Industry Summary:

The objectives of this study were three-fold: (i) develop a national estimate for peelout prevalence in swine carcasses, (ii) determine if common respiratory pig pathogens are associated with peelouts (specifically *Streptococcus suis*, *Pasteurella multocida*, *Bordetella bronchiseptica*, *Actinobacillus suis*, *Actinobacillus pleuropneumoniae*, and *Haemophilus parasuis*) and (iii) determine if peelouts are associated with *Salmonella* contamination. Six abattoirs were selected from different geographical areas of the United States, and samples were evaluated at two time periods. At each abattoir visit, 50 lesioned (peel-out present) and 50 non-lesioned (peel-out absent) carcasses were sampled. Lung samples and pleural swabs were taken from each carcass. A standard bacteriological identification and culture was performed. A national prevalence estimate was obtained. Peelout prevalence ranged from 2.64% to 28.39%, with an average of 9.78% (95% CI 5.33% to 14.23%). Contamination rates for respiratory pathogens varied greatly, and there was no consistent pattern among lesioned/non-lesioned carcasses. The prevalence of respiratory contamination for lesioned and non-lesioned carcasses was as follows: *Streptococcus suis*, 5.45% to 50%, 0.04% to 56.76%, *Pasteurella multocida*, 0% to 33.33%, 0% to 42%, and *Bordetella bronchiseptica* 0% to 6.12%, 0% to 2.22%. *Salmonella* prevalence ranged from 0% to 23.53% in lesioned carcasses, and 0% to 16% in non-lesioned carcasses. While there appears to be little association between respiratory bacterial contamination and peelouts, these pathogens still play a significant role in swine health. While a significant association was not found between peelouts and *Salmonella* contamination in all abattoirs, the effect that peelouts can have on animal health and carcass contamination, and therefore public health, should not be ruled out. This is especially true in abattoirs that have a high *Salmonella* prevalence.

Keywords: *Salmonella*, peelout, prevalence, food safety, swine, abattoir, respiratory

Scientific Abstract:

The objectives of this study were three-fold: (i) develop a national estimate for peelout prevalence in swine carcasses, (ii) determine if common respiratory pig pathogens are associated with peelouts (specifically *Streptococcus suis*, *Pasteurella multocida*, *Bordetella bronchiseptica*, *Actinobacillus suis*, *Actinobacillus pleuropneumoniae*, and *Haemophilus parasuis*) and (iii) determine if peelouts are associated with *Salmonella* contamination. Six abattoirs were selected from different geographical areas of the United States, and samples were evaluated at two time periods. At each abattoir visit, 50 lesioned (peel-out present) and 50 non-lesioned (peel-out absent) carcasses were sampled. Lung samples and pleural swabs were taken from each carcass. A standard bacteriological identification and culture was performed. A national prevalence estimate was obtained. Association between *Salmonella* contamination and peelouts and respiratory pathogens and peelouts was analyzed using logistic regression, 1,228 carcasses were analyzed: 623...
lesioned carcasses and 605 non-lesioned carcasses. Peelout prevalence ranged from 2.64% to 28.39%, with an average of 9.78% (95% CI 5.33% to 14.23%). Contamination rates for respiratory pathogens varied greatly, and there was no consistent pattern among lesioned/non-lesioned carcasses. The prevalence of respiratory contamination for lesioned and non-lesioned carcasses was as follows: *Streptococcus suis*, 5.45% to 50%, 2.04% to 56.76%, *Pasteurella multocida*, 0% to 33.33%, 0% to 42%, and *Bordetella bronchiseptica* 0% to 6.12%, 0% to 2.22%. *Salmonella* prevalence ranged from 0% to 23.53% in lesioned carcasses, and 0% to 16% in non-lesioned carcasses. The association between *Salmonella* contamination and peelouts was not statistically significant, except in abattoirs with a higher prevalence of *Salmonella* contamination.

**Introduction:**

Healthy livestock are vital in ensuring food safety. With increased scrutiny being placed on management practices such as housing and antibiotic usage, it has become more important than ever to study how changes in these practices could affect animal health, and, in turn, affect public health.

Previous modeling in chickens has suggested that even small changes in animal health can have a significant impact on food safety, and therefore human health (Singer et al. 2007). However, this model was limited by a scarce amount of data available to obtain parameter estimates. This model also does not take into account the effect of post-harvest interventions on reducing bacterial contamination. Post-harvest interventions have been repeatedly shown to be effective in reducing bacterial contamination, thus bringing the validity of this assumption into question.

