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Tracking of *Salmonella* through the Pork Slaughter Process

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Tracking of *Salmonella* through the Pork Slaughter Process

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Summary

To help address the problem of salmonellosis in the Republic of Ireland (RoI), a national *Salmonella* control programme was introduced in 1997 with a view to reducing the prevalence of *Salmonella* in pigs on the farm and on pig carcasses. The primary objective of this present study was to determine the correlation between the *Salmonella* serological and bacteriological status of pigs presented for slaughter and the *Salmonella* status of pork cuts following slaughter, dressing and chilling. Two additional studies investigated the prevalence and numbers of *Salmonella* spp. in the boning halls of four commercial pork abattoirs and at retail level in butcher shops and supermarkets in the RoI. The results indicated that categorisation of pig herds on the basis of a historical serological test for *Salmonella* was not a good predictor of the bacteriological *Salmonella* status of individual pigs at time of slaughter. However, it is acknowledged that serological testing does help in giving a rough estimate of the overall *Salmonella* status of a pig herd. There was a linear correlation between prevalence of *Salmonella* in caecal contents and on pork cuts at factory level; therefore, if the number of herds presented for slaughter with high levels of *Salmonella* (category 3) was reduced, there would be less potential for contamination of the lairage, equipment etc. and so less likelihood of *Salmonella* contamination on pork. The impact of cross-contamination during transport, lairage, processing and distribution cannot be ignored and measures to diminish this would significantly reduce the dissemination of *Salmonella* in the chain and the consequent risk posed. A key finding was the considerable variation in the incidence of *Salmonella* on different sampling days and in different slaughter plants.

Introduction

Salmonella spp. are the second most common cause of bacterial food borne illness and pork is now recognised as one of the most important food borne sources of *Salmonella*. Pigs are normally asymptomatic carriers and the major contamination sources of pig carcasses are rectal and caecal contents, lymph nodes and the environment. In the RoI, there is an ongoing *Salmonella* pig herd monitoring programme operated by the Department of Agriculture, Fisheries and Food. Every pig herd is tested on an on-going basis. Twenty-four (24) pigs from each herd are tested three times a year 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% positive), category 2 (> 10% ≤ 50% positive) or category 3 (> 50% positive). At slaughter, pigs from category 3 herds are slaughtered separately from other pigs and in a manner that minimises the risk of contamination.

While there is a considerable amount of information available on the occurrence of *Salmonella* in pork on the island of Ireland, this has not been amalgamated and there are many knowledge gaps. Therefore, this study employed a quantitative risk assessment approach to (1) track *Salmonella* from different herd serological categories through the pork slaughter process, (2) determine the numbers and types of *Salmonella* spp. on pork cuts in the boning hall environment and (3) determine the numbers and types of *Salmonella* spp. on pork samples in retail and butcher shops in the RoI.

Objectives

The main objectives of this study were to determine:

- the correlation between the *Salmonella* serological and bacteriological status of pigs presented for slaughter and the *Salmonella* status of pork cuts following slaughter and dressing operations;
- the prevalence and numbers of *Salmonella* spp. on pork cuts in boning halls, and
- the prevalence and numbers of *Salmonella* spp. at retail.

Tracking of Salmonella through the pork slaughter process

Pigs from thirteen different herds were tracked through four commercial pork abattoirs. Four category 1, four category 2 and five category 3 herds were selected and sampled between November 2005 and March 2007. Each pig to be tracked was slap marked for identification purposes. The number of individual pigs from each herd selected for tracking varied between thirteen and twenty-one and was dictated by the number of pigs per pen in addition to other practical constraints. 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. In total, 193 animals were tracked and rectal samples (193), caecal samples (193), pre-chill carcass swabs (191), post-chill carcass swabs (161) and pork primals cuts (135) were sampled from all tracked animals. In addition, swabs were taken from equipment and personnel along the slaughter line and in the boning hall. Samples were analysed for *Salmonella* spp. and *Salmonella* most probable numbers (MPN) using the method described in Figure 1.

