ATTRIBUTION OF POTENTIALLY FOODBORNE ENTERIC DISEASES:

HUMAN SALMONELLOSIS – AN EPIDEMIOLOGICAL APPROACH

Prepared for the New Zealand Food Safety Authority under
project MRP/09/02 – Risk Profiles,
as part of overall contract for scientific services

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April 2010

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ACKNOWLEDGEMENTS

We would like to thank the staff of the Public Health Units who provided copies of outbreak reports.

We would also like to thank the following ESR employees:

Helen Heffernan who provided advice on testing of multiresistant salmonellae.
Muriel Dufour for provision of archived serotype data of human and non-human *Salmonella* isolates.
Beverley Horn of the ESR Food Safety Group who provided helpful advice on statistical methods and prepared the box plots.
Catherine Tisch of the ESR Population and Environmental Health Group who provided copies of outbreak reports.
Carolyn Nicol who provided advice on molecular typing of salmonellae.

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EXECUTIVE SUMMARY

The New Zealand Food Safety Authority (NZFSA) has set itself a goal of achieving a 30% reduction in the incidence of foodborne salmonellosis by 2013. As part of their *Salmonella* Risk Management Strategy, the NZFSA aims to quantify the proportion of foodborne salmonellosis cases attributable to specific foods, animal feeds, domestically produced versus imported foods, and multi-resistant and virulent *Salmonella* genotypes associated with foods. This study analysed New Zealand human salmonellosis surveillance data with the aim of attributing the proportion of non-typhoid salmonellosis to these (and other) pathways, building on previous attribution studies. The study has identified areas where salmonellosis reporting could be improved and options for sentinel surveillance.

All 15,040 cases of non-typhoid salmonellosis notified between 2000 and 2009 were compared to other enteric disease cases for the same time period. The comparator diseases were campylobacteriosis, cryptosporidiosis, giardiasis, shigellosis, yersiniosis and VTEC/STEC infection. People aged less than five years or of European ethnicity were over-represented in the salmonellosis dataset when compared to the national population. There were significantly more salmonellosis cases than campylobacteriosis cases or giardiasis cases in the less than five years and five to 16 years age groups. There were significantly fewer salmonellosis cases than cryptosporidiosis cases in the same age groups. These results were reversed for the adult age group (17 years or older). A higher proportion of salmonellosis cases were of Maori ethnicity when compared to all other enteric diseases except for shigellosis and VTEC/STEC infection, which were not significantly different. Pacific peoples were more frequently represented amongst shigellosis cases than salmonellosis cases, and people of Asian origin were more highly represented in the shigellosis and yersiniosis case datasets. More than one in ten salmonellosis cases lived in rural environments. This was higher than for the other enteric diseases, except for cryptosporidiosis and VTEC/STEC infection where one in five lived in rural areas.

Nine risk factors were compared by case-case analysis between the enteric diseases. Salmonellosis was the reference for these analyses. The risk factors investigated were overseas travel, food consumption from a food premise, consumption of untreated drinking water, contact with recreational water, contact with farm animals, contact with sick animals, and person-to-person transmission factors (contact with symptomatic people, contact with confirmed cases and contact with human faeces). Salmonellosis was more strongly associated with overseas travel than the other enteric diseases, except for giardiasis and shigellosis. Salmonellosis and campylobacteriosis were similarly associated with consumption of food from a premise, and both were more strongly associated than the other enteric diseases. The only enteric diseases with a greater association with consumption of untreated drinking water than salmonellosis were giardiasis and cryptosporidiosis. Campylobacteriosis, cryptosporidiosis and VTEC/STEC infection had greater associations with farm animal contact than salmonellosis, but only cryptosporidiosis was more associated with sick animal contact than salmonellosis. With the exception of campylobacteriosis and yersiniosis, the association of salmonellosis with person-to-person factors was lower than for other enteric diseases. There were only minor variations in these results when cases were stratified by sex or age. The risk factor analyses suggest that the important pathways for *Salmonella* infection in New Zealand are foodborne (as indicated by premises data), consumption of untreated drinking water and contact with sick animals. These are not necessarily mutually exclusive, since cases living in rural environments could be exposed to all of these risk factors. The southern South Island regions of New Zealand have higher salmonellosis rates compared with the rest of the country, which suggests rurality is important.

There were 11,554 salmonellosis cases between 2000 and 2009 which had a laboratory-confirmed *Salmonella* serotype. There were over 400 serotypes identified but 35 accounted for 80% of the cases. *S.* Typhimurium DT160 caused 19% of all the cases. Males were over-represented compared to females in the full dataset of 11,554 cases, as were cases aged under five years when compared to the national population. Significantly more females were associated with person-to-person transmission and the serotypes *S.* Typhimurium DT9, *S.* Typhimurium DT12a and *S.* Saintpaul were associated with this risk factor. *S.* Brandenburg, *S.* Typhimurium DT101 and *S.* Saintpaul were statistically associated with cases living in rural regions; most non-human isolates of *S.* Brandenburg have been from bovine and ovine samples, *S.* Typhimurium DT101 has largely been isolated from bovine and poultry samples, and *S.* Saintpaul has most often been isolated from reptile samples. *S.* Typhimurium DT160 and *S.* Infantis were statistically associated with cases living in urban areas, although the proportion of cases from rural areas was not markedly different. *S.* Typhimurium DT160 has been isolated from a wide variety of animal and environmental samples. Most non-human *S.* Infantis isolates have been from poultry samples.

Cases with a known *Salmonella* serotype were compared by case-case analysis based on risk factors. The reference was *Salmonella* Typhimurium DT160, which caused the highest number of notified cases during this period. The risk factors investigated were the same as those used for the case-case analysis between the enteric diseases, excluding contact with symptomatic people and contact with confirmed cases. A high number of serotypes were significantly associated with cases that had travelled overseas during their incubation period. Some of these serotypes also produced higher odds ratios for contact with recreational water. There was a lack of significant associations with consumption of food from a food premise which implies that the serotypes are similarly represented among cases exposed to this risk factor. Four serotypes (*S.* Saintpaul, *S.* Typhimurium DT23, *S.* Typhimurium DT9 and *S.* Brandenburg) were positively associated with consumption of untreated drinking water and contact with farm animals. The latter two serotypes were also associated with contact with sick animals. The odds ratios for contact with human faeces were fairly similar, confirming that this is a risk factor for all salmonellosis.

S. Typhimurium DT160 was significantly associated with male infants and children, and female adults. This serotype appears well spread through the community and was more likely to be domestically-acquired. *S.* Typhimurium DT1 was significantly associated with males aged five to 16 years, and male adults in rural areas. The latter group are most likely to contract this serotype from farm animals, sick animals or contact with recreational water. *S.* Brandenburg was significantly associated with rural risk factors, which supports its well-known role as a cause of disease in livestock. *S.* Saintpaul was associated with rural risk factors but also with consumption of food from food premises, recreational water, overseas travel and person-to-person contact. Similar results were found for *S.* Typhimurium DT9. Notifications of *S.* Infantis have recently increased but it was not possible to identify key risk factors.

It was not possible to attribute salmonellosis to specific foods using the notification data. There were no sporadic case reports with a food or drink confirmed as the source of infection by laboratory testing. A sample of notified cases where probable foods were reported was reviewed and this provided a long list of foods, with chicken and other meats most frequently reported.

Data from all reported outbreaks of non-typhoid salmonellosis between 2000 and 2009 were cleaned, augmented with additional information (particularly serotypes), and analysed. There were 204 outbreaks involving 1,426 probable and confirmed cases. The annual number of salmonellosis outbreaks has declined over the last decade; in 2009, 3% of all enteric outbreaks (1% of cases associated with enteric outbreaks) were caused by *Salmonella*. From 2000 to 2009,

S. Typhimurium DT160, DT135 and DT1 serotypes caused half of the total outbreaks and outbreak cases for which serotypes have been identified, although the proportion of outbreaks and outbreak cases caused by these serotypes has decreased over this period. The West Coast, Wanganui and Auckland health districts had the highest rates of reported outbreaks and Nelson and Gisborne health districts had the highest reported outbreak case rates. However, the number of outbreaks in each region was low, and it is likely that factors influencing reporting and investigation are significant. The seasonal pattern, with both number of outbreaks and number of outbreak cases being highest in summer and lowest in winter, is consistent with notifications for salmonellosis and other bacterial enteric illnesses.

The outbreaks were analysed for strength of evidence for transmission by food, person-to-person, animals, water and environmental factors. Outbreaks with multiple transmission routes were also analysed, particularly food/person-to-person and zoonotic/person-to-person. There was evidence for the importance of foodborne transmission in outbreaks where infection was acquired domestically. Foodborne transmission was implicated in 64% of the outbreaks, involving 84% of the outbreak cases. Considering only outbreaks with strong evidence (i.e. laboratory confirmed) for a mode of transmission, and excluding multi-modal outbreaks, 17/18 (94%) of these outbreaks were either foodborne or associated with an infected food handler. There is at least some evidence of foodborne transmission in 74% of outbreaks with only one implicated mode of transmission. The laboratory-confirmed food sources were diverse and included potato salad, raw egg mayonnaise, palusami, tahini and flour.

The data analysed in this study did not allow quantitative attribution of proportions of non-typhoid salmonellosis to the pathways of importance to the NZFSA. However, all the analyses did provide evidence to show that food is the most important route of *Salmonella* transmission. There were insufficient foods associated with cases or outbreaks and confirmed by laboratory evidence to attribute human salmonellosis cases to specific foods. Outbreaks were the only source of these data, and the confirmed foods were variable and a mix of domestic and imported. The analyses of probable foods (i.e. foods that are implicated but unconfirmed) reveal possible bias in reporting and we recommend caution in the use of these data. Infected food handlers were identified in half of the outbreaks with strong evidence for a mode of transmission. While it is acknowledged that infected food handlers are important in transmission of salmonellosis there was insufficient information in these outbreaks to determine whether the handlers contaminated food or became ill as a result of handling or consuming contaminated food.

Salmonellosis was not strongly associated with person-to-person transmission. There was good evidence that contact with farm animals and sick animals can lead to human salmonellosis. Consumption of untreated drinking water and contact with recreational water appeared to be less important transmission routes, but these findings were confounded by cases having contact with other risk factors, such as contact with farm animals. Salmonellosis was associated with overseas travel, but for only a small proportion of cases and involved less common serotypes. These results generally support a recent review of salmonellosis aetiology in New Zealand (Wilson and Baker, 2009), though our findings suggest that person-to-person transmission is less important and direct animal contact more important.

Demographic information on notified cases was complete for almost all cases; the completeness of reporting for risk factors was much lower (17-86% depending on the risk factor and Public Health Unit). Salmonellosis reporting could be improved by changes to the way foodborne risk factors are collected for sporadic cases, standardisation in data recording and establishing a food categorisation system. Some of these options are being considered in a current review of the outbreak report form.

Sentinel surveillance focusing on a New Zealand geographical region has been useful in elucidating campylobacteriosis transmission pathways; a similar approach would likely yield useful information on sources and transmission pathways for human salmonellosis, but would require greater resources.

1 INTRODUCTION

Salmonella is one of the three priority enteric pathogens for the New Zealand Food Safety Authority (NZFSA). The NZFSA has set itself a goal of achieving a 30% reduction in the incidence of foodborne salmonellosis by 2013. To support this goal the NZFSA have developed the *Salmonella* Risk Management Strategy 2009-2012.[1] The first listed objective of this strategy is to quantify the proportion of foodborne cases attributable to specific foods, animal feeds, domestically produced versus imported foods, and multi-resistant and virulent *Salmonella* genotypes associated with foods.

This project was commissioned with the following objectives:

- To build on previous attribution studies in alignment with the NZFSA Science, the Human Enteric Disease Surveillance and *Salmonella* strategies;
- To quantify the proportions of human salmonellosis cases attributable to a range of pathways including those identified in the *Salmonella* strategy; and,
- To inform future improvements in salmonellosis reporting, and potential sentinel surveillance.

The project had two major tasks:

1. Case-case analysis of ten years of salmonellosis notification data based on a previously reported analysis of data from 2006 (Wilson *et al*., 2008).
2. Analysis of approximately ten years of reported salmonellosis outbreaks, building on an earlier report (King and Lake, 2007).

Results have been presented in three sections, all based on data collated from surveillance of New Zealand enteric disease for the years 2000 to 2009. Section 2 presents the results of case-case analyses that compare salmonellosis with other enteric diseases. Section 3 presents an analysis of *Salmonella* serotypes and includes case-case analyses based on these serotypes. Section 4 presents analyses of salmonellosis outbreak data. Each section concludes with some discussion, but the overall findings in terms of the objectives are summarised in Section 5.

The case and outbreak data used in this report was obtained from EpiSurv, New Zealand's national notifiable diseases database, which is managed by ESR. Public Health Officers (PHOs) electronically report notifiable disease cases and outbreaks into EpiSurv on standardised case report forms and outbreak forms.[2] It is acknowledged that these data only represent a fraction of the burden of illness in the New Zealand population. Approximately 22% of cases in the community with acute gastrointestinal illness will visit their GP. Only a proportion of these cases will receive a faecal specimen request, and only some of these samples will yield a positive test result that is notified. It has been estimated that for every notified case there are 222 community cases (Lake *et al*., 2010).

[1] http://www.nzfsa.govt.nz/foodborne-illness/salmonella/strategy.htm

[2] We use the title "Public Health Officers" to encompass personnel who investigate and report surveillance information, e.g. Health Protection Officers, Environmental Health Officers.

2 CASE-CASE ANALYSIS: COMPARISON WITH ENTERIC DISEASES

2.1 Introduction

Analytical studies of infectious diseases using cases routinely reported to surveillance systems require an awareness of selection biases inherent in the reporting process (McCarthy and Giesecke, 1999). There are also difficulties in selecting suitable controls should a comparator group be required, as in a case-control study. Ideally the same selection biases should be reproduced in the control group, but this is challenging.

To at least partially overcome these difficulties the case-case methodology has been developed. Advances in microbiological typing have enabled the segregation of reported cases of the same disease (i.e. acute gastrointestinal illness) into subgroups based on etiological agent, which can then be compared. The reporting system selection biases are thus reproduced across these groups (O'Brien and Halder, 2007). The biases will include interactions with the health system, case exposure history, as well as how the history is recalled (McCarthy and Giesecke, 1999).

The use of reported cases of the same disease caused by a different agent as a control group can have disadvantages. Exposures which are a risk for infection for both groups will not be identified or may be underestimated. Secondly, general risk factors or exposures for the disease that apply to all the etiological agents will also not be identified. One example is the use of medicines which lower gastric acidity and increase the risk from a given dose of any enteric pathogen (McCarthy and Giesecke, 1999). Case-case comparisons cannot be used to make statements about the magnitude or direction of population risk (O'Brien and Halder, 2007). Case-case analyses of cases routinely reported to surveillance systems will also be restricted to those risk factors for which data are routinely collected, which may also be lacking in detail (Wilson *et al*., 2008).

However, case-case comparisons have been described as useful for generating hypotheses. For example, a comparison of infections with *Campylobacter jejuni* and *Campylobacter coli* identified exposures that were more likely for *C. Coli* infections, such as eating pâté, which is biologically plausible given the association of that species with pork (Gillespie *et al*., 2002). Case-case comparisons can also be useful in efficiently identifying exposures associated with outbreaks. Reported cases of infection with a particular *Salmonella* serotype in Germany were compared to those caused by all other serotypes to identify associations with consumption of beef and pork (Krumkamp *et al*., 2008).

Case-case analysis of reported cases of enteric disease has been illustrated using New Zealand data from 2006 (Wilson *et al*., 2008). Using cases of campylobacteriosis as the reference, odds ratios for reported risk factors were calculated for cases of shigellosis, giardiasis, salmonellosis, cryptosporidiosis and yersiniosis. The risk factors used were those routinely collected on the case report forms for the national notification surveillance database EpiSurv. A number of risk factors were identified as associated with particular enteric diseases, and these were consistent with data from other studies.

In this section we have applied the case-case methodology to a larger New Zealand dataset, being the ten years from 2000 – 2009, and used salmonellosis as the reference. Further analysis of the dataset of reported cases of salmonellosis has been conducted on the basis of serotype (see Section 3).

Demographic information on salmonellosis cases is collected as part of the notification process and should be reasonably complete. PHOs collect information on risk factors during the investigation process. Public Health Units (PHUs) have different policies and approaches to case investigations (Whyte, 2003) and this can influence the level of detail recorded in EpiSurv, and hence the results of any analyses. In this section the completeness of demographic and risk factor information recorded by each PHU for the salmonellosis dataset is also compared.

2.2 Method

All cases of notified salmonellosis with a status of "confirmed", "probable", "suspect", "under investigation" and "unknown" (default) were extracted on 22 February 2010 for the period 2000 to 2009.

Case demographics were assigned as follows:

- Sex: As recorded in EpiSurv.
- Age: Cases were grouped into three age groups based on their age or date of birth recorded in EpiSurv. The groups were less than five years, five to 16 years and 17 years or older.
- Ethnicity: EpiSurv can record multiple ethnicities. Cases were assigned a single ethnicity using a prioritised ethnicity approach. Ethnicities were prioritised in the following order: Maori, Pacific peoples, Asian, European and 'Other'. The 'Other' ethnic group includes any person who had an ethnicity (or ethnicities) recorded that was not Maori, Pacific peoples or Asian, and at least one of their ethnicities was not European.
- Rurality: Cases were assigned as rural or urban based on Statistics New Zealand's Urban Rural Profile 2006.[3] For this profile, Statistics New Zealand assigns home and workplace addresses from the 2006 Census to urban/rural categories. Only cases living in strongly rural or strongly urban domiciles were included in this report's analysis (Table 1). Cases from the other categories were grouped with cases that could not be assigned an urban/rural category and are collectively referred to as 'Unknown' in the relevant parts of this report.

Table 1: Statistics NZ Urban Rural Profile 2006 categories, their assignment for the case-case analysis and 2006 New Zealand population estimates

Category	Rural/Urban assignment	NZ population in each category[1]	
		No.	%
Area outside urban/rural profile	Not used	915	<0.01
Highly rural/remote area	**Rural**	**64,182**	**1.6**
Rural area with low urban influence	**Rural**	**220,470**	**5.5**
Rural area with moderate urban influence	Not used	154,968	3.8
Rural area with high urban influence	Not used	124,251	3.1
Independent urban area	**Urban**	**442,260**	**11.0**
Main urban area	**Urban**	**2,892,810**	**71.8**
Satellite urban area	**Urban**	**128,094**	**3.2**

1. *Sourced from the Statistics NZ updated urban/rural tables based on the 2006 census (released December 2006) (http://www.stats.govt.nz/Publications/BusinessPerformanceEnergyAndAgriculture/urban-rural-profile-update.aspx). Total population = 4,027,947 people.*

[3] http://www.stats.govt.nz/Publications/BusinessPerformanceEnergyAndAgriculture/urban-rural-profile-experimental-class-categories.aspx

Cases were assigned as outbreak-associated if the case report form section relating to outbreaks indicated that they were part of an outbreak. An outbreak number was not required.

The enteric disease case report form includes a section where PHOs can record risk factors for the case. These risk factors include:

- Food consumption from a food premises
- Consumption of untreated drinking water
- Contact with recreational water
- Contact with symptomatic people or human faeces
- Contact with farm animals or sick animals
- Overseas travel during the incubation period.

These risk factors were used for case-case analyses.

All confirmed cases of campylobacteriosis, cryptosporidiosis, giardiasis, shigellosis, yersiniosis and verocytotoxin-producing *Escherichia coli* (VTEC)/shiga-toxigenic *E. coli* (STEC) infection, for the period 2000 to 2009, were extracted from EpiSurv on 22 February 2010. These cases were assigned demographics as described above and used for the case-case analyses.

For the case-case analyses, the chi-square test (Hennekens and Buring, 1987) was used to determine the statistical significance of differences in the proportions of cases in various demographic groups between salmonellosis and the other enteric diseases. Odds ratios (ORs) and 95 percent confidence intervals (CI) were calculated according to methods described in Hennekens and Buring (1987). There are several potential confounders in such aggregated data, so a stratified analysis was undertaken by three age strata and by sex. Regression analysis was considered, but was not carried out due to the high number of "unknowns" in the risk factor data. From the data available, crude ORs and confidence intervals were calculated.

Salmonellosis cases were used as the reference group in all of the case-case analyses.

To measure the completeness of the information on each demographic and risk factor for the cases investigated by each PHU, the salmonellosis records were first grouped by PHU based on the EpiSurv number. For each PHU, the proportion of cases with completed information was calculated for each demographic factor:

- Sex: Number of cases with a recorded sex.
- Age: Number of cases with a recorded age.
- Ethnicity: Number of cases for which a prioritised ethnicity could be assigned.
- Rurality: Number of cases for which an urban/rural profile could be assigned.

For each PHU, the proportion of cases with completed information was also calculated for each risk factor:

- Overseas travel: Number of cases with "yes" or "no" against the question "Was the case overseas during the incubation period for this disease?"
- Food premises: Number of cases with "yes" or "no" against the question "Did the case consume food from a food premise during the incubation period?"
- Drinking water: Number of cases with "yes" or "no" against the question "did the case consume untreated surface water, bore water or rain water during the incubation period?"
- Recreational water contact: Number of cases with "yes" or "no" against the question "Did the case have recreational contact with water during the incubation period?"
- Animal contact: Number of cases with "yes" or "no" against the question "Did the case have contact with farm animals during the incubation period?"

- Sick animal contact: Number of cases with "yes" or "no" against the question "Did the case have contact with sick animals during the incubation period?"
- Contact with symptomatic people: Number of cases with "yes" or "no" against the question "Did the case have contact with other symptomatic people during the incubation period?"
- Contact with confirmed cases of the same disease: Number of cases with "yes" or "no" against this statement.
- Contact with human faeces: Number of cases with "yes" or "no" against the question "Did the case have contact with children in nappies, sewage or other types of faeces or vomit during the incubation period?"

2.3 Results: Summary of Cases

2.3.1 Number of cases

A total of 159,709 enteric disease cases were included in this case-case analysis. Over the ten-year study period, the highest number of reported cases occurred for campylobacteriosis (114,418 cases), which is over seven times more than the next highest disease giardiasis (15,068 cases). VTEC/STEC infection caused the lowest number of reported cases (955) (Table 2).

Table 2: Number of reported enteric disease cases by disease, 2000 to 2009

Disease	No. cases
Campylobacteriosis	114,418
Giardiasis	15,068
Salmonellosis	**15,040**
Cryptosporidiosis	8,554
Yersiniosis	4,417
Shigellosis	1,257
VTEC/STEC infection	955
Total	**159,709**

2.3.2 Hospitalisations and fatalities

There were 1,656 people with salmonellosis who were admitted to hospital over the period 2000-2009, ranging from 111 cases in 2007 to 282 cases in 2001. The PHO records hospitalisations when they interview cases. If a case is hospitalised after the interview the EpiSurv information may not be updated so the data on hospitalisations may be an underestimate. Twenty-seven salmonellosis cases died over the ten-year period. Five deaths were directly attributed to salmonellosis. These five fatal cases all occurred between 2005 and 2009 (one case each year).

2.3.3 Demographics

Of the 15,040 salmonellosis cases:

- Sex was not recorded for 216 (1.4%) cases.
- Age was not recorded for 47 (0.3%) cases.
- The ethnicity for 2,449 (16.3%) cases was unknown or could not be assigned.
- A Statistics NZ Urban Rural Profile 2006 score could not be applied to 830 (5.5%) cases.

Table 3 displays the completeness of this demographic information by PHU. Demographic data on sex, age and residence are reasonably complete across the PHUs. Ethnicity information is less readily available, particularly in northern regions of New Zealand.

Table 3: The percentage of salmonellosis cases logged in EpiSurv by each Public Health Unit (2000-2009) which had demographic information available for analysis

Public Health Unit	No. cases	% cases demographic information was available			
		Sex	Age	Ethnicity	Urban/rural profile
Northland District Health Board	486	99.2	100.0	74.7	87.7
Auckland Regional Public Health Service	3,766	97.7	99.5	70.9	96.8
Population Health Service Waikato	1,353	99.1	99.9	91.2	91.9
Toi Te Ora - Public Health	954	98.1	99.5	86.5	90.7
Tairawhiti DHB	168	98.8	98.8	92.3	93.5
Taranaki Health Protection Unit	367	99.7	100.0	84.5	97.0
Hawke's Bay Public Health Unit	670	99.3	99.9	79.7	97.9
MidCentral Public Health Service	702	99.4	100.0	83.8	89.9
Regional Public Health	1,798	98.2	99.6	89.6	95.8
Nelson Marlborough Public Health Service	656	98.9	99.5	85.2	87.2
Community and Public Health	2,369	99.4	99.8	90.3	96.2
Public Health South	1,751	98.3	99.9	91.5	94.6
All PHUs	**15,040**	**98.6**	**99.7**	**83.7**	**94.5**

Based on the cases where demographic data were recorded:

- 48.2% were female and 51.8% were male (n=14,824).
- 26.3% were aged less than five years, 15.1% five to 16 years, and 58.5% 17 years or older (n=14,993).
- 10.1% were Maori, 2.9% Pacific peoples, 4.2% of Asian origin, 82.0% European and 0.8% Other (n=12,591).
- 10.1% were classified as rural and 81.8% as urban (n=14,210). Without the 1,146 cases that were weakly rural or weakly urban (see Table 1), these percentages become 11.0% rural and 89.0% urban (n=13,064).

2.3.4 Salmonellosis cases associated with outbreaks

Overall, 6.2% (927/15,040) of salmonellosis cases were reported to be associated with an outbreak. The annual number and proportion of salmonellosis cases associated with an outbreak varied considerably over the ten-year study period. The number of outbreak-associated cases ranged from seven cases in 2004 to 177 in 2000, whereas the percentage of outbreak cases ranged from 0.6% in 2004 to 11.8% in 2008 (Table 4).

Table 4: Number and proportion of salmonellosis cases associated with an outbreak, 2000-2009

Year	No. outbreak cases	Total cases	% outbreak cases
2000	177	1,795	9.9
2001	119	2,417	4.9
2002	146	1,880	7.8
2003	56	1,401	4.0
2004	7	1,081	0.6
2005	93	1,382	6.7
2006	32	1,335	2.4
2007	81	1,275	6.4
2008	159	1,345	11.8
2009	177	1,129	5.0
Total	**927**	**15,040**	**6.2**

2.4 Results: Case-case Analysis of Enteric Diseases

2.4.1 Demographic variables

Sex, age (less than five years, five to 16 years and 17 years or older), ethnicity and rurality of domicile were compared between the enteric disease cases (Table 5). The salmonellosis cases were the reference group.

Sex was not reported for 9 (0.9%) VTEC/STEC infection cases and 2,569 (1.8%) of other enteric disease cases. Age was not reported for 3 (0.3%) VTEC/STEC infection cases and 958 (0.7%) of the remaining cases. Prioritised ethnicity could not be assigned for 197 (9.5%) VTEC/STEC infection cases and 31,681 (22.0%) of other enteric disease cases. A Statistics NZ Urban Rural Profile 2006 score was not available for 71 (7.4%) VTEC/STEC infection cases and 7,175 (5.0%) of the remaining cases. A Statistics NZ Urban Rural Profile 2006 score was rural with moderate or high urban influence (Table 1) for 1,146 (7.6%) of salmonellosis cases, 126 (0.8%) of VTEC/STEC infection cases, and 9,901 (7.8%) of the remaining cases. These are reported as 'unknown' in Table 5.

Table 5: Comparison of the demographic variables of enteric disease cases from 2000-2009, salmonellosis cases as the reference group

Demographic variable (DV) and enteric disease	% salmonellosis cases with DV	% other disease cases with DV	P-value	Significance[1]
Sex: Female				
Campylobacteriosis	48.2	45.9	0.000	***
Cryptosporidiosis	48.2	51.0	0.000	***
Giardiasis	48.2	48.0	0.777	n/s
Shigellosis	48.2	52.9	0.001	**
Yersiniosis	48.2	46.3	0.028	*
VTEC/STEC infection	48.2	53.7	0.001	**
Age: Less than five years				
Campylobacteriosis	26.3	11.4	0.000	***
Cryptosporidiosis	26.3	42.8	0.000	***
Giardiasis	26.3	22.5	0.000	***
Shigellosis	26.3	15.2	0.000	***
Yersiniosis	26.3	29.8	0.068	n/s
VTEC/STEC infection	26.3	51.2	0.000	***
Age: Five to 16 years				
Campylobacteriosis	15.1	11.4	0.000	***
Cryptosporidiosis	15.1	22.8	0.000	***
Giardiasis	15.1	10.8	0.000	***
Shigellosis	15.1	14.8	0.751	n/s
Yersiniosis	15.1	10.1	0.000	***
VTEC/STEC infection	15.1	14.1	0.370	n/s
Age: 17 years or older				
Campylobacteriosis	58.5	77.2	0.000	***
Cryptosporidiosis	58.5	35.1	0.000	***
Giardiasis	58.5	66.7	0.000	***
Shigellosis	58.5	70.0	0.000	***
Yersiniosis	58.5	60.1	0.068	n/s
VTEC/STEC infection	58.5	34.8	0.000	***
Ethnicity: Maori				
Campylobacteriosis	10.1	6.0	0.000	***
Cryptosporidiosis	10.1	8.4	0.000	***
Giardiasis	10.1	6.3	0.000	***
Shigellosis	10.1	11.1	0.295	n/s
Yersiniosis	10.1	8.4	0.004	**
VTEC/STEC infection	10.1	10.1	0.999	n/s
Ethnicity: Pacific peoples				
Campylobacteriosis	2.9	1.6	0.000	***
Cryptosporidiosis	2.9	1.4	0.000	***
Giardiasis	2.9	1.0	0.000	***
Shigellosis	2.9	25.2	0.000	***
Yersiniosis	2.9	2.5	0.186	n/s
VTEC/STEC infection	2.9	1.4	0.009	**

Table 5 continued…

Demographic variable (DV) and enteric disease	% salmonellosis cases with DV	% other disease cases with DV	P-value	Significance[1]
Ethnicity: Asian origin				
Campylobacteriosis	4.2	3.6	0.002	**
Cryptosporidiosis	4.2	2.0	0.000	***
Giardiasis	4.2	4.2	0.912	n/s
Shigellosis	4.2	10.1	0.000	***
Yersiniosis	4.2	11.5	0.000	***
VTEC/STEC infection	4.2	2.9	0.060	n/s
Ethnicity: European				
Campylobacteriosis	82.0	88.1	0.000	***
Cryptosporidiosis	82.0	87.7	0.000	***
Giardiasis	82.0	86.5	0.000	***
Shigellosis	82.0	52.1	0.000	***
Yersiniosis	82.0	76.7	0.000	***
VTEC/STEC infection	82.0	84.7	0.046	*
Ethnicity: Other				
Campylobacteriosis	0.8	0.7	0.197	n/s
Cryptosporidiosis	0.8	0.5	0.008	**
Giardiasis	0.8	1.9	0.000	***
Shigellosis	0.8	1.5	0.019	*
Yersiniosis	0.8	0.9	0.393	n/s
VTEC/STEC infection	0.8	0.9	0.635	n/s
Rurality: Rural[2]				
Campylobacteriosis	11.0	7.3	0.000	***
Cryptosporidiosis	11.0	21.0	0.000	***
Giardiasis	11.0	7.0	0.000	***
Shigellosis	11.0	4.0	0.000	***
Yersiniosis	11.0	6.9	0.000	***
VTEC/STEC infection	11.0	21.9	0.000	***

*1. Levels of statistical significance: n/s not significant; * p<0.05, ** p<0.01, *** p<0.001*

2. For the "Rural" analysis, only cases classified as highly urban or highly rural have been included. See Section 2.2 for further detail.

When comparing salmonellosis cases with cases of the other enteric diseases, significant differences were identified for both sex and age. The proportion of cases that were female was significantly higher for VTEC/STEC infection, shigellosis, and cryptosporidiosis compared with salmonellosis, whereas campylobacteriosis and yersiniosis had a significantly lower proportion of female cases. Both cryptosporidiosis and VTEC/STEC infection had a significantly higher proportion of cases aged less than five years compared with salmonellosis cases. Cases from all the other enteric diseases, except yersiniosis, had a significantly lower proportion in this age group. For the five to 16 years age group, cryptosporidiosis was the only disease that had a significantly higher proportion in this age group than salmonellosis, and the proportions for campylobacteriosis, giardiasis, and yersiniosis were significantly lower. Finally, three diseases, campylobacteriosis, giardiasis, and shigellosis, had a significantly higher proportion of cases aged 17 years or over compared with salmonellosis; the proportions for cryptosporidiosis and VTEC/STEC infection were significantly lower than salmonellosis.

There were significant differences in the ethnicity of cases between the enteric diseases. A statistically significant lower proportion of Maori cases was found for campylobacteriosis, cryptosporidiosis, giardiasis, and yersiniosis cases compared with salmonellosis cases. The proportion of shigellosis cases who were Pacific peoples (25.2%) was significantly higher than for salmonellosis (2.9%). For almost all of the other enteric diseases, other than yersiniosis, the proportion of cases that were Pacific peoples was significantly lower compared with salmonellosis cases. In terms of Asian ethnicity, the proportion was significantly higher for shigellosis and yersiniosis cases, and significantly lower for campylobacteriosis and cryptosporidiosis cases compared with the reference group. The enteric diseases which had a significantly higher proportion of European cases compared with salmonellosis were campylobacteriosis, cryptosporidiosis, and giardiasis. The proportion of European cases was significantly lower for shigellosis and yersiniosis. Three diseases showed a significant difference in the proportion of cases who were of 'Other' ethnicity compared with salmonellosis. For both giardiasis and shigellosis the proportion was significantly higher whereas for cryptosporidiosis the proportion was significantly lower.

Significant differences were also identified between the enteric diseases in terms of the proportion of cases that lived in a rural area. The proportion of rural cases for VTEC/STEC infection (21.9%) and cryptosporidiosis (21.0%) was significantly higher than for salmonellosis (11.0%). For all of the other diseases the proportion of cases living in a rural area (range 4.0-7.3%) was significantly lower than for salmonellosis.

2.4.2 Risk factor variables

Of the 15,040 salmonellosis cases:

- Overseas travel was not recorded for 4,312 (28.7%) cases.
- Food consumption from a food premises was not recorded for 7,785 (51.8%) cases.
- Consumption of untreated drinking water was not recorded for 7,666 (51.0%) cases.
- Contact with recreational water was not recorded for 6,384 (42.4%) cases.
- Contact with farm animals was not recorded for 6,104 (40.6%) cases.
- Contact with sick animals was not recorded for 7,241 (48.1%) cases.
- Contact with symptomatic people was not recorded for 6,701 (44.6%) cases.
- Contact with confirmed cases (of the same specific disease) was not recorded for 7,089 (47.1%) cases.
- Contact with human faeces was not recorded for 6,888 (45.8%) cases.

Table 6 displays the completeness of this risk factor information by PHU.

The completeness of information on risk factors is low across all PHUs. The highest completion rate was for overseas travel.

If "yes" or "no" is not recorded the record defaults to "unknown". It is not possible to separate out cases where the answer was actually "unknown" (i.e. the case could not recall the correct response to this question) from situations where this information was not gathered from the case.

Table 6: The percentage of salmonellosis cases logged in EpiSurv by each Public Health Unit (2000-2009) with completed risk factor information available for analysis

Public Health Unit	No. cases	% cases where risk factor information was available[1]								
		Overseas travel	Food premises	Untreated drinking water	Contact recreational water	Contact farm animals	Contact sick animals	Contact symptom. people	Contact confirmed cases	Contact faeces
Northland District Health Board	486	68.3	65.0	59.1	66.5	66.3	61.3	61.3	24.7	63.4
Auckland Regional Public Health Service	3,766	57.5	31.0	35.2	41.2	40.2	36.7	38.6	26.7	36.6
Population Health Service Waikato	1,353	68.1	17.4	22.2	22.7	56.2	38.1	52.3	76.9	51.1
Toi Te Ora - Public Health	954	80.8	71.9	62.8	79.1	76.1	69.9	73.2	78.3	71.0
Tairawhiti DHB	168	72.0	44.0	62.5	68.5	72.0	57.7	50.6	51.2	59.5
Taranaki Health Protection Unit	367	86.9	27.0	60.8	82.0	83.9	74.1	74.9	71.4	77.9
Hawke's Bay Public Health Unit	670	60.7	36.9	47.2	34.5	56.3	36.7	48.4	46.6	45.4
MidCentral Public Health Service	702	78.8	65.5	59.0	75.5	68.4	64.2	64.5	72.4	59.0
Regional Public Health	1,798	76.2	58.9	52.0	63.0	56.6	52.7	51.4	33.4	53.3
Nelson Marlborough Public Health Service	656	72.7	61.3	57.3	65.9	66.5	63.7	65.7	65.7	63.1
Community and Public Health	2,369	85.7	59.5	61.4	70.6	68.3	58.6	67.4	70.2	63.2
Public Health South	1,751	71.9	62.9	59.3	74.6	71.7	63.8	62.4	67.2	64.0
All PHUs	**15,040**	**71.3**	**48.2**	**49.0**	**57.6**	**59.4**	**51.9**	**55.4**	**52.9**	**54.2**

1. For a full description of risk factors see text in Section 2.4.2.

2.4.3 Unstratified, unadjusted risk factor analysis

In the unstratified risk factor case-case analysis there were significant differences in the reported exposure to risk factors between salmonellosis cases and other enteric disease cases (Table 7). The ORs in Table 7 have not been adjusted for any potential confounding factors.

Cases who travelled overseas were significantly less likely to have campylobacteriosis, cryptosporidiosis, yersiniosis or VTEC/STEC infection than to have salmonellosis, but more likely to have shigellosis or giardiasis.

In the food premises analysis, only campylobacteriosis had a significantly elevated OR. For all other diseases, except VTEC/STEC infection, the ORs were significantly reduced. This risk factor is not collected for VTEC/STEC infection cases.

Consumption of untreated drinking water was associated with a significantly increased risk of cryptosporidiosis and giardiasis and a significantly lower risk of campylobacteriosis and shigellosis compared with salmonellosis.

Cases that had contact with recreational water were less likely to be notified with salmonellosis than any of the other enteric diseases except for campylobacteriosis. Recreational water exposure was associated with a significantly lower risk of campylobacteriosis.

Contact with farm animals was associated with a significantly elevated OR for cryptosporidiosis and VTEC/STEC infection (OR=3.5 for both), and campylobacteriosis (OR=1.2) and significantly reduced OR for shigellosis (OR=0.24), and giardiasis (OR=0.91).

Exposure to a sick animal was associated with a 4.2 times increased risk of cryptosporidiosis compared with salmonellosis. For all other diseases where data on this risk factor is collected the OR were significantly reduced (variable not collected on the VTEC/STEC case report form).

Cases that had contact with a symptomatic person during their incubation period were significantly less likely to have cryptosporidiosis or yersiniosis than salmonellosis cases. All other diseases had a significantly elevated OR (OR range 1.9–3.3).

Contact with a confirmed case of the same disease during the disease incubation period was associated with elevated OR for giardiasis, shigellosis, and cryptosporidiosis cases (3.8, 3.1, and 1.2 respectively). Both yersiniosis and campylobacteriosis had significantly lower OR (29 and 0.49 respectively). This risk factor is not collected for VTEC/STEC infection cases.

Analysis of exposure to human faeces found significantly elevated OR for giardiasis and cryptosporidiosis compared with salmonellosis cases whereas for campylobacteriosis the OR was significantly lower.

Table 7: Case-case analysis of the exposure to risk factors for enteric disease cases from 2000-2009, salmonellosis cases as the reference group

Risk factor (RF) and enteric disease	Cases with reported exposure to the RF					Odds ratio (OR)[2]	
	Yes	No	Unknown	% reported the RF[1]	% Unknown	OR	95% CI[3]
Overseas travel							
Campylobacteriosis	2,967	39,381	72,070	7.0	63.0	**0.40**	**0.37-0.42**
Cryptosporidiosis	386	5,727	2,441	6.3	28.5	**0.36**	**0.32-0.40**
Giardiasis	1,541	5,937	7,590	20.6	50.4	**1.4**	**1.3-1.5**
Shigellosis	504	433	320	53.8	25.5	**6.1**	**5.3-7.0**
Yersiniosis	142	2,132	2,143	6.2	48.5	**0.35**	**0.29-0.42**
VTEC/STEC infection	29	712	214	3.9	22.4	**0.21**	**0.15-0.31**
Salmonellosis	*1,711*	*9,017*	*4,312*	*15.9*	*28.7*	*1.0*	-
Food consumption from a food premises							
Campylobacteriosis	15,815	15,157	83,446	51.1	72.9	**1.2**	**1.1-1.3**
Cryptosporidiosis	971	2,669	4,914	26.7	57.4	**0.42**	**0.39-0.46**
Giardiasis	1,158	2,925	10,985	28.4	72.9	**0.46**	**0.42-0.50**
Shigellosis	199	337	721	37.1	57.4	**0.68**	**0.57-0.82**
Yersiniosis	609	932	2,876	39.5	65.1	**0.75**	**0.67-0.84**
VTEC/STEC infection	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Salmonellosis	*3,367*	*3,888*	*7,785*	*46.4*	*51.8*	*1.0*	-
Consumption of untreated drinking water							
Campylobacteriosis	6,254	23,901	84,263	20.7	73.6	**0.89**	**0.84-0.95**
Cryptosporidiosis	1,901	2,961	3,692	39.1	43.2	**2.2**	**2.0-2.4**
Giardiasis	1,767	3,116	10,185	36.2	67.6	**1.9**	**1.8-2.1**
Shigellosis	88	387	782	18.5	62.2	**0.77**	**0.61-0.98**
Yersiniosis	373	1,268	2,776	22.7	62.8	1.0	0.88-1.1
VTEC/STEC infection	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Salmonellosis	*1,673*	*5,701*	*7,666*	*22.7*	*51.0*	*1.0*	-
Contact with recreational water							
Campylobacteriosis	4,948	29,824	79,646	14.2	69.6	**0.88**	**0.82-0.94**
Cryptosporidiosis	1,805	3,726	3,023	32.6	35.3	**2.6**	**2.4-2.8**
Giardiasis	1,966	3,953	9,149	33.2	60.7	**2.6**	**2.4-2.9**
Shigellosis	113	494	650	18.6	51.7	1.2	0.98-1.5
Yersiniosis	321	1,521	2,575	17.4	58.3	1.1	0.98-1.3
VTEC/STEC infection	187	511	257	26.8	26.9	**1.9**	**1.3-2.2**
Salmonellosis	*1,373*	*7,283*	*6,384*	*15.9*	*42.4*	*1.0*	-
Contact with farm animals							
Campylobacteriosis	11,548	23,647	79,223	32.8	69.2	**1.2**	**1.1-1.3**
Cryptosporidiosis	3,580	2,474	2,500	59.1	29.2	**3.5**	**3.3-3.8**
Giardiasis	1,580	4,233	9,255	27.2	61.4	**0.91**	**0.85-0.98**
Shigellosis	54	547	656	9.0	52.2	**0.24**	**0.18-0.32**
Yersiniosis	595	1,416	2,406	29.6	54.5	1.0	0.92-1.1
VTEC/STEC infection	313	217	425	59.1	44.5	**3.5**	**2.9-4.2**
Salmonellosis	*2,597*	*6,339*	*6,104*	*29.1*	*40.6*	*1.0*	-

Table 7 continued…

Risk factor (RF) and enteric disease	Cases with reported exposure to the RF					Odds ratio (OR)[2]	
	Yes	No	Unknown	% reported the RF[1]	% Unknown	OR	95% CI[3]
Contact with sick animals							
Campylobacteriosis	1,781	27,269	85,368	6.1	74.6	**0.85**	**0.77-0.94**
Cryptosporidiosis	1,160	3,605	3,789	24.3	44.3	**4.2**	**3.8-4.7**
Giardiasis	213	4,834	10,021	4.2	66.5	**0.57**	**0.49-0.67**
Shigellosis	9	528	720	1.7	57.3	**0.22**	**0.11-0.43**
Yersiniosis	97	1,606	2,714	5.7	61.4	**0.78**	**0.63-0.98**
VTEC/STEC infection	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Salmonellosis	*558*	*7,241*	*7,241*	*7.2*	*48.1*	*1.0*	-
Contact with symptomatic people							
Campylobacteriosis	3,888	29,354	81,176	11.7	70.9	**0.78**	**0.73-0.84**
Cryptosporidiosis	1,440	4,032	3,082	26.3	36.0	**2.1**	**1.9-2.3**
Giardiasis	2,017	3,586	9,465	36.0	62.8	**3.3**	**3.1-3.6**
Shigellosis	162	462	633	26.0	50.4	**2.1**	**1.7-2.5**
Yersiniosis	196	1,658	2,563	10.6	58.0	**0.70**	**0.59-0.82**
VTEC/STEC infection	165	501	289	24.8	30.3	**1.9**	**1.6-2.3**
Salmonellosis	*1,210*	*7,129*	*6,701*	*14.5*	*44.6*	*1.0*	-
Contact with confirmed cases (of the same specific disease)							
Campylobacteriosis	1,724	38,067	74,627	4.3	65.2	**0.49**	**0.44-0.53**
Cryptosporidiosis	501	4,397	3,656	10.2	42.7	**1.2**	**1.08-1.38**
Giardiasis	1,580	4,418	9,070	26.3	60.2	**3.8**	**3.5-4.2**
Shigellosis	121	423	713	22.2	56.7	**3.1**	**2.5-3.8**
Yersiniosis	45	1,645	2,727	2.7	61.7	**0.29**	**0.22-0.40**
VTEC/STEC infection	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Salmonellosis	*677*	*7,274*	*7,089*	*8.5*	*47.1*	*1.0*	-
Contact with human faeces							
Campylobacteriosis	3,956	27,214	83,248	12.7	72.8	**0.80**	**0.75-0.86**
Cryptosporidiosis	1,614	3,764	3,176	30.0	37.1	**2.4**	**2.2-.2.6**
Giardiasis	2,089	3,239	9,740	39.2	64.6	**3.6**	**3.3-3.9**
Shigellosis	73	494	690	12.9	54.9	0.82	0.63-1.05
Yersiniosis	304	1,527	2,586	16.6	58.5	1.10	0.96-1.26
VTEC/STEC infection	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Salmonellosis	*1,251*	*6,901*	*6,888*	*15.3*	*45.8*	*1.0*	-

1. The percentage of cases that reported "Yes" from the total cases reporting "Yes" or "No".

2. Crude OR unadjusted for sex, age, ethnicity, rurality of domicile and other potential confounders. OR significantly different from salmonellosis are bold and shaded.

3. 95% confidence interval

n/a, Not applicable as not collected on VTEC/STEC case report form.

2.4.4 Unadjusted risk factor analysis, stratified by sex

A stratified analysis was undertaken to remove sex as a potential confounding variable and also to assess effect modification by sex (Table 8).

In general, the patterns of elevated or reduced OR were consistent between the unstratified and stratified analyses (see Table 7 and Table 8). A notable exception was a reduced OR (0.87) for contact with recreational water and yersiniosis in females compared with an OR of 1.1 in the unstratified analysis. However, neither OR were statistically significant. Similarly, for contact with sick animals, for females the OR for campylobacteriosis was 1.0, whereas the unstratified analysis gave an OR of 0.85 (95%CI: 0.77-0.94).

When comparing OR between the female and male strata, there was little variation (see Table 8). This indicates that there was minimal effect modification, with some exceptions. In the analysis of consumption of untreated drinking water for cryptosporidiosis, in females the OR was 2.5 compared with 1.9 for males. Similarly, for giardiasis this OR was higher in females (OR=2.3) compared with males (OR=1.7). The OR for exposure to recreational water of yersiniosis cases compared to salmonellosis was lower for females (0.87) but elevated for males (1.3). The OR for cryptosporidiosis and contact with farm animals was 4.0 in females and 3.2 in males. There were two results of note in the analysis of contact with sick animals. The OR for campylobacteriosis and females was 1.0 whereas the OR in the male analysis was 0.73, and for cryptosporidiosis the corresponding OR were 5.7 and 3.1. Finally, contact with human faeces and risk of giardiasis versus salmonellosis produced an OR of 4.5 for females and 2.8 for males.

Table 8: Case-case analysis of the exposure to risk factors for enteric disease cases from 2000-2009, stratified by sex, salmonellosis cases as the reference group

Risk factor (RF) and enteric disease	Female cases							Male cases						
	Reported exposure to the RF					Crude odds ratio (OR)		Reported exposure to the RF					Crude OR	
	Yes (Y)	No (N)	Unk[1]	Y/Y+N (%)	% Unk[1]	OR[2]	95% CI[3]	Yes (Y)	No (N)	Unk	Y/Y+N (%)	% Unk	OR	95% CI
Overseas travel														
Campylobacteriosis	1,427	18,438	31,649	7.2	61.4	**0.41**	**0.38-0.45**	1,510	20,529	38,800	6.9	63.8	**0.38**	**0.35-0.42**
Cryptosporidiosis	191	2,918	1,206	6.1	27.9	**0.35**	**0.30-0.41**	191	2,752	1210	6.5	29.1	**0.36**	**0.31-0.43**
Giardiasis	754	2,912	3,433	20.6	48.4	**1.4**	**1.2-1.5**	777	2,934	3,967	20.9	51.7	**1.4**	**1.3-1.5**
Shigellosis	264	218	168	54.8	25.8	**6.5**	**5.3-7.9**	236	205	137	53.5	23.7	**6.0**	**4.9-7.4**
Yersiniosis	64	1,011	925	6.0	46.3	**0.34**	**0.26-0.44**	75	1,100	1,144	6.4	49.3	**0.36**	**0.28-0.46**
VTEC/STEC infection	19	372	117	4.9	23.0	**0.27**	**0.17-0.44**	10	335	93	2.9	21.2	**0.16**	**0.08-0.29**
Salmonellosis	*816*	*4,358*	*1,972*	*15.8*	*27.6*	*1.0*	-	*873*	*4,567*	*2,238*	*16.0*	*29.1*	*1.0*	**-**
Food consumption from a food premises														
Campylobacteriosis	8,199	6,771	36,544	54.8	70.9	**1.3**	**1.2-1.4**	7,468	8,209	45,162	47.6	74.2	**1.2**	**1.1-1.3**
Cryptosporidiosis	532	1,345	2,438	28.3	56.5	**0.41**	**0.36-0.46**	430	1,300	2,423	24.9	58.3	**0.42**	**0.37-0.48**
Giardiasis	605	1,430	5,064	29.7	71.3	**0.44**	**0.39-0.49**	537	1,449	5,692	27.0	74.1	**0.47**	**0.42-0.53**
Shigellosis	108	175	367	38.2	56.5	**0.64**	**0.50-0.82**	89	157	332	36.2	57.4	**0.72**	**0.55-0.95**
Yersiniosis	295	442	1,263	40.0	63.2	**0.69**	**0.59-0.81**	305	484	1,530	38.7	66.0	**0.81**	**0.69-0.94**
VTEC/STEC infection	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Salmonellosis	*1759*	*1821*	*3566*	*49.1*	*49.9*	*1.0*	-	*1,582*	*2,021*	*4,075*	*43.9*	*53.1*	*1.0*	-

Table 8 continued…

Risk factor (RF) and enteric disease	Female cases							Male cases						
	Reported exposure to the RF					Crude odds ratio (OR)		Reported exposure to the RF					Crude OR	
	Yes (Y)	No (N)	Unk[1]	Y/Y+N (%)	% Unk[1]	OR[2]	95% CI[3]	Yes (Y)	No (N)	Unk	Y/Y+N (%)	% Unk	OR	95% CI
Consumption of untreated drinking water														
Campylobacteriosis	2,740	11,650	37,124	19.0	72.1	0.96	0.87-1.1	3,440	12,017	45,382	22.3	74.6	**0.84**	**0.77-0.91**
Cryptosporidiosis	966	1,550	1,799	38.4	41.7	**2.5**	**2.3-2.9**	919	1,383	1,851	39.9	44.6	**1.9**	**1.7-2.2**
Giardiasis	880	1,549	4,670	36.2	65.8	**2.3**	**2.1-2.6**	859	1,517	5,302	36.2	69.1	**1.7**	**1.5-1.9**
Shigellosis	47	197	406	19.3	62.5	0.97	0.70-1.4	40	185	353	17.8	61.1	**0.63**	**0.45-0.90**
Yersiniosis	165	608	1,227	21.3	61.4	1.1	0.9-1.3	203	647	1,469	23.9	63.3	0.92	0.77-1.1
VTEC/STEC infection	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Salmonellosis	*700*	*2,849*	*3,597*	*19.7*	*50.3*	*1.0*	-	*959*	*2,801*	*3,918*	*25.5*	*51.0*	*1.0*	**-**
Contact with recreational water														
Campylobacteriosis	2,173	14,349	34,992	13.2	67.9	**0.86**	**0.78-0.94**	2,724	15,147	42,968	15.2	70.6	**0.91**	**0.83-0.99**
Cryptosporidiosis	882	1,971	1,462	30.9	33.9	**2.5**	**2.3-2.9**	908	1,715	1,530	34.6	36.8	**2.7**	**2.4-3.0**
Giardiasis	936	1,966	4,197	32.3	59.1	**2.7**	**2.4-3.0**	1,004	1,924	4,750	34.3	61.9	**2.6**	**2.4-2.9**
Shigellosis	57	251	342	18.5	52.6	1.3	0.95-1.7	55	234	289	19.0	50.0	1.2	0.9-1.6
Yersiniosis	114	740	1,146	13.3	57.3	0.87	0.70-1.1	203	765	1,351	21.0	58.3	**1.3**	**1.1-1.6**
VTEC/STEC infection	101	269	138	27.3	27.2	**2.1**	**1.7-2.7**	86	236	116	26.7	26.5	**1.8**	**1.4-2.4**
Salmonellosis	*632*	*3,582*	*2,932*	*15.0*	*41.0*	*1.0*	-	*720*	*3,628*	*3,330*	*16.6*	*43.4*	*1.0*	**-**
Contact with farm animals														
Campylobacteriosis	4,860	11,826	34,828	29.1	67.6	**1.2**	**1.1-1.5**	6,559	11,582	42,698	36.2	70.2	**1.2**	**1.1-1.3**
Cryptosporidiosis	1,809	1,290	1,216	58.4	28.2	**4.0**	**3.6-4.4**	1,735	1,162	1,256	59.9	30.2	**3.2**	**2.9-3.5**
Giardiasis	760	2,116	4,223	26.4	59.5	1.0	0.91-1.2	798	2,044	4,836	28.1	63.0	**0.83**	**0.75-0.92**
Shigellosis	30	276	344	9.8	52.9	**0.31**	**0.21-0.45**	24	260	294	8.5	50.9	**0.20**	**0.13-0.30**
Yersiniosis	250	704	1,046	26.2	52.3	1.0	0.85-1.2	336	699	1,284	32.5	55.4	1.0	0.89-1.2
VTEC/STEC infection	150	109	249	57.9	49.0	**3.9**	**3.0-5.0**	160	107	171	59.9	39.0	**3.2**	**2.5-4.1**
Salmonellosis	*1,129*	*3,181*	*2,836*	*26.2*	*39.7*	*1.0*	-	*1,450*	*3,089*	*3,139*	*31.9*	*40.9*	*1.0*	-

Table 8 continued…

Risk factor (RF) and enteric disease	Female cases							Male cases						
	Reported exposure to the RF					Crude odds ratio (OR)		Reported exposure to the RF					Crude OR	
	Yes (Y)	No (N)	Unk[1]	Y/Y+N (%)	% Unk[1]	OR[2]	95% CI[3]	Yes (Y)	No (N)	Unk	Y/Y+N (%)	% Unk	OR	95% CI
Contact with sick animals														
Campylobacteriosis	830	13,243	37,441	5.9	72.7	1.0	0.88-1.2	935	13,747	46,157	6.4	75.9	**0.73**	**0.64-0.83**
Cryptosporidiosis	644	1,846	1,825	25.9	42.3	**5.7**	**4.8-6.7**	505	1,726	1,922	22.6	46.3	**3.1**	**2.7-3.7**
Giardiasis	103	2,441	4,555	4.0	64.2	**0.69**	**0.54-0.88**	106	2,319	5,253	4.4	68.4	**0.49**	**0.39-0.62**
Shigellosis	5	269	376	1.8	57.8	**0.30**	**0.12-0.74**	4	250	324	1.6	56.1	**0.17**	**0.06-0.46**
Yersiniosis	46	771	1,183	5.6	59.2	0.97	0.70-1.4	49	817	1,453	5.7	62.7	**0.64**	**0.47-0.88**
VTEC/STEC infection	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Salmonellosis	*219*	*3,574*	*3,353*	*5.8*	*46.9*	*1.0*	-	*334*	*3,590*	*3,754*	*8.5*	*48.9*	*1.0*	-
Contact with symptomatic people														
Campylobacteriosis	1,968	13,832	35,714	12.5	69.3	**0.81**	**0.74-0.90**	1,878	15,228	43,733	11.0	71.9	**0.76**	**0.69-0.84**
Cryptosporidiosis	795	2,021	1,499	28.2	34.7	**2.3**	**2.0-2.5**	637	1,968	1548	24.5	37.3	**2.0**	**1.8-2.3**
Giardiasis	1,040	1,708	4,351	37.8	61.3	**3.5**	**3.1-3.9**	941	1,822	4,915	34.1	64.0	**3.2**	**2.8-3.6**
Shigellosis	94	227	329	29.3	50.6	**2.4**	**1.8-3.1**	64	228	286	21.9	49.5	**1.7**	**1.3-2.3**
Yersiniosis	93	792	1,115	10.5	55.8	**0.67**	**0.53-0.85**	101	846	1,372	10.7	59.2	**0.73**	**0.59-0.92**
VTEC/STEC infection	79	265	164	23.0	32.3	**1.7**	**1.3-2.2**	84	235	119	26.3	27.2	**2.2**	**1.69-2.9**
Salmonellosis	*600*	*3,426*	*3,120*	*14.9*	*43.7*	*1.0*	-	*593*	*3,643*	*3,442*	*14.0*	*44.8*	*1.0*	**-**
Contact with confirmed cases (of the same specific disease)														
Campylobacteriosis	825	17,582	33,107	4.5	64.3	**0.47**	**0.41-0.53**	883	20,094	39,862	4.2	65.5	**0.52**	**0.46-0.60**
Cryptosporidiosis	262	2,208	1,845	10.6	42.8	1.2	1.0-1.4	235	2,155	1,763	9.8	42.5	**1.3**	**1.1-1.5**
Giardiasis	797	2,162	4,140	26.9	58.3	**3.7**	**3.2-4.2**	761	2,194	4,723	25.8	61.5	**4.1**	**3.6-4.7**
Shigellosis	71	214	365	24.9	56.2	**3.3**	**2.5-4.4**	44	205	329	17.7	56.9	**2.5**	**1.8-3.6**
Yersiniosis	19	773	1,208	2.4	60.4	**0.24**	**0.15-0.39**	25	858	1,436	2.8	61.9	**0.35**	**0.23-0.52**
VTEC/STEC infection	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Salmonellosis	*352*	*3,500*	*3294*	*9.1*	*46.1*	*1.0*	-	*313*	*3,709*	*3,656*	*7.8*	*47.6*	*1.0*	-

Table 8 continued…

Risk factor (RF) and enteric disease	Female cases							Male cases						
	Reported exposure to the RF					Crude odds ratio (OR)		Reported exposure to the RF					Crude OR	
	Yes (Y)	No (N)	Unk[1]	Y/Y+N (%)	% Unk[1]	OR[2]	95% CI[3]	Yes (Y)	No (N)	Unk	Y/Y+N (%)	% Unk	OR	95% CI
Contact with human faeces														
Campylobacteriosis	2,131	12,739	36,644	14.3	71.1	**0.89**	**0.81-0.98**	1,783	14,205	44,851	11.2	73.7	**0.72**	**0.65-0.79**
Cryptosporidiosis	872	1,889	1,554	31.6	36.0	**2.5**	**2.2-2.8**	727	1,837	1,589	28.4	38.3	**2.3**	**2.0-2.6**
Giardiasis	1,216	1,443	4,440	45.7	62.5	**4.5**	**4.0-5.1**	840	1,744	5,094	32.5	66.3	**2.8**	**2.4-3.1**
Shigellosis	44	244	362	15.3	55.7	0.96	0.69-1.3	28	242	308	10.4	53.3	**0.66**	**0.44-0.98**
Yersiniosis	144	727	1,129	16.5	56.5	1.1	0.87-1.3	156	785	1378	16.6	59.4	1.1	0.94-1.4
VTEC/STEC infection	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Salmonellosis	*622*	*3321*	*3,203*	*15.8*	*44.8*	*1.0*	-	*616*	*3,512*	*3,550*	*14.9*	*46.2*	*1.0*	-

1. Unk, Unknown

2. Crude OR unadjusted for age, ethnicity, rurality of domicile and other potential confounders. OR significantly different from salmonellosis are bold and shaded.