With 48 million illnesses annually attributable to foodborne pathogens, even small increases in illness rates can causes thousands of additional illnesses. According to CDC estimates, a 10% reduction in foodborne illness would result in 5 million less cases of foodborne illness nationwide annually (CDC 2011).

While there has been a reduction in human illnesses attributable to foodborne infectious agents such as *E. coli* from 1996-2012, illnesses attributable to *Salmonella* have remained steady over the same time period (CDC 2013). While found in many foods, meat and poultry continue to be common sources of *Salmonella* (Hald et al., 2007; Painter et al., 2013). Pork is not as likely as other meats to cause Salmonella illness; however its importance cannot be overlooked (Painter et al. 2013). According to estimates by Hald et al. (2007) 10.5% (95% CI 9.1%-11.9%) of clinical human *Salmonella* infections in Denmark could be attributed to pork. In the United States, this percentage was much less at <1% (Guo et al., 2011.) This may seem like a small percentage, however, with the millions of hogs slaughtered annually, (USDA, 2012a) it is still important to explore interventions to reduce the number of illnesses attributable to pork.

Animals can be asymptomatic carriers of the *Salmonella* bacteria, such as *Salmonella typhimurium*, and thus carry it off the farm (Lo Fo Wang et al., 2002). In addition to Salmonella, respiratory pathogens are common in swine herds. While clinically ill animals will not pass ante-mortem inspection, it is possible that animals with subclinical illness or lesions from previous illness could pass inspection and be harvested.

One type of lesion that could possibly harbor these respiratory pathogens is what is referred to as a peelout, or a pleural or peritoneal adhesion which does not allow for complete removal of the viscera. Mortem inspection procedures, if these peelouts are severe, they are often retained for further veterinary inspection (USDA-FSIS, 2012b).

A previous study found that for each percentage increase in carcass adhesions, the percentage of *Enterococcus* and *Campylobacter* went up 4.4% and 5.1% respectively (Hurd et al 2008.) Another study found that approximately 7% or 1 in 15 carcasses had some degree of pleural adhesions, and carcasses with peel-outs were 90% more likely to be contaminated with *Salmonella* (Hurd et al., 2012.)

To our knowledge, these are the only two studies conducted on peelouts in swine, and in each study the findings were isolated to one abattoir. No studies to our knowledge have been conducted examining which respiratory pathogens are associated with peelouts at slaughter. The hypothesis is that swine respiratory pathogens such as *Streptococcus suis*, *Pasteurella multocida*, *Actinobacillus pleuropneumoniae*, *Haemophilus parasuis*, *Actinobacillus suis* and *Bordetella bronchiseptica* may be associated with peelouts, as these pathogens are associated with pleuritis and respiratory illness (MacInnes, et al, 2008; Olson et al., 2001;
Brockmeier et al., 2001; Brockmeier, 2004; Mattoo et al., 2005; MacInnes et al., 1999).

The objectives of this project are to 1) estimate the prevalence of peelouts across the United States, 2) determine what common respiratory pig pathogens are more likely to be associated with peelouts, and 3) determine if peelouts are associated with an increase in food-borne pathogens (specifically *Salmonella*).

**Objectives:**
1. Estimate the national prevalence of peelouts in larger processing facilities.
2. Determine what pig respiratory pathogens are more highly associated with peelouts.
3. Determine if peel-outs are associated with an increase in food-borne pathogens (*Salmonella*).

**Materials & Methods:**

**Abattoir Selection**

A search was conducted on several swine companies to find the locations of large abattoirs in different geographical locations of the United States. After examining this data, a preliminary list was made of ten abattoirs. This list was then finalized down to six abattoirs: three in the Midwest, and one each in the South, East Coast, and West Coast. Originally the protocol called for only four abattoirs, but with additional funding, we were able to increase this number to six abattoirs, and chose to sample two additional abattoirs in the Midwest. Factors influencing what abattoirs were chosen included logistics, ease of contacting abattoir personnel, budget, and time constraints. Identifying information was omitted at the abattoirs’ request to protect confidentiality. Each abattoir was operated by a different company. All abattoirs were USDA inspected facilities, processing approximately 1,000 carcasses per hour. Samples were evaluated during two different time periods. The first sampling period went from December through April, while the second sampling period went from May through August. The rationale for two sampling time periods was to capture possible differences in peelout and pathogen prevalence for market hogs raised in the winter compared to summer months.

