonella* on-farm control programs, not associated with antibodies and gut-associated lymph nodes.

**Materials and Methods**

**Study population**

This study was conducted in compliance with guidelines detailed in the Iowa State University Committee for Animal Care No. 5-05-5897-S application.

Candidate farms were identified based on geographic location. The project was described to owners/managers of 130 premises who were invited to participate. In the year before the study, these 130 premises slaughtered between 8 and 103,000 swine, with an average of 3200 swine. Twenty-seven premises in the U.S. Midwest agreed to participate. For owners/managers who declined to participate, no further contact was made. For owners who agreed to participate the next step in enrollment was to identify when the producers would ship pigs to the study abattoir during the study period of September 2006 to February 2009.

Once a farm had notified the team that a cohort of pigs was ready for slaughter, a farm visit was scheduled. At the farms, sampling frames were not available; therefore, a formal random selection process was not used to identify study units. Instead, before selecting animals, farm staff marked those to be marketed, and the team walked the barn and selected marked animals based on convenience. The team was instructed to sample from multiple pens, excluding recumbent pigs.

The slaughter plant used in the present study has a capacity of 17,000 hogs per day. Processing steps included CO₂ euthanasia, bleeding, stunning, scalding, dehairing, singeing, polishing, evisceration, decapitation, washing, and blast chilling of carcass halves upon entry to the cooler.

**Sampling**

One to three days before slaughter, farm fecal samples (around 10 g) were collected from the rectum of 30 pigs by digital extraction and left on the gloves that were placed in a WhirlPak bag (Nasco, Ft. Atkinson, WI). Sterile gloves for collecting the feces were changed between pigs. The study pigs were tattooed on the left flank with a unique code that enabled tracking and identification at the plant. The pigs were shipped to slaughter using normal marketing channels. At the abattoir, the pigs were held in a pen until slaughter that same day. Sub-iliac lymph nodes were collected from the tattooed carcasses after blast chilling in the cooler room, using a sterile scalpel and placed in sterile tubes. Further, from June 2007 a second set of matching sub-iliac lymph nodes were collected immediately after the decapitation point, from the carcasses while they were still on the processing rail. The additional samples were collected to increase the opportunity to obtain sub-iliac lymph nodes matching with farm fecal samples. All samples were refrigerated on wet ice and transported to the lab where they were refrigerated until processing the next day. Samples were expected to be collected from four cohorts of each farm.

**Salmonella determination**

Sub-iliac lymph nodes and fecal samples were cultured for the presence of *Salmonella enterica* as follows. Sub-iliac lymph nodes were surface sterilized by flaming, macerated in sterile bags (Nasco), combined with 25 mL phosphate-buffered saline, and homogenized for 1 min with a stomacher (Seward, Worthing, West Sussex, United Kingdom). Ten grams fecal samples or 10 mL aliquots from lymph node homogenates was added to 90 mL of tetrathionate broth (Tet, Remel Co., Philadelphia, PA) supplemented with novobiocin and incubated (24 h at 37 °C) (Gray et al., 1996; Hurd et al., 2002; Bahnson et al., 2006a); another 10 g fecal sample or 10 mL aliquot from lymph node homogenates was added to 90 mL buffer peptone water broth (Remel Co., Philadelphia, PA) supplemented with novobiocin and incubated (24 h at 42 °C) (Taft, 1966; Smyser and Snoeyenbos, 1969; Davies et al., 2000; Love and Rostagno, 2008). One hundred microliters each of Tet and buffer peptone water broth preenrichment culture was inoculated into 9 mL of Rappaport-Vassiliadis R 10 broth (BD Co., Franklin Lakes, MD) and incubated (24 h at 42 °C). Rappaport-Vassiliadis R 10 broth samples were streaked for isolation both on Xylose-Lysine-Tergitol™ 4 agar (BD Co.) and Brilliant Green agar (BD Co.). After 24 h of growth at 37 °C, one colony per plate exhibiting morphology typical of *Salmonella* was inoculated to Triple Sugar Iron slant (BD Co.) and Lysine Iron slant (Oxoid, Basingstoke, Hampshire, United Kingdom), and incubated (24 h at 37 °C). Isolates with characteristic *Salmonella* reactions in Triple Sugar Iron slant (alkaline slant, acid butt, and gas with H2S) and Lysine Iron slants (alkaline with H2S) were verified by *Salmonella* O Antiserum Poly A-I and Vi (BD Co.).

