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The impact of pig health on public health: quantitative data for risk assessments

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The impact of pig health on public health: quantitative data for risk assessments

by

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A thesis submitted to the graduate faculty in partial fulfillment for the degree of

MASTER OF SCIENCE

Major: Veterinary Preventive Medicine

Program of Study Committee

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Ames, Iowa

2014

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DEDICATION

Dedicated to my husband and my parents with love.

In loving memory of Dr. H. Scott Hurd

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ABSTRACT

A safe food supply is essential to public health. Changes in management practices affecting animal health could significantly impact public health. While animals with clinical illness will not pass ante-mortem inspection, animals with subclinical illness could be harvested. These animals could have peelouts, or pleural/peritoneal lesions that do not allow for complete viscera removal, requiring extra trimming. Swine are commonly asymptomatic carriers of *Salmonella* infection. If animals are also infected with respiratory pathogens, it is possible that peelouts could lead to carcass contamination.

This study has three objectives: to obtain a peelout prevalence estimate, determine if common swine respiratory pathogens are associated with peelouts (*Streptococcus suis*, *Pasteurella multocida*, *Bordetella bronchiseptica*, *Haemophilus parasuis*, *Actinobacillus suis*, *Actinobacillus pleuropneumoniae*), and determine if carcasses with peelouts are more likely to have *Salmonella* contamination.

Six abattoirs from different geographical locations in the United States were chosen, and two different sampling periods were run. Samples were taken from 50 lesioned carcasses and 50 non-lesioned carcasses. Two sets of samples were taken: a lung sample immediately after evisceration and a pleural swab from the corresponding carcass after trimming and before the final carcass rinse. The pleural swabs were tested for *Salmonella* and the lung samples tested for respiratory pathogens using a standard bacteriological isolation and culture protocol. Data was analyzed using logistic regression.

The prevalence of peelouts by abattoir visit ranged from 2.64% to 28.39%, with a national prevalence estimate of 9.77% (95% CI 5.31% to 14.22%). *Salmonella* contamination rates ranged from 0% to 23.53% for lesioned and 0% to 16% for non-lesioned carcasses. Respiratory pathogen contamination rates for lesioned and non-lesioned carcasses ranged as following: *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%. No significant association was found between peelouts and respiratory pathogens. There was no strong association between *Salmonella* contamination and peelouts, except in abattoirs with significant *Salmonella* contamination (22.77% lesioned carcasses, 8% non-lesioned carcasses). Therefore, we cannot ignore the role that pig health could have on public health, especially in herds with higher amounts of bacterial contamination.

CHAPTER 1. INTRODUCTION AND LITERATURE REVIEW

Introduction

Maintaining healthy livestock is vital in ensuring a safe food supply. While management practices such as antibiotic use, animal housing, and biosecurity remain under scrutiny, it is important to examine what effect that changing these practices could have on animal health.

Any changes that could affect animal health have the potential to significantly impact human health. Foodborne illness due to certain pathogens such as *E. coli* has decreased from 1996-2012, however, the amount of foodborne illness attributed to *Salmonella* has remained steady, if not slightly increased, during this same time period (CDC, 2013). *Salmonella* continues to be one of the top pathogens implicated in foodborne illness. It is estimated to cause approximately 11% of illnesses, 35% of hospitalizations, and 28% of deaths (CDC, 2011).

Meat and poultry products continue to be a common *Salmonella* source. Using data from the Danish *Salmonella* surveillance program, Hald et al. (2007) developed a Bayesian model to estimate the attribution of pork to foodborne illness, and estimated that 10.5% of *Salmonella* illnesses could be attributed to domestic pork (95% CI 9.1%-11.9%). An adaption of this model done by Guo et al. (2011) using data from the United States attributed <1% of illnesses due to pork (no 95% CI was given, as this estimate was not significantly affected by changing model inputs). Even though this number may seem small, considering the millions of hogs processed each year (USDA, 2012), and the possibility of underestimating the attribution of pork to foodborne illness, *Salmonella* in

pork still poses a significant public health risk.

Objective and Topic Overview

The overall objective of this thesis is to examine the relationship between animal health and carcass contamination (in this case, examining peelouts as an indicator of animal health), and the effect that this carcass contamination could have on public health risk (in the form of foodborne illness). In this literature review, the following topics will be discussed, as well as their importance to the overall research question: the epidemiology of *Salmonella*, changes in *Salmonella* prevalence from on-farm to slaughter, *Salmonella* control and surveillance, epidemiology and prevalence of common swine respiratory pathogens, slaughter checks, examining the relationship between on-farm animal health and carcass contamination, and examining the relationship between animal health and human health. The study itself is divided into three objectives, which are designed to expand on the findings of the previous peelout studies in swine, as well as address some of the limitations posed in those studies.

1. The first objective was to estimate a national prevalence estimate of peelouts. We hypothesized that there would be a difference in peelout prevalence between geographical location as well as sampling period.

2. The second objective was to determine if common respiratory pig pathogens (*Streptococcus suis*, *Pasteurella multocida*, *Bordetella bronchiseptica*, *Haemophilus parasuis*, *Actinobacillus suis*, and *Actinobacillus pleuropneumoniae*) are more likely to be associated with peelouts. Our hypothesis is that carcasses with peelouts were more likely to belong to swine that were positive for these respiratory pathogens. We chose

these pathogens as they are commonly associated with respiratory illness (MacInnes et al., 1999; MacInnes et al., 2008; Olson et al., 2000; Brockmeier et al., 2001; Brockmeier, 2004; Mattoo et al., 2005).

3. The third and final objective was to determine if peelouts are associated with foodborne pathogens, specifically *Salmonella*. Our hypothesis for this objective was that peelout positive carcasses would be more likely to be contaminated with *Salmonella* than peelout negative carcasses, and that there would be a statistically significant association between peelouts and carcass contamination.

Literature Search Methods

An informal literature search method was used, beginning with the three studies relating to peelouts (Russell, 2003; Hurd et al., 2008a, Hurd et al., 2012). These papers were then cross-referenced to other papers with pertinent material. An outline was made of the topics to be discussed in the literature review, and from there a list of search terms was developed. These search terms included: *Salmonella* (prevalence on-farm, carcass prevalence, prevalence during processing, lairage, transport, attribution, cross contamination, modeling), surveillance programs (Danish *Salmonella* control program, PigMON), and the respiratory pathogens *Streptococcus suis*, *Pasteurella multocida*, *Bordetella bronchiseptica*, *Haemophilus parasuis*, *Actinobacillus suis*, and *Actinobacillus pleuropneumoniae* (symptoms, pathogenesis, prevalence, zoonotic, control). While efforts were made to find as much pertinent and current literature as possible, the literature referenced may not be an exhaustive list of all available literature.

Epidemiology of *Salmonella*

Research by Foley et al. (2008) and The National Animal Health Monitoring System (USDA-APHIS, 2008) have found that *Salmonella typhimurium* is one of the main serotypes found in swine in North America. Asymptomatic carriers of *S. typhimurium* continue to be a concern, as *S. typhimurium* which comes off of the farm can then be spread at the abattoir (Hurd et al., 2001a; Hurd et al., 2001b; Wang et al., 2002; Rostagno et al., 2003). This topic will be more thoroughly covered in the next section.

The epidemiology of *Salmonella* from the farm to retail is complex. There are many points both on-farm and post-harvest that influence *Salmonella* prevalence in the animal or the carcass. Figure 1 demonstrates different points in the processing chain where *Salmonella* contamination can occur, as well as possible factors that could contribute to *Salmonella* contamination (Adapted from Dickson et al., 2010). Factors that can affect the on-farm prevalence of positive animals can include type of feed, water contamination, pen contamination, stocking density, pests such as mice and birds, comingling, improperly sanitized boots, farm personnel, and more (Dickson et al., 2010; Fosse et al., 2009; Wang et al., 2002). Points of possible contamination post-harvest can include trailers and transport, stress, lairage, contaminated holding pens, evisceration, carcass splitting, comingling, and more (Dickson et al., 2010; Hurd et al., 2001a; Rostagno et al., 2003). Both on-farm and post-harvest interventions are regarded as important. The consensus of the majority of scientific literature is that the most effective way to reduce foodborne disease has been to focus on post-harvest interventions, or a

combination of pre-harvest and post-harvest interventions (Alban et al., 2005; Hurd et al., 2008b; Arguello et al., 2013; O'Connor et al., 2012).

***Salmonella* Prevalence On-Farm and At Slaughter**

Longitudinal studies conducted on the farm generally find a lower *Salmonella* prevalence compared to the prevalence at slaughter. In a cohort study by (Hurd et al., 2001a), fecal samples were taken on a farrow-to-finish operation with approximately 600 sows. Ten groups of thirty market hogs were sampled, and 3.4% of fecal samples tested were positive for *Salmonella*. Hurd et al. (2004) also conducted another study to estimate the on-farm prevalence of *Salmonella*, using a cohort of 100 finishers from six swine herds. In this study, fecal samples, caecal contents, and lymph nodes were tested. This study found an on-farm prevalence of 5.3% (95% CI 2.7%-8.0%). A cohort study conducted by Bahson et al. (2005) on 30 finishers on 30 different Midwestern farms found that 11.7% (n=105) of fecal samples tested positive for *Salmonella*.

After the animals were taken to slaughter at a Midwestern abattoir, the same cohort study from Hurd et al. (2001a) then found that 71.8% of fecal samples from these pigs test positive during lairage. The second study by Hurd et al. (2004) found that 39.9% (95% CI 34.2%-45.5%) of samples collected at lairage (fecal samples, caecal contents, and lymph nodes) were positive for *Salmonella*.

In an experimental study conducted by Hurd et al. (2001b), pigs that were previously negative for *Salmonella* could become infected in as little as two hours. This was tested by taking 5 trials with 8 market hogs in each trial, by putting hogs in a setting that imitated conditions at lairage. Even though this study had a small sample size, the findings of other scientific literature support the findings of this study, as the *Salmonella*

prevalence increases from on-farm to lairage. Rostagno et al. (2003) surveyed two Midwestern abattoirs to determine if holding pens could be a source of *Salmonella* infection. At each abattoir, four groups of approximately 150 pigs were sampled, and three replicates were performed. Six pooled fecal samples of 10 samples per pool were collected from transport trailers and six pooled samples were collected from each holding pen. At abattoir A 34.7% of transport trailer samples tested positive for *Salmonella*, compared to 52.8% at abattoir B. In addition, 65.3% and 90.3% of holding pen samples tested positive for *Salmonella* in abattoir A and B respectively. There were different serovars detected from pens, trailers, and pigs, which was indicative of cross-contamination, and suggested that pens and trailers could be a source of infection in addition to other animals.