**Sample population**

At each abattoir, 100 market hogs total were selected for analysis: 50 lesioned carcasses (carcasses with peelouts) and 50 non-lesioned carcasses (carcasses without peelouts), for a total of 1,200 samples. Originally our protocol was to sample 25 lesioned and 25 non-lesioned carcasses at four abattoirs, for a total of 400 samples. This sample size was chosen as a previous study by Hurd et al. (2012) found a statistically significant relationship with a sample size of 358 carcasses. With additional funding, we were able to significantly increase our sample size. The hypothesis is that this increased sample size would allow for a better detection of a statistically significant relationship between peelouts and bacterial contamination.

**Sample collection**

Three non-experts (students and abattoir staff) conducted the sample collection and carcass characteristic identification, as a previous study by Hurd et al. (2012) determined that a non-expert assessment is adequate in identifying peelouts. Sample collection took place early in the morning to reduce the risk of abattoir cross-contamination. Whenever possible, sample collection took place at the beginning of the week, as Arguello et al. 2012 found that more cross-contamination was found at the middle and end of the work week versus the beginning of the work week. A possible reason for this difference in cross-contamination could be due to cleaning and disinfection procedures performed at the end of the work week.

To estimate the peelout prevalence at each plant, one student counted the total number of carcasses observed as well as the number of peelouts observed. This student also identified the carcasses with and without peelouts for sample collection, and labeled with either numbered tags or food-grade markers, depending on the individual abattoir’s preference. This student also recorded on a separate sheet if the carcass was a lesioned or non-lesioned carcass, allowing for blinding during bacteriological analysis.

From each selected carcass two sets of samples were collected: lung samples immediately after evisceration and pleural/peritoneal swabs from the interior of the carcass after the final trimming and before the final carcass wash and USDA inspection. Carcasses were selected haphazardly and separated by at least 10-15 non-selected carcasses. Sample collection was performed at the abattoir normal line speed so true random sampling was not feasible. The rationale for
the spacing of carcass selection was for two main reasons: to give the people collecting lung samples and pleural swabs adequate time between samples, and to minimize cross contamination. Furthermore, According to Berend et al. (1996), if the carcass following a Salmonella positive carcass is swabbed, that carcass is 28% likely to be positive for Salmonella as well. Additional research, Arguello et al. 2012 estimated that 50% of contaminated carcasses are a result of cross-contamination, whereas a study conducted by Bottledoorn et al. (2003) in Belgian abattoirs estimated that 29% of carcass contamination is due to cross-contamination. Therefore, it would be difficult to determine if the carcass was truly positive for Salmonella, or if the carcass was positive due to cross contamination.

To collect the lung samples for respiratory pathogen analysis a second person (either a student or staff member, depending on the abattoir’s preference) collected a piece of lung measuring approximately 5-10 cm in diameter from the corresponding viscera pan after the lesioned/non-lesioned carcass was identified. Because of the carcasses moving along at line speed, it was not possible to take a piece of lung from either each lung lobe or the same lobe each time. Scissors were dipped in either 180°F water or 70% alcohol after each sample was taken, depending on what was permitted at each abattoir.

For the pleural swab collection, 18 oz Whirl-Pak© bags with Speci-Sponge were used (Nasco, Ft. Atkinson, Wisconsin). Each sponge was hydrated with 10 ml of buffered peptone water (Thermo Scientific) one to two days before sample collection took place, and was kept refrigerated. This was done to help reduce the possibility of unwanted bacterial growth. After the final trimming and before the final carcass wash, both sides of the inside of the carcass were swabbed utilizing a zigzag motion in order to swab as much of the interior of the carcass surface area as possible. The exterior of the carcass is inspected according to FSIS inspection procedures (USDA-FSIS, 2012b). Gloves were changed after each swab to minimize the possibility of cross contamination. For quality control purposes and to minimize selection bias, lesioned and non-lesioned carcasses were selected in a haphazard pattern to blind the person doing the pleural/peritoneal swabs. Both sets of samples were kept on ice until they could be analyzed.