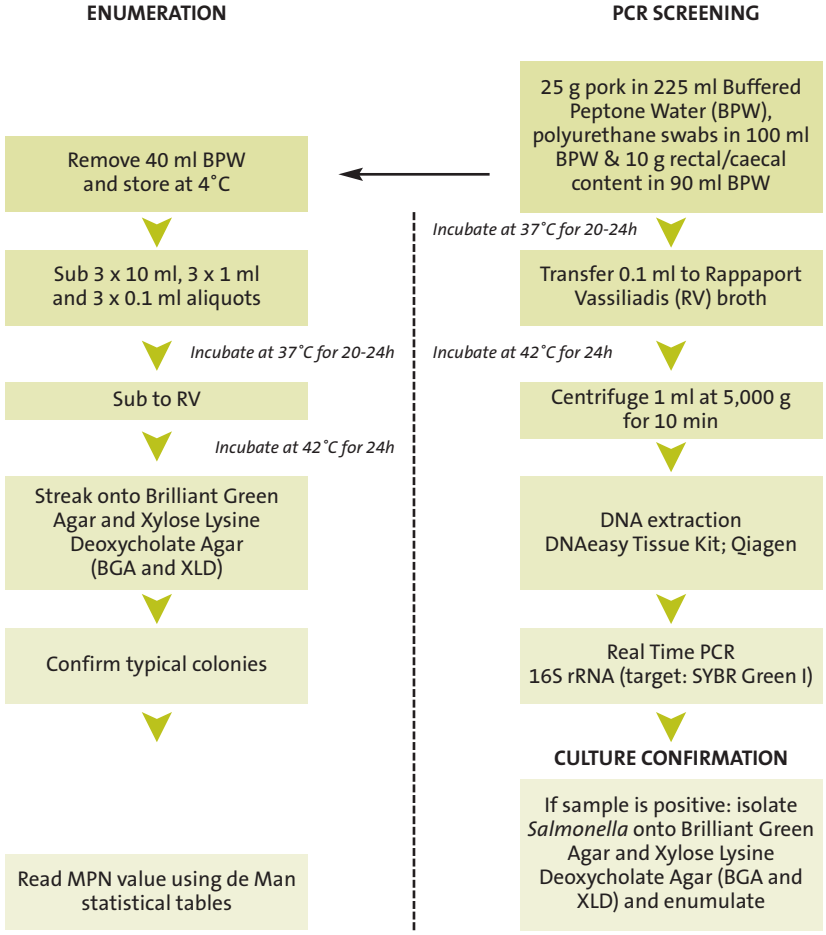

Figure 1: Methodology used for the isolation, detection and enumeration of *Salmonella* spp. from samples (Reprinted with permission from Prendergast *et al*., 2008; Wiley-Blackwell, UK)

The total number of samples taken at each stage along with the number of *Salmonella* positive samples is shown in Table 1. Of the 193 pigs tracked, 59 (31.0%) had *Salmonella* in their rectal faeces and 87 (45.0%) had *Salmonella* in their caecal content. As the pigs progressed through the slaughter and dressing processes, there was a marked decrease in the incidence of *Salmonella* with 29 (15.2%) pork carcasses examined before chilling testing positive for *Salmonella* and decreasing further to 5 (3.1%) after chilling. Only 2 (1.1%) pork primal cuts were positive for *Salmonella*.

Table 1: Total number of animals sampled along with the number of *Salmonella* positive samples in the slaughter process.

Stage	*Total no. samples*	*Total no. Salmonella positive (%)*
No. animals sampled	193	
Rectal content	193	59 (31)
Caecal content	193	87 (45)
Pre-chill carcass swabs	191	29 (15.2)
Post-chill carcass swabs	161	5 (3.1)
Pork primal cuts	135	2 (1.1)

Table 2 summarises the serological and bacteriological status of each herd through the process. 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 while all their caecal contents tested negative.

Table 2. Overview of the category and number of pigs tracked from each herd through the four slaughter plants. Results are shown for each sample type that tested positive for the presence of *Salmonella* sp. at the key stages investigated.

Category and rolling average (%)	*1 (6.7)*	*1 (7.3)*	*1 (0)*	*1 (6.7)*	*Total Cat 1 (%)*	*2 (49)*	*2 (21)*	*2 (44)*	*2 (36)*	*Total Cat 2 (%)*	*3 (62)*	*3 (95)*	*3 (83)*	*3 (59)*	*3 (51)*	*Total Cat 3 (%)*
Abbatoir	C	A	B	D		A	A	A	D		B	C	B	B	D	
Herd	7	8	9	12		1	2	3	13		4	5	6	10	11	
No. animals tested	14	16	16	10	56	16	21	13	10	60	19	16	16	16	10	77
No. pos caecal	0	2	1	6	9 (16)	16	17	4	6	43 (72)	6	17	5	16	1	35 (45)
No. pos rectal	3	2	0	2	7 (12)	10	11	1	4	26 (43)	5	2	2	16	1	26 (34)
No. pos pre-chill	1	1	0	1	3 (5)	0	0	0	0	0 (0)	7	2	11	5	1	26 (34)
No. pos. post-chill	0	0	0	0	0 (0)	1	0	0	0	1 (2)	0	1	NS	2	1	4 (7)
No. pos pork cuts	0	0	0	NS	0 (0)	0	0	0	NS	0 (0)	0	2	NS	0	NS	2 (4)

Note: the rolling average is the result of a national programme which serologically tests 24 pigs from each herd three times per year.
NS = Not Sampled

In total, ninety-nine environmental swabs were taken in the slaughter lines and boning halls. Out of these, six *Salmonella* positive samples were obtained from herds 7 (three conveyors in boning hall), 8 (hands of operator who carried out the debunging) and 10 (hands of operator who carried out the debunging and the conveyor in the boning hall) highlighting the potential role of the plant environment and operators in dissemination of the pathogen.