All suspect *Salmonella* isolates were sent to the National Veterinary Services Laboratories for serotyping (USDA NVSL, Ames, IA). Samples were classified as positive or negative based on serotyping results. In this article, *Salmonella enterica* subsp. *enterica* is abbreviated *Salmonella*, followed by the serotype name. For example, *Salmonella enterica* subsp. *enterica* serotype Derby is designated *Salmonella* Derby.

**Quality control procedures**

Several quality control procedures were employed during the study. Throughout the entire project a set of known
positive and known negative ground pork samples were included with each batch of samples being processed. Further, a group of known positive and known negative ground pork samples were randomly ordered, sequentially numbered, and referred to as the blinded control set. The master key identifying these blind controls was maintained by staff not performing the culture steps. Each week the laboratory staff selected the next blinded control in the sequence for inclusion with the farm samples, the abattoir samples, and the known positive and negative samples. Each week after the blinded sample had been processed, the outcome of the culture of that sample was compared to the key. Positive samples were spiking with ATCC 14028 *Salmonella* Typhimurium with a final concentration of 10 cfu per mL. The number of colony-forming units of *Salmonella* per mL in these samples after enrichment was not determined.

Because of the large number of negative samples noticed in the early stages of the project, several steps were taken during the process to verify the culture results. Six hundred and ninety-six samples were sent to another laboratory for polymerase chain reaction (PCR) determination of *Salmonella* status over 10 weeks from 4/14/08 to 08/28/08 using the BAX® system PCR for *Salmonella* (Bennett et al., 1998; Franchin et al., 2006). The BAX system PCR for *Salmonella* is reported to reliably detect $10^4$ cfu per mL in enriched samples (DuPont Qualicon BAX System, PCR assay for *Salmonella* product description). Of these 696 samples, 265 were gut-associated lymph nodes collected for another purpose. These samples were included in the quality control samples as they were more likely to be positive based on prior research (Hurd et al., 2001; Bahnson et al., 2006b) and therefore suitable for assessing detection ability of *Salmonella* in lymph node tissue using culture method compared with PCR detection. The other 431 were sub-iliac lymph node samples from both processing and cooler.

**Data analysis**

For each farm, the percentages of positive farm fecal samples and positive lymph nodes were calculated. Further, the percentages of positive fecal and lymph node sample were calculated using only those animals for which on-farm and at-slaughter matched data were available. The average farm level and slaughter cohort prevalence of *Salmonella* and corresponding 95% confidence interval (CI) were also calculated. The proposed analysis was a correlation analysis using Pearson correlation, that is, the proportion of positive samples in farm feces regressed against the proportion of positive samples in the lymph nodes. Two units of analyses were planned, the farm and the slaughter cohort. The correlation analysis used all samples, not just matched samples.

**Results**

**Results of quality control comparison between PCR and microbiological culture method**

No blinded controls were misidentified during the study period. Of the 265 gut-associated lymph node samples tested both by culture method and PCR, 25 of 265 were positive by PCR detection and 19 of 25 were positive based on culture method. A higher number of PCR-positive results may have been due to the presence of DNA from dead or nonculturable cells (Bennett et al., 1998). PCR and cultural methods for 431 sub-iliac lymph nodes resulted in 100% *Salmonella*-negative samples, suggesting that the cultural method utilized in this study was as sensitive as PCR for *Salmonella* detection. During the time prechill and postchill samples were collected, there was 100% agreement between both methods; that is, all samples were negative.

**Salmonella prevalence and serotypes**

Of the 27 farms that agreed to participate, three subsequently declined as they were unable to provide pigs to the requested abattoir at the time required. Twenty-four farms with 50 slaughter cohorts (1–4 cohorts per farm) were visited to collect farm fecal samples. The final dataset included fecal samples from 21 farms and sub-iliac lymph nodes from 24 farms. Results from fecal samples were missing from two farm visits (Farm 1 and 4) because the original study design proposed testing fecal samples from lymph-node-positive farms only. Later this approach was modified and all farm fecal samples were cultured regardless of lymph node status. Results from fecal cultures from the other farm (Farm 22) were excluded as processing errors resulted in lost sample identification. After slaughter, carcasses from within a cohort were lost to follow-up for the following reasons: “railed” off during processing, not placed on correct rail in the cooler, sample could not be collected from a hot carcass sample due to the rail speed, and sample missing due to the routine in-plant carcass “cleaning” process to remove extraneous materials.