**Bacteriological Analysis**

Samples were submitted for bacteriological isolation at the Iowa State University College of Veterinary Medicine Veterinary Diagnostic Laboratory in Ames, IA. Lung and pleural swabs were initially set up on 5% sheep blood agar (Thermo Scientific) and incubated aerobically with 10% CO₂, as well as incubated anaerobically. Additionally, samples were streaked onto 4% bovine blood agar (BD Diagnostic Systems) and Tergitol 7 (Thermo Scientific) and incubated aerobically without CO₂. A Staph nurse colony was added to the sheep blood agar plate and 4% bovine blood agar plate. Plates were examined once a day for one to three days. Typical Haemophilus parasuis, Actinobacillus pleuropneumoniae, Pasteurella multocida, Streptococcus suis, Bordetella bronchiseptica, and Actinobacillus suis isolates were identified with biochemical testing, gram stain, and matrix-assisted laser desorption time of flight mass spectrometry. Additional bacterial populations were identified if they had significant growth.

For Salmonella isolation, 100 ml of buffered peptone water (BPW) (Thermo Scientific) was homogenized in the Whirl-Pak bag with Speci-Sponge (Nasco, Ft. Atkinson, Wisconsin) and incubated for 18hrs at 35°C. Subsequently, 0.1 ml of BPW was transferred to 10 ml of Rappaport-Vassiliadis (RV) broth (Thermo Scientific) and incubated for 18 hours at 42°C. Aliquots (10µl) of RV broth were streaked onto XLT4 and Brilliant Green with Novobiocin agars (BD Diagnostic Systems) Suspect colonies were confirmed as Salmonella with biochemical analysis (lysine-iron agar (BD Diagnostic Systems), motility-indole-lysine agar (BD Diagnostic Systems)) and slide agglutination with polyvalent anti-O sera (BD Diagnostic Systems.)

**Statistical Analysis**

In order to address the 1st objective and obtain a national peelout prevalence estimate, first the individual abattoir’s peelout prevalence was calculated by dividing the number of peelouts observed by the total number of carcasses observed. These prevalence percentages were added, and then the average was calculated, as well as the standard deviation, and 95% confidence interval. The individual animal prevalence estimate was obtained by taking the sum of all peelouts observed divided by the sum of all carcasses observed. This prevalence estimate was compared to the average national prevalence estimate. These calculations were done in Microsoft Excel 2007.

To address the relationship between peelouts and respiratory pathogens data was analyzed using the statistical program SAS 9.2©. A logistic regression model was used as the outcome (peelouts) was a binary categorical variable. Carcasses with peelouts were coded “1” while carcasses without peelout were coded “0”. The explanatory variable
(respiratory bacterial pathogens) was also categorical (positive or negative), was coded “1” for positive and “0” for negative. Therefore, this model is the logit of the probability of being positive for peelouts in carcasses contaminated with respiratory bacterial pathogen compared to being negative for peelouts in carcasses contaminated with respiratory bacterial pathogens (Kleinbaum and Klein 2010, Kleinbaum et al. 2003). A model was run for each of the different respiratory pathogens. Each abattoir had a separate variable (letters A through F), and each sampling period also had a separate variable (X and Y), and were run as fixed effects in the model. The measure of association was the prevalence odds ratios.

The model was first tested for interaction between the explanatory variables and each of the fixed effects, and if the interaction term was significant at a cutoff of p=0.05, the model was stratified by that variable. If the interaction term was not significant, the model remained unstratified. Also, if there was a quasi-complete separation of points, a “firth” adjustment was used to obtain a prevalence ratio estimate (Heinze et al 2002, SAS 2013). If the prevalence odds ratio estimate obtained was not interpretable, a sensitivity analysis was conducted to see if this data could be omitted from the model. The unadjusted prevalence odds ratio estimates, adjusted prevalence odds ratio estimates (adjusting for the fixed effects of abattoir and sampling period), 95% confidence intervals, and p-values were calculated.

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Results:

Objective 1. Estimate the national prevalence of peelouts in larger processing facilities.