Overall, for herd categories 1 and 2 there was no significant association between *Salmonella* infection of the pig and the *Salmonella* status of its carcass. However, there was a significant correlation ($p < 0.05$) between rectal carriage and pre-chill carcass contamination of pigs originating from category 3 herds. In general, when all herd categories were analysed together at individual pig level, no association between internal contamination or infection (caecal, rectal carriage) with external contamination (pre-chill, post-chill, pork cut) was found. It appears there was little correlation between the *Salmonella* serological status and bacteriological status of caecal and rectal contents when an animal was presented for slaughter.

Table 3 A, B and C present an overview of the tracking of *Salmonella* on individually tracked pigs and demonstrate the routes and sources of contamination. Genetic finger printing (PFGE) was used to confirm that the *Salmonella* tracked were identical ($p \geq 80\%$ similarity).

For example, for herd 5, which was tracked through Abattoir C, the same *S.* Typhimurium was recovered from the caecal contents, rectal faeces, the carcass pre-chill and a pork cut from one particular animal. From herd 10, tracked through abattoir B, *S.* Derby was recovered from three pre-chill carcass, 1 post-chill carcass and one environmental swab. From herd 7, tracked through abattoir C, *S.* Typhimurium DT208 was recovered from the lairage area both before and after the herd had passed through, from the rectal faeces of 3 animals, from the pre-chill carcass of one animal and from 3 different swabs of conveyor belts in the boning hall. The isolates were shown by PFGE to be genetically similar, indicating the likelihood that pigs became infected with this strain of *Salmonella* in the lairage area and during the slaughter process there was cross-contamination to both meat and equipment, thus posing a reservoir for further contamination. The study showed that contamination could be transmitted from one contaminated carcass or meat cut to another and that equipment and surfaces play a very important role in cross-contamination. High variability in cross-contamination from day to day and abattoir to abattoir was observed.

Prevalence and numbers of Salmonella on pork cuts in abattoirs

Samples of pork (n = 720) were taken at random from trays in the boning halls of four commercial pork abattoirs (A, B, C and D). The cut sampled in each plant was the oyster (Figure 2) which remained on the leg in abattoirs A, B and D and on the loin in abattoir C. To ensure that the samples taken were representative of all production times, the day of sampling and the time in the production shifts at which samples were taken was randomised. In each abattoir, a total of sixty samples were taken over the entire working day; sampling started 2 h after a shift commenced. Thirty samples were taken in the morning and thirty samples in the afternoon.

Table 3A: *Salmonella* serotypes / phage types recovered from each sampling stage for category 1 herds.

Plant	*Herd*	*Sample [Positive Samples / Tested (n)]*	*Serovars and Phage Types (n)*	*Pig ID number*	*PFGE profile [Serotype (number related/isolated, profile ID number)]*
Category 1					
C	7	L_1 (10/10)	DT208 (7), DT193 (1), PTU311 (1), Bredeney (1)	-	T (6/8, P0008)
		L_2 (10/10)	DT208 (10)	-	T (9/10, P0008)
		Environmental (3/6)	Unnamed (2)[a,b], DT208 (1)[c]	-	T (3/3, P0008)
		Caecal (0/14)	All Negative	-	-
		Rectal (3/14)	DT208 (3)	4, 5, 6	T (3/3, P0008)
		Carcass Pre-Chill (1/14)	DT208 (1)	17	T (1/1, P0008)
		Carcass Post-Chill (0/8)	All Negative	-	-
		Pork Cut (0/8)	All Negative	-	-
A	8	L_1 (5/5)	DT104b (5)	-	T (5/5, P0010)
		L_2 (5/5)	Kimuenza (4), Infantis (1)	-	K (4/4, P0009)
		Environmental (1/12)	DT104b (1)[d]	-	T (1/1, P0010)
		Caecal (2/16)	Kimuenza (2)	8, 17	K (2/2, P0009)
		Rectal (2/16)	DT104b (2)	1, 15	T (2/2, P0010)
		Carcass Pre-Chill (1/16)	DT104b (1)	3	T (1/1, P0010)
		Carcass Post-Chill (0/16)	All Negative	-	-
		Pork Cut (0/16)	All Negative	-	-
B	9	L_1 (9/9)	DT143 (4), DT104 (2), Manhattan (2), DT193 (1)	-	-

Table 3A: *Salmonella* serotypes / phage types recovered from each sampling stage for category 1 herds... *continued*

Plant	*Herd*	*Sample [Positive Samples / Tested (n)]*	*Serovars and Phage Types (n)*	*Pig ID number*	*PFGE profile [Serotype (number related/isolated, profile ID number)]*
Category 1					
		L_2 (10/10)	DT143 (9), DT193 (1)	-	-
		Environmental (0/9)	All Negative	-	-
		Caecal (1/16)	DT104 (1)	1	-
		Rectal (0/16)	All Negative	-	-
		Carcass Pre-Chill (0/16)	All Negative	-	-
		Carcass Post-Chill (0/16)	All Negative	-	-
		Pork Cut (0/16)	All Negative	-	-
D	12	L_1 (0/0)	Not Sampled	-	-
		L_2 (0/0)	Not Sampled	-	-
		Environmental (0/2)	All Negative	-	-
		Caecal (6/10)	Unnamed (6)	1 - 4, 7, 9	-
		Rectal (2/10)	Unnamed (2)	3, 4	-
		Carcass Pre-Chill (1/10)	DT104b (1)	2	-
		Carcass Post-Chill (0/10)	All Negative	-	-
		Pork Cut (0/0)	Not Sampled	-	-