During the slaughter process, there are also many other points of possible contamination, including scalding, dehairing, singeing, polishing, evisceration, dressing, and splitting. Reviews by both Arguello et al. (2013) and O'Connor et al. (2012) discuss the impacts of these different processing points in either increasing or decreasing *Salmonella* prevalence. Proper scalding, singeing, and carcass rinses can effectively decrease carcass prevalence. Evisceration, post splitting, dehairing, improper scalding temperature, and inadequate carcass rinse procedures have been shown to increase *Salmonella* prevalence (Arguello et al., 2013).

Bolton et al. (2003) examined the ability for *Salmonella* to survive different scalding temperatures, and found that a temperature of at least 60°C is required in order to reduce *Salmonella* by 1 log unit per 10 ml. In a study of 2211 pigs, Davies et al. 1999 found a *Salmonella* prevalence of 82.9% post-bleeding. This prevalence decreased after

scalding to 5.7%, subsequently increased to 42% after dehairing, and decreased to 0% after singeing. Pearce et al. (2004) sampled carcasses over 8 abattoir visits and found a similar trend, with 31% *Salmonella* prevalence post-bleeding, a decrease to 1% after scalding, and then a subsequent increase to 7% after dehairing.

The majority of published literature has found that by the time the carcasses reach the cooler, there has been a drastic reduction in the prevalence of *Salmonella* (O'Connor et al., 2012; Arguello et al., 2013). For example, a study conducted by which sampled 28 lots over 10 visits, Tamplin et al. (2001) found a mean *Salmonella* prevalence on 0.7% of chilled carcasses. In addition, the most recent data from the USDA-FSIS Microbiological Baseline Data Collection Program sampled 1,960 pre-evisceration and 1,960 carcasses post-chill from 2010-2011 to find the *Salmonella* prevalence. The percent positive rate declined from 69.64% pre-evisceration, to 2.7% post chill, with the *Salmonella* prevalence being 1.66% (95% CI 0.82% to 2.51%) post-chill (USDA-FSIS, 2011).

***Salmonella* Surveillance**

Surveillance programs both on-farm and at harvest have been utilized to examine disease patterns in animal populations. One example of an on-farm surveillance program that has been adopted to look for *Salmonella* is the Danish *Salmonella* control program. The program was adopted in 1993, and looks into decreasing *Salmonella* both on the farm, as well as at slaughter. The primary motivating factor for adoption of this program was an outbreak attributed to pork in Denmark.

With the Danish *Salmonella* control program, blood samples are taken on-farm

and meat juice samples (exudates containing serum) are taken at slaughter to determine *Salmonella* seroprevalence. Seroprevalence is used to identify if herds have a *Salmonella* problem. Herds with continuing *Salmonella* problems are fined (Alban et al., 2002; Nielsen et al., 2001). Recommendations to change feed, hygiene, and other management practices are also been made. Post-harvest interventions include limiting fecal contamination by covering intestinal tracts pre-evisceration (Hurd et al., 2008b).

Initially, the Danish *Salmonella* control program had a significant impact on the pork industry. From 1993 to 1997, the herd prevalence *Salmonella* in pork declined from 3.5% to 0.7% (Nielsen et al., 2001.) From 1993-2001, human illness attributable to pork is estimated to have dropped from 22% to 3%. The economic impact was significant as well. An estimated \$25.5 million in 2001 was saved as a result of livestock *Salmonella* control programs (Wegener et al., 2003).

The focus of this program was interventions both on the farm and at slaughter. Alban et al. (2005) developed a stochastic model using data from the *Salmonella* control program to determine what pre-harvest and post-harvest interventions were most effective in reducing *Salmonella* prevalence. The results indicated that the most effective interventions were lowering the proportion of herds highly contaminated with *Salmonella*, while concurrently increasing singeing efficacy, reducing cross-contamination during handling, and reducing cross-contamination at evisceration.

According to Dahl (2013) on-farm interventions have not been effective, as the percentage of positive breeding herds increased from 25% in 1998 to 50% in 2012. This is problematic, as the early stages of the *Salmonella* surveillance program focused mainly on pre-harvest interventions, and 95 million Euros were spent on this program from

1995-2005 (Hurd et al., 2008b.) Data also suggests an increase in positive sow herds as well. Carcass prevalence has remained low, under 2%, and the amount of human attributable cases to pork has remained low (Dahl, 2013), reinforcing the scientific literature stating that post-harvest interventions are most effective in controlling *Salmonella*.

Epidemiology of Respiratory Diseases

In addition to *Salmonella* being an important pathogen to the swine industry, there are other common pathogens which are important, including pathogens which can cause respiratory problems. Examples of these pathogens in swine include *Streptococcus suis*, *Pasteurella multocida*, *Bordetella bronchiseptica*, *Actinobacillus suis*, *Actinobacillus pleuropneumoniae*, and *Haemophilus parasuis*. While many of these pathogens are not of zoonotic concern (Olvera et al., 2007; Mattoo et al., 2005) they are important because of the potential impact on animal health. Respiratory diseases can cause significant economic losses for producers due to increased morbidity and mortality, treatment costs, and decreased weight gain (Olson et al., 2000; Oliveria et al., 2004; Stärk, 2000). Mixed infections are quite common, and often clinical signs are quite similar (Brockmeir et al., 2001). Infections with multiple pathogens tend to be more severe than those with one pathogen (Van Reeth et al., 1994). General symptoms of respiratory infections include rhinitis, pneumonia, and pleuritis (Olson et al., 2000; Stärk, 2000; MacInnes et al., 2008). Because eradication of these diseases can be difficult, producers are encouraged to focus on control measures instead.

Streptococcus suis can often be found in healthy animals in their tonsils as well as intestinal tract and is found in almost all herds (Devriese et al., 1994). Clinical signs of *S.*

suis infection can include fever, septicemia, bacteremia, rhinitis, pneumonia, endocarditis, and neurological problems (Coulter et al., 2003). Often, several *S. suis* serotypes can be seen in an infection (MacInnes et al., 2008.)

In addition to being economically important to the swine industry, *S. suis* also has the potential to be a causative agent in zoonotic infections. *S. suis* generally causes disease in humans through skin wounds, and most cases are isolated to persons who work in the swine industry or abattoirs. *S. suis* infections can cause purulent meningitis, endocarditis, cellulitis, peritonitis, rhabdomyolysis, and other conditions (Hughes et al., 2009).

In swine herds, disease incidence is low, even with a high amount of carrier animals. According to Coulter et al. (2003), the mortality rate can reach 20% if animals are left untreated. Infections can be treated with antibiotics, such as ceftiofur and amoxicillin; however, vaccination generally isn't effective (MacInnes et al., 2009).

Pasteurella multocida is a cause of pneumonia in addition to PAR, or progressive atrophic rhinitis. Two main serotypes are found in swine: types A and D. Type A is generally associated with pneumonia, whereas type D is generally associated with PAR (Davies et al., 2003; MacInnes et al., 2008) *P. multocida* is rarely a primary pathogen; rather it is considered an opportunistic pathogen. Like *Streptococcus suis*, it is often seen concurrently with *Bordetella bronchiseptica* (Brockmeier et al., 2001).

P. multocida is generally found in respiratory tract as well as the tonsils of swine, and younger pigs are affected more severely than older pigs (Ackermann et al., 1991; Scheidt, no date). Pulmonary abscesses and pleuritis can result from some strains of *P. multocida*. Pneumonia due to *P. multocida* tends to affect growing and finishing pigs.

When PAR is observed, the lesions tend to be isolated to the nasal cavity (Ackermann et al., 1994).

P. multocida is of zoonotic concern because humans can contract *P. multocida* through animal bites and scratches. Persons who are exposed to pigs can become carriers of *P. multocida*, and tend to remain healthy. However, acute and chronic respiratory disease can occur with *P. multocida* infection, especially in those who are immunocompromised (Marois et al., 2009; Migliore et al., 2009.)

Bordetella bronchiseptica is often seen as a part of the normal flora in swine, but can also cause respiratory illness. It promotes the growth of *Pasteurella multocida*, and when seen with *Pasteurella multocida*, results in more severe respiratory disease (Brockmeier et al., 2001). In addition, *Bordetella bronchiseptica* can make animals more susceptible to co-infection with *Haemophilus parasuis* and *Streptococcus suis*. (Brockmeier, 2004; Vecht et al., 1992).

The severity of disease can range from asymptomatic to lethal. Clinical signs can include progressive atrophic rhinitis (especially when seen with *Pasteurella multocida*), bronchopneumonia, and systemic infection, and co-infection causes more severe disease. Morbidity tends to be high, but mortality tends to be low. Lesions are generally found in the nasal cavity (Mattoo et al., 2005; Brockmeier et al., 2001).

Bordetella bronchiseptica can cause respiratory disease in humans. However, no cases have been reported from exposure to swine. Instead, zoonotic illness results from exposure to dogs, cats, or rabbits (Mattoo et al., 2005). It may be possible for wild animals and domesticated pets can spread *Bordetella bronchiseptica* to swine, underlying the importance for biosecurity. Like other respiratory pathogens, it can be difficult to

eradicate.

Actinobacillus pleuropneumoniae is the causative agent of pleuropneumoniae, and causes pneumonia along with pleuritis. Among different strains of *Actinobacillus pleuropneumoniae*, there is a significant difference in virulence. Outbreaks of *Actinobacillus pleuropneumoniae* with high mortality continue to remain a problem in Europe, Asia, and Latin America; however, they are not seen as often in the United States and Canada (Gottschalk et al., 2003).

Peracute, acute, and chronic infection can be seen with *Actinobacillus pleuropneumoniae*. Virulent infection can be fatal within a few hours, and acute infections cause severe respiratory and cardiovascular problems. Pigs infected with *Actinobacillus pleuropneumoniae* that survive infection can remain subclinical carriers, and can exhibit lung lesions and severe pulmonary tissue damage (Bossé et al., 2002).

At slaughter, lesions appear such as fibrinous pleuritis, which can make complete lung removal difficult. Enøe et al. (2002) found that 51% of pigs seropositive for *Actinobacillus pleuropneumoniae* had pleuritis at slaughter. The efficacy treatment with antibiotics remains variable, and antibiotics must be administered early in the course of the disease. (Marsteller et al., 1999).