Farm fecal samples ($n = 1490$) and sub-iliac lymph node samples ($n = 2621$) from 1739 carcasses (961 sub-iliac lymph nodes from carcasses during processing and 1660 sub-iliac lymph nodes from chilled carcasses) were processed, for an average 71 farm feces and 109 sub-iliac lymph nodes from 72.5 carcasses per farm. Not all the farm feces and sub-iliac lymph nodes were matched. Sub-iliac lymph nodes were harvested from pigs of 24 farms with 69 cohorts (1–4 cohorts per farm). In the year prior to the study, these 24 premises slaughtered between 1684 and 102,840 swine, with an average of 14,883 swine slaughtered per farm. Individual animal-matched fecal samples and lymph nodes were collected from 1337 animals/carasses from 50 cohorts of 21 farms.

*Salmonella* were detected in 51 of 1490 fecal samples (3.4%; 95% CI: 2.6–4.5%) and in a single lymph node sample from the 1739 carcasses (0.06%; 95% CI: 0.01–0.3%). One or more *Salmonella*-positive isolates in feces were identified from pigs on 15 of 21 farms (71.4%; 95% CI: 49.8–86.1%) and 20 of 50 cohorts (40%; 95% CI: 27.4–53.9%). *Salmonella* was detected in one sub-iliac lymph node from 1 of 24 farms (4.2%; 95% CI: 1.0–20.3%) and 1 of 69 cohorts (1.4%; 95% CI: 0.3–7.7%).

*Salmonella* prevalence in all fecal samples and sub-iliac lymph nodes and matched samples are summarized for farm and cohort level in Table 1. The *Salmonella* prevalence in farm feces and sub-iliac lymph nodes for individual farm and cohort is shown in Table 2. The median within-farm prevalence was 1.7% for fecal samples (range: 0%–38.3%) and 0% for sub-iliac lymph nodes (range: 0%–1.1%), and median within-cohort prevalence was 0% from fecal samples (range: 0%–43.3%) and 0% for sub-iliac lymph nodes (range: 0%–4%).

We were able to match farm feces and sub-iliac lymph node samples for 1337 animals from 21 farms and 50 slaughter...
coyghs. For the matched animals, *Salmonella* was detected in 48 of 1337 fecal samples (3.6%; 95% CI: 2.7–4.7%) and in 1 of 1337 lymph nodes (0.07%; 95% CI: 0.02–0.4%). For the matched animals, the median within-farm prevalence of *Salmonella* was 1.9% for fecal samples (range: 0%–40.4%) and 0% for lymph nodes (range: 0%–1.1%). For the 50 slaughter cohorts, the median prevalence of *Salmonella* was 0% for fecal samples (range: 0%–44.8%) and 0% for lymph nodes (range: 0%–4%).

High serotype diversity was detected (15 serotypes overall, 14 in farm feces and 1 in lymph nodes; Table 3). *Salmonella* Derby was the predominant serotype in farm feces (15 of 52 [28.8%; 95% CI: 18.3–42.3%], followed by *Salmonella Anatum* (7 of 52 [13.5%]; 95% CI: 6.7–25.3%) and *Typhimurium* (Copenhagen) (7 of 52 [13.5%; 95% CI: 6.7–25.3%). The only *Salmonella*-positive sub-iliac lymph node yielded *Salmonella Braenderup*.

### Table 2. The Prevalence of *Salmonella enterica* in Farm Feces (n = 21 Farms) and Sub-Iliac Lymph Nodes (n = 24 Farms)