Key: Where *S.* Typhimurium was isolated the phage type is displayed.
L1, lairage before pigs; L2, lairage after pigs.
a =conveyor primal stage; b=conveyor leg drop; c=conveyor after leg drop; d=hands of debung operative. - = Not Applicable. T = *S.* Typhimurium; K = *S.* Kimeunza

Table 3B: *Salmonella* serotypes / phage types recovered from each sampling stage for category 2 herds

Plant	*Herd*	*Sample [Positive Samples / Tested (n)]*	*Serovars and Phage Types (n)*	*Pig ID number*	*PFGE profile [Serotype (number related/isolated, profile ID number)]*
Category 2					
A	1	L_1 (10/10)	Derby (10)	-	-
		L_2 (9/10)	Derby (7), DT104 (1), Unnamed (1)	-	T (2/2, P0001)
		Environmental (0/12)	All Negative	-	-
		Caecal (16/16)	[e]DT104 (15), [f]Unnamed (1)	[e](1 - 9, 12 - 15, 17 - 18) [f](16)	T (15/16, P0001)
		Rectal (10/16)	[e]DT104 (7), [f]Unnamed (3)	[e](2, 4, 6 - 7, 9, 12, 16) [f](1, 5, 17)	T (9/10, P0001)
		Carcass Pre-Chill (0/16)	All Negative	-	-
		Carcass Post-Chill (1/16)	DT104 (1)	7	T (1/1, P0001)
		Pork Cut (0/16)	All Negative	-	-
A	2	L_1 (7/10)	PTU302 (3), DT104b (3), Derby (1)	-	-
		L_2 (9/10)	Derby (8), Goldcoast (1)	-	-
		Environmental (0/12)	All Negative	-	-
		Caecal (17/21)	Derby (12), Goldcoast (4), DT104b (1)	-	-
		Rectal (11/21)	Derby (11)	-	-
		Carcass Pre-Chill (0/21)	All Negative	-	-
		Carcass Post-Chill (0/16)	All Negative	-	-
		Pork Cut (0/21)	All Negative	-	-
A	3	L_1 (3/5)	Derby (2), PTU288 (1)	-	-
		L_2 (0/5)	All Negative	-	-

Table 3B: *Salmonella* serotypes / phage types recovered from each sampling stage for category 2 herds... *continued*

Plant	*Herd*	*Sample [Positive Samples / Tested (n)]*	*Serovars and Phage Types (n)*	*Pig ID number*	*PFGE profile [Serotype (number related/isolated, profile ID number)]*
Category 2					
		Environmental (0/12)	All Negative	-	-
A	3	L_1 (3/5)	Derby (2), PTU288 (1)	-	-
		L_2 (0/5)	All Negative	-	-
		Environmental (0/12)	All Negative	-	-
		Caecal (4/13)	DT104b (4)	14, 15, 17, 24	-
		Rectal (1/13)	DT104b (1)	14	-
		Carcass Pre-Chill (0/13)	All Negative	-	-
		Carcass Post-Chill (0/13)	All Negative	-	-
		Pork Cut (0/13)	All Negative	-	-
D	13	L_1 (0/0)	Not Sampled	-	-
		L_2 (0/0)	Not Sampled	-	-
		Environmental (0/2)	All Negative	-	-
		Caecal (6/10)	U310 (5), Derby (1)	-	-
		Rectal (4/10)	U310 (4)	-	-
		Carcass Pre-Chill (0/10)	All Negative	-	-
		Carcass Post-Chill (0/10)	All Negative	-	-
		Pork Cut (0/0)	Not Sampled	-	-

Key: Where *S.* Typhimurium was isolated the phage type is displayed.
L1, lairage before pigs; L2, lairage after pigs.
e, f=the serotype or phage type was isolated from the pig ID number indicated.
- = Not Applicable. T = *S.* Typhimurium

Table 3C: *Salmonella* serotypes / phage types recovered from each sampling stage for category 3 herds.