Actinobacillus suis is quite similar to *Actinobacillus pleuropneumoniae*, but tends to be less virulent. It is an opportunistic pathogen and is found in the upper respiratory tract. It can be found in many herds, especially high health herds. Clinical manifestations of *A. suis* include septicemia and localized infections. The disease occurs in three main forms: acute septicemia in piglets, respiratory disease in high health herds, and acute septicemia in adults. Treatment with antibiotics should begin early in the onset of disease

(MacInnes et al., 1999).

Haemophilus parasuis is the causative agent in Glässer's disease. Polyserositis and arthritis are common manifestations of Glässer's disease. It is part of the normal flora that is found in the respiratory tract. When causing illness, *Haemophilus parasuis* is often seen as a secondary pathogen to *Actinobacillus pleuropneumoniae*; however, it can also act as a primary pathogen (Oliveria et al., 2004; MacInnes et al., 2008; Mousing, 1991). Animals affected with *Bordetella bronchiseptica* can be at an increased risk for *Haemophilus parasuis* colonization (Brockmeier, 2004). *Haemophilus parasuis* is not of zoonotic concern, as swine are the only known reservoir (Olvera et al., 2007).

High health herds tend to be affected most severely, and nurseries are the main source of infection (Oliveria et al., 2004). In herds exposed to *Haemophilus parasuis*, mortality and morbidity rates are relatively low, between 5%-10%. However, in herds where *Haemophilus parasuis* is not normally present, morbidity and mortality rates can reach up to 75% (Wiseman et al., 1989). Peracute infection can cause mortality quickly after incubation. In acute infection, polyserositis, arthritis, and meningitis are some of the clinical signs that can be seen. Animals with chronic infection will exhibit chronic arthritis, as well as fibrosis in the pleura, peritoneum, or pericardium. It is important to differentiate *Haemophilus parasuis* infection from *S. suis*, as they cause similar lesions and affect pigs of similar age (Olvera et al., 2007).

Like other respiratory pathogens discussed, it is difficult to eradicate *Haemophilus parasuis* completely. Vaccination can prove effective in preventing mortality, and antibiotics are also effective in the prevention and control of *Haemophilus parasuis*. However, exposure to virulent *Haemophilus parasuis* early in life while still

receiving maternal immunity can protect against morbidity and mortality later in life (Oliveria et al., 2004).

Prevalence of Respiratory Diseases

The respiratory pathogens described above can commonly be found on swine farms. A study conducted by Brisebois et al. (1990) examined 388 piglets from 49 different farms in Quebec to determine the prevalence of *S. suis*. Nasal swabs were taken from each of the piglets, and *S. suis* was isolated from 94% of piglets and 98% of farms.

Enøe et al. (2002) examined 4800 pigs at one Danish abattoir from 623 herds, with 240 samples being taken twice weekly over a 10-week period. Blood samples were taken from each animal. The prevalence of positive piglets in affected with *Actinobacillus pleuropneumoniae* was 20%-76%, depending on serotype. The prevalence of positive pigs in herds affected by *Haemophilus parasuis* was 56%, with 70% of herds being positive for *Haemophilus parasuis*.

To obtain prevalence data on *S. suis*, *P. multocida*, *H. parasuis*, *A. suis*, and *A. pleuropneumoniae*, MacInnes et al. (2008) took nasal and tonsil swabs of 6 week old pigs from 50 swine herds in Ontario. Several different types of farms (for example, farrow-to-finish, multi-site, and farrow-to-feeder) were included. PCR, serology, and selective media were utilized to find the herd prevalence. All but one of the herds tested positive for *S. suis* (98%), and *H. parasuis* was detected in 96% of herds. *A. suis* was detected in 8 herds, and 78% of the herds tested were positive for *Actinobacillus pleuropneumoniae*. Only one herd tested positive for toxicogenic *P. multocida*.

Slaughter Checks/Surveillance

Surveillance programs also exist to check for lesions at slaughter. They first started in Scandinavia, where lesions were recorded in all herds. Early programs included the Danish Swine Slaughter Inspection Data System, which was implemented in 1978 (Willeberg et al., 1984). These programs led to the development of similar programs in other countries.

In performing surveillance at slaughter (also known as slaughter checks), there are several types of lesions to check for including: papular dermatitis, liver white spots, nephritis, ileitis, peritonitis, pericarditis, atrophic rhinitis, pleuritis, and pneumonia (Davies et al., 1995). Because the focus of this paper pertains mainly to respiratory diseases and their associated lesions, the main focus of discussion will be slaughter checks monitoring for pleuritis, pneumonia, and atrophic rhinitis.

Morrison et al. (1985) proposed four possible methods of examining pneumonia prevalence. These techniques included the following: (1) examine the percentage of lung involved and calculating a mean percentage and standard deviation, (2) determining first an amount of pneumonia, then counting the number of lungs above this amount, (3) scoring the lung most severely affected by pneumonia, and (4) categorizing lungs by how much of the lung is affected. The contribution of each of the seven lung lobes to lung weight (right cranial, right middle, right caudal, accessory, left cranial, left middle and left caudal) are 11.9%, 7.5%, 30%, 4.6%, 7.1%, 6.9%, and 31.6% respectively. Other slaughter check methods, such as PigMON use different percentages for lung lobe weights, which will be discussed later.

The first method, which calculates a mean and standard deviation, is preferred in

the respect that it provides the most information. However, the drawbacks are that it can be time and labor intensive. Also, in herds with a higher mean percentage of pneumonia, a larger sample size is needed.

The third method (also known as the maximum percentage pneumonia technique) of scoring the most affected lung is also effective. It has the advantage over the first method in that it takes much less time to perform, and is informative at the herd level. A clear set of guidelines set by Conover (1971) states the sample size needed to detect disease in a certain percentage of the herd at a certain confidence level. For example, a sample size of 59 is required to state at a 95% confidence level, 95% of the herd is less affected than what was observed in the most severely affected lung. The drawbacks are in order for this method to work, the worst lung must be chosen, and data gathered provides little value in comparing between herds.

The second method is less labor intensive in that only pneumonic lungs are counted. This method, however, requires setting a baseline as to what percentage of the lung needs to be affected in order to be considered pneumonic. The authors found that setting $\leq 5\%$ as the baseline was just as informative as setting the baseline to $>0\%$, and fewer lungs needed to be counted. The problem with this is that the person examining the lungs needs to be able to accurately identify the percentage of lung affected each time. This could present problems, for instance, if the percent of a certain lung affected was slightly fewer than 5% and was counted as pneumonic, or, conversely, if slightly more than 5% of a lung was affected and was not counted as pneumonic. If any other value than $>0\%$ is chosen, there can be problems with inaccuracy and subjectivity.

The fourth method poses similar problems as the second method. Lungs are put

into categories (the suggested categories are 0%, >0%-≤5%, >5%-≤10%, and ≥10% for no lesions, mild, moderate, and severe respectively.) When the percentage of lung affected lies close to the cutoff of one of these categories, the difficulty comes in deciding which category to put the lung in. This could lead to a less precise estimation, and difficulty in interpretation.

Another method proposed by Bollo et al. (2010) is the “0 to 5 scoring method” to look for enzootic pneumonia in Spanish abattoirs. In this instance, lesion scores range from 0 to 5. For each increase in number, it is estimated that approximately 10% of the individual lung lobe is affected. The breakdown of the amount of lung involved by lesion scores from 1 to 5 is as follows: >5%-≤15%, <15%-≤25%, >25%≤35%, >35%-≤45%, and >45%-≤55%. In this case, the weights of each lung lobe differ from Morrison et al (1985): right and left cranial lobes 10%, right and left middle lobes 7%, accessory lobe 6%, and right and left caudal lobes, 30%. Calculations are then performed measuring the percentage of pigs presenting lesions, the percentage of pigs presenting lesions scored 4 or 5, and the total average score. Using statistical analysis such as a t-test or rank-sum test (Fay and Proschan 2010), comparisons can be made between different populations of animals. The advantages of this method are the ease in learning and execution. However, as discussed with previous methods, subjectivity can be an issue.

Programs that have been developed from the Scandinavian slaughter surveillance include PigMON in the United States, and PHMS, or the Pig Health Monitoring Scheme, in Australia (Pointon et al.,1999). As with similar schemes, inspection is done visually and by palpation. With PigMON, lung lesions are scored by determining the lesion amount in each lung lobe. These scores are then put into a formula where the contribution

of each individual lung lobe is calculated based on the area of the lung. The contribution of each lung lobe is as follows: right and left cranial lobes 10% each, right and left middle lobes 10% each, right and left caudal lobes 25% each, and accessory lobe 10% (Thacker et al., 2010), differing from the contribution of lung lobes estimated by Morrison and Bollo. The data is then recorded into a computer software program, and the results are sent back to veterinarians and producers.

Similar to other surveillance programs, PigMON also records lesions due to pleuritis and atrophic rhinitis. Pleuritis is scored 1 if found between lobes and 2 if found between the parietal and visceral pleura, or the lungs are attached to the chest wall. It is also noted if the pleuritis comes from normal or pneumonic lungs. Atrophic rhinitis is scored on a scale from 0-5. One limitation, however, is that viscera from condemned carcasses were not able to be examined (Davies et al., 1995).

From 1990-1993, 49,256 pigs were tested using the PigMON system. This data was taken in Minnesota to test if this program should be extended to other areas of the United States. This data was used to build a database which veterinarians and producers could use as a reference in comparison to their own herd. In this three year period, pneumonic lesions were found in 64.7% of carcasses, pleuritis was found in 9.1% of carcasses, and atrophic rhinitis was found in 11.4% of snouts (Davies et al., 1995). The response to this program was very positive, with 86% the United States producers that were surveyed stated they viewed this program as beneficial in increasing herd profitability. Veterinarians surveyed also viewed the PigMON program as beneficial (Davies et al., 1992; Davies et al., 1996).

Two main health schemes are used in Great Britain: the BPEX Pig Health Scheme

(BPHS) and Wholesome Pigs Scotland (WPS) (Sanchez-Vazquez et al., 2011). These schemes look for both respiratory and non-respiratory conditions (twelve conditions total) by examining the skin as well as the pluck. Lesions associated with pleuropneumoniae are scored as either absent or present. Lesions due to enzoonotic pneumonia are scored from 0-55 (the percentage of lung affected). Three scores are possible for lesions associated with pleuritis: 0 for absent, 1 for lesions between lung lobes, and 2 for lesions involving both pleural surfaces (parietal and visceral), similar to the scoring system in PigMON. WPS was first developed in 2003 to examine commercial Scottish herds, and BPHS was developed in 2005, as a larger scale version of WPS.