3. 95% confidence interval

n/a, Not applicable as not collected on VTEC/STEC case report form.

2.4.5 Unadjusted risk factor analysis, stratified by age

As for Section 2.4.4, in most instances in the analysis stratified by age the direction of the OR for a particular risk factor and disease combination (i.e. elevated or reduced) was the same as in the unstratified analysis (see Table 7 and Table 9). However, there were more age related OR differences in this analysis than occurred with stratification by sex. This discussion uses the terms 'infants', 'children' and 'adults' to describe the age groups of less than five years, five to 16 years and 17 years or older, respectively.

When stratified by age, the OR for campylobacteriosis for consumption of food from a food premises changed from significantly increased, to significantly reduced in infants, and was no longer significantly different to salmonellosis for the remaining two age groups. The OR for consumption of untreated drinking water and campylobacteriosis in infants was 1.7 whereas the OR was reduced in the unstratified analysis (0.89). The same was true for shigellosis in adults, which had an elevated but not significant OR (1.2) compared to a significant and reduced OR in the unstratified analysis (0.77). There were two age related differences in the analysis of contact with recreational water. The OR for campylobacteriosis in both infants and children was significantly elevated at 1.2 compared with a significantly reduced OR of 0.88 in the unstratified analysis, and the corresponding OR for shigellosis were 0.34 (children) and 1.2 (unstratified). A significantly reduced OR (0.91) for contact with farm animals and giardiasis in the unstratified analysis became non-significant (ORs: 1.1 and 1.0) in the child and adult analysis. The OR for contact with sick animals and campylobacteriosis was 1.6 for infants but 0.85 in the unstratified analysis. Similarly for contact with symptomatic people and campylobacteriosis a significantly reduced OR in the unstratified analysis (0.78) became non-significantly elevated for infants in the stratified analysis. Conversely, for contact with confirmed cases of the same disease and cryptosporidiosis, a significantly elevated OR (1.2) in the unstratified analysis became significantly reduced (0.75) for children in the stratified analysis.

When comparing the three age strata, the ORs for the same risk factor and disease combinations were largely similar (see Table 9). Some notable exceptions are listed below. Consumption of untreated water and risk of campylobacteriosis was associated with a significantly elevated OR in infants (1.7) but a significantly reduced OR in adults (0.83). The converse was true for shigellosis where the infants' and children's ORs were 0.30 and 0.25 respectively and significant whereas the adult's OR was 1.2 but not significant. Differences between age groups were also seen for contact with recreational water and the same two diseases; for campylobacteriosis the infants' and children's ORs were both 1.2 compared with the adult's OR of 0.91, and for shigellosis the infants' OR was 1.1, children's OR was 0.34 and the adult's OR was 2.0. In the analysis of contact with farm animals, higher ORs were seen in infants and children compared with adults for campylobacteriosis, cryptosporidiosis, and VTEC/STEC infection, but all of the ORs were elevated compared with salmonellosis. For contact with sick animals and campylobacteriosis infants had a significantly elevated OR (1.6) whereas the adult OR was significantly reduced (0.74). For the combination of contact with symptomatic people and cryptosporidiosis the infants' and children's ORs were 1.5 and 1.3 compared with an OR of 3.0 in the adult analysis. Noteworthy child/adult differences relating to contact with confirmed cases of the same disease occurred for campylobacteriosis, giardiasis, and shigellosis. For campylobacteriosis the infants' OR was 0.91 compared with ORs of 0.49 and 0.46 for children and adults respectively. For giardiasis the corresponding OR were 6.8, 4.1 and 2.9 respectively and for shigellosis they were 5.0, 3.0, and 2.8. Finally, exposure to human faeces was associated with an OR of 1.5 and 1.7 for infants and children respectively and an OR of 3.9 for adults with cryptosporidiosis, and ORs of 2.0, 3.1, and 5.2 for the same age strata with giardiasis.

Table 9: Case-case analysis of the exposure to risk factors for enteric disease cases from 2000-2009, stratified by age group, salmonellosis cases as the reference group

Risk factor (RF) and enteric disease	Cases aged less than five years					Cases ages five to 16 years					Cases aged 17 years or older				
	Reported exposure to the risk factor			Crude Odds Ratio (OR)		Reported exposure to the risk factor			Crude Odds Ratio (OR)		Reported exposure to the risk factor			Crude Odds Ratio (OR)	
	Yes (Y)	No (N)	% Unk[1]	OR[2]	95% CI[3]	Yes (Y)	No (N)	% Unk	OR	95% CI	Yes (Y)	No (N)	% Unk	OR	95% CI
Overseas travel															
Campylobacteriosis	129	4,956	60.7	**0.37**	**0.29-0.46**	176	4331	65.2	**0.45**	**0.36-0.57**	2,655	30,026	62.7	**0.31**	**0.28-0.33**
Cryptosporidiosis	94	2,544	27.8	**0.52**	**0.41-0.68**	60	1,344	28.0	**0.50**	**0.36-0.68**	231	1,834	29.6	**0.43**	**0.37-0.50**
Giardiasis	193	1,868	39.0	**1.5**	**1.2-1.8**	116	607	55.1	**2.1**	**1.6-2.8**	1,228	3,440	53.3	**1.2**	**1.1-1.4**
Shigellosis	35	90	34.2	**5.5**	**3.6-8.4**	37	93	29.7	**4.4**	**2.9-6.7**	432	250	22.0	**6.0**	**5.1-7.1**
Yersiniosis	16	570	55.2	**0.40**	**0.24-0.67**	12	233	44.7	0.57	0.31-1.1	114	1,327	45.3	**0.30**	**0.24-0.36**
VTEC/STEC infection	11	372	21.4	**0.42**	**0.23-0.78**	1	103	22.4	**0.11**	**0.01-0.78**	17	235	23.9	**0.25**	**0.15-0.41**
Salmonellosis	*191*	*2,710*	*26.5*	*1.0*	-	*138*	*1,531*	*26.5*	*1.0*	-	*1,380*	*4,762*	*30.0*	*1.0*	-
Food consumption from a food premises															
Campylobacteriosis	890	2,667	72.5	**0.75**	**0.67-0.85**	1,413	1,803	75.2	0.92	0.81-1.1	13,488	10,665	72.5	1.1	1.0-1.2
Cryptosporidiosis	291	1,272	57.2	**0.52**	**0.44-0.61**	220	573	59.3	**0.45**	**0.37-0.55**	459	821	56.4	**0.47**	**0.42-0.54**
Giardiasis	187	829	69.9	**0.51**	**0.42-0.61**	87	306	75.6	**0.34**	**0.26-0.44**	878	1,781	73.4	**0.42**	**0.38-0.46**
Shigellosis	22	60	56.8	0.83	0.50-1.4	25	53	57.8	**0.56**	**0.34-0.91**	152	224	57.0	**0.58**	**0.46-0.71**
Yersiniosis	102	289	70.1	0.80	0.62-1.0	63	97	63.9	0.77	0.55-1.1	443	546	62.4	**0.69**	**0.60-0.79**
VTEC/STEC infection	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Salmonellosis	616	1,390	49.2	1.0	-	506	597	51.4	1.0	-	2,235	1,898	52.9	1.0	-

Table 9 continued…

Risk factor (RF) and enteric disease	Cases aged less than five years					Cases ages five to 16 years					Cases aged 17 years or older				
	Reported exposure to the risk factor			Crude Odds Ratio (OR)		Reported exposure to the risk factor			Crude Odds Ratio (OR)		Reported exposure to the risk factor			Crude Odds Ratio (OR)	
	Yes (Y)	No (N)	% Unk[1]	OR[2]	95% CI[3]	Yes (Y)	No (N)	% Unk	OR	95% CI	Yes (Y)	No (N)	% Unk	OR	95% CI
Consumption of untreated drinking water															
Campylobacteriosis	1,344	2,373	71.3	**1.7**	**1.5-1.9**	928	2,217	75.7	1.1	0.94-1.3	3,977	19,270	73.5	**0.83**	**0.77-0.91**
Cryptosporidiosis	955	1,194	41.2	**2.4**	**2.1-2.7**	445	663	43.2	**1.8**	**1.5-2.1**	499	1,101	45.4	**1.8**	**1.6-2.1**
Giardiasis	537	884	57.9	**1.8**	**1.6-2.1**	179	280	71.5	**1.7**	**1.3-2.1**	1,048	1,940	70.1	**2.2**	**2.0-2.4**
Shigellosis	8	79	54.2	**0.30**	**0.14-0.62**	6	63	62.7	**0.25**	**0.11-0.58**	74	245	63.5	1.2	0.93-1.6
Yersiniosis	101	304	69.0	0.98	0.77-1.3	43	119	63.4	0.94	0.65-1.4	229	843	59.3	1.1	0.93-1.3
VTEC/STEC infection	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Salmonellosis	541	1,601	45.7	1.0	-	331	861	47.5	1.0	-	799	3228	54.1	1.0	-
Contact with recreational water															
Campylobacteriosis	835	3,479	66.7	**1.2**	**1.1-1.4**	1,340	2,422	70.9	**1.2**	**1.1-1.4**	2,768	23,875	69.6	0.91	0.83-1.0
Cryptosporidiosis	777	1,601	35.0	**2.5**	**2.2-2.9**	627	673	33.3	**2.1**	**1.8-2.4**	400	1,448	37.0	**2.2**	**1.9-2.5**
Giardiasis	666	1,069	48.6	**3.2**	**2.8-3.7**	293	261	65.6	**2.5**	**2.0-3.0**	1,005	2,603	63.9	**3.0**	**2.7-3.4**
Shigellosis	17	78	50.0	1.1	0.6-1.9	12	78	51.4	**0.34**	**0.18-0.63**	84	338	51.7	**2.0**	**1.5-2.5**
Yersiniosis	88	371	64.9	1.2	0.94-1.6	73	132	53.7	1.2	0.90-1.7	160	1,016	55.3	1.2	1.0-1.5
VTEC/STEC infection	92	264	26.9	**1.8**	**1.4-2.3**	54	50	22.4	**2.4**	**1.6-3.6**	41	196	28.4	**1.6**	**1.2-2.3**
Salmonellosis	402	2,068	37.4	1.0	-	432	951	39.1	1.0	-	539	4,250	45.4	1.0	-
Contact with farm animals															
Campylobacteriosis	2,460	1,962	65.9	**2.5**	**2.2-2.7**	1,689	2,069	71.0	**1.4**	**1.3-1.6**	7,382	19,574	69.3	**1.2**	**1.1-1.2**
Cryptosporidiosis	1,708	936	27.7	**3.6**	**3.2-4.0**	927	494	27.1	**3.3**	**2.8-3.9**	941	1,042	32.4	**2.8**	**2.5-3.1**
Giardiasis	489	1,213	49.6	**0.8**	**0.69-0.91**	215	336	65.8	1.1	0.92-1.4	874	2,666	64.6	1.0	0.91-1.1
Shigellosis	11	84	50.0	**0.26**	**0.14-0.48**	11	80	50.8	**0.24**	**0.13-0.46**	32	383	52.5	**0.26**	**0.18-0.37**
Yersiniosis	186	316	61.6	1.2	0.95-1.4	87	128	51.5	1.2	0.89-1.6	322	971	50.9	1.0	0.88-1.2
VTEC/STEC infection	197	105	38.0	**3.7**	**2.9-4.7**	46	31	42.5	**2.6**	**1.6-4.2**	69	81	54.7	**2.6**	**1.9-3.6**
Salmonellosis	856	1,682	35.7	1.0	-	510	897	38.0	1.0	-	1,227	3,749	43.3	1.0	-

Table 9 continued…

Risk factor (RF) and enteric disease	Cases aged less than five years					Cases ages five to 16 years					Cases aged 17 years or older				
	Reported exposure to the risk factor			Crude Odds Ratio (OR)		Reported exposure to the risk factor			Crude Odds Ratio (OR)		Reported exposure to the risk factor			Crude Odds Ratio (OR)	
	Yes (Y)	No (N)	% Unk[1]	OR[2]	95% CI[3]	Yes (Y)	No (N)	% Unk	OR	95% CI	Yes (Y)	No (N)	% Unk	OR	95% CI
Contact with sick animals															
Campylobacteriosis	352	3,007	74.1	**1.6**	**1.3-2.0**	219	2,749	77.1	0.88	0.69-1.1	1,209	21,465	74.1	**0.74**	**0.65-0.84**
Cryptosporidiosis	527	1,522	44.0	**4.9**	**4.0-5.9**	286	783	45.2	**4.0**	**3.2-5.1**	347	1,295	44.0	**3.5**	**3.0-4.1**
Giardiasis	74	1,381	56.9	0.75	0.56-1.0	15	438	71.9	**0.38**	**0.22-0.66**	124	2,997	68.8	**0.54**	**0.44-0.67**
Shigellosis	2	86	53.7	0.33	0.08-1.3	2	73	59.5	0.30	0.07-1.3	5	369	57.2	**0.18**	**0.07-0.43**
Yersiniosis	27	373	69.4	1.0	0.66-1.6	9	169	59.8	0.59	0.29-1.2	61	1,063	57.3	0.75	0.57-1.0
VTEC/STEC infection	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Salmonellosis	142	1,994	45.9	1.0	-	102	1,124	46.0	1.0	-	314	4,108	49.6	1.0	-
Contact with symptomatic people															
Campylobacteriosis	954	3,105	68.7	1.25	1.0-1.3	551	2,955	72.9	**0.74**	**0.63-0.87**	2,380	23,240	70.8	0.93	0.84-1.0
Cryptosporidiosis	664	1,671	36.1	**1.5**	**1.3-1.7**	317	954	34.8	**1.3**	**1.1-1.6**	459	1,402	36.5	**3.0**	**2.6-3.5**
Giardiasis	853	768	52.0	**4.2**	**3.7-4.9**	263	295	65.4	**3.5**	**2.9-4.4**	896	2,507	65.9	**3.3**	**2.9-3.7**
Shigellosis	42	51	51.1	**3.1**	**2.1-4.8**	25	60	54.1	1.7	1.0-2.7	95	351	49.0	**2.5**	**1.9-3.2**
Yersiniosis	81	381	64.7	0.81	0.63-1.1	22	173	56.0	**0.50**	**0.32-0.80**	93	1,102	54.6	0.77	0.61-1.0
VTEC/STEC infection	105	234	30.4	**1.7**	**1.3-2.2**	23	71	29.9	1.3	0.79-2.1	36	195	30.2	**1.7**	**1.2-2.4**
Salmonellosis	476	1818	41.9	1.0	-	266	1,053	41.9	1.0	-	464	4,245	46.3	1.0	-
Contact with confirmed cases (of the same specific disease)															
Campylobacteriosis	457	4,645	60.6	0.91	0.76-1.1	315	4,197	65.1	**0.49**	**0.40-0.60**	952	29,159	65.7	**0.46**	**0.41-0.53**
Cryptosporidiosis	257	1,907	40.8	1.2	1.0-1.5	118	1,028	41.2	**0.75**	**0.59-0.97**	126	1,455	46.1	1.2	0.99-1.5
Giardiasis	714	967	50.2	**6.8**	**5.7-8.1**	246	398	60.0	**4.1**	**3.2-5.1**	614	3,038	63.4	**2.9**	**2.5-3.3**
Shigellosis	31	57	53.7	**5.0**	**3.2-8.0**	22	49	61.6	**3.0**	**1.7-5.0**	63	316	56.6	**2.8**	**2.1-3.8**
Yersiniosis	15	383	69.5	**0.36**	**0.21-0.62**	8	174	58.9	**0.30**	**0.15-0.62**	21	1,087	57.9	**0.27**	**0.18-0.43**
VTEC/STEC infection	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Salmonellosis	208	1,920	46.1	1.0	-	166	1,090	44.7	1.0	-	299	4,254	48.1	1.0	-

Table 9 continued…

Risk factor (RF) and enteric disease	Cases aged less than five years					Cases ages five to 16 years					Cases aged 17 years or older				
	Reported exposure to the risk factor			Crude Odds Ratio (OR)		Reported exposure to the risk factor			Crude Odds Ratio (OR)		Reported exposure to the risk factor			Crude Odds Ratio (OR)	
	Yes (Y)	No (N)	% Unk[1]	OR[2]	95% CI[3]	Yes (Y)	No (N)	% Unk	OR	95% CI	Yes (Y)	No (N)	% Unk	OR	95% CI
Contact with human faeces															
Campylobacteriosis	981	2,791	70.9	0.95	0.85-1.1	248	3,040	74.6	0.83	0.66-1.4	2,721	21,338	72.6	0.98	0.88-1.1
Cryptosporidiosis	824	1477	37.1	**1.5**	**1.3-1.7**	180	1,070	35.9	**1.7**	**1.3-2.2**	610	1,211	37.9	**3.9**	**3.4-4.4**
Giardiasis	609	847	56.9	**2.0**	**1.7-2.2**	119	388	68.5	**3.1**	**2.4-4.1**	1,356	1,992	66.5	**5.2**	**4.7-5.8**
Shigellosis	18	65	56.3	0.75	0.44-1.3	6	70	58.9	0.87	0.37-2.1	49	359	53.3	1.0	0.8-1.4
Yersiniosis	132	311	66.1	1.2	0.92-1.4	18	180	55.3	1.0	0.60-1.7	154	1,034	54.9	1.1	0.94-1.4
VTEC/STEC infection	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
Salmonellosis	*601*	*1,630*	*43.5*	*1*	-	*114*	*1,157*	*44.0*	*1.0*	-	*536*	*4,099*	*47.2*	*1.0*	-

1. Unk, Unknown

2. Crude OR unadjusted for age, ethnicity, rurality of domicile and other potential confounders. OR significantly different from salmonellosis are bold and shaded.

3. 95% confidence interval

n/a, Not applicable as not collected on VTEC/STEC case report form.

2.5 Discussion

For the period 2000 to 2009, *Salmonella* caused the third-highest number of enteric disease cases notified in New Zealand; over 15,000 people. This is slightly less than the number of notified cases of giardiasis but almost eight times more people were notified with campylobacteriosis than salmonellosis for the same time period.

2.5.1 Limitations

The demographic detail for most salmonellosis cases was complete and analyses based on these data will be more reliable. Conversely, detailed reporting of risk factors is much less complete. The percentage of cases for which risk factors were reported ranged from 22% (VTEC/STEC infection, overseas travel) to 75% (campylobacteriosis, contact with sick animals). For salmonellosis, 71% of cases reported on overseas travel was a risk factor, but the percentage of cases for which the risk factors were reported ranged from 48% (consumption of food from a food premises) to 59% (contact with farm animals). As a result, the analyses based on risk factors should be considered indicative only, despite the application of statistical methods.

The case-case analyses based on consumption of food from food premises only provides an indication of the relative importance of this pathway for *Salmonella* infection compared with other enteric diseases. It does not attribute salmonellosis to specific foods. It should be noted that the proportion of salmonellosis cases associated with outbreaks is small (6.2%) so the signals resulting from the case-case analyses should be indicative of sporadic disease. Multivariable analysis could not be undertaken to control for the effects of any likely confounding variables on the overall results due to the incomplete nature of the dataset.

2.5.2 Salmonellosis case demographics

The comparison of demographic variables between salmonellosis cases and the other enteric disease cases identified many significant differences across all of the demographic categories studied. However, it is plausible that these demographic variables are independently associated with the risk factors being studied (e.g. rural males and contact with farm animals), so the crude ORs are likely to be influenced by confounding and should be viewed with some caution.

Looking solely at the salmonellosis data, there are some indicators of the demographic more likely to be infected by *Salmonella* spp. Based on the average New Zealand resident population for the years 2000-2009, 7.0% of the population were aged 0-4 years, 17.6% 5-16 years and 75.4% 17 years or older.[4] The proportion of reported salmonellosis cases aged under five years is 26.3%, 15.1% of cases were aged five to 16 years and 58.5% of cases were aged 17 years or older. This indicates that salmonellosis is more likely to be reported for infants than adults.

A higher than expected proportion of the salmonellosis cases were European (82% versus 67%, for the usually resident population in the 2006 Census). All other ethnic groups were under-represented based on expected proportions from the 2006 Census. It is possible that barriers to accessing healthcare influence the pathway to disease notification disproportionately for other ethnic groups. However, a community survey found that the percentage of Maori acute gastrointestinal illness (AGI) cases that reported attending their GP was higher than non-Maori

[4] Calculated from Statistics New Zealand National Population Estimates at 30 June, http://www.stats.govt.nz/methods_and_services/access-data/tables/national-pop-estimates.aspx

respondents (32% vs. 20%), although a low response rate meant that this result should be treated with caution (Adlam *et al*., 2010).

More than one in ten salmonellosis cases lived in rural environments (as categorised in Table 1); this is not as a high a proportion as for cryptosporidiosis or VTEC/STEC infection (both are around one in five cases), but this is still an indication of the importance of rural factors on acquiring *Salmonella* infection. Compared to the national data on rural/urban split (Table 1), rural cases are slightly over-represented (10% salmonellosis cases compared with 7% of the NZ population, or 11% salmonellosis cases compared with 8% of the NZ population when the rural with moderate and high urban influence residents are excluded). Urban cases are slightly under-represented (82% salmonellosis cases compared with 86% of the NZ population, or 89% salmonellosis cases compared with 92% of the NZ population when the rural with moderate or high urban influence residents are excluded).

2.5.3 Salmonellosis risk factors

The findings of the case-case analysis of enteric disease are consistent with a similar study referenced to campylobacteriosis (Wilson *et al*., 2008). For most risk factors, the enteric diseases remain in the same relative order to each other.

The analysis of risk factors indicates that there is a greater association between salmonellosis and overseas travel than for campylobacteriosis, cryptosporidiosis, VTEC/STEC infection or yersiniosis. However, overseas travel is associated with a greater risk of giardiasis and, in particular, shigellosis than of salmonellosis. This result did not change when the data were stratified by sex or age.

People who were reported as consuming food from a food premise were associated more with salmonellosis than any of the other enteric diseases, except for campylobacteriosis. The OR confidence interval for campylobacteriosis was 1.1-1.3, so the difference between these two diseases was minimal. In fact, when the data were stratified by age, the age group of less than five years had a reduced OR of campylobacteriosis for this risk factor compared with salmonellosis and the OR for the other two age groups were not significantly different between the two diseases. This suggests that food consumed from a food premises is an important pathway of infection for both *Salmonella* spp. and *Campylobacter* spp.

Salmonellosis is proportionately more strongly associated with consumption of untreated drinking water than the other enteric diseases, apart from the largely waterborne giardiasis and cryptosporidiosis. When stratified by age, the results show a stronger association between people aged less than five years consuming untreated drinking water and campylobacteriosis, when compared with salmonellosis. However, the proportion of cases with an unknown exposure to this risk factor is high (e.g. 72% unknown for campylobacteriosis), so it is possible this result is affected by incomplete reporting.

Campylobacteriosis, cryptosporidiosis and VTEC/STEC infection have greater associations with farm animal contact than salmonellosis. However, salmonellosis was more strongly associated with contact with sick animals than all other enteric diseases, except for cryptosporidiosis. When stratified by age, campylobacteriosis has a higher OR than salmonellosis for infants aged less than five years who have contact with sick animals.

Compared with other enteric diseases, salmonellosis is less associated with people who have been in contact with symptomatic people or confirmed cases, or have had contact with human faeces. Only campylobacteriosis and yersiniosis have lower associations with these cases.

When stratified by age, campylobacteriosis and salmonellosis show fewer significant differences for these risk factors (e.g. no significant difference between the diseases in any age group for contact with human faeces). Also, cryptosporidiosis in those aged five to 16 years who had contact with confirmed cases has a significantly lower OR than salmonellosis, and the OR is no longer significantly elevated for the other age groups.

The risk factor analyses suggest that the important pathways for *Salmonella* infection in New Zealand are foodborne (as indicated by the premises data), consumption of untreated drinking water and contact with sick animals, though these are not necessarily mutually exclusive since cases living in rural environments could be exposed to all of these risk factors.

3 SEROTYPE ANALYSIS

3.1 Introduction

The Enteric Reference Laboratory (ERL) at ESR undertakes national reference laboratory services for human, animal and environmental enteric bacterial pathogens including *Salmonella*. Human *Salmonella* isolates are referred to the ERL for confirmatory testing and further typing. Non-human *Salmonella* isolates may be referred to ERL for typing or may be tested by other laboratories (Lake and Sexton, 2009). The ERL reports human and non-human *Salmonella* serotypes annually and the non-human data used for this report are summarised in Appendix 1. It should be noted that these data are not the result of a formal sampling programme but provide a useful source of information on non-human serotypes in New Zealand. Over the last five years, the *Salmonella* serotypes most commonly isolated from the non-human sources were:

- *S.* Brandenburg (1,027 isolates; 64% from ovine samples, 15% from bovine samples, 7% from food samples (including animal carcasses))
- *S.* Typhimurium DT101 (654 isolates; 70% poultry-related (40% poultry product including neckflaps, 29% poultry environmental samples and 2% poultry feed), 26% bovine)
- *S.* Hindmarsh (469 isolates; 87% ovine, 8% bovine)
- *S.* Typhimurium DT160 (247 isolates; 34% poultry-related (5% poultry product, 14% poultry environmental samples and 15% poultry feed), 15% avian, 15% bovine, 13% equine, 10% feline, 7% environmental)
- *S.* Typhimurium DT1 (242 isolates; 81% bovine)
- *S.* Infantis (238 isolates; 44% poultry-related (10% poultry product, 24% poultry environmental samples and 11% poultry feed), 22% animal feed including meat/bone meal, 14% food, 8% environmental)

A total of 257 *S.* Typhimurium RDNC isolates were also detected from a variety of samples (mostly bovine and poultry-related samples), though this is a category of *S.* Typhimurium serotypes that do not correspond to a recognised phage type. The most common *Salmonella* serotypes isolated by the ERL from a selection of non-human sources are summarised in Table 10 (see Appendix 1 for the full data).

In New Zealand, the prevalence of different *Salmonella* serotypes in humans has been observed to rise and fall over time. Sneyd and Baker (2003) documented the emergence of *S.* Typhimurium DT160, which in 2009 was still the isolate most frequently isolated from humans with salmonellosis, the peak of *S.* Brandenburg and the decline of *S.* Enteritidis PT4 (Sneyd and Baker, 2003). In this section we have applied the case-case methodology to human salmonellosis cases for the period 2000–2009 for which the serotypes have been identified. *S.* Typhimurium DT160 is used as the reference.

Table 10: *Salmonella* serotypes most commonly isolated from non-human sources by the ERL, 2005-2009

Source of sample	Total *Salmonella* serotypes[1]	*Salmonella* serotypes most commonly isolated (>10% of all serotypes from source)[2]
Avian	92	Typhimurium DT160 (40%), Brandenburg (17%)
Bovine	1,551	Typhimurium DT1 (13%), Typhimurium DT101 (11%), Brandenburg (10%)
Canine	68	Brandenburg (15%), Typhimurium DT160 (13%), Typhimurium DT1 (10%)
Equine	115	Typhimurium DT160 (29%)
Feline	90	Typhimurium DT160 (28%)
Ovine	1,120	Brandenburg (59%), Hindmarsh (37%)
Porcine	20	Brandenburg (15%), Typhimurium DT135 (10%), Bovismorbificans (10%), Group B 4,12:-:1,2 (10%)
Reptile	252	Saintpaul (16%), Mississippi (11%)
Shellfish	19	Brandenburg (21%), Oslo (11%), Thompson (11%), Weltevreden (11%)
Poultry[3] - Poultry product - Environmental - Feed	1,634 (438) (645) (551)	Typhimurium DT101 (28%) - Typhimurium DT101 (59%) - Typhimurium DT101 (29%), Agona (14%) - Derby (17%)
Animal feed[4]	298	Infantis (18%), Anatum (13%), Montevideo (13%), Tennessee (12%)
Environmental	315	Brandenburg (11%), Urbana (10%)
Food[5]	294	Brandenburg (26%), Infantis (11%)
Total	**5,868**	**Brandenburg (18%), Typhimurium DT101 (11%)**

Source: Enteric Reference Laboratory Annual Reports, ESR, Kenepuru Science Centre/NCBID

1. *Total number of isolates from each sample type.*
2. *Only serotypes that make up 10% or more of the isolates are listed, excluding S. Typhimurium RDNC. For full details see Appendix 1.*
3. *Combined results for poultry-related products are presented with separate results for "miscellaneous poultry samples including product" (this includes 10 neckflap samples), poultry environmental samples and poultry feed.*
4. *Includes 7 samples of animal feed and 291 samples of meat/bone meal.*
5. *Includes animal carcasses from meat works and food samples from outbreaks of salmonellosis in humans. In 2005 and 2006, 24 samples of sesame seed products and 3 spice samples were specifically tested and these have been included. For full details see Appendix 1.*

3.2 Method

This section also analysed the dataset of salmonellosis cases for the period 2000 to 2009, as described in Section 2.

The following cases were removed from the total of 15,040 salmonellosis cases for 2000-2009:

- 927 cases linked to outbreaks.
- 2,462 cases for which the *Salmonella* was not typed or not able to be typed.
- 34 cases for which samples not sent to ESR for further analysis
- Three cases for which there were no ESR laboratory records of the isolates.
- Seven cases caused by *Salmonella* Typhi and 11 by *Salmonella* Paratyphi.

- Nine cases that were notified as "Salmonellosis" but for which another bacterial species was identified.
- 33 cases that had been assigned a serotype group (e.g. Group C), but the specific serotype was not available.

The final dataset was 11,554 cases.

The cases associated with each serotype were summed for the analyses. Unless specified, use of the word 'serotype' in this section should be interpreted to mean the collective serotype and phage type of a *Salmonella* species. The abbreviations 'PT' and 'DT' stand for provisional phage type and definitive phage type (Bell and Kyriakides, 2002). These terms are used interchangeably in current literature.

Case-case analyses used the same methods as described in Section 2.

The full dataset was used for demographic analyses. The risk factor case-case analysis (Section 3.4), excluded 374 cases that reportedly became ill through person-to-person transmission (Section 3.3.6). The risk factors were analysed by *Salmonella* serotypes that caused 50 or more notifications over the ten-year period between 2000 and 2009. *S.* Typhimurium DT160 cases were used as the reference group in all of the case-case analyses.

The case report form includes a section on source of infection, including a specific tick box to check if a contaminated food or drink was confirmed as the source. This tick box was used to identify cases with a potentially confirmed food source for the attribution to food analysis (Section 3.5). Cases with a confirmed food source were extracted from the total 15,040 salmonellosis cases over the period 2000–2009. Of the 36 cases reported with a confirmed food source, 33 were associated with outbreaks and were excluded from further analysis. The remaining three sporadic salmonellosis cases are examined separately in Section 3.5.1. Cases where the "Probable Food Source" tick box had been selected were then extracted from the 11,554 salmonellosis cases for which serotype data was available. From these, the ten serotypes causing the highest number of cases were identified. To select cases for detailed analysis, every *n*th case was chosen from within the group of cases associated with each serotype, where *n* was a number that, when divided into the total number of cases associated with that serotype, would yield approximately 20 cases per serotype. The case report for each of these cases was reviewed, including any free-text entered by the PHO. From this information risk factors were tabulated, premises identified and food recorded and grouped (Section 3.5.2).

3.3 Results: Summary of Serotypes

3.3.1 Frequency of serotypes

There were 420 different *Salmonella* serotypes associated with 11,554 cases. Ignoring phage typing, the 10 serotypes causing the largest number of cases are shown in Table 11. These serotypes caused 85% of all cases with a known serotype.

Table 11: The ten *Salmonella* serotypes (disregarding phage typing) that caused the most notified salmonellosis cases, 2000 to 2009

Salmonella serotype	No. cases	% cases (n=11,554)
Typhimurium	6,724	58.2
Enteriditis	1,012	8.8
Brandenburg	700	6.1
Infantis	523	4.5
Saintpaul	249	2.2
Heidelberg	150	1.3
Virchow	141	1.2
Mississippi	95	0.8
Agona	92	0.8
Thompson	92	0.8
Total	**9,778**	**84.6**

Table 12 lists the 35 serotypes that have caused 50 or more cases over the ten-year period, excluding 232 cases caused by *S.* Typhimurium but where phage typing was either not done or not able to be done. The table displays the peak years for each of these serotypes and the total number of cases over this time period (for the annual number of cases, see Appendix 2). Together, these 35 serotypes caused 80% (9,290) of the 11,554 cases. *S.* Typhimurium DT160 alone caused 19% of the cases.

Table 12: *Salmonella* serotypes that caused 50 or more cases over the years 2000 to 2009 – peak occurrence and total cases

Salmonella serotype	Peak occurrence[1]										Total cases
	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	
Typhimurium DT160		+									**2,147**
Typhimurium DT1	+	+	+								**729**
Brandenburg	+	+									**700**
Typhimurium DT135	+	+									**698**
Typhimurium DT156	+	+									**562**
Infantis									+	+	**523**
Typhimurium DT101	+										**505**
Enteritidis PT9a	+	+									**432**
Typhimurium DT42	+										**257**
Saintpaul						+					**249**
Typhimurium DT12a							+				**237**
Typhimurium DT9	+										**182**
Typhimurium RDNC-May 06									+		**154**
Heidelberg		+									**150**
Virchow					+			+			**141**
Typhimurium DT74							+				**139**
Typhimurium DT23		+									**138**
Typhimurium RDNC[2]				+						+	**137**

Table 12 continued…

***Salmonella* serotype**	**Peak occurrence[1]**										**Total cases**
	2000	**2001**	**2002**	**2003**	**2004**	**2005**	**2006**	**2007**	**2008**	**2009**	
Mississippi						+					**95**
Enteritidis PT4	+		+								**95**
Thompson							+				**92**
Agona							+				**92**
Weltevreden		+					+				**88**
Montevideo			+	+							**79**
Mbandaka							+		+		**76**
Newport		+					+				**68**
Stanley									+		**65**
Enteritidis PT6a									+		**62**
Corvallis							+				**61**
Salmonella sp. 4,5,12:d :-					+			+			**59**
Typhimurium DT8								+			**58**
Enteritidis PT1		+									**58**
Enteritidis PT1b									+		**57**
Hadar	+	+	+								**55**
Typhimurium RDNC Aug-01				+							**50**

1. + denotes where number of cases exceeds ten year mean plus one standard deviation for a given serotype.

2. Typhimurium RDNC is not a single serotype, but a grouping of serotypes. RDNC stands for 'reaction does not conform' and indicates that the isolate does not match any recognised serotypes. RDNC can sometimes be followed by the month and year of isolation.

3.3.2 Hospitalisations and fatalities

Hospitalisation was either not recorded, or recorded as "unknown", for 2,520 (22%) of cases. Of the remaining 9,035 cases with hospital admission recorded as "Yes" or "No", 1,288 were admitted to hospital for salmonellosis; a rate of 14%.

Different serotypes may result in more severe illness and result in hospitalisation. Of the 420 serotypes, infection by 283 (67%) did not result in the hospitalisation of any of the associated 488 cases. The median hospitalisation rate for the 137 serotypes that caused one or more cases to be admitted to hospital was 20%. The minimum hospitalisation rate was 2% (*S.* Hadar, 1/42 cases) and 22 serotypes hospitalised all of the one or two cases they infected (i.e. hospitalisation rate of 100%).

Table 13 shows the percentage of cases admitted to hospital by serotype, for those serotypes where the hospitalisation status of 50 or more people was known. The median hospitalisation rate for these 26 serotypes is 13% (range 7-20%). Higher hospitalisation rates were associated with *S.* Typhimurium (DT160, DT135, DT23, DT74 and RDNC), *S.* Infantis, *S.* Virchow and *S.* Thompson.

Table 13: Hospitalisation rates for *Salmonella* serotypes where the hospitalisation status of 50 or more cases is known, 2000 to 2009

Salmonella serotype	No. cases	No. cases with known status[1]	No. hospitalised	% hospitalised
Typhimurium DT160	2,147	1,745	304	17.4
Typhimurium DT1	729	598	85	14.2
Typhimurium DT135	698	573	91	15.9
Brandenburg	700	573	86	15.0
Typhimurium DT156	562	454	55	12.1
Infantis	523	400	61	15.3
Typhimurium DT101	505	398	55	13.8
Enteritidis PT9a	432	359	39	10.9
Saintpaul	249	211	22	10.4
Typhimurium DT42	257	207	28	13.5
Typhimurium DT12a	237	185	23	12.4
Typhimurium DT9	182	153	20	13.1
Typhimurium DT23	138	120	23	19.2
Heidelberg	150	115	16	13.9
Typhimurium DT74	139	108	22	20.4
Typhimurium RDNC	137	103	21	20.4
Virchow	141	99	17	17.2
Typhimurium RDNC-May 06	154	98	11	11.2
Mississippi	95	79	6	7.6
Enteritidis PT4	95	76	8	10.5
Thompson	92	68	12	17.6
Agona	92	68	9	13.2
Weltevreden	88	64	8	12.5
Montevideo	79	58	5	8.6
Mbandaka	76	55	5	9.1
Newport	68	55	4	7.3

1. The number of cases for which the hospitalisation status has been recorded as either "Yes" or "No".

Twenty-five deaths have been directly attributed or associated with salmonellosis over the ten-year period (Table 14). The highest number of deaths were associated with *S.* Brandenburg and *S.* Typhimurium DT160 (five deaths each). The highest case fatality rate was 2.3% for *S.* Weltevreden, though this should be accepted with caution as the total number of cases is smaller than for most other serotypes associated with mortality. Salmonellosis was the primary cause of death for four people; the serotypes were *S.* Typhimurium DT9, *S.* Brandenburg, *S.* Mbandaka and *S.* Infantis.

Table 14: Deaths attributed to or associated with *Salmonella* serotypes, 2000-2009

Salmonella serotype	No. cases	No. deaths	Death rate (%)
Weltevreden	88	2	2.3
Stanley	65	1	1.5
Mbandaka	76	1	1.3
Typhimurium DT74	139	1	0.7
Brandenburg	700	5	0.7
Enteritidis PT9a	432	3	0.7
Typhimurium Not Typed	144	1	0.7
Typhimurium DT9	182	1	0.5
Infantis	523	2	0.4
Typhimurium DT12a	237	1	0.4
Typhimurium DT160	2,147	5	0.2
Typhimurium DT1	729	1	0.1
Typhimurium DT135	698	1	0.1
Total	**6,160**	**25**	**0.4**

3.3.3 Demographics

Sex was recorded for 98.6% (11,393/11,554) of cases and an age group could be assigned for 98.4% (11,373/11,554) of cases (Table 15). There were significantly more males (51.9%) than females (48.1%) in this dataset ($p<0.001$). People aged 17 years or older (58.0%) are under-represented compared to the New Zealand average for 2000-2009, and cases less than five years old are over-represented (27.2%).[5] There were significantly more males than females in the two youngest age strata.

Table 15: Sex and age of the cases in the salmonellosis serotype dataset

Demographic	% Female	% Male	Sig[1]
Sex (n=11,393)	48.1	51.9	***
Age (n=11,373)			
Less than five years (n=3,091)	48.3	51.7	**
Five to 16 years (n=1,683)	42.4	57.6	***
17 years or older (n=6,599)	49.4	50.6	n/s

*1. Levels of statistical significance: n/s not significant; * p<0.05, ** p<0.01, *** p<0.001*

Table 16 shows the 15 serotypes causing the highest number of cases, with the cases broken down by age and sex. Of interest is that in the 17 years or older group, the serotypes *S.* Typhimurium DT160 and *S.* Heidelberg are significantly associated with females but are

[5] Based on the average New Zealand resident population for the years 2000-2009, 7.0% of the population were aged 0-4 years, 17.6% 5-16 years and 75.4% 17 years or older. Calculated from Statistics New Zealand National Population Estimates at 30 June, http://www.stats.govt.nz/methods_and_services/access-data/tables/national-pop-estimates.aspx

significantly associated with males in the other age groups. The only other significant association between females and a serotype is for *S.* Virchow in the under five age group. The proportions of males compared with females were notably higher across the serotypes in the five to 16 year old age group (the proportion male in nine of the 11 significant results for this age group was 60% or more).

Ethnicity was recorded for 84% (9,681/11,554) of cases. Of the cases with a recorded ethnicity, the majority (82.4%) were European, followed by Maori (9.6%), people of Asian origin (4.5%), Pacific peoples (2.8%) and Other (0.8%). European cases were over-represented in comparison with 2006 Census data whereas the other ethnic groups were under-represented.[6]

[6] Based on the 2006 New Zealand census, 64.8% of the NZ population were European, 14.0% Maori, 8.8% of Asian origin and 6.6% Pacific peoples. Data obtained using the Statistics New Zealand Table Builder, based on the "Ethnic group, 2006 census" data (http://www.stats.govt.nz/methods_and_services/access-data/TableBuilder.aspx)

Table 16: Cases associated with 15 *Salmonella* serotypes causing the highest number of salmonellosis cases (2000-2009), broken down by age and sex

Salmonella serotype	Cases aged less than five years				Cases aged five to 16 years				Cases aged 17 years or over			
	% female	% male	p-value	Sig[1]	% female	% male	p-value	Sig	% female	% male	p-value	Sig
Typhimurium DT160	47	53	0.0099	**	46	54	0.0180	*	53	47	0.0180	*
Typhimurium DT1	50	50	1.0000	n/s	39	61	0.0006	***	47	53	0.0688	n/s
Brandenburg	45	55	0.0274	*	43	57	0.0744	n/s	40	60	0.0000	***
Typhimurium DT135	43	57	0.0135	*	46	54	0.2281	n/s	49	51	0.5738	n/s
Typhimurium DT156	51	49	0.5659	n/s	44	56	0.0426	*	46	54	0.0808	n/s
Infantis	57	43	0.0875	n/s	41	59	0.1153	n/s	46	54	0.0199	*
Typhimurium DT101	48	52	0.3862	n/s	40	60	0.0088	**	49	51	0.5795	n/s
Enteritidis PT9a	46	54	0.2361	n/s	38	63	0.0048	**	44	56	0.0133	*
Typhimurium DT42	42	58	0.0374	*	36	64	0.0110	*	51	49	0.6955	n/s
Saintpaul	48	52	0.6464	n/s	44	56	0.1917	n/s	55	45	0.1299	n/s
Typhimurium DT12a	47	53	0.4598	n/s	33	67	0.0072	**	50	50	0.8935	n/s
Typhimurium DT9	56	44	0.3211	n/s	38	63	0.0472	*	49	51	0.7915	n/s
Typhimurium RDNC-May 06	52	48	0.6207	n/s	35	65	0.0280	*	57	43	0.1759	n/s
Heidelberg	37	63	0.0405	*	32	68	0.0056	**	60	40	0.0068	**
Virchow	68	32	0.0117	*	9	91	0.0002	***	46	54	0.2065	n/s

*1. Levels of statistical significance: n/s not significant; * p<0.05, ** p<0.01, *** p<0.001*

3.3.4 Geographical distribution

3.3.4.1 Rurality

From the sporadic salmonellosis cases for which the serotype is known (11,554 cases), 8,932 (77.3%) cases lived in highly urban areas and 1,184 (10.2%) lived in highly rural areas (using the categories as described in Table 1). The proportion of serotypes infecting these urban and rural cases is shown in Table 17. *S.* Infantis is strongly associated with highly urban cases and *S.* Saintpaul is strongly associated with highly rural cases. *S.* Brandenburg is also associated with rural cases. While *S.* Typhimurium DT160 and DT101 are respectively associated with urban and rural cases, the proportion of cases split between these two geographical categories differs very little.

Table 17: Proportion of *Salmonella* serotypes infecting cases living in highly rural and highly urban locations (2000-2009)

***Salmonella* serotype**	**Rural cases (%)**	**Urban cases (%)**	**p-value**	**Sig.[1]**
Typhimurium DT160	16.5	18.5	0.033	*
Typhimurium DT1	7.0	5.9	0.294	n/s
Brandenburg	22.9	3.6	0.002	**
Typhimurium DT135	4.0	6.3	0.593	n/s
Typhimurium DT156	4.1	4.9	0.205	n/s
Infantis	2.5	5.0	0.000	***
Typhimurium DT101	5.6	4.3	0.043	*
Enteritidis PT9a	4.1	3.6	0.803	n/s
Typhimurium DT42	2.9	2.1	0.059	n/s
Saintpaul	4.6	1.7	0.000	***
Typhimurium DT12a	1.9	2.1	0.832	n/s

*1. Levels of statistical significance: n/s not significant, * p<0.05, ** p<0.01, *** p<0.001*

A stratified analysis of the serotypes by rurality, age and sex (Table 18) shows very few statistically-significant relationships. Most notably, stratification of the under five years age group by rural/urban setting resulted in only one significant association (rural males and *S.* Typhimurium DT42). There were significant differences between males and females for six serotypes when rural/urban stratification was not applied to this age group (Table 16). This suggests that within a rural or urban setting, infant males and infant females are infected at similar rates by these serotypes. However, the results are also influenced by overall lower case numbers when stratification is applied (e.g. of the rural cases aged less than five years and infected by *S.* Typhimurium DT12a, 70% were male, but there was no significant difference between the sexes because the total number of cases was ten).

Table 18 further investigates the unstratified urban/rural results in Table 17. *S.* Typhimurium DT160, weakly associated with cases from urban settings, was significantly associated with urban males aged five to 16 years and urban females aged 17 years or older. There were no significant differences between the sexes in any of the rural age groups for this serotype. For *S.* Brandenburg, there were no significant differences between the sexes in any of the urban age groups, but this serotype was significantly associated with males aged five to 16 and aged 17 years or older from rural settings. For *S.* Infantis, there was a significantly higher proportion of

males with this serotype compared with their female counterparts in the adult age groups in both settings, but in the five to 16 years age group this serotype was associated more with males from urban settings (64% male) and more with females from rural settings (89% female). For *S.* Typhimurium DT101 there were no significant differences between the sexes in any of the urban age groups, but there were significantly more males than females in the two older rural age groups. While *S.* Saintpaul was strongly associated with rural cases (Table 17), adult females (61%) from urban settings were also significantly associated with this serotype. For cases from rural settings, the only significant difference between the sexes associated with *S.* Saintpaul was in the five to 16 years age group (82% male).

Table 18: Proportion of *Salmonella* serotypes infecting cases living in highly rural and highly urban locations (2000-2009), by age and sex

Setting, *Salmonella* serotype	Cases of all ages				Cases aged less than five years				Cases aged five to 16 years				Cases aged 17 years or older			
	% female	% male	p-value	Sig[1]	% female	% male	p-value	Sig	% female	% male	p-value	Sig	% female	% male	p-value	Sig
Urban																
Typhimurium DT160	49.4	50.6	0.528	n/s	47.5	52.5	0.098	n/s	43.2	56.8	0.001	**	52.9	47.1	0.020	*
Typhimurium DT1	48.0	52.0	0.195	n/s	50.6	49.4	0.823	n/s	42.3	57.7	0.066	n/s	48.0	52.0	0.323	n/s
Brandenburg	46.2	53.8	0.055	n/s	42.6	57.4	0.088	n/s	54.8	45.2	0.386	n/s	45.5	54.5	0.074	n/s
Typhimurium DT135	48.5	51.5	0.308	n/s	45.9	54.1	0.178	n/s	48.1	51.9	0.638	n/s	49.6	50.4	0.818	n/s
Typhimurium DT156	48.7	51.3	0.452	n/s	52.5	47.5	0.342	n/s	45.1	54.9	0.183	n/s	46.5	53.5	0.215	n/s
Infantis	46.4	53.6	0.035	*	55.2	44.8	0.267	n/s	36.4	63.6	0.028	*	45.9	54.1	0.032	*
Typhimurium DT101	48.9	51.1	0.560	n/s	47.2	52.8	0.381	n/s	42.3	57.7	0.066	n/s	52.8	47.2	0.290	n/s
Enteritidis PT9a	43.6	56.4	0.001	**	44.0	56.0	0.067	n/s	39.5	60.5	0.054	n/s	44.4	55.6	0.045	*
Typhimurium DT42	46.5	53.5	0.179	n/s	46.4	53.6	0.396	n/s	36.7	63.3	0.041	*	50.0	50.0	1.000	n/s
Saintpaul	52.6	47.4	0.360	n/s	44.4	55.6	0.250	n/s	51.4	48.6	0.817	n/s	60.7	39.3	0.019	*
Typhimurium DT12a	46.7	53.3	0.209	n/s	50.0	50.0	1.000	n/s	27.3	72.7	0.003	**	48.9	51.1	0.764	n/s
Rural																
Typhimurium DT160	49.5	50.5	0.839	n/s	43.5	56.5	0.127	n/s	56.4	43.6	0.261	n/s	51.2	48.8	0.761	n/s
Typhimurium DT1	43.2	56.8	0.085	n/s	62.1	37.9	0.068	n/s	33.3	66.7	0.110	n/s	32.5	67.5	0.002	**
Brandenburg	37.3	62.7	0.000	***	43.7	56.3	0.052	n/s	27.8	72.2	0.000	***	33.3	66.7	0.000	***
Typhimurium DT135	37.0	63.0	0.013	*	33.3	66.7	0.073	n/s	27.3	72.7	0.037	*	45.0	55.0	0.532	n/s
Typhimurium DT156	42.9	57.1	0.159	n/s	35.7	64.3	0.138	n/s	41.7	58.3	0.424	n/s	47.8	52.2	0.771	n/s
Infantis	41.4	58.6	0.193	n/s	50.0	50.0	1.000	n/s	88.9	11.1	0.028	*	30.4	69.6	0.009	**
Typhimurium DT101	35.4	64.6	0.001	***	40.0	60.0	0.162	n/s	27.3	72.7	0.037	*	34.5	65.5	0.019	*

Table 18 continued…

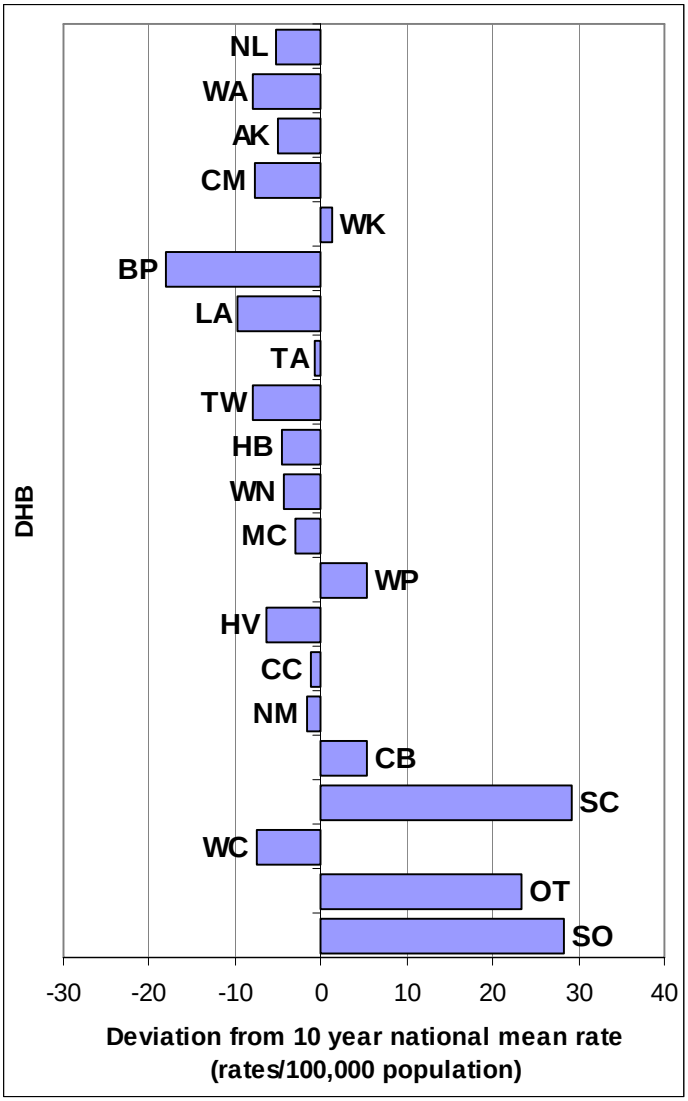
Setting, *Salmonella* serotype	Cases of all ages				Cases aged less than five years				Cases aged five to 16 years				Cases aged 17 years or older			
	% female	% male	p-value	Sig[1]	% female	% male	p-value	Sig	% female	% male	p-value	Sig	% female	% male	p-value	Sig
Enteritidis PT9a	34.7	65.3	0.003	**	41.7	58.3	0.424	n/s	25.0	75.0	0.053	n/s	34.5	65.5	0.019	*
Typhimurium DT42	39.4	60.6	0.087	n/s	20.0	80.0	0.009	**	20.0	80.0	0.072	n/s	55.6	44.4	0.511	n/s
Saintpaul	42.6	57.4	0.125	n/s	45.0	55.0	0.532	n/s	18.2	81.8	0.004	**	52.2	47.8	0.771	n/s
Typhimurium DT12a	34.8	65.2	0.041	*	30.0	70.0	0.081	n/s	20.0	80.0	0.072	n/s	50.0	50.0	1.000	n/s

*1. Levels of statistical significance: n/s not significant, * p<0.05, ** p<0.01, *** p<0.001*

3.3.4.2 District Health Boards

Figure 1 shows the ten-year mean rate per 100,000 population for sporadic salmonellosis by each District Health Board (DHB), relative to the ten-year mean of all DHBs (28.5 per 100,000). The average notification rates were considerably higher than the national average in the South Island DHBs of Canterbury, South Canterbury, Otago and Southland. The West Coast DHB was below average. In the North Island, the Waikato and Wairarapa DHBs are the only DHBs to have higher average notification rates than the national average. The Bay of Plenty DHB was most below average. The annual rates for each DHB are detailed in Appendix 3.[7] There is also geographical variation by serotype across DHBs. Most notable are higher rates of *S.* Brandenburg and *S.* Typhimurium DT135 in the lower half of the South Island. The geographical spread of the top 15 serotypes is shown in Table 19.