Plant	*Herd*	*Sample [Positive Samples / Tested (n)]*	*Serovars and Phage Types (n)*	*Pig ID number*	*PFGE profile [Serotype (number related/isolated, profile ID number)]*
Category 3					
B	4	L_1 (10/10)	Manhattan (7), Reading (1), Anatum (1), Derby (1)	-	D (1/1, P0002) M (5/7, P0003)
		L_2 (10/10)	DT193 (9), Derby (1)	-	T (9/9, P0004)
		Environmental (0/9)	All Negative	-	-
		Caecal (6/19)	DT193 (6)	5, 8, 9, 16, 17, 23	T (6/6, P0004)
		Rectal (5/19)	[g]DT193 (4), [h]Manhattan (1)	[g](3, 5, 8, 9) [h](19)	T (4/4, P0004) M (1/1, P0003)
		Carcass Pre-Chill (7/19)	[g]DT193 (5), [i]Anatum (1), [j]Derby (1)	[g](3, 9, 17, 19, 23) [i](1), [j](5) D (1/1, P0002)	T (4/5, P0004)
		Carcass Post-Chill (0/16)	All Negative	-	-
		Pork Cut (0/15)	All Negative	-	-
C	5	L_1 (5/10)	Panama (2), DT104 (2), PTU288 (1)	-	T (3/3, P0005)
		L_2 (10/10)	DT104b (8), Manhattan (2)	-	T (7/8, P0005) T (1/8, P0006)
		Environmental (0/9)	All Negative	-	-
		Caecal (7/16)	DT104b (7)	2 -4, 8, 13, 15 -16	T (7/7, P0005)
		Rectal (2/16)	DT104b (2)	3, 18	T (2/2, P0005)
		Carcass Pre-Chill (2/15)	DT104b (2)	3, 17	T (2/2, P0006)
		Carcass Post-Chill (1/15)	DT104b (1)	14	T (1/1 P0006)
		Pork Cut (2/15)	DT104b (2)	3, 12	T (2/2, P0005)

Table 3C: *Salmonella* serotypes / phage types recovered from each sampling stage for category 3 herds... *continued*

Plant	*Herd*	*Sample [Positive Samples / Tested (n)]*	*Serovars and Phage Types (n)*	*Pig ID number*	*PFGE profile [Serotype (number related/isolated, profile ID number)]*
Category 3					
B	6	L_1 (10/10)	Derby (5), Derby (2), London (2), Manhattan (1)	-	-
		L_2 (10/10)	Bredeney (3), London (2), PTU302 (2), Reading (1), Anatum (1), Manhattan (1)	-	T (1/2, P0007)
		Environmental (0/9)	Not Sampled	-	-
		Caecal (5/16)	[k]PTU302 (4), [l]DT193 (1)	[k](5, 15 - 16, 20) [l](8)	T (4/5, P0007)
		Rectal (2/16)	PTU302 (2)	20, 21	T (2/2, P0007)
		Carcass Pre-Chill (11/16)	[k]PTU302 (10), [m]Manhattan (1)	[k](4, 7, 13, 15, 17, 19, 20, 21, 24, 25) [m](9)	T (10/10, P0007)
		Carcass Post-Chill (0/16)	Not Sampled	-	-
		Pork Cut (0/15)	Not Sampled	-	-
B	10	L_1 (5/8)	Agona (2), Derby (1), DT193 (1), Rough (1)	-	-
		L_2 (8/8)	Reading (8)	-	R (7/8, P0011)
		Environmental (2/9)	[d]Derby (1), [b]Typhimurium (1)	-	D (1/1, P0012)
		Caecal (16/16)	Reading (16)	-	R (1/16, P0011)
		Rectal (16/16)	Reading (16)	-	R (4/16, P0011)
		Carcass Pre-Chill (5/15)	[n]Derby (4), [o]Reading (1)	[n](3, 7, 8, 15) [o](2)	D (4/4, P0012) R (1/1, P0011)

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Table 3C: *Salmonella* serotypes / phage types recovered from each sampling stage for category 3 herds... *continued*

Plant	*Herd*	*Sample [Positive Samples / Tested (n)]*	*Serovars and Phage Types (n)*	*Pig ID number*	*PFGE profile [Serotype (number related/isolated, profile ID number)]*
Category 3					
		Carcass Post-Chill (2/15)	[n]Derby (1), [p]Manhattan (1)	[n](4) [p](7)	D (1/1, P0012)
		Pork Cut (0/15)	All Negative	-	-
D	11	L_1 (0/0)	Not Sampled	-	-
		L_2 (0/0)	Not Sampled	-	-
		Environmental (0/3)	All Negative	-	-
		Caecal (1/10)	Typhimurium (1)	5	-
		Rectal (1/10)	Derby (1)	2	D (1/1, P0013)
		Carcass Pre-Chill (1/10)	Derby (1)	2	D (1/1, P0013)
		Carcass Post-Chill (1/10)	Unnamed (1)	4	D (1/1, P0013)
		Pork Cut (0/0)	Not Sampled	-	-

Key: Where *S.* Typhimurium was isolated the phage type is displayed.
L1, lairage before pigs; L2, lairage after pigs.
b=conveyor leg drop; d=hands of debung operative.
g – p=the serotype or phage type was isolated from the pig ID number indicated.
- = Not Applicable. D = *S.* Derby; M = *S.* Manhattan; T = *S.* Typhimurium; R = *S.* Reading