One limitation with BPEX is that the lungs are not able to be incised by the assessors, so inspections must be done by palpitation and examining the surface (Holt et al. 2011). This is because the assessors are not official meat inspectors. Despite the limitations, these programs have been viewed as beneficial. BPEX recorded that 60% of the 55 producers and 80% of 42 veterinarians surveyed used the data obtained at slaughter to implement changes to improve herd health.

Holt et al. (2011) also looked at the efficacy of BPEX in providing information to producers, by determining if the respiratory lung lesions found at slaughter were associated with pathogens found on the farm. Serology was used on the farm to test for several respiratory pathogens including PRRS, H1N2, swine influenza, *Mycoplasma hyopneumoniae*, porcine parvovirus, porcine circovirus, and *Actinobacillus pleuropneumoniae*. Because some herds may vaccinate for the tested pathogens, it is important to distinguish if antibodies present are due to disease or vaccination. The authors found a statistically significant relationship between pleurisy and the viral

pathogens PRRS and H1N2. However, not all respiratory pathogens were tested for, especially bacterial respiratory pathogens, and the pigs that were tested on farm were not the same pigs tested at slaughter.

Andreasen et al. (2001) conducted a longitudinal study of 830 pigs from eight herds by bleeding piglets monthly until slaughter and testing for *Mycoplasma hypopneumoniae* and *A. pleuropneumoniae*, then examining for respiratory lesions at slaughter. There was some association between the seroprevalence of *M. hypopneumoniae* the lesions found at slaughter; however, there was no association between *A. pleuropneumoniae* seroprevalence and slaughter lesions. These findings suggest while there is some evidence that lesions found at slaughter can correspond with pathogens found on the farm, more research is needed.

As noted earlier, initially swine slaughter checks were met with much enthusiasm. The desire for such programs in swine, rather than in poultry and beef was for two main reasons: more swine were housed in confinement systems, and necropsy was not feasible to look for disease in subclinical or healthy pigs, due to the individual animal's economic value (Pointon et al., 1999; Davies et al., 1995). The majority of producers involved in the PHMS and PigMON programs consulted veterinarians with their results, and the majority of producers involved implemented changes on-farm to help control disease. Most also felt that participation in such programs could help increase profits.

However, the value of slaughter checks has been called into question, and they are no longer commonly performed for several reasons. One reason is the inability of slaughter checks to be performed at line speed. Also, animals from the same herd often do not come to slaughter at the same time. If slaughter checks are only performed on the

best performing (animals finishing first) or worst performing animals (animals finishing last), this data may not be representative of the whole herd.

Another limitation is that often by the time the animal reaches slaughter it may be too late to detect lesions, especially if disease has an early on-set. Also, if the animal dies before it reaches slaughter, the data obtained at slaughter may not be truly representative of the herd (Bollo et al., 2010; Pointon et al., 1999; Sanchez-Vazquez et al., 2011).

A cohort study conducted by Regula et al. (2000) compared using serological data versus evaluation of the lungs, liver, skin, and nasal turbinates at slaughter, and found that serology is better at detecting subclinical disease.

Animal Health and Carcass Contamination

While the effect of *Salmonella* on animal and public health has been widely studied, the link between animal health due to infection with respiratory pathogens and public health has not been widely explored. In 2003, Russell conducted a study in poultry examining the effect of airsacculitis, or inflammation of the air sacs, on possible carcass contamination. Two hundred birds positive for airsacculitis (ASP) as well as two hundred birds negative for airsacculitis (ASN) were analyzed over five replicates. Only 20 of the ASP birds and 20 ASN were chosen for bacteriological evaluation during each replicate. Russell found that birds with lesions due to airsacculitis were more likely to be contaminated with *Campylobacter*. This was thought to be because animals that were positive for airsacculitis may not have been the same size or weight as negative birds, and processing errors such as digestive tears could have caused increased fecal contamination.

While Russell's study demonstrating the effect of airsacculitis on bacterial contamination focused on *Campylobacter* in poultry, it is reasonable to assume that such lesions would have a similar effect on *Salmonella* contamination in swine. Expanding on the findings of Russell, two studies have been conducted on the effect of similar lesions in swine on foodborne bacterial contamination. These lesions in swine are referred to as peelouts, or a peritoneal or pleural adhesion that does not allow for complete removal of viscera, requiring extra trimming. Generally the lung tissue is involved. (See figure 2). They are one of the most frequently observed lesions in swine (Enøe et al., 2002; USDA-APHIS, 2008). However, the specific pathology of a peelout has not been described, and is only specific from a meat inspection standpoint, underlying the need for more information on the topic (Hurd et al., 2008a).

The first study done by Hurd et al. (2008a) involved taking samples at one abattoir over the course of eight visits. The researchers took 280 samples, which were then tested for *Campylobacter*, *Enterococcus*, and *Salmonella*. Samples were taken from the skin at pre-scald, the bung/pelvic cavity after removal of the distal colon and rectum, and at the pleural cavity before the final carcass rinse. Samples were pooled in groups of five resulting in 56 pools. Peelouts were identified as a health indicator, as well as abscessed heads and fatigued animals. On-farm antibiotic usage also considered.

The study found approximately 7% of carcasses had some sort of adhesions. A linear regression model showed that for each increase in peelout percentage, the amount of *Enterococcus* and *Campylobacter* contamination increased by 4.4% and 5.1% respectively.

Salmonella was isolated from 8.9% of the bung and pleural cavities, and 17.9% of

the carcasses pre-scald. This makes sense, as one would expect the prevalence of *Salmonella* to decrease after scalding. However, there was no meaningful association detected between *Salmonella* contamination and the prevalence of peelouts. The variance of peelouts and bacterial contamination varied from replicate as well as antibiotic usage.

One of the strengths of the study is that carcasses were sampled with the healthiest first to minimize cross contamination. Also, sampling over several visits helped account for the variance of peelouts/bacterial contamination that was found each day. Using animals that had the same management practices (with the exception of antibiotic use) helped minimize differences in prevalence that could have been attributed to on-farm practices. Also, serotyping was used to identify *Salmonella* strains, as certain strains pose more of a public health risk than others, such as *Salmonella typhimurium* (Foley et al., 2008).

One of the limitations of this study is that the sample size was relatively small. A total of only 280 carcasses were sampled, and for the pleural cavity, one sponge was used to swab five carcasses, resulting in a total of 56 pools. This method is commonly used in Denmark. The rationale for pooling the pleural swabs together was to enable better detection of *Salmonella* (Sørensen et al., 2004).

Interestingly, a statistically significant relationship ($p < 0.05$) was found between peelouts as *Campylobacter* in the pleural cavity, as well as peelouts and *Enterococcus* in the bung/pelvic cavity. This could be due to the higher numbers of positive pools. If, on the other hand, we had a smaller number of positive pools, we would not have seen as high of an association. If the samples had not been pooled, there may have not been as strong of a statistical association. For example, if hypothetically only one of the samples

in the pool was truly positive, the fact that it is pooled with four other samples would make all of them appear positive, therefore, there would be a stronger association.

Another limitation is that the carcasses were not labeled after the first sets of samples were taken, making it likely that samples were not all taken from the same carcasses. While this method possibly allowed for the testing of different pigs, it makes it difficult to trace the bacterial contamination at a pig/herd level. Antibiotic usage was also studied as a secondary objective in this study, as it was found to be a confounder (Kleinbaum et al., 2003).

However, as pointed out in the study, one limitation is that antimicrobial-free pigs represent a different population from the conventional pigs. Because the antimicrobial-free pigs have never been treated with antibiotics, and the conventional may have been treated, they may represent a healthier herd. Therefore, it should not be surprising that there may be more contamination in the conventional group. Finally, the study outlines that there is a need to further examine the association between peelouts and bacterial contamination.

The second study by Hurd et al. (2012) had two objectives: determine if peelouts were associated with *Salmonella* contamination, and determine the ability of non-experts to assess and identify peelouts. Like the previous study, samples were taken at one abattoir. Four replicates were run, with 358 total carcasses sampled: 202 conventionally raised pigs and 156 antimicrobial-free pigs. As with the previous study, sampling was taken at the beginning of the day to reduce the possibility of cross-contamination. Carcasses were selected 10-15 carcasses apart in order to minimize the chance of cross contamination, as it has been found that the carcass following a *Salmonella* positive

carcass has a 28% chance of being contaminated as well (Berend et al., 1996). Pictures were taken of the interior of the carcasses for lesion scoring. Pleural swabs were taken after the final USDA inspection point just before the carcass rinse. The exterior of carcasses are swabbed according to FSIS procedure, however, the interior of carcasses are not (USDA-FSIS, 2012).

At each visit, 25 lesioned and 25 non-lesioned carcasses were sampled from each group. The pleural swab samples were then tested for *Enterococcus* and *Salmonella*. Photographs of the carcasses were studied and scored by three veterinary pathologists, as well as one non-expert. To test agreement between the expert and non-expert assessors, the Fleiss κ was calculated. An ROC curve and LR plot were also used (Dohoo et al., 2003; Fleiss, 1981).

Enterococcus was isolated from 10.9% of carcasses, while *Salmonella* was isolated from 10.1% of carcasses. Of the carcasses sampled, 182 were positive for lesions, and 12% of those were positive for *Salmonella* and *Enterococcus*. Pigs raised without antimicrobials were more likely to be contaminated with *Salmonella* (17.3%) versus conventionally raised pigs (4.5%). *Enterococcus* contamination was slightly higher in the conventionally raised pigs. The probability of *Salmonella* contamination from antimicrobial free swine was significantly higher than from conventional swine (POR 6.7, 95% CI 2.7-16.9). Therefore, on-farm antibiotic use was found to be a significant confounder in this case. After controlling for replicate and on-farm antimicrobial use, statistical analysis found that carcasses with lesions were 90% more likely to be contaminated with *Salmonella*. In addition, statistical analysis found that there was a very close agreement between non-expert assessment and expert assessment.

This indicates that non-expert assessment is adequate to determine peelout status.