A total of 29,962 carcasses were observed, with 2,486 carcasses of these carcasses having peelouts. At each abattoir visit, approximately 2,000-3,000 carcasses were observed. This number varied depending on the amount of peelouts, as fewer carcasses needed to be observed in order to obtain 50 lesioned carcasses in abattoirs that had higher peelout prevalence. Data from 1,228 carcasses were analyzed: 623 lesioned carcasses and 605 non-lesioned carcasses. Some carcasses did not have a matching lung (22 lesioned carcasses and 17 non-lesioned carcasses) or pleural swab (26 lesioned carcasses and 11 non-lesioned carcasses) due either to misclassification or the carcass being railed off, as carcasses with severe pleuritis can have either the viscera condemned or the entire carcass railed off for further inspection (USDA-FSIS 2012b). This could lead to two types of bias. The missing lung samples could lead to information bias in the form of non-differential misclassification of exposure, i.e., the respiratory pathogen prevalence, and the missing pleural swabs could lead to selection bias due to loss to follow-up (Kleinbaum, 2003). Table 1 shows a descriptive analysis of peelout prevalence, Salmonella contamination, and respiratory pathogen contamination by each abattoir visit.

For the first objective, prevalence estimates were obtained. The prevalence of peelouts ranged from 2.64% to 28.39% with an average national abattoir estimate of 9.78% (95% CI 5.33% to 14.23%). The prevalence at the individual animal level was found to be 8.30%; however, this data does not take into account the effects of plant, as well as sampling period. Figure 1 shows a frequency distribution of peelout prevalence per abattoir visit, and Table 1 shows the peelout prevalence by abattoir.
Figure 1. Peelout frequency by abattoir

- Peelout percentage
- Plant

- December-April
- May-August
<table>
<thead>
<tr>
<th>Abattoir visit</th>
<th>Peelout %</th>
<th><em>Salmonella</em> contamination</th>
<th><em>S. suis</em> contamination</th>
<th><em>P. multocida</em> contamination</th>
<th><em>B. bronchiseptica</em> contamination</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Lesioned</td>
<td>Non-lesioned</td>
<td>Lesioned</td>
<td>Non-lesioned</td>
<td>Lesioned</td>
</tr>
<tr>
<td>A</td>
<td>5.05%</td>
<td>0.00% (n=0)</td>
<td>0.00% (n=0)</td>
<td>46.15% (n=18)</td>
<td>56.76% (n=21)</td>
</tr>
<tr>
<td>B</td>
<td>2.64%</td>
<td>8.00% (n=4)</td>
<td>4.08% (n=2)</td>
<td>7.84% (n=4)</td>
<td>2.04% (n=1)</td>
</tr>
<tr>
<td>C</td>
<td>4.18%</td>
<td>4.00% (n=2)</td>
<td>8.00% (n=4)</td>
<td>15.39% (n=11)</td>
<td>22.00% (n=6)</td>
</tr>
<tr>
<td>D</td>
<td>8.26%</td>
<td>0.00% (n=0)</td>
<td>0.00% (n=0)</td>
<td>43.14% (n=18)</td>
<td>30.00% (n=17)</td>
</tr>
<tr>
<td>E</td>
<td>28.39%</td>
<td>0.00% (n=0)</td>
<td>2.00% (n=1)</td>
<td>14.00% (n=7)</td>
<td>6.00% (n=3)</td>
</tr>
<tr>
<td>F</td>
<td>7.23%</td>
<td>22.00% (n=11)</td>
<td>12.00% (n=6)</td>
<td>20.00% (n=10)</td>
<td>6.00% (n=3)</td>
</tr>
<tr>
<td>G</td>
<td>8.53%</td>
<td>3.33% (n=2)</td>
<td>6.52% (n=3)</td>
<td>18.37% (n=9)</td>
<td>31.11% (n=14)</td>
</tr>
<tr>
<td>H</td>
<td>5.98%</td>
<td>4.44% (n=1)</td>
<td>1.96% (n=1)</td>
<td>5.45% (n=3)</td>
<td>7.27% (n=4)</td>
</tr>
<tr>
<td>I</td>
<td>4.08%</td>
<td>11.11% (n=5)</td>
<td>8.16% (n=3)</td>
<td>27.78% (n=15)</td>
<td>28.85% (n=15)</td>
</tr>
<tr>
<td>J</td>
<td>10.96%</td>
<td>8.00% (n=4)</td>
<td>0.00% (n=0)</td>
<td>50.00% (n=15)</td>
<td>44.00% (n=15)</td>
</tr>
<tr>
<td>K</td>
<td>22.86%</td>
<td>8.16% (n=4)</td>
<td>16.00% (n=8)</td>
<td>20.00% (n=10)</td>
<td>28.00% (n=14)</td>
</tr>
<tr>
<td>L</td>
<td>9.12%</td>
<td>23.53% (n=12)</td>
<td>4.00% (n=2)</td>
<td>18.00% (n=9)</td>
<td>26.00% (n=13)</td>
</tr>
</tbody>
</table>
Objective 2. Determine what pig respiratory pathogens are more highly associated with peelouts.