Figure 1: Average notification rate of salmonellosis per 100,000 population (2000-2009) for each District Health Board (DHB), relative to the average of all DHBs*



DHB abbreviations:
NL, Northland
WA, Waitemata
AK, Auckland
CM, Counties Manukau
WK, Waikato
BP, Bay of plenty
LA, Lakes
TA, Taranaki
TW, Tairawhiti
HB, Hawke's Bay
WN, Whanganui
MC, MidCentral
WP, Wairarapa
HV, Hutt Valley
CC, Capital and Coast
NM, Nelson Marlborough
CB, Canterbury
SC, South Canterbury
WC, West Coast
OT, Otago
SO, Southland

** Only cases with known serotypes have been used to calculate these rates (n=11,554).*

[7] This analysis is based on the cases with known serotypes. Regional rates for all salmonellosis cases are published annually in ESR's surveillance reports (http://www.surv.esr.cri.nz/surveillance/annual_surveillance.php).

Table 19: Rates of salmonellosis per 100,000 population by District Health Board (2000-2009)

Salmonella serotype	NL	WA	AK	CM	WK	BP	TW	RO	TA	HB	WN	MC	WP	CC	HV	NM	WC	CB	SC	OT	SO	All NZ
Typhimurium DT 160	37.5	49.3	41.3	38.3	41.4	19.0	54.6	39.5	48.6	66.9	46.5	70.5	101.3	51.4	42.2	64.6	53.9	72.8	155.1	69.1	71.4	**52.5**
Typhimurium DT 1	29.4	9.2	9.3	9.7	28.3	5.7	34.9	14.8	50.5	18.6	34.1	14.7	30.4	12.2	6.4	26.6	25.4	26.7	51.1	17.5	9.2	**17.8**
Brandenburg	1.3	2.7	3.8	3.9	6.4	1.5	0.0	1.0	4.7	4.0	3.1	3.1	0.0	3.3	0.0	3.0	0.0	18.8	63.9	94.9	273.6	**17.1**
Typhimurium DT135	6.0	11.3	10.3	15.2	20.7	8.7	41.5	9.9	26.2	13.3	15.5	24.5	27.9	20.7	18.6	20.5	9.5	10.2	29.2	58.1	15.6	**17.1**
Typhimurium DT 156	26.8	8.8	5.2	9.5	23.6	5.7	6.6	3.9	32.7	11.3	17.1	31.9	60.8	29.9	27.2	9.9	0.0	6.0	5.5	6.6	2.7	**13.8**
Infantis	12.7	12.5	12.4	14.1	11.1	7.7	8.7	14.8	16.8	13.9	32.6	7.4	2.5	8.1	12.9	13.7	12.7	13.2	18.2	19.2	14.6	**12.8**
Typhimurium DT 101	18.7	7.0	5.7	5.8	11.7	3.6	4.4	4.9	12.2	7.3	10.9	8.6	12.7	3.7	4.3	28.1	19.0	29.3	21.9	34.5	17.4	**12.4**
Enteritidis PT 9a	10.7	7.6	4.1	1.8	21.6	9.3	6.6	12.8	24.3	4.6	15.5	18.4	12.7	6.7	8.6	8.4	6.3	13.5	27.4	18.6	11.9	**10.6**
Typhimurium DT 42	0.7	2.7	2.4	2.5	6.1	1.5	2.2	4.9	2.8	2.7	4.7	6.1	12.7	8.1	4.3	12.9	6.3	17.5	34.7	8.2	3.7	**6.3**
Saintpaul	0.0	0.8	0.5	0.2	1.8	0.5	0.0	2.0	1.9	6.6	3.1	7.4	0.0	2.2	2.1	6.1	6.3	11.5	36.5	43.9	31.1	**6.1**
Typhimurium DT 12a	2.7	2.7	2.9	4.4	5.5	3.1	2.2	2.0	1.9	2.7	6.2	4.9	0.0	1.5	4.3	6.8	9.5	13.7	56.6	8.2	10.1	**5.8**
Typhimurium DT 9	2.0	1.2	1.7	0.7	5.8	0.5	6.6	2.0	0.9	3.3	10.9	0.6	2.5	1.8	2.1	4.6	6.3	2.3	14.6	35.1	21.0	**4.5**
Typhimurium RDNC-May 06	12.7	4.7	4.1	6.0	8.5	2.1	0.0	7.9	1.9	5.3	6.2	1.2	5.1	0.7	2.9	0.0	0.0	0.6	0.0	0.5	0.0	**3.8**
Heidelberg	2.0	2.5	4.1	2.5	4.4	2.1	4.4	5.9	0.9	3.3	1.6	3.7	0.0	1.8	1.4	8.4	6.3	5.8	1.8	6.6	6.4	**3.7**
Virchow	0.7	3.7	7.6	4.8	3.5	2.1	0.0	2.0	0.0	1.3	0.0	2.5	2.5	4.4	2.9	1.5	0.0	3.2	3.6	2.7	3.7	**3.5**

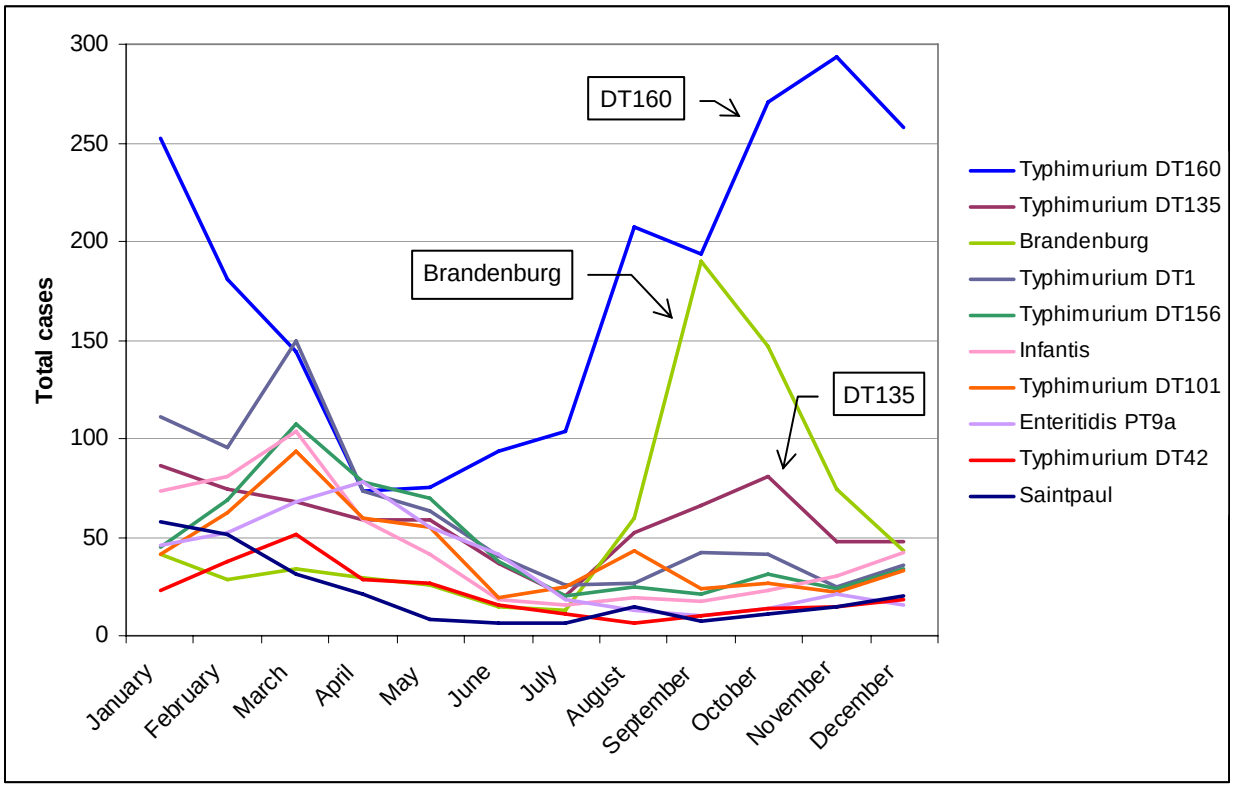
Notes to table:

1. *Only cases with known serotypes have been used to calculate these rates (n=11,554).*
2. *Rates per100,000 population referenced to Statistics NZ estimated population for 2004 for each DHB.*
3. *Shaded areas signify where rates of Salmonella serotype for a given DHB exceeds mean rate + 1 SD for that serotype across all of NZ.*
4. *For DHB abbreviations, see Figure 1.*

3.3.5 Seasonality

Salmonellosis shows a season variation with peaks generally occurring in February/March and then later in the spring between August and October. The data from 2000-2009 for the ten serotypes causing the highest number of notifications suggests that the timing of these peaks can vary with serotype (Figure 2). *S.* Typhimurium DT160 peaks in the late spring/summer months (November-January) and re-emerges first in late winter. As a result of its aetiology, *S.* Brandenburg peaks in spring (coinciding with birthing ewes) and *S.* Typhimurium DT135 shows a similar pattern. Section 4.3.4 has further information on outbreaks of illness by these serotypes. *S.* Saintpaul peaks in January/February and *S.* Enteritidis PT9a only shows a peak in autumn. The remaining five serotypes all show a clear peak in March.

Figure 2: Notifications of *Salmonella* serotypes by month, for the ten serotypes causing the most notifications across the years 2000-2009



3.3.6 Person-to-person transmission

Of the 11,554 serotype cases, 373 (3.2%) recorded person-to-person transmission as the confirmed source. The sex was recorded for the majority (97.5%) of these cases and this showed more females (54%) than males (46%) were infected by person-to-person transmission (p=0.05). However, when broken down by two age strata (16 years or younger, 17 years or older), a statistically significant difference was only observed for the 16 years or younger group, where 56% females contracted salmonellosis through person-to-person transmission versus 44% males (p=0.008).

The 15 serotypes linked to the most confirmed person-to-person cases during 2000-2009 were analysed to determine if there were gender differences in the 16 years or younger age group and the 17 years or older age group.

In the 16 years or younger age group, there were significant statistical differences between males and females for four serotypes. Females more likely than males to contract salmonellosis by person-to-person transmission for *S*. Typhimurium DT9 (p=0.02), *S*. Typhimurium DT12a (p=0.009) and *S*. Saintpaul (p=0.003). Males were more likely than females to contract *S*. Infantis (p=0.03) by person to person transmission but as numbers are very low this should be accepted with some caution

In the 17 years or older age group there was no significant difference between males and females for any of these 15 serotypes.

3.4 Results: Attribution of Risk Factors Using Case-case Analysis

The case-case analysis included all serotypes causing 50 cases or more over 2000-2009 (see Table 12). The results for the seven risk factors for which data are routinely collected and entered on the case report form are summarised in Table 20 for cases aged less than five years, in Table 21 for cases aged five to 16 years, and in Table 22 for cases aged 17 years or older. Only those ORs that have confidence intervals that would suggest significance are included. For the full results please see Appendices 4, 5 and 6.

3.4.1 Salmonellosis cases less than five years old

The results are presented in Table 20 for cases aged less than five years.

For cases under the age of 16, only 1.2% of cases with *S.* Typhimurium DT160 reported overseas travel as a risk factor. This serotype is less likely than most of the other serotypes to be acquired overseas, which supports a likely domestic source. Those much more likely to be acquired overseas in this age group include *S.* Newport (OR=152.4), *S.* Enteritidis PT6a (OR=225.8) and *S.* Hadar (OR=112.9).

For the remaining risk factors, there were very few serotypes with significantly different ORs to *S.* Typhimurium DT160.

Significant ORs for the risk factor food consumption from a premise (reported by 36% of *S.* Typhimurium DT160 cases) are all reduced (OR≤0.5) except for males with this risk factor infected with *S.* Typhimurium DT42 (OR=4.8).

Only two serotypes had significant ORs for consumption of untreated drinking water when referenced to *S.* Typhimurium DT160 (25% *S.* Typhimurium DT160 cases). *S.* Typhimurium DT1 had an elevated OR for females (OR=2.1) but reduced OR for males (OR=0.5). The ORs for *S.* Brandenburg were similarly elevated for both sexes (OR=2.3 for females, OR=2.8 for males).

Contact with recreational water, where this was reported as a risk factor in 16% of cases of *S.* Typhimurium DT160, showed increased ORs for the serotypes *S.* Saintpaul (OR=3.4) and *S.* Heidelberg (OR=3.1). Recreational water was also a more likely source of *S.* Typhimurium DT156 for males (OR=2.0).

Contact with farm animals was reported to be associated with 33% of cases for *S.* Typhimurium DT160. This risk factor is more likely to be a source of *S.* Brandenburg for both sexes (OR=3.0 for females, OR=5.1 for males). A notable increased OR was also observed for *S.* Typhimurium DT9 in females (OR=5.5).

Contact with sick animals was a reported risk factor for only 5% of cases of *S.* Typhimurium DT160. Four serotypes had elevated ORs, of which *S.* Brandenburg (risk factor reported by 21% of cases with this serotype) was significantly elevated for males (OR=5.0) and females OR=5.1). *S.* Typhimurium DT156 had an elevated OR for females (OR=4.0).

ORs for contact with human faeces which was reported to be associated with 27% of cases for *S.* Typhimurium DT160 are only elevated for two serotypes when the sexes are combined. The OR for *S.* Typhimurium DT156 remains elevated in females (OR=2.2). *S.* Typhimurium 42 (OR=0.3) has less association with this risk factor than *S.* Typhimurium DT160, but when males and females are separated out this significant difference is lost.

Table 20: Salmonellosis serotype case-case analysis for risk factors referenced to *S*. Typhimurium DT160, for cases aged less than five years[1]

Risk factor, *Salmonella* serotype	Males and females less than five years			Females less than five years			Males less than five years		
	% with risk factor	Crude odds ratio	95% CI[2]	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Overseas travel									
Typhimurium DT160	**1.2**	**1(ref)**		**1.3**	**1.0**		**1.1**	**1(ref)**	
Saintpaul	5.3	**4.7**	1.3-17.1	5.6	4.6	0.74-28.3	5.0	4.8	0.78-29.8
Typhimurium RDNC	15.4	**15.4**	4.1-58.5	22.2	**22.2**	3.2-154.5	11.8	**12.2**	1.9-78.8
Typhimurium DT23	13.9	**13.7**	4.1-45.8	19.2	**18.5**	4.1-82.8	3.7	3.5	0.17-74.1
Typhimurium DT9	7.3	**6.7**	1.1-42.4	9.1	7.8	0.74-81.4	5.3	5.1	0.24-109.3
Heidelberg	11.6	**11.1**	2.4-52.2	7.7	6.5	0.29-143.9	13.3	**14.1**	2.2-91.8
Virchow	45.0	**69.3**	21.0-228.5	35.7	**43.1**	8.9-209.2	66.7	**183.3**	23.8-1,414.8
Agona	53.3	**96.8**	26.5-353.3	50.0	**77.7**	10.9-553.7	55.6	**114.6**	20.1-652.0
Typhimurium Untypable	25.0	**28.2**	6.1-131.0	16.7	**15.5**	1.4-176.5	33.3	**45.8**	5.9-353.7
Newport	64.3	**152.4**	39.2-592.3	50.0	**77.7**	8.1-749.4	70.0	**213.9**	36.5-1,252.5
Enteritidis PT1	42.9	**63.5**	11.6-347.5	50.0	**77.7**	3.9-1,554.8	40.0	**61.1**	7.3-509.3
Thompson	14.3	**14.1**	1.5-135.9	9.1	7.8	0.34-176.3	33.3	**45.8**	1.3-1,644.9
Montevideo	33.3	**42.3**	7.6-236.0	14.3	12.9	0.53-318.6	50.0	**91.7**	9.5-884.0
Mbandaka	16.7	**16.9**	1.7-167.7	14.3	12.9	0.53-318.6	20.0	22.9	0.84-622.1
Stanley	44.4	**67.7**	8.9-513.7	33.3	**38.8**	2.7-553.5	66.7	**183.3**	5.1-6,579.5
Enteritidis PT6a	72.7	**225.8**	29.3-1,739.7	80.0	**310.7**	11.4-8,437.1	66.7	**183.3**	12.9-2,611.8
Weltevreden	44.4	**67.7**	8.9-513.7	33.3	**38.8**	2.7-553.5	66.7	**183.3**	5.1-6,579.5
Enteritidis PT1b	50.0	**84.7**	10.2-704.5	50.0	**77.7**	3.9-1,554.8	50.0	**91.7**	4.6-1,834.3
Corvallis	37.5	**50.8**	5.8-448.7	20.0	19.4	0.71-527.3	66.7	**183.3**	5.1-6,579.5
Enteritidis PT4	42.9	**63.5**	6.6-611.5	50.0	**77.7**	3.9-1,554.8	33.3	**45.8**	1.3-1,644.9
Salmonella species 4,5,12 : d :-	37.5	**50.8**	5.8-448.7	66.7	**155.3**	4.3-5,576.6	20.0	22.9	0.84-622.1
Hadar	57.1	**112.9**	11.7-1,087.1	66.7	**155.3**	4.3-5,576.6	50.0	**91.7**	4.6-1,834.3

Table 20 continued…

Risk factor, *Salmonella* serotype	Males and females less than five years			Females less than five years			Males less than five years		
	% with risk factor	Crude odds ratio	95% CI[2]	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Food consumption from a premise									
Typhimurium DT160	**35.6**	**1(ref)**		**37.4**	**1(ref)**		**34.1**	**1(ref)**	
Typhimurium DT1	20.4	**0.5**	0.27-0.80	17.0	**0.3**	0.16-0.75	24.4	0.6	0.30-1.3
Brandenburg	14.7	**0.3**	0.18-0.53	15.3	**0.3**	0.14-0.66	14.3	**0.3**	0.16-0.65
Typhimurium DT12a	20.8	**0.5**	0.23-0.99	15.8	0.3	0.09-1.1	24.1	0.6	0.25-1.5
Typhimurium DT42	48.8	1.7	0.91-3.3	27.3	0.6	0.23-1.7	71.4	**4.8**	1.8-13.1
Infantis	20.0	0.5	0.20-1.0	33.3	0.8	0.32-2.2	5.3	**0.1**	0.01-0.82
Typhimurium DT101	30.4	0.8	0.47-1.3	22.0	**0.5**	0.21-1.1	39.5	1.3	0.61-2.6
Consumption of untreated drinking water									
Typhimurium DT160	**25.4**	**1(ref)**		**21.6**	**1(ref)**		**28.5**	**1(ref)**	
Typhimurium DT1	25.7	1.0	0.63-1.6	36.4	**2.1**	1.1-4.0	15.5	**0.5**	0.21-0.99
Brandenburg	46.7	**2.6**	1.7-3.9	39.0	**2.3**	1.2-4.3	52.6	**2.8**	1.6-4.7
Contact with recreational water									
Typhimurium DT160	**15.8**	**1(ref)**		**15.8**	**1(ref)**		**15.8**	**1(ref)**	
Typhimurium DT156	21.8	1.5	0.90-2.43	16.9	1.1	0.51-2.3	27.1	**2.0**	1.0-3.9
Saintpaul	39.1	**3.4**	2.0-5.9	44.1	**4.2**	1.9-9.1	34.3	**2.8**	1.3-6.1
Heidelberg	36.8	**3.1**	1.2-8.2	40.0	3.5	0.57-22.1	35.7	3.0	0.94-9.3
Contact with farm animals									
Typhimurium DT160	**32.6**	**1(ref)**		**32.6**	**1(ref)**		**32.7**	**1(ref)**	
Brandenburg	65.8	**4.0**	2.7-5.8	58.8	**3.0**	1.7-5.2	71.1	**5.1**	3.0-8.6
Infantis	12.2	**0.3**	0.11-0.75	16.0	0.4	0.13-1.2	6.3	0.1	0.02-1.1
Typhimurium DT23	50.0	2.1	0.96-4.4	58.8	**3.0**	1.1-8.1	36.4	1.2	0.34-4.1
Typhimurium DT9	65.0	**3.8**	1.5-9.8	72.7	**5.5**	1.4-21.4	55.6	2.6	0.67-9.8

Table 20 continued…

Risk factor, *Salmonella* serotype	Males and females less than five years			Females less than five years			Males less than five years		
	% with risk factor	Crude odds ratio	95% CI[2]	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Contact with sick animals									
Typhimurium DT160	**5.1**	**1(ref)**		**3.2**	**1(ref)**		**6.7**	**1(ref)**	
Typhimurium DT156	10.2	2.1	0.95-4.6	11.8	**4.0**	1.2-13.0	8.5	1.3	0.41-4.1
Brandenburg	20.8	**4.8**	2.6-8.9	14.5	**5.1**	1.7-15.0	26.5	**5.0**	2.4-10.6
Typhimurium RDNC-May 06	13.8	**3.0**	1.0-8.8	4.3	1.4	0.07-26.0	19.0	3.3	0.97-10.9
Typhimurium DT23	17.4	**3.9**	1.2-12.5	15.4	5.5	0.98-30.2	20.0	3.5	0.68-17.8
Contact with human faeces									
Typhimurium DT160	**26.7**	**1(ref)**		**23.9**	**1(ref)**		**29.2**	**1(ref)**	
Typhimurium DT156	36.4	**1.6**	1.0-2.4	40.4	**2.2**	1.2-4.0	32.1	1.1	0.60-2.2
Typhimurium DT42	10.0	**0.3**	0.11-0.87	5.3	0.2	0.02-1.4	14.3	0.4	0.12-1.4
Typhimurium RDNC-May 06	43.8	**2.1**	1.0-4.4	46.7	2.8	0.96-8.1	41.2	1.7	0.62-4.7

1. Only those ORs that have confidence intervals that would suggest significance are included (bold and shaded). Full tables are in Appendix 4.

2. 95% confidence interval.

3.4.2 Salmonellosis cases aged five to 16 years

The results are presented in Table 21 for cases aged five to 16 years.

For cases aged five to 16 years, only 0.4% of cases with *S.* Typhimurium DT160 reported overseas travel as a risk factor. There were 24 serotypes more likely to be associated with this risk factor than *S.* Typhimurium DT160, many with ORs over 100.

For the remaining risk factors, there were very few serotypes with significantly different ORs to *S.* Typhimurium DT160.

Food consumption from a premise was reported by 50% of *S.* Typhimurium DT160 cases. *S.* Brandenburg had significantly reduced ORs (OR=0.3, OR=0.2 females). *S.* Saintpaul is more likely to be associated with this risk factor (RO=2.3), particularly males infected by this serotype (OR=3.2).

ORs for consumption of untreated drinking water, which was reported to be associated with 27% of cases for *S.* Typhimurium DT160, were elevated for three serotypes; *S.* Typhimurium DT9 (OR=3.4), *S.* Brandenburg (OR=2.0) and *S.* Typhimurium DT23 (OR=3.0). ORs for the latter two serotypes remained elevated for males.

Contact with recreational water where this was reported as a risk factor in 29% of cases of *S.* Typhimurium DT160, showed increased ORs for the serotypes *S.* Saintpaul (OR=3.0) and *S.* Mississippi (OR=5.9). Females infected with *S.* Typhimurium DT9 were also more associated with this risk factor than those infected with *S.* Typhimurium DT160 (OR=9.9 for *S.* Typhimurium DT9 females).

Contact with farm animals was reported to be associated with 42% of cases for *S.* Typhimurium DT160. This risk factor is more likely to be a source of *S.* Brandenburg for males (OR=5.7), but less likely to be a source of *S.* Typhimurium DT156 (OR=0.5).

Contact with sick animals was a reported risk factor for only 7.3% of cases of *S.* Typhimurium DT160. Four serotypes were more likely to be associated with this risk factor. The OR for *S.* Brandenburg was significantly elevated for males (OR=5.1) and females OR=5.6). *S.* Enteritidis PT9a showed an increased OR for females only (OR=4.4). The serotypes *S.* Typhimurium DT12a and DT9 both showed elevated ORs for males (OR=7.2 and OR=9.0, respectively).

There were no serotypes with significantly different ORs for the risk factor contact with human faeces which was reported to be associated with 10% of *S.* Typhimurium DT160 cases.

Table 21: Salmonellosis serotype case-case analysis for risk factors referenced to *S*. Typhimurium DT160 for cases aged five to 16 years[1]

Risk factor, *Salmonella* serotype	Males and females five to 16 years			Females five to 16 years			Males five to 16 years		
	% with risk factor	Crude odds ratio	95% CI[2]	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Overseas travel									
Typhimurium DT160	**0.4**	**1(ref)**		**0.4**	**1(ref)**		**0.3**	**1(ref)**	
Typhimurium DT135	3.8	**11.3**	1.2-110.4	5.6	14.9	0.66-339.1	2.4	7.6	0.25-230.8
Typhimurium DT42	4.5	**13.3**	1.0-171.0	8.3	23.1	0.73-727.6	2.3	7.4	0.14-384.4
Heidelberg	10.6	**33.7**	3.2-357.2	7.7	21.2	0.39-1,161.0	11.8	**41.6**	1.8-965.0
Typhimurium RDNC-May 06	8.3	**25.7**	1.5-438.8	20.0	63.5	0.99-4,074.3	5.3	17.3	0.32-925.0
Typhimurium DT9	8.7	**27.0**	2.4-309.6	16.7	**50.8**	1.5-1,700.0	5.9	19.5	0.63-604.3
Typhimurium Not Typed	7.7	**23.6**	1.8-309.6	9.1	25.4	0.46-1,415.6	7.1	24.0	0.77-749.7
Typhimurium RDNC	8.6	**26.5**	2.0-350.1	7.7	21.2	0.39-1,161.0	9.1	31.2	0.99-987.3
Virchow	58.3	**396.2**	31.0-5,061.2	50.0	**254.0**	2.1-30,992.0	60.0	**468.0**	17.2-12,725.6
Enteritidis PT4	76.2	**905.6**	80.3-10,217.1	88.9	**2032.0**	35.6-115,978.6	66.7	**624.0**	24.1-16,158.9
Mississippi	9.1	**28.3**	1.7-485.7	9.1	25.4	0.46-1,415.6	9.1	31.2	0.56-1,737.7
Stanley	75.0	**849.0**	67.4-10,690.3	80.0	**1016.0**	29.5-34,938.6	66.7	**624.0**	15.9-24,497.6
Typhimurium Untypable	27.3	**106.1**	7.0-1,604.6	20.0	63.5	0.99-4,074.3	33.3	**156.0**	4.0-6,124.4
Salmonella species 4,5,12 : d :-	76.9	**943.3**	64.7-13,764.2	66.7	**508.0**	6.3-40,807.6	80.0	**1248.0**	36.3-42,882.6
Weltevreden	61.5	**452.8**	36.4-5,629.7	60.0	**381.0**	14.0-10,368.8	66.7	**624.0**	7.8-50,093.8
Newport	80.0	**1132.0**	59.7-21,462.2	80.0	**1016.0**	15.8-65,189.4	80.0	**1248.0**	19.5-80,021.1
Enteritidis PT1b	60.0	**424.5**	29.8-6,047.0	50.0	**254.0**	5.0-12,851.2	66.7	**624.0**	15.9-24,497.6
Agona	63.6	**495.3**	36.0-6,814.5	75.0	**762.0**	21.2-27,408.9	33.3	**156.0**	1.9-12,523.4
Thompson	33.3	**141.5**	6.4-3,144.9	33.3	**127.0**	1.6-10,201.9	33.3	**156.0**	1.9-12,523.4
Mbandaka	50.0	**283.0**	17.7-4,535.8	50.0	**254.0**	5.0-12,851.2	50.0	**312.0**	6.2-15,774.4
Corvallis	50.0	**283.0**	14.1-5,662.7	50.0	**254.0**	2.1-30,992.0	50.0	**312.0**	6.2-15,774.4
Montevideo	42.9	**212.3**	11.8-3,809.1	33.3	**127.0**	1.6-10,201.9	50.0	**312.0**	6.2-15,774.4

Table 21 continued…

Risk factor, *Salmonella* serotype	Males and females five to 16 years			Females five to 16 years			Males five to 16 years		
	% with risk factor	Crude odds ratio	95% CI[2]	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Overseas travel *continued…*									
Hadar	57.1	**377.3**	21.0-6,771.8	66.7	**508.0**	6.3-40,807.6	50.0	**312.0**	6.2-15,774.4
Enteritidis PT1	66.7	**566.0**	25.5-12,579.4	66.7	**508.0**	6.3-40,807.6	66.7	**624.0**	7.8-50,093.8
Enteritidis PT6a	40.0	**188.7**	7.7-4,641.4	50.0	**254.0**	2.1-30,992.0	33.3	**156.0**	1.9-12,523.4
Food consumption from a premise									
Typhimurium DT160	**45.9**	**1(ref)**		**46.5**	**1(ref)**		**45.4**	**1(ref)**	
Brandenburg	22.2	**0.3**	0.15-0.78	17.6	**0.2**	0.07-0.92	26.3	0.4	0.14-1.3
Saintpaul	65.7	**2.3**	1.1-4.8	53.8	1.3	0.42-4.3	72.7	**3.2**	1.2-8.8
Consumption of untreated drinking water									
Typhimurium DT160	**27.0**	**1(ref)**		**24.5**	**1(ref)**		**29.0**	**1(ref)**	
Brandenburg	42.0	**2.0**	1.0-3.7	21.7	0.9	0.29-2.5	59.3	**3.6**	1.5-8.4
Typhimurium DT23	52.9	**3.0**	1.1-8.2	37.5	1.8	0.41-8.3	66.7	**4.9**	1.2-20.6
Typhimurium DT9	56.0	**3.4**	1.1-10.9	66.7	6.2	0.20-189.2	54.5	2.9	0.84-10.2
Contact with recreational water									
Typhimurium DT160	**28.9**	**1(ref)**		**28.8**	**1(ref)**		**29.0**	**1(ref)**	
Saintpaul	55.3	**3.0**	1.5-6.1	28.6	1.0	0.29-3.4	70.8	**5.9**	2.3-15.5
Typhimurium DT9	28.6	1.0	0.37-2.6	80.0	**9.9**	1.1-91.7	12.5	0.3	0.08-1.6
Mississippi	70.6	**5.9**	1.3-26.5	85.7	14.8	0.7-303.9	60.0	3.7	0.59-22.9
Contact with farm animals									
Typhimurium DT160	**42.0**	**1(ref)**		**46.2**	**1(ref)**		**38.6**	**1(ref)**	
Typhimurium DT156	28.4	**0.5**	0.31-0.96	29.0	0.5	0.20-1.1	27.9	0.6	0.29-1.3
Typhimurium DT1	35.6	0.8	0.42-1.4	16.7	**0.2**	0.06-0.85	43.9	1.2	0.62-2.5
Brandenburg	71.9	**3.5**	1.9-6.6	64.0	2.1	0.85-5.1	78.1	**5.7**	2.3-14.0

Table 21 continued…

Risk factor, *Salmonella* serotype	Males and females five to 16 years			Females five to 16 years			Males five to 16 years		
	% with risk factor	Crude odds ratio	95% CI[2]	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Contact with sick animals									
Typhimurium DT160	**7.3**	**1(ref)**		**8.3**	**1(ref)**		**6.5**	**1.0**	
Brandenburg	29.5	**5.3**	2.4-12.0	33.3	**5.6**	1.8-17.3	26.1	**5.1**	1.6-16.4
Enteritidis PT9a	17.6	2.7	0.99-7.5	28.6	**4.4**	1.2-17.1	10.0	1.6	0.31-8.1
Typhimurium DT12a	28.6	**5.1**	1.4-17.8	20.0	2.8	0.28-27.6	33.3	**7.2**	1.5-34.2
Typhimurium DT9	33.3	**6.3**	2.0-19.7	14.3	1.9	0.09-39.9	38.5	**9.0**	2.4-33.9

1. Only those ORs that have confidence intervals that would suggest significance are included (bold and shaded). Full tables are in Appendix 5.
2 . 95% confidence interval.

3.4.3 Salmonellosis cases aged 17 years or older

The results are presented in Table 22 for cases aged 17 years or older.

Overseas travel was a reported risk factor for 2% of *S.* Typhimurium DT160 cases aged 17 years or older. Similar to the findings of the other age groups, *S.* Typhimurium DT160 is less likely than most of the serotypes to be acquired overseas. There were 28 serotypes more likely to be associated with overseas travel, ten with ORs exceeding 100.

Food consumption from a premise was reported to be an associated risk factor in 54% of *S.* Typhimurium DT160 cases. An elevated OR was observed for *S.* Typhimurium DT135 (OR=1.5) but the ORs were no longer significantly different when the cases were separated by gender. This was also a more likely attributable source for *S.* Heidelberg and *S.* Montevideo if cases were male (OR=3.4 and OR=4.1, respectively). *S.* Brandenburg was less likely to be associated with this risk factor (OR=0.4, OR=0.4 females, OR=0.5 males). Males infected with *S.* Typhimurium DT9 were also less likely to be significantly associated with this risk factor (OR=0.4).

Consumption of untreated drinking water was reported by 20% of *S.* Typhimurium DT160 cases. ORs were increased for *S.* Brandenburg (OR=2.4), *S.* Saintpaul (OR=2.4), *S.* Typhimurium DT23 (OR=2.2) and *S.* Typhimurium DT9 (OR=3.2). The OR was also elevated for males with *S.* Enteritidis PT1 who reported this risk factor (OR=10.7). This risk factor is a less likely source of attribution for *S.* Infantis (OR=0.5).

Contact with recreational water was a reported risk factor in only 7% of cases of *S.* Typhimurium DT160 aged 17 years or older. The equivalent value for the group aged under five years was 16% and was 29% for cases aged between five and 16 years. There were increased ORs with a wider group of serotypes than for the younger age groups, with a trend towards increased ORs for males. These results suggest that other serotypes are more likely to be acquired through contact with recreational water than *S.* Typhimurium DT160. There were no significantly reduced ORs.

There are a number of serotypes more likely to be acquired through contact with farm animals than *S.* Typhimurium DT160 (risk factor reported by 25% of *S.* Typhimurium DT160 cases). As with the younger age groups, this is a more likely source of *S.* Brandenburg (OR=4.6), particularly for males (OR=3.1 for females, OR=5.8 for males). Serotypes with increased ORs that only remained elevated in males were *S.* Typhimurium DT1 (OR=1.7, OR=2.3 in males), *S.* Typhimurium DT9 (OR=2.8, OR=4.8 in males) and *S.* Saintpaul (OR=1.8, OR=2.9 in males). The OR for *S.* Typhimurium DT23 (OR=2.5) remained elevated in females only (OR=2.6). This was a less likely source of attribution for four serotypes (*S.* Virchow, *S.* Agona, *S.* Mbandaka and *S.* Weltevreden).

Contact with sick animals was only reported as a risk factor in 6% of cases of *S.* Typhimurium DT160. The pattern of significant ORs was similar to that seen in contact with farm animals for the serotypes *S.* Brandenburg (OR=8.2, OR=4.4 for females, OR=10.2 for males), *S.* Typhimurium DT1 (OR=2.8, OR=3.8 in males) and *S.* Typhimurium DT156 (OR=2.3). *S.* Typhimurium DT9 remained elevated for both sexes (OR=6.0 females, OR=8.3 males). *S.* Typhimurium DT23, which had an elevated OR for females who had contact with farm animals, only had an elevated OR for males who had contact with sick animals (OR=4.8). *S.* Virchow was significantly less likely than *S.* Typhimurium DT160 to be acquired through contact with

farm animals, but females who had contact with sick animals had an elevated OR for this serotype (OR=3.6).

Only one serotype had a significant OR for the risk factor contact with human faeces when compared to the 13% of *S.* Typhimurium DT160 cases reporting this risk factor. *S.* Typhimurium DT74 was significantly more likely to be acquired by females through contact with human faeces (OR=3.8).

Table 22: Salmonellosis serotype case-case analysis for risk factors referenced to *S*. Typhimurium DT160 for cases aged 17 years or older[1]

Risk factor, *Salmonella* serotype	Males and females 17 years or older			Females 17 years or older			Males 17 years or older		
	% with risk factor	Crude odds ratio	95% CI[2]	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Overseas Travel									
Typhimurium DT160	**1.9**	**1(ref)**		**1.5**	**1(ref)**		**2.3**	**1(ref)**	
Infantis	6.5	**3.7**	1.8-7.6	7.6	**5.4**	1.9-15.3	5.5	2.5	0.88-7.0
Typhimurium DT135	9.3	**5.4**	2.8-10.6	10.2	**7.6**	2.8-20.1	8.5	**3.9**	1.6-9.9
Typhimurium DT1	4.3	**2.4**	1.1-5.4	3.3	2.3	0.63-8.2	5.3	2.4	0.85-6.7
Typhimurium DT42	4.3	2.4	0.72-7.8	7.3	**5.2**	1.3-21.8	1.2	0.5	0.03-9.5
Typhimurium DT12a	14.1	**8.7**	3.8-19.9	17.5	**14.1**	4.5-44.3	10.5	**5.0**	1.4-17.6
Typhimurium DT9	8.2	**4.7**	1.8-12.7	10.0	**7.4**	2.0-27.3	6.1	2.8	0.56-13.6
Saintpaul	13.6	**8.3**	3.6-19.0	8.7	**6.3**	1.7-23.3	20.0	**10.7**	3.6-31.6
Virchow	76.1	**167.9**	78.6-358.8	63.3	**114.6**	38.3-342.9	85.4	**249.4**	81.8-759.9
Heidelberg	11.7	**7.0**	2.7-18.0	5.0	3.5	0.68-17.9	25.0	**14.3**	4.2-48.8
Typhimurium RDNC	30.2	**22.9**	10.4-50.3	19.2	**15.8**	4.5-56.0	40.7	**29.4**	10.4-83.1
Thompson	10.0	**5.9**	2.0-17.0	8.0	**5.8**	1.1-30.2	12.0	**5.8**	1.4-23.5
Weltevreden	77.6	**182.6**	77.7-429.1	83.9	**344.9**	98.7-1,205.6	66.7	**85.5**	25.6-285.3
Enteritidis PT4	80.3	**215.8**	94.7-491.8	85.3	**384.7**	110.8-1,336.5	74.1	**122.1**	40.3-370.7
Typhimurium Not Typed	15.9	**10.0**	3.8-26.3	8.7	**6.3**	1.2-33.2	23.8	**13.4**	3.9-45.5
Agona	60.0	**79.3**	35.7-175.9	66.7	**132.7**	39.4-446.6	54.2	**50.5**	17.4-146.7
Typhimurium DT23	5.6	3.1	0.79-12.5	8.7	**6.3**	1.2-33.2	2.3	1.0	0.06-18.3
Mbandaka	34.2	**27.5**	11.7-64.5	50.0	**66.3**	20.8-211.9	12.5	**6.1**	1.2-31.5
Montevideo	44.1	**41.7**	17.7-98.5	54.5	**79.6**	24.9-254.9	25.0	**14.3**	3.2-62.8
Typhimurium Untypable	46.2	**45.3**	19.9-103.1	50.0	**66.3**	19.5-226.1	42.9	**32.1**	10.5-97.6
Mississippi	17.5	**11.2**	4.2-29.6	33.3	**33.2**	8.7-127.0	8.0	3.7	0.75-18.5
Enteritidis PT6a	92.8	**676.6**	168.3-2,720.4	97.4	**2520.7**	135.7-46,807.7	86.7	**277.9**	53.6-1,440.4

Table 22 continued…

Risk factor, *Salmonella* serotype	Males and females 17 years or older			Females 17 years or older			Males 17 years or older		
	% with risk factor	Crude odds ratio	95% CI[2]	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Overseas Travel *continued…*									
Corvallis	88.2	**396.4**	123.1-1,276.8	88.2	**497.5**	92.6-2,672.9	88.2	**320.6**	62.6-1,642.2
Salmonella species 4,5,12 : d :-	83.3	**264.3**	95.0-735.6	78.6	**243.2**	53.7-1,100.9	86.4	**270.8**	66.4-1,103.5
Stanley	76.7	**173.7**	64.0-471.0	72.2	**172.5**	46.6-638.6	83.3	**213.8**	40.2-1,138.0
Enteritidis PT1b	77.2	**178.9**	64.4-497.3	94.1	**1061.3**	54.5-20,661.0	70.0	**99.8**	30.5-326.5
Hadar	80.0	**211.4**	79.1-564.8	78.9	**248.8**	63.5-975.2	81.3	**185.3**	44.0-780.2
Newport	53.1	**59.9**	25.0-143.4	31.6	**30.6**	8.7-107.9	84.6	**235.1**	44.6-1,238.8
Enteritidis PT1	83.3	**264.3**	88.3-790.9	86.7	**431.2**	79.3-2,343.7	80.0	**171.0**	40.3-726.4
Food consumption from a premise									
Typhimurium DT160	**54.3**	**1(ref)**		**58.7**	**1(ref)**		**49.2**	**1(ref)**	
Typhimurium DT135	63.6	**1.5**	1.1-2.1	69.1	1.6	0.97-2.6	57.8	1.4	0.87-2.3
Brandenburg	33.7	**0.4**	0.30-0.61	37.1	**0.4**	0.24-0.71	31.5	**0.5**	0.30-0.76
Typhimurium DT9	43.3	0.6	0.38-1.1	57.6	1.0	0.46-2.0	25.9	**0.4**	0.15-0.88
Heidelberg	61.7	1.4	0.73-2.5	53.3	0.8	0.38-1.7	76.5	**3.4**	1.1-10.6
Virchow	46.2	0.7	0.38-1.4	38.1	**0.4**	0.17-1.1	55.6	1.3	0.49-3.4
Montevideo	63.6	1.5	0.61-3.6	50.0	0.7	0.22-2.2	80.0	**4.1**	0.86-19.8
Consumption of untreated drinking water									
Typhimurium DT160	**20.0**	**1(ref)**		**18.3**	**1(ref)**		**21.8**	**1(ref)**	
Infantis	10.9	**0.5**	0.30-0.81	12.4	0.6	0.32-1.2	9.2	**0.4**	0.17-0.79
Brandenburg	37.7	**2.4**	1.7-3.4	25.7	1.5	0.85-2.8	44.8	**2.9**	1.9-4.6
Typhimurium DT9	44.7	**3.2**	1.8-6.0	42.3	**3.3**	1.4-7.5	47.6	**3.3**	1.3-8.0
Saintpaul	37.7	**2.4**	1.4-4.2	25.0	1.5	0.67-3.3	56.0	**4.6**	2.0-10.5
Typhimurium DT23	35.5	**2.2**	1.0-4.7	42.1	**3.3**	1.3-8.4	25.0	1.2	0.31-4.5
Enteritidis PT1	38.5	2.5	0.81-7.8	22.2	1.3	0.26-6.3	75.0	**10.7**	1.1-105.0

Table 22 continued…

Risk factor, *Salmonella* serotype	Males and females 17 years or older			Females 17 years or older			Males 17 years or older		
	% with risk factor	Crude odds ratio	95% CI[2]	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Contact with recreational water									
Typhimurium DT160	**6.7**	**1(ref)**		**6.7**	**1(ref)**		**6.6**	**1(ref)**	
Typhimurium DT156	13.9	**2.3**	1.2-4.2	12.2	1.9	0.75-5.0	15.3	**2.5**	1.1-5.9
Typhimurium DT1	10.4	1.6	0.95-2.8	5.7	0.8	0.33-2.1	15.1	**2.5**	1.3-5.1
Enteritidis PT9a	11.3	1.8	0.96-3.3	14.5	**2.4**	1.0-5.4	8.5	1.3	0.50-3.4
Typhimurium DT12a	17.5	**3.0**	1.4-6.3	21.4	**3.8**	1.4-10.3	13.8	2.3	0.72-7.1
Virchow	33.3	**7.0**	3.3-15.0	26.3	**5.0**	1.7-15.0	41.2	**9.9**	3.4-28.8
Heidelberg	11.5	1.8	0.74-4.5	5.9	0.9	0.20-3.9	22.2	**4.0**	1.2-13.4
Typhimurium RDNC	19.4	**3.4**	1.3-8.6	11.1	1.7	0.38-8.0	30.8	**6.3**	1.8-22.2
Weltevreden	31.0	**6.3**	2.7-14.7	35.3	**7.6**	2.6-22.4	25.0	**4.7**	1.2-18.8
Enteritidis PT4	21.2	**3.8**	1.6-9.2	16.7	2.8	0.75-10.3	26.7	**5.1**	1.5-17.6
Typhimurium Not Typed	15.4	**2.5**	1.0-6.4	10.0	1.5	0.34-7.1	21.1	**3.8**	1.2-12.4
Mbandaka	27.6	**5.3**	2.2-12.8	33.3	**7.0**	2.4-20.2	18.2	3.1	0.64-15.5
Salmonella species 4,5,12 : d :-	31.6	**6.5**	2.3-17.9	37.5	**8.3**	1.9-37.1	27.3	**5.3**	1.3-21.6
Stanley	26.3	**5.0**	1.7-14.6	21.4	3.8	0.99-14.6	40.0	**9.4**	1.5-59.7
Enteritidis PT1b	22.6	**4.1**	1.2-14.0	11.1	1.7	0.09-33.9	27.3	**5.3**	1.3-21.6
Hadar	25.0	**4.7**	1.5-15.1	22.2	4.0	0.78-20.2	28.6	**5.7**	1.0-31.0
Enteritidis PT1	40.0	**9.3**	3.2-27.5	20.0	3.5	0.70-17.3	80.0	56.6	6.0-530.5

Table 22 continued…

Risk factor, *Salmonella* serotype	Males and females 17 years or older			Females 17 years or older			Males 17 years or older		
	% with risk factor	Crude odds ratio	95% CI[2]	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Contact with farm animals									
Typhimurium DT160	**24.5**	**1(ref)**		**23.6**	**1(ref)**		**25.6**	**1(ref)**	
Typhimurium DT1	36.2	**1.7**	1.3-2.4	27.6	1.2	0.76-2.0	43.7	**2.3**	1.5-3.5
Brandenburg	59.8	**4.6**	3.4-6.2	48.9	**3.1**	1.9-5.0	66.7	**5.8**	3.8-8.9
Typhimurium DT156	34.2	**1.6**	1.1-2.4	31.6	1.5	0.81-2.7	36.5	1.7	0.94-3.0
Typhimurium DT9	48.0	**2.8**	1.6-5.1	34.6	1.7	0.74-4.0	62.5	**4.8**	2.0-11.5
Saintpaul	36.6	**1.8**	1.1-3.0	26.8	1.2	0.57-2.5	50.0	**2.9**	1.4-6.2
Virchow	9.1	**0.3**	0.11-0.87	12.5	0.5	0.13-1.6	5.0	0.2	0.02-1.2
Agona	6.7	**0.2**	0.05-0.93	7.1	0.2	0.03-1.9	6.3	0.2	0.03-1.5
Typhimurium DT23	44.7	**2.5**	1.3-4.8	45.0	**2.6**	1.1-6.6	44.4	2.3	0.89-6.1
Mbandaka	6.5	**0.2**	0.05-0.90	5.3	0.2	0.02-1.4	8.3	0.3	0.03-2.1
Weltevreden	9.1	**0.3**	0.09-1.0	10.0	0.4	0.08-1.6	7.7	0.2	0.03-1.9
Contact with sick animals									
Typhimurium DT160	**5.7**	**1(ref)**		**5.0**	**1(ref)**		**6.6**	**1(ref)**	
Typhimurium DT1	14.7	**2.8**	1.7-4.8	7.5	1.5	0.62-3.8	21.2	**3.8**	2.0-7.4
Brandenburg	33.2	**8.2**	5.2-12.8	18.9	**4.4**	2.1-9.4	41.6	**10.2**	5.7-18.3
Typhimurium DT156	12.0	**2.3**	1.2-4.4	9.8	2.1	0.72-5.9	14.0	2.3	0.97-5.6
Typhimurium DT9	29.5	**6.9**	3.3-14.3	24.0	**6.0**	2.1-16.9	36.8	**8.3**	2.9-23.6
Typhimurium DT23	14.3	2.7	0.96-7.9	3.2	0.6	0.04-11.0	25.0	**4.8**	1.4-16.2
Virchow	10.5	1.9	0.65-5.8	15.8	**3.6**	0.94-13.4	5.3	0.8	0.10-6.3
Contact with human faeces									
Typhimurium DT160	**13.2**	**1(ref)**		**13.7**	**1(ref)**		**12.7**	**1(ref)**	
Typhimurium DT74	21.3	1.8	0.73-4.4	37.5	**3.8**	1.3-10.9	3.4	0.2	0.01-4.2

1. Only those ORs that have confidence intervals that would suggest significance are included (bold and shaded). Full tables are in Appendix 6.
2. 95% confidence interval.

3.5 Results: Attribution to Food

3.5.1 Sporadic salmonellosis cases with a confirmed food source

Out of the 15,040 salmonellosis cases there were only 38 (0.3%) case reports with a food or drink confirmed as the source of infection. Thirty-five cases were associated with outbreaks, of which 27 cases were linked by laboratory confirmation to the 2008 flour outbreak. The cases associated with outbreaks were excluded. The case report forms for the remaining three cases were reviewed and none of the foods were confirmed by laboratory testing:

- one case of *S.* Typhimurium DT42 was epidemiologically linked to the consumption of contaminated flour;
- one case of *S.* Enteritidis RDNC was epidemiologically linked to fish. This case had also been overseas ten days prior to the approximate date of illness onset;
- one case of *S.* Typhimurium DT1 was linked to drinking tank water with suspected bird/ animal contamination.

3.5.2 Cases with a probable food source

From the 11,554 sporadic salmonellosis cases for which serotype data was available there were 8,508 cases (74%) reported in EpiSurv where the Probable Food Source check box had been selected. The ten serotypes causing the highest number of cases were *S.* Brandenburg, *S.* Enteritidis PT9a, *S.* Infantis, *S.* Saintpaul, *S.* Typhimurium DT1, *S.* Typhimurium DT101, *S.* Typhimurium DT135, *S.* Typhimurium DT156, *S.* Typhimurium DT160 and *S.* Typhimurium DT42. Using the selection method detailed in Section 3.2, 208 case report forms were examined in further detail.

Food and premises were recorded as risk factors in all 208 cases, but specific foods were not recorded in 37 (18%) of the cases. Four of the cases were overseas during the incubation period. Of the 171 cases with a record of at least one probable food, 49 (29%) listed two probable foods, 30 (18%) listed three probable foods and 6 (4%) listed four probable foods. Eighteen cases also had contact with farm animals or pets and 14 reported consuming water from untreated water supplies such as bore, well or tank (Table 23).

Table 23: Food-related risk factors recorded for a sample of cases associated with ten serotypes causing the highest number of salmonellosis cases, 2000-2009

Food-related risk factors	**No. cases**	**% cases (n=208)**
Case report forms in sample	208	100
No record of any probable foods	37	18
Shared food with others	27	13
Shared food that caused illness in others	11	5
Also has contact with farm animals/pets	18	9
Also consumed water from bore/well/tank	14	7
Number of recorded foods	***No. cases***	***% cases (n=171)***
One or more probable foods recorded	171	100
Two probable foods recorded	49	29
Three probable foods recorded	30	18
Four probable foods recorded	6	4

There were 27 cases who shared their food with others, and in 11 of these cases those they shared the foods with also became unwell (Table 24).

Table 24: Cases that shared foods that resulted in illness in others, from a sample of salmonellosis cases, 2000-2009

Shared foods that made others unwell	No. cases
Meat cooked cold sandwich	1
Barbeque (food unspecified)	2
Cakes/muffins	1
Cooked chicken	1
Deep fried chicken nuggets	1[1]
Cooked beef	1
Mass catering (food unspecified)	1
Hummus/tahini	1
Beef cheeseburger	2[2]

1. One also had contact with pets
2. One also consumed drinking water from a bore, well or tank.

Table 25 summarises the reported premises where the cases consumed food. Fast food takeaway outlets, café's/restaurants and supermarkets are most associated with these salmonellosis cases.

Table 25: Type of premises where food was consumed by a sample of salmonellosis cases, 2000-2009

Premises type reported	No. cases	% cases (n=208)
Fast food/takeaway	61	29
Café/Restaurant	46	22
Supermarket	26	13
Bakery	11	5
Lunch bar	8	4
Mass catering	6	3
Hotel/Bar	6	3
School/University cafeteria	4	2
Barbeque	4	2
Chinese takeaway	3	1
Work cafeteria	3	1
Sports club	2	1
Overseas food/water	2	1
Dairy	2	1
Resthome	1	0.5
Butcher	1	0.5
Premises not stated	21	10
Not a premise[1]	1	0.5

1. Case had contact with farm animals with confirmed Salmonella

Table 26 displays the *Salmonella* serotypes that caused illness in each case against the associated premises. There are no strong associations between premises type and *Salmonella* serotype, though over half of the salmonellosis cases caused by *S.* Typhimurium DT42 consumed food from a fast food or takeaway outlet.

Table 26: Percentage of salmonellosis cases (from a sample of salmonellosis cases, 2000-2009) associated with each premises type and *Salmonella* serotype

Premises type reported	***Salmonella* serotype**										
	Brandenburg (n=20)	**Enteritidis PT9a (n=22)**	**Infantis (n=22)**	**Saintpaul (n=16)**	**Typhimurium DT1 (n=21)**	**Typhimurium DT101 (n=23)**	**Typhimurium DT135 (n=21)**	**Typhimurium DT156 (n=23)**	**Typhimurium DT160 (n=21)**	**Typhimurium DT42 (n=19)**	**All serotypes (n=108)**
Fast food/takeaway	30	32	23	25	29	30	29	26	14	58	**29**
Café/Restaurant	25	23	27	31	29	17	10	26	24	11	**22**
Supermarket	5	14	14	13	5	13	24	9	24	5	**13**
Bakery/lunch bar	-	18	9	6	5	4	-	-	-	11	**5**
Lunchbar	5	-	5	6	5	4	14	-	-	-	**4**
Mass catering	-	-	-	-	5	13	-	4	-	5	**3**
Hotel/Bar	5	-	5	-	-	-	-	4	14	-	**3**
School/University cafeteria	5	-	-	-	-	4	-	4	-	5	**2**
Barbeque	5	5	5	-	-	-	5	-	-	-	**2**
Chinese takeaway	-	-	-	-	5	-	5	4	-	-	**1**
Work cafeteria	5	-	-	-	5	4	-	-	-	-	**1**
Sports Club	-	-	-	-	5	-	-	-	5	-	**1**
Overseas food/water	-	-	-	13	-	-	-	-	-	-	**1**
Dairy	-	-	5		-	4	-	-	-	-	**1**
Resthome	-	-	-	-	-	-	-	4	-	-	**0**
Butcher	-	-	-	-	-	-	-	4	-	-	**0**
Premises not stated	10	9	9	6	10	4	14	13	19	5	**10**
Not a premise*	5	-	-	-	-	-	-	-	-	-	**0**

A hyphen (-) indicates zero percent.