One strength that this study had over the previous was that the carcasses identified at evisceration were the carcasses that were swabbed before the final rinse. In the previous study, it was addressed that the rationale for pooling *Salmonella* samples was for increased sensitivity to detect *Salmonella*. In order to increase the possibility of detecting *Salmonella* from each pleural swab, an extended enrichment protocol was performed. The isolation protocol called first for enrichment at 24 hours, incubation on selective agar for 48 hours, and then subculture into media for an additional 6-8 days for enrichment.

Another strength of this study is that the ability of non-experts to detect peelouts was tested. Determining that non-experts can detect peelouts enables future research to be done without having to rely on experts, therefore, saving time, money, and labor. Also, for quality control purposes, the person collecting the pleural swabs was blinded to the whether or not the carcass was lesioned or non-lesioned, as was the bacteriological laboratory. This reduced the possibility of information bias (Kleinbaum et al., 2003). For example, if the person taking carcasses swabs knew which carcasses had peelouts or not, they may have been inclined to swab peelout carcasses more heavily with the goal of detecting *Salmonella*.

One limitation to the study, as in the previous peelout study, was the sample size. The total number of carcasses sampled was 358, with 182 exhibiting lesions. Furthermore, 156 swine were sampled that were raised without antimicrobials, and 202 from conventionally raised swine. Spread out over four visits, this is slightly less than 100 pigs per visit. Also, findings were isolated to one barn. While this controlled for the

possibility of barn being a confounding variable, it is possible that the results may not be representative of not only that particular abattoir, but other abattoirs as well.

Other limitations that are pointed out include that the on-farm history is possibly different between the antimicrobial-free and conventionally raised pigs. For instance, because the antimicrobial-free pigs sent to slaughter were never given antimicrobials, they are most likely the best performing pigs out of the herd, whereas the conventional pigs may have been administered antibiotics in their lifetime, perhaps due to a previous illness, and could be a source of bias (more specifically, selection bias) (Kleinbaum et al., 2003). Also, even though the pleural swabs had an extended enrichment period, it is possible that there was a low sensitivity with *Salmonella* detection.

Human Health and Animal Health

The literature referenced above has studied how animal health on the farm could affect carcass contamination, and how carcass contamination could affect public health. However, little work has been done to examine the direct relationship between animal health and public health. Singer et al. 2007 proposed a model using *Campylobacter* infections in chickens to model the potential impact of illness rates on the farm to public health. The authors utilized a dynamic systems approach, and mathematical models were used to build several equations to analyze the direct effect of animal illness rates and public health. Also the effects of pre-harvest interventions, such as changing antimicrobial usage on farm, were modeled. The authors estimated that as little as a 1% increase in animal illness rates on the farm had the potential to increase human health risk by 4%. On the other hand, reducing the animal illness rates, even slightly, had the

potential significantly decrease human health risk. One limitation to this model is that there was very little data available to obtain parameter estimates for the model.

A key assumption that was made in building these models is that there was little effect of post-harvest interventions on decreasing carcass contamination. However, this is not likely a valid assumption, as the main consensus of scientific literature suggests that post-harvest interventions can have a significant impact in decreasing carcass contamination. A more valid approach in studying how animal health can affect public health risk would be to first examine the effect of animal health on carcass contamination, and then the effect of carcass contamination on public health risk.

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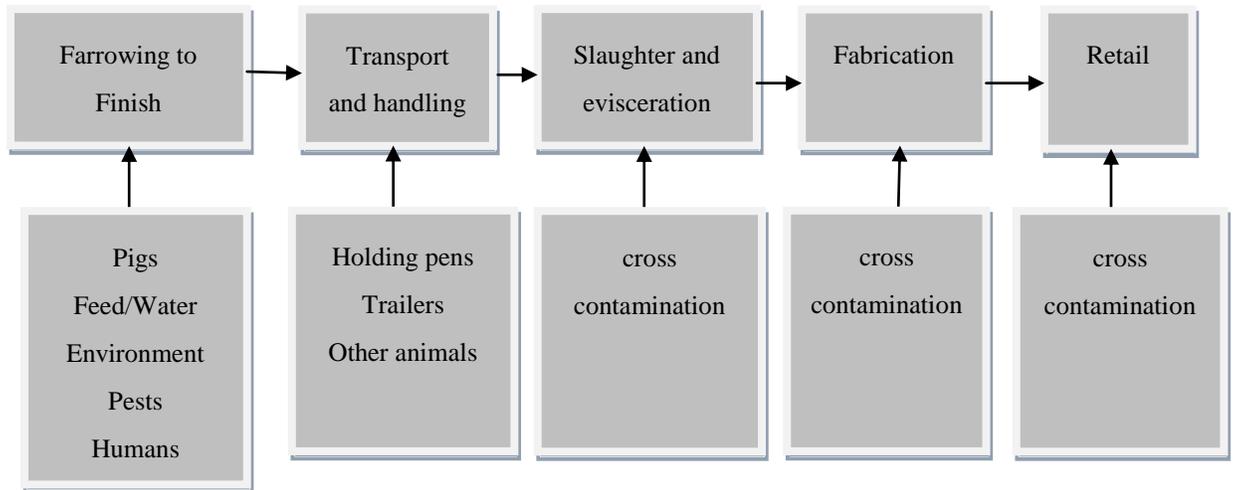


Figure 1. Sources of *Salmonella* contamination during different stages of production and processing. (Adapted from Dickson et al., 2010).

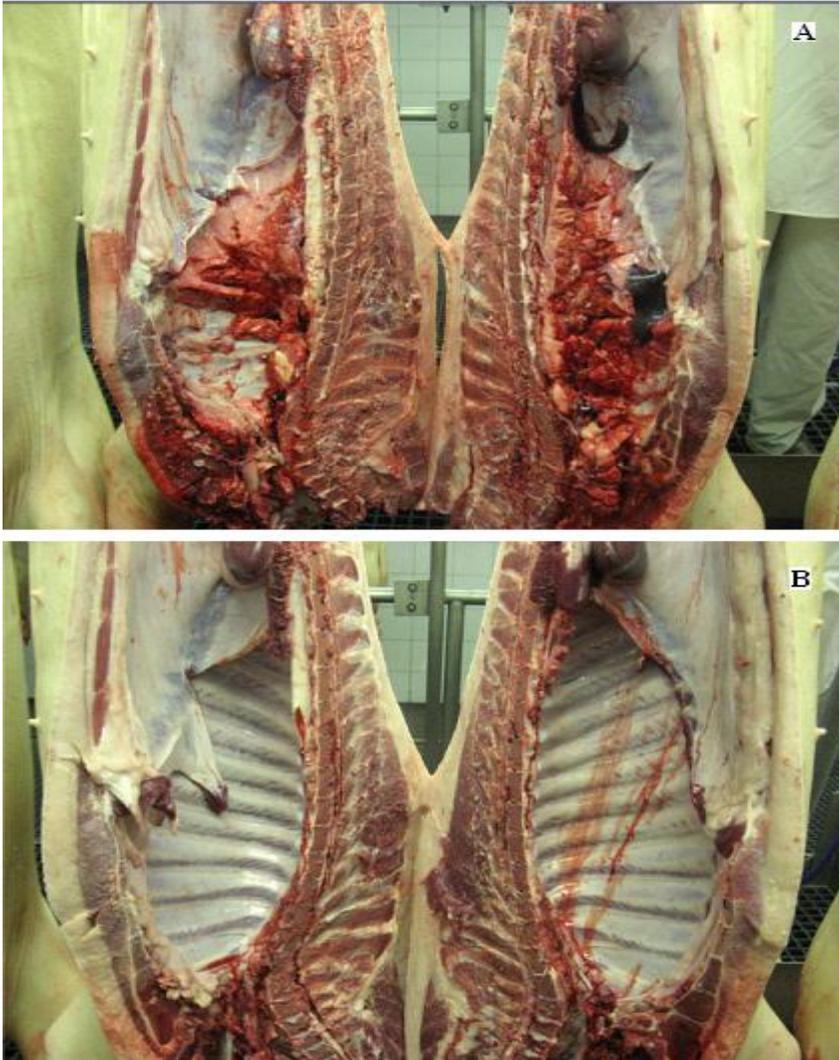


Figure 2. A lesioned carcass positive for *Salmonella* (top) and a lesioned carcass negative for *Salmonella* (bottom) (Source: Hurd et al., 2012)

**CHAPTER 2. THE IMPACT OF PIG HEALTH ON PUBLIC HEALTH:
QUANTITATIVE DATA FOR RISK ASSESSMENTS.**

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A MANUSCRIPT TO BE SUBMITTED TO **FOODBORNE PATHOGENS AND
DISEASE**

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 (peelout present) and 50 non-lesioned (peelout 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 9.77% (95% CI 5.31% to 14.22%). 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 (Alban et al., 2005; Arguello et al.,

2013; O'Connor et al., 2012).

With 48 million illnesses annually attributable to foodborne pathogens, even small increases in illness rates can cause 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).

From 1996-2012 there has been a reduction in human illnesses attributable to foodborne infectious agents such as *E. coli*. However, 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, 2012) 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 (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 (Figure 1.) As a result, extra trimming and handling is required. In accordance with post-mortem inspection procedures, if these peelouts are severe, they are often retained for further veterinary inspection (USDA-FSIS, 2012).

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 peelouts 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., 1999; MacInnes, et al., 2008; Olson et al., 2001; Brockmeier et al., 2001; Brockmeier, 2004; Mattoo et al., 2005).

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*).

Materials and 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 by Arguello et al. (2012) estimated that 50% of contaminated carcasses are a result of cross-contamination, whereas a study conducted by Botteldoorn 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-Sponges 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, 2012). Gloves were changed after each swab to minimize the possibility of cross contamination. For quality control purposes and to minimize information, 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, 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), and 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.

To address the relationship between *Salmonella* contamination and peelouts, a similar logistic regression model was used, however, in this model, the binary categorical outcome was *Salmonella* contamination, and the explanatory variable was carcass lesions. Therefore, in this instance, this model is the logit of the probability of being *Salmonella* positive in lesion carcasses compared to being *Salmonella* positive in non-lesioned carcasses. (Kleinbaum and Klein, 2010; Kleinbaum et al., 2003). Abattoir and sampling period were run again as fixed effects. The coding scheme was the same as the previous models. As with the previous model, interaction was tested for between the fixed effects and explanatory variable, and stratified if significant. Again, a fifth adjustment was used (Heinze, et al. 2002; SAS, 2013) and a sensitivity analysis conducted if needed. The unadjusted prevalence odds ratios, adjusted prevalence odds ratios, 95% confidence intervals, and p-values were calculated.