For the second objective, respiratory pathogen contamination rates were obtained. Respiratory pathogen contamination rates for lesioned and non-lesioned carcasses ranged as following (Table 1): *Streptococcus suis*, 5.45% to 50%, 2.04% to 56.76%, *Pasteurella multocida*, 0% to 33.33%, 0% to 42% and *Bordetella bronchiseptica*, 0% to 6.12%, 0% to 2.22%. *Actinobacillus suis*, *Actinobacillus pleuropneumoniae*, and *Haemophilus parasuis* were only found in one carcass each, so they were not included in the descriptive or statistical analysis, as they would not provide any meaningful statistical data.

In analyzing the respiratory pathogen contamination data, each bacteria (*Streptococcus suis*, *Pasteurella multocida*, and *Bordetella bronchiseptica*) was run separately. In testing for interaction, no significant interaction (p =0.05) was found between either bacteria and sampling period, or bacteria and plant, except for between *Pasteurella multocida* and sampling period. This model was stratified by sampling period, while the other models remained unstratified. No statistically significant association was found between peelouts and respiratory pathogen contamination. Table 2 presents the unadjusted prevalence odds ratios, adjusted prevalence odds ratios (adjusting for the fixed effects of plant and sampling period), 95% confidence intervals, and p-values.

<table>
<thead>
<tr>
<th>Explanatory variable</th>
<th>% contaminated carcasses</th>
<th>% non-contaminated carcasses</th>
<th>POR</th>
<th>Adjusted POR</th>
<th>95% confidence interval</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>S. suis</em></td>
<td>23.29% (n=140)</td>
<td>23.13% (n=136)</td>
<td>1.00</td>
<td>1.00</td>
<td>(0.76-1.33)</td>
<td>0.98</td>
</tr>
<tr>
<td><em>P. multocida</em></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sampling Period X</td>
<td>10.58% (n=31)</td>
<td>14.34% (n=41)</td>
<td>0.71</td>
<td>0.69</td>
<td>(0.41-1.17)</td>
<td>0.17</td>
</tr>
<tr>
<td>Sampling Period Y</td>
<td>9.42% (n=29)</td>
<td>6.29% (n=19)</td>
<td>1.55</td>
<td>1.58</td>
<td>(0.86-2.90)</td>
<td>0.14</td>
</tr>
<tr>
<td><em>B. bronchiseptica</em></td>
<td>1.16% (n=7)</td>
<td>0.68% (n=4)</td>
<td>1.72</td>
<td>1.69</td>
<td>(0.49-5.86)</td>
<td>0.41</td>
</tr>
</tbody>
</table>

Objective 3. Determine if peel-outs are associated with an increase in food-borne pathogens (*Salmonella*).

For the third objective, the *Salmonella* contamination rates were obtained. *Salmonella* contamination rates ranged from 0% to 23.53% for lesioned and 0% to 16% for non-lesioned carcasses.

In analyzing the *Salmonella* data, the model was tested for interaction between peelout and plant, as well as sampling period and plant. A significant interaction was found between peelout and plant, so the model was stratified by plant.

Because abattoir D did not have any non-lesioned carcasses positive for *Salmonella*, the Firth
adjustment was used to calculate the odds ratio estimate of 9.71 (95% CI 0.57-165.73, p=0.12). This number does not provide any interpretable data, therefore it was decided post-hoc to omit this abattoir from the model. To compare the effect of removing this data, a sensitivity analysis was conducted by comparing the unstratified model and with the model using the Firth adjustment. With the data from abattoir 4 the adjusted POR 1.56 (95% CI 0.97-2.52, p=0.07) and without the data the adjusted POR was 1.41 (95% CI 0.87-2.31, p=0.17). This is not surprising, as the odds ratio of 9.37 skewed our data, giving a bias away from the null (Kleinbaum, 2003). Table 3 presents the unadjusted prevalence odds ratios, adjusted prevalence odds ratios, 95% confidence intervals, and p-values. With the exception of abattoir 6, no statistically significant association was found between Salmonella contamination and peelouts.

Table 3. Association between Salmonella contamination by abattoir

<table>
<thead>
<tr>
<th>Explanatory variable</th>
<th>Peelout %</th>
<th>% contamination lesioned carcasses</th>
<th>% contamination non-lesioned carcasses</th>
<th>Un-adjusted POR</th>
<th>Adjusted POR</th>
<th>95% confidence interval</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Overall (including abattoir 4)</td>
<td>9.77% (n=46)</td>
<td>7.71%</td>
<td>5.22 (n=31)</td>
<td>1.52</td>
<td>1.56</td>
<td>(0.97-2.52)</td>
<td>0.07</td>
</tr>
<tr>
<td>Overall (excluding abattoir 4)</td>
<td>9.81% (n=42)</td>
<td>8.45%</td>
<td>6.28% (n=31)</td>
<td>1.38</td>
<td>1.41</td>
<td>(0.87-2.31)</td>
<td>0.17</td>
</tr>
<tr>
<td>Abattoir 1 (Visits A and G)</td>
<td>6.83% (n=2)</td>
<td>1.87%</td>
<td>3.16% (n=3)</td>
<td>0.58</td>
<td>0.53</td>
<td>(0.11-2.70)</td>
<td>0.45</td>
</tr>
<tr>
<td>Abattoir 2 (Visits B and H)</td>
<td>4.30% (n=6)</td>
<td>6.32%</td>
<td>3.00% (n=3)</td>
<td>2.18</td>
<td>1.98</td>
<td>(0.53-7.34)</td>
<td>0.31</td>
</tr>
<tr>
<td>Abattoir 3 (Visits C and I)</td>
<td>4.13% (n=7)</td>
<td>7.37%</td>
<td>8.08% (n=8)</td>
<td>0.91</td>
<td>0.92</td>
<td>(0.33-2.56)</td>
<td>0.88</td>
</tr>
<tr>
<td>Abattoir 4 (Visits D and J)*</td>
<td>9.35% (n=4)</td>
<td>4.00%</td>
<td>0.00% (n=0)</td>
<td>*</td>
<td>*</td>
<td>*</td>
<td>*</td>
</tr>
<tr>
<td>Abattoir 5 (Visits E and K)</td>
<td>25.11% (n=4)</td>
<td>4.04%</td>
<td>9.00% (n=9)</td>
<td>0.43</td>
<td>0.44</td>
<td>(0.14-1.42)</td>
<td>0.17</td>
</tr>
<tr>
<td>Abattoir 6 (Visits F and L)</td>
<td>8.04% (n=23)</td>
<td>22.77%</td>
<td>8.00% (n=8)</td>
<td>3.39</td>
<td>3.25</td>
<td>(1.41-7.54)</td>
<td>0.01</td>
</tr>
</tbody>
</table>

*data from abattoir 4 not included in analysis
Discussion:

The objectives of this study were to develop a national prevalence estimate for peelout prevalence, (ii) determine if common respiratory pig pathogens are associated with peelouts and (iii) determine if peelouts are associated with *Salmonella* contamination. As there is limited research in this area, this study was designed with the goal of expanding on the previous research. In both previous peelout studies, sample size was an issue, as each study was only conducted in one abattoir. Our study sampled over two sampling periods, and at different geographical locations, in order to address this limitation.

The first study by Hurd et al. (2008) obtained a peelout prevalence of 7.1% at one abattoir. Expanding on these findings, we found a national peelout prevalence of 9.78% (95% CI 5.33% to 14.23%). Most abattoirs had a peelout prevalence between approximately 5% to 10%, which was consistent with the previous studies’ findings. However, one abattoir had a peelout prevalence of 28.39% for the first sampling period and 22.87% for the second sampling period, possibly skewing our data. Also, in five out of the six abattoirs the peelout prevalence was slightly higher during the second abattoir sampling period, suggesting that there may be a seasonal effect on prevalence of peelouts in market hogs raised in the winter months versus summer months. However, because we were only able to spend one day at each abattoir during each sampling period, these results should be interpreted with caution. In sampling for respiratory pathogens, there was little association between contamination and peelout status. Some abattoirs had higher contamination in lesioned carcasses, while others had higher contamination in non-lesioned carcasses. This could be for a number of reasons. Many of these pathogens that we tested for are common in swine herds, and can be part of the normal flora (Brockmeier et al 2001; Oliviera et al, 2004; Olvera et al, 2007; MacInnes et al, 2008).

There could have been high amounts of healthy carrier animals. Lesions could have been left over from a previous infection, and the bacteria may no longer be present. This is common when younger animals have these infections. Because we only looked for bacterial pathogens, this study could be repeated to look for common viral respiratory pathogens.

As many respiratory infections are mixed infections, (Brockmeier et al., 2001; Brockmeier et al., 2004; Olson et al, 2000) it was not surprising that we found more than one type of bacteria in several of our samples. We found several samples that were positive for both *Streptococcus suis* and *Pasteurella multocida*, (20 lesioned carcasses and 17 non-lesioned carcasses) which is consistent with the literature. *Pasteurella multocida* is often seen with *Bordetella bronchiseptica*; however, we found very few samples that contained both bacteria (1 lesioned and 1 non-lesioned carcass), but this is not surprising considering the small amount of samples that tested positive for *Bordetella bronchiseptica*. Also, we had 5 lesioned carcasses and 1 non-lesioned carcass test positive for both *Streptococcus suis* and *Bordetella bronchiseptica*.

The data collected from this study represents the best available estimate of the peelout prevalence and bacterial contamination in abattoirs. However, it is limited since we only sampled one day during each sampling period at each abattoir. Personnel at the abattoirs have pointed out that peelout prevalence (and the possible resulting bacterial contamination) can vary from day to day. Sampling over multiple days may result in more accurate estimations of carcass lesions and contamination. Also, in this study, we visited three abattoirs in the Midwest versus one abattoir in each of the other geographical locations. This could have led to a selection bias, and an overrepresentation of the effect of geographical location on peelouts in the Midwest, and an underrepresentation of the effect of geographical location on peelouts in the other abattoirs. To address this, this study could be repeated by sampling fewer abattoirs in the Midwest, or more abattoirs in other areas of the country for a more even distribution of geographical location.

In Hurd et al. (2008), samples were not taken from the same carcass, and were pooled together. Thus, it may have been more difficult to track contamination on an individual animal level. A strength in
our study was that we took both sets of samples from the same carcass, therefore being able to look at contamination on the individual animal, as well as looking at the contamination at the abattoir level.

At most abattoirs, a statistically significant relationship between peelout status and Salmonella contamination was not found. This could be for several reasons. Because samples were taken at line speed, there may not have been enough time to adequately swab the pleural/peritoneal cavity, or a large enough surface area may not have been swabbed. For example, the EU ordered an increased carcass swabbing area in its Salmonella control program. This increase in the swabbing area of swine carcasses from 3x100 cm² to 4x400 cm² showed a prevalence increase in the first year it was performed from a 1.2% to 1.7% (Dahl 2013). However, it is possible that this is not a result of the increase in swabbing area, but simply an increase in the number of carcasses contaminated or cross-contaminated at slaughter. Also, the person swabbing may not have applied adequate pressure to the swab in order to make adequate contact with the interior of the carcass, which may possibly contribute to fewer Salmonella organisms being picked up. Another explanation is that the prevalence of Salmonella has truly decreased by the time the carcass gets to the final USDA inspection, demonstrating the efficacy of post-harvest interventions or Hazard Analysis of Critical Control Points (HAACP). Conversely, high Salmonella contamination rates could also be a result of cross contamination due to failure of post-harvest interventions/HAACP.

Because we found a significant association between Salmonella contamination and peelouts at abattoirs that had more samples positive for Salmonella, it may be beneficial to repeat this experiment with a focus on these abattoirs. If possible, swabbing methods that are more sensitive should be adapted (for example, swabbing a larger surface area), to increase the likelihood of detecting Salmonella. Also, it may be beneficial to modify the study design take samples at other points in the processing chain in order to obtain differences in contamination rates, as well as collecting data on animal selection and processing procedures. This may help determine where other risks for contamination exist.

While there was no clear evidence of an association between respiratory bacterial contamination and peelouts, these pathogens still play a significant role in swine health. While a significant association was not found between peelouts and Salmonella contamination in all abattoirs, the effect that peelouts can have on public health with even a small number of abattoirs, should not be ruled out. This is especially true in abattoirs that have a high Salmonella prevalence.

References:


