Risk-factors for positive carcass swabs in Danish slaughterhouses

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Abstract

Pooled swab sample results were obtained from 22 different Danish slaughterhouses of varying sizes from July 2002 to June 2008. The smallest slaughterhouse slaughtered 242 pigs per day on average, and the largest slaughterhouse slaughtered 11,200 pigs per day. A full dataset could be obtained for 17,180 swab pools. Five carcasses were swabbed with a gauze swab after cooling and pooled into one sample which was analysed for salmonella.

For each pool, serological results from the herds represented in the pool were obtained from the Danish Zoonoses register. One year’s data from each herd was used to assign a seroprevalence for each carcass. For each slaughterhouse we calculated the salmonella “burden” of the slaughter day by multiplying the number of pigs transported to the slaughterhouse and the serological prevalence of the particular herd. The results were analysed using a generalised, linear mixed model with serological status of the herds of origin for the sampled pool, salmonella burden of the day as fixed effects, and slaughterhouse as a random effect.

The results clearly indicated, that pool positivity could be explained by number of carcasses from seropositive herds presented in the pool, salmonella burden of day and a random slaughterhouse effect, which probably reflects slaughter hygiene.

Salmonella burden of the day was highly influential up until 40 seropositive pigs introduced to the slaughterhouse. From 40 seropositive pigs and upwards there was no further effect of introducing more positive pigs.

The results have important implications for the effect of herd based salmonella-programmes. For medium to high prevalence countries even very drastic reductions on herd level will only result in limited effects on positive carcasses on large slaughterhouses, whereas in small slaughterhouses a herd based intervention is highly effective.

Introduction

Salmonella control in the pig and pork production has traditionally been seen as something that has to be conducted at every level of the production from feed to slaughterhouse and processing. We claim that in order to be cost effective, control at all levels may be less cost-effective in some situations. And that some interventions may be cost effective under certain conditions, while others may be cost effective under other conditions.

This study try to analyse the association between salmonella level in the primary production and the risk of carcasses being bacteriologically positive at the slaughterhouse (here measured as pool prevalence of 5 carcasses).

In this study we found, that in small slaughterhouse, or regions with a very low prevalence of positive herds there is a very direct association between level in primary production and bacteriologcal results from carcasses, whereas in large slaughterhouses in medium to high prevalence areas this effect is relatively weak, indicating that for a large slaughterhouse, a very large and costly intervention in primary production is needed, in order to achieve even moderate reductions at carcass level.
Material and Methods

Pooled swab sample results were obtained from 22 different slaughterhouses of varying sizes from July 2002 to June 2008. The smallest slaughterhouse slaughtered 242 pigs per day on average, and the largest slaughterhouse slaughtered 11,200 pigs per day.

A full dataset could be obtained for 17,180 swab pools. Five carcasses were swabbed with a gauze swab after cooling and pooled into one sample which was analysed for salmonella. For each carcass, 300 cm² from three predefined areas was swabbed using the methodology described in the US regulations for slaughterhouses authorised for export to the US.

Each pool is marked with the Central Herd Register (CHR) number of the herds of origin. For each pool, serological results from the herds represented in the pool were obtained from the Danish Zoonoses register. One year’s data from each herd was used to assign a sero prevalence for each carcass. Initial analyses showed that the discriminatory power of the test in this situation was improved by using a cut off of 40 OD% instead of 20 OD%. Consequently, we used 40 OD% in this study.

For each slaughterhouse we calculated the salmonella “burden” of the slaughter day by multiplying the number of pigs transported to the slaughterhouse and the serological prevalence of the particular herd. A full dataset for a swab pool would then include the result of the bacteriological examination, the seroprevalence of the herd of origin for each carcass in the swab pool, and the number of serologically positive pigs transported to the slaughterhouse on the day in question.

Data were explored in a number of cross-tabulations.

The final analysis was performed with the use of a generalised linear mixed model (Glimmix, SAS Institute). The dependent variable was swab positivity, and the explanatory variables were the serological status of the herds of origin of the 5 carcasses in the pool and the serological status of the total number of pigs delivered to the slaughterhouse on the day in question. Random effects were the slaughterhouse and to allow for variation of the explanatory variables, the coefficients of the explanatory variables were allowed to vary between slaughterhouses.

Results

50% of the analysed herds were serologically positive in this study. Average prevalence in positive herds was 7.5%.

Initial exploratory analyses showed a clear effect of the serological status of the herds that contributed carcasses to the pool (table 1).

Table 1. Association between serological status of the carcasses in the pool and the risk of bacteriological positivity

<table>
<thead>
<tr>
<th>Positive herds in the pool</th>
<th>Positive pools</th>
<th>Negative pools</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>5</td>
<td>88 (4.4%)</td>
<td>1,895</td>
<td>1,983</td>
</tr>
<tr>
<td>4</td>
<td>135 (4.9%)</td>
<td>2,642</td>
<td>2,777</td>
</tr>
<tr>
<td>3</td>
<td>166 (4.18%)</td>
<td>3,809</td>
<td>3,975</td>
</tr>
<tr>
<td>2</td>
<td>122 (3.14%)</td>
<td>3,767</td>
<td>3,889</td>
</tr>
<tr>
<td>1</td>
<td>85 (3.13%)</td>
<td>2,634</td>
<td>2,719</td>
</tr>
<tr>
<td>0</td>
<td>38 (2.07%)</td>
<td>1,799</td>
<td>1,837</td>
</tr>
<tr>
<td>Total</td>
<td>634 (3.69%)</td>
<td>16,546</td>
<td>17,180</td>
</tr>
</tbody>
</table>

The association between the risk of the pool being salmonella-positive and the number of salmonella-positive pigs transported to the slaughterhouse on the day in question showed a complex pattern (figure 1). It could best be described as an increasing risk up to 40 sero-positive pigs, and then a flat line from 40 pigs and upwards.