Results

Study population and general results

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 2012). 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 et al., 2003). Table 1 shows a descriptive analysis of peelout prevalence, *Salmonella* contamination, and respiratory pathogen contamination by each abattoir visit.

Prevalence estimates

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 9.77% (95% CI 5.31% to 14.22%). The prevalence at the individual animal level was found to be 8.29%; however, this data is not very useful, as it fails to take into account the effects of abattoir and sampling period. Figure 2 shows a frequency distribution of peelout prevalence per abattoir visit, and Table 1 shows the peelout prevalence by abattoir.

Bacteriology

For the second objective, respiratory pathogen contamination rates were obtained. Figures 3-5 show this data for each abattoir visit. Respiratory pathogen contamination rates for lesioned and non-lesioned carcasses ranged as following: *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.

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. Figure 6 shows this data at each abattoir visit.

Statistical analysis

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 abattoir, 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.

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

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 9.71 skewed our data, giving a bias away from the null (Kleinbaum et al., 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. A Forrest plot was also ran (Figure 7) to further illustrate this data.

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 9.77% (95% CI 5.31% to 14.22%). 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).

In addition, 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. Also, animals that had severe clinical infections likely did not make it to slaughter, or they failed to pass ante-mortem inspection. (Bollo et al., 2010; Davies et al., 1995; Sanchez-Vazquez et al., 2011). This is an example of selection bias, which can occur with cross-

sectional studies (Kleinbaum et al., 2003). 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 may not be a true representation of the peelout prevalence and bacterial contamination at each abattoir, as 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. In our study, 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. 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 to take samples at other points in the processing chain in order to obtain differences in contamination rates, and thus determine where other risks for contamination exist.

Conclusions

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.

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CHAPTER 3. GENERAL DISCUSSION AND CONCLUSIONS

The overall objective of this thesis was to examine how *Salmonella* and respiratory pathogens affect both pig health and public health risk, first by reviewing the available literature, then by reporting our study conducted, and finally, discussing how the literature relates to our findings.

By examining the available literature, it is clear that both *Salmonella* and the respiratory pathogens that we tested for are of significant importance in the swine industry. While the slaughter checks for respiratory described previously were seen as beneficial from a producer standpoint, they may not be a true representation of disease patterns in a herd, which was discussed in the literature review.

In our study we did not find any consistent pattern between respiratory pathogen contamination and peelouts, suggesting that there is little association. If there truly is an association between respiratory pathogen contamination and lesion status, there could be a few possible explanations for why an association was not found. One explanation is that infection can be isolated to one lobule without affecting the others. Also, the entirety of one lung lobe may not be affected. Therefore, it is possible that the pig may have had an infection, but we selected either an unaffected lobe, or an unaffected portion of a lobe. For example, pleuritis is often found with the ventro-cranial portion of the lung (Sørensen et al., 2011). This could be a possible source of information bias, specifically a non-differential misclassification of exposure (in this case the exposure was the respiratory pathogen contamination (Kleinbaum et al., 2003).

As discussed earlier, another reason is that many of the pathogens we tested for

are often common in herds. In affected herds, there could have been many carriers, and these carriers may have not developed any sort of infection or lesions. Even if an animal still had residual lesions, it is possible that the bacteria would have been cleared from the lung tissue by the time the animal went to slaughter. This could be a source of information bias, and we could have misclassification of disease as well as exposure. This is because often animals that had infections at a younger age will test negative for the bacteria. Animals that had severe infections probably had higher rates of morbidity and mortality, and may have not made it to slaughter or passed inspection (Bollo et al., 2010; Pointon et al., 1999; Sanchez-Vazquez et al., 2011.)

As previously discussed, many respiratory infections involve more than one pathogen; for example *Pasteurella multocida* and *Bordetella bronchiseptica* (Brockmeier et al., 2001; Olson et al., 2000). However, we did not find many samples that contained both *Pasteurella multocida* and *Bordetella bronchiseptica*. This is not surprising considering how few samples we had that were positive for *Bordetella bronchiseptica*. We found many samples with *Streptococcus suis* and *Pasteurella multocida* in the same lung sample.

Hurd et al. (2008) and Hurd et al. (2012) found evidence that swine carcasses exhibiting pleural/peritoneal lesions were more likely to be contaminated with pathogens. While there were many strengths in these studies, there were limitations posed as well, which our study aimed to address. To address the issue with sample size, we expanded our study to different geographical locations in the United States, and sampled over two sampling periods to possibly account for seasonal differences in peelout and pathogen prevalence.

As discussed in the previous chapter, this study found a national abattoir peelout prevalence of 9.77% (95% CI 5.31% to 14.22%). The prevalence obtained of Hurd et al. (2008) of 7.1% was lower than this estimate; however, this estimate was only taken at one abattoir. In order to compare our data to this previous study, an individual animal prevalence of 8.29% was calculated.

One possible reason for our estimates being higher could be because one abattoir had much higher peelout prevalence versus the other abattoirs: 28.39% for the first sampling period and 22.87% for the second sampling period. The peelout prevalence at this particular abattoir was over 10% higher compared to the other abattoirs (see Table 1). This possibly significantly increased the average peelout prevalence.

As mentioned in the literature review, the sets of samples in the first peelout study (Hurd et al., 2008) were not taken from the same carcass. Also, the same pleural swab was used for five animals, pooling results together. This may have made it harder to detect bacterial contamination at an individual level. In our study, the two sets of samples were both taken from the same carcass, and each pleural swab was only used on one carcass. This allowed us to get a more complete picture of the bacterial contamination, or lack of, found in each individual animal, as well as a possible increase in sensitivity.

Even though this study had a larger sample size versus the previous peelout studies, we still were only able to spend one day at each abattoir during each sampling period. Because the peelout and pathogen prevalence can vary significantly from day to day, the results should be interpreted with caution, as this could be a source of information bias and data may not truly be representative of each abattoir. Some abattoirs reported that they tend to have more lesioned animals on certain days of the

week, due to having more sick animals on certain days.

Collecting samples at line speed best simulated real-life conditions. However, there was only approximately three seconds to sample each carcass as line speeds are reported as approximately 1,000 per hour. As a result, the pleural/peritoneal swabbing may not have been adequate enough to detect bacterial contamination, possibly serving as a source of information bias. Also, we were unable to sample the same lung lobule each time, or take a sample of each lung lobule. Because we found little association between peelout prevalence and respiratory pathogen contamination, it could be argued that further research should be done either testing for the same pathogens to reaffirm our results, or to test for different pathogens altogether.

While we did find some association between *Salmonella* contamination and peelouts, there are several questions we were unable to answer given the limitations of our study. First, we obtained a relatively low number of positive *Salmonella* samples. The low number of positives could be due to a number of reasons. For example, it is possible that our sampling method was not sensitive enough to detect *Salmonella* present in the pleural/peritoneal cavity. Also the enrichment method that was used at bacteriological analysis may not have been adequate to detect *Salmonella*. At abattoirs that had higher numbers of *Salmonella* positive samples there was a significant association between *Salmonella* contamination and peelouts. If this experiment were to be repeated, it would be beneficial to utilize a more sensitive swabbing and culture method to detect more *Salmonella*.

As discussed earlier, the epidemiology of *Salmonella* infection in swine is very complex from farm-to-fork, and contamination or cross-contamination can occur at many

points during either pre-harvest or post-harvest. The animal could have been positive for *Salmonella* contamination while still on the farm, or could have picked up *Salmonella* at transport or lairage (Hurd et al., 2001a; Hurd et al., 2001b; Rostagno et al., 2003). The *Salmonella* contamination could have happened post-mortem as well, for example, during evisceration, carcass splitting, dehairing, contamination from equipment, personnel, etc. As outlined in reviews by Arguello et al. (2013) and O'Connor et al. (2012), several studies have tried to examine the prevalence of *Salmonella* contamination at different points in the processing chain, thus identifying possible areas where improved hygienic measures could be implemented. Arguello et al. (2013) focused on prevalence at farm and slaughter, while O'Connor et al. (2012) focused on prevalence at slaughter. Much of the literature referenced in these reviews emphasizes lairage (by environmental contamination or pig-to-pig contamination) as well as evisceration and carcass splitting as areas where *Salmonella* prevalence increases. Figure 1 in the introduction also illustrates a simplified diagram of possible sources of *Salmonella* contamination at different points in the processing chain.

The proposed next phase for the data gathered in this study is to build a mathematical model for possible use in a risk assessment, i.e. using the peelout prevalence as a parameter estimate. This data has also been disseminated to each of the abattoirs where sampling was done. They can utilize this data to determine if additional interventions at the abattoir need to be taken to reduce bacterial contamination, or determine where problems may be at the herd level.

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TABLES AND FIGURES

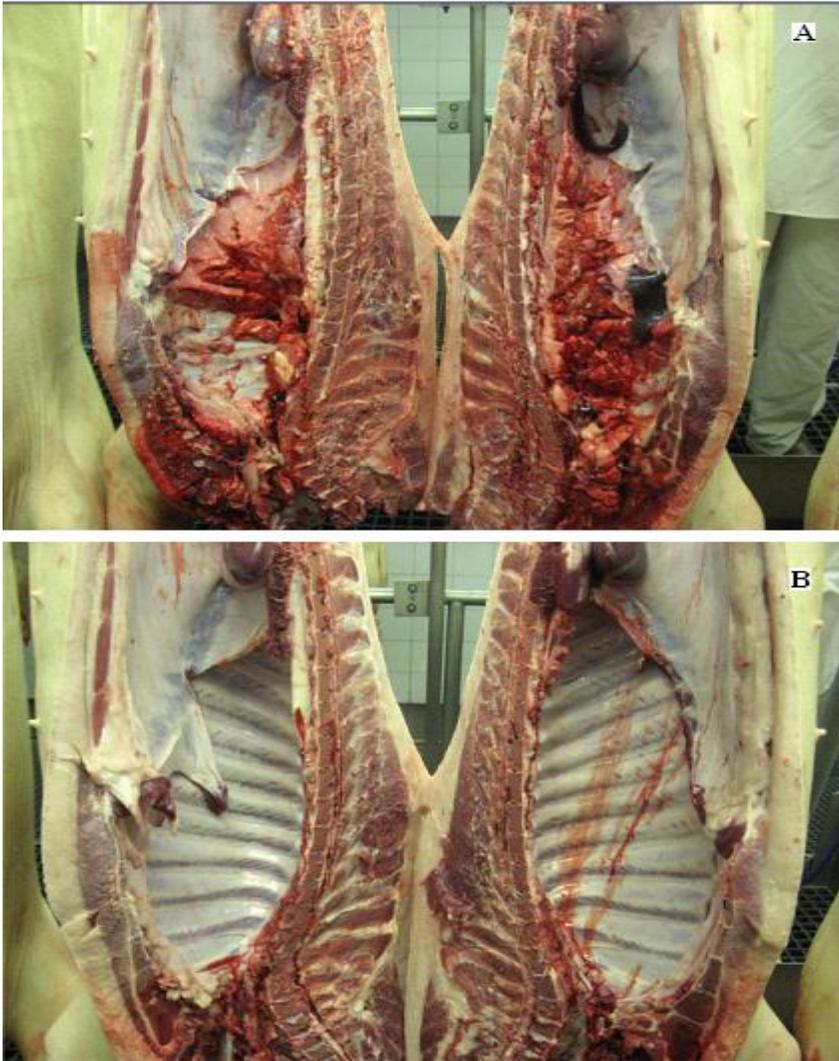


Figure 1. A lesioned carcass positive for *Salmonella* (top) and a lesioned carcass negative for *Salmonella* (bottom)

