Tracking of *Salmonella* Positive Pigs from Farm to Fork in the Republic of Ireland


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Abstract

In this study, individual pigs from selected herds of known *Salmonella* serological status were tracked through the slaughter and dressing process. From all tracked animals, caecal contents, rectal faeces, carcasses (before washing and chilling and after chilling) and pork primal cuts were examined for the presence of *Salmonella*. All samples were screened for *Salmonella* using real-time PCR and all suspect positive samples were confirmed using the ISO 6579 method for *Salmonella*. To determine the relationship between *Salmonella* isolates from different parts of the chain, all isolates are being characterised by Pulse Field Gel Electrophoresis (PFGE). The results suggest that the slaughter and dressing operations have a significant effect on the incidence of *Salmonella* and that even if pigs are presented for slaughter with caecal or rectal carriage of *Salmonella* then good slaughter practices can prevent carcass contamination. All data generated in the study is being fed into a quantitative risk assessment model for *Salmonella* in pork.

Introduction

In Ireland, salmonellosis is one of the most common zoonotic diseases in humans and the two predominant serovars associated with human illness are *S. Enteritidis* and *S. Typhimurium* (Health Protection Surveillance Centre). Recent surveillance data indicates that *S. Enteritidis* was identified in 3 and 2% of raw pork respectively in 2002 and 2003 (FSAI, 2005) and in 2.3% of raw pork in 2004 (FSAI, 2006). In keeping with this trend, at retail level, *S. Enteritidis* was identified in 3 and 0% of raw pork respectively in 2002 and 2003 (FSAI, 2005) and 0.2% of raw pork in 2004 (FSAI, 2006).

In the Republic of Ireland there is an ongoing *Salmonella* pig herd monitoring programme which is operated by the Department of Agriculture and Food (DAF). The meat juice from twenty four pigs in each herd are tested serologically three times a year at slaughter plants and herds are assigned a category (1-3) based on a calculated weighted average of the three most recent tests. A certificate is issued grading the herd as Category 1 (< 10% of herd serologically positive for *Salmonella*), Category 2 (≥ 10%, ≤ 50% positive) or Category 3 (> 50% positive). Category 3 herds are slaughtered separately from other pigs to minimise the risk of cross contamination. The head meat and offals of category 3 pigs may not be sold in the raw state and must be heat treated in an approved manner before being passed fit for human consumption or else it must be destroyed. Pigs with no valid certificate are treated as category 3 pigs at slaughter.

The aim of this study was to determine the correlation between the *Salmonella* status of the pigs presented for slaughter and the *Salmonella* status of the pork following slaughter and dressing operations.
Materials and Methods

Pigs from nine different herds were tracked through three commercial pork abattoirs. Each pig to be tracked was slap marked for identification purposes. The serological status of each herd presented for slaughter was a historical value based on the rolling average of the three most recent serological tests. Each marked pig was examined for the presence of *Salmonella* at key stages during slaughter and dressing, namely, caecal contents, rectal faeces, carcasses (left side before washing and chilling and right side after overnight chilling) and pork primal cuts.

All samples were screened for *Salmonella* using real time PCR based on the method developed by Catarame *et al.*, 2005, for the detection of the 16S rRNA gene (Trkov and Avgustin, 2003). Suspect positive samples were plated from the enrichment broth (Rappaport Vassiliadis Soya broth) onto brilliant green agar and xylose lysine desoxycholate (BGA and XLD; Merck, Germany) and incubated for 24 h at 37°C. Suspect positives were confirmed using the ISO 6579 method for the detection of *Salmonella*. Figure 1 below outlines the method employed in this study.

![Flowchart showing the method for detecting Salmonella.](attachment:method_flowchart.png)

**Figure 1:** *Salmonella* detection method

Results

The summarised results are shown below in Table 1. The historical serological *Salmonella* status of the nine herds tracked in this study ranged from 0% to 95%. The number of pigs tracked from each herd ranged between thirteen and twenty one animals.

Of the 147 pigs tracked only 69 (46.9%) had *Salmonella* in their caecal contents and 50 (34.0%) had *Salmonella* in their rectal faeces. In general, if a pig showed rectal carriage of *Salmonella* then it was also present in the caecal contents, the exception being the pigs tracked from herd six, from which three pigs tested positive for *Salmonella* in rectal faeces but all their caecal contents tested negative.

As the pigs progressed through the slaughter and dressing procedures there was a marked decrease in the incidence of *Salmonella*. Only sixteen pork carcasses examined after evisceration and before chilling and washing tested positive for *Salmonella* and this decreased to only four
Salmonella positive carcasses after chilling. Only two pork primal cuts were positive for Salmonella. This suggests that the slaughter and dressing operations significantly reduce the incidence of Salmonella.

Table 1: Number of Salmonella positive animals as they were tracked from individual pig herds through the slaughter process at different plants.

<table>
<thead>
<tr>
<th>Abattoir</th>
<th>A Herd 1</th>
<th>A Herd 2</th>
<th>A Herd 3</th>
<th>A Herd 4</th>
<th>B Herd 5</th>
<th>C Herd 6</th>
<th>A Herd 7</th>
<th>B Herd 8</th>
<th>B Herd 9</th>
<th>Total no. sampled</th>
<th>Total no. positive (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Category (rolling average of herd)</td>
<td>2 (49%)</td>
<td>2 (21%)</td>
<td>2 (62%)</td>
<td>3 (62%)</td>
<td>3 (95%)</td>
<td>1 (6.7%)</td>
<td>1 (7.3%)</td>
<td>1 (0%)</td>
<td>3 (60%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>No. animals sampled</td>
<td>16</td>
<td>21</td>
<td>13</td>
<td>19</td>
<td>16</td>
<td>14</td>
<td>16</td>
<td>16</td>
<td>16</td>
<td>147</td>
<td></td>
</tr>
<tr>
<td>No. positive rectal samples</td>
<td>10</td>
<td>11</td>
<td>1</td>
<td>5</td>
<td>2</td>
<td>3</td>
<td>2</td>
<td>0</td>
<td>16</td>
<td>147</td>
<td>50 (34.0)</td>
</tr>
<tr>
<td>No. positive caecal samples</td>
<td>16</td>
<td>17</td>
<td>4</td>
<td>6</td>
<td>7</td>
<td>0</td>
<td>2</td>
<td>1</td>
<td>16</td>
<td>147</td>
<td>69 (46.9)</td>
</tr>
<tr>
<td>No. positive carcasses (pre-chill)</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>7</td>
<td>2</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>5</td>
<td>145</td>
<td>16 (11.0)</td>
</tr>
<tr>
<td>No. positive carcasses (post-chill)</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>2</td>
<td>131</td>
<td>4 (3.05)</td>
</tr>
<tr>
<td>No. positive pork primal cuts</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>2</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>135</td>
<td>2 (1.48)</td>
</tr>
</tbody>
</table>

Discussion

Overall, 46.9% of the caecal samples tested positive for Salmonella in relation to 11.0 and 3.05% of carcasses before washing and chilling, and after chilling respectively. These results are in agreement with other workers who found a poor correlation between caecal carriage and carcass contamination (Davies et al., 2004; Vieira-Pinto et al., 2005). A larger study carried out in the UK (Davies et al., 2004), reported a carriage of Salmonella in 23% of caecal contents but on only 5.3% of carcasses.

In the present study, all pigs tracked from herds 1 (n=16) and 9 (n=16) had Salmonella in their caecal contents. Of the corresponding carcasses none of the pigs from herd 1 had a positive carcass pre washing and chilling and only one carcass was positive post chilling while from herd 9, five of the pre washing and chilling carcasses and two of the post chill carcasses tested positive for Salmonella. Of these, only one animal was positive for Salmonella at both stages of carcass sampling. It should be noted that herds 1 and 9 were slaughtered at different pork plants with differences in abattoir practices and production days.

The tracking study on pigs from herd 5 (n=16) showed Salmonella was present on the pork primal cuts with two of the sixteen animals testing positive. One of these contaminated pork primal cuts was also positive at the pre chill carcass stage, however the second positive pork cut was not positive at the pre or post chill carcass stage. This would indicate that cross contamination may have occurred. When complete, molecular characterisation will inform us if the Salmonella strains carried by the pigs are the same Salmonella strains recovered from the carcass or if contamination is as a result of cross contamination within the pork slaughter process.

Other workers concluded that cross contamination accounted for 29% of the entire carcass contamination and that improvements in slaughter house hygiene as well as measures to decrease the Salmonella contamination both in the slaughterhouse and at pig level was needed (Botteldoorn et al., 2003).

According to Giovannacci et al., 2001, Salmonella transmission to carcasses occurs by pig to pig contact and exposure to the contaminated physical environment and as long as contaminated carcasses are being processed, about 90% of cross contamination that occurs is unavoidable.
Conclusions

The results of this present study suggest that the slaughter and dressing operations have a significant effect on the incidence of *Salmonella* and that even if pigs presented for slaughter have caecal or rectal carriage then good slaughter practices can prevent carcass contamination.

References