** Case had contact with farm animals with confirmed Salmonella*

Table 27 summarises the principal foods suspected as causing illness for the 208 cases. Meat products, primarily chicken, were reported most often. Table 28 lists these suspected foods against the *Salmonella* serotype. There are no strong associations between food and serotype, which is expected as none of these foods were confirmed as being the source of salmonellosis.

Table 27 Foods consumed by a sample of salmonellosis cases, 2000-2009

Food type reported	No. cases	% cases (n=208)
Chicken	56	27.0
Beef/probable beef	29	14.0
Fish	20	9.6
Processed meats	16	7.7
Ham	10	4.8
Pork	5	2.4
Cakes	4	1.9
Lamb	4	1.9
Quiche	4	1.9
Bacon	3	1.4
Pizza	3	1.4
Vegetables/salad	2	1.0
Chips	2	1.0
Coffee	2	1.0
Hangi/mass catering	2	1.0
Pasta/noodles	2	1.0
Water	2	1.0
Cheese	1	0.5
Fruit	1	0.5
Hummus/tahini	1	0.5
Icecream	1	0.5
Wild game	1	0.5
No foods reported	37	17.8

Table 28 Foods consumed by a sample of salmonellosis cases (2000-2009) reported against the *Salmonella* serotypes that caused illness in these cases

Food type reported	*Salmonella* serotype										
	Brandenburg (n=20)	Enteritidis PT9a (n=22)	Infantis (n=22)	Saintpaul (n=16)	Typhimurium DT1 (n=21)	Typhimurium DT101 (n=23)	Typhimurium DT135 (n=21)	Typhimurium DT156 (n=23)	Typhimurium DT160 (n=21)	Typhimurium DT42 (n=19)	All serotypes (n=108)
Chicken	45.0	36.4	22.7	37.5	33.3	17.4	19.0	8.7	19.0	36.8	**26.9**
Beef/probable beef	20.0	13.6	18.2	6.3	14.3	13.0	19.0	13.0	4.8	15.8	**13.9**
Fish	5.0	-	13.6	6.3	-	13.0	19.0	17.4	9.5	10.5	**9.6**
Processed Meats	-	9.1	4.5	12.5	9.5	4.3	4.8	8.7	14.3	10.5	**7.7**
Ham	-	4.5	4.5	6.3	4.8	13.0	4.8	0.0	4.8	5.3	**4.8**
Pork	5.0	-	4.5	-	-	-	9.5	4.3	-	-	**2.4**
Cakes	5.0	4.5	-	-	-	4.3	-	-	-	5.3	**1.9**
Lamb	-	-	4.5	-	4.8	4.3	4.8	-	-	-	**1.9**
Quiche	-	-	-	6.3	4.8	4.3	-	-	-	5.3	**1.9**

Table 28 continued…

Food type reported	*Salmonella* serotype										
	Brandenburg (n=20)	Enteritidis PT9a (n=22)	Infantis (n=22)	Saintpaul (n=16)	Typhimurium DT1 (n=21)	Typhimurium DT101 (n=23)	Typhimurium DT135 (n=21)	Typhimurium DT156 (n=23)	Typhimurium DT160 (n=21)	Typhimurium DT42 (n=19)	All serotypes (n=108)
Bacon	-	-	4.5	-	4.8	-	-	-	-	5.3	**1.4**
Pizza	-	-	-	-	4.8	4.3	4.8	-	-	-	**1.4**
Vegetables/salad	-	-	4.5	-	-	-	-	-	4.8	-	**1.0**
Chips	5.0	-	-	-	-	-	-	-	4.8	-	**1.0**
Coffee	-	4.5	-	-	-	-	-	4.3	-	-	**1.0**
Hangi and mass catering	-	-	-	-	4.8	4.3	-	-	-	-	**1.0**
Pasta/noodles	-	4.5	-	-	-	-	-	-	-	5.3	**1.0**
Water	-	-	-	12.5	-	-	-	-	-	-	**1.0**
Cheese	-	-	-	-	-	-	-	-	4.8	-	**0.5**
Fruit	-	-	-	-	-	-	-	4.3	-	-	**0.5**
Hummus/tahini	-	-	-	-	-	4.3	-	-	-	-	**0.5**
Icecream	-	-	-	-	-	4.3	-	-	-	-	**0.5**
Wild game	-	-	-	-	-	-	-	4.3	-	-	**0.5**
No foods reported	15.0	22.7	18.2	12.5	14.3	8.7	14.3	34.8	33.3	-	**17.8**

A hyphen (-) indicates zero percent.

Taking into account all the foods reported for each case (not just the principal implicated food as above), Table 29 presents some key food groups consumed by the cases against other risk factors. For the cases that reported chicken, 45% of the chicken consumed was deep fried, 14% of cases also had contact with animals and 7% also had untreated water supplies.

Table 29: Key food groups consumed by a sample of salmonellosis cases (2000-2009) presented against multiple risk factors

Food type reported	No. cases recording food	Risk factors					
		deep fried food	uncooked/ fresh or frozen	other risk foods reported	contact with animals	bore/well/ tank water	other risk factor
Chicken	56	45	11	4	14	7	0
Beef/probable beef	27	0	0	30	7	0	4
Fish/Seafood	20	35	20	25	0	5	10
Cheerios/hot dogs/ salami/frankfurters	16	38	0	56	13	0	0
Bacon/Ham	13	0	0	62	15	0	0
Savouries/cakes/pizza/ icecream/breads	12	0	0	33	0	0	0
Eggs	9	0	0	100	0	11	0
Pork	5	0	0	60	20	20	0
Lamb	4	0	0	50	0	0	0
Vegetables	4	0	0	100	0	0	0
Hummus/dips/tahini	2	0	0	50	0	0	0

3.6 Discussion

3.6.1 Data limitations

The analyses in this section are primarily limited by:

- Case report forms that did not have a recorded serotype (23% of salmonellosis cases): In most cases where a serotype was not available it was because the *Salmonella* was not typed or not able to be typed.
- Case report forms that did not hold complete risk factor information: For a large proportion of the cases the relevance of one or more risk factors was reported as "unknown" rather than "Yes" or "No". Some of these records will be genuine responses where the case could not recall exposure to a risk factor or the information could not be gathered by the PHO, but it is expected that this would be a small proportion of cases. Using the 1,022 adult cases of *S.* Typhimurium DT160 as an example, it was not known whether 26% travelled overseas, whether 46% consumed food at a food premise, whether 40% consumed untreated water nor whether between 32% and 38% had contact with recreational water, farm animals, sick animals or human faeces.
- Lack of laboratory-confirmed *Salmonella* strains from foods implicated as a source of infection.

3.6.2 Signals from serotype analysis

The review of the serotype information over ten years shows the rise and peak of a number of serotypes before they return to lower baseline levels (Table 12). It also shows the emergence of some new serotypes in humans. Although over 400 serotypes have been isolated from New Zealanders in the last decade, 35 of these are associated with 80% of the salmonellosis cases, and the predominant domestic strain *S.* Typhimurium DT160 is responsible for 19% of all cases. It is interesting to observe that the five dominant serotypes in terms of frequency (*S.* Typhimurium DT160, DT1, DT135 and DT156, and *S.* Brandenburg) all peaked between 2000 and 2002. It is not possible to predict how the pattern of serotypes will change in future years, though it looks likely that *S.* Typhimurium DT160 will be surpassed by other serotypes.

Hospitalisation is a reasonable surrogate for severity of illness with rates ranging between 7% and 20% (Table 13). Not only is *S.* Typhimurium DT160 New Zealand's most frequently occurring serotype but it is also responsible for considerable morbidity with higher rates of hospitalisation (17%). The serotypes *S.* Typhimurium DT23, *S.* Typhimurium DT74 and *S.* Virchow had similar or higher hospitalisation rates than *S.* Typhimurium DT160, but 15 times less cases.

Males are over represented in salmonellosis (52% vs. 48% female) but this is mostly accounted for by cases aged 16 years or under (Table 15). Males aged between five and 16 years ("children") were associated with seven *S.* Typhimurium phage types (including DT160) plus *S.* Heidelberg, *S.* Enteritidis 9a and *S.* Virchow (Table 16). There were no serotypes associated with female children. Males aged less than five years ("infants") were associated with two of the same *S.* Typhimurium serotypes as male children and *S.* Heidelberg, plus *S.* Typhimurium DT135 and *S.* Brandenburg. Infant females were associated with *S.* Virchow. In the "adult"

age group (aged 17 years or older) there was no significant difference between the numbers of salmonellosis cases of each sex (Table 15). *S.* Brandenburg and *S.* Enteritidis 9a were also significant for males in this age group, but in contrast to younger males, adult females were more associated with *S.* Typhimurium DT160 and *S.* Heidelberg.

Adults were under-represented and infants were over-represented in salmonellosis cases compared with the New Zealand population.

Salmonellosis in New Zealand has a geographical distribution favouring the lower half of the South Island. Over the last decade, South Canterbury, Otago and Southland have dominated other regions with high annual salmonellosis rates (Figure 1), despite changing *Salmonella* serotypes. These regions are characterised by high agricultural activity (pastoral, dairy and cropping).

Only five serotypes were significantly associated with rural or urban cases (Table 17). This increased to ten serotypes when cases were stratified by age and sex, though for six of these there were only one or two associations with a rurality/age/sex group. *S.* Brandenburg, *S.* Typhimurium DT135 and *S.* Typhimurium DT101 were associated with rural males (children and adults) but were not associated with cases from urban areas. *S.* Typhimurium DT160 was not associated with cases from rural areas but was associated with male children and female adults from urban areas.

Only 373 (3.2%) of the salmonellosis cases reported contact with confirmed cases. Significantly more females (54%) were infected by person-to-person transmission. Usually this is explained by mothers attending to sick children but this difference was maintained (56% female) in the 16 years or younger age group. *S.* Typhimurium DT9, *S.* Typhimurium DT12a and *S.* Saintpaul had the greatest association with person-to-person transmission in females.

3.6.2.1 Association with risk factors

With the exception of overseas travel, there were few significant associations between serotypes and each of the risk factors (Tables 20-22). Following is some general commentary for each risk factor, but we have separated out some specific serotypes for further discussion below.

A high number of serotypes were significantly associated with cases that had travelled overseas during their incubation period. Serotypes with the highest ORs tended to be those that caused lower numbers of cases over the study period (e.g. *S.* Newport, *S.* Enteritidis 6a and *Salmonella* sp. 4,5,12:d:-). There were 12 serotypes that also had elevated ORs for the risk factor contact with recreational water, particularly adult cases (e.g. *S.* Enteritidis 1 and 1b, *S.* Hadar and *S.* Stanley). An analysis of cases that had been exposed to both risk factors might separate serotypes more likely to be acquired from recreational water overseas from those more likely to be acquired from New Zealand recreational waters.

There were 12 serotypes that were significantly associated with the risk factor consumption of food from a premise in one or more age/sex groups (five with an OR>1). Only *S.* Brandenburg showed any notable pattern, being negatively associated for all sex/age groups except female children (OR also reduced but not significantly). The lack of significant associations when referenced to *S.* Typhimurium DT160 implies that commercial food is a potential vehicle for a large variety of serotypes, which appears logical given the variety of foods consumed by New Zealanders.

Seven serotypes were positively associated with the risk factor consumption of untreated drinking water in one or more age/sex groups. Of these, *S.* Saintpaul, *S.* Typhimurium DT23, *S.* Brandenburg and *S.* Typhimurium DT9 were also positively associated with equivalent age/sex strata who reported contact with farm animals (mostly adult cases). People living in rural environments are more likely to consume water from private (and possibly untreated) supplies, so it is difficult to separate this potential *Salmonella* source from other rural risk factors.

The risk factor contact with sick animals highlights *S.* Brandenburg and *S.* Typhimurium DT9 as key serotypes, which suggests transmission of these serotypes from sick farm animals to farm workers or farm residents.

The ORs for contact with human faeces were fairly even, confirming that this is a risk factor for all salmonellosis.

3.6.2.2 S. Typhimurium DT160

This serotype was significantly associated with male infants and children and female adults. It was also significantly associated with cases living in urban areas, though there was little difference between the proportions of urban and rural cases. Given the large number of cases, if there were strong patterns in terms of exposure by age, gender or rurality, these would have been detected in the analyses. The lack of patterns suggests that this serotype is well spread through the New Zealand environment and among the New Zealand population.

Further evidence of the widespread nature of this serotype is its isolation from samples from birds, a variety of domestic and farm animals, food and the environment. Forty percent of the 92 avian serotypes isolated by the ERL between 2005 and 2009 were *S.* Typhimurium DT160, followed by 29% of the equine serotypes (n=115) and 28% of the feline serotypes (n=90). Only 5% (83/1,634) of the combined poultry-related serotypes (neckflaps, environmental samples, feed and miscellaneous poultry including product) were *S.* Typhimurium DT160. However, of all 247 *S.* Typhimurium DT160 isolates from 2005-2009, 34% were poultry-related (15% from poultry feed, 14% from poultry environmental samples and 5% from the poultry product group). The next highest proportions were avian (15%), bovine (15%) and equine (13%).

Because *S.* Typhimurium DT160 was used as the reference in case-case analyses, its association with risk factors can only be inferred when reflected against the other serotypes with significant results. This serotype is less likely than most others to infect people who have travelled overseas during the incubation period, which infers that the source of *S.* Typhimurium DT160 is domestic. There are not enough significant results for the other risk factors to draw further conclusions on the aetiology of *S.* Typhimurium DT160.

A case-control study of *S.* Typhimurium DT160 identified contact with people with diarrhoea, handling of dead wild birds and consumption of fast food as the primary, albeit wide-ranging, risk factors (Thornley *et al*., 2003). The 1999 emergence of *S.* Typhimurium DT160 in humans corresponded with an outbreak of this serotype in wild birds (mainly sparrows). Interestingly, the total notifications of this serotype between 2000 and 2009 show a peak in November (Figure 2), which differs from the other serotypes and possibly reflects a surge in the avian population as chicks leave their nests. The case control study did not investigate human exposure to urban environments contaminated by wild bird faeces such as parks and play areas, and the authors acknowledged that they may have underestimated the avian contribution to human illness. It has been reported that sparrows infected with *S.* Typhimurium DT160 can excrete the pathogen for 10 days after infection (Connolly *et al*., 2006).

3.6.2.3 S. Typhimurium DT1

This serotype is significantly associated with male children, and male adults from rural areas. Despite the high number of cases in New Zealand there are no strong indications of its source, though male adults are more likely to contract this serotype and have contact with farm animals, sick animals or contact with recreational water compared with *S.* Typhimurium DT160. These results suggest that rural environments are important for this serotype. Most isolates of *S.* Typhimurium DT1 are from bovine samples, though the serotype has been isolated from a variety of other sources.

3.6.2.4 S. Brandenburg

The aetiology of *S.* Brandenburg is well known and the serotype analyses support this. This serotype was first diagnosed in an aborted ewe in Canterbury in 1996, and quickly spread through South Island livestock populations, including sheep, cattle, deer, pigs, and horses (Clark *et al*., 2004). The outbreak and epidemic pattern observed in sheep corresponded with increased *S.* Brandenburg notifications in humans, and human infection was significantly associated with occupational contact with sheep or contact with a household member who had occupational contact with sheep (Baker *et al*., 2007).

In this analysis, *S.* Brandenburg was significantly associated with male children and adults from rural areas. This serotype caused the highest salmonellosis rates of any serotype in Otago and South Canterbury. Notifications peaked in September which corresponds with the birthing of livestock. *S.* Brandenburg was relatively unconnected with consumption of food from a food premise, but had strong associations with the rural risk factors of consuming untreated drinking water and contact with farm or sick animals.

3.6.2.5 S. Infantis

S. Infantis was significantly associated with adult males. Interestingly, this serotype was significantly associated with urban cases, yet when age/sex stratification was applied the serotype had a more significant association with rural adult males ($p<0.01$) than with urban adult males ($p<0.05$). The serotype was also associated with male children from urban areas, but female children from rural areas. The highest rates of this serotype were in Whanganui and Otago.

This serotype had very few significant associations with risk factors. The serotype was more likely than *S.* Typhimurium DT160 to be associated with adult females who had travelled overseas, but was less likely to be associated with untreated drinking water for the same demographic. These inconclusive results raise questions on what the transmission pathways might be for this serotype, given its relatively recent emergence. Most of the non-human isolates have been from poultry-related samples and animal feed.

3.6.2.6 S. Saintpaul

This serotype was associated with cases living in rural environments, particularly male children, but was also associated with female adults from urban areas. The highest rates were in the largely rural areas of South Canterbury, Otago and Southland. Further evidence of this serotype's 'rurality' is the positive associations with consumption of untreated drinking water and farm animals when compared with *S.* Typhimurium DT160. However, *S.* Saintpaul is also positively associated with recreational water, overseas travel and person-to-person contact, so its source may be more widespread than just rural areas. The highest number of *S.* Saintpaul non-

human isolates were from reptiles, though it has also been isolated from farm and domestic animals. Interestingly notifications of this serotype peak in January, but given the lack of information on the source of this serotype we can draw no meaning from this.

3.6.2.7 S. Typhimurium DT9

There is some suggestion that this serotype is also associated with rural cases. The highest rates are in South Canterbury, Otago and Southland, and there are associations with consumption of untreated drinking water, contact with farm animals and contact with sick animals (particularly for adults). Most non-human isolates are from cattle and sheep. However, *S.* Typhimurium DT9 is also linked person-to-person transmission in female children and overseas travel (particularly females), neither of which are necessarily connected to rural environments.

3.6.3 Attribution to food

It is not possible to attribute salmonellosis to specific foods using the notification data. There were no sporadic case reports with a food or drink confirmed as the source of infection by laboratory testing. The sample of notifications with a recorded probable food is small at 208 (2.5%). These notifications also have risk factors associated with other foods, farm animals or pets, untreated water supplies from bore/wells tanks and other potential risk factors such as person-to-person transmission.

It is not possible to attribute serotypes to foods from these data. Salmonellosis occurring sporadically over the last ten years was associated with various food groups, with various meats reported most often. Twenty-seven percent of cases reported chicken. Meats, fish and processed meats were also frequently reported. Lamb and porcine meats were less likely to be reported as the probable cause of salmonellosis.

Chicken was often incriminated as a potential source but it is noted that 45% of chicken consumed was deep fried. Most of the larger food chains have strict quality control around cooking temperatures and times and while cross-contamination is a possibility, it is more likely this 45% reflects reporter bias by PHOs and/or recall bias on the part of the subject. Additionally, chicken is usually served with salad or vegetables but these foods were listed as possible risk factors in only 4% of cases. Eggs however seem to have a "good" reputation by public perception in New Zealand and in 100% of cases where eggs were recorded, these were reported as being consumed with other foods and were not raised as the principal risk food. The public perception of chicken does not appear to have extended to beef yet beef rates quite highly as a recorded food. Foods containing beef were possibly involved in half of the cases where shared food resulted in others becoming unwell (6/11 cases).

4 OUTBREAK ANALYSIS

The analysis in this section is an update and extension of an earlier report which analysed data from outbreaks that were reported from 1997 – 2006 (King and Lake, 2007). The 2007 report was reviewed as part of an overview of salmonellosis aetiology in New Zealand (Wilson and Baker, 2009). That overview suggested some additional analyses, and extended the scope by adding the outbreaks from 2007 which had become available. The analysis of the 2007 outbreaks was described as consistent with the conclusion that most outbreaks of salmonellosis were foodborne.

The literature section from the earlier report has been updated, as follows.

4.1 Literature Review: Attribution of Salmonellosis Using Outbreak Data

The use of outbreak data for attribution is often complicated by the identification of a complex or mixed food as the vehicle, where a number of food components have the potential to be the specific source of contamination (Pires *et al*., 2009). The US Centers for Disease Control (CDC) have published a food categorisation system for use with outbreak data, as well as a method for dealing with attribution to complex foods (Painter *et al*., 2009). Essentially outbreak illnesses attributed to complex foods are partitioned to each commodity in that food according to the proportion of illnesses attributed to each of those commodities in outbreaks caused by simple foods.

An alternative food classification scheme has been published for an analysis of Canadian outbreak data (Ravel *et al*., 2009). This system had three levels of food categories, which were aggregated into classifications used for analysis. This was a less detailed system; for instance multi-ingredient foods were only classified as "cooked" or "other".

4.1.1 Attribution studies

A number of international agencies have utilised outbreak data for source attribution of salmonellosis. Published reports up to 2006 were summarised in the 2007 report. These studies were from the USA, England and Wales, Australia, Sweden and the Netherlands. A common feature was that a high proportion of salmonellosis outbreaks were attributed to poultry and eggs. *S.* Enteritidis (particularly phage type 4) was strongly associated with eggs in several countries. *S.* Enteritidis PT4 is not endemic in eggs (or other foods) in New Zealand and the serotype of more importance is *S.* Typhimurium (Lake *et al*., 2004).

Since the 2007 report, three studies have been published which (in part) examined the attribution of salmonellosis using outbreak data.

A dataset of outbreaks from Canada has been analysed, including 6,908 foodborne outbreaks from 1976 to 2005 (Ravel *et al*., 2009). Both the agent and food were identified as confirmed in only 158 (2.29%) of these. Considering only the most recent data (1996 – 2005), and including all outbreaks where a pathogen and a vehicle were identified (whatever the level of evidence) there were 76 outbreaks caused by *Salmonella.* Of these, 22 (28.9%) were attributed to produce, 11 (14.5%) to meat: poultry, 11 (14.5%) to meat: other, 6 (7.9%) to multi-ingredient foods: cooked, and 4 (5.3%) each to multi-ingredient foods: other, and eggs.

The Canadian analysis has been extended to an international perspective (Greig and Ravel, 2009). Foodborne outbreaks from the USA, European Union, Australia and New Zealand,

Canada, and "other countries" were collated. The exact source of the New Zealand data is not given, although both the scientific literature and government reports were canvassed. Overall 4093 outbreaks were collated, mostly from government reports (86.1%), and mostly from the USA. A total of 246 outbreaks from Australia and New Zealand were identified.

Of the 4093 outbreaks, 46.9% were caused by *Salmonella*, and 24.1% by *S*. Enteritidis (none of these were from Australia or New Zealand). Of the 113 *S*. Typhimurium outbreaks identified from Australia-New Zealand between 1996 and 2005, 31 were attributed to eggs, followed by multi-ingredient foods (17), bakery items (14), chicken (14), and seafood (8). These foods were the most common for *S*. Typhimurium outbreaks across all countries, except that dairy food, beef pork, and produce were also identified in approximately 10% of total outbreaks in regions outside Australia-New Zealand.

A doctoral thesis has examined source attribution using a number of approaches, with a focus on campylobacteriosis and salmonellosis (Pires, 2009). European data from 2005 and 2006 were used to attribute outbreak associated salmonellosis cases to specific sources. The food categorisation system was similar to that used by CDC with recipes used to attribute complex foods on the basis of major ingredients (Painter *et al*., 2009).

The largest category was "unknown" (42% of cases, 55% of outbreaks). Of the identified sources, the most common were "eggs" (32% of cases, 26% of outbreaks), and "meat and poultry" (11% of cases, 9% of outbreaks).

The US Center for Science in the Public Interest (CSPI) combines outbreak data from the CDC with scientific articles, federal government publications, state health department postings, and newspaper reports verified by public health officials. The most recent report is for outbreaks that occurred from 1998 – 2007 (Smith De Waal *et al*., 2009). Non-CDC data makes up about 2% of the database (for outbreaks from 1998 – 2007), and waterborne outbreaks or outbreaks with no identifiable aetiology or food vehicle are excluded. For the years 1998 to 2007 there were 4,638 foodborne outbreaks (117,136 cases) in the CSPI database. *Salmonella* was the pathogen identified in 18% of the outbreaks. Outbreaks of *Salmonella* were most often associated with multi-ingredient (non-meat) foods, produce (sprouts, tomato, melon, greens-based salads), eggs/egg dishes (*S*. Enteritidis), dairy, breads and bakery products (e.g. filled rolls), beverages, poultry/poultry dishes, and beef/beef dishes.

In late 2008 – early 2009 a major outbreak in the US of salmonellosis was linked to peanut butter and peanut butter containing products (Medus *et al*., 2009). The outbreak involved over 500 cases in 43 states. The contamination with *S*. Typhimurium was traced to a single plant, and highlighted the complexity of an ingredient based outbreak, where that ingredient (peanut paste) had been used in a wide variety of foods (e.g. cookies, crackers, cereal, candy, ice cream, pet treats).

Another example of an ingredient based outbreak appears to be currently occurring in the US. In early 2010 a major outbreak of infection with S. Montevideo has been investigated (238 cases as of February 23). Preliminary reports have linked infection with consumption of salami, and the source may be black pepper used as an ingredient.

Both these US outbreaks illustrate the difficulty of attributing sources where a multi-component food is the vehicle, and that attribution at the point of consumption may not be the most useful point in the food chain.

In Australia in 2006 and 2007, there were a 38 outbreaks of infection with *S*. Typhimurium reported that were linked with eggs (OzFoodNet Working Group, 2007, 2008). *S*. Enteritidis is not endemic in Australian egg layer flocks. *S*. Typhimurium DT 9, 197, U302, 135a, and 44 were the specific serotypes identified in outbreaks associated with eggs in 2007. An investigation in Queensland into five outbreaks of S. Typhimurium DT 197 identified the source as a single egg farm, and was followed by a prosecution of the owner for selling cracked and dirty eggs to a retailer (OzFoodNet Working Group, 2008).

In the previous report (King and Lake, 2007) the importance of infected food handlers as a source was identified. A series of papers in the Journal of Food Protection has reviewed the data on outbreaks where food workers were implicated in the spread of foodborne disease (Greig *et al*., 2007). Of the bacterial outbreaks of this type identified, most (151/280) were attributed to *Salmonella*. Another paper in the series noted that *Salmonella* continues to be shed in faeces for long periods (up to 100 days) after illness (Todd *et al*., 2007).

4.2 Method

All salmonellosis outbreaks from 2000 to 2009 were extracted from the outbreak module of EpiSurv on 21 January 2010. Supplementary information was gathered from the outbreak-associated case report forms (identifiable either from the outbreak field in the case report form or from case numbers included in the outbreak record).

This section refers to field codes in the outbreak report form. A copy of the outbreak report, with codes, is included in Appendix 7.

The outbreak records were reviewed and the following data cleaning and augmentation conducted:

- Eighteen outbreaks caused by *Salmonella* Typhi or *Salmonella* Paratyphi were removed;
- A further two outbreaks were removed. One record that had initially been treated as an outbreak but on further investigation by the PHO did not meet the definition of an outbreak (this information was found in the comments field), and a second outbreak was coded as salmonellosis but the causative organism was norovirus (discovered during discussion with the PHO);
- Five outbreaks were added. These did not appear in the initial outbreak extract due to errors in filling out the fields in the outbreak report.[8] They were identified through the review of the individual case report forms;
- Only 30% of the outbreaks in the raw outbreak extract specified a *Salmonella* serotype, and only a few also specified a phage type. The percentage of outbreaks with an identified serotype was increased to 91% by examining individual case report forms linked to each outbreak and retrieving serotype information from those;
- The onset date of symptoms for the index case in each outbreak (either reported in the 'FirstDate' field, or identified from linked individual case report forms) was assigned as the date for the outbreak. This differs from King and Lake (2007) where analyses were based on the reporting date, and resulted in the reassignment of two outbreaks from the dataset which were reported in 2000 but began in 1999;

[8] Errors included only putting the serotype in the 'PathogenName' field without *Salmonella*, specifying *Salmonella* in the 'OthrIllspec' field rather than the 'PathogenName' field, and selecting an unknown illness ('Gastro') when the implicated pathogen was *Salmonella*.

- The free text fields of each outbreak record (primarily comments ('OthComm'), description of the exposure event ('DesExEvent') and source ('SourVeh')) were examined to provide additional information relevant to serotype, setting, implicated source and mode of transmission.
- Records from ESR's laboratory testing of food samples submitted by PHUs were examined for any positive *Salmonella* results from 2000–2009. These were linked back to outbreak records to ensure any laboratory-confirmed foods were captured;
- Separate outbreak reports written by ESR or PHUs were retrieved where readily available (e.g. from the New Zealand Public Health Surveillance reports) and examined for any supplementary information. Attempts were made to obtain reports for 14 outbreaks where there were more than ten cases but very little information in the EpiSurv record; unfortunately the reports were not available for most of these;

There are 12 PHUs in New Zealand who provide services for the 21 DHBs. The PHUs report outbreaks by health district rather than by DHB. There are 24 health districts. The outbreaks were analysed for geographical distribution based on the health districts. The relationship between PHUs, health districts and DHBs has been included in Appendix 8 for reference.

Additional methods are described alongside the relevant results in Section 4.3 and Section 4.4.

4.3 Results: Summary of outbreaks and cases

This analysis only considers non-typhoid salmonellosis outbreaks and excludes outbreaks from *Salmonella* Typhi and *Salmonella* Paratyphi. Unless specified, the use of '*Salmonella*' or '*Salmonella* spp.' in this section should be interpreted as non-typhoid *Salmonella* only.

Where the word "cases" is used, unless otherwise specified it refers to the total of confirmed and probable cases.

4.3.1 Number of outbreaks and cases

In the final dataset there were 204 salmonellosis outbreaks reported between 2000 and 2009 (Table 30). Between 2000 and 2006 there were 169 outbreaks, which is less than the 182 outbreaks analysed by King and Lake (2007) for the same period. The number of outbreaks in the final dataset is also less than the 209 outbreaks reported in ESR's annual outbreak summaries for the years 2000 to 2009.[9] These differences are due to the data cleaning and augmentation described in Section 4.2; the removal of outbreaks caused by *S.* Typhi and *S.* Paratyphi accounted for most of the difference between the 2007 report and this report.

[9] ESR produces an annual summary of outbreaks for the Ministry of Health (http://www.surv.esr.cri.nz/surveillance/annual_outbreak.php).

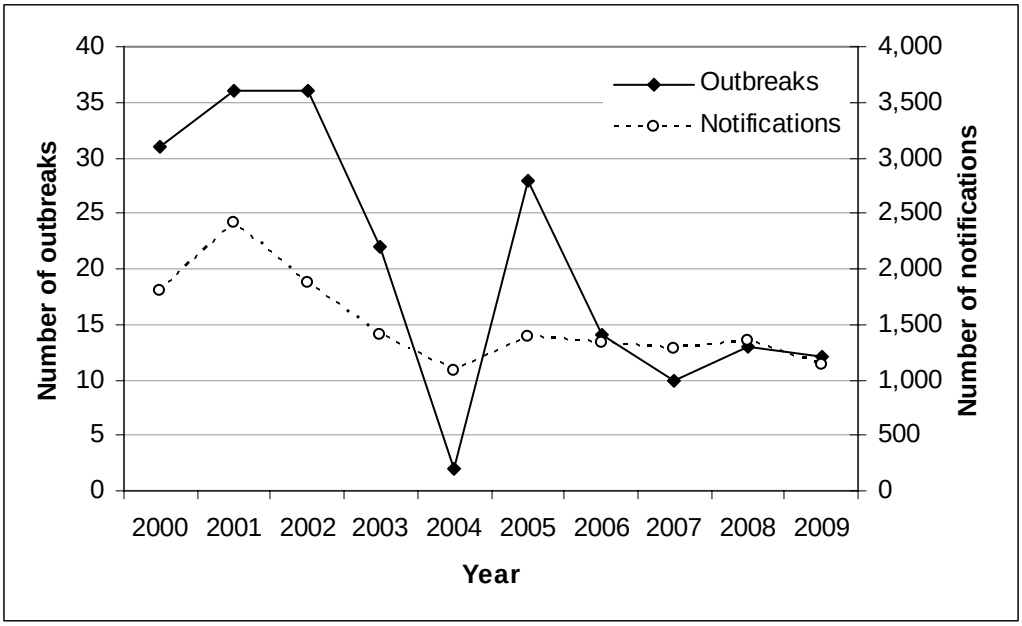
Table 30: The number of salmonellosis outbreaks for each year between 2000 and 2009

Year	No. outbreaks	% all salmonellosis outbreaks 2000-09
2000	31	15.2
2001	36	17.6
2002	36	17.6
2003	22	10.8
2004	2	1.0
2005	28	13.7
2006	14	6.9
2007	10	4.9
2008	13	6.4
2009	12	5.9
All years	**204**	**100**

The 2004 Annual Summary of Outbreaks in New Zealand (ESR, 2005) reports six salmonellosis outbreaks; five from *Salmonella* spp. and one from *Salmonella* paratyphi. Of the five *Salmonella* spp. outbreaks, two were caused by *Salmonella* Typhi and one was later found to be caused by norovirus. This leaves only two outbreaks relevant to this report.

The year 2004 is anomalous, but otherwise the number of reported outbreaks in 2006–2009 is approximately half the number reported in 2000–2005. The number of salmonellosis notifications per year has also declined, with numbers in 2000–2002 being higher than for 2003–2009. These data are presented in Figure 3.

Figure 3: Number of salmonellosis outbreaks between 2000 and 2009 considered in this report, compared to the number of salmonellosis notifications



Notes to graph:

1. *Source of notification data: ESR's Annual NZ Notifiable Disease Reports, http://www.surv.esr.cri.nz/surveillance/annual_surveillance.php.*
2. *A small proportion of the notification data is cases associated with outbreaks (see Section 4.3.2).*

In four of the outbreaks, a non-*Salmonella* pathogen was also isolated from clinical samples:

- In 2002, *S.* Typhimurium DT101 and *Campylobacter* were isolated from the clinical samples from two people involved in a household outbreak. It was suspected that one case became ill through contact with chickens or drinking contaminated water and the second became ill through person-to-person infection;
- In 2002, *S.* Typhimurium DT160 was isolated from clinical samples of 17 people associated with a cruise ship outbreak, and norovirus from the clinical samples of a further six people (the norovirus status of the *Salmonella*-positive samples was not reported). The suspected vehicle was club sandwiches with mayonnaise.
- In 2008 *S.* Derby was isolated from clinical samples from three people involved in a household outbreak. A fourth person involved in the outbreak was diagnosed with campylobacteriosis. The suspected sources of infection were a pet duck and person-to-person transmission.
- An outbreak on a farm in 2009 involved four cases and implicated the drinking water supply. Two of the cases had campylobacteriosis. *S.* Typhimurium RDNC Aug 09 was isolated from clinical samples of the other two cases, one of whom was also reported to have campylobacteriosis.

The six norovirus cases from the 2002 cruise ship outbreak, the *Campylobacter* case from the 2008 outbreak and the two *Campylobacter* cases from the 2009 outbreak have been excluded from the analyses in this report.

There were 1,426 cases associated with the 204 outbreaks between 2000 and 2009 (Table 31). Confirmed cases are usually people who have submitted clinical samples that were found to be positive for *Salmonella*. Probable cases are usually people who have been exposed to the same conditions as confirmed cases and exhibit symptoms of salmonellosis (e.g. diarrhoea, vomiting) over a similar time period. Note that these figures differ to those presented in Table 4 as not all outbreak cases are reported in EpiSurv's sporadic notification dataset (see Section 4.3.2).

Table 31: Cases associated with 204 salmonellosis outbreaks between 2000 and 2009

Year	No. cases[1]			Cases per outbreak	Hospitalisations		No. who died
	Confirmed	Probable	Total		No.	%[2]	
2000	172	61	233	7.5	23	9.9	1
2001	134	81	215	6.0	15	7.0	0
2002	214	56	270	7.5	18	6.7	0
2003	76	43	119	5.4	6	5.0	0
2004	5	0	5	2.5	1	20.0	0
2005	110	34	144	5.1	4	2.8	0
2006	29	25	54	3.9	6	11.1	0
2007	172	13	185	18.5	13	7.0	1
2008	100	23	123	9.5	14	11.4	0
2009	70	8	78	6.5	13	16.7	0
All years	**1,082**	**344**	**1,426**	**7.0**	**113**	**7.9**	**2**

1. *Due to the data cleaning described in Section 4.2, the number of salmonellosis outbreaks and associated cases differs to that reported in ESR's annual outbreak summaries.*
2. *Percentage based on total cases.*

There was an average of seven cases per outbreak for the entire period. The two lowest number of cases per outbreak were in 2004 (2.5 cases per outbreak) when there were only two outbreaks, and in 2006 (3.9 cases per outbreak). In 2006 ten of the 14 outbreaks only involved two people. The highest number of cases per outbreak occurred in 2007 (18.5 cases per outbreak). Of the ten outbreaks during this year, one involved 85 people (46% of the cases reported).

On average, 8% of all cases were hospitalised (range 3-20%). The salmonellosis outbreak hospitalisation rates are similar to rates from outbreaks of Hepatitis A and shigellosis, but are higher than rates from outbreaks of norovirus infection, rotovirus infection, cryptosporidiosis and campylobacteriosis.[10] Hospitalisation rates for sporadic cases of salmonellosis have been between 12 and 14% since 2005, with the exception of 2009 where the hospitalisation rate rose to 18.7%.

Two deaths were recorded. The death in 2000 was part of a two-person *S.* Typhimurium 12a outbreak set in a residential care home. The death in 2007 was a 74-year-old woman, who was part of 30-person national *S.* Mbandaka outbreak. The sources of infection for these outbreaks were not confirmed.

There were 123 outbreaks that included a figure for the total number of people exposed to the same conditions as the confirmed and probable cases ('ExposeNo'). A total of 5,078 people were exposed, which is an average of 41 per outbreak. This number is skewed by two outbreaks which involved large numbers of potentially exposed people. One outbreak was set in a prison, where approximately 1,000 inmates were potentially exposed, and the other was set on a cruise ship carrying approximately 2,000 people. The number of people exposed provides some indication of the potential for unreported illness as not all cases will seek medical attention, and PHOs cannot always locate or identify all of the cases associated with an outbreak.

Table 32 presents the salmonellosis outbreaks as a percentage of total enteric outbreaks for the years 2005-2009, and the number of outbreaks expressed per 100,000 population. Table 33 presents the same information using the number of outbreak cases. Different analytical methods for reporting outbreaks were used prior to 2005 (ESR, 2009a) so data from earlier years are not comparable and have been omitted. These tables provide comparisons with outbreaks caused by *Campylobacter*, a pathogen of importance to New Zealand public health (NZFSA, 2008), and by norovirus which is the causative organism of the largest number of outbreaks (and cases) in New Zealand each year. The increases in these parameters for norovirus after 2005 probably reflect improvements in detection methods.

[10] Compared with outbreak hospitalisation rates as reported in ESR's Annual Summary of Outbreaks http://www.surv.esr.cri.nz/surveillance/annual_outbreak.php

Table 32: Outbreaks of salmonellosis, campylobacteriosis and norovirus infection as a proportion of total enteric outbreaks in New Zealand and relative to the New Zealand population, 2005-2009[1]

Year	Outbreaks as a percentage of total enteric outbreaks[2]			Outbreaks per 100,000 population[3]		
	Salmonellosis	Campylobac-teriosis	Norovirus infection	Salmonellosis	Campylobac-teriosis	Norovirus infection
2005	12.6	21.1	27.4	0.7	1.1	1.5
2006	4.4	14.8	49.1	0.3	1.1	3.7
2007	3.0	6.1	62.8	0.2	0.5	4.9
2008	4.7	5.8	55.1	0.3	0.4	3.6
2009	3.0	3.0	66.7	0.3	0.3	6.3
All years	**5.0**	**9.2**	**54.5**	**0.4**	**0.7**	**4.0**

1. *Data on outbreaks of campylobacteriosis and norovirus infection were from ESR's Annual Summary of Outbreaks in New Zealand (http://www.surv.esr.cri.nz). New Zealand population data were Statistics New Zealand's national population estimates at 30 June (http://www.stats.govt.nz).*
2. *Total enteric outbreaks comprises outbreaks caused by Bacillus cereus, Campylobacter spp., Clostridium perfringens, Cryptosporidium spp., Giardia spp., Hepatitis A, Norovirus, Rotavirus, Salmonella Typhi/Paratyphi, Shigella spp., Staphylococcus aureus, Vibrio parahaemolyticus, VTEC/STEC and Yersinia spp., plus the salmonellosis outbreaks from the cleaned dataset used for this study.*
3. *For each year, the value is calculated based on the population for that year. The value for all years is based on average annual population 2005-2009.*

Table 33: Cases associated with outbreaks of salmonellosis, campylobacteriosis and norovirus infection as a proportion of total enteric outbreak cases in New Zealand and relative to the New Zealand population, 2005-2009[1]

Year	Cases as a percentage of total enteric outbreak cases			Outbreak cases per 100,000 population		
	Salmonella spp.	*Campylobacter spp.*	Norovirus	*Salmonella spp.*	*Campylobacter spp.*	Norovirus
2005	7.4	13.1	60.1	3.5	6.1	28.0
2006	1.1	4.7	83.6	1.3	5.3	94.3
2007	2.8	0.8	88.8	4.4	1.3	139.6
2008	2.6	2.3	81.7	2.9	2.6	91.8
2009	1.0	0.8	88.7	1.8	1.5	164.9
All years	**2.2**	**2.7**	**84.3**	**2.8**	**3.3**	**104.3**

1. *See footnotes for Table 32.*

Since 2006, salmonellosis outbreaks accounted for less than 5% of the annual number of notified enteric outbreaks and less than 3% of the annual number of notified enteric outbreak cases. Table 32 and Table 33 indicate that outbreaks of salmonellosis are less important in terms of the total incidence of enteric disease in New Zealand than outbreaks caused by norovirus. Other important causative organisms of New Zealand outbreaks are *Cryptosporidium* and *Giardia*. Together, norovirus, *Campylobacter*, *Cryptosporidium* and *Giardia* were the causative

organisms of 81% of the outbreaks (91% of outbreak cases) between 2005 and 2009.[11] However, *Cryptosporidium* and *Giardia* are the causative agents of very few foodborne outbreaks.

The proportion of outbreaks of campylobacteriosis amongst all enteric outbreaks is unusually high by international standards (Lake *et al*., 2007b).

4.3.2 Outbreak cases as a proportion of all salmonellosis notifications

To understand the weight that can be given to findings from analyses of outbreaks, it is important to determine the contribution outbreaks make to the incidence of disease relative to sporadic illness. A proportion of the individual salmonellosis notifications extracted from EpiSurv will be cases linked to the outbreaks being analysed in this report. Additionally, not all of the cases associated with an outbreak will be individually notified to EpiSurv. Once PHOs identify an outbreak they may cease to report individual cases, and instead capture the full number of cases in the outbreak report.

Outbreak records and individual notifications were reviewed to identify the overlap between outbreak and sporadic cases of salmonellosis. Table 34 presents the number of salmonellosis notifications and the proportion of these attributable to salmonellosis outbreaks. Note that the total notifications (15,037) differs from the set of 15,040 notifications analysed in Sections 2 and 3. This is due to the extensive data cleaning that was made possible because of the small dataset (204 outbreaks). For the same reason, the notified outbreak cases in Table 34 (831) also differ from the 927 outbreak cases removed from analyses in Section 3. These numerical differences make a negligible difference to the calculations in Table 34 (equation 1 would produce 9.7% and equation 2 would produce 6.2%) and do not influence the overall findings.

[11] Data compiled from ESR's Annual Summary of Outbreaks in New Zealand (http://www.surv.esr.cri.nz).

Table 34: Percentage of New Zealand's total reported salmonellosis cases that are associated with outbreaks, based on notified cases and all known cases

Year	A	B	C	% of cases associated with outbreaks	
	No. salmonellosis notifications[1]	No. notified outbreak cases	No. outbreak-only cases	Equation 1	Equation 2
2000	1,802	139	94	12.3	7.7
2001	2,417	80	135	8.4	3.3
2002	1,870	147	123	13.5	7.9
2003	1,401	50	69	8.1	3.6
2004	1,080	5	0	0.5	0.5
2005	1,383	91	53	10.0	6.6
2006	1,335	28	26	4.0	2.1
2007	1,274	152	33	14.2	11.9
2008	1,346	92	31	8.9	6.8
2009	1,129	47	31	6.7	4.2
All years	**15,037**	**831**	**595**	**9.1**	**5.5**

1. Notification data are from ESR's Annual Surveillance Reports (http://www.surv.esr.cri.nz).

Key to table:

A = the number of notified cases (cases with EpiSurv numbers) with non-typhoid *Salmonella* ('Salmonellosis'). A proportion of these make up B, below.

B = the number of notified cases (cases with EpiSurv numbers) with non-typhoid *Salmonella* ('Salmonellosis') that are associated with the salmonellosis outbreaks being analysed in this report.

C = "outbreak-only" cases, i.e. the number of cases associated with the salmonellosis outbreaks that were not notified as separate cases and have no EpiSurv number. This is calculated by subtracting B (above) from the total number of confirmed and probable cases.

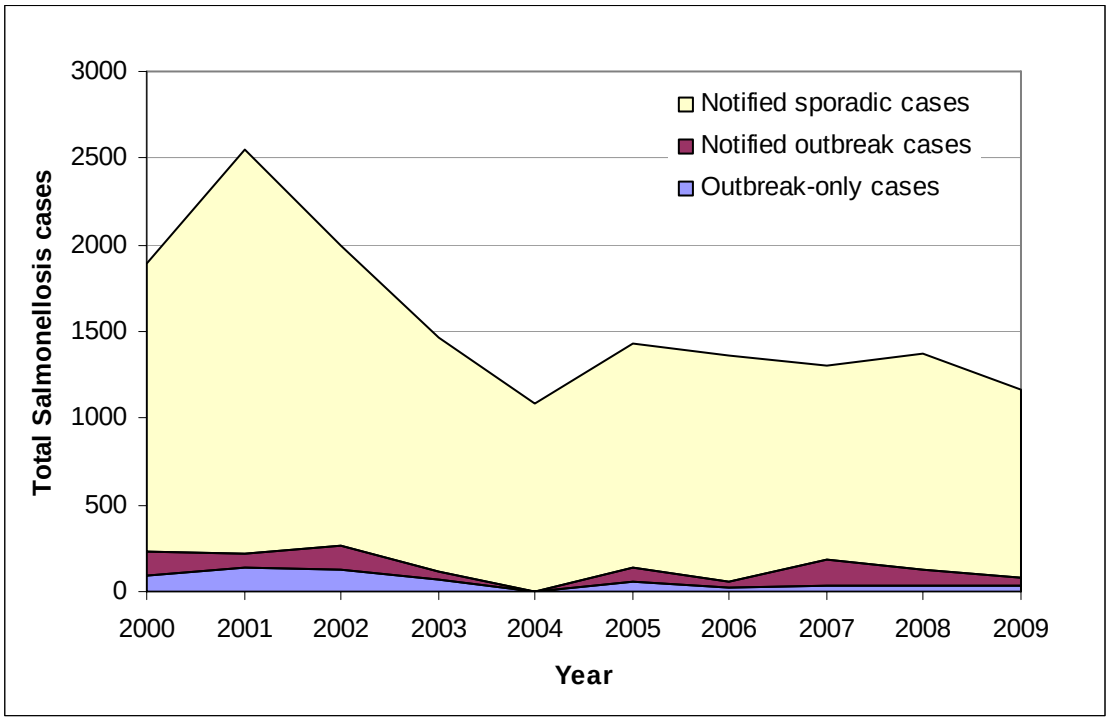
Equation 1 = (B+C)/(A+C)*100 (calculates the proportion of all known cases, notified and outbreak-only, that are associated with the outbreaks)

Equation 2 = B/A*100 (calculates the proportion of notified cases that are associated with the outbreaks)

Of the cases identified in outbreak reports (B+C), 58% are notified as individual cases. The 595 outbreak-only cases add an extra 3.6% to the total number of salmonellosis cases in the period 2000-2009.

Based on equation 2, outbreak cases make up between 0.5 and 11.9% of all notified cases, an average of 5.5% over the years 2000 to 2009. Equation 1 takes account of all known salmonellosis cases, including those that were not notified as separate sporadic cases (i.e. outbreak-only cases). Equation 1 provides an estimate of the contribution outbreaks make to the total salmonellosis incidence in New Zealand, ranging from 0.5 to 14.2% of cases, or an average of 9.1% across the years 2000 to 2009. These data are displayed in Figure 4.

Figure 4: Number of salmonellosis cases per year separated into those that are notified but not linked to outbreaks (sporadic cases), notified and linked to outbreaks, and reported as part of outbreak reports only



4.3.3 Overseas-acquired outbreaks

There were 14 outbreaks where the cases were reported as infected either while travelling overseas or on an airline travelling back to New Zealand, though the mode of transmission was not confirmed for any of these outbreaks. The overseas-acquired outbreaks represent 7% of all salmonellosis outbreaks between 2000 and 2009, and 1% of the outbreak-related cases (Table 35).

Overseas-acquired infections can introduce new strains of *Salmonella* into New Zealand and outbreaks associated with airlines have the potential for spreading infection to a number of regions. Of the 11 overseas-acquired outbreaks with known serotypes, the ERL had isolated all but two of these serotypes from human clinical samples prior to the date of the outbreaks, indicating they were already present in New Zealand.[12] Of the remaining two serotypes, *S.* Ferruch has not been isolated from any other New Zealand source except the one outbreak case, and *S.* Alachua has been isolated only twice from New Zealanders since the outbreak of this serotype. The ERL has not detected these serotypes in any non-human samples over this period.

These 14 overseas-acquired outbreaks will not be included in further analyses. This reduces the salmonellosis outbreak dataset to a total of 190 outbreaks.

[12] The Enteric Reference Laboratory reports *Salmonella* serotypes and phage types isolated from human and non-human samples. Records from 2000 to 2009 were examined for isolations of the overseas-acquired outbreaks (http://www.surv.esr.cri.nz/enteric_reference/enteric_reference.php). It should be noted that this information does not consider different strains within a serotype that may be identified through molecular typing methods.

Table 35: Summary of overseas-acquired salmonellosis outbreaks

Month, year	Country acquired	*Salmonella* serotype(s)	No. cases	Suspected source of infection
Oct. 2002	India	Alachua, Bareilly	2	Exposure to infected people
Dec. 2002	India	*Not available*	2	Unpasteurised milk
Jan. 2005	Australia	Typhimurium DT41	2	Chicken burger
Jul. 2005	Fiji	Typhimurium DT41	3	Exposure to infected people
Jul. 2005	Sri Lanka	(Not available)	2	Exposure to infected people
Oct. 2005	Rarotonga	(Not available)	2	None reported
Oct. 2005	India[1]	Mbandaka	3	Airline meal
Feb. 2006	Malaysia	Enteritidis PT1	2	None reported
Sep. 2006	Fiji	species 3,10:r:-	2	Exposure to infected people
Jun. 2008	USA[1]	Enteritidis PT8	2	Airline meal, exposure to infected people
Nov. 2008	Samoa[1]	Weltevreden	5	Exposure to infected people, water or food
Nov. 2008	China	Thompson	4	Exposure to infected people
Apr. 2009	Fiji	Ferruch	2	Poor hygiene, exposure to untreated recreational water
Oct. 2009	Australia[1]	Typhimurium DT12a variant 09	13	Exposure to infected people

1. May have been infected on the airline while travelling back to New Zealand.

4.3.4 Serotypes and phage types

The serotypes were identified for 172/190 outbreaks (91%). More than one *Salmonella* serotype was identified from clinical samples in five outbreaks:

- 2000: A five-person outbreak where three people were clinically positive for *Salmonella* Typhimurium DT9 and one for *Salmonella* Agona.
- 2002: An outbreak involving 77 people, of whom *Salmonella* Typhimurium DT1 was isolated from 57 clinical samples and *Salmonella* Typhimurium DT160 from 1 clinical sample.
- 2003: An outbreak involving 64 people. *Salmonella* Typhimurium DT8 variant was isolated from six clinical samples, *Salmonella* Typhimurium (phage type not known) from one clinical sample and *Salmonella* Infantis from one clinical sample.
- 2005: An outbreak involving 25 people. *Salmonella* Typhimurium DT9a was isolated from 21 clinical samples, *Salmonella* Enteritidis was isolated from one clinical sample and *Salmonella* Heidelberg was isolated from another clinical sample.
- 2009: A three-person outbreak with two *Salmonella* Typhimurium DT42 cases and one *Salmonella* Typhimurium DT160.

Further analysis of these multi-serotype outbreaks uses the serotype most frequently isolated in each outbreak.

There were over 30 *Salmonella* serotypes involved in the 172 outbreaks, involving 1,320 cases (see Appendix 9). *Salmonella* Typhimurium was the causative agent of 78% of these outbreaks (71% of cases), with the Typhimurium phage types 160, 135 and 1 together accounting for 53% of all outbreaks and 49% of all cases (Figure 5). Thus these three phage types dominate the aggregate picture for 2000-2009.

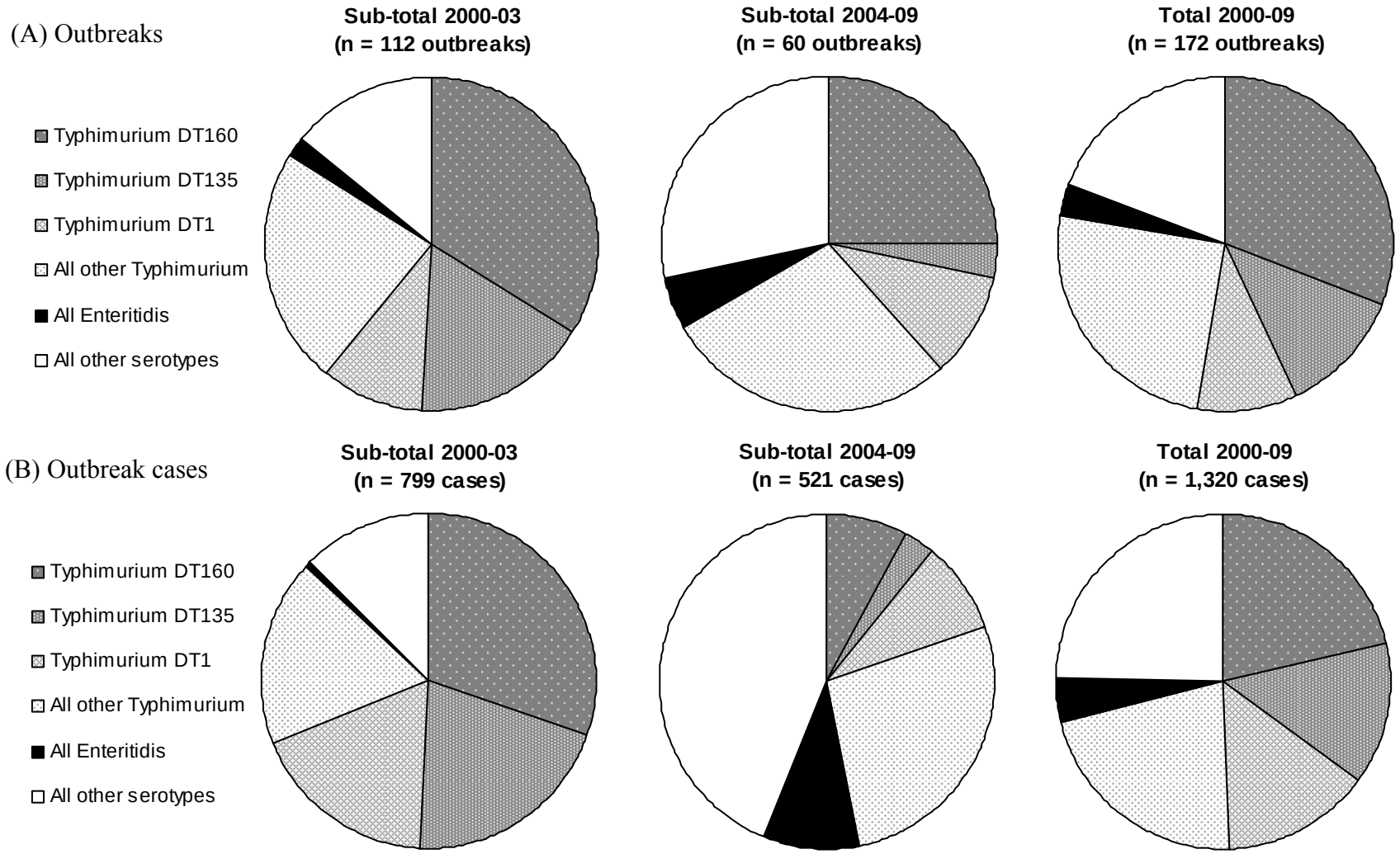
The tables in Appendix 9 provide subtotals for the periods 2000-2003 and 2004-2009. These time periods were chosen because three particular serotypes (*S*. Typhimurium DT160, *S*. Typhimurium DT135 and *S*. Brandenburg) dominated human salmonellosis in New Zealand during the earlier period but have declined in prevalence since 2004. The notifications over time for these serotypes can be viewed in Appendix 10.