<table>
<thead>
<tr>
<th>Farm</th>
<th>*Salmonella prevalence in farm feces, positive/tested (%)</th>
<th>*Salmonella prevalence in sub-iliac lymph nodes, positive/tested (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>NA</td>
<td>0/83 (0)</td>
</tr>
<tr>
<td>2</td>
<td>3/59 (5.1, 1.8–13.9)</td>
<td>0/106 (0)</td>
</tr>
<tr>
<td>3</td>
<td>2/60 (3.3, 1.0–11.3)</td>
<td>0/110 (0)</td>
</tr>
<tr>
<td>4</td>
<td>NA</td>
<td>0/76 (0)</td>
</tr>
<tr>
<td>5</td>
<td>0/60 (0)</td>
<td>0/74 (0)</td>
</tr>
<tr>
<td>6</td>
<td>0/30 (0)</td>
<td>0/76 (0)</td>
</tr>
<tr>
<td>7</td>
<td>0/90 (0)</td>
<td>0/107 (0)</td>
</tr>
<tr>
<td>8</td>
<td>1/30 (3.3, 0.8–16.7)</td>
<td>0/48 (0)</td>
</tr>
<tr>
<td>9</td>
<td>2/120 (1.7, 0.5–5.8)</td>
<td>0/68 (0)</td>
</tr>
<tr>
<td>10</td>
<td>23/60 (38.3, 27.1–51.0)</td>
<td>0/82 (0)</td>
</tr>
<tr>
<td>11</td>
<td>1/60 (1.7, 0.4–8.8)</td>
<td>0/53 (0)</td>
</tr>
<tr>
<td>12</td>
<td>2/119 (1.7, 0.5–5.9)</td>
<td>0/108 (0)</td>
</tr>
<tr>
<td>13</td>
<td>2/120 (1.7, 0.5–5.8)</td>
<td>1/91 (1.1, 0.3–5.9)</td>
</tr>
<tr>
<td>14</td>
<td>1/120 (0.8, 0.2–4.5)</td>
<td>0/101 (0)</td>
</tr>
<tr>
<td>15</td>
<td>1/29 (3.5, 0.8–17.2)</td>
<td>0/52 (0)</td>
</tr>
<tr>
<td>16</td>
<td>0/30 (0)</td>
<td>0/53 (0)</td>
</tr>
<tr>
<td>17</td>
<td>0/117 (0)</td>
<td>0/101 (0)</td>
</tr>
<tr>
<td>18</td>
<td>0/90 (0)</td>
<td>0/69 (0)</td>
</tr>
<tr>
<td>19</td>
<td>4/57 (7.0, 2.9–16.7)</td>
<td>0/52 (0)</td>
</tr>
<tr>
<td>20</td>
<td>1/119 (0.8, 0.2–4.6)</td>
<td>0/106 (0)</td>
</tr>
<tr>
<td>21</td>
<td>3/60 (5.0, 1.8–13.7)</td>
<td>0/51 (0)</td>
</tr>
<tr>
<td>22</td>
<td>NA</td>
<td>0/21 (0)</td>
</tr>
<tr>
<td>23</td>
<td>2/30 (6.7, 2.0–21.4)</td>
<td>0/24 (0)</td>
</tr>
<tr>
<td>24</td>
<td>3/30 (10.0, 3.6–25.8)</td>
<td>0/27 (0)</td>
</tr>
</tbody>
</table>

NA indicates data not available because original study design proposed testing fecal samples from lymph-node-positive farms only or because of processing errors in lab.

*Correlation between Salmonella contamination in live animals on farm and in carcasses at slaughter*

The planned correlation analysis between *Salmonella* prevalence in farm feces and in sub-iliac lymph nodes was not conducted due to the limited number of positive samples. The fecal sample from the animal with the only *Salmonella*-positive sub-iliac lymph node sample was *Salmonella*-negative on the premises, Farm 13. The average *Salmonella*-fecal-positive prevalence at Farm 13 (1.7%) was lower than the average prevalence of the 21 enrolled farms (3.4%). There was no evidence of an association detected between the *Salmonella* contamination of deep systemic sub-iliac lymph nodes and from farm feces.

### Discussion

We had hypothesized that if there was a strong association between the presence of *Salmonella* in sub-iliac lymph nodes and the prevalence of on-farm *Salmonella* shedding in the feces, then this readily collected tissue might be a useful screening tool. We chose to study these tissues, as prior studies had shown that the number of high prevalence *Salmonella* farms in the United States is low, and therefore a screening tissue collected at slaughter must also have low *Salmonella* prevalence, if the correlation was to be strong. However, the prevalence of 0.06% from 1739 carcasses was too low and suggests that this tissue is not a candidate for
Table 3. Salmonella Serotypes Found in Sampled Farm Feces and Sub-Iliac Lymph Nodes