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Several other models were tried, for example sero-prevalence of pigs transported to the slaughterhouse, but the best fit was obtained by using the number of sero-positive pigs.

In order to describe this, we performed a spline regression in which two parameters for the effect of the number of salmonella-positive pigs were evaluated, the effect up to 40 pigs and the effect above 40 pigs (table 2). Up to 40 seropositive pigs, each additional seropositive pig increased the proportion of positive pools by 2% (OR=1.02). Above 40 seropositive pigs there was no effect of an increased number of seropositive pigs.

**Figure 1.** Number of salmonella-positive pigs transported to the slaughterhouse and the risk of bacteriologically positive swab pools.

![Graph showing the relationship between salmonella sero-positive pigs and percent positive pool swabs.](image)

**Table 2. Results of the generalised linear mixed model.**

<table>
<thead>
<tr>
<th></th>
<th>Estimate</th>
<th>OR</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Intercept</td>
<td>-4.5124</td>
<td></td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Increase of one positive herd in pool sample</td>
<td>0.1504</td>
<td>1.16</td>
<td>0.0002</td>
</tr>
<tr>
<td>Increase of 1 sero-positive pig delivered to the slaughterhouse up to 40</td>
<td>0.02365</td>
<td>1.024</td>
<td>0.0007</td>
</tr>
<tr>
<td>Increase above 40</td>
<td>0</td>
<td>1</td>
<td>1</td>
</tr>
</tbody>
</table>

Random effects

<table>
<thead>
<tr>
<th></th>
<th>Estimate</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Slaughterhouse</td>
<td>0.1463</td>
<td>0.03</td>
</tr>
<tr>
<td>Increase in positive herds in sample*slaughterhouse</td>
<td>0.00267</td>
<td>0.31</td>
</tr>
<tr>
<td>Increase in the number of positive pigs delivered to the slaughterhouse*</td>
<td>0</td>
<td>1</td>
</tr>
</tbody>
</table>

The results show that there is a significant effect of the serological status of the pigs in the pool, and there is an effect of the status of other pigs slaughtered on that particular day, possibly due to cross contamination. The analyses of the random effects show an effect of slaughterhouse. The effects of the fixed effects could be assumed to be identical across all herds since the estimates from the random coefficients were far from significant.

In order to evaluate whether the model described the data adequately, residuals of the random slaughterhouse effect was plotted against slaughterhouse size (figure 2).

**Discussion**

The model showed a clear association between sero-positivity of the herds of origin included in the swab pool. However, it also clearly indicated that the serological status of other pigs delivered on the specific day was a clear risk. Many studies have shown that transport trucks and lairage pens often are highly
contaminated. The effect of the other pigs is probably due to cross contamination, either during transport, in lairage (Swanenburg, 2001) or during slaughter.
This effect is probably the reason why many studies have found it difficult to find a clear association between the serological status of the herd and the risk of carcass positivity.
The significant effect of slaughterhouse probably reflects the hygiene level of the slaughterhouse. A lot can be achieved, if the slaughterhouses with the highest prevalence would be able to reduce the level by improved hygiene. This result is very much in concordance with the results from the European baseline study (Anon, 2008), where there were large differences in carcass prevalence between slaughterhouses, even when controlling for the effect of differences in prevalence in primary production.
Figure 2 shows no serious deviations for the random effects compared to slaughterhouse size. Two of the small slaughterhouses show the largest deviation, one is above and one is below. Both slaughterhouses were represented by fewer swab-samples than the majority of the slaughterhouses, which can explain the deviation since the swab prevalence is based on fewer samples.
Based on the results from the logistic regression, it is possible to calculate the expected effect of reducing the number of positive herds. For a large slaughterhouse (more than 5000 pigs slaughtered pr day) in a region with 50% positive herds, a reduction to 25% positive herds will reduce the level measured on carcasses from app. 4% positive pools to app. 3.4% positive pools, a relative reduction of 15%, whereas the same reduction on a small slaughterhouse (less than 1000 pigs killed pr day) will reduce the number of positive pools from 3.8% to 2%, a relative reduction of 47%.

Conclusion

The risk of bacteriologically positive carcasses depend on the serological status of the herds of origin of the carcasses, the status of other pigs slaughtered on the same day, and a "random" slaughterhouse effect, which probably reflects hygiene.
For small slaughterhouses and regions with low salmonella prevalence carcass positivity is very much a result of the level in primary production. For large slaughterhouses cross contamination accounts for a large proportion of the positive, reducing the effect of the level in primary production.

References