Notifications of *S.* Typhimurium DT160 were first recorded in 1999 and rose to a peak of almost 800 cases in 2001. The emergence in humans corresponded with an outbreak of this serotype in wild birds (mainly sparrows). In a case-control study human infections were significantly associated with contact with people with diarrhoea, handling of dead wild birds and consumption of fast food (Thornley *et al*., 2003). Human notifications of *S.* Typhimurium DT160 have declined since 2001 but this phage type remains the single most frequently isolated type from salmonellosis cases in New Zealand (ESR, 2009b). The trends in outbreaks and outbreak cases since 2003 are largely a reflection of the changes in prevalence of *S.* Typhimurium DT160.

Notifications of *S.* Typhimurium DT135 reached a peak of 459 in 1999 but have since declined; only 20 cases were notified in 2009. This has been reflected in the outbreak data, with only two outbreaks caused by this serotype after 2003, but 17 between the years 2000 and 2003.

The aetiology of *S.* Brandenburg has been described in Section 3.6.2.4. Human notifications of *S.* Brandenburg were at their highest levels between 1998 and 2001, and have since declined to a low but steady state. There were two outbreaks caused by this serotype across the years 2000-2009, involving 23 cases.

Figure 5: Proportion of salmonellosis outbreaks (A) and outbreak cases (B) caused by different serotypes



The frequency of outbreaks associated with each serotype shows some similarities with frequencies observed in sporadic notification data (Table 36).

Table 36: Comparison between the number of salmonellosis outbreak cases (2000-2009) and the number of salmonellosis notifications (2000-2009)

Serotype	% outbreak cases (n=1,320)[1]	Rank[2]	% surveillance cases (n=11,554)[3]	Rank[4]
Typhimurium DT160	21.4	1	18.6	1
Typhimurium DT1	14.2	2	6.3	2
Typhimurium DT135	13.7	3	6.0	4
Chester	6.7	4	-	-
Typhimurium DT42	5.5	5	2.2	9
Typhimurium DT8 variant	4.8	6	-	-
Enteritidis PT9a	3.1	7	3.7	8
Infantis	3.0	8	4.5	6
Typhimurium DT156	2.7	9	4.9	5
Mbandaka	2.6	10	0.7	23
Thompson	2.4	11	0.8	20=
Montevideo	2.2	12	0.7	22

1. *2000-09 outbreak data: There were 172 salmonellosis outbreaks with an identified serotype, involving 1,320 cases. The percentages represent the proportion of cases caused by each serotype. Only serotypes causing 2% or more of the outbreak cases are shown.*
2. *The serotypes were ranked by the number of outbreak cases they represent.*
3. *Surveillance data from EpiSurv (2000-2009): Based on the serotype dataset analysed in Section 3 of this report (see also Appendix 2). The percentages represent the proportion of cases caused by each serotype. Hyphens (-) indicate an outbreak serotype that caused less than 50 cases during this time period.*
4. *The serotypes were ranked by the number of cases they represent. Only serotypes corresponding to the top 12 outbreak serotypes are shown.*

While *S.* Typhimurium DT160, DT135 and DT1 are important in terms of the total incidence of salmonellosis in New Zealand, a few other serotypes are also important given the large numbers of people they have affected through only one or two outbreaks. When comparing the ratio of cases per outbreak, the highest values are observed for *S.* Typhimurium DT8 variant, *S.* Chester and *S.* Typhimurium DT42 (Table 37). This result is due to these serotypes being responsible for some of the largest outbreaks of salmonellosis between 2000 and 2009 (Table 38).

Table 37: Serotypes causing an average of ten or more cases per outbreak over the years 2000 to 2009

Serotype and phage type	No. outbreaks	Cases/outbreak
Typhimurium DT8 variant	1	64
Chester	2	44
Typhimurium DT42	2	37
Mbandaka	1	34
Salmonella Group C 6,7:k:-	1	25
Typhimurium DT150	1	16
Typhimurium RDNC Aug 08	1	14
Saintpaul	2	13
Typhimurium DT1	16	12
Brandenburg	2	12
Enteritidis PT26	1	11
Enteritidis PT9a	4	10
All serotypes[1]	**172**	**8**

1. This is not the sum of the rows above, but values across all serotypes (Appendix 9).

Table 38: The eight largest outbreaks of salmonellosis between 2000 and 2009

Year	No. cases	Serotype	Location	Reported vehicle
2007	85	Chester	Multi-district	Infected food handler*
2002	77	Typhimurium DT1	Nelson	Unknown
2001	70	Typhimurium DT160	South Auckland	Potato salad*
2008	67	Typhimurium DT42	Multi-district	Flour*
2003	64	Typhimurium DT8 variant	South Auckland	Infected food handler*
2000	40	Typhimurium DT135	Wairarapa	Infected food handler*
2007	34	Mbandaka	Multi-district	Chicken, eggs
2000	30	Typhimurium DT135	Manawatu	Infected food handler*

** Confirmed by laboratory evidence. All others are suspected.*

4.3.5 Geographical distribution

There were 173 outbreaks (91%) that reported one or more health districts as the location of the outbreak. Eight of these outbreaks spanned two or more health districts (multi-district outbreaks) and involved 261 cases (Table 39).

Table 39: Outbreaks that involved more than one health district

Month, year	Health districts	No. cases
Jul. 2001	Manawatu, Hutt	2
Feb. 2002	North West Auckland, South Auckland	25
Aug. 2003	Central Auckland, South Auckland	4
Jan. 2005	North West Auckland, South Auckland, Central Auckland	25
Apr. 2005	North West Auckland, South Auckland, Central Auckland, Waikato	19
Oct. 2007	Tauranga, Waikato	85
Dec. 2007	South Auckland, Waikato, Rotorua, Taupo, Wellington, Nelson-Marlborough, Canterbury, South Canterbury, West Coast, Otago, Southland	34
Oct. 2008	Waikato, Rotorua, Taupo, Bay of Plenty, Taranaki, Hawke's Bay, Hutt, Nelson-Marlborough, West Coast, Canterbury, Otago, Southland.	67

Most of the single district outbreaks were located in the Auckland region, which includes the North West, Central and South Auckland health districts (Figure 6). Only two outbreaks were recorded for the Nelson region but these involved 102 people. These outbreaks were caused by *S.* Typhimurium DT1 and were thought to be related to a third outbreak in the Marlborough region involving a further 11 people. The source of these outbreaks was thought to be a contaminated food distributed in the community, but PHOs were unable to confirm this.

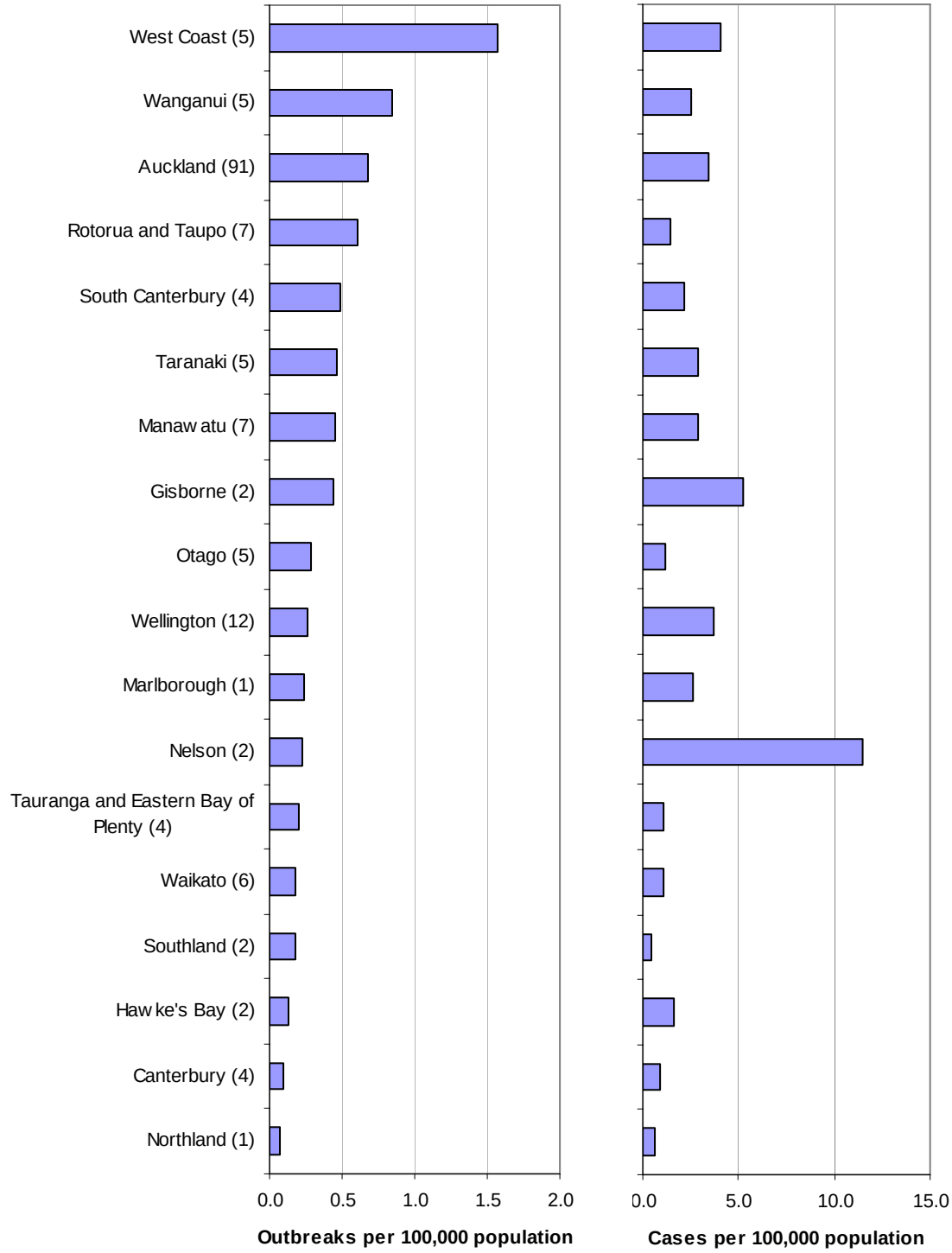
Figure 7 shows the number of outbreaks and outbreak cases by geographical region, normalised for population. The populations have been calculated from the populations of Territorial Authority areas. Appendix 8 shows the relationship between Territorial Authorities, health districts and PHUs. The highest outbreak rates were in the West Coast, Wanganui and Auckland regions, however Nelson, Gisborne and the West Coast had the highest case rates per head of population.

Figure 6: Total outbreaks and outbreak cases by geographical region (2000-2009)[1,2]

Notes to graphs:

1. *The geographical regions presented are the same as those used for the annual summary of outbreaks (http://www.surv.esr.cri.nz/surveillance/annual_outbreak.php). Most regions represent a health district, except: Auckland includes Northwest Auckland, Central Auckland and South Auckland health districts (as served by the Auckland Regional Public Health Service), Wellington includes Wellington, Hutt and Wairarapa health districts (as served by Regional Public Health) and Nelson and Marlborough are analysed separately.*
2. *Outbreaks associated with multiple health districts have not been included (see Table 39).*

Figure 7: Total outbreaks and outbreak cases by geographical region (2000-2009), per 100,000 population[1,2]



Notes to graphs:

1. *The geographical regions presented are the same as those used for the annual summary of outbreaks (http://www.surv.esr.cri.nz/surveillance/annual_outbreak.php). Most regions represent a health district, except: Auckland includes Northwest Auckland, Central Auckland and South Auckland health districts (as served by the Auckland Regional Public Health Service), Wellington includes Wellington, Hutt and Wairarapa health districts (as served by Regional Public Health) and Nelson and Marlborough are analysed separately.*
2. *Outbreaks associated with multiple health districts have not been included (see Table 39).*
3. *Numbers in parenthesis indicate the total number of outbreaks per region from 2000-2009.*
4. *Population data were sourced from Statistics New Zealand (www.stats.co.nz).*

4.3.6 Seasonality

All of the outbreaks and associated cases were grouped by season based on the month and year symptoms commenced for the index case, where:

- Summer: December, January and February
- Autumn: March, April and May
- Winter: June, July and August
- Spring: September, October and November.

The summer 2000 data includes one salmonellosis outbreak in December 1999 that involved two cases.

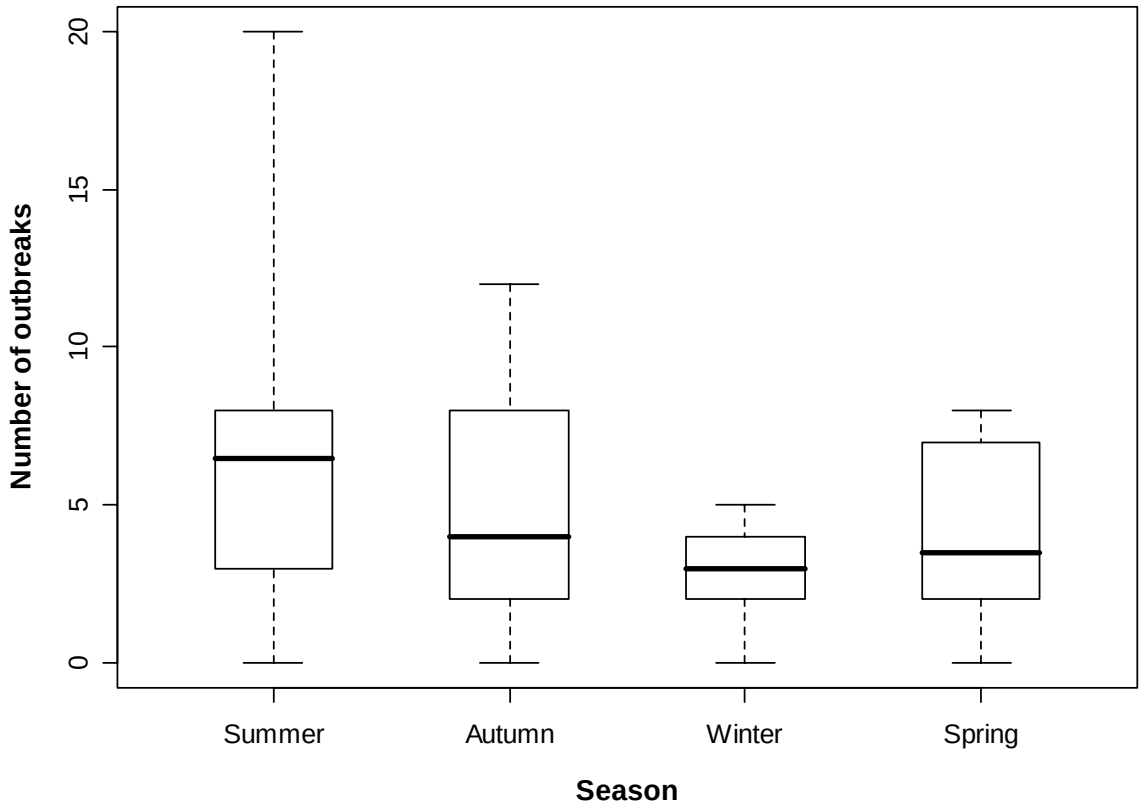
Table 40 shows the total number of outbreaks, outbreak cases and cases per outbreak, by season. While it is apparent that there are more outbreaks and cases in summer and less in winter, there is considerable year-to-year variability (Figure 8).

Using a Poisson distribution (mean 47.75 outbreaks per season, 95% CI 26.891-52.158), there are significantly more outbreaks in summer (71>52.158) and less in winter (29<26.891). However, these data are limited and influenced by outliers so should be interpreted with caution. Appendix 11 presents some analyses of the distribution of cases between seasons.

Table 40: Total number of outbreaks and cases per season, 2000-2009

Season	Months	No. outbreaks	No. cases	Cases/outbreak
Summer	Dec-Feb	71	624	8.8
Autumn	Mar-May	50	335	6.7
Winter	Jun-Aug	29	86	3.0
Spring	Sep-Nov	41	337	8.2

Figure 8: Box plot showing variability between years for each season



Notes to graph:

1. *Data: Box plot is based on the number of outbreaks per season, per year (i.e. Summer = No. outbreaks in summer 2000, summer 2001, summer 2002, etc.)*
2. *Box: Values between the 25th (lower) and 75th (upper) percentiles*
3. *Solid line in box: Median*
4. *Whiskers: Maximum and minimum values*

4.4 Results: Attribution to Food

4.4.1 Outbreak settings

At least one setting was reported for 175 (92%) of the outbreaks, with more than one setting reported for 28 of these. Where more than one setting was implicated, information in the outbreak report and associated case reports were reviewed to decide on the most likely setting of exposure or transmission ('primary setting').

The 15 outbreaks without a reported setting represented 116 (8%) of all outbreak cases.

The most commonly reported setting was the home (47%) (Table 41). Commercial food operator was the next most frequently reported setting (31%), with restaurants/cafés and takeaways being reported most often. In terms of cases, more are associated with commercial food operators (39%) than the home setting (30%). Outbreaks set in the home are usually confined to household members (46% of all outbreaks in the home only involved two people), whereas outbreaks set in commercial food operations can affect multiple households, and thus more people. Home-based outbreaks that are an exception to this are those where the source of the outbreak is distributed in the community. There were two outbreaks set in the home that involved large numbers of

people; one in 2007 (34 cases) which, through a case-control study, was thought to be from chicken or eggs and a second in 2008 (67 cases) that was caused by contaminated flour.

While community events represented 5% of the total outbreaks, 15% of outbreak cases were associated with these events. The mode of transmission for all of these events was foodborne, which illustrates the importance of safe food practices where large numbers of people are gathering.

Table 41: Number of outbreaks and outbreak cases for each primary setting

Outbreak setting	No. outbreaks	% outbreaks (n=175)	No. cases	% cases (n=1,264)
Commercial food operators	**54**	**30.9**	**488**	**38.6**
Restaurant/café	33	18.9	286	22.6
Takeaway	11	6.3	72	5.7
Other food outlet	7	4.0	116	9.2
Supermarket	2	1.1	4	0.3
Caterers	1	0.6	10	0.8
Institutions	**17**	**9.7**	**126**	**10.0**
Camp	3	1.7	52	4.1
Hostel/Boarding house	3	1.7	8	0.6
Workplace	3	1.7	25	2.0
Childcare centre	2	1.1	7	0.6
Prison	2	1.1	20	1.6
Rest home	1	0.6	2	0.2
Hospital (acute care)	1	0.6	2	0.2
Hospital (continuing care)	1	0.6	2	0.2
Hotel/Motel	1	0.6	8	0.6
Community	**8**	**4.6**	**193**	**15.3**
Community/church gathering	6	3.4	184	14.6
Tangi	2	1.1	9	0.7
Farm	**9**	**5.1**	**25**	**2.0**
Home	**83**	**47.4**	**380**	**30.1**
Other setting	**4**	**2.3**	**52**	**4.1**

4.4.2 Factors contributing to the outbreaks

The outbreak report form offers 37 factors that could contribute to an outbreak. PHOs are able to select one or more of these. These factors have been categorised as:

- Food factors, e.g. inadequate thawing of food, undercooking, cross contamination;
- Water factors, e.g. untreated water supply, contamination of source water;
- Person-to-person factors, e.g. exposure to infected people, poor hygiene of cases;
- Environmental factors, e.g. exposure to infected animals or animal products, exposure to contaminated environments.

At least one factor was reported in 129 outbreaks (68%). Table 42 presents a summary of all the factors reported by these 129 outbreaks. Food and person-to-person factors were most frequently reported. Cross-contamination, temperature abuse and contamination from an infected food handler were the most frequently reported food-related risk factors. Exposure to infected people is also commonly reported, which is not unexpected given this is an analysis of outbreaks.

Table 42: Summary of reported factors contributing to outbreaks (n=129)

Factors contributing to the outbreak	No. outbreaks recording this factor	% outbreaks recording at least one factor (n=129)
Food factors ***At least one food factor:***	***65***	50.4
Cross contamination	27	20.9
Inadequate cooling or refrigeration	21	16.3
Contamination from an infected food handler	17	13.2
Use of ingredients from unsafe sources	11	8.5
Improper storage prior to preparation	9	7.0
Consumption of raw food	8	6.2
Inadequate reheating of previously cooked food	6	4.7
Inadequate thawing	6	4.7
Improper hot holding	4	3.1
Undercooking	2	1.6
Use of untreated water in food preparation	2	1.6
Consumption of unpasteurised milk	1	0.8
Other food factors	6	4.7
Water factors ***At least one water factor:***	***11***	8.5
Untreated water supply	9	7.0
Contamination of source water	6	4.7
Contamination of reservoir/holding tank	2	1.6
Other water factors	2	1.6
Person-to-person factors ***At least one P2P factor:***[1]	***60***	46.5
Exposure to infected people	56	43.4
Poor hygiene of cases	12	9.3
Other person-to-person factors	3	2.3
Environmental factors ***At least one Env. factor:***[2]	***17***	13.2
Exposure to infected animals or animal products	13	10.1
Exposure to contaminated environment	9	7.0

1. P2P, person-to-person.
2. Env, environmental.

4.4.3 Mode of transmission

At least one mode of transmission was reported in 169 (89%) of the outbreaks. The 21 outbreaks with no reported mode of transmission represents 186 (13%) of all outbreak cases. Of the 169 outbreaks reporting at least one mode of transmission, the majority (73%) listed only one mode. Two modes were reported for 37 (22%) of these outbreaks, seven outbreaks (4%) recorded three

modes and two outbreaks recorded four modes. Table 43 summarises all reported modes of transmission.

Table 43: Summary of reported modes of transmission for outbreaks that listed at least one mode (n=169)

Mode of transmission	No. outbreaks reporting this mode	% outbreaks reporting this mode (n = 169)
Foodborne	108	63.9
Person to person	82	48.5
Zoonotic	17	10.1
Waterborne	13	7.7
Environmental	5	3.0
Other mode[1]	1	0.6

1. The other mode was transfer from soiled linen while doing laundry.

The 46 outbreaks where more than one mode (multi-modal) was reported were examined in more detail. Written comments in the outbreak report and information in the associated case reports provided more context to help decide the most likely mode of transmission from those reported (the 'primary mode'). Table 44 shows the proportion of outbreaks and cases attributed to each mode when considering just the primary mode for the 46 multi-modal outbreaks and the single mode listed for the other 123 outbreaks.

Table 44: Number of outbreaks and outbreak cases associated with each mode of transmission

Primary mode of transmission[1]	No. outbreaks	No. cases	% cases
Foodborne	102	1,000	83.8
Person to person	43	122	10.2
Zoonotic	13	43	3.6
Waterborne	10	27	2.3
Environmental	0	0	0
Other mode	1	2	0.2
Total	**169**	**1,194**	**100**

1. The mode of transmission for 123 outbreaks reporting only one mode, or the most likely mode of transmission for 46 outbreaks reporting more than one mode.

When considering only the primary mode, person-to-person transmission decreases in importance. This reflects a plausible chain of events for the multi-modal outbreaks, whereby initial cases are infected through consumption of contaminated food, water or contact with animals or a contaminated environment, and subsequent cases are infected through person-to-person transmission.

Table 45 demonstrates the relationship between the primary and secondary modes for the 46 multi-modal outbreaks.

Table 45: Number of multi-modal outbreaks associated with each primary and secondary mode of transmission

Primary mode[1]	Secondary mode	No. outbreaks	% outbreaks	No. cases	% cases
Foodborne	Person-to-person	24	52.2	172	70.2
Zoonotic	Person-to-person	9	19.6	28	11.4
Waterborne	Person-to-person	1	2.2	3	1.2
Person-to-person	Foodborne	2	4.3	6	2.4
Person-to-person	Waterborne	1	2.2	3	1.2
Person-to-person	Environmental	1	2.2	2	0.8
Foodborne	Zoonotic	1	2.2	16	6.5
Waterborne	Zoonotic	2	4.3	5	2.0
Waterborne	Foodborne	2	4.3	4	1.6
Zoonotic	Waterborne	2	4.3	4	1.6
Waterborne	Environmental	1	2.2	2	0.8
Total		**45**	**100**	**243**	**100**

1. Shaded cells indicate a likely pathway of events. Unshaded cells are outbreaks where the mode of transmission was not certain and the primary mode is the most likely source.

A comparison between the primary setting and the primary mode of transmission provides an indication on the source of transmission (Table 46). Foodborne outbreaks are most associated with restaurants/cafés and the home environment.

Table 46: Comparison between the primary outbreak setting and primary mode of transmission, based on the percentage of outbreaks (OBs) and percentage of cases (2000-2009; 162 outbreaks, 1,178 cases)[1]

Primary outbreak setting	Foodborne		Person to person		Zoonotic		Waterborne		Other mode		All modes	
	% OBs[2]	% cases	% OBs	% cases	% OBs	% cases	% OBs	% cases	% OBs	% cases	% OBs	% cases
Com. food operators[3]	**31.5**	**39.6**	**-**	**-**	**0.6**	**0.8**	**-**	**-**	**-**	**-**	**32.1**	**40.4**
Restaurant/café	19.1	23.0	-	-	0.6	0.8	-	-	-	-	19.8	23.8
Takeaway	6.2	5.6	-	-	-	-	-	-	-	-	6.2	5.6
Other food outlet	4.3	9.8	-	-	-	-	-	-	-	-	4.3	9.8
Supermarket	1.2	0.3	-	-	-	-	-	-	-	-	1.2	0.3
Caterers	0.6	0.8	-	-	-	-	-	-	-	-	0.6	0.8
Institutions	**3.7**	**5.2**	**3.7**	**2.0**	**-**	**-**	**-**	**-**	**0.6**	**0.2**	**8.0**	**7.3**
Camp	0.6	1.4	-	-	-	-	-	-	-	-	0.6	1.4
Hostel/Boarding house	0.6	0.3	1.2	0.3	-	-	-	-	-	-	1.9	0.7
Workplace	1.2	1.3	0.6	0.8	-	-	-	-	-	-	1.9	2.1
Childcare centre	-	-	1.2	0.6	-	-	-	-	-	-	1.2	0.6
Prison	0.6	1.5	-	-	-	-	-	-	0.6	0.2	1.2	1.7
Rest home	-	-	0.6	0.2	-	-	-	-	-	-	0.6	0.2
Hotel/Motel	0.6	0.7	-	-	-	-	-	-	-	-	0.6	0.7
Community	**4.9**	**16.4**	**-**	**-**	**-**	**-**	**-**	**-**	**-**	**-**	**4.9**	**16.4**
Com./church gathering	3.7	15.6	-	-	-	-	-	-	-	-	3.7	15.6
Tangi	1.2	0.8	-	-	-	-	-	-	-	-	1.2	0.8
Farm	**-**	**-**	**0.6**	**0.2**	**3.7**	**1.5**	**1.2**	**0.4**	**-**	**-**	**5.6**	**2.1**
Home	**20.4**	**20.1**	**19.1**	**7.4**	**3.7**	**1.4**	**4.3**	**1.7**	**-**	**-**	**47.5**	**30.6**
Other setting	**1.2**	**3.1**	**-**	**-**	**-**	**-**	**0.6**	**0.2**	**-**	**-**	**1.9**	**3.2**
Total	**61.7**	**84.4**	**23.5**	**9.5**	**8.0**	**3.7**	**6.2**	**2.3**	**0.6**	**0.2**	**100**	**100**

1. Excludes 28 outbreaks where the setting or mode of transmission was unknown.
2. OBs, outbreaks.
3. Commerical food operators.

4.4.4 Strength of evidence for the mode of transmission

For each outbreak, information provided in the outbreak form, including the PHOs comments, and any available written investigation reports were scrutinised to determine the strength of evidence for the mode (or modes) of transmission. The evidence was classified as:

- Weak: Where cases had a history of exposure to the implicated source ('EvTrnEpiHist');
- Moderate: Where there were critical control point failures linked to the implicated source ('EvTrnEnvInv') or a case control or cohort study showed an elevated risk for cases exposed to the implicated source ('EvTrnEpiRisk');
- Strong: Where the same *Salmonella* serotype was isolated from one or more cases, and the implicated source or from a food handler ('EvTrnLabPTC' or 'EvTrnLabP').

The strength of evidence for the 169 outbreaks that reported one or more modes of transmission are presented in Table 47. This table differs to that of King and Lake (2007) in two ways:

- An additional category has been added to the 'moderate' evidence category, namely 'Hist. + CCP'. Outbreaks were scored in this category where the PHO had indicated that cases had a history of exposure to the implicated source ('EvTrnEpiHist'), but had then specified CCP failures they identified as a result of their investigation in the free text fields and/or by selecting 'EvImpEnvInv';

- The 'other evidence' category has been removed. The decision was taken that strong evidence should only include evidence supported by a positive laboratory test and should not include implicit evidence.

Of the 169 outbreaks where one or more mode of transmission was reported, 107 outbreaks (63%) had weak or no evidence for the mode of transmission.

There were 53 outbreaks with a reported foodborne mode of transmission and weak or moderate evidence (31.4%). For 48 of these, a suspected food or food type was also reported. For 22/48 (45.8%) of these outbreaks, chicken or chicken as an ingredient was suspected, in 7/48 (14.6%) egg or egg as an ingredient was suspected and 3/48 (6.3%) implicated both chicken and eggs.

Five outbreaks were investigated using epidemiological studies. A cohort study linked 16 cases of *S.* Typhimurium DT160 infection to a camp where poor handwashing, an infected food handler, temperature abuse of food and the presence of ducks around the food preparation area may have all contributed to the outbreak. The other four oubreaks were investigated by case-control studies. Consumption of food from a Middle Eastern restaurant was strongly associated with *S*. Enteritidis 9a infection in one outbreak but no single food item was identified from a number of significant foods (chicken, hummus, flatbread, lettuce, tomato, onions and cabbage). *S*. Mbandaka infection was statistically associated with consumption of chicken breast prepared at home, of eggs prepared away from the home and purchase of iceberg lettuce from a specific supermarket (poultry sold through a specific supermarket was implicated but not able to be confirmed). Raw carrots from a produce packer and distributor were a statistically significant source of *S*. Saintpaul infection. Consumption of watermelon purchased from roadside stalls was associated with *S*. Typhimurium DT1 infection.

There were 22 outbreaks (13%) where laboratory evidence confirmed the source of infection, which involved 497 cases. In 11 of these outbreaks (313 cases) an infected food handler was identified and these outbreaks are summarised in Table 48.

Salmonella was isolated from a source in the remaining 11 outbreaks (184 cases) with strong evidence (Table 49). Seven of these outbreaks were caused by a contaminated food, two by contact with infected calves and one from contaminated drinking water. The remaining outbreak was caused either by consumption of contaminated raw milk, contact with the farm environment or contact with bovine faecal material (all of these samples were *Salmonella*-positive).

The 147 outbreaks with at least one suspected mode of transmission and weak or moderate evidence are summarised in Appendix 12, with an indication of the strength of evidence for the transmission mode or source.

4.4.5 Attribution of salmonellosis.

There were only 21 laboratory-confirmed outbreaks that could be used to estimate the proportions of human salmonellosis cases attributable to different sources. This excludes the laboratory-confirmed outbreak that could have been caused by exposure to a number of rural sources. Of these 21 outbreaks, 18 (86%) were either foodborne or associated with an infected food handler, and involved all but nine of the cases (98%). Ten percent of the outbreaks, but only 1.4% of the cases, were attributed to contact with animals. Contact with drinking water caused the remaining outbreak and contributed 0.4% of cases.

Table 47: Strength of evidence for the implicated modes of transmission for salmonellosis outbreaks between 2000 and 2009, by number of outbreaks

Implicated mode of transmission	No. outbreaks	No evidence[3]	Strength of evidence					
			Weak	Moderate			Strong	
			History[4]	Hist.+ CCP[5]	Environ.[6]	Elev. risk[7]	Source[8]	Handler[9]
Foodborne	77	7	29	10	10	4	7	10
Zoonotic	2	0	1	0	0	0	1	0
Person-to-person	39	22	17	0	0	0	0	0
Waterborne	4	0	1	2	1	0	0	0
Other[1]	1	0	0	0	1	0	0	0
Multi-modal[2]	46	9	21	10	1	1	3	1
Food-P2P	24	6	9	7	1	0	0	1
Zoo-P2P	9	0	5	2	0	0	2	0
Total	**169**	**38**	**69**	**22**	**13**	**5**	**11**	**11**

1. *Transfer from soiled linen while doing laundry.*
2. *Where more than one mode of transmission was implicated (see page 26). The shaded lines are subsets of these, and show the number of outbreaks where the likely pathway of transmission was initial infection from contaminated food followed by person-to-person infection (Food-P2P) or initial contamination from contact with an infected animal following by person-to-person infection (Zoo-P2P).*
3. *No evidence was reported.*
4. *Epidemiological evidence: Cases had history of exposure to implicated source.*
5. *Epidemiological evidence and evidence from environmental investigation: Cases had history of exposure to implicated source but the PHO specified critical control point failures linked to the implicated source.*
6. *Evidence from environmental investigation: Identified critical control point failures linked to implicated source.*
7. *Epidemiological evidence: Case control or cohort study showed elevated risk for cases exposed to implicated source.*
8. *Laboratory evidence: The same serotype of Salmonella identified in implicated source, e.g. food, water, animal or environmental source.*
9. *Laboratory evidence: The same serotype of Salmonella identified in a food handler responsible for the implicated foods.*

Table 48: Summary of outbreaks where a food handler or food handlers tested positive for *Salmonella*

Setting	Year	*Salmonella* serotype	No. cases[1]			Suspected source(s)	Other contributing factors
			Conf	Prob	Exp		
Restaurant	2000	Typhimurium DT150	14	2	?	Unknown	Inadequate thawing Cross-contamination
Café	2000	Typhimurium DT 135	17	3	?	Unknown	Cross contamination
Restaurant/café	2000	Typhimurium DT 135	27	13	?	Unknown	Cross-contamination
Bakery	2000	Typhimurium DT 135	25	5	?	Unknown	Inadequate cooling/refrigeration Cross-contamination
Takeaway	2000	Montevideo	11	0	?	Chicken and lamb kebabs	Inadequate reheating of previously cooked food Cross-contamination
Restaurant	2000	Typhimurium DT 135	11	0	?	Honey chicken, barbequed pork and rice	Improper hot holding Inadequate cooling/refrigeration
RSA afternoon tea	2001	Brandenburg	11	10	55	Egg and salmon sandwiches	Cross-contamination
Restaurant[2]	2002	Typhimurium DT 160	4	0	?	Chocolate mousse containing raw egg	Inadequate cooling/refrigeration Use of ingredients from unsafe sources
Bakery	2002	Typhimurium DT 160	7	4	?	Various bakery goods	(none recorded)
Hangi	2003	Typhimurium DT 8 variant	36	28	150	Hangi-cooked kumara, pork, potato and pumpkin	Inadequate thawing (of meat) Undercooking Inadequate cooling/refrigeration Cross-contamination
Restaurant[3]	2007	Chester	84	1	?	Unknown	Use of ingredients from unsafe sources

1. *Conf., confirmed cases, Prob., probable cases; Exp., exposed people; ?, unknown (data not available).*
2. *While two food handlers were carriers of Salmonella, both had also consumed the chocolate mousse so it could not be ascertained if the illness was caused by temperature abuse of the mousse or contamination by a food handler (or both). There is no information to indicate that the chocolate mousse was tested.*
3. *In this outbreak four food handlers were asymptomatic carriers of Salmonella and one was symptomatic. However this was a multi-district outbreak and only 46% of cases had actually eaten at the implicated restaurant. Some of the cases not associated with this premises became ill before those that were. Because this was a new strain of S. Chester in New Zealand and the cases were widespread, it is possible that the outbreak was caused by an imported food. Despite widespread testing no food was identified. It is possible that the food handlers of the implicated premises had become ill through contact with contaminated ingredients.*

Table 49: Summary of outbreaks where *Salmonella* was isolated from an implicated source

Setting	Year	*Salmonella* serotype	No. cases[1]			Confirmed source(s)	Evidence	Other contributing factors
			Conf	Prob	Exp			
Farm	2000	Typhimurium DT 9	3	2	?	Sick calves	Calves also positive for *S.* Typhimurium 9	Exposure to contaminated environment
Umu	2001	Typhimurium DT 160	27	43	99	Potato salad	*Salmonella* isolated from potato salad	Inadequate cooling/refrigeration
Home	2001	Typhimurium DT 160	2	0	2	Raw egg mayonnaise	*Salmonella* isolated from mayonnaise	(none reported)
Home	2002	Weltevreden	5	8	20	Palusami[2]	*Salmonella* isolated from palusami	Inadequate cooling/refrigeration Inadequate reheating of previously cooked food
Home	2002	Typhimurium DT 160	2	0	4	Drinking water	Sewage overflow into drinking water, *Salmonella* isolated from water	Untreated water supply
Restaurant	2003	Montevideo	4	0	?	Tahini paste	*Salmonella* isolated from tahini	(none reported)
Farm	2003	Typhimurium DT 9	2	0	6	Sick calves	Calves positive for *Salmonella*	(none reported)
Restaurant	2003	Montevideo	2	0	2	Tahini in hummus	*Salmonella* isolated from tahini paste	(none reported)
Café/bakery	2005	Thompson	9	4	13	Chicken sandwich, bacon and egg pie, panini, fried chicken, chicken roll	*Salmonella* isolated from food (does not specify which food) and family member of food handler	Improper storage prior to preparation Improper cooling or refrigeration Cross contamination
Home	2008	Typhimurium DT 42	67	0	?	Flour	*Salmonella* isolated from flour	Consumption of raw food
Farm	2009	Typhimurium DT 156	4	0	8	Raw milk, dirt, bovine faecal material	*Salmonella* isolated from unpasteurised milk, cows and environmental samples	Exposure to infected people

1. Conf., confirmed cases, Prob., probable cases; Exp., exposed people; ?, unknown (data not available).

2. Umu-cooked packs of taro in coconut milk wrapped in taro leaves, privately imported from Samoa.

4.5 Discussion

The findings in this report are consistent with the previous analysis of data from 1997 – 2006 i.e. in New Zealand salmonellosis is principally a foodborne disease. However, the estimated proportion attributable to foodborne transmission has considerable uncertainty, and the information to identify specific foods is sparse. There are few confirmed food sources, and of the suspected food sources, some can be discounted on the basis of other evidence. This particularly applies to eggs; the importance of eggs as a source of salmonellosis overseas can influence the views of those proposing suspected food vehicles in New Zealand, where *Salmonella* contamination of eggs is low and confined to the external shell surface (Wilson, 2007). However, it is noteworthy that a number of *S.* Typhimurium outbreaks in Australia in 2007 and 2008 have been linked to eggs.

4.5.1 Limitations

The 204 salmonellosis outbreaks over the period 2000-2009 that are available for analysis is still modest in comparison with some of the databases collated overseas; see Section 4.1 and (King and Lake, 2007). In addition the database may be subject to selection bias i.e. outbreaks associated with a food premise may be more likely to be investigated and reported, and food and waterborne outbreaks are potentially larger and more likely to be investigated. PHOs are not required to record in EpiSurv person-to-person outbreaks set in home settings, but this practice varies between PHUs (39 were reported, Table 46). The high proportion of outbreaks with a home setting (Table 41) and an average of only seven cases per outbreak (Table 31) suggests that selection bias is not occurring.

A food categorisation scheme to classify foods implicated in outbreaks has been published by CDC (Painter *et al*., 2009). The scheme includes options to assign outbreaks linked to mixed foods on the basis of ingredient mixes (recipes), and proportions of outbreaks attributed to those ingredients as single foods. CDC has applied this scheme to an analysis of outbreaks in 2006 (Ayers *et al*., 2009).[13] Although potentially valuable, this scheme was not employed for this New Zealand analysis. It was considered that the number of outbreaks for which there was strong evidence linking a food source was too small to warrant this analysis.

4.5.2 Foodborne transmission

Outbreaks excluded from this analysis were those caused by *S.* Typhi or *S.* Paratyphi, and those where the infection was apparently acquired overseas. The evidence for the importance of foodborne transmission in outbreaks where infection was acquired domestically derives from the following data:

- The commercial food operator setting for outbreaks was the second most common in terms of outbreaks (54/175, 30.9%) after homes (83/175, 47.4%), but in terms of number of cases commercial food operators was the most common setting (38.6% of cases) (Table 41).
- Of the reported factors contributing to outbreaks, food factors were reported more often than water, person to person, or environmental factors (Table 42).
- Of the reported modes of transmission, 108 outbreaks (64%) reported foodborne, the next most common mode reported was person-to-person (82 outbreaks, 49%) (Table 43);

[13] Table available at http://www.cdc.gov/outbreaknet/pdf/surveillance/2006_reported_outbreaks_illnesses.pdf

- Of the reported modes of transmission, when multi-modal outbreaks are restricted to just the primary mode, 102/169 (60%) were foodborne and involved 84% of cases; the next most common mode was person to person at 43/168 (25%; 10% of cases) (Table 44);
- Excluding multi-modal outbreaks, there is at least some evidence of foodborne transmission in 70/94 (74%) outbreaks with weak, moderate or strong evidence (Table 47);
- Of the 22 outbreaks where there was strong evidence for a mode of transmission, four involved multiple modes of transmission. Of the 18 outbreaks with a single mode of transmission, seven involved food, while in the other ten an infected food handler was identified. For one multi-modal outbreak the primary transmission mode was identified as an infected food handler (Table 47). Together, these foodborne outbreaks with strong evidence for a mode of transmission involved 484 (35%) of the total outbreak cases (29% excluding the multi-modal outbreak; Table 48 and Table 49);
- Of 21 outbreaks with an identified laboratory-confirmed source, 18 (86%) were either foodborne or associated with an infected food handler, and involved all but nine of the cases (98%).

Estimates of the proportion of salmonellosis outbreaks that are foodborne could be made from several of these data points. Considering only outbreaks with a single mode of transmission and strong evidence for that mode of transmission, and excluding multi-modal outbreaks, 17/18 outbreaks (94%) are either foodborne or associated with an infected food handler, and involved all but two of the cases. Still excluding multi-modal outbreaks, there is at least some evidence of foodborne transmission in 70/94 outbreaks (74%).

The identification of an infected food handler associated with an outbreak does not automatically identify this person as the source of contamination of food; the food handler may simply have become infected from the food source themselves, or acted as an amplifier by becoming infected from a food source and then spreading contamination.

The confirmed food sources identified are quite various: potato salad, raw egg mayonnaise, palusami, tahini paste, tahini in hummus, flour and one unidentified food of the following: chicken sandwich, bacon and egg pie, panini, fried chicken, chicken roll. The inconsistency of these foods suggests that quantitative estimates should be treated with considerable caution.

4.5.3 Serotypes

The serotypes identified in outbreaks are dominated by *S*. Typhimurium. In particular, *S*. Typhimurium DT160, DT135 and DT1 were associated with over half the total outbreaks and total outbreak cases. The importance of these three phage types has reduced in the period 2004-2009, as the numbers of outbreaks and cases associated with DT160 and DT135 have diminished.

S. Typhimurium DT160 was investigated in a case control study (Thornley *et al*., 2003) and there was some evidence for foodborne transmission. The strongest finding was that there was an association between infection with *S*. Typhimurium DT160 and direct contact with wild birds (matched Odds Ratio (mOR)=12.3, CI: 2.8-54.6). However, this high risk activity was associated with only a few cases. Consumption of takeaway food had a weakly positive association with infection (mOR=1.7, CI: 1.04-2.8), but consumption of whole chicken was less common amongst cases than controls (mOR=0.4, CI: 0.2-0.6). Contact with another individual with diarrhoea and vomiting was also associated with *S*. Typhimurium DT160 infection (mOR=3.1, CI: 1.7-5.7). Population attributable ratios (PAR) were calculated and the largest

PAR% was demonstrated for consumption of takeaway food (26.1%). However, no single type of takeaway outlet was significantly associated with illness.

S. Typhimurium DT135 and DT1 are not clearly linked to particular food sources.

The information on serotypes is not particularly informative regarding attribution. However, the similarity between the list of important serotypes in outbreaks and those identified from sporadic cases (Table 36) suggests that attribution for outbreaks may be similar to that for sporadic cases.

4.5.4 Geography and seasonal patterns

While the geographical distribution of outbreaks and cases has interest, no conclusions have been drawn for this report. Given the low numbers of outbreaks in each region it is likely that factors influencing reporting and investigation are the primary drivers of the data, rather than any epidemiological patterns.

The seasonal pattern, with both numbers of outbreaks, and numbers of cases being highest in summer and lowest in winter, is consistent with notifications for other bacterial enteric illnesses, notably campylobacteriosis.

5 SUMMARY

The NZFSA *Salmonella* Risk Management Strategy (2009-2012) aims to quantify the proportion of foodborne salmonellosis cases attributable to the following pathways: animal feeds, specific foods, and domestically produced versus imported foods. NZFSA also aims to quantify the proportion of foodborne salmonellosis cases attributable to multi-resistant and virulent *Salmonella* genotypes associated with foods. This project intended to support these aims.

This report has addressed foodborne salmonellosis within the boundaries of the information available from EpiSurv. The results do not allow accurate quantification of foodborne salmonellosis, but clearly show that food is an important route of *Salmonella* transmission:

- Notified salmonellosis cases had a greater association with consuming food from food premises than any of the other enteric diseases, except for campylobacteriosis;
- 46% of sporadic salmonellosis cases had reported consuming food from food premises;
- Very few of the serotypes isolated from sporadic salmonellosis cases who had reported consuming food from food premises were significantly different to the most frequently isolated serotype, *S.* Typhimurium DT160. This implies that commercial food is a potential vehicle for a large variety of serotypes;
- 74% of salmonellosis cases for which serotypes were known reported a probable food source;
- Foodborne transmission was the most common mode reported in outbreak reports (64% of reports);
- The commercial food operator setting for outbreaks was the second most common in terms of outbreaks, but the most common setting in terms of number of outbreak cases;
- Of the reported factors contributing to outbreaks, food factors were reported more often than water, person-to-person or environmental factors;
- Of the 22 outbreaks where there was strong evidence for a mode of transmission, seven involved food and eleven were associated with an infected food handler. These 18 foodborne outbreaks involved around a third of the total outbreak cases.

There were no sporadic case reports with a food or drink confirmed as the source of infection by laboratory testing, therefore it is not possible to quantify the proportions of human salmonellosis cases attributable to specific foods. There were seven outbreaks where specific foods were the source. These foods and the proportion of outbreak cases associated with them are potato salad (5.1%), raw egg mayonnaise (0.1%), palusami (0.9%), tahini (two outbreaks; 0.4%), flour (4.9%) and an unspecified bakery product (0.9%). The palusami and tahini were both imported foods and there was no evidence to indicate whether the flour was contaminated during milling in New Zealand or from imported contaminated wheat. Given these minimal findings, it is not sensible to draw conclusions on which specific foods present higher risks for foodborne salmonellosis. The analyses of probable foods (i.e. foods that are implicated but unconfirmed) suggest bias in reporting and we recommend caution in the use of these data.

Infected food handlers are important in foodborne transmission of salmonellosis. However, the isolation of the same serotype from a potential source does not indicate the direction of transmission, which is particularly important where infected food handlers are identified. There is often not enough evidence to know whether the handlers contaminated food or became ill as a result of handling (or consuming) contaminated food. Other outbreak analyses have shown that infected food handlers are frequently identified in outbreaks of salmonellosis (Greig *et al*., 2007) and that *Salmonella* continues to be shed in faeces for long periods (up to 100 days) after illness (Todd *et al*., 2007).

A recent Risk Profile concluded that animal feed is not considered a significant source of human salmonellosis in New Zealand, but that the available information on the *Salmonella* status of feed and feed ingredients in New Zealand is not sufficiently comprehensive to exclude animal feed as a source of human salmonellosis cases (Cressey *et al*., 2010) (Note: this Risk Profile draft is with the NZFSA for review).

Each year ESR's Antibiotic Reference Laboratory tests the antimicrobial susceptibility of a representative sample (approx. 20%) of human and non-human non-typhoidal *Salmonella* isolates routinely referred to ESR for serotyping.[14] This work has not identified any clear associations of multidrug resistance with particular serotypes, except for the internationally recognised multiresistant clones, such as *S*. Typhimurium DT104 and U302. The incidence of these international multiresistant clones in New Zealand is very low and almost all cases have been sporadic. An analysis of 3,065 *Salmonella* isolates from human and non-human sources over the period 2002-2007 found increasing non-suceptibility to streptomycin and sulfonamides by isolates from both sources, and increasing non-susceptibility to ampicillin and tetracycline by isolates from human sources (Broughton *et al*., 2010). There was also an increase in multidrug non-susceptibility (non-susceptibility to three or more antibiotics) by isolates from humans over this period. However, as the isolates from humans cannot be divided into foodborne and non-foodborne, any trends in antimicrobial susceptibility cannot be determined.

5.1 Non-foodborne Pathways

Person-to-person:
Salmonellosis was not strongly associated with contact with symptomatic or confirmed cases, or contact with human faeces when compared to other enteric diseases. The serotype analysis signalled this to be a risk factor for all serotypes. Person-to-person transmission was implicated in almost half of the outbreaks and was the single implicated mode of infection in 23% of the outbreaks, but these were either not supported by any evidence, or only weak evidence.

Zoonotic
Salmonellosis was associated with contact with farm animals and sick animals. *S.* Brandenburg, *S.* Saintpaul, *S.* Typhimurium DT9 and *S.* Typhimurium DT23 were the serotypes that showed a significantly elevated OR for such contact, compared to *S*. Typhimurium DT160. Zoonotic transmission was reported for 10% of outbreaks, and was the primary mode in 8% of outbreaks. There were three outbreaks with confirmed zoonotic transmission, two from contact with sick calves (*S.* Typhimurium DT9) and one where cows were positive for *S.* Typhimurium DT156. Case-control studies of sporadic cases have confirmed zoonotic transmission of salmonellosis in New Zealand for other serotypes (Baker *et al*., 2007; Thornley *et al*., 2003).

Drinking water
The four serotypes with elevated ORs for zoonotic transmission, also had significantly elevated ORs for consumption of untreated drinking water. People living in rural environments are more likely to consume water from private (and possibly untreated) supplies. Together these results suggest transmission pathways associated with rural environments for these serotypes. Salmonellosis from untreated drinking water was implicated in 6% of outbreaks and confirmed in one, where a sewage overflow had contaminated the water source. It has been estimated that 8% of the New Zealand population (mostly rural) receive their drinking water from unregistered supplies (Ball *et al*., 2007).

[14] Reports on antimicrobial susceptibility of *Salmonella* can be found at http://www.surv.esr.cri.nz/antimicrobial/salmonella.php

Overseas travel
Salmonellosis was more strongly associated with overseas travel than other enteric disease apart from campylobacteriosis. Overseas travel within the incubation period was reported for 16% of notified cases and is associated with less common serotypes (e.g. *S.* Enteritidis PT6a, *S.* Newport). There were 14 outbreaks where salmonellosis was acquired overseas, representing only 1% of outbreak cases. Of the ten serotypes identified in these outbreaks, four also caused 50 or more sporadic notifications in the last decade.

Recreational water
Salmonellosis was associated with contact with recreational water but only 16% of cases reported this activity. The serotypes show similarity to that of cases travelling overseas and detailed investigation is needed to determine if these factors were linked. Recreational water was not implicated in any outbreaks.

These results generally support a recent review of salmonellosis aetiology in New Zealand (Wilson and Baker, 2009), though our findings suggest that person-to-person transmission is less important and direct animal contact more important.

5.2 Reporting Quality and Data Gaps

This report aimed to inform future improvements in salmonellosis reporting. The study has identified areas where salmonellosis reporting could be improved:

- The details recorded for risk factors were not well completed in sporadic case report forms. The completeness of entries in the case report depends on the availability and willingness of the case to provide this information, and the policies and priorities of each PHU.
- Attribution of foodborne salmonellosis for sporadic cases could only be approximated by analysing consumption of food from premises. Foods consumed in the home, and any potential risky food preparation practices, are not recorded in case report forms.
- Outbreak reports were often incomplete, though the fields that were incomplete varied. There was also an apparent lack of standardisation in how information was recorded, e.g. how the type of outbreak was defined. PHOs made good use of the comments section, but this suggests that the forms do not support collection of all the information they consider important for investigation. As a consequence, this information will be missed in any data analysis, e.g. annual outbreak reporting.
- There is no agreed food categorisation which makes analysis of implicated foods difficult.
- Separate written outbreak reports are often compiled by PHUs but do not appear to be routinely collated. In this analysis these have been a valuable source of additional information, but some older reports were unable to be retrieved due to archiving.

ESR is currently working with the PHUs and the Ministry of Health to improve the outbreak report form. Key changes to the form are:

- A greater focus on strength of evidence: Risk factors will be listed against the strength of evidence to support them (e.g. history of exposure, laboratory confirmation);
- Food categorisation: A food categorisation scheme will be adopted that aligns with that used for Information Leader, the software system recently introduced as a replacement for

FoodNet. This categorisation scheme has been adapted from the Australia New Zealand Food Standards Code;[15]

- Revision of questions: Any ambiguous questions will be rewritten to ensure it is clear what information should be collected, for example, separate questions will now be asked about the setting of exposure/transmission and the setting of contamination.

Roll-out of the new form is expected in the latter half of 2010.

5.3 Sentinel Surveillance

This report aimed to inform potential sentinel surveillance. Sentinel surveillance could involve monitoring specific *Salmonella* serotypes or enhancing surveillance of salmonellosis in a geographical region.

The case-case analysis of serotypes did not suggest any particular serotypes that could be confidently used to monitor general salmonellosis rates or salmonellosis linked to particular pathways in New Zealand. Short-term surveillance (i.e. 1-2 years) might focus on a few serotypes of interest, but the serotype patterns change too rapidly over time for this method to be of use in longer-term surveillance. There may be some value in tracking the potential changes in relationships between serotypes and risk factors through a repeated case-case analysis, but this would rely on improved reporting against risk factors.

Enhanced surveillance of campylobacteriosis has recently been reported for the Manawatu region (French 2008). The research group combined molecular genotyping and modelling to estimate the relative contribution of different food and environmental sources to human infection with *Campylobacter jejuni*. The project involved considerable resources but was able to draw conclusions on important sources and pathways for campylobacteriosis. A similar study focused on salmonellosis is likely to yield similar insights but would be more challenging given the lower notification rate and poorly defined food sources for this disease.

At a national level, monitoring of salmonellosis would benefit from better integration of human and non-human surveillance information. The options for a national *Salmonella* surveillance programme that integrates human and non-human surveillance information from existing data systems have been investigated (Lake and Sexton, 2009). An example of an integrated system is provided by the Danish Zoonosis Centre, which compiles and reports annually Denmark's surveillance data on foodborne zoonoses through close collaboration with all relevant institutions and authorities along the farm-to-fork chain.[16]

[15] Available at http://www.foodstandards.gov.au/foodstandards/foodstandardscode/
[16] See http://www.food.dtu.dk/Default.aspx?ID=8573

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7.1 Appendix 1: *Salmonella* serotypes isolated from non-human sources by the Enteric Reference Laboratory, 2005-2009.