<table>
<thead>
<tr>
<th>Rank</th>
<th>Serotype</th>
<th>Farm feces</th>
<th>Sub-iliac lymph nodes</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Number of overall</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>positive isolates</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>% Positive</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>(n = 52)</td>
<td>% Positive</td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>Derby</td>
<td>15</td>
<td>28.8</td>
</tr>
<tr>
<td>2</td>
<td>Anatum</td>
<td>7</td>
<td>13.5</td>
</tr>
<tr>
<td>2</td>
<td>Typhimurium (Copenhagen)</td>
<td>7</td>
<td>13.5</td>
</tr>
<tr>
<td>4</td>
<td>Agona</td>
<td>5</td>
<td>9.6</td>
</tr>
<tr>
<td>5</td>
<td>Typhimurium</td>
<td>4</td>
<td>7.7</td>
</tr>
<tr>
<td>6</td>
<td>Uganda var. 15+</td>
<td>3</td>
<td>5.8</td>
</tr>
<tr>
<td>7</td>
<td>Infantis</td>
<td>2</td>
<td>3.8</td>
</tr>
<tr>
<td>7</td>
<td>Uganda</td>
<td>2</td>
<td>3.8</td>
</tr>
<tr>
<td>9</td>
<td>4,5,12: poorly motile</td>
<td>1</td>
<td>1.9</td>
</tr>
<tr>
<td>9</td>
<td>Livingstone</td>
<td>1</td>
<td>1.9</td>
</tr>
<tr>
<td>9</td>
<td>Mbandaka</td>
<td>1</td>
<td>1.9</td>
</tr>
<tr>
<td>9</td>
<td>Newport</td>
<td>1</td>
<td>1.9</td>
</tr>
<tr>
<td>9</td>
<td>Worthington</td>
<td>1</td>
<td>1.9</td>
</tr>
<tr>
<td>9</td>
<td>Braenderup</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>9</td>
<td>Salmonella untypable</td>
<td>1</td>
<td>1.9</td>
</tr>
</tbody>
</table>

*The overall positive isolates are from both Salmonella-positive farm fecal and sub-iliac lymph node samples.

Screening swine at slaughter to identify farms with a high prevalence of Salmonella. Serotyping indicated that Derby was predominant, followed by Anatum and Typhimurium (Copenhagen), which is consistent with the serotype profile of the swine population in the United States (FSIS USDA, 2008). The only Salmonella isolated in systemic sub-iliac lymph node was Braenderup, which was not found in any farm feces. Salmonella Typhimurium is the major cause of human salmonellosis (Olsen et al., 1997; Fullerton et al., 2007). Salmonella Derby has been frequently associated with pork (Jayarao et al., 1990; Davies et al., 1997; Valdezate et al., 2005; Lomonaco et al., 2009), but not human infections.

Although other studies have correlated Salmonella prevalence on farm with abattoir-collected samples from naturally infected farms (Hurd et al., 2001, 2002; Korsak et al., 2003; Kranker et al., 2005; Larsen et al., 2003), the present study is unique because it matched individual pigs on the basis of fecal samples collected on farm with sub-iliac lymph node samples collected at slaughter. To the best of our knowledge, this type of individual animal sample matching in Salmonella and swine-production-related research has not been reported previously.

Our objective was to determine if sub-iliac lymph nodes represent a readily accessible tissue that could be used for accurate identification of high-prevalence Salmonella farms. This study suggests that it is not the case since only 0.06% sub-iliac lymph nodes harbored Salmonella. The single isolation of Salmonella in sub-iliac lymph nodes precludes a statistically valid hypothesis test. As shown in this study, although a total of 2621 sub-iliac lymph node samples from 1739 carcasses were tested, the one positive isolate in sub-iliac lymph node was quantitatively inadequate to determine the on-farm and at-slaughter association. However, given the large number of samples tested, the use of multiple farms, with multiple slaughter cohorts and the laboratory quality control system utilized, we conclude that since sub-iliac lymph nodes are rarely Salmonella culture positive, they are not appropriate candidates for surveillance as a means to assess safety and quality of meat or meat products for the consumer food chain.

Conclusions

The low frequency of Salmonella in sub-iliac lymph nodes suggests that these samples are not useful predictors of Salmonella contamination on farm under the conditions evaluated.

Acknowledgments

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Disclaimer

Mention of trade names or commercial products in this article is solely for the purpose of providing specific information and does not imply recommendation or endorsement.

Disclosure Statement

No competing financial interests exist.

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