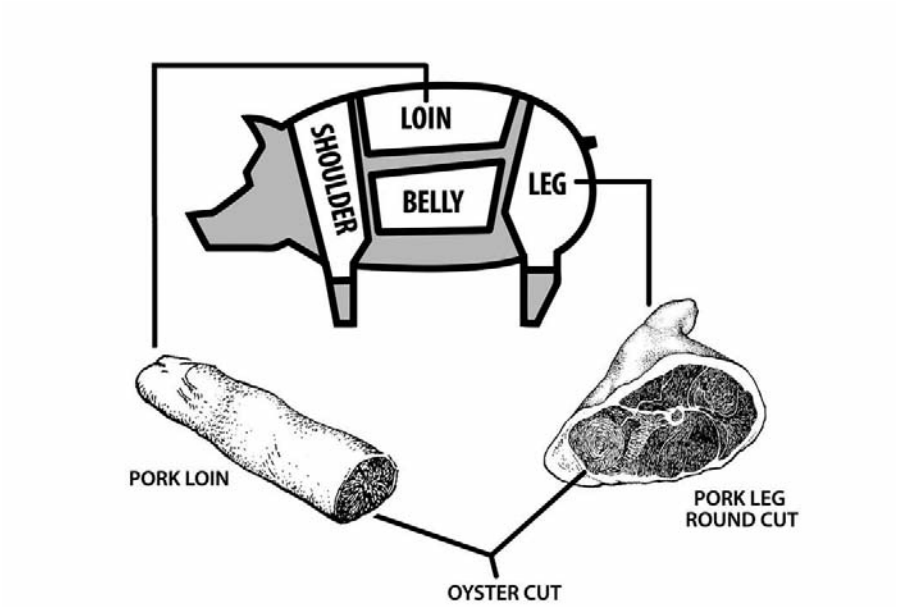

Figure 2: Oyster cut on pork loin and leg after processing

Samples (25 g) were examined for the presence of *Salmonella* using the method described in Figure 1. In addition, an estimation of the number of *Salmonella* spp. in all *Salmonella* positive samples was made using a 3-tube MPN method.

The mean prevalence (%) of *Salmonella* on the oyster cuts taken on each of three visits to four commercial pork abattoirs was 24/720 (3.3%), as shown in Table 4. The confidence limit for this data set calculated at the 95% confidence limit was 2.02 to 4.64%. There was considerable variation in the incidence of *Salmonella* on different sampling days ranging from 0 to as high as 33.3% over the 12 visits. *Salmonella* was not detected on 9 of the 12 visits while on three visits, incidences of 6.7% (abattoir B), 31.7% (abattoir D) and 1.7% (abattoir D) were recorded.

Analysis of the data using the Chi-square test revealed significant differences in the prevalence of *Salmonella* between the four abattoirs ($P<0.001$). Over six visits to abattoirs A and C, *Salmonella* were not recovered from any of the samples. *Salmonella* spp. were recovered during one of three visits to abattoir B, with a higher incidence in the afternoon (10%) compared to the morning (3.3%). In abattoir D, *Salmonella* spp. was recovered on 2 of 3 visits at levels of 1.7 and 31.7%. On one of these visits, the incidence was lower in the morning (30%) than in the afternoon (33.3%). On another occasion, just one positive was found during morning production.

Table 4: Prevalence (%) of *Salmonella* spp. on the oyster cut in the boning halls of four commercial pork abattoirs

Abattoir	*Number tested*			*Number positive (%)*		
	a.m.	*p.m.*	*total*	*a.m.*	*p.m.*	*Total*
A	30	30	60	0	0	0
A	30	30	60	0	0	0
A	30	30	60	0	0	0
B	30	30	60	0	0	0
B	30	30	60	1 (3.3)	3 (10)	4 (6.7)
B	30	30	60	0	0	0
C	30	30	60	0	0	0
C	30	30	60	0	0	0
C	30	30	60	0	0	0
D	30	30	60	9 (30)	10 (33.3)	19 (31.7)
D	30	30	60	1 (3.3)	0	1 (1.7)
D	30	30	60	0	0	0
Total	**360**	**360**	**720**	**11 (3.06)**	**13 (3.61)**	**24 (3.3)**

The characteristics and numbers of *Salmonella* (MPN g^{-1}) on pork are shown in Table 5. Of the 24 *Salmonella* isolates from pork in abattoirs B and D, the serotypes and / or phage types were *S.* Derby (n = 4), *S.* Livingstone (n = 1), *S.* Typhimurium U310 (n = 17), *S.* Typhimurium U302 (n = 1) and one isolate was untypable. Three *S.* Derby isolates were resistant to two antimicrobials, one *S.* Typhimurium U310 was shown to have intermediate sensitivity to minocycline, *S.* Typhimurium U302 was resistant to seven antimicrobials, one *S.* Derby isolate was resistant to four antimicrobials and the untypable isolate was resistant to five antimicrobials. The other *S.* Typhimurium U310 and the *S.* Livingstone isolate were not resistant to any of the antimicrobials tested. The calculated MPN values from the *Salmonella* positive samples in abattoirs ranged from $\log_{10}$ <-0.52 to -0.44 MPN g^{-1} for the 24 isolates.