This table only lists serotypes that were isolated ten or more times from all sources, over the period 2005-09. An additional 135 serotypes (278 isolates) were also detected by the laboratory during this period.

Salmonella serotype	Avian	Bovine	Canine	Equine	Feline	Ovine	Porcine	Reptile	Environmental	Food[1]	Spice	Sesame seed	Meat/bone meal	Feed	Shellfish	Poultry neckflaps	Poultry feed	Poultry environmental	Poultry product	All sources
Brandenburg	16	155	10	2	0	658	3	0	36	75	0	0	14	1	4	0	30	8	15	**1,027**
Typhimurium 101	5	167	6	5	0	2	1	0	3	6	0	0	0	0	0	1	13	188	257	**654**
Hindmarsh	1	37	3	1	2	409	1	0	2	4	0	0	0	0	0	0	8	1	0	**469**
Typhimurium RDNC	8	95	6	18	31	2	2	0	20	2	0	0	1	0	2	0	15	34	21	**257**
Typhimurium 160	37	37	9	33	25	1	1	0	17	2	0	0	1	0	1	1	37	34	11	**247**
Typhimurium 1	0	196	7	10	1	5	0	1	4	6	0	0	0	0	1	0	0	10	1	**242**
Infantis	0	8	2	0	1	1	0	16	19	33	0	0	52	1	0	7	25	56	17	**238**
Typhimurium 156	0	142	2	6	1	0	0	1	8	9	0	0	0	0	0	0	3	5	1	**178**
Derby	0	0	1	0	0	0	1	0	7	1	0	0	16	0	1	0	94	27	3	**151**
Agona	0	8	3	0	0	0	1	0	8	7	0	0	7	2	0	0	16	87	3	**142**
Typhimurium 12a	4	87	3	7	3	0	0	0	1	5	0	0	0	0	0	0	2	1	7	**120**
Typhimurium 42	0	55	0	1	2	0	0	0	12	21	0	0	0	0	0	0	12	9	7	**119**
Typhimurium 9	1	78	1	7	0	25	0	0	1	5	0	0	0	0	0	0	0	0	0	**118**
Senftenberg	0	19	0	0	0	0	0	0	27	5	0	0	7	0	0	0	36	13	3	**110**
Tennessee	0	1	1	0	1	0	0	0	4	0	0	2	37	0	0	0	22	21	15	**104**
Typhimurium 135	5	62	1	3	6	4	2	3	0	5	0	0	3	0	0	0	1	7	1	**103**

Salmonella serotype	Avian	Bovine	Canine	Equine	Feline	Ovine	Porcine	Reptile	Environmental	Food[1]	Spice	Sesame seed	Meat/bone meal	Feed	Shellfish	Poultry neckflaps	Poultry feed	Poultry environmental	Poultry product	All sources
Typhimurium 8	0	90	0	3	4	4	1	0	0	1	0	0	0	0	0	0	0	0	0	**103**
Mbandaka	0	1	0	0	1	0	0	0	24	4	0	0	7	0	0	0	31	18	3	**89**
Anatum	0	11	0	0	0	0	0	0	3	1	0	0	39	1	0	0	15	5	9	**84**
Typhimurium 74	0	57	1	7	1	0	0	0	1	4	0	0	0	0	0	0	2	1	2	**76**
Montevideo	0	0	0	0	0	0	0	0	2	4	0	11	38	0	0	0	10	6	1	**72**
Saintpaul	2	6	1	3	0	0	0	41	1	3	0	0	0	0	0	0	2	0	0	**59**
Typhimurium 23	0	49	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	**50**
Thompson	2	2	0	0	0	0	0	10	2	10	0	0	4	0	2	0	4	5	2	**43**
Havana	0	0	0	0	0	0	0	0	6	1	0	0	11	0	0	0	9	8	4	**39**
Anatum 15+	0	3	0	0	0	0	0	0	0	0	0	0	4	0	0	0	18	7	5	**37**
Give 15+	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	31	2	0	**33**
Urbana	0	0	0	0	0	0	0	0	32	0	0	0	0	0	0	0	0	0	0	**32**
Enteritidis 9a	0	8	4	1	6	3	0	0	0	0	0	0	0	0	0	0	1	4	1	**28**
Mississippi	0	0	0	0	0	0	0	26	0	0	0	0	0	0	0	0	1	0	1	**28**
Heidelberg	0	12	0	1	0	0	1	0	0	1	0	0	0	0	0	0	11	1	0	**27**
Kiambu	0	4	0	1	0	0	0	0	0	2	0	0	13	0	0	0	6	0	0	**26**
Typhimurium 89	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	23	1	**24**
Kentucky	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	12	8	**23**
Onderstepoort	0	0	0	0	0	0	0	23	0	0	0	0	0	0	0	0	0	0	0	**23**
Ruiru	1	17	0	0	1	0	0	0	0	2	0	0	0	0	0	0	1	1	0	**23**
Group C 6,7 : k : -	0	0	0	0	0	0	0	1	1	3	0	0	0	0	0	0	6	8	4	**23**

Salmonella serotype	Avian	Bovine	Canine	Equine	Feline	Ovine	Porcine	Reptile	Environmental	Food[1]	Spice	Sesame seed	Meat/bone meal	Feed	Shellfish	Poultry neckflaps	Poultry feed	Poultry environmental	Poultry product	All sources
Bousso	0	0	0	0	0	0	0	22	0	0	0	0	0	0	0	0	0	0	0	**22**
Emek	0	10	0	0	0	0	0	0	3	2	0	0	1	0	0	0	2	1	0	**19**
Typhimurium 154	0	15	0	1	0	0	0	0	1	0	0	0	1	0	0	0	0	0	1	**19**
Typhimurium Untypable	1	12	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	4	**19**
Typhimurium 41	0	0	0	0	0	0	0	0	15	1	0	0	2	0	0	0	0	0	0	**18**
Typhimurium Rough	2	12	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	1	**18**
Oranienburg	0	0	0	0	0	0	0	0	1	6	0	0	0	0	0	0	5	1	4	**17**
London	0	6	0	0	0	1	1	0	1	0	0	0	1	0	0	0	6	0	0	**16**
Orion 15+	0	0	0	0	0	0	0	0	0	0	0	3	10	0	0	0	2	1	0	**16**
Typhimurium U310	0	15	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**16**
Warragul	0	0	0	0	0	0	0	16	0	0	0	0	0	0	0	0	0	0	0	**16**
Group B 4,12 : - : 1,2	0	4	0	2	0	0	2	4	0	2	0	0	0	0	0	0	2	0	0	**16**
Subspecies I 13,23 : - : 1,5	0	0	0	0	0	0	0	16	0	0	0	0	0	0	0	0	0	0	0	**16**
Zanzibar	0	7	0	0	0	0	0	0	2	0	0	0	4	1	0	0	0	0	0	**14**
Group E 3,19 : - : -	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	12	1	0	**14**
Typhimurium 195	5	7	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	**13**
Group N 30 : - : - (non-motile)	0	0	0	0	0	0	0	0	13	0	0	0	0	0	0	0	0	0	0	**13**
Potsdam	0	0	0	0	0	0	0	12	0	0	0	0	0	0	0	0	0	0	0	**12**
Rissen	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	10	0	1	**12**
Adelaide	0	0	0	0	0	0	0	2	0	0	0	0	8	0	0	0	0	1	0	**11**
Paratyphi B var Java	0	0	0	0	0	0	0	0	9	2	0	0	0	0	0	0	0	0	0	**11**

***Salmonella* serotype**	**Avian**	**Bovine**	**Canine**	**Equine**	**Feline**	**Ovine**	**Porcine**	**Reptile**	**Environmental**	**Food[1]**	**Spice**	**Sesame seed**	**Meat/bone meal**	**Feed**	**Shellfish**	**Poultry neckflaps**	**Poultry feed**	**Poultry environmental**	**Poultry product**	**All sources**
Subspecies IV 43 : z4,z23 : -	0	0	0	0	0	0	0	11	0	0	0	0	0	0	0	0	0	0	0	**11**
Livingstone	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	8	0	0	**10**
Typhimurium 126	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	1	**10**
Typhimurium 193	0	8	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	**10**
TOTAL[2]	**92**	**155**	**68**	**115**	**90**	**1,120**	**20**	**252**	**315**	**267**	**3**	**24**	**291**	**7**	**9**	**10**	**551**	**645**	**428**	**5,868**

Source: Enteric Reference Laboratory Annual Reports, ESR, Kenepuru Science Centre/NCBID

1. *Includes animal carcasses from meat works and food samples from outbreaks of salmonellosis in humans.*
2. *Total isolates 2005-2009 (including serotypes isolated less than ten times over that time period).*

7.2 Appendix 2: *Salmonella* serotypes that caused 50 or more cases over the years 2000 to 2009

***Salmonella* serotype**	**2000**	**2001**	**2002**	**2003**	**2004**	**2005**	**2006**	**2007**	**2008**	**2009**	**Total**
Typhimurium DT160	150	576	353	171	158	183	201	125	132	98	**2,147**
Typhimurium DT1	106	94	95	67	40	71	67	51	61	77	**729**
Brandenburg	164	113	76	48	81	61	48	37	36	36	**700**
Typhimurium DT135	231	199	101	49	21	34	13	10	21	19	**698**
Typhimurium DT156	82	83	50	48	32	50	66	39	64	48	**562**
Infantis	24	57	50	55	48	40	47	52	79	71	**523**
Typhimurium DT101	104	57	25	33	22	48	60	27	72	57	**505**
Enteritidis PT9a	55	62	44	41	32	33	45	37	47	36	**432**
Typhimurium DT42	52	24	21	18	18	25	26	7	36	30	**257**
Saintpaul	18	14	24	24	27	39	30	17	30	26	**249**
Typhimurium DT12a	21	19	25	23	17	23	39	14	29	27	**237**
Typhimurium DT9	69	26	12	9	5	4	10	9	18	20	**182**
Typhimurium RDNC-May 06	0	0	0	0	0	0	14	45	57	38	**154**
Heidelberg	0	105	12	4	2	3	11	6	3	4	**150**
Virchow	16	8	12	10	20	14	9	27	13	12	**141**
Typhimurium DT74	0	0	0	0	28	21	36	21	21	12	**139**
Typhimurium DT23	15	48	13	16	2	13	17	1	5	8	**138**
Typhimurium RDNC	3	18	13	24	5	8	15	8	19	24	**137**
Mississippi	5	8	7	10	9	17	11	4	10	14	**95**
Enteritidis PT4	30	17	21	11	5	0	6	2	2	1	**95**
Thompson	7	12	11	6	12	6	16	6	8	8	**92**
Agona	9	15	6	3	3	6	23	8	9	10	**92**
Weltevreden	6	15	3	8	9	6	16	8	7	10	**88**
Montevideo	6	3	19	19	8	4	8	3	0	9	**79**
Mbandaka	1	10	4	3	8	1	13	11	17	8	**76**
Newport	4	11	10	4	7	6	12	5	7	2	**68**
Stanley	9	8	1	0	2	9	4	11	12	9	**65**
Enteritidis PT6a	1	1	1	4	4	8	5	11	17	10	**62**
Corvallis	0	0	0	2	4	12	17	11	11	4	**61**
Salmonella sp. 4,5,12:d :-	0	5	6	8	11	4	8	11	6	0	**59**
Typhimurium DT8	8	4	3	3	4	4	2	12	9	9	**58**
Enteritidis PT1	3	16	9	3	2	10	2	6	3	4	**58**
Enteritidis PT1b	0	0	0	0	7	5	10	11	19	5	**57**
Hadar	12	11	13	4	2	2	0	6	3	2	**55**
Typhimurium RDNC Aug-01	0	2	7	40	1	0	0	0	0	0	**50**
Total[1]	**1,408**	**1,913**	**1,256**	**974**	**818**	**979**	**1,126**	**869**	**1,163**	**1,048**	**11,554**

1. Total number of cases per year for all serotypes in the full dataset of 11,554 cases, not just those causing 50 cases or more between 2000 and 2009.

7.3 Appendix 3: Rates of sporadic salmonellosis per 100,000 population by District Health Board (2000-2009)

District Health Board	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009
Northland	22.9	39.5	8.2	12.9	23.4	30.5	28.2	33.8	27.8	20.5
Waitemata	22.6	40.1	29.3	18.7	17.5	14.5	24.4	16.8	19.6	16.1
Auckland	22.4	44.2	32.4	22.7	22.9	22.0	23.1	15.9	19.9	23.4
Counties Manukau	18.3	43.4	28.0	24.4	17.3	19.1	20.2	12.3	18.6	19.9
Waikato	32.0	54.8	9.3	40.2	23.3	30.3	37.1	26.3	31.7	28.1
Bay of Plenty	19.8	22.4	3.2	0.5	5.1	5.1	4.0	16.2	23.9	18.8
Tairawhiti	34.7	13.2	76.9	15.3	0.0	6.6	6.5	13.1	15.3	39.0
(Rotorua) Lakes	11.1	31.2	22.0	17.8	14.8	20.7	11.8	24.6	24.6	24.6
Taranaki	16.9	52.9	34.8	20.6	28.1	26.2	40.0	23.3	32.5	17.6
Hawke's Bay	31.1	50.0	17.4	26.7	21.9	16.5	16.4	24.2	22.2	26.6
Whanganui	15.0	44.4	38.4	26.2	26.4	37.4	15.6	12.6	22.1	19.0
MidCentral	46.5	52.4	31.1	21.6	12.3	19.0	22.6	22.6	24.3	16.3
Wairarapa	53.8	38.3	43.2	33.0	2.5	20.2	37.9	22.8	55.3	45.0
Capital and Coast	43.0	60.9	43.0	12.4	1.8	14.2	35.6	26.6	30.2	19.8
Hutt Valley	29.9	38.7	26.1	15.9	1.4	18.5	27.0	22.6	31.0	23.8
Nelson Marlborough	36.1	78.6	31.4	13.9	9.1	16.6	15.0	20.8	33.9	27.0
West Coast	12.7	38.6	35.3	12.8	12.7	15.7	6.2	37.2	24.7	27.6
Canterbury	56.0	46.7	47.2	35.3	27.3	36.8	28.3	17.5	30.0	27.3
South Canterbury	66.7	87.3	73.9	60.6	52.9	52.8	67.2	5.4	63.3	61.2
Otago	99.0	90.9	55.9	35.4	38.9	44.7	45.4	29.0	53.9	39.8
Southland	118.3	78.3	60.7	40.6	64.1	45.7	62.9	38.1	31.6	42.9
All New Zealand	**36.5**	**49.3**	**31.8**	**24.2**	**20.0**	**23.7**	**26.9**	**20.6**	**27.2**	**24.3**

Notes to table:

1. *Only cases with known serotypes have been used to calculate these rates (n=11,554).*
2. *Rates of 50 or more people per 100,000 have been shaded.*
3. *Rates are 100,000 population referenced to NZStats estimated population 2004 for each DHB.*

7.4 Appendix 4: *Salmonella* serotype case-case analysis for each risk factor, referenced to *S.* Typhimurium DT160 in cases aged less than five years

(A) Overseas travel

Salmonella serotype	Males and females less than five years			Females less than five years			Males less than five years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT160	**1.2**	**1(ref)**		**1.3**	**1.0**		**1.1**	**1(ref)**	
Typhimurium DT1	0.9	0.8	0.13-4.82	1.2	0.9	0.10-9.23	0.6	0.6	0.03-12.01
Typhimurium DT156	1.4	1.2	0.23-5.89	1.3	1.0	0.10-9.97	1.4	1.3	0.14-13.16
Brandenburg	0.9	0.8	0.13-4.79	0.7	0.6	0.03-11.21	1.1	1.0	0.10-9.91
Typhimurium DT135	1.5	1.3	0.21-7.78	1.2	0.9	0.05-19.26	1.7	1.6	0.16-15.46
Typhimurium DT101	1.3	1.1	0.19-6.87	0.9	0.7	0.03-13.55	1.8	1.7	0.17-16.63
Enteritidis PT9a	0.9	0.8	0.10-6.70	1.0	0.8	0.04-15.44	0.9	0.8	0.04-16.87
Typhimurium DT12a	1.5	1.3	0.16-11.16	1.8	1.4	0.07-29.48	1.3	1.2	0.06-25.22
Typhimurium DT42	2.4	2.1	0.35-12.92	3.3	2.7	0.27-26.60	1.6	1.5	0.07-30.20
Saintpaul	5.3	4.7	1.30-17.07	5.6	4.6	0.74-28.34	5.0	4.8	0.78-29.81
Typhimurium RDNC-May 06	2.3	2.0	0.23-16.73	2.3	1.8	0.09-38.16	2.2	2.1	0.10-42.92
Infantis	2.1	1.8	0.21-15.28	1.9	1.5	0.07-30.64	2.3	2.2	0.11-45.02
Typhimurium DT74	4.3	3.8	0.62-23.84	3.0	2.4	0.12-50.56	5.6	5.4	0.53-54.63
Typhimurium Not Typed	2.7	2.4	0.28-20.07	3.0	2.4	0.12-50.56	2.4	2.3	0.11-47.34
Typhimurium RDNC	15.4	15.4	4.05-58.51	22.2	22.2	3.19-154.54	11.8	12.2	1.90-78.76
Typhimurium DT23	13.9	13.7	4.09-45.84	19.2	18.5	4.13-82.83	3.7	3.5	0.17-74.09
Typhimurium DT9	7.3	6.7	1.05-42.38	9.1	7.8	0.74-81.44	5.3	5.1	0.24-109.34
Heidelberg	11.6	11.1	2.38-52.22	7.7	6.5	0.29-143.91	13.3	14.1	2.17-91.84
Mississippi	4.5	4.0	0.46-35.01	4.3	3.5	0.17-74.87	4.8	4.6	0.21-97.72
Virchow	45.0	69.3	21.01-228.45	35.7	43.1	8.90-209.20	66.7	183.3	23.76-1,414.82
Agona	53.3	96.8	26.50-353.25	50.0	77.7	10.89-553.70	55.6	114.6	20.14-652.00
Typhimurium Untypable	25.0	28.2	6.08-130.95	16.7	15.5	1.37-176.52	33.3	45.8	5.94-353.71
Newport	64.3	152.4	39.21-592.34	50.0	77.7	8.05-749.40	70.0	213.9	36.53-1,252.50
Enteritidis PT1	42.9	63.5	11.60-347.47	50.0	77.7	3.88-1,554.84	40.0	61.1	7.33-509.30
Thompson	14.3	14.1	1.47-135.89	9.1	7.8	0.34-176.29	33.3	45.8	1.28-1,644.87
Montevideo	33.3	42.3	7.59-236.03	14.3	12.9	0.53-318.59	50.0	91.7	9.51-884.00

Salmonella serotype	Males and females less than five years			Females less than five years			Males less than five years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Mbandaka	16.7	16.9	1.71-167.71	14.3	12.9	0.53-318.59	20.0	22.9	0.84-622.13
Stanley	44.4	67.7	8.93-513.74	33.3	38.8	2.72-553.49	66.7	183.3	5.11-6,579.48
Enteritidis PT6a	72.7	225.8	29.30-1,739.65	80.0	310.7	11.44-8,437.07	66.7	183.3	12.87-2,611.78
Weltevreden	44.4	67.7	8.93-513.74	33.3	38.8	2.72-553.49	66.7	183.3	5.11-6,579.48
Enteritidis PT1b	50.0	84.7	10.17-704.54	50.0	77.7	3.88-1,554.84	50.0	91.7	4.58-1,834.34
Corvallis	37.5	50.8	5.75-448.69	20.0	19.4	0.71-527.32	66.7	183.3	5.11-6,579.48
Enteritidis PT4	42.9	63.5	6.59-611.50	50.0	77.7	3.88-1,554.84	33.3	45.8	1.28-1,644.87
Salmonella species 4,5,12 : d :-	37.5	50.8	5.75-448.69	66.7	155.3	4.33-5,576.58	20.0	22.9	0.84-622.13
Hadar	57.1	112.9	11.72-1,087.12	66.7	155.3	4.33-5,576.58	50.0	91.7	4.58-1,834.34

(B) Food consumption from a premise

Salmonella serotype	Males and females less than five years			Females less than five years			Males less than five years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT160	**35.6**	**1(ref)**		**37.4**	**1(ref)**		**34.1**	**1(ref)**	
Typhimurium DT1	20.4	0.5	0.27-0.80	17.0	0.3	0.16-0.75	24.4	0.6	0.30-1.32
Typhimurium DT156	35.3	1.0	0.62-1.57	33.3	0.8	0.44-1.59	37.8	1.2	0.60-2.31
Brandenburg	14.7	0.3	0.18-0.53	15.3	0.3	0.14-0.66	14.3	0.3	0.16-0.65
Typhimurium DT135	34.6	1.0	0.57-1.61	40.5	1.1	0.55-2.37	29.3	0.8	0.38-1.68
Typhimurium DT101	30.4	0.8	0.47-1.34	22.0	0.5	0.21-1.06	39.5	1.3	0.61-2.59
Enteritidis PT9a	35.3	1.0	0.57-1.70	40.0	1.1	0.50-2.48	31.6	0.9	0.42-1.89
Typhimurium DT12a	20.8	0.5	0.23-0.99	15.8	0.3	0.09-1.12	24.1	0.6	0.25-1.52
Typhimurium DT42	48.8	1.7	0.91-3.27	27.3	0.6	0.23-1.69	71.4	4.8	1.79-13.09
Saintpaul	31.6	0.8	0.46-1.52	42.9	1.3	0.55-2.84	20.7	0.5	0.20-1.30
Typhimurium RDNC-May 06	33.3	0.9	0.42-1.93	25.0	0.6	0.17-1.81	41.2	1.4	0.49-3.73
Infantis	20.0	0.5	0.20-1.01	33.3	0.8	0.32-2.19	5.3	0.1	0.01-0.82
Typhimurium DT74	52.0	2.0	0.87-4.43	54.5	2.0	0.59-6.87	50.0	1.9	0.65-5.77
Typhimurium Not Typed	38.7	1.1	0.54-2.43	35.7	0.9	0.30-2.91	41.2	1.4	0.49-3.73
Typhimurium RDNC	35.7	1.0	0.33-3.07	20.0	0.4	0.05-3.83	44.4	1.5	0.40-5.97
Typhimurium DT23	31.6	0.8	0.31-2.25	44.4	1.3	0.35-5.18	20.0	0.5	0.10-2.35

Salmonella serotype	Males and females less than five years			Females less than five years			Males less than five years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT9	17.6	0.4	0.11-1.38	22.2	0.5	0.10-2.38	12.5	0.3	0.03-2.30
Heidelberg	25.0	0.6	0.16-2.27	50.0	1.7	0.10-27.25	20.0	0.5	0.10-2.35
Mississippi	27.3	0.7	0.18-2.60	40.0	1.1	0.18-6.87	16.7	0.4	0.04-3.39
Virchow	24.1	0.6	0.17-1.96	33.3	0.8	0.20-3.47	9.1	0.2	0.01-3.60
Agona	17.6	0.4	0.07-2.29	11.1	0.2	0.01-4.03	25.0	0.6	0.07-6.33
Typhimurium Untypable	20.0	0.5	0.05-4.09	14.3	0.3	0.01-5.66	33.3	1.0	0.03-29.25
Newport	25.0	0.6	0.12-3.03	25.0	0.6	0.06-5.49	25.0	0.6	0.07-6.33
Enteritidis PT1	25.0	0.6	0.06-5.86	33.3	0.8	0.03-25.32	20.0	0.5	0.02-10.89
Thompson	44.4	1.4	0.22-9.41	33.3	0.8	0.07-9.43	66.7	3.9	0.13-117.00
Montevideo	46.2	1.6	0.33-7.36	80.0	6.7	0.30-150.90	25.0	0.6	0.07-6.33
Mbandaka	40.0	1.2	0.10-15.29	33.3	0.8	0.03-25.32	50.0	1.9	0.04-98.72
Stanley	28.6	0.7	0.07-7.43	20.0	0.4	0.02-9.43	50.0	1.9	0.04-98.72
Enteritidis PT6a	50.0	1.8	0.11-29.17	50.0	1.7	0.03-85.43	50.0	1.9	0.04-98.72
Weltevreden	33.3	0.9	0.08-10.08	33.3	0.8	0.03-25.32	33.3	1.0	0.03-29.25
Enteritidis PT1b	42.9	1.4	0.16-11.40	33.3	0.8	0.03-25.32	50.0	1.9	0.12-31.47
Corvallis	40.0	1.2	0.10-15.29	33.3	0.8	0.03-25.32	50.0	1.9	0.04-98.72
Enteritidis PT4	40.0	1.2	0.10-15.29	33.3	0.8	0.03-25.32	50.0	1.9	0.04-98.72
Salmonella species 4,5,12 : d :-	28.6	0.7	0.07-7.43	50.0	1.7	0.03-85.43	20.0	0.5	0.02-10.89
Hadar	60.0	2.7	0.21-34.40	50.0	1.7	0.03-85.43	66.7	3.9	0.13-117.00

(C) Consumption of untreated drinking water

Salmonella serotype	Males and females less than five years			Females less than five years			Males less than five years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT160	**25.4**	**1(ref)**		**21.6**	**1(ref)**		**28.5**	**1(ref)**	
Typhimurium DT1	25.7	1.0	0.63-1.64	36.4	2.1	1.08-3.95	15.5	0.5	0.21-0.99
Typhimurium DT156	30.0	1.3	0.78-2.04	23.1	1.1	0.52-2.25	37.5	1.5	0.78-2.89
Brandenburg	46.7	2.6	1.73-3.85	39.0	2.3	1.24-4.32	52.6	2.8	1.64-4.72
Typhimurium DT135	19.7	0.7	0.39-1.33	16.1	0.7	0.25-1.92	22.2	0.7	0.34-1.53
Typhimurium DT101	18.3	0.7	0.36-1.20	10.3	0.4	0.14-1.23	25.6	0.9	0.41-1.81

Salmonella serotype	Males and females less than five years			Females less than five years			Males less than five years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Enteritidis PT9a	23.0	0.9	0.49-1.58	17.1	0.7	0.29-1.92	28.2	1.0	0.46-2.09
Typhimurium DT12a	22.4	0.9	0.42-1.73	16.7	0.7	0.20-2.62	25.8	0.9	0.37-2.05
Typhimurium DT42	30.2	1.3	0.64-2.54	31.6	1.7	0.60-4.66	29.2	1.0	0.41-2.61
Saintpaul	35.7	1.6	0.91-2.95	32.1	1.7	0.72-4.07	39.3	1.6	0.72-3.65
Typhimurium RDNC-May 06	34.4	1.5	0.72-3.30	31.3	1.6	0.54-5.00	37.5	1.5	0.53-4.31
Infantis	15.8	0.6	0.22-1.36	16.7	0.7	0.23-2.23	14.3	0.4	0.09-1.92
Typhimurium DT74	9.4	0.3	0.08-1.15	4.3	0.2	0.01-2.86	13.3	0.4	0.08-1.76
Typhimurium Not Typed	18.5	0.7	0.25-1.81	14.3	0.6	0.13-2.80	23.1	0.8	0.20-2.82
Typhimurium RDNC	37.9	1.8	0.61-5.31	7.7	0.3	0.02-5.51	62.5	4.2	0.97-18.00
Typhimurium DT23	37.5	1.8	0.75-4.15	41.7	2.6	0.78-8.56	33.3	1.3	0.36-4.31
Typhimurium DT9	44.4	2.4	0.91-6.12	45.5	3.0	0.88-10.37	42.9	1.9	0.41-8.64
Heidelberg	15.4	0.5	0.12-2.45	25.0	1.2	0.12-11.90	11.1	0.3	0.04-2.56
Mississippi	29.0	1.2	0.39-3.69	5.9	0.2	0.01-4.02	57.1	3.3	0.73-15.35
Virchow	13.0	0.4	0.08-2.49	12.5	0.5	0.06-4.32	14.3	0.4	0.02-8.46
Agona	33.3	1.5	0.32-6.82	20.0	0.9	0.04-20.44	40.0	1.7	0.27-10.24
Typhimurium Untypable	42.9	2.2	0.49-10.02	33.3	1.8	0.16-20.45	50.0	2.5	0.35-18.18
Newport	15.8	0.6	0.10-3.20	11.1	0.5	0.02-8.73	20.0	0.6	0.07-5.72
Enteritidis PT1	25.0	1.0	0.10-9.53	33.3	1.8	0.06-54.87	20.0	0.6	0.03-14.09
Thompson	25.0	1.0	0.15-6.31	11.1	0.5	0.02-8.73	66.7	5.0	0.17-151.33
Montevideo	16.7	0.6	0.07-5.10	14.3	0.6	0.03-12.28	20.0	0.6	0.03-14.09
Mbandaka	28.6	1.2	0.11-12.10	20.0	0.9	0.04-20.44	50.0	2.5	0.05-127.73
Stanley	40.0	2.0	0.15-24.88	33.3	1.8	0.06-54.87	50.0	2.5	0.05-127.73
Enteritidis PT6a	50.0	2.9	0.18-47.48	50.0	3.6	0.07-185.13	50.0	2.5	0.05-127.73
Weltevreden	28.6	1.2	0.11-12.10	20.0	0.9	0.04-20.44	50.0	2.5	0.05-127.73
Enteritidis PT1b	28.6	1.2	0.11-12.10	50.0	3.6	0.07-185.13	20.0	0.6	0.03-14.09
Corvallis	28.6	1.2	0.11-12.10	20.0	0.9	0.04-20.44	50.0	2.5	0.05-127.73
Enteritidis PT4	60.0	4.4	0.35-55.98	66.7	7.2	0.24-219.49	50.0	2.5	0.05-127.73
Salmonella species 4,5,12 : d :-	40.0	2.0	0.15-24.88	50.0	3.6	0.07-185.13	33.3	1.3	0.04-37.83
Hadar	33.3	1.5	0.13-16.40	33.3	1.8	0.06-54.87	33.3	1.3	0.04-37.83

(D) Contact with recreational water

Salmonella serotype	Males and females less than five years			Females less than five years			Males less than five years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT160	**15.8**	**1(ref)**		**15.8**	**1(ref)**		**15.8**	**1(ref)**	
Typhimurium DT1	16.0	1.0	0.60-1.69	20.8	1.4	0.71-2.77	11.1	0.7	0.29-1.50
Typhimurium DT156	21.8	1.5	0.90-2.43	16.9	1.1	0.51-2.29	27.1	2.0	1.01-3.87
Brandenburg	11.0	0.7	0.37-1.15	7.6	0.4	0.16-1.17	13.5	0.8	0.41-1.67
Typhimurium DT135	17.0	1.1	0.60-1.98	16.7	1.1	0.43-2.60	17.3	1.1	0.50-2.47
Typhimurium DT101	15.8	1.0	0.55-1.81	19.6	1.3	0.59-2.85	12.0	0.7	0.29-1.82
Enteritidis PT9a	14.1	0.9	0.46-1.66	11.1	0.7	0.24-1.81	17.0	1.1	0.47-2.52
Typhimurium DT12a	14.0	0.9	0.39-1.91	12.5	0.8	0.21-2.70	15.2	0.9	0.34-2.61
Typhimurium DT42	10.9	0.7	0.27-1.58	11.1	0.7	0.19-2.34	10.7	0.6	0.18-2.22
Saintpaul	39.1	3.4	1.98-5.90	44.1	4.2	1.93-9.11	34.3	2.8	1.27-6.05
Typhimurium RDNC-May 06	9.1	0.5	0.17-1.64	16.7	1.1	0.29-3.88	2.4	0.1	0.01-2.25
Infantis	11.6	0.7	0.27-1.84	4.3	0.2	0.03-1.86	20.0	1.3	0.42-4.19
Typhimurium DT74	18.6	1.2	0.47-3.18	4.0	0.2	0.01-3.84	29.4	2.2	0.74-6.65
Typhimurium Not Typed	22.6	1.6	0.64-3.74	13.3	0.8	0.18-3.80	31.3	2.4	0.79-7.35
Typhimurium RDNC	25.7	1.8	0.61-5.54	6.7	0.4	0.02-6.85	40.0	3.5	0.95-13.16
Typhimurium DT23	15.8	1.0	0.35-2.82	3.0	0.2	0.01-2.84	33.3	2.7	0.76-9.27
Typhimurium DT9	7.3	0.4	0.08-2.26	8.3	0.5	0.06-3.87	5.9	0.3	0.02-5.91
Heidelberg	36.8	3.1	1.18-8.15	40.0	3.5	0.57-22.05	35.7	3.0	0.94-9.30
Mississippi	25.0	1.8	0.56-5.65	25.0	1.8	0.34-9.17	25.0	1.8	0.34-9.11
Virchow	30.8	2.4	0.71-7.88	22.2	1.5	0.30-7.64	50.0	5.3	0.73-38.90
Agona	9.1	0.5	0.07-4.22	11.1	0.7	0.03-12.87	7.7	0.4	0.02-8.10
Typhimurium Untypable	14.3	0.9	0.11-7.47	14.3	0.9	0.04-18.10	14.3	0.9	0.04-18.04
Newport	15.8	1.0	0.17-5.81	25.0	1.8	0.18-17.57	9.1	0.5	0.03-9.93
Enteritidis PT1	28.6	2.1	0.21-21.92	50.0	5.3	0.10-272.66	20.0	1.3	0.06-30.05
Thompson	30.8	2.4	0.44-12.74	20.0	1.3	0.14-12.27	66.7	10.6	0.35-322.56
Montevideo	23.1	1.6	0.25-10.06	14.3	0.9	0.04-18.10	33.3	2.7	0.24-30.05
Mbandaka	40.0	3.5	0.28-45.07	33.3	2.7	0.09-80.86	50.0	5.3	0.10-272.05
Stanley	28.6	2.1	0.21-21.92	20.0	1.3	0.06-30.14	50.0	5.3	0.10-272.05
Enteritidis PT6a	50.0	5.3	0.33-85.97	50.0	5.3	0.10-272.66	50.0	5.3	0.10-272.05
Weltevreden	50.0	5.3	0.54-51.83	50.0	5.3	0.32-87.14	50.0	5.3	0.10-272.05
Enteritidis PT1b	25.0	1.8	0.18-17.28	33.3	2.7	0.09-80.86	20.0	1.3	0.06-30.05

Salmonella serotype	Males and females less than five years			Females less than five years			Males less than five years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Corvallis	37.5	3.2	0.41-24.53	20.0	1.3	0.06-30.14	66.7	10.6	0.35-322.56
Enteritidis PT4	40.0	3.5	0.28-45.07	33.3	2.7	0.09-80.86	50.0	5.3	0.10-272.05
Salmonella species 4,5,12 : d :-	40.0	3.5	0.28-45.07	50.0	5.3	0.10-272.66	33.3	2.7	0.09-80.64
Hadar	33.3	2.7	0.24-29.70	33.3	2.7	0.09-80.86	33.3	2.7	0.09-80.64

(E) Contact with farm animals

Salmonella serotype	Males and females less than five years			Females less than five years			Males less than five years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT160	**32.6**	**1(ref)**		**32.6**	**1(ref)**		**32.7**	**1(ref)**	
Typhimurium DT1	37.7	1.2	0.83-1.87	38.5	1.3	0.73-2.29	36.9	1.2	0.68-2.13
Typhimurium DT156	27.9	0.8	0.51-1.24	26.2	0.7	0.39-1.39	29.5	0.9	0.47-1.59
Brandenburg	65.8	4.0	2.72-5.82	58.8	3.0	1.69-5.17	71.1	5.1	3.00-8.58
Typhimurium DT135	30.7	0.9	0.56-1.49	31.4	0.9	0.44-2.04	30.2	0.9	0.47-1.69
Typhimurium DT101	34.0	1.1	0.67-1.69	21.7	0.6	0.27-1.22	45.1	1.7	0.92-3.12
Enteritidis PT9a	34.0	1.1	0.67-1.70	31.3	0.9	0.48-1.84	37.0	1.2	0.63-2.32
Typhimurium DT12a	28.6	0.8	0.45-1.52	18.2	0.5	0.15-1.41	35.3	1.1	0.53-2.38
Typhimurium DT42	40.4	1.4	0.76-2.59	45.0	1.7	0.67-4.27	37.0	1.2	0.53-2.76
Saintpaul	42.4	1.5	0.90-2.57	48.4	1.9	0.91-4.14	37.1	1.2	0.58-2.54
Typhimurium RDNC-May 06	31.1	0.9	0.48-1.80	45.5	1.7	0.71-4.18	17.4	0.4	0.14-1.32
Infantis	12.2	0.3	0.11-0.75	16.0	0.4	0.13-1.19	6.3	0.1	0.02-1.06
Typhimurium DT74	22.2	0.6	0.26-1.32	27.8	0.8	0.27-2.32	16.7	0.4	0.12-1.46
Typhimurium Not Typed	24.2	0.7	0.29-1.50	37.5	1.2	0.43-3.55	11.8	0.3	0.06-1.23
Typhimurium RDNC	42.9	1.5	0.64-3.75	50.0	2.1	0.50-8.51	38.5	1.3	0.41-4.06
Typhimurium DT23	50.0	2.1	0.96-4.44	58.8	3.0	1.08-8.08	36.4	1.2	0.34-4.13
Typhimurium DT9	65.0	3.8	1.50-9.80	72.7	5.5	1.42-21.42	55.6	2.6	0.67-9.84
Heidelberg	15.8	0.4	0.11-1.35	33.3	1.0	0.19-5.78	7.7	0.2	0.02-1.34
Mississippi	35.5	1.1	0.39-3.27	5.9	0.1	0.01-2.28	71.4	5.2	0.98-27.11
Virchow	25.9	0.7	0.21-2.48	27.3	0.8	0.20-3.01	20.0	0.5	0.02-11.55
Agona	9.1	0.2	0.03-1.63	14.3	0.3	0.02-6.98	6.7	0.1	0.01-2.62

Salmonella serotype	Males and females less than five years			Females less than five years			Males less than five years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium Untypable	50.0	2.1	0.66-6.51	57.1	2.8	0.60-12.66	40.0	1.4	0.23-8.38
Newport	14.3	0.3	0.06-1.96	11.1	0.3	0.01-4.96	16.7	0.4	0.05-3.58
Enteritidis PT1	33.3	1.0	0.14-7.40	33.3	1.0	0.03-31.21	33.3	1.0	0.09-11.52
Thompson	27.3	0.8	0.12-5.11	25.0	0.7	0.07-6.75	33.3	1.0	0.03-31.02
Montevideo	12.5	0.3	0.04-2.42	14.3	0.3	0.02-6.98	11.1	0.3	0.01-4.93
Mbandaka	55.6	2.6	0.40-16.73	66.7	4.1	0.37-46.40	33.3	1.0	0.03-31.02
Stanley	37.5	1.2	0.16-9.46	20.0	0.5	0.02-11.62	66.7	4.1	0.14-124.08
Enteritidis PT6a	60.0	3.1	0.24-39.17	50.0	2.1	0.04-105.36	66.7	4.1	0.14-124.08
Weltevreden	28.6	0.8	0.08-8.46	20.0	0.5	0.02-11.62	50.0	2.1	0.04-104.75
Enteritidis PT1b	25.0	0.7	0.07-6.67	33.3	1.0	0.03-31.21	20.0	0.5	0.02-11.55
Corvallis	25.0	0.7	0.07-6.67	20.0	0.5	0.02-11.62	33.3	1.0	0.03-31.02
Enteritidis PT4	50.0	2.1	0.21-20.01	66.7	4.1	0.14-124.82	33.3	1.0	0.03-31.02
Salmonella species 4,5,12 : d :-	40.0	1.4	0.11-17.41	50.0	2.1	0.04-105.36	33.3	1.0	0.03-31.02
Hadar	33.3	1.0	0.09-11.47	33.3	1.0	0.03-31.21	33.3	1.0	0.03-31.02

(F) Contact with sick animals

Salmonella serotype	Males and females less than five years			Females less than five years			Males less than five years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT160	**5.1**	**1(ref)**		**3.2**	**1(ref)**		**6.7**	**1(ref)**	
Typhimurium DT1	5.2	1.0	0.40-2.58	3.6	1.1	0.22-5.77	6.7	1.0	0.32-3.10
Typhimurium DT156	10.2	2.1	0.95-4.62	11.8	4.0	1.23-12.99	8.5	1.3	0.41-4.08
Brandenburg	20.8	4.8	2.63-8.92	14.5	5.1	1.73-14.96	26.5	5.0	2.35-10.58
Typhimurium DT135	9.8	2.0	0.84-4.80	1.7	0.5	0.03-9.51	14.9	2.4	0.93-6.33
Typhimurium DT101	5.8	1.1	0.42-3.11	2.2	0.7	0.08-5.81	9.8	1.5	0.47-4.77
Enteritidis PT9a	5.2	1.0	0.34-3.04	2.6	0.8	0.09-6.75	7.9	1.2	0.33-4.32
Typhimurium DT12a	6.7	1.3	0.38-4.61	5.9	1.9	0.21-16.55	7.1	1.1	0.23-4.93
Typhimurium DT42	3.5	0.7	0.13-3.65	5.0	1.6	0.18-13.82	2.2	0.3	0.02-5.46
Saintpaul	4.3	0.8	0.22-3.15	7.1	2.3	0.44-12.04	1.6	0.2	0.01-3.97
Typhimurium RDNC-May 06	13.8	3.0	1.00-8.81	4.3	1.4	0.07-26.02	19.0	3.3	0.97-10.93

Salmonella serotype	Males and females less than five years			Females less than five years			Males less than five years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Infantis	2.6	0.5	0.06-3.72	2.1	0.7	0.04-12.06	3.2	0.5	0.03-8.12
Typhimurium DT74	4.8	0.9	0.17-5.04	6.3	2.0	0.23-17.72	3.2	0.5	0.03-8.12
Typhimurium Not Typed	5.9	1.2	0.21-6.37	8.3	2.7	0.30-24.68	3.7	0.5	0.03-9.43
Typhimurium RDNC	9.1	1.8	0.33-10.47	7.7	2.5	0.12-50.09	10.0	1.5	0.18-12.98
Typhimurium DT23	17.4	3.9	1.21-12.46	15.4	5.5	0.98-30.22	20.0	3.5	0.68-17.79
Typhimurium DT9	14.3	3.1	0.75-12.60	5.3	1.7	0.09-32.22	25.0	4.6	0.86-24.90
Heidelberg	16.1	3.6	0.86-14.74	14.3	5.0	0.22-111.26	16.7	2.8	0.56-13.82
Mississippi	7.7	1.5	0.19-12.41	6.7	2.1	0.11-42.28	9.1	1.4	0.07-26.60
Virchow	12.0	2.5	0.43-14.67	10.0	3.3	0.36-30.70	20.0	3.5	0.15-80.34
Agona	12.5	2.6	0.31-22.45	20.0	7.5	0.30-184.73	9.1	1.4	0.07-26.60
Typhimurium Untypable	14.3	3.1	0.35-26.76	14.3	5.0	0.22-111.26	14.3	2.3	0.11-48.29
Newport	11.1	2.3	0.28-19.33	20.0	7.5	0.30-184.73	7.7	1.2	0.06-21.69
Enteritidis PT1	33.3	9.2	0.80-106.02	33.3	15.0	0.46-492.23	33.3	6.9	0.22-215.16
Thompson	20.0	4.6	0.49-43.17	14.3	5.0	0.22-111.26	33.3	6.9	0.22-215.16
Montevideo	14.3	3.1	0.35-26.76	14.3	5.0	0.22-111.26	14.3	2.3	0.11-48.29
Mbandaka	28.6	7.4	0.70-78.30	20.0	7.5	0.30-184.73	50.0	13.9	0.27-723.68
Stanley	28.6	7.4	0.70-78.30	20.0	7.5	0.30-184.73	50.0	13.9	0.27-723.68
Enteritidis PT6a	40.0	12.3	0.94-160.64	50.0	30.0	0.55-1,643.69	33.3	6.9	0.22-215.16
Weltevreden	28.6	7.4	0.70-78.30	20.0	7.5	0.30-184.73	50.0	13.9	0.27-723.68
Enteritidis PT1b	28.6	7.4	0.70-78.30	50.0	30.0	0.55-1,643.69	20.0	3.5	0.15-80.34
Corvallis	25.0	6.2	0.61-61.76	20.0	7.5	0.30-184.73	33.3	6.9	0.22-215.16
Enteritidis PT4	40.0	12.3	0.94-160.64	50.0	30.0	0.55-1,643.69	33.3	6.9	0.22-215.16
Salmonella species 4,5,12 : d :-	28.6	7.4	0.70-78.30	50.0	30.0	0.55-1,643.69	20.0	3.5	0.15-80.34
Hadar	33.3	9.2	0.80-106.02	33.3	15.0	0.46-492.23	33.3	6.9	0.22-215.16

(G) Contact with human faeces

Salmonella serotype	Males and females less than five years			Females less than five years			Males less than five years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT160	**26.7**	**1(ref)**		**23.9**	**1(ref)**		**29.2**	**1(ref)**	
Typhimurium DT1	26.8	1.0	0.63-1.60	25.5	1.1	0.55-2.16	28.1	0.9	0.50-1.80
Typhimurium DT156	36.4	1.6	1.01-2.43	40.4	2.2	1.16-4.00	32.1	1.1	0.60-2.18
Brandenburg	28.5	1.1	0.70-1.70	29.8	1.4	0.70-2.60	27.3	0.9	0.50-1.67
Typhimurium DT135	30.6	1.2	0.70-2.08	34.6	1.7	0.71-4.02	28.3	1.0	0.48-1.93
Typhimurium DT101	19.3	0.7	0.37-1.16	14.3	0.5	0.21-1.33	23.9	0.8	0.37-1.59
Enteritidis PT9a	26.4	1.0	0.58-1.66	19.5	0.8	0.33-1.78	32.6	1.2	0.60-2.31
Typhimurium DT12a	15.2	0.5	0.21-1.13	13.3	0.5	0.11-2.25	16.1	0.5	0.17-1.27
Typhimurium DT42	10.0	0.3	0.11-0.87	5.3	0.2	0.02-1.36	14.3	0.4	0.12-1.42
Saintpaul	22.6	0.8	0.43-1.50	22.2	0.9	0.35-2.38	22.9	0.7	0.31-1.66
Typhimurium RDNC-May 06	43.8	2.1	1.03-4.42	46.7	2.8	0.96-8.07	41.2	1.7	0.62-4.65
Infantis	20.5	0.7	0.32-1.58	28.0	1.2	0.49-3.14	7.1	0.2	0.02-1.46
Typhimurium DT74	31.3	1.2	0.57-2.71	31.3	1.4	0.48-4.37	31.3	1.1	0.37-3.29
Typhimurium Not Typed	33.3	1.4	0.60-3.13	33.3	1.6	0.52-4.88	33.3	1.2	0.35-4.16
Typhimurium RDNC	33.3	1.4	0.52-3.59	6.7	0.2	0.01-4.08	50.0	2.4	0.76-7.79
Typhimurium DT23	29.2	1.1	0.46-2.79	26.7	1.2	0.35-3.80	33.3	1.2	0.30-4.99
Typhimurium DT9	29.4	1.1	0.39-3.31	20.0	0.8	0.16-3.87	42.9	1.8	0.40-8.35
Heidelberg	45.0	2.2	0.91-5.54	33.3	1.6	0.28-8.96	50.0	2.4	0.82-7.18
Mississippi	10.3	0.3	0.06-1.74	11.1	0.4	0.05-3.26	9.1	0.2	0.01-4.50
Virchow	44.4	2.2	0.73-6.54	36.4	1.8	0.51-6.48	80.0	9.7	0.43-218.13
Agona	52.9	3.1	0.79-12.05	20.0	0.8	0.04-17.95	66.7	4.9	0.87-27.13
Typhimurium Untypable	13.0	0.4	0.07-2.32	7.7	0.3	0.01-4.84	20.0	0.6	0.07-5.53
Newport	13.0	0.4	0.07-2.32	11.1	0.4	0.02-7.66	14.3	0.4	0.05-3.42
Enteritidis PT1	16.7	0.5	0.06-4.74	33.3	1.6	0.05-48.18	11.1	0.3	0.02-5.82
Thompson	27.3	1.0	0.16-6.79	25.0	1.1	0.11-10.44	33.3	1.2	0.04-36.61
Montevideo	14.3	0.5	0.05-3.83	20.0	0.8	0.04-17.95	11.1	0.3	0.02-5.82
Mbandaka	30.0	1.2	0.17-8.04	14.3	0.5	0.03-10.78	66.7	4.9	0.16-146.45
Stanley	37.5	1.6	0.21-12.58	20.0	0.8	0.04-17.95	66.7	4.9	0.16-146.45
Enteritidis PT6a	40.0	1.8	0.14-23.14	50.0	3.2	0.06-162.58	33.3	1.2	0.04-36.61
Weltevreden	37.5	1.6	0.21-12.58	33.3	1.6	0.14-17.93	50.0	2.4	0.05-123.62
Enteritidis PT1b	28.6	1.1	0.11-11.25	50.0	3.2	0.06-162.58	20.0	0.6	0.03-13.63

Salmonella serotype	Males and females less than five years			Females less than five years			Males less than five years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Corvallis	25.0	0.9	0.09-8.86	20.0	0.8	0.04-17.95	33.3	1.2	0.04-36.61
Enteritidis PT4	50.0	2.7	0.17-44.15	50.0	3.2	0.06-162.58	50.0	2.4	0.05-123.62
Salmonella species 4,5,12 : d :-	28.6	1.1	0.11-11.25	50.0	3.2	0.06-162.58	20.0	0.6	0.03-13.63
Hadar	40.0	1.8	0.14-23.14	50.0	3.2	0.06-162.58	33.3	1.2	0.04-36.61

7.5 Appendix 5: *Salmonella* serotype case-case analysis for each risk factor, referenced to *S.* Typhimurium DT160 in cases aged five to 16 years

(A) Overseas travel

Salmonella serotype	Males and females five to 16 years			Females five to 16 years			Males five to 16 years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT160	**0.4**	**1(ref)**		**0.4**	**1(ref)**		**0.3**	**1(ref)**	
Typhimurium DT156	1.7	4.8	0.38-60.57	2.6	6.7	0.22-203.13	1.0	3.1	0.06-156.14
Typhimurium DT135	3.8	11.3	1.16-110.39	5.6	14.9	0.66-339.06	2.4	7.6	0.25-230.82
Typhimurium DT1	2.2	6.3	0.50-80.68	2.1	5.5	0.11-285.37	2.2	7.1	0.23-214.88
Typhimurium DT101	2.3	6.5	0.51-83.20	2.0	5.1	0.10-262.09	2.4	7.8	0.26-236.67
Brandenburg	2.7	7.7	0.60-98.53	2.1	5.5	0.11-285.37	3.0	9.8	0.32-296.88
Enteritidis PT9a	2.3	6.7	0.41-109.78	3.0	7.9	0.15-414.03	1.9	6.0	0.12-309.11
Saintpaul	3.5	10.4	0.81-132.79	5.9	15.9	0.51-492.33	2.0	6.2	0.12-321.71
Typhimurium DT42	4.5	13.3	1.03-171.02	8.3	23.1	0.73-727.56	2.3	7.4	0.14-384.41
Infantis	4.3	12.9	0.78-212.73	5.9	15.9	0.30-853.48	3.4	11.1	0.21-583.33
Heidelberg	10.6	33.7	3.18-357.20	7.7	21.2	0.39-1,161.00	11.8	41.6	1.79-964.97
Typhimurium DT12a	4.8	14.2	0.85-234.73	6.7	18.1	0.33-983.83	3.7	12.0	0.23-629.88
Typhimurium DT23	4.5	13.5	0.81-223.19	5.3	14.1	0.26-753.58	4.0	13.0	0.25-684.49
Typhimurium RDNC-May 06	8.3	25.7	1.51-438.83	20.0	63.5	0.99-4,074.34	5.3	17.3	0.32-925.01
Typhimurium DT9	8.7	27.0	2.35-309.56	16.7	50.8	1.52-1,699.96	5.9	19.5	0.63-604.26
Typhimurium DT74	5.3	15.7	0.94-261.80	7.7	21.2	0.39-1,161.00	4.0	13.0	0.25-684.49
Typhimurium Not Typed	7.7	23.6	1.80-309.62	9.1	25.4	0.46-1,415.61	7.1	24.0	0.77-749.72
Typhimurium RDNC	8.6	26.5	2.01-350.13	7.7	21.2	0.39-1,161.00	9.1	31.2	0.99-987.25
Virchow	58.3	396.2	31.02-5,061.17	50.0	254.0	2.08-30,991.97	60.0	468.0	17.21-12,725.59
Enteritidis PT4	76.2	905.6	80.27-10,217.14	88.9	2032.0	35.60-115,978.56	66.7	624.0	24.10-16,158.94
Mississippi	9.1	28.3	1.65-485.69	9.1	25.4	0.46-1,415.61	9.1	31.2	0.56-1,737.65
Stanley	75.0	849.0	67.43-10,690.27	80.0	1016.0	29.54-34,938.57	66.7	624.0	15.89-24,497.61
Typhimurium Untypable	27.3	106.1	7.02-1,604.58	20.0	63.5	0.99-4,074.34	33.3	156.0	3.97-6,124.40
Salmonella species 4,5,12 : d :-	76.9	943.3	64.65-13,764.15	66.7	508.0	6.32-40,807.63	80.0	1248.0	36.32-42,882.57
Weltevreden	61.5	452.8	36.42-5,629.69	60.0	381.0	14.00-10,368.75	66.7	624.0	7.77-50,093.78

Salmonella serotype	Males and females five to 16 years			Females five to 16 years			Males five to 16 years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Newport	80.0	1132.0	59.71-21,462.21	80.0	1016.0	15.83-65,189.42	80.0	1248.0	19.46-80,021.11
Enteritidis PT1b	60.0	424.5	29.80-6,047.02	50.0	254.0	5.02-12,851.18	66.7	624.0	15.89-24,497.61
Agona	63.6	495.3	35.99-6,814.53	75.0	762.0	21.18-27,408.94	33.3	156.0	1.94-12,523.44
Thompson	33.3	141.5	6.37-3,144.85	33.3	127.0	1.58-10,201.91	33.3	156.0	1.94-12,523.44
Mbandaka	50.0	283.0	17.66-4,535.78	50.0	254.0	5.02-12,851.18	50.0	312.0	6.17-15,774.39
Corvallis	50.0	283.0	14.14-5,662.74	50.0	254.0	2.08-30,991.97	50.0	312.0	6.17-15,774.39
Montevideo	42.9	212.3	11.83-3,809.14	33.3	127.0	1.58-10,201.91	50.0	312.0	6.17-15,774.39
Hadar	57.1	377.3	21.03-6,771.80	66.7	508.0	6.32-40,807.63	50.0	312.0	6.17-15,774.39
Enteritidis PT1	66.7	566.0	25.47-12,579.40	66.7	508.0	6.32-40,807.63	66.7	624.0	7.77-50,093.78
Enteritidis PT6a	40.0	188.7	7.67-4,641.39	50.0	254.0	2.08-30,991.97	33.3	156.0	1.94-12,523.44

(B) Food consumption from a premise

Salmonella serotype	Males and females five to 16 years			Females five to 16 years			Males five to 16 years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT160	**45.9**	**1(ref)**		**46.5**	**1(ref)**		**45.4**	**1(ref)**	
Typhimurium DT156	39.7	0.8	0.44-1.38	44.4	0.9	0.39-2.19	36.1	0.7	0.31-1.48
Typhimurium DT135	39.3	0.8	0.42-1.40	40.0	0.8	0.31-1.90	38.7	0.8	0.34-1.72
Typhimurium DT1	45.8	1.0	0.53-1.88	53.3	1.3	0.44-3.95	42.4	0.9	0.40-1.95
Typhimurium DT101	48.8	1.1	0.58-2.18	66.7	2.3	0.73-7.29	39.3	0.8	0.33-1.82
Brandenburg	22.2	0.3	0.15-0.78	17.6	0.2	0.07-0.92	26.3	0.4	0.14-1.28
Enteritidis PT9a	64.5	2.1	0.98-4.72	53.8	1.3	0.42-4.32	72.2	3.1	1.04-9.39
Saintpaul	65.7	2.3	1.07-4.80	53.8	1.3	0.42-4.32	72.7	3.2	1.17-8.83
Typhimurium DT42	58.3	1.7	0.70-3.90	87.5	8.1	0.95-68.27	43.8	0.9	0.33-2.70
Infantis	47.8	1.1	0.33-3.56	11.1	0.1	0.01-2.80	71.4	3.0	0.56-16.20
Heidelberg	46.7	1.0	0.36-2.96	33.3	0.6	0.10-3.31	55.6	1.5	0.38-5.91
Typhimurium DT12a	56.3	1.5	0.54-4.24	60.0	1.7	0.27-10.85	54.5	1.4	0.42-5.02
Typhimurium DT23	30.8	0.5	0.16-1.76	40.0	0.8	0.12-4.82	25.0	0.4	0.08-2.08
Typhimurium RDNC-May 06	43.8	0.9	0.22-3.82	50.0	1.2	0.02-59.30	42.9	0.9	0.19-4.23

Salmonella serotype	Males and females five to 16 years			Females five to 16 years			Males five to 16 years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT9	43.8	0.9	0.33-2.56	75.0	3.5	0.35-34.50	33.3	0.6	0.17-2.12
Typhimurium DT74	28.0	0.5	0.13-1.63	11.1	0.1	0.01-2.80	37.5	0.7	0.16-3.18
Typhimurium Not Typed	58.3	1.7	0.51-5.39	75.0	3.5	0.35-34.50	50.0	1.2	0.29-5.07
Typhimurium RDNC	55.6	1.5	0.38-5.66	50.0	1.2	0.07-18.99	57.1	1.6	0.34-7.52
Virchow	50.0	1.2	0.20-6.97	50.0	1.2	0.02-59.30	50.0	1.2	0.16-8.86
Enteritidis PT4	40.0	0.8	0.13-4.81	50.0	1.2	0.07-18.99	33.3	0.6	0.05-6.84
Mississippi	70.6	2.8	0.63-12.72	85.7	6.9	0.34-141.93	60.0	1.8	0.29-11.25
Stanley	50.0	1.2	0.12-11.54	50.0	1.2	0.07-18.99	50.0	1.2	0.02-61.80
Typhimurium Untypable	33.3	0.6	0.08-4.27	20.0	0.3	0.01-6.56	50.0	1.2	0.07-19.75
Salmonella species 4,5,12 : d :-	40.0	0.8	0.06-10.03	50.0	1.2	0.02-59.30	33.3	0.6	0.02-18.33
Weltevreden	50.0	1.2	0.12-11.54	50.0	1.2	0.07-18.99	50.0	1.2	0.02-61.80
Newport	42.9	0.9	0.10-7.49	50.0	1.2	0.07-18.99	33.3	0.6	0.02-18.33
Enteritidis PT1b	44.4	0.9	0.14-6.19	66.7	2.3	0.08-70.39	33.3	0.6	0.05-6.84
Agona	33.3	0.6	0.05-6.61	33.3	0.6	0.02-17.60	33.3	0.6	0.02-18.33
Thompson	60.0	1.8	0.14-22.58	50.0	1.2	0.02-59.30	66.7	2.4	0.08-73.31
Mbandaka	75.0	3.5	0.36-34.63	66.7	2.3	0.08-70.39	80.0	4.8	0.21-109.30
Corvallis	60.0	1.8	0.14-22.58	50.0	1.2	0.02-59.30	66.7	2.4	0.08-73.31
Montevideo	66.7	2.4	0.21-26.46	66.7	2.3	0.08-70.39	66.7	2.4	0.08-73.31
Hadar	50.0	1.2	0.12-11.54	33.3	0.6	0.02-17.60	66.7	2.4	0.08-73.31
Enteritidis PT1	40.0	0.8	0.06-10.03	50.0	1.2	0.02-59.30	33.3	0.6	0.02-18.33
Enteritidis PT6a	40.0	0.8	0.06-10.03	50.0	1.2	0.02-59.30	33.3	0.6	0.02-18.33

(C) Consumption of untreated drinking water

Salmonella serotype	Males and females five to 16 years			Females five to 16 years			Males five to 16 years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT160	**27.0**	**1(ref)**		**24.5**	**1(ref)**		**29.0**	**1(ref)**	
Typhimurium DT156	32.4	1.3	0.72-2.33	29.6	1.3	0.51-3.32	34.1	1.3	0.60-2.69
Typhimurium DT135	18.8	0.6	0.29-1.36	23.8	1.0	0.32-2.89	14.8	0.4	0.14-1.32

Salmonella serotype	Males and females five to 16 years			Females five to 16 years			Males five to 16 years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT1	32.7	1.3	0.67-2.55	26.7	1.1	0.33-3.83	35.3	1.3	0.60-2.98
Typhimurium DT101	18.2	0.6	0.26-1.37	11.8	0.4	0.09-1.92	22.2	0.7	0.26-1.87
Brandenburg	42.0	2.0	1.04-3.69	21.7	0.9	0.29-2.54	59.3	3.6	1.50-8.40
Enteritidis PT9a	29.0	1.1	0.48-2.54	14.3	0.5	0.11-2.45	41.2	1.7	0.60-4.85
Saintpaul	38.2	1.7	0.79-3.55	33.3	1.5	0.43-5.55	40.9	1.7	0.66-4.31
Typhimurium DT42	18.2	0.6	0.20-1.85	16.7	0.6	0.07-5.53	18.8	0.6	0.15-2.10
Infantis	18.9	0.6	0.19-2.10	42.9	2.3	0.48-11.03	4.3	0.1	0.01-1.94
Heidelberg	25.0	0.9	0.28-2.90	28.6	1.2	0.22-6.75	22.2	0.7	0.14-3.52
Typhimurium DT12a	17.2	0.6	0.14-2.27	9.1	0.3	0.02-5.84	22.2	0.7	0.14-3.52
Typhimurium DT23	52.9	3.0	1.12-8.24	37.5	1.8	0.41-8.29	66.7	4.9	1.16-20.62
Typhimurium RDNC-May 06	31.3	1.2	0.27-5.64	50.0	3.1	0.06-159.30	28.6	1.0	0.18-5.27
Typhimurium DT9	56.0	3.4	1.08-10.92	66.7	6.2	0.20-189.19	54.5	2.9	0.84-10.22
Typhimurium DT74	33.3	1.4	0.39-4.65	40.0	2.1	0.32-13.00	28.6	1.0	0.18-5.27
Typhimurium Not Typed	25.7	0.9	0.31-2.85	14.3	0.5	0.02-10.60	28.6	1.0	0.29-3.32
Typhimurium RDNC	33.3	1.4	0.39-4.65	66.7	6.2	0.54-70.85	22.2	0.7	0.14-3.52
Virchow	30.0	1.2	0.17-8.03	50.0	3.1	0.06-159.30	25.0	0.8	0.08-8.10
Enteritidis PT4	50.0	2.7	0.28-26.50	66.7	6.2	0.20-189.19	33.3	1.2	0.04-37.25
Mississippi	66.7	5.4	0.97-30.29	50.0	3.1	0.19-51.07	75.0	7.3	0.74-72.87
Stanley	33.3	1.4	0.12-15.19	33.3	1.5	0.05-47.30	33.3	1.2	0.04-37.25
Typhimurium Untypable	50.0	2.7	0.28-26.50	50.0	3.1	0.19-51.07	50.0	2.4	0.05-125.58
Salmonella species 4,5,12 : d :-	50.0	2.7	0.17-43.92	50.0	3.1	0.06-159.30	50.0	2.4	0.05-125.58
Weltevreden	28.6	1.1	0.10-11.21	20.0	0.8	0.03-17.64	50.0	2.4	0.05-125.58
Newport	33.3	1.4	0.12-15.19	33.3	1.5	0.05-47.30	33.3	1.2	0.04-37.25
Enteritidis PT1b	33.3	1.4	0.19-9.81	33.3	1.5	0.05-47.30	33.3	1.2	0.11-13.91
Agona	40.0	1.8	0.14-23.03	33.3	1.5	0.05-47.30	50.0	2.4	0.05-125.58
Thompson	50.0	2.7	0.28-26.50	33.3	1.5	0.05-47.30	66.7	4.9	0.16-148.99
Mbandaka	25.0	0.9	0.09-8.83	33.3	1.5	0.05-47.30	20.0	0.6	0.03-13.88
Corvallis	40.0	1.8	0.14-23.03	50.0	3.1	0.06-159.30	33.3	1.2	0.04-37.25
Montevideo	25.0	0.9	0.09-8.83	33.3	1.5	0.05-47.30	20.0	0.6	0.03-13.88
Hadar	66.7	5.4	0.48-60.74	66.7	6.2	0.20-189.19	66.7	4.9	0.16-148.99

Salmonella serotype	Males and females five to 16 years			Females five to 16 years			Males five to 16 years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Enteritidis PT1	33.3	1.4	0.12-15.19	33.3	1.5	0.05-47.30	33.3	1.2	0.04-37.25
Enteritidis PT6a	40.0	1.8	0.14-23.03	50.0	3.1	0.06-159.30	33.3	1.2	0.04-37.25

(D) Contact with recreational water

Salmonella serotype	Males and females five to 16 years			Females five to 16 years			Males five to 16 years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT160	**28.9**	**1(ref)**		**28.8**	**1(ref)**		**29.0**	**1(ref)**	
Typhimurium DT156	23.8	0.8	0.43-1.37	18.9	0.6	0.23-1.44	27.9	0.9	0.44-2.04
Typhimurium DT135	25.0	0.8	0.44-1.54	21.4	0.7	0.25-1.81	27.8	0.9	0.41-2.14
Typhimurium DT1	40.7	1.7	0.92-3.10	46.7	2.2	0.73-6.43	38.5	1.5	0.72-3.23
Typhimurium DT101	26.4	0.9	0.45-1.72	33.3	1.2	0.46-3.33	21.9	0.7	0.27-1.72
Brandenburg	18.6	0.6	0.28-1.15	20.0	0.6	0.21-1.78	17.6	0.5	0.20-1.37
Enteritidis PT9a	28.9	1.0	0.47-2.13	26.7	0.9	0.27-3.02	30.4	1.1	0.41-2.81
Saintpaul	55.3	3.0	1.51-6.09	28.6	1.0	0.29-3.37	70.8	5.9	2.28-15.49
Typhimurium DT42	33.3	1.2	0.53-2.86	42.9	1.9	0.39-8.72	30.0	1.0	0.38-2.93
Infantis	33.3	1.2	0.44-3.40	42.9	1.9	0.39-8.72	27.3	0.9	0.23-3.65
Heidelberg	22.2	0.7	0.22-2.21	28.6	1.0	0.18-5.34	18.2	0.5	0.11-2.64
Typhimurium DT12a	16.7	0.5	0.14-1.75	16.7	0.5	0.06-4.39	16.7	0.5	0.10-2.34
Typhimurium DT23	23.5	0.8	0.24-2.40	25.0	0.8	0.16-4.28	22.2	0.7	0.14-3.52
Typhimurium RDNC-May 06	10.0	0.3	0.03-2.20	33.3	1.2	0.04-37.69	5.9	0.2	0.01-2.73
Typhimurium DT9	28.6	1.0	0.37-2.63	80.0	9.9	1.07-91.65	12.5	0.3	0.08-1.61
Typhimurium DT74	14.3	0.4	0.09-1.88	25.0	0.8	0.08-8.20	10.0	0.3	0.03-2.22
Typhimurium Not Typed	18.9	0.6	0.17-1.90	9.1	0.2	0.01-4.65	23.1	0.7	0.19-2.82
Typhimurium RDNC	21.4	0.7	0.18-2.47	66.7	4.9	0.43-56.31	9.1	0.2	0.03-1.98
Virchow	70.0	5.7	0.83-39.61	50.0	2.5	0.05-127.06	75.0	7.3	0.74-72.83
Enteritidis PT4	61.5	3.9	0.79-19.56	66.7	4.9	0.16-150.76	60.0	3.7	0.59-22.85
Mississippi	70.6	5.9	1.32-26.46	85.7	14.8	0.72-303.86	60.0	3.7	0.59-22.85
Stanley	50.0	2.5	0.34-17.79	50.0	2.5	0.15-40.64	50.0	2.4	0.15-40.14

Salmonella serotype	Males and females five to 16 years			Females five to 16 years			Males five to 16 years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium Untypable	66.7	4.9	0.68-35.58	50.0	2.5	0.15-40.64	80.0	9.8	0.43-222.12
Salmonella species 4,5,12 : d :-	40.0	1.6	0.13-20.89	50.0	2.5	0.05-127.06	33.3	1.2	0.04-37.25
Weltevreden	28.6	1.0	0.10-10.16	20.0	0.6	0.03-14.05	50.0	2.4	0.05-125.60
Newport	62.5	4.1	0.53-31.60	80.0	9.9	0.43-224.82	33.3	1.2	0.04-37.25
Enteritidis PT1b	25.0	0.8	0.08-8.01	33.3	1.2	0.04-37.69	20.0	0.6	0.03-13.88
Agona	33.3	1.2	0.11-13.77	33.3	1.2	0.04-37.69	33.3	1.2	0.04-37.25
Thompson	33.3	1.2	0.11-13.77	33.3	1.2	0.04-37.69	33.3	1.2	0.04-37.25
Mbandaka	75.0	7.4	0.75-72.08	66.7	4.9	0.16-150.76	80.0	9.8	0.43-222.12
Corvallis	40.0	1.6	0.13-20.89	50.0	2.5	0.05-127.06	33.3	1.2	0.04-37.25
Montevideo	57.1	3.3	0.39-27.71	66.7	4.9	0.16-150.76	50.0	2.4	0.15-40.14
Hadar	33.3	1.2	0.11-13.77	33.3	1.2	0.04-37.69	33.3	1.2	0.04-37.25
Enteritidis PT1	50.0	2.5	0.25-24.03	66.7	4.9	0.16-150.76	33.3	1.2	0.04-37.25
Enteritidis PT6a	40.0	1.6	0.13-20.89	50.0	2.5	0.05-127.06	33.3	1.2	0.04-37.25

(E) Contact with farm animals

Salmonella serotype	Males and females five to 16 years			Females five to 16 years			Males five to 16 years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT160	**42.0**	**1(ref)**		**46.2**	**1(ref)**		**38.6**	**1(ref)**	
Typhimurium DT156	28.4	0.5	0.31-0.96	29.0	0.5	0.20-1.12	27.9	0.6	0.29-1.30
Typhimurium DT135	39.0	0.9	0.49-1.57	34.6	0.6	0.25-1.49	42.4	1.2	0.54-2.52
Typhimurium DT1	35.6	0.8	0.42-1.37	16.7	0.2	0.06-0.85	43.9	1.2	0.62-2.51
Typhimurium DT101	34.0	0.7	0.37-1.36	38.9	0.7	0.27-2.04	31.0	0.7	0.30-1.68
Brandenburg	71.9	3.5	1.89-6.61	64.0	2.1	0.85-5.05	78.1	5.7	2.30-13.99
Enteritidis PT9a	50.0	1.4	0.70-2.72	43.8	0.9	0.32-2.59	54.5	1.9	0.77-4.71
Saintpaul	34.1	0.7	0.36-1.43	26.7	0.4	0.13-1.40	38.5	1.0	0.42-2.34
Typhimurium DT42	34.8	0.7	0.30-1.79	42.9	0.9	0.19-4.07	31.3	0.7	0.24-2.19
Infantis	23.8	0.4	0.15-1.21	33.3	0.6	0.14-2.44	16.7	0.3	0.07-1.50
Heidelberg	20.0	0.3	0.11-1.06	14.3	0.2	0.02-1.66	23.1	0.5	0.13-1.81

Salmonella serotype	Males and females five to 16 years			Females five to 16 years			Males five to 16 years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT12a	45.0	1.1	0.45-2.81	28.6	0.5	0.09-2.49	53.8	1.9	0.59-5.80
Typhimurium DT23	33.3	0.7	0.25-1.89	37.5	0.7	0.16-3.05	30.0	0.7	0.17-2.74
Typhimurium RDNC-May 06	15.8	0.3	0.04-1.50	33.3	0.6	0.02-17.68	12.5	0.2	0.03-1.89
Typhimurium DT9	52.9	1.6	0.58-4.15	25.0	0.4	0.04-3.84	61.5	2.5	0.79-8.16
Typhimurium DT74	38.9	0.9	0.33-2.33	66.7	2.3	0.41-13.20	25.0	0.5	0.14-2.04
Typhimurium Not Typed	17.6	0.3	0.08-1.05	20.0	0.3	0.03-2.68	16.7	0.3	0.07-1.50
Typhimurium RDNC	25.0	0.5	0.14-1.46	50.0	1.2	0.23-6.00	10.0	0.2	0.02-1.43
Virchow	22.2	0.4	0.04-3.68	50.0	1.2	0.02-59.63	14.3	0.3	0.01-5.39
Enteritidis PT4	20.0	0.3	0.04-3.13	20.0	0.3	0.01-6.59	20.0	0.4	0.02-8.97
Mississippi	28.6	0.6	0.11-2.89	50.0	1.2	0.07-19.04	20.0	0.4	0.04-3.65
Stanley	33.3	0.7	0.10-4.97	20.0	0.3	0.01-6.59	50.0	1.6	0.10-25.93
Typhimurium Untypable	30.0	0.6	0.09-4.06	66.7	2.3	0.08-70.71	14.3	0.3	0.01-5.39
Salmonella species 4,5,12 : d :-	28.6	0.6	0.05-5.68	50.0	1.2	0.02-59.63	20.0	0.4	0.02-8.97
Weltevreden	22.2	0.4	0.04-3.68	14.3	0.2	0.01-3.96	50.0	1.6	0.03-81.25
Newport	25.0	0.5	0.05-4.48	20.0	0.3	0.01-6.59	33.3	0.8	0.03-24.08
Enteritidis PT1b	42.9	1.0	0.12-8.71	33.3	0.6	0.02-17.68	50.0	1.6	0.10-25.93
Agona	33.3	0.7	0.06-7.70	33.3	0.6	0.02-17.68	33.3	0.8	0.03-24.08
Thompson	50.0	1.4	0.14-13.43	33.3	0.6	0.02-17.68	66.7	3.2	0.10-96.32
Mbandaka	25.0	0.5	0.05-4.48	33.3	0.6	0.02-17.68	20.0	0.4	0.02-8.97
Corvallis	60.0	2.1	0.16-26.27	50.0	1.2	0.02-59.63	66.7	3.2	0.10-96.32
Montevideo	25.0	0.5	0.05-4.48	33.3	0.6	0.02-17.68	20.0	0.4	0.02-8.97
Hadar	33.3	0.7	0.06-7.70	33.3	0.6	0.02-17.68	33.3	0.8	0.03-24.08
Enteritidis PT1	33.3	0.7	0.06-7.70	33.3	0.6	0.02-17.68	33.3	0.8	0.03-24.08
Enteritidis PT6a	40.0	0.9	0.07-11.68	50.0	1.2	0.02-59.63	33.3	0.8	0.03-24.08

(F) Contact with sick animals

Salmonella serotype	Males and females five to 16 years			Females five to 16 years			Males five to 16 years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT160	**7.3**	**1(ref)**		**8.3**	**1(ref)**		**6.5**	**1.0**	
Typhimurium DT156	9.0	1.2	0.47-3.29	12.0	1.5	0.38-6.06	7.1	1.1	0.28-4.38
Typhimurium DT135	4.0	0.5	0.12-2.36	4.8	0.6	0.07-4.63	3.4	0.5	0.06-4.28
Typhimurium DT1	13.0	1.9	0.74-4.80	12.5	1.6	0.31-8.11	13.2	2.2	0.67-7.11
Typhimurium DT101	8.2	1.1	0.34-3.77	3.0	0.3	0.02-6.29	11.5	1.9	0.46-7.61
Brandenburg	29.5	5.3	2.35-11.97	33.3	5.6	1.79-17.29	26.1	5.1	1.57-16.42
Enteritidis PT9a	17.6	2.7	0.99-7.45	28.6	4.4	1.16-17.06	10.0	1.6	0.31-8.13
Saintpaul	4.0	0.5	0.10-2.90	3.4	0.4	0.02-7.23	4.3	0.7	0.08-5.49
Typhimurium DT42	4.8	0.6	0.08-5.00	7.7	0.9	0.05-17.95	3.4	0.5	0.03-9.43
Infantis	5.3	0.7	0.09-5.59	6.7	0.8	0.04-15.15	4.3	0.7	0.04-12.16
Heidelberg	10.3	1.5	0.25-8.49	20.0	2.8	0.28-27.57	5.3	0.8	0.04-15.06
Typhimurium DT12a	28.6	5.1	1.43-17.84	20.0	2.8	0.28-27.57	33.3	7.2	1.51-34.21
Typhimurium DT23	9.7	1.4	0.23-7.84	14.3	1.9	0.20-17.12	5.9	0.9	0.05-17.09
Typhimurium RDNC-May 06	15.8	2.4	0.39-14.53	33.3	5.6	0.17-177.23	12.5	2.1	0.22-18.80
Typhimurium DT9	33.3	6.3	2.03-19.70	14.3	1.9	0.09-39.92	38.5	9.0	2.38-33.88
Typhimurium DT74	6.3	0.8	0.10-6.77	11.1	1.4	0.07-28.41	4.3	0.7	0.04-12.16
Typhimurium Not Typed	5.9	0.8	0.10-6.33	11.1	1.4	0.07-28.41	4.0	0.6	0.03-11.09
Typhimurium RDNC	10.3	1.5	0.25-8.49	9.1	1.1	0.06-22.01	11.1	1.8	0.20-16.20
Virchow	22.2	3.6	0.37-35.21	50.0	11.1	0.21-593.98	14.3	2.4	0.11-52.05
Enteritidis PT4	20.0	3.2	0.33-29.89	20.0	2.8	0.12-66.34	20.0	3.6	0.15-86.49
Mississippi	11.1	1.6	0.19-13.39	14.3	1.9	0.09-39.92	9.1	1.4	0.07-28.71
Stanley	25.0	4.2	0.42-42.75	20.0	2.8	0.12-66.34	33.3	7.2	0.22-230.90
Typhimurium Untypable	25.0	4.2	0.42-42.75	33.3	5.6	0.17-177.23	20.0	3.6	0.15-86.49
Salmonella species 4,5,12 : d :-	28.6	5.1	0.47-54.18	50.0	11.1	0.21-593.98	20.0	3.6	0.15-86.49
Weltevreden	28.6	5.1	0.47-54.18	20.0	2.8	0.12-66.34	50.0	14.4	0.27-773.14
Newport	25.0	4.2	0.42-42.75	20.0	2.8	0.12-66.34	33.3	7.2	0.22-230.90
Enteritidis PT1b	25.0	4.2	0.42-42.75	33.3	5.6	0.17-177.23	20.0	3.6	0.15-86.49
Agona	33.3	6.3	0.55-73.34	33.3	5.6	0.17-177.23	33.3	7.2	0.22-230.90
Thompson	33.3	6.3	0.55-73.34	33.3	5.6	0.17-177.23	33.3	7.2	0.22-230.90

Salmonella serotype	Males and females five to 16 years			Females five to 16 years			Males five to 16 years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Mbandaka	25.0	4.2	0.42-42.75	33.3	5.6	0.17-177.23	20.0	3.6	0.15-86.49
Corvallis	40.0	8.4	0.64-111.06	50.0	11.1	0.21-593.98	33.3	7.2	0.22-230.90
Montevideo	25.0	4.2	0.42-42.75	33.3	5.6	0.17-177.23	20.0	3.6	0.15-86.49
Hadar	33.3	6.3	0.55-73.34	33.3	5.6	0.17-177.23	33.3	7.2	0.22-230.90
Enteritidis PT1	40.0	8.4	0.64-111.06	33.3	5.6	0.17-177.23	50.0	14.4	0.27-773.14
Enteritidis PT6a	40.0	8.4	0.64-111.06	50.0	11.1	0.21-593.98	33.3	7.2	0.22-230.90

(G) Contact with human faeces

Salmonella serotype	Males and females five to 16 years			Females five to 16 years			Males five to 16 years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT160	**10.1**	**1(ref)**		**9.3**	**1(ref)**		**10.9**	**1(ref)**	
Typhimurium DT156	5.9	0.6	0.19-1.66	10.3	1.1	0.29-4.41	2.6	0.2	0.03-1.70
Typhimurium DT135	10.5	1.0	0.41-2.69	15.4	1.8	0.51-6.21	6.5	0.6	0.12-2.63
Typhimurium DT1	7.5	0.7	0.24-2.18	5.6	0.6	0.07-4.80	8.6	0.8	0.21-2.85
Typhimurium DT101	5.1	0.5	0.11-2.12	6.7	0.7	0.08-5.89	4.2	0.4	0.04-2.85
Brandenburg	8.0	0.8	0.24-2.51	15.0	1.7	0.43-6.94	2.1	0.2	0.01-3.11
Enteritidis PT9a	8.6	0.8	0.24-2.92	6.3	0.7	0.08-5.48	10.5	1.0	0.20-4.63
Saintpaul	3.9	0.4	0.07-1.94	3.4	0.4	0.02-6.33	4.2	0.4	0.04-2.85
Typhimurium DT42	11.1	1.1	0.28-4.41	7.7	0.8	0.04-15.72	12.5	1.2	0.24-5.71
Infantis	12.8	1.3	0.32-5.26	5.9	0.6	0.03-11.47	18.2	1.8	0.36-9.31
Heidelberg	8.6	0.8	0.15-4.67	9.1	1.0	0.05-19.28	8.3	0.7	0.09-6.23
Typhimurium DT12a	15.8	1.7	0.45-6.13	16.7	2.0	0.21-18.48	15.4	1.5	0.30-7.44
Typhimurium DT23	5.6	0.5	0.07-4.10	5.9	0.6	0.03-11.47	5.3	0.5	0.03-8.30
Typhimurium RDNC-May 06	16.7	1.8	0.29-10.77	66.7	19.6	0.62-621.50	6.7	0.6	0.03-10.90
Typhimurium DT9	22.6	2.6	0.73-9.16	20.0	2.5	0.10-58.13	23.1	2.5	0.60-10.04
Typhimurium DT74	5.9	0.6	0.07-4.37	7.7	0.8	0.04-15.72	4.8	0.4	0.02-7.42
Typhimurium Not Typed	8.6	0.8	0.15-4.67	25.0	3.3	0.31-34.42	3.7	0.3	0.02-5.62
Typhimurium RDNC	6.3	0.6	0.07-4.68	9.1	1.0	0.05-19.28	4.8	0.4	0.02-7.42

Salmonella serotype	Males and females five to 16 years			Females five to 16 years			Males five to 16 years		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Virchow	37.5	5.3	0.67-42.11	50.0	9.8	0.18-521.14	33.3	4.1	0.35-48.26
Enteritidis PT4	16.7	1.8	0.20-15.83	20.0	2.5	0.10-58.13	14.3	1.4	0.07-28.76
Mississippi	23.1	2.7	0.41-17.32	20.0	2.5	0.10-58.13	25.0	2.7	0.27-28.15
Stanley	33.3	4.4	0.39-50.78	33.3	4.9	0.15-155.38	33.3	4.1	0.13-128.07
Typhimurium Untypable	20.0	2.2	0.24-20.67	33.3	4.9	0.15-155.38	14.3	1.4	0.07-28.76
Salmonella species 4,5,12 : d :-	28.6	3.6	0.34-37.49	50.0	9.8	0.18-521.14	20.0	2.1	0.09-47.84
Weltevreden	22.2	2.5	0.26-24.35	14.3	1.6	0.08-34.97	50.0	8.2	0.16-430.50
Newport	25.0	3.0	0.30-29.57	20.0	2.5	0.10-58.13	33.3	4.1	0.13-128.07
Enteritidis PT1b	25.0	3.0	0.30-29.57	33.3	4.9	0.15-155.38	20.0	2.1	0.09-47.84
Agona	40.0	5.9	0.45-76.94	33.3	4.9	0.15-155.38	50.0	8.2	0.16-430.50
Thompson	33.3	4.4	0.39-50.78	33.3	4.9	0.15-155.38	33.3	4.1	0.13-128.07
Mbandaka	25.0	3.0	0.30-29.57	33.3	4.9	0.15-155.38	20.0	2.1	0.09-47.84
Corvallis	28.6	3.6	0.34-37.49	50.0	9.8	0.18-521.14	20.0	2.1	0.09-47.84
Montevideo	42.9	6.7	0.77-57.64	33.3	4.9	0.15-155.38	50.0	8.2	0.49-138.76
Hadar	33.3	4.4	0.39-50.78	33.3	4.9	0.15-155.38	33.3	4.1	0.13-128.07
Enteritidis PT1	40.0	5.9	0.45-76.94	33.3	4.9	0.15-155.38	50.0	8.2	0.16-430.50
Enteritidis PT6a	40.0	5.9	0.45-76.94	50.0	9.8	0.18-521.14	33.3	4.1	0.13-128.07

7.6 Appendix 6: *Salmonella* serotype case-case analysis for each risk factor, referenced to *S.* Typhimurium DT160 in cases aged 17 years or older

(A) Overseas travel

Salmonella serotype	Males and females 17 years or older			Females 17 years or older			Males 17 years or older		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT160	**1.9**	**1(ref)**		**1.5**	**1(ref)**		**2.3**	**1(ref)**	
Infantis	6.5	3.7	1.80-7.61	7.6	5.4	1.94-15.26	5.5	2.5	0.88-6.96
Typhimurium DT135	9.3	5.4	2.79-10.56	10.2	7.6	2.84-20.07	8.5	3.9	1.58-9.87
Typhimurium DT1	4.3	2.4	1.08-5.36	3.3	2.3	0.63-8.17	5.3	2.4	0.85-6.74
Brandenburg	1.9	1.0	0.35-2.98	0.5	0.4	0.02-6.51	2.8	1.2	0.36-4.09
Typhimurium DT101	3.1	1.7	0.59-4.71	3.8	2.7	0.65-10.84	2.4	1.0	0.21-4.94
Enteritidis PT9a	3.7	2.0	0.76-5.34	3.9	2.7	0.66-10.99	3.5	1.5	0.40-5.95
Typhimurium DT156	1.1	0.6	0.11-3.17	0.7	0.5	0.03-8.97	1.4	0.6	0.08-5.03
Typhimurium DT42	4.3	2.4	0.72-7.83	7.3	5.2	1.26-21.78	1.2	0.5	0.03-9.48
Typhimurium DT12a	14.1	8.7	3.79-19.87	17.5	14.1	4.47-44.30	10.5	5.0	1.44-17.57
Typhimurium DT9	8.2	4.7	1.76-12.72	10.0	7.4	1.99-27.33	6.1	2.8	0.56-13.56
Saintpaul	13.6	8.3	3.63-18.99	8.7	6.3	1.71-23.29	20.0	10.7	3.61-31.63
Virchow	76.1	167.9	78.57-358.80	63.3	114.6	38.29-342.85	85.4	249.4	81.84-759.88
Heidelberg	11.7	7.0	2.70-18.04	5.0	3.5	0.68-17.90	25.0	14.3	4.16-48.81
Typhimurium RDNC	30.2	22.9	10.38-50.34	19.2	15.8	4.46-55.98	40.7	29.4	10.39-83.12
Thompson	10.0	5.9	2.03-17.03	8.0	5.8	1.10-30.17	12.0	5.8	1.44-23.53
Weltevreden	77.6	182.6	77.71-429.08	83.9	344.9	98.69-1,205.62	66.7	85.5	25.63-285.27
Enteritidis PT4	80.3	215.8	94.73-491.76	85.3	384.7	110.75-1,336.52	74.1	122.1	40.25-370.66
Typhimurium Not Typed	15.9	10.0	3.81-26.26	8.7	6.3	1.20-33.21	23.8	13.4	3.93-45.46
Agona	60.0	79.3	35.73-175.93	66.7	132.7	39.41-446.55	54.2	50.5	17.40-146.69
Typhimurium DT23	5.6	3.1	0.79-12.52	8.7	6.3	1.20-33.21	2.3	1.0	0.06-18.33
Mbandaka	34.2	27.5	11.70-64.54	50.0	66.3	20.77-211.85	12.5	6.1	1.19-31.45
Montevideo	44.1	41.7	17.68-98.51	54.5	79.6	24.86-254.86	25.0	14.3	3.23-62.78
Typhimurium Untypable	46.2	45.3	19.91-103.09	50.0	66.3	19.46-226.08	42.9	32.1	10.54-97.57
Mississippi	17.5	11.2	4.24-29.64	33.3	33.2	8.66-126.99	8.0	3.7	0.75-18.52

Salmonella serotype	Males and females 17 years or older			Females 17 years or older			Males 17 years or older		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium RDNC-May 06	3.7	2.0	0.26-16.05	3.7	2.6	0.14-48.14	3.7	1.6	0.09-30.19
Enteritidis PT6a	92.8	676.6	168.26-2,720.42	97.4	2520.7	135.74-46,807.73	86.7	277.9	53.61-1,440.42
Typhimurium DT74	6.5	3.6	0.79-16.79	6.3	4.4	0.50-39.08	6.7	3.1	0.36-26.12
Corvallis	88.2	396.4	123.08-1,276.82	88.2	497.5	92.60-2,672.88	88.2	320.6	62.60-1,642.18
Salmonella species 4,5,12 : d :-	83.3	264.3	94.95-735.61	78.6	243.2	53.74-1,100.85	86.4	270.8	66.43-1,103.50
Stanley	76.7	173.7	64.04-471.01	72.2	172.5	46.58-638.62	83.3	213.8	40.15-1,138.02
Enteritidis PT1b	77.2	178.9	64.36-497.30	94.1	1061.3	54.52-20,661.03	70.0	99.8	30.47-326.51
Hadar	80.0	211.4	79.14-564.83	78.9	248.8	63.45-975.18	81.3	185.3	43.98-780.22
Newport	53.1	59.9	25.03-143.38	31.6	30.6	8.69-107.85	84.6	235.1	44.63-1,238.78
Enteritidis PT1	83.3	264.3	88.31-790.92	86.7	431.2	79.32-2,343.70	80.0	171.0	40.26-726.38

(B) Food consumption from a premise

Salmonella serotype	Males and females 17 years or older			Females 17 years or older			Males 17 years or older		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT160	**54.3**	**1(ref)**		**58.7**	**1(ref)**		**49.2**	**1(ref)**	
Infantis	52.5	0.9	0.66-1.31	52.6	0.8	0.49-1.24	52.4	1.1	0.69-1.87
Typhimurium DT135	63.6	1.5	1.05-2.07	69.1	1.6	0.97-2.56	57.8	1.4	0.87-2.29
Typhimurium DT1	51.6	0.9	0.63-1.27	58.2	1.0	0.59-1.62	45.1	0.8	0.51-1.40
Brandenburg	33.7	0.4	0.30-0.61	37.1	0.4	0.24-0.71	31.5	0.5	0.30-0.76
Typhimurium DT101	52.9	0.9	0.64-1.41	55.9	0.9	0.51-1.57	50.0	1.0	0.59-1.81
Enteritidis PT9a	53.3	1.0	0.65-1.43	59.6	1.0	0.58-1.85	47.6	0.9	0.54-1.63
Typhimurium DT156	55.1	1.0	0.66-1.61	60.5	1.1	0.56-2.07	50.0	1.0	0.55-1.93
Typhimurium DT42	55.2	1.0	0.62-1.73	65.7	1.4	0.65-2.82	43.8	0.8	0.38-1.68
Typhimurium DT12a	54.5	1.0	0.54-1.87	50.0	0.7	0.31-1.62	60.0	1.5	0.61-3.91
Typhimurium DT9	43.3	0.6	0.38-1.10	57.6	1.0	0.46-1.98	25.9	0.4	0.15-0.88
Saintpaul	47.5	0.8	0.44-1.30	55.3	0.9	0.44-1.72	33.3	0.5	0.20-1.32
Virchow	46.2	0.7	0.38-1.38	38.1	0.4	0.17-1.08	55.6	1.3	0.49-3.37
Heidelberg	61.7	1.4	0.73-2.50	53.3	0.8	0.38-1.71	76.5	3.4	1.06-10.56

Salmonella serotype	Males and females 17 years or older			Females 17 years or older			Males 17 years or older		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium RDNC	66.7	1.7	0.74-3.81	73.3	1.9	0.60-6.23	58.3	1.4	0.45-4.67
Thompson	59.4	1.2	0.59-2.54	55.0	0.9	0.35-2.14	66.7	2.1	0.61-7.03
Weltevreden	52.2	0.9	0.40-2.11	53.8	0.8	0.27-2.51	50.0	1.0	0.29-3.65
Enteritidis PT4	51.9	0.9	0.42-1.96	42.9	0.5	0.18-1.56	61.5	1.7	0.53-5.18
Typhimurium Not Typed	67.6	1.8	0.84-3.68	73.3	1.9	0.60-6.23	63.2	1.8	0.67-4.64
Agona	48.0	0.8	0.35-1.73	45.5	0.6	0.18-1.97	50.0	1.0	0.35-3.03
Typhimurium DT23	65.4	1.6	0.70-3.62	66.7	1.4	0.42-4.78	64.3	1.9	0.61-5.70
Mbandaka	58.3	1.2	0.51-2.69	60.0	1.1	0.37-3.05	55.6	1.3	0.34-4.91
Montevideo	63.6	1.5	0.61-3.56	50.0	0.7	0.22-2.24	80.0	4.1	0.86-19.82
Typhimurium Untypable	45.0	0.7	0.28-1.69	60.0	1.1	0.29-3.82	30.0	0.4	0.11-1.75
Mississippi	52.2	0.9	0.40-2.11	75.0	2.1	0.42-10.65	40.0	0.7	0.24-1.99
Typhimurium RDNC-May 06	55.6	1.1	0.41-2.70	60.0	1.1	0.29-3.82	50.0	1.0	0.25-4.22
Enteritidis PT6a	58.8	1.2	0.45-3.20	70.0	1.6	0.42-6.48	42.9	0.8	0.17-3.53
Typhimurium DT74	42.9	0.6	0.26-1.52	54.5	0.8	0.25-2.83	30.0	0.4	0.11-1.75
Corvallis	38.5	0.5	0.17-1.63	33.3	0.4	0.09-1.44	50.0	1.0	0.14-7.44
Salmonella species 4,5,12 : d :-	58.3	1.2	0.37-3.75	60.0	1.1	0.17-6.42	57.1	1.4	0.30-6.27
Stanley	44.4	0.7	0.26-1.73	53.8	0.8	0.27-2.51	20.0	0.3	0.03-2.34
Enteritidis PT1b	61.5	1.3	0.43-4.16	66.7	1.4	0.13-15.71	60.0	1.5	0.43-5.62
Hadar	47.4	0.8	0.21-2.73	66.7	1.4	0.25-7.81	14.3	0.2	0.01-3.47
Newport	64.3	1.5	0.50-4.57	63.6	1.2	0.35-4.30	66.7	2.1	0.18-23.05
Enteritidis PT1	50.0	0.8	0.27-2.64	44.4	0.6	0.15-2.14	66.7	2.1	0.18-23.05

(C) Consumption of untreated drinking water

Salmonella serotype	Males and females 17 years or older			Females 17 years or older			Males 17 years or older		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT160	**20.0**	**1(ref)**		**18.3**	**1(ref)**		**21.8**	**1(ref)**	
Infantis	10.9	0.5	0.30-0.81	12.4	0.6	0.32-1.23	9.2	0.4	0.17-0.79
Typhimurium DT135	15.8	0.8	0.49-1.16	11.0	0.6	0.28-1.10	20.8	0.9	0.54-1.66

Salmonella serotype	Males and females 17 years or older			Females 17 years or older			Males 17 years or older		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT1	23.7	1.2	0.84-1.84	23.1	1.3	0.76-2.36	24.2	1.1	0.66-1.97
Brandenburg	37.7	2.4	1.71-3.43	25.7	1.5	0.85-2.80	44.8	2.9	1.85-4.55
Typhimurium DT101	16.7	0.8	0.47-1.36	13.2	0.7	0.29-1.58	19.7	0.9	0.44-1.75
Enteritidis PT9a	26.1	1.4	0.89-2.26	20.8	1.2	0.57-2.41	31.0	1.6	0.86-3.00
Typhimurium DT156	24.2	1.3	0.76-2.15	20.9	1.2	0.54-2.60	27.1	1.3	0.66-2.66
Typhimurium DT42	17.7	0.9	0.44-1.71	25.8	1.6	0.66-3.65	9.7	0.4	0.11-1.30
Typhimurium DT12a	14.9	0.7	0.31-1.60	8.7	0.4	0.10-1.87	20.8	0.9	0.34-2.62
Typhimurium DT9	44.7	3.2	1.76-5.95	42.3	3.3	1.43-7.51	47.6	3.3	1.32-8.00
Saintpaul	37.7	2.4	1.39-4.22	25.0	1.5	0.67-3.34	56.0	4.6	1.97-10.52
Virchow	10.6	0.5	0.13-1.80	4.3	0.2	0.01-3.51	16.7	0.7	0.15-3.35
Heidelberg	10.4	0.5	0.18-1.20	12.1	0.6	0.21-1.82	6.7	0.3	0.03-1.98
Typhimurium RDNC	6.7	0.3	0.07-1.22	6.3	0.3	0.04-2.30	7.1	0.3	0.04-2.14
Thompson	10.8	0.5	0.17-1.40	10.0	0.5	0.11-2.20	11.8	0.5	0.11-2.14
Weltevreden	17.1	0.8	0.26-2.65	25.0	1.5	0.39-5.68	5.9	0.2	0.01-3.95
Enteritidis PT4	12.0	0.5	0.16-1.86	6.7	0.3	0.04-2.48	20.0	0.9	0.19-4.32
Typhimurium Not Typed	20.0	1.0	0.43-2.35	22.2	1.3	0.41-4.02	17.6	0.8	0.21-2.75
Agona	12.0	0.5	0.16-1.86	8.3	0.4	0.05-3.21	15.4	0.7	0.14-3.01
Typhimurium DT23	35.5	2.2	1.03-4.72	42.1	3.3	1.25-8.44	25.0	1.2	0.31-4.54
Mbandaka	4.5	0.2	0.03-1.43	3.4	0.2	0.01-2.72	6.7	0.3	0.01-4.56
Montevideo	22.7	1.2	0.43-3.26	27.3	1.7	0.43-6.52	18.2	0.8	0.17-3.77
Typhimurium Untypable	30.4	1.8	0.71-4.36	33.3	2.2	0.65-7.68	27.3	1.3	0.35-5.20
Mississippi	20.8	1.1	0.39-2.88	20.0	1.1	0.23-5.40	21.4	1.0	0.26-3.60
Typhimurium RDNC-May 06	16.7	0.8	0.23-2.81	10.0	0.5	0.06-4.00	25.0	1.2	0.24-6.05
Enteritidis PT6a	12.0	0.5	0.10-3.04	14.3	0.7	0.09-6.31	9.1	0.4	0.02-6.64
Typhimurium DT74	16.7	0.8	0.27-2.39	23.1	1.3	0.36-5.03	9.1	0.4	0.04-2.85
Corvallis	9.1	0.4	0.05-3.16	7.7	0.4	0.02-6.77	11.1	0.4	0.02-8.57
Salmonella species 4,5,12 : d :-	16.1	0.8	0.20-3.03	7.7	0.4	0.02-6.77	22.2	1.0	0.21-5.04
Stanley	12.0	0.5	0.10-3.04	11.1	0.6	0.07-4.56	14.3	0.6	0.03-12.06
Enteritidis PT1b	33.3	2.0	0.59-6.76	66.7	8.9	0.80-100.34	22.2	1.0	0.21-5.04
Hadar	20.0	1.0	0.21-4.78	16.7	0.9	0.10-7.80	25.0	1.2	0.12-11.66

Salmonella serotype	Males and females 17 years or older			Females 17 years or older			Males 17 years or older		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Newport	24.1	1.3	0.38-4.32	27.3	1.7	0.43-6.52	14.3	0.6	0.03-12.06
Enteritidis PT1	38.5	2.5	0.81-7.79	22.2	1.3	0.26-6.31	75.0	10.7	1.10-104.96

(D) Contact with recreational water

Salmonella serotype	Males and females 17 years or older			Females 17 years or older			Males 17 years or older		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT160	**6.7**	**1(ref)**		**6.7**	**1(ref)**		**6.6**	**1(ref)**	
Infantis	9.5	1.5	0.85-2.54	11.3	1.8	0.87-3.63	7.5	1.2	0.49-2.71
Typhimurium DT135	9.4	1.5	0.86-2.47	8.9	1.4	0.64-2.87	9.9	1.6	0.74-3.29
Typhimurium DT1	10.4	1.6	0.95-2.80	5.7	0.8	0.33-2.13	15.1	2.5	1.25-5.06
Brandenburg	4.1	0.6	0.30-1.22	3.2	0.5	0.13-1.54	4.7	0.7	0.29-1.70
Typhimurium DT101	7.6	1.2	0.57-2.37	10.9	1.7	0.70-4.17	4.5	0.7	0.19-2.30
Enteritidis PT9a	11.3	1.8	0.96-3.31	14.5	2.4	1.04-5.38	8.5	1.3	0.50-3.38
Typhimurium DT156	13.9	2.3	1.21-4.23	12.2	1.9	0.75-5.04	15.3	2.5	1.10-5.91
Typhimurium DT42	12.7	2.0	0.95-4.37	15.2	2.5	0.88-7.04	10.5	1.7	0.54-5.16
Typhimurium DT12a	17.5	3.0	1.41-6.31	21.4	3.8	1.40-10.28	13.8	2.3	0.72-7.14
Typhimurium DT9	2.3	0.3	0.06-1.68	1.4	0.2	0.01-3.25	3.3	0.5	0.06-3.77
Saintpaul	10.1	1.6	0.68-3.67	9.5	1.5	0.48-4.46	11.1	1.8	0.49-6.38
Virchow	33.3	7.0	3.28-14.98	26.3	5.0	1.65-15.01	41.2	9.9	3.41-28.79
Heidelberg	11.5	1.8	0.74-4.52	5.9	0.9	0.20-3.86	22.2	4.0	1.22-13.43
Typhimurium RDNC	19.4	3.4	1.31-8.64	11.1	1.7	0.38-8.03	30.8	6.3	1.78-22.22
Thompson	4.1	0.6	0.11-3.17	2.3	0.3	0.02-5.65	6.7	1.0	0.13-8.08
Weltevreden	31.0	6.3	2.71-14.70	35.3	7.6	2.57-22.37	25.0	4.7	1.18-18.81
Enteritidis PT4	21.2	3.8	1.55-9.19	16.7	2.8	0.75-10.31	26.7	5.1	1.50-17.62
Typhimurium Not Typed	15.4	2.5	1.01-6.42	10.0	1.5	0.34-7.07	21.1	3.8	1.15-12.43
Agona	13.3	2.2	0.72-6.46	13.3	2.1	0.46-10.06	13.3	2.2	0.46-10.32
Typhimurium DT23	6.8	1.0	0.28-3.86	9.5	1.5	0.32-6.68	3.2	0.5	0.03-8.19
Mbandaka	27.6	5.3	2.24-12.77	33.3	7.0	2.39-20.23	18.2	3.1	0.64-15.54

Salmonella serotype	Males and females 17 years or older			Females 17 years or older			Males 17 years or older		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Montevideo	9.8	1.5	0.40-5.83	13.3	2.1	0.46-10.06	4.8	0.7	0.04-12.56
Typhimurium Untypable	3.7	0.5	0.07-4.07	3.7	0.5	0.03-9.31	3.7	0.5	0.03-9.51
Mississippi	9.4	1.5	0.42-4.95	18.2	3.1	0.63-15.15	4.8	0.7	0.09-5.55
Typhimurium RDNC-May 06	10.5	1.6	0.37-7.38	10.0	1.5	0.19-12.74	11.1	1.8	0.21-14.85
Enteritidis PT6a	18.8	3.2	0.89-11.79	20.0	3.5	0.70-17.34	16.7	2.8	0.32-25.40
Typhimurium DT74	13.0	2.1	0.60-7.36	15.4	2.5	0.53-12.10	10.0	1.6	0.19-13.04
Corvallis	12.5	2.0	0.44-9.10	11.1	1.7	0.21-14.51	14.3	2.4	0.27-20.55
Salmonella species 4,5,12 : d :-	31.6	6.5	2.34-17.87	37.5	8.3	1.88-37.14	27.3	5.3	1.31-21.57
Stanley	26.3	5.0	1.72-14.56	21.4	3.8	0.99-14.56	40.0	9.4	1.49-59.74
Enteritidis PT1b	22.6	4.1	1.20-14.00	11.1	1.7	0.09-33.91	27.3	5.3	1.31-21.57
Hadar	25.0	4.7	1.45-15.11	22.2	4.0	0.78-20.24	28.6	5.7	1.03-31.03
Newport	10.0	1.6	0.35-6.94	7.7	1.2	0.14-9.31	14.3	2.4	0.27-20.55
Enteritidis PT1	40.0	9.3	3.18-27.48	20.0	3.5	0.70-17.34	80.0	56.6	6.04-530.48

(E) Contact with farm animals

Salmonella serotype	Males and females 17 years or older			Females 17 years or older			Males 17 years or older		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT160	**24.5**	**1(ref)**		**23.6**	**1(ref)**		**25.6**	**1(ref)**	
Infantis	19.6	0.8	0.52-1.09	16.7	0.6	0.38-1.11	23.1	0.9	0.52-1.47
Typhimurium DT135	26.7	1.1	0.79-1.57	21.0	0.9	0.51-1.45	31.7	1.3	0.85-2.13
Typhimurium DT1	36.2	1.7	1.26-2.41	27.6	1.2	0.76-2.02	43.7	2.3	1.45-3.50
Brandenburg	59.8	4.6	3.35-6.23	48.9	3.1	1.94-4.96	66.7	5.8	3.80-8.87
Typhimurium DT101	29.9	1.3	0.88-1.97	22.2	0.9	0.49-1.76	36.5	1.7	0.98-2.85
Enteritidis PT9a	28.8	1.2	0.83-1.85	21.4	0.9	0.48-1.64	35.5	1.6	0.94-2.72
Typhimurium DT156	34.2	1.6	1.05-2.42	31.6	1.5	0.81-2.74	36.5	1.7	0.94-2.95
Typhimurium DT42	22.2	0.9	0.49-1.57	22.9	1.0	0.42-2.19	21.6	0.8	0.35-1.82
Typhimurium DT12a	33.3	1.5	0.88-2.70	31.0	1.5	0.64-3.32	35.5	1.6	0.73-3.47
Typhimurium DT9	48.0	2.8	1.59-5.08	34.6	1.7	0.74-3.98	62.5	4.8	2.04-11.47

Salmonella serotype	Males and females 17 years or older			Females 17 years or older			Males 17 years or older		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Saintpaul	36.6	1.8	1.06-2.97	26.8	1.2	0.57-2.47	50.0	2.9	1.36-6.20
Virchow	9.1	0.3	0.11-0.87	12.5	0.5	0.13-1.59	5.0	0.2	0.02-1.16
Heidelberg	19.3	0.7	0.37-1.45	13.9	0.5	0.20-1.38	28.6	1.2	0.44-3.09
Typhimurium RDNC	16.7	0.6	0.27-1.41	13.0	0.5	0.14-1.67	21.1	0.8	0.25-2.40
Thompson	17.4	0.6	0.30-1.42	16.7	0.6	0.22-1.95	18.2	0.6	0.21-1.96
Weltevreden	9.1	0.3	0.09-1.02	10.0	0.4	0.08-1.58	7.7	0.2	0.03-1.89
Enteritidis PT4	17.1	0.6	0.26-1.56	17.4	0.7	0.23-2.06	16.7	0.6	0.12-2.70
Typhimurium Not Typed	15.0	0.5	0.22-1.32	23.8	1.0	0.36-2.84	5.3	0.2	0.02-1.23
Agona	6.7	0.2	0.05-0.93	7.1	0.2	0.03-1.93	6.3	0.2	0.03-1.49
Typhimurium DT23	44.7	2.5	1.28-4.83	45.0	2.6	1.06-6.60	44.4	2.3	0.89-6.08
Mbandaka	6.5	0.2	0.05-0.90	5.3	0.2	0.02-1.37	8.3	0.3	0.03-2.08
Montevideo	12.3	0.4	0.14-1.34	21.4	0.9	0.24-3.24	3.4	0.1	0.01-1.76
Typhimurium Untypable	34.6	1.6	0.71-3.72	35.7	1.8	0.59-5.51	33.3	1.5	0.43-4.95
Mississippi	14.3	0.5	0.19-1.41	4.8	0.2	0.01-2.80	19.0	0.7	0.22-2.09
Typhimurium RDNC-May 06	29.2	1.3	0.52-3.11	25.0	1.1	0.29-4.08	33.3	1.5	0.43-4.95
Enteritidis PT6a	5.0	0.2	0.02-1.22	4.3	0.1	0.01-2.53	5.9	0.2	0.01-3.19
Typhimurium DT74	31.0	1.4	0.62-3.10	20.0	0.8	0.22-2.93	42.9	2.2	0.73-6.46
Corvallis	8.6	0.3	0.05-1.55	9.1	0.3	0.04-2.57	7.7	0.2	0.01-4.38
Salmonella species 4,5,12 : d :-	11.6	0.4	0.11-1.53	5.3	0.2	0.01-3.13	16.7	0.6	0.12-2.70
Stanley	8.1	0.3	0.05-1.45	9.1	0.3	0.04-2.57	6.7	0.2	0.01-3.69
Enteritidis PT1b	18.8	0.7	0.20-2.52	25.0	1.1	0.11-10.51	16.7	0.6	0.12-2.70
Hadar	20.0	0.8	0.21-2.76	20.0	0.8	0.17-3.88	20.0	0.7	0.08-6.59
Newport	26.1	1.1	0.42-2.80	25.0	1.1	0.34-3.43	28.6	1.2	0.22-6.10
Enteritidis PT1	5.3	0.2	0.02-1.29	4.3	0.1	0.01-2.53	6.7	0.2	0.01-3.69

(F) Contact with sick animals

Salmonella serotype	Males and females 17 years or older			Females 17 years or older			Males 17 years or older		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT160	**5.7**	**1(ref)**		**5.0**	**1(ref)**		**6.6**	**1(ref)**	
Infantis	3.0	0.5	0.21-1.21	3.7	0.7	0.24-2.19	2.2	0.3	0.07-1.37
Typhimurium DT135	6.9	1.2	0.64-2.31	4.0	0.8	0.26-2.40	9.7	1.5	0.69-3.42
Typhimurium DT1	14.7	2.8	1.69-4.77	7.5	1.5	0.62-3.84	21.2	3.8	1.97-7.42
Brandenburg	33.2	8.2	5.23-12.79	18.9	4.4	2.07-9.44	41.6	10.2	5.66-18.25
Typhimurium DT101	5.1	0.9	0.37-2.16	5.2	1.0	0.29-3.64	5.1	0.8	0.22-2.67
Enteritidis PT9a	3.9	0.7	0.26-1.73	6.2	1.2	0.40-3.82	1.6	0.2	0.03-1.72
Typhimurium DT156	12.0	2.3	1.15-4.41	9.8	2.1	0.72-5.85	14.0	2.3	0.97-5.62
Typhimurium DT42	10.6	2.0	0.83-4.58	10.0	2.1	0.58-7.64	11.1	1.8	0.57-5.57
Typhimurium DT12a	9.3	1.7	0.63-4.48	7.4	1.5	0.33-6.93	11.1	1.8	0.49-6.46
Typhimurium DT9	29.5	6.9	3.33-14.33	24.0	6.0	2.12-16.91	36.8	8.3	2.94-23.58
Saintpaul	3.9	0.7	0.18-2.46	1.3	0.2	0.01-4.12	8.0	1.2	0.27-5.66
Virchow	10.5	1.9	0.65-5.76	15.8	3.6	0.94-13.38	5.3	0.8	0.10-6.26
Heidelberg	2.9	0.5	0.09-2.54	1.5	0.3	0.02-5.04	5.0	0.8	0.10-5.91
Typhimurium RDNC	4.0	0.7	0.13-3.64	2.2	0.4	0.03-7.41	6.7	1.0	0.13-8.17
Thompson	4.1	0.7	0.13-3.74	4.8	0.9	0.12-7.48	3.2	0.5	0.03-8.27
Weltevreden	5.3	0.9	0.17-4.90	5.9	1.2	0.15-9.46	4.3	0.6	0.04-11.46
Enteritidis PT4	9.4	1.7	0.50-5.86	9.5	2.0	0.43-9.27	9.1	1.4	0.17-11.74
Typhimurium Not Typed	2.6	0.4	0.06-3.34	2.4	0.5	0.03-8.17	2.9	0.4	0.02-7.26
Agona	3.3	0.6	0.08-4.29	3.4	0.7	0.04-11.85	3.2	0.5	0.03-8.27
Typhimurium DT23	14.3	2.7	0.96-7.87	3.2	0.6	0.04-11.02	25.0	4.8	1.40-16.16
Mbandaka	4.9	0.9	0.16-4.55	5.3	1.1	0.13-8.36	4.3	0.6	0.04-11.46
Montevideo	4.2	0.7	0.09-5.45	4.0	0.8	0.04-13.93	4.3	0.6	0.04-11.46
Typhimurium Untypable	6.1	1.1	0.20-5.80	3.7	0.7	0.04-12.80	9.1	1.4	0.17-11.74
Mississippi	3.4	0.6	0.08-4.45	4.8	0.9	0.05-16.90	2.7	0.4	0.02-6.84
Typhimurium RDNC-May 06	7.0	1.2	0.23-6.72	9.1	1.9	0.23-15.67	4.8	0.7	0.04-12.68
Enteritidis PT6a	5.3	0.9	0.12-7.05	4.3	0.9	0.05-15.27	6.7	1.0	0.06-18.64
Typhimurium DT74	10.2	1.9	0.48-7.23	4.0	0.8	0.04-13.93	16.7	2.9	0.58-13.96
Corvallis	6.3	1.1	0.14-8.55	5.3	1.1	0.06-18.92	7.7	1.2	0.06-22.09