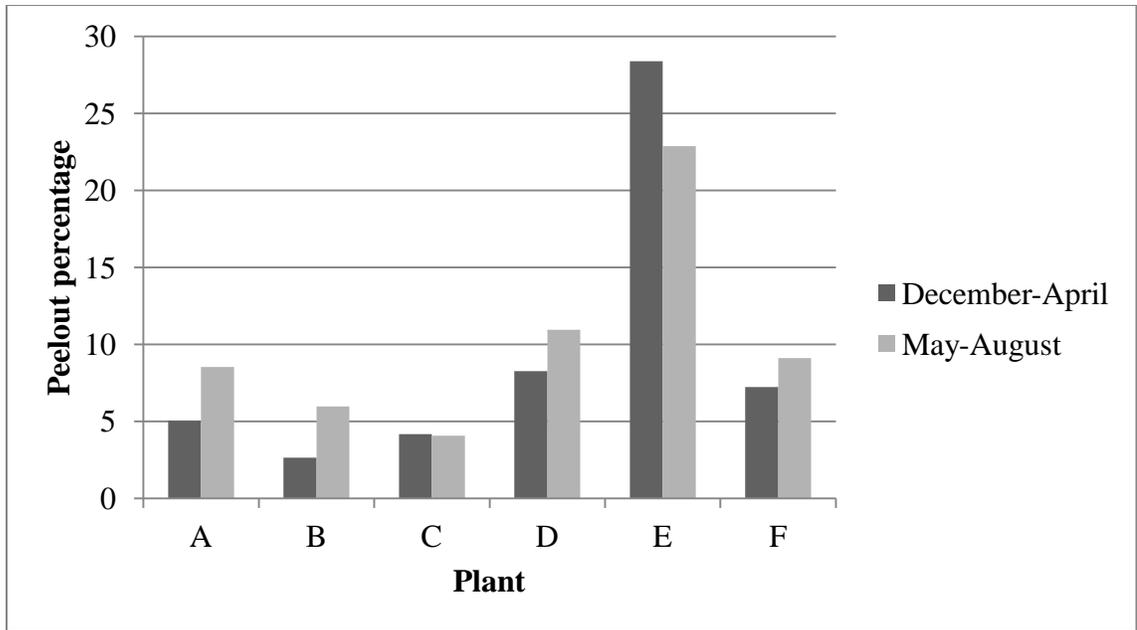


Figure 2. Peelout frequency by abattoir

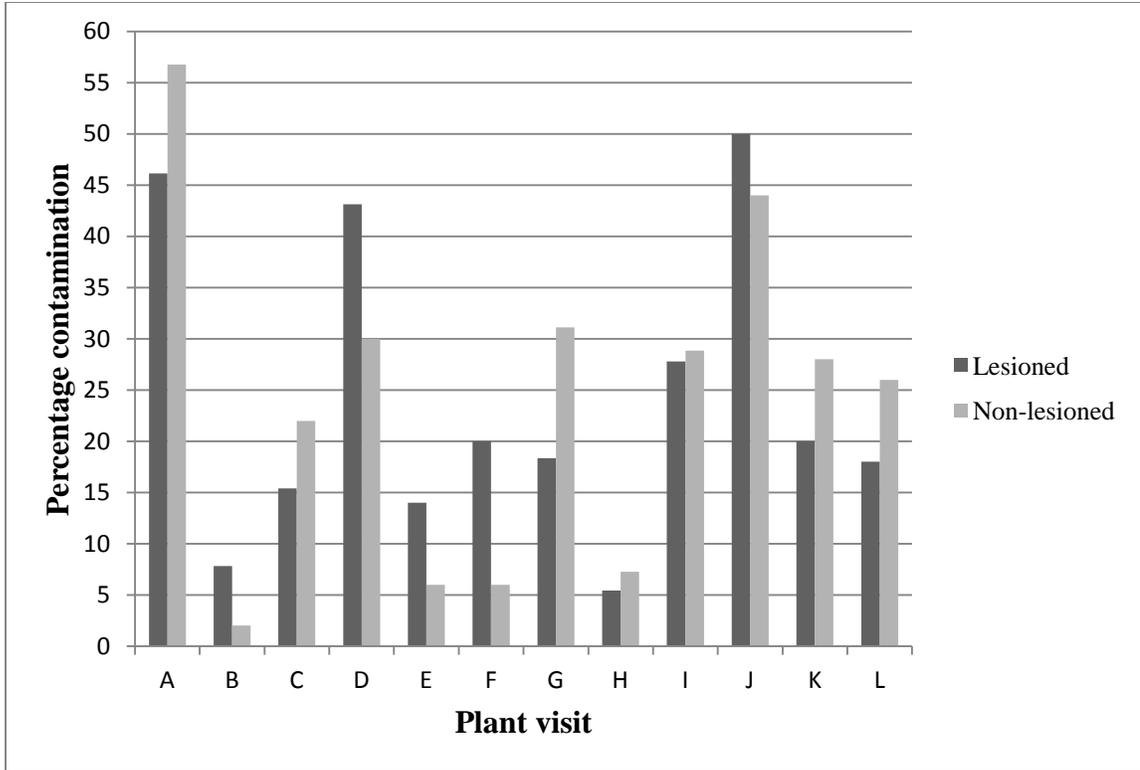


Figure 3. *Streptococcus suis* contamination by abattoir visit

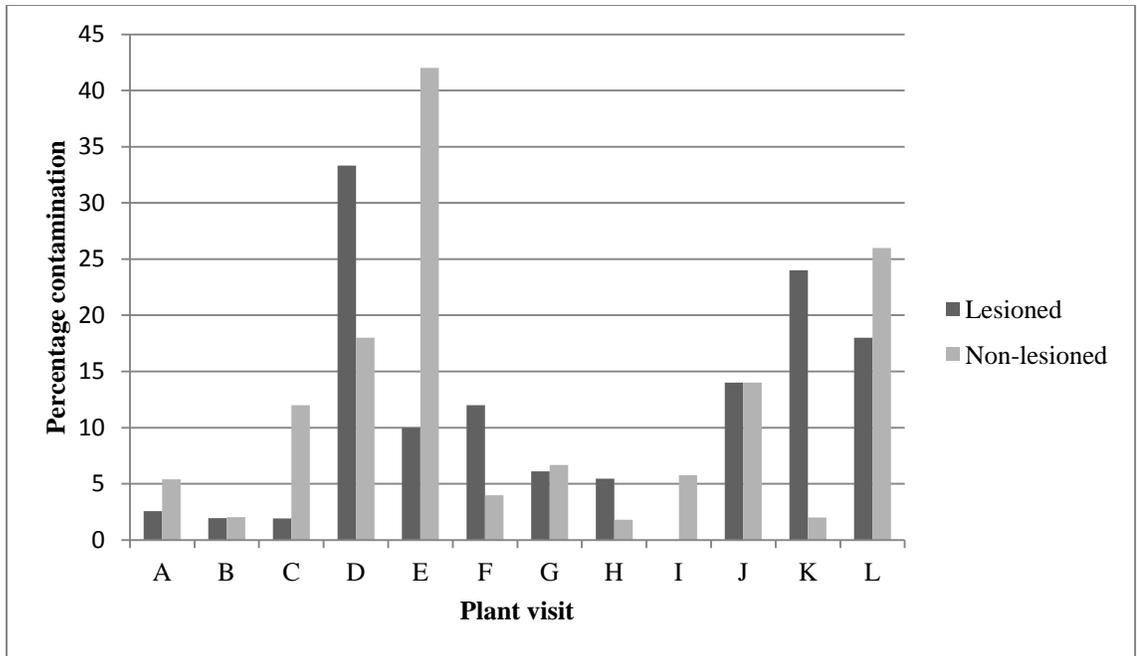


Figure 4. *Pasteurella multocida* contamination by abattoir visit

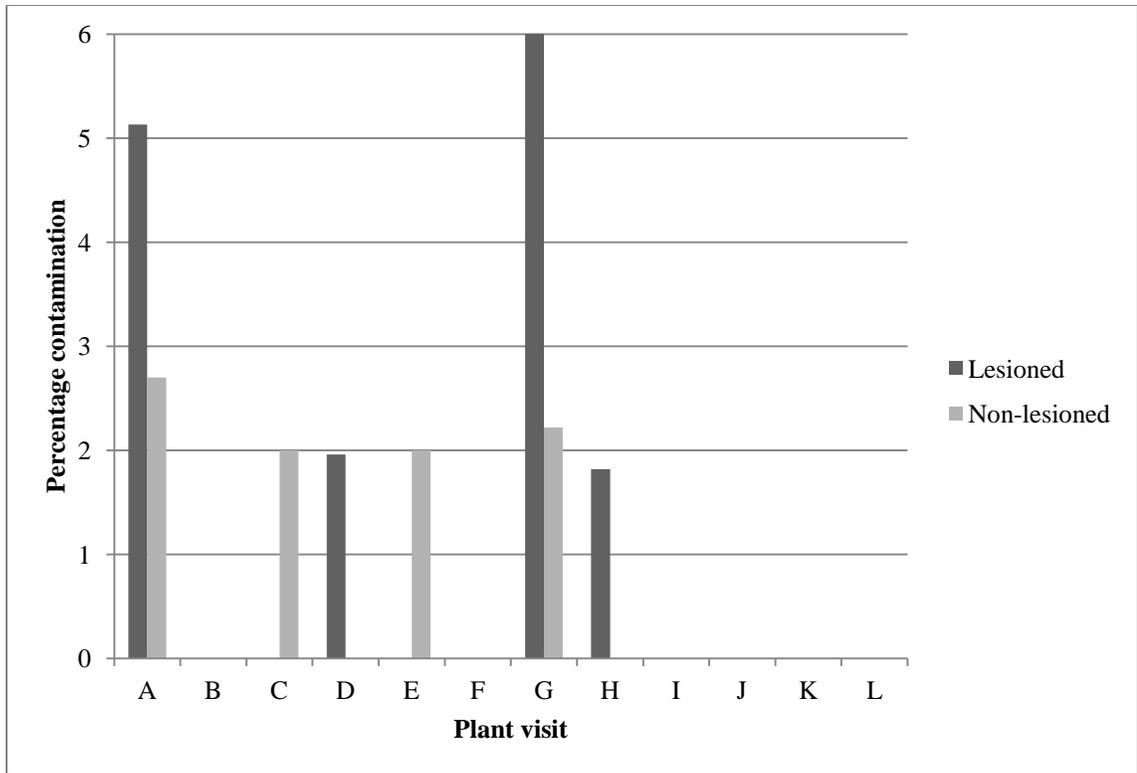


Figure 5. *Bordetella bronchiseptica* contamination by abattoir visit

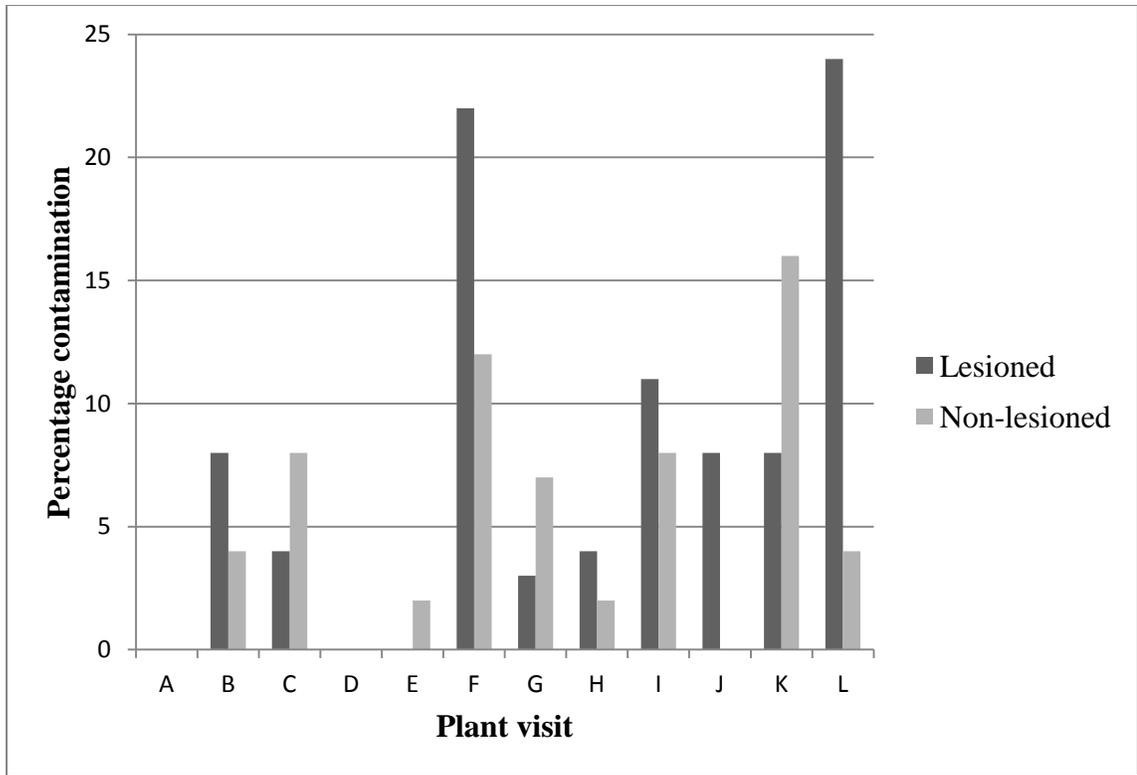


Figure 6. *Salmonella* contamination by abattoir visit

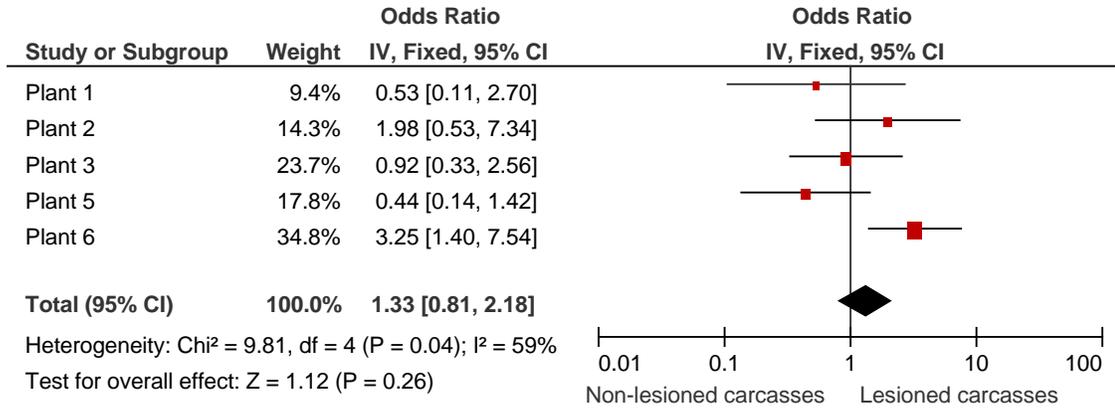


Figure 7. Forrest plot examining *Salmonella* contamination by abattoir visit while controlling for season

Abattoir visit	Peelout %	<i>Salmonella</i> contamination		<i>S. suis</i> contamination		<i>P. multocida</i> contamination		<i>B. bronchiseptica</i> contamination	
		Lesioned	Non-lesioned	Lesioned	Non-lesioned	Lesioned	Non-lesioned	Lesioned	Non-lesioned
A	5.05%	0.00% (n=0)	0.00% (n=0)	46.15% (n=18)	56.76% (n=21)	2.56% (n=1)	5.41% (n=2)	5.13% (n=2)	2.70% (n=1)
B	2.64%	8.00% (n=4)	4.08% (n=2)	7.84% (n=4)	2.04% (n=1)	1.96% (n=1)	2.04% (n=1)	0.00% (n=0)	0.00% (n=0)
C	4.18%	4.00% (n=2)	8.00% (n=4)	15.39% (n=8)	22.00% (n=11)	1.92% (n=1)	12.00% (n=6)	0% (n=0)	2.00% (n=1)
D	8.26%	0.00% (n=0)	0.00% (n=0)	43.14% (n=22)	30.00% (n=15)	33.33% (n=17)	18.00% (n=9)	1.96% (n=1)	0.00% (n=0)
E	28.39%	0.00% (n=0)	2.00% (n=1)	14.00% (n=7)	6.00% (n=3)	10.00% (n=5)	42.00% (n=21)	0.00% (n=0)	2.00% (n=1)
F	7.23%	22.00% (n=11)	12.00% (n=6)	20.00% (n=10)	6.00% (n=3)	12.00% (n=6)	4.00% (n=2)	0.00% (n=0)	0.00% (n=0)
G	8.53%	3.33% (n=2)	6.52% (n=3)	18.37% (n=9)	31.11% (n=14)	6.12% (n=3)	6.67% (n=3)	6.12% (n=3)	2.22% (n=1)
H	5.98%	4.44% (n=2)	1.96% (n=1)	5.45% (n=3)	7.27% (n=4)	5.45% (n=3)	1.82% (n=1)	1.82% (n=1)	0.00% (n=0)
I	4.08%	11.11% (n=5)	8.16% (n=4)	27.78% (n=15)	28.85% (n=15)	0.00% (n=0)	5.77% (n=3)	0.00% (n=0)	0.00% (n=0)
J	10.96%	8.00% (n=4)	0.00% (n=0)	50.00% (n=25)	44.00% (n=22)	14.00% (n=7)	14.00% (n=7)	0.00% (n=0)	0.00% (n=0)
K	22.86%	8.16% (n=4)	16.00% (n=8)	20.00% (n=10)	28.00% (n=14)	24.00% (n=12)	2.00% (n=1)	0.00% (n=0)	0.00% (n=0)
L	9.12%	23.53% (n=12)	4.00% (n=2)	18.00% (n=9)	26.00% (n=13)	18.00% (n=4)	26.00% (n=4)	0.00% (n=0)	0.00% (n=0)

Table 1. Descriptive analysis of peelout prevalence, *Salmonella* contamination, and respiratory pathogen contamination

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

Table 2. Association between bacterial pig pathogens and peelouts

Explanatory variable	Peelout percentage	% contamination lesioned carcasses	% contamination non-lesioned carcasses	Unadjusted POR	Adjusted POR	95% confidence interval	p-value
Overall (including abattoir 4)	9.77%	7.71% (n=46)	5.22 (n=31)	1.52	1.56	(0.97-2.52)	0.07
Overall (excluding abattoir 4)	9.80%	8.45% (n=42)	6.28% (n=31)	1.38	1.41	(0.87-2.31)	0.17
Abattoir 1 (Visits A and G)	6.83%	1.87% (n=2)	3.16% (n=3)	0.58	0.53	(0.11-2.70)	0.45
Abattoir 2 (Visits B and H)	4.30%	6.32 % (n=6)	3.00% (n=3)	2.18	1.98	(0.53-7.34)	0.31
Abattoir 3 (Visits C and I)	4.13%	7.37% (n=7)	8.08% (n=8)	0.91	0.92	(0.33-2.56)	0.88
Abattoir 4 (Visits D and J)*	9.35%	4.00% (n=4)	0.00% (n=0)	*	*	*	*
Abattoir 5 (Visits E and K)	25.11%	4.04% (n=4)	9.00% (n=9)	0.43	0.44	(0.14-1.42)	0.17
Abattoir 6 (Visits F and L)	8.04%	22.77% (n=23%)	8.00% (n=8)	3.39	3.25	(1.41-7.54)	0.01

Table 3. Association between *Salmonella* contamination by abattoir
*data from abattoir 4 not included in analysis