

Copyright is owned by the Author of the thesis. Permission is given for a copy to be downloaded by an individual for the purpose of research and private study only. The thesis may not be reproduced elsewhere without the permission of the Author.

Estimating the contribution of different sources to the  
burden of human campylobacteriosis and salmonellosis

A thesis submitted in partial fulfilment of the  
requirements for the degree of  
Doctor of Philosophy  
at Massey University, Palmerston North,  
New Zealand,

by

Petra Müllner

2009



# Preface

It was both odd and unjust, said Gauss, a real example of the pitiful arbitrariness of existence, that you were born into a particular time and held prisoner there whether you wanted it or not. It gave you an indecent advantage over the past and made you a clown vis-à-vis the future.

*Measuring the World*, Daniel Kehlmann 2005.

Seltsam sei es und ungerecht, sagte Gauss, so recht ein Beispiel für die erbärmliche Zufälligkeit der Existenz, da man in einer bestimmten Zeit geboren und ihr verhaftet sei, ob man wolle oder nicht. Es verschaffe einem einen unziemlichen Vorteil vor der Vergangenheit und mache einen zum Clown der Zukunft.

*Die Vermessung der Welt*, Daniel Kehlmann 2005.



# Abstract

This thesis is concerned with the molecular epidemiology of *Campylobacter jejuni* and *Salmonella* in New Zealand and the development of source attribution tools for these pathogens. Although campylobacteriosis is the leading enteric zoonosis worldwide, the pathogen's complex epidemiology and difficulties with existing typing schemes, have posed challenges for the control of this disease.

The first study of this thesis gives an overview of existing approaches to microbial risk assessment and source attribution, with particular respect to campylobacteriosis, and describes their advantages and shortcomings. Further, the chapter discusses pheno- and genotyping techniques for *Campylobacter* spp. and the value of including microbial typing data in risk assessments. In the second study, data from a sentinel surveillance site in the Manawatu region was used to investigate the molecular epidemiology of human campylobacteriosis cases. This analysis revealed the presence of a dominant *C. jejuni* clone, namely sequence type (ST) 474, which accounted for 30.7 % of human cases in the study and identified risk factors for infection with ruminant and poultry associated STs. The third study investigated the link between *C. jejuni* in human cases and samples taken from poultry. By applying epidemiological and population genetic techniques this part of the thesis provided further evidence that poultry is a major contributor to human infection. In the fourth study an existing Bayesian source attribution model was modified and consecutively applied to New Zealand's major foodborne zoonoses: campylobacteriosis and salmonellosis. The majority (80 %) of human campylobacteriosis cases attributable to *C. jejuni* were estimated to have been acquired from poultry sources, whereas wildlife source were estimated to contribute only a minor proportion of cases. In the fifth study the *Salmonella* dataset was descriptively analysed and a large proportion of human cases was found to be caused by 'exotic' *Salmonella* types. In the final study of this thesis four different genetic and epidemiological source attribution methodologies were applied to the same dataset in a comparative modelling framework.

The studies in this thesis show that epidemiological studies combined with molecular tools and modeling can provide valuable risk-based tools to inform the surveillance and control of zoonotic pathogens. Methods from these studies may be readily applied to the control of other (food borne) zoonoses and provide new opportunities for epidemiological investigations and source attribution modelling of major pathogens.

# Acknowledgements

I learned many things while working on this thesis and greatly appreciate the excellent training I received at Massey University. But it feels the most valuable improvement has not come from the technical side of things but from a new appreciation I acquired for other disciplines and my colleagues. Clearly my mind has become a broader one in the process.

I owe a lot to my main supervisor Nigel French. You have taught me a great many things and moved me out of my comfort zone to reach peak performance. Thank you for your kindness and encouragement in difficult times, your contagious enthusiasm and guidance.

I would like to thank the New Zealand Food Safety Authority for funding this project as part of their postgraduate programme and for the help of all those I came to know in the process. You provided valuable input for my thesis and it was great to learn from your expertise. Special thanks to the Science Group for their support in the last four years, in particular Steve Hathaway for initiating the program and taking the time to supervise and guide me. To Donald Campbell, Terry Ryan and Roger Cook for their advice, Peter van der Logt for his help and kindness, Paul Dansted for the invaluable noise cancelling headphones, Bob Jackman for his helpfulness, David Tisdall for making me laugh when it was much needed and Audrey Taulalo for those hours of ‘girls time’ in and out of the office. Thanks all for your annual (failed) attempts to make me understand your sense of humour for the Christmas skit.

Thanks to my supervisor Cord Heuer for getting me over here and started, and always being there when I needed his advice. Thanks to all my fellow students at the Epicentre and Hopkirk Institute for sharing their experiences with me. Thanks to Colleen Blair, Julie Dunlop, Wendy Maharey, Chris Cunningham and Simon Verschaffelt from the EpiCentre for their administrative and computing support and Bruce White for his help with EndNote. Thanks to the many people who made my project possible: the Hopkirk Lab Team (in particular Julie Collins-Emerson, Ann Midwinter, Errol Kwan, Rhukshana Akhter, Rebecca Pattison, Sarah Moore, Isabel Li and Diane



Richardson), MedLab Central (in particular Lynn Rogers), and Tui Shadbolt and her colleagues from MidCentral Public Health. A special thanks to the team at ESR in Kenepuru, in particular Phil Carter, for their help with the project. I owe the Hopkirk Team and Tui some special words for all the hard work and extra hours they put into the project. We pushed through hard times until my German directness and your Kiwi ingenuity melted us into a great team. I will miss working with you.

Thanks to Simon Spencer, Geoff Jones and Alasdair Noble for guiding me through the ups and downs of applied statistics and being key