Salmonella serotype	Males and females 17 years or older			Females 17 years or older			Males 17 years or older		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Salmonella species 4,5,12 : d :-	5.0	0.9	0.11-6.66	5.3	1.1	0.06-18.92	4.8	0.7	0.04-12.68
Stanley	5.9	1.0	0.13-7.98	4.8	0.9	0.05-16.90	7.7	1.2	0.06-22.09
Enteritidis PT1b	9.7	1.8	0.32-9.83	11.1	2.4	0.12-46.62	9.1	1.4	0.17-11.74
Hadar	6.7	1.2	0.15-9.20	5.3	1.1	0.06-18.92	9.1	1.4	0.08-27.09
Newport	17.6	3.5	0.97-12.84	15.4	3.4	0.71-16.78	25.0	4.8	0.47-47.92
Enteritidis PT1	6.7	1.2	0.15-9.20	5.3	1.1	0.06-18.92	9.1	1.4	0.08-27.09

(G) Contact with human faeces

Salmonella serotype	Males and females 17 years or older			Females 17 years or older			Males 17 years or older		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium DT160	**13.2**	**1(ref)**		**13.7**	**1(ref)**		**12.7**	**1(ref)**	
Infantis	12.1	0.9	0.57-1.44	14.5	1.1	0.59-1.95	9.2	0.7	0.32-1.50
Typhimurium DT135	9.3	0.7	0.40-1.13	10.3	0.7	0.35-1.49	8.3	0.6	0.29-1.34
Typhimurium DT1	13.7	1.0	0.66-1.64	15.0	1.1	0.59-2.09	12.4	1.0	0.50-1.91
Brandenburg	10.5	0.8	0.47-1.25	9.6	0.7	0.31-1.48	10.9	0.8	0.45-1.60
Typhimurium DT101	10.2	0.7	0.40-1.38	13.8	1.0	0.45-2.26	7.1	0.5	0.20-1.40
Enteritidis PT9a	15.4	1.2	0.72-1.98	13.9	1.0	0.49-2.12	16.9	1.4	0.69-2.85
Typhimurium DT156	11.0	0.8	0.43-1.54	11.8	0.8	0.34-2.08	10.3	0.8	0.32-1.98
Typhimurium DT42	13.8	1.1	0.50-2.21	16.1	1.2	0.44-3.31	11.8	0.9	0.31-2.75
Typhimurium DT12a	15.5	1.2	0.57-2.54	10.7	0.8	0.22-2.61	20.0	1.7	0.66-4.49
Typhimurium DT9	15.9	1.2	0.54-2.88	15.4	1.1	0.38-3.48	16.7	1.4	0.38-4.99
Saintpaul	14.9	1.2	0.57-2.34	16.7	1.3	0.50-3.19	12.9	1.0	0.34-3.08
Virchow	4.9	0.3	0.08-1.42	4.5	0.3	0.04-2.29	5.3	0.4	0.05-2.95
Heidelberg	9.6	0.7	0.27-1.81	12.1	0.9	0.29-2.59	5.3	0.4	0.05-2.95
Typhimurium RDNC	7.5	0.5	0.16-1.77	8.7	0.6	0.14-2.65	5.9	0.4	0.06-3.34
Thompson	12.8	1.0	0.37-2.54	14.3	1.1	0.30-3.71	11.1	0.9	0.19-3.90
Weltevreden	4.5	0.3	0.06-1.61	5.3	0.4	0.05-2.69	3.4	0.2	0.01-4.22
Enteritidis PT4	7.7	0.5	0.15-2.03	2.4	0.2	0.01-2.65	16.7	1.4	0.29-6.54

Salmonella serotype	Males and females 17 years or older			Females 17 years or older			Males 17 years or older		
	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI	% with risk factor	Crude odds ratio	95% CI
Typhimurium Not Typed	23.5	2.0	0.89-4.61	22.2	1.8	0.57-5.71	25.0	2.3	0.71-7.49
Agona	6.9	0.5	0.11-2.08	7.1	0.5	0.06-3.80	6.7	0.5	0.06-3.85
Typhimurium DT23	8.6	0.6	0.18-2.06	10.0	0.7	0.16-3.12	6.7	0.5	0.06-3.85
Mbandaka	12.3	0.9	0.29-2.88	16.7	1.3	0.35-4.52	4.8	0.3	0.02-6.02
Montevideo	5.3	0.4	0.07-1.92	6.7	0.5	0.06-3.51	3.7	0.3	0.02-4.56
Typhimurium Untypable	9.8	0.7	0.19-2.69	3.7	0.2	0.01-4.16	16.7	1.4	0.29-6.54
Mississippi	4.9	0.3	0.06-1.78	5.9	0.4	0.02-6.98	4.5	0.3	0.04-2.51
Typhimurium RDNC-May 06	11.6	0.9	0.23-3.29	4.8	0.3	0.02-5.49	18.2	1.5	0.32-7.36
Enteritidis PT6a	8.6	0.6	0.11-3.33	9.1	0.6	0.08-5.04	7.7	0.6	0.03-10.49
Typhimurium DT74	21.3	1.8	0.73-4.36	37.5	3.8	1.32-10.90	3.4	0.2	0.01-4.22
Corvallis	6.3	0.4	0.06-3.36	5.3	0.4	0.02-6.15	7.7	0.6	0.03-10.49
Salmonella species 4,5,12 : d :-	7.7	0.5	0.10-2.94	12.5	0.9	0.11-7.49	4.3	0.3	0.02-5.44
Stanley	5.0	0.3	0.05-2.62	4.0	0.3	0.02-4.53	6.7	0.5	0.03-8.85
Enteritidis PT1b	15.2	1.2	0.30-4.59	11.1	0.8	0.04-15.16	16.7	1.4	0.29-6.54
Hadar	13.0	1.0	0.17-5.56	12.5	0.9	0.11-7.49	14.3	1.1	0.06-23.39
Newport	6.7	0.5	0.09-2.50	6.7	0.5	0.06-3.51	6.7	0.5	0.03-8.85
Enteritidis PT1	7.1	0.5	0.07-3.91	5.3	0.4	0.02-6.15	11.1	0.9	0.04-16.63

7.7 Appendix 7: Outbreak report form with data codes

OUTBREAK REPORT FORM

Outbreak Summary **Outbreak No.** OutbreakNumber

Reporting Authority

Name of public health officer responsible for case OfficerName

Date outbreak reported ReportDate ○ **Interim report** ○ **Final report - date finalised** DtReportFinalised RptType

Disease and Implicated Pathogen, Toxin or Chemical

Name of implicated pathogen, toxin or chemical (if known) PathogenName

Subtype PathSubtype

Other known pathogen OtherKnownPathogen

Unknown pathogen

☐ Gastroenteritis Gastro

☐ Other illness (specify) OthrIllness OthrIllSpec

CASE DEFINITION(S)

Laboratory-confirmed case DefnLabConfirm

Other confirmed case DefnConfirm

Probable case DefnProbable

Outbreak Demographics

Number of cases

Lab confirmed (as per case defn above) NoLabConfirmed ____ Number Hospitalised NoHospital ____

Other confirmed (as per case defn above) NoConfirmed ____ Number Died NoDied ____

Probable (as per case defn above) NoProbable ____

Total NoTotal ____

Outbreak dates

Onset of illness in first case FirstDate ____

Onset of illness in last case LastDate ____ or ☐ Outbreak ongoing Ongoing

Age of cases Median age (years) AgeMedian ____ Range (years) AgeRange ____

Sex of cases Number of males NoMales ____ Number of females NoFemales ____

Incubation period Median IncMedian ○ days ○ hrs IncMedianDayHr Range IncRange ○ days ○ hrs IncRangeDayHr

Duration of illness Median DurMedian ○ days ○ hrs DurMedianDayHr Range DurRan... ○ days ○ hrs DurRangeDayHr

Circumstances of Exposure/Transmission

How was the outbreak recognised and links among cases established? (tick all that apply)

☐ Increase in disease incidence Incidence

☐ Cases attended common event ComEvent

☐ Cases linked to common source (eg food, water, environmental site) ComSource

☐ Cases had person to person contact with other cases(s) PersPers

☐ Common organism type/strain characteristics between cases CommOrg

☐ Other means (specify) OthMeaSpec ____

Outbreak Summary **Outbreak No.** OutbreakNumber

Circumstances of Exposure/Transmission contd

Type of outbreak (tick one) TypeOutbreak

- ○ Common event
- ○ Common source dispersed in community (eg food, water)
- ○ Common source in specific place (eg environmental site, farm animals)
- ○ Community-wide, person to person transmission
- ○ Institutional (transmission within a defined setting)
- ○ Household (transmission within a single household)
- ○ Other outbreak type (specify) TypeOutbreakSpec _____
- ○ Unknown outbreak type

Were these cases part of a well-defined exposed group (eg Common event, institutional, environmental, household) Exposed ○ Yes ○ No ○ Unknown

If yes, number exposed _____ ExposeNo

Date of exposure ExpoDate _____ If exposure >1 day, date exposure ended DateExpEnd _____

Description of exposure event DesExEvent _____

Setting where exposure transmission occurred or contaminated food/beverage was prepared for consumption (Tick all that apply).Note - if food was prepared at a different place to where it was consumed, tick each box that applies.

☐ Home Home	☐ Tangi/hui Tangi	☐ Restaurant/café Cafe
☐ Hostel/boarding house Hostel	☐ Camp Camp	☐ Takeaway Takeaway
☐ Hotel/motel HotelMotel	☐ Community/church gathering Community	☐ Supermarket/delicatessen Supermarket
☐ Rest home RestHome	☐ Childcare centre ChildCare	☐ Caterers Caterers
☐ Hospital (continuing care) HospCont	☐ School School	☐ Abattoir/meat processing plant Abattoir
☐ Hospital (acute care) HospAcute	☐ Swimming/spa pool SwimSpa	☐ Other food outlet OthFood
☐ Prison Prison	☐ Workplace (specify type of workplace) WorkPlace	_____ WorkPlSpec
☐ Farm Farm		

☐ Other setting (specify) _____ OthrStSpec

☐ Unknown SetUnkn

Name of setting (if applicable) _____ Setting

Address Number housenumber Street streetname Suburb suburb

Town/City towncity PostCode postcode

Geographic location where exposure/transmission occurred (tick one) loctrans

○ Single health district (specify) _____ HDName1 _____ HDName2 _____ HDName3

○ Multiple health districts _____ HDName4 _____ HDName5

TLA (specify) _____ TAName

○ Overseas (specify country) _____ Overseas

○ Unknown

Outbreak Summary **Outbreak No.** OutbreakNumber

Circumstances of Exposure/Transmission contd

Mode of transmission (tick all that apply)

- ☐ Foodborne, from consumption of contaminated food or drink (excluding water) **Foodborne**
- ☐ Waterborne, from consumption of contaminated drinking water **Waterborne**
- ☐ Person to person spread, from (non-sexual) contact with an infected person (including droplets) **PersToPers**
- ☐ Sexual, from sexual contact with an infected person **SexualContact**
- ☐ Parenteral, from needle stick injury or reuse of contaminated injection equipment **Parenteral**
- ☐ Environmental, from contact with an environmental source (eg swimming) **Environmental**
- ☐ Zoonotic, from contact with an infected animal **Zoonotic**
- ☐ Vectorborne, from contact with an insect vector **Vectorborne**
- ☐ Other mode of transmission (specify) **OthMode** _____ **OthModSpec**
- ☐ Unknown mode of transmission **ModeUnknown**

Vehicle/source of common source outbreak

Was a specific contaminated food, water or environmental vehicle/source identified? **WatEnvSource** ○ Definite ○ Suspect ○ No ○ Unknown

If suspected or definite, list all vehicles/sources in detail **SourVeh**

_____

Was the vehicle/source linked to a commercial operator? **VehComm** ○ Yes ○ No

If yes, list all the operators and record whether each had a Ministry of Health approved food safety plan (FSP) in place.

Name of food operators	MoH approved FSP in place?		
_____ **NameOp1**	○ Yes	○ No	○ Unknown **FSPPla1**
_____ **NameOp1**	○ Yes	○ No	○ Unknown **FSPPla2**
_____ **NameOp3**	○ Yes	○ No	○ Unknown **FSPPla3**

Evidence for mode of transmission (tick all that apply)

- ☐ Epidemiological - case had history of exposure to implicated source **EvTrnEpiHist**
- ☐ Epidemiological - case control or cohort study showed elevated risk for cases exposed to implicated source **EvTrnEpiRisk**
- ☐ Laboratory - pathogen/toxin/chemical suspected to have caused illness identified in implicated source eg leftover food, water, animal or environmental source **EvTrnLabPTC**
- ☐ Laboratory - pathogen suspected to have caused illness identified in food handler **EvTrnLabP**
- ☐ Environmental investigation - identified critical control point failures linked to implicated source **EvTrnEnvInv**
- ☐ Other evidence (specify) **EvTrnOthEv** _____ **EvTrnOthSpec**
- ☐ No evidence obtained **EvTrnNoEv**

Outbreak Summary **Outbreak No.** OutbreakNumber

Factors Contributing to Outbreak

Foodborne outbreak (tick all that apply)

Time/temperature abuse

- ☐ Inadequate reheating of previously cooked food **Reheat**
- ☐ Improper storage prior to preparation **StorPrior**
- ☐ Inadequate thawing **Thaw**
- ☐ Preparation too far in advance **Prepar**
- ☐ Undercooking **UnderCook**
- ☐ Improper hot holding **Warming**
- ☐ Inadequate cooling or refrigeration **Refridg**

Contamination of food

- ☐ Cross contamination **XcontaIm**
- ☐ Contamination from an infected food handler **Handler**
- ☐ Chemical contamination **ChemCon**

Unsafe sources

- ☐ Use of ingredients from unsafe sources **UnsafeIng**
- ☐ Use of untreated water in food preparation **UntrWat**
- ☐ Consumption of unpasteurised milk **UnPastMilk**
- ☐ Consumption of raw food **RawF**

☐ Other factor (specify) **FOthFac** _____ ***FOthFacSpec***

☐ Unknown factors **FUnknFac**

Waterborne outbreak (tick all that apply)

- ☐ Contamination of source water **InadSource**
- ☐ Treatment process failure **TreatFail**
- ☐ Post treatment contamination **PostCont**
- ☐ Untreated water supply **UntrWSupp**
- ☐ Contamination of reservoir(s)/holding tank(s) **ConReservoir**

☐ Other factor (specify) **wOthFac** _____ **WOthFacSpec**

☐ Unknown factors **WUnknFac**

Specify the implicated supply distribution zone Zone code **WSZone** _____ ☐ Unknown **WSZoneUn**

Other outbreak (tick all that apply)

Person to person

- ☐ Inadequate vaccination coverage **InAdVac**
- ☐ Inadequate vaccination effectiveness **VacEff**
- ☐ Exposure to infected people **ExPeople**
- ☐ Poor hygiene of cases **PoorHy**
- ☐ Excessively crowded living conditions **Crowd**
- ☐ Unprotected sexual activity **UnprSex**
- ☐ Needle/syringe reuse by injecting drug users **NeddleUse**

Environmental

- ☐ Exposure to contaminated environment(s) **ExpEnv**
- ☐ Exposure to infected animals or animal products **ExpAnimal**
- ☐ Exposure to untreated recreational water **ExpRecWater**
- ☐ Exposure to contaminated swimming pool **ExpContPool**
- ☐ Exposure to inadequately maintained swimming pool **ExpInadPool**

☐ Other factor (specify) **OOthFac** _____ **OOthFacSpec**

☐ Unknown factors **OUnknFac**

Evidence for implicating a contributing factor

☐ Environmental investigation - identified critical point failure(s) **EvImpEnvInv**

☐ Other evidence for factor contributing to outbreak (specify) **EvImpOthEv** _____ **EvImpOthSpec**

Outbreak Summary **Outbreak No.** OutbreakNumber

Management of the Outbreak

Was there any specific action taken to control the outbreak? SpecAction ○ Yes ○ No ○ Unknown

If yes, list the control measures undertaken (tick all that apply)

Source	Specify
☐ Closure SrcCls	SrcClsSpec
☐ Modification of procedures SrcMod	SrcModSpec
☐ Cleaning, disinfection SrcClean	SrcCleanSpec
☐ Removal SrcRem	SrcRemSpec
☐ Treatment SrcTreat	SrcTreatSpec
☐ Exclusion SrcExcl	SrcExclSpec
☐ Isolation SrcIso	SrcIsoSpec
☐ Health education and advice SrcHealth	SrcHealthSpec
☐ Health warning SrcHealthWarn	SrcHealthWarnSpec

Vehicles and vectors

☐ Removal VehVecRem	VehVecRemSpec
☐ Treatment VehVecTreat	VehVecTreatSpec

Contacts and potential contacts

☐ Chemoprophylaxis ContChem	ContChemSpec
☐ Vaccination ContVac	ContVacSpec
☐ Health education and advice ContHealth	ContHealthSpec

Other control measures (specify)

OutCont

Other comments on outbreak

OthComm

Has a written outbreak report been prepared? ReportWritten ○ Yes ○ No

If yes, please send a copy to ESR

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7.8 Appendix 8: Relationship between PHUs, health districts, DHBs and Territorial Authorities

Public Health Units (n=12)	District Health Boards (n=21)	Health districts (n=24)	Territorial Authorities (n=74)
Northland District Health Board	Northland	Northland	Far North District Whangarei District Kaipara District
Auckland Regional Public Health Service	Waitemata	North West Auckland	Rodney District North Shore City Waitakere City
Auckland Regional Public Health Service	Auckland	Central Auckland	Auckland City
Auckland Regional Public Health Service	Counties Manukau	South Auckland	Manukau City Papakura District Franklin District
Population Health Service Waikato	Waikato	Waikato	Thames-Coromandel District Hauraki District Waikato District Matamata-Piako District Hamilton City Waipa District Otorohanga District South Waikato District Waitomo District
Toi Te Ora - Public Health	Bay of plenty	Tauranga and Eastern Bay of Plenty	Whakatane District Kawerau District Opotiki District Western Bay of Plenty District Tauranga City
Tairawhiti DHB	Tairawhiti	Gisborne	Gisborne district
Toi Te Ora - Public Health	Lakes	Rotorua, Taupo and Ruapehu[1]	Rotorua District Taupo District Ruapehu District
Taranaki Health Protection Unit	Taranaki	Taranaki	New Plymouth District Stratford District South Taranaki District
Hawke's Bay Public Health Unit	Hawke's Bay	Hawke's Bay	Wairoa District Hastings District Napier City Central Hawke's Bay District Chatham Islands
MidCentral Public Health Service	Whanganui	Wanganui	Wanganui District Rangitikei District
MidCentral Public Health Service	MidCentral	Manawatu[2]	Manawatu District Palmerston North City Tararua District Horowhenua District
Regional Public Health	Wairarapa	Wairarapa	Masterton District Carterton District South Wairarapa District
Regional Public Health	Capital and Coast	Wellington	Kapiti Coast District Porirua City Wellington City
Regional Public Health	Hutt	Hutt	Upper Hutt City Lower Hutt City
Nelson Marlborough Public Health Service	Nelson Marlborough	Nelson-Marlborough	Tasman District Nelson city Marlborough District

Public Health Units (n=12)	District Health Boards (n=21)	Health districts (n=24)	Territorial Authorities (n=74)
Community and Public Health	West Coast	West Coast	Buller District Grey District Westland District
Community and Public Health	Canterbury	Canterbury	Kaikoura District Hurunui District Waimakariri District Christchurch City Selwyn District Banks Peninsula District
Community and Public Health	South Canterbury	South Canterbury	Ashburton District Timaru District Mackenzie District Waimate District
Public Health South	Otago	Otago	Waitaki District Central Otago District Dunedin City Clutha District
Public Health South	Southland	Southland	Queenstown-Lakes District Southland District Gore District Invercargill City

1. *Responsibility for the Ruapehu health district is actually split between Toi Te Ora PHU (northern Ruapehu region) and MidCentral PHU (southern Ruapehu region). For simplicity, the Ruapehu District has been included as part of the Lakes District Health Board (Toi Te Ora PHU).*
2. *Regional Public Health also covers Otaki, which is part of the Manawatu District.*

7.9 Appendix 9: Outbreaks and cases by *Salmonella* serotype

(A) Number of outbreaks caused by each *Salmonella* serotype, per year

The percentage of total outbreaks per year are presented for some serotypes at the end of the table.
Subtotals for 2000-03 and 2004-09 account for peaks in notifications due to S. Typhimurium DT135, S. Typhimurium DT160 and S. Brandenburg (see text, Section 4.3.4).

Serotype and phage type	2000	2001	2002	2003	*Subtotal 2000-03*	2004	2005	2006	2007	2008	2009	*Subtotal 2004-09*	Total 2000-09
***S.* Typhimurium**	**22**	**32**	**28**	**12**	***94***	**2**	**13**	**6**	**4**	**6**	**9**	***40***	**134**
DT160	1	14	16	7	***38***		8	4	1	2		***15***	**53**
DT135	13	4	2		***19***		1			1		***2***	**21**
DT1[1]	3	2	4	2	***11***	1	1		1		3	***6***	**17**
Unknown[2]	2	5			***7***							***0***	**7**
DT156		1			***1***	1	1	1	1		2	***6***	**7**
DT9	1	1	1	1	***4***						1	***1***	**5**
RDNC[3]			2	1	***3***					1	2	***2***	**5**
DT12a	1	1	1		***3***					1		***1***	**4**
DT101		1	1		***2***		1	1				***2***	**4**
DT42[4]		1			***1***					1	1	***2***	**3**
DT8[5]			1	1	***2***				1			***1***	**3**
DT23		1			***1***							***0***	**1**
DT26		1			***1***							***0***	**1**
DT150	1				***1***							***0***	**1**
DT193					***0***		1					***1***	**1**
DT195					***0***					1		***1***	**1**
S. Enteritidis	**1**	**0**	**0**	**1**	***2***	**0**	**1**	**1**	**1**	**0**	**0**	***3***	**5**
PT9a	1			1	***2***		1	1				***2***	**4**
PT26					***0***				1			***1***	**1**

Serotype and phage type	2000	2001	2002	2003	*Subtotal 2000-03*	2004	2005	2006	2007	2008	2009	*Subtotal 2004-09*	Total 2000-09
Other serotypes	**2**	**3**	**4**	**7**	***16***	**0**	**4**	**5**	**4**	**4**	**0**	***17***	**33**
Infantis		1		2	***3***		2	1	1	1		***5***	**8**
Montevideo	1			3	***4***				1			***1***	**5**
Thompson		1	1		***2***		1	1				***2***	**4**
Weltevreden [6]			1		***1***			2				***2***	**3**
Chester					***0***				1	1		***2***	**2**
Saintpaul					***0***		1			1		***2***	**2**
Virchow	1				***1***			1				***1***	**2**
Brandenburg		1	1		***2***							***0***	**2**
Derby					***0***					1		***1***	**1**
Mbandaka					***0***				1			***1***	**1**
Mississippi				1	***1***							***0***	**1**
Heidelberg				1	***1***							***0***	**1**
Salmonella Group C,6,7:k:-			1		***1***							***0***	**1**
All serotypes	**25**	**35**	**32**	**20**	***112***	**2**	**18**	**12**	**9**	**10**	**9**	***60***	**172**
All Typhimurium	**88%**	**91%**	**88%**	**60%**	***84%***	**100%**	**72%**	**50%**	**44%**	**60%**	**100%**	***67%***	**78%**
DT160	4%	40%	50%	35%	*34%*	0%	44%	33%	11%	20%	0%	*25%*	**31%**
DT135	52%	11%	6%	0%	*17%*	0%	6%	0%	0%	10%	0%	*3%*	**12%**
DT1[a]	12%	6%	13%	10%	*10%*	50%	6%	0%	11%	0%	33%	*10%*	**10%**
All Enteritidis	**4%**	**0%**	**0%**	**5%**	***2%***	**0%**	**6%**	**8%**	**11%**	**0%**	**0%**	***5%***	**3%**
All other serotypes	**8%**	**9%**	**13%**	**35%**	***14%***	**0%**	**22%**	**42%**	**44%**	**40%**	**0%**	***28%***	**19%**

1. *Includes one outbreak of S. Typhimurium DT1 variant in 2003.*
2. *Phage type unknown.*
3. *Includes one outbreak of S. Typhimurium RDNC in 2002, one of S. Typhimurium RDNC Aug 01 in each of 2002 and 2003, and one of each of S. Typhimurium RDNC Aug 08 and RDNC Aug 09 in 2009.*
4. *Includes one outbreak of S. Typhimurium DT42 variant in 2009.*
5. *Includes one outbreak of S. Typhimurium DT8 variant in 2003.*
6. *Includes one outbreak of S. Weltevreden 15+ in 2006.*

(B) Number of outbreak cases caused by each *Salmonella* serotype, per year

The percentage of total outbreak cases per year are presented for some serotypes at the end of the table.
Subtotals for 2000-03 and 2004-09 account for peaks in notifications due to S. Typhimurium DT135, S. Typhimurium DT160 and S. Brandenburg (see text, Section 4.3.4).

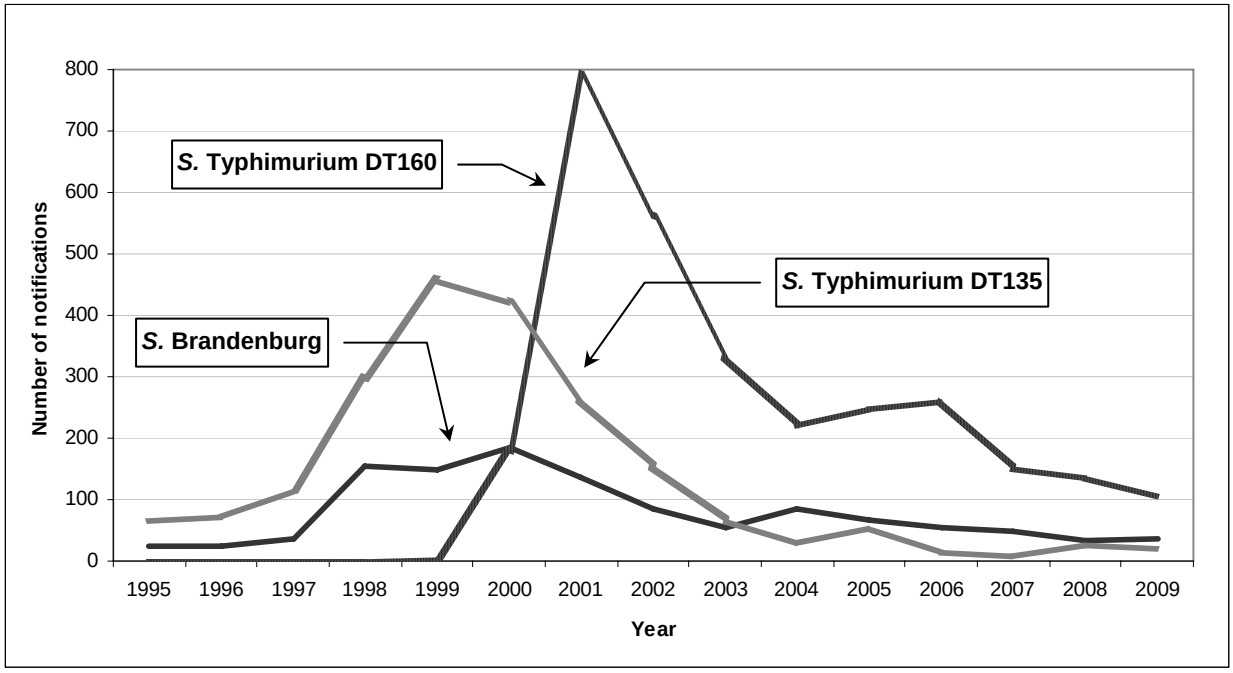
Serotype and phage type	2000	2001	2002	2003	*Subtotal 2000-03*	2004	2005	2006	2007	2008	2009	*Subtotal 2004-09*	Total 2000-09
***S.* Typhimurium**	**196**	**188**	**219**	**92**	***695***	**5**	**50**	**14**	**36**	**82**	**58**	***245***	**940**
DT160	4	134	87	16	***241***		25	10	2	4		***41***	**282**
DT135	145	17	4		***166***		9			6		***15***	**181**
DT1[1]	16	4	115	8	***143***	2	2		10		31	***47***	**190**
Unknown[2]	8	12			***20***							***0***	**20**
DT156		3			***3***	3	2	2	19		6	***32***	**35**
DT9	5	3	3	2	***13***						2	***2***	**15**
RDNC[3]			4	2	***6***						16	***16***	**22**
DT12a	2	3	2		***7***					3		***3***	**10**
DT101		2	2		***4***		3	2				***5***	**9**
DT42[4]		6			***6***					67	3	***70***	**76**
DT8[5]			2	64	***66***				5			***5***	**71**
DT23		2			***2***							***0***	**2**
DT26		2			***2***							***0***	**2**
DT150	16				***16***							***0***	**16**
DT193					***0***		7					***7***	**7**
DT195					***0***					2		***2***	**2**
***S.* Enteritidis**	**3**	**0**	**0**	**2**	***5***	**0**	**25**	**11**	**11**	**0**	**0**	***47***	**52**
PT9a	3			2	***5***		25	11				***36***	**41**
PT26					***0***				11			***11***	**11**
Other serotypes	**13**	**25**	**42**	**19**	***99***	**0**	**40**	**25**	**134**	**30**	**0**	***229***	**328**
Infantis		2		4	***6***		8	2	5	18		***33***	**39**
Montevideo	11			8	***19***				10			***10***	**29**

Serotype and phage type	2000	2001	2002	2003	*Subtotal 2000-03*	2004	2005	2006	2007	2008	2009	*Subtotal 2004-09*	Total 2000-09
Thompson		2	2		***4***		13	15				***28***	**32**
Weltevreden[6]			13		***13***			6				***6***	**19**
Chester					***0***				85	3		***88***	**88**
Saintpaul					***0***		19			6		***25***	**25**
Virchow	2				***2***			2				***2***	**4**
Brandenburg		21	2		***23***							***0***	**23**
Derby					***0***					3		***3***	**3**
Mbandaka					***0***				34			***34***	**34**
Mississippi				2	***2***							***0***	**2**
Heidelberg				5	***5***							***0***	**5**
Salmonella Group C,6,7:k:-			25		***25***							***0***	**25**
All serotypes	**212**	**213**	**261**	**113**	***799***	**5**	**115**	**50**	**181**	**112**	**58**	***521***	**1,320**
***S.* Typhimurium**	**92%**	**88%**	**84%**	**81%**	***87%***	**100%**	**43%**	**28%**	**20%**	**73%**	**100%**	***47%***	**71%**
DT160	2%	63%	33%	14%	*30%*	0%	22%	20%	1%	4%	0%	*8%*	**21%**
DT135	68%	8%	2%	0%	*21%*	0%	8%	0%	0%	5%	0%	*3%*	**14%**
DT1[a]	8%	2%	44%	7%	*18%*	40%	3%	0%	6%	0%	53%	*9%*	**14%**
***S.* Enteritidis**	**1%**	**0%**	**0%**	**2%**	***1%***	**0%**	**22%**	**22%**	**6%**	**0%**	**0%**	***9%***	**4%**
All other serotypes	**6%**	**12%**	**16%**	**17%**	***12%***	**0%**	**35%**	**50%**	**74%**	**27%**	**0%**	***44%***	**25%**

1. *Includes one outbreak of S. Typhimurium DT1 variant in 2003 (2 cases).*
2. *Phage type unknown.*
3. *Includes one outbreak of S. Typhimurium RDNC in 2002 (2 cases), one of S. Typhimurium RDNC Aug 01 in each of 2002 and 2003 (2 cases in each), and one of each of S. Typhimurium RDNC Aug 08 (14 cases) and RDNC Aug 09 (2 cases) in 2009.*
4. *Includes one outbreak of S. Typhimurium DT42 variant in 2009 (3 cases).*
5. *Includes one outbreak of S. Typhimurium DT8 variant in 2003 (64 cases).*
6. *Includes one outbreak of S. Weltevreden 15+ in 2006 (2 cases).*

7.10 Appendix 10: New Zealand notifications of four *Salmonella* serotypes

This graph shows the number of notifications associated with three *Salmonella* serotypes that are frequently isolated from humans in New Zealand. Data are from ESR's ERL Annual Reports on Human *Salmonella* Isolates (years 2002-2008).



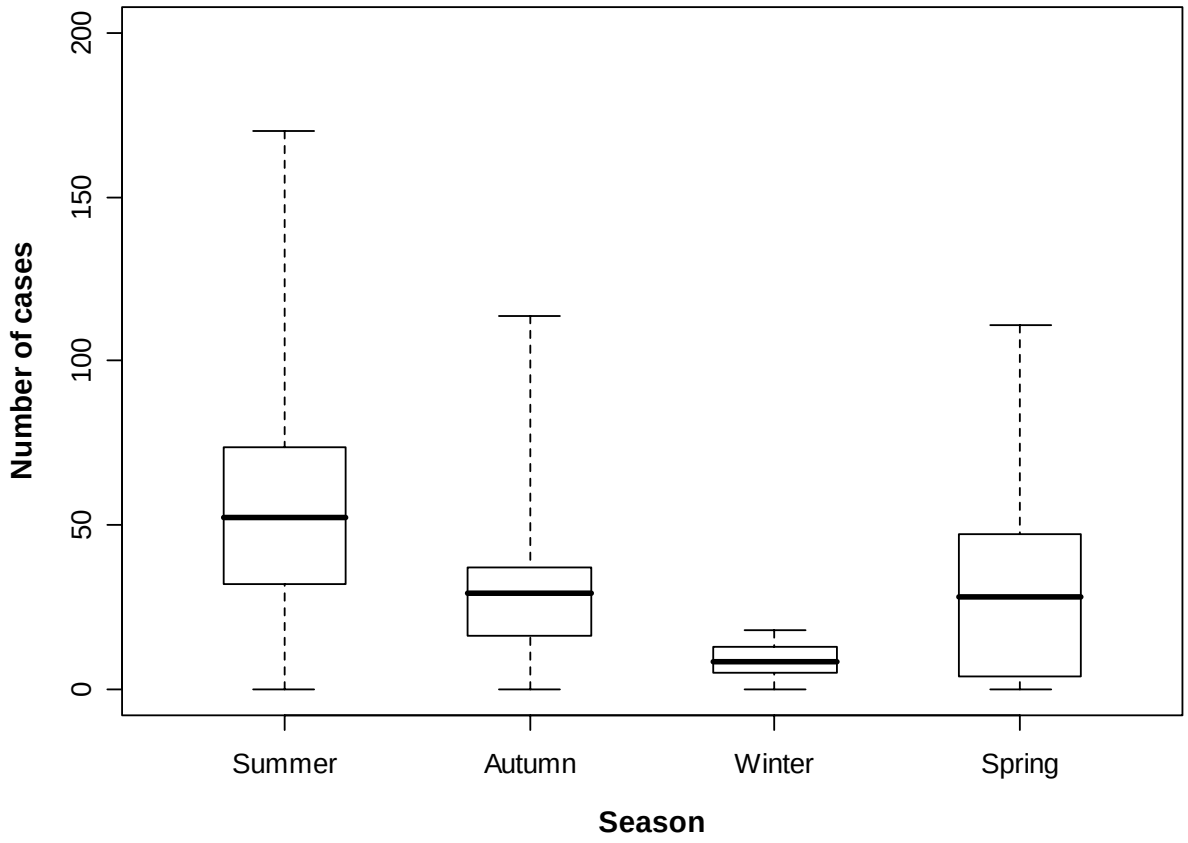
7.11 Appendix 11: Seasonal patterns in salmonellosis outbreak cases

This appendix presents:

(A) Box plot showing the year-to-year variability in the number of cases per season: This graph only considers the total cases for each season (per year), and does not take account of variability in the number of cases per outbreak.

(B) Box plot showing seasonal differences when the number of cases associated with each outbreak are grouped by season (rather than summed). This graph shows that, irrespective of season, the majority of outbreaks involve small numbers of people (2-3 people) and that larger outbreaks have not occurred in winter.

Box plot (A)



Notes to graph:

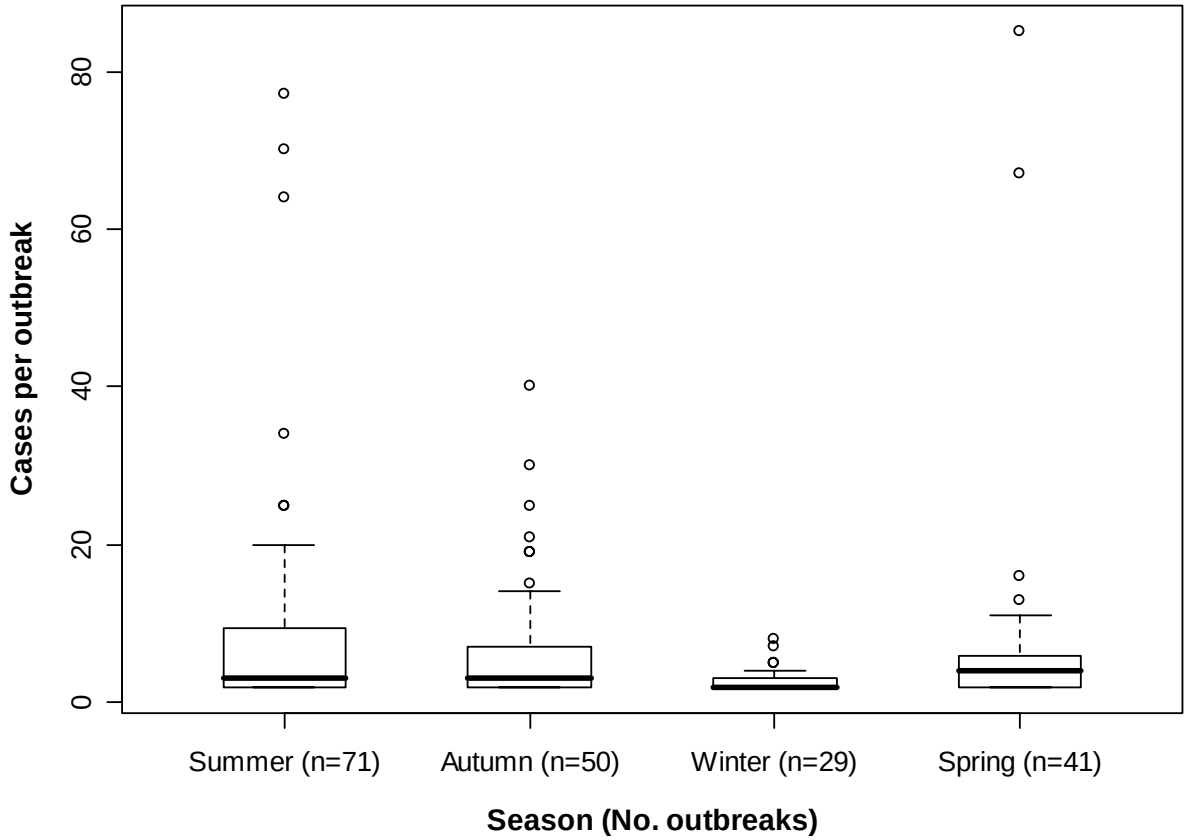
Data: Box plot is based on the number of outbreak cases per season, per year (i.e. Summer = No. outbreak cases in summer 2000, summer 2001, summer 2002, etc.)

Box: Values between the 25th (lower) and 75th (upper) percentiles

Solid line in box: Median

Whiskers: Maximum and minimum values

Box plot (B)



Notes to graph:

Data: Box plot is based on the number of cases per outbreak, per season (ie. Summer = No. cases for each of the outbreaks in summer 2000, summer 2001, summer 2002, etc.)

Box: Values between the 25th (lower) and 75th (upper) percentiles

Solid line in box: Median

Whiskers: Values between the 10th (lower) and 90th (upper) percentiles

Dots: Outliers

7.12 Appendix 12: Summary of salmonellosis outbreaks for which the mode of transmission was not confirmed by laboratory evidence

Level of evidence:

a. No evidence was reported.
b. Epidemiological evidence: Cases had history of exposure to implicated source.
c. Epidemiological evidence and evidence from environmental investigation: Cases had history of exposure to implicated source but the PHO specified critical control point failures linked to the implicated source.
d. Evidence from environmental investigation: Identified critical control point failures linked to implicated source.
e. Epidemiological evidence: Case control or cohort study showed elevated risk for cases exposed to implicated source.

(A) Summary of outbreaks with a suspected foodborne mode of transmission (n=60)

Setting	Year	*Salmonella* serotype	No. cases			Suspected food(s)	Level of evidence
			Conf	Prob	Exp		
Workplace	2000	Virchow	2	0	?	Surimi seafood salad	a
Supermarket, home	2000	Not known	1	1	2	hot spicy chicken nibbles	a
Restaurant/café	2000	Typhimurium DT135	6	0	?	Unknown	a
Restaurant/café	2001	Typhimurium DT160	2	0	?	Unknown	a
Unknown	2002	Typhimurium DT160	2	2	4	Antipasto platter, homemade mayonnaise (raw egg).	a
Takeaway, home, café	2002	Typhimurium DT160	2	1	4	Takeaway meal	a
Bakery	2007	Infantis	5	0	?	Unknown	a
Restaurant/café	2000	Not known	0	2	2	Chicken burritos	b
Bakery	2000	Typhimurium DT135	11	0	?	Country fried chicken, chicken rolls and sandwiches	b
Fundraising dinner	2000	Not known	0	8	304	Unknown	b
Home	2000	Typhimurium DT135	7	7	10	Chicken, apple pie	b
Takeaway, home	2000	Not known	0	5	7	Fish and chips (batter)	b
Home	2000	Typhimurium DT	1	2	3	Home-cooked chicken breast in stir-fry chicken	b
Caterers	2000	Typhimurium DT1	4	6	120	Ham in filled rolls provided to bus tour	b
Restaurant/café	2001	Typhimurium DT135	3	0	15	Barbeque food	b
Restaurant/café	2001	Typhimurium DT	1	1	2	Chicken nuggets	b
Restaurant/café	2001	Typhimurium DT160	1	3	?	Unknown	b
Home	2001	Typhimurium DT160	2	1	3	Barbeque (steak), smoked chicken, luncheon	b
Home	2002	Typhimurium DT160	1	2	3	beef schnitzel with egg batter, home-grown vegetables possibly contaminated with animal faeces	b
Takeaway	2002	Typhimurium DT160	2	0	2	Ham roll	b

Setting	Year	*Salmonella* serotype	No. cases			Suspected food(s)	Level of evidence
			Conf	Prob	Exp		
Supermarket, home	2002	Thompson	1	1	3	Raw fresh mussels	b
Home	2002	Typhimurium DT160	1	1	2	Scrambled eggs	b
Home	2002	Typhimurium DT160	2	7	13	Barbeque chicken	b
Home	2003	Not known	1	2	7	Roast chicken	b
Restaurant/café	2003	Infantis	1	1	2	Chicken broth	b
Hangi	2003	Typhimurium DT160	2	0	30	Hangi food	b
Unknown	2005	Typhimurium DT160	2	0	?	shredded chicken noodle salad, chocolate cake	b
Restaurant/café	2005	Typhimurium DT160	1	1	2	raw egg aeoli	b
Tangi (hangi)	2005	Typhimurium DT193	5	2	?	Hangi foods	b
Hangi	2005	Typhimurium DT160	3	5	30	Chicken	b
Restaurant/café	2007	Typhimurium DT8	5	0	?	Unknown	b
Fundraising event	2007	Typhimurium DT156	11	8	125	Chicken, taro, chop suey, sweet and sour mince, egg fu yong	b
Home	2007	Not known	1	3	27	Savories, chicken nibbles, Bacon and egg pies, sandwiches	b
Home	2007	Enteritidis PT26	11	0	?	Seafood, infected food handler	b
Home	2008	Saintpaul	5	1	30	Smoked trout, infected food handler	b
Prison	2008	Infantis	8	12	1000	Contaminated food, infected food handler	b
Restaurant/café	2000	Typhimurium DT135	1	2	2	Chicken satay	c
Restaurant/café	2001	Typhimurium DT160	2	0	4	Butter chicken	c
Restaurant/café	2003	Typhimurium DT160	3	0	3	Eggs benedict with raw egg hollandaise sauce	c
Restaurant/café	2005	Not known	3	0	?	Club sandwiches	c
Restaurant/café	2005	Not known	2	0	2	smoked chicken lettuce and tomato sandwich	c
Home	2005	Typhimurium DT135	7	2	?	Home kill pork	c
Takeaway	2006	Typhimurium DT156	1	1	2	Pizza	c
Market	2006	Thompson	11	4	?	Taro in coconut cream, BBQ lamb flaps, chop suey in coconut cream, taro and vermicelli, pork buns	c
Takeaway	2007	Typhimurium DT160	1	1	2	BBQ chicken bacon pizza	c
Takeaway	2007	Montevideo	10	0	?	chicken kebabs, lamb kebabs or vegetarian falafels	c
Restaurant/café	2001	Typhimurium DT160	4	5	13	Hollandaise sauce with raw egg, rotisserie chicken	d
Takeaway	2001	Infantis	1	1	2	Egg fu yong, curry beef, chicken fried rice	d
Home	2001	Typhimurium DT160	1	4	7	Turkey, chicken and avocado salad	d

Setting	Year	*Salmonella* serotype	No. cases			Suspected food(s)	Level of evidence
			Conf	Prob	Exp		
Bakery, manufacturer of bakery products	2002	Group C 6,7:k:-	24	1	24	Potato-topped savories, infected food handler	d
House	2002	Typhimurium DT160	4	0	4	Roast chicken	d
Workplace	2002	Typhimurium DT160	6	7	?	Tuna sandwiches with raw egg mayonnaise, asymptomatic food handler	d
Restaurant/café	2003	Heidelberg	3	2	5	Shanghai style sliced chicken, braised gluten, salty pork and winter melon soup, Shanghai style rice with vegetables in soup, deep fried pork chops	d
Restaurant/café	2005	Not known	2	0	?	Beef lasagne	d
Restaurant/café	2006	Infantis	1	1	2	Egg sandwiches	d
Restaurant/café	2009	Typhimurium DT1	10	0	?	Infected food handler	d
Takeaway	2005	Enteritidis PT9a	25	0	?	Middle Eastern food: chicken, hummus, flat bread, lettuce, tomato, onions, cabbage. Tahini was negative.	e
Food packers and distributers	2005	Saintpaul	19	0	?	Raw carrots	e
Home	2007	Mbandaka	30	0	?	Chicken, eggs	e
Grower's roadside stalls	2009	Typhimurium DT1	19	0	?	Watermelon, ham	e

(B) Summary of outbreaks with a suspected zoonotic mode of transmission (n=1)

Setting	Year	*Salmonella* serotype	No. cases			Suspected source	Level of evidence
			Conf	Prob	Exp		
Restaurant/café	2001	Typhimurium DT160	4	5	231	Sparrows	b

(C) Summary of outbreaks with a suspected waterborne mode of transmission (n=4)

Setting	Year	*Salmonella* serotype	No. cases			Suspected source	Level of evidence
			Conf	Prob	Exp		
Farm	2008	Typhimurium RDNC Aug 09	2*	0	16	Reticulated drinking water on a farm	b
Home	2002	Typhimurium DT160	4	0	4	Contaminated water supply	c
Home	2002	Not known	1	1	?	Untreated water supply	c
Home, farm	2002	Typhimurium DT160	4	1	6	Contaminated water supply	d

(D) Summary of outbreaks with a suspected person-to-person mode of transmission (n=39)

Setting	Year	*Salmonella* serotype	No. cases			Level of evidence
			Conf	Prob	Exp	
Hostel/boarding house	2000	Typhimurium DT12a	2	0	?	a
Childcare centre, home	2000	Not known	1	4	5	a
Home	2000	Typhimurium DT135	2	0	4	a
Home	2001	Typhimurium DT135	1	1	4	a

Setting	Year	*Salmonella* serotype	No. cases			Level of evidence
			Conf	Prob	Exp	
Home	2001	Typhimurium DT135	2	0	4	a
Home	2001	Typhimurium	2	0	3	a
Farm, home	2001	Typhimurium DT1	2	0	4	a
Home	2001	Typhimurium DT1	2	0	?	a
Home	2001	Typhimurium DT156	1	2	5	a
Unknown	2001	Typhimurium DT160	2	0	?	a
Unknown	2001	Not known	2	0	?	a
Home	2002	Typhimurium DT1	2	0	3	a
Home	2005	Typhimurium DT156	2	0	4	a
Unknown	2005	Typhimurium DT160	2	0	3	a
Unknown	2006	Virchow	1	1	?	a
Home	2006	Enteritidis 9a	3	8	?	a
Home	2008	Chester	2	1	3	a
Home	2008	Typhimurium DT160	2	0	?	a
Childcare centre, home	2008	Typhimurium DT160	1	1	?	a
Home	2009	Not known	1	4	?	a
Home	2009	Typhimurium DT156	2	0	7	a
Home	2009	Typhimurium DT1	1	1	?	a
Home	2000	Typhimurium DT1	2	0	4	b
Workplace (supermarket)	2001	Typhimurium DT135	10	0	107	b
Rest home	2002	Typhimurium DT160	2	0	?	b
Home	2002	Not known	2	0	?	b
Home	2003	Mississippi	2	0	2	b
Home	2003	Not known	1	2	3	b
Home	2003	Typhimurium DT160	2	0	2	b
Unknown	2003	Infantis	2	0	?	b
Home	2003	Typhimurium DT1	2	4	8	b
Home	2003	Typhimurium DT1 variant	1	1	?	b
Home	2003	Montevideo	1	1	?	b
Home	2003	Typhimurium DTRDNC Aug 01	2	0	?	b
Home	2004	Typhimurium DT156	3	0	?	b
Home	2004	Typhimurium DT1	2	0	?	b
Home	2006	Typhimurium DT160	1	3	5	b
Home	2009	Typhimurium DT9	1	1	2	b
Home	2005	Infantis	1	1	4	c

(E) Summary of outbreaks with one or more suspected modes of transmission (n=42)

Setting	Year	*Salmonella* serotype	No. cases			Suspected sources	Level of evidence
			Conf	Prob	Exp		
Home	2000	Enteritidis PT9a	3	0	3	"blowing" free range eggs, organic produce purchased from roadside stalls, pre-cooked supermarket chicken	a

Setting	Year	*Salmonella* serotype	No. cases			Suspected source/vehicle	Level of evidence
			Conf	Prob	Exp		
Home	2000	Typhimurium	1	4	5	Unknown – possible infected person or food	a
Mental health hostel	2001	Typhimurium DT160	4	0	5	Unknown – possible infected person or inadequately reheated food	a
Home	2001	Typhimurium	3	0	7	Unknown – possible infected person or food or animals	a
Home	2001	Typhimurium DT160	1	3	4	Unknown – possible infected person or food	a
Home	2002	Typhimurium RDNC	2	0	4	Poultry water, poultry, infected person	a
Home	2005	Typhimurium DT160	1	1	?	Ham, infected person	a
Home	2006	Typhimurium DT101	2	0	3	Untreated water supply, infected person, use of untreated water in food preparation	a
Home	2008	Typhimurium DT195	2	0	0	Undercooked cake mixture containing raw eggs, infected person	a
Tangi, home	2000	Not known	2	0	30	Feral shellfish and kina, farm kill turkey, infected person	b
Farm, home	2000	Not known	2	0	2	Cows (calving, milking), sub-standard water supply, infected person	b
Restaurant/café, hostel	2000	Typhimurium DT135	3	1	?	Seafood, BBQ, pub meals, infected person	b
Home	2000	Typhimurium DT160	2	2		Home-cooked barbeque meal, including pork chops and lettuce salad	b
Home	2001	Thompson	2	0	?	Saveloys, infected person	b
Farm	2001	Typhimurium DT12a	3	0	?	Farm water supply, infected person	b
Restaurant, home	2001	Typhimurium	2	1	3	Chicken panini, infected person	b
Home, farm	2001	Typhimurium DT9	2	1	6	Farm animals, sick puppy, infected person	b
Home	2001	Typhimurium DT160	2	0	?	Ducks/duck faeces	b
Farm	2001	Typhimurium DT101	2	0	4	Calves	b
Mental health hostel	2001	Typhimurium DT26	2	0	2	Infected person, dirt	b
Home	2002	Typhimurium DT101	2**	0	?	Water supply, chickens, infected person	b
Farm	2002	Typhimurium DT9	3	0	11	Farm animals, infected person	b
Home	2002	Not known	3	0	4	Farm animals, untreated water supply, infected person	b
Holiday home	2003	Enteritidis PT9a	2	0	2	Untreated roof water supply, filo pastry pie	b

Setting	Year	*Salmonella* serotype	No. cases			Suspected source/vehicle	Level of evidence
			Conf	Prob	Exp		
Home	2005	Not known	3	2	5	Chicken satay, infected person	b
Home	2005	Typhimurium DT101	1	2	?	Home-cooked meal, infected person	b
Home	2006	Typhimurium DT160	1	1	?	Consumption of pet food, infected person	b
Home	2006	Typhimurium DT160	1	1	3	Unknown – possible infected person or food	b
Home	2008	Derby	3	0	3	Faeces from pet duck, infected person	b
Home	2009	Typhimurium DT42 variant	2	1*	3	Underheated precooked sausage, infected person	b
Home	2000	Typhimurium DT1	4	0	5	Bird faeces, infected person	c
Restaurant/café	2001	Typhimurium DT23	2	0	2	Satay chicken, infected person	c
Home	2002	Typhimurium RDNC Aug 01	2	0	3	Chicken giblets	c
Home	2003	Typhimurium DT160	3	0	5	Infected person, contaminated drinking water	c
Takeaway	2005	Typhimurium DT1	3	1	4	Chicken drumsticks, infected person	c
Home	2005	Typhimurium DT160	2	2	4	Roast chicken, infected person	c
Home	2005	Not known	1	1	?	Ill calf, infected person	c
Home	2005	Not known	1	4	5	Barbeque, infected person	c
Home	2006	Weltevreden	1	3	4	Fish imported from Tonga, infected person	c
Restaurant/café	2006	Weltevreden 15+	1	1	?	Unknown	c
Cruise ship	2002	Typhimurium DT160	23	0	2000	Club sandwiches with mayonnaise	d
Camp	2001	Typhimurium DT160	16	0	32	Lasagne, ducks, infected food handler	e

(F) Summary of outbreaks with a mode of transmission that does not belong in tables A-E above ('other' mode) (n=1)

Setting	Year	*Salmonella* serotype	No. cases			Suspected source	Level of evidence
			Conf	Prob	Exp		
Prison	2000	Typhimurium DT135	2	0	100	Handling soiled linen	d