Table 5: Characteristics and numbers of *Salmonella* (MPN g^{-1}) on pork from four commercial abattoirs

Plant	*Visit*	*Time*	*Serotype*	*Phage*	*Antibiotic type*	*MPN g^{-1} resistance*
B	2	a.m.	*S.* Derby	-	TMn	< 0.30
B	2	p.m.	*S.* Livingstone	-	None	<0.30
B	2	p.m.	*S.* Derby	-	TMn	<0.30
B	2	p.m.	*S.* Derby	-	TMn	<0.30
D	1	a.m.	*S.* Typhimurium	U310	None*	0.36
D	1	a.m.	*S.* Typhimurium	U310	None	<0.30
D	1	a.m.	*S.* Typhimurium	U310	None	0.36
D	1	a.m.	*S.* Typhimurium	U310	None	0.36
D	1	a.m.	*S.* Typhimurium	U310	None	<0.30
D	1	a.m.	*S.* Typhimurium	U310	None	<0.30
D	1	a.m.	*S.* Typhimurium	U302	ACSSuTTmMn	0.36
D	1	a.m.	*S.* Typhimurium	U310	None	<0.30
D	1	a.m.	*S.* Typhimurium	U310	None	<0.30
D	1	p.m.	*S.* Typhimurium	U310	None	<0.30
D	1	p.m.	*S.* Typhimurium	U310	None	<0.30
D	1	p.m.	*S.* Typhimurium	U310	None	<0.30
D	1	p.m.	*S.* Typhimurium	U310	None	<0.30
D	1	p.m.	*S.* Typhimurium	U310	None	<0.30
D	1	p.m.	*S.* Derby	-	SuTTmMn	<0.30
D	1	p.m.	*S.* Typhimurium	U310	None	<0.30
D	1	p.m.	*S.* Typhimurium	U310	None*	<0.30
D	1	p.m.	*S.* Typhimurium	U310	None	<0.30
D	1	p.m.	*S.* Typhimurium	U310	None	<0.30
D	2	a.m.	Untypable	-	SSuTTmMn†	<0.30

* = intermediate sensitivity to minocycline; †= rough isolate, intermediate susceptibility to kanamycin; T = tetracycline (30 µg), Mn = minocycline (30 µg), A = ampicillin (10 µg), C = Chloramphenicol (30 µg), S = streptomycin (10 µg), Su = sulphonamides (300 µg), Tm = trimethoprim (5 µg).

Prevalence and numbers of Salmonella spp. from butcher shops and supermarkets

Pork samples (n = 500) were collected at random in butcher shops and supermarkets in the RoI between January and November 2007. During each sampling at each sampling location, three pork sample types, i.e. mince, pieces and chops, were purchased. However, it was not possible to obtain all three sample types during each sampling occasion as this was dependent on their availability. The number of each sample type along with the number taken in each province i.e., Connacht, Leinster, Munster and Ulster is shown in Table 6. The same methods employed for the detection and enumeration of *Salmonella* spp. in the boning hall study were used in this study. The mean prevalence (%) of *Salmonella* on pork samples taken in butcher shops and supermarkets in the RoI was 13/500 (2.60%). The highest incidence of *Salmonella* in pork was observed in Ulster (8%) followed by Leinster (2.2%) and Munster (1.2%). No *Salmonella* positive samples were isolated from any of the samples in Connacht. Out of the pork types, the highest incidence of *Salmonella* was observed in pieces [4/128 (3.13%)] followed by mince [2/85 (2.35%)] and chops [7/287 (2.44%)]. The number of *Salmonella* positive samples classified by pork type, region and by outlet within pork type is shown in Table 6.

Table 6: Number of *Salmonella* positive samples from butcher shops and supermarkets the RoI

Factor	*Pork type, and region*	*No. samples taken*	*Salmonella positive %*
Pork type	Chop	287	7 (2.44)
	Mince	85	2 (2.35)
	Pieces	128	4 (3.13)
Outlet	Butcher	223	4 (1.77)
	Supermarket	277	9 (3.28)
Region	Connacht	74	0 (0)
	Leinster	273	6 (2.20)
	Munster	75	1 (1.28)
	Ulster	78	6 (8.00)
Pork type - chop	Butcher	90	1 (1.11)
	Supermarket	197	6 (3.05)
Pork type - mince	Butcher	53	2 (3.77)
	Supermarket	32	0 (0)
Pork type - pieces	Butcher	80	1 (1.20)
	Supermarket	48	3 (6.67)
Total		**500**	**13 (2.6%)**

Characteristics and numbers of *Salmonella* (MPN g^{-1}) on pork from butcher shops and supermarkets in the RoI are shown in Table 7. Out of the 13 *Salmonella* isolates recovered from pork samples, the serotypes and/or phagetypes were *S.* Typhimurium DT193 (n=7), *S.* Typhimurium DT120 (n=1), *S.* Typhimurium DT104 (n=1), *S.* Typhimuruim DT104b (n=1), *S.* Typhimurium U310 (n=1), *S.* Derby (n=1) and *S.* Rissen (n=1). Three of the *S.* Typhimuruim DT193 were resistant to five antimicrobials (chloramphenicol, streptomycin, sulphonamides, tetracycline and trimethoprim) and four were resistant to seven antimicrobials (ampicillin, chloramphenicol, streptomycin, sulphonamides, tetracycline, trimethoprim and kanamycin). *S.* Typhimuruim DT104 and DT104b were resistant to 5 antimicrobial agents (ampicillin, chloramphenicol, streptomycin, sulphonamides and tetracycline). The calculated *Salmonella* MPN value for all samples ranged from <0.30 to 2.10 g^{-1}.

Table 7: Characteristics and numbers of *Salmonella* (MPNg-1) on pork from butcher shops and supermarkets in the RoI.

Pork type	*Province*	*Supermarket/ butcher*	*Serotype*	*Phagetype*	*Antibiotic resistance*	*MPN g-1*
Mince	Leinster	Butcher	Rissen	-	T 0.30	
Mince	Leinster	Butcher	Typhimurium	DT193	CSSuTTm	0.92
Pieces	Leinster	Butcher	Typhimurium	DT193	CSSuTTm	1.10
Chop	Leinster	Butcher	Typhimurium	DT193	CSSuTTm	0.36
Pieces	Leinster	Supermarket	Typhimurium	DT120	ACSSuT	<0.30
Chop	Munster	Supermarket	Derby	-	SSuT	<0.30
Chop	Leinster	Supermarket	Typhimurium	U310	STTm	<0.30
Pieces	Ulster	Supermarket	Typhimurium	DT193	ACSSuTTmK	2.10
Chop	Ulster	Supermarket	Typhimurium	DT193	ACSSuTTmK	1.50
Pieces	Ulster	Supermarket	Typhimurium	DT193	ACSSuTTmK	<0.30
Chop	Ulster	Supermarket	Typhimurium	DT193	ACSSuTTmK	0.92
Chop	Ulster	Supermarket	Typhimurium	DT104b	ACSSuT	<0.30
Chop	Ulster	Supermarket	Typhimurium	DT104	ACSSuT	<0.30

T = tetracycline (30 µg); C = chlorampenicol (30 µg); S = streptomycin (10 µg); Su = sulphonamides (300 µg); Tm = trimethoprim (5 µg); A = ampicillin (10 µg); K = kanamycin (30 µg).

Conclusions

Tracking the *Salmonella* status of pigs from farm through to boned-out cuts highlighted that, at an individual pig level, there was little correlation between the *Salmonella* serological status and bacteriological status of caecal and rectal contents when the animal was presented for slaughter. This indicates that logistic slaughter based on this historical data is unlikely to be an effective control strategy.

The study showed that contamination could be transmitted from one contaminated carcass or meat cut to another and that equipment and surfaces played a very important role in cross-contamination. There was high variability in cross-contamination from day-to-day and abattoir-to-abattoir. This study has shown that lairage was a major source of cross-contamination with *Salmonella* as were the hands of evisceration operatives employed in debunging and conveyor belts and equipment in the boning hall. Cross-contamination within the slaughter plant environment can account for up to 73.5 % of contamination on carcasses and pork cuts. There was a strong association found between Enterobacteriaceae counts (hygiene indicators) and *Salmonella* status on pre-chill carcass swab and also a significant association between Enterobacteriaceae counts and the *Salmonella* status of pork cut samples.

Recommendations to industry

During the slaughter process, *Salmonella* can be transferred to pork meat. Categorising the pig herd based on a historical serological testing for the presence of *Salmonella* was not shown to be a good predictor of the bacteriological *Salmonella* status of individual pigs at time of slaughter. However, it is acknowledged that serological testing does help in giving a rough estimate of the overall *Salmonella* status of a pig herd with a linear correlation shown between prevalence of *Salmonella* in caecal contents and on pork cuts at factory level.

Salmonella has the potential to enter and spread at all stages of the pork supply chain and therefore control must involve a farm-to-fork approach.The impact of cross-contamination during transport, lairage, processing and distribution cannot be ignored and measures to reduce this would significantly reduce the dissemination of *Salmonella* in the chain and the risk posed.

Publications from this project

Prendergast, D.M., Duggan, S.J., Fanning, S., Cormican, M., Gonzales-Barron, U., Butler, F. and Duffy, G. 2008. Prevalence and numbers of *Salmonella* spp. and Enterobacteriaceae on pork cuts in abattoirs in the Republic of Ireland. *J Applied Microbiology*, **105**(4), 1209-1219.

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Gonzales-Barron, U., Soumpasis, I., Butler, F. and Duffy, G. 2009. A comparison between herd-level and animal-level simulation for estimation of prevalence of *Salmonella* in caecal contents of slaughter pigs in Ireland from meat juice serology. *Risk Analysis.* In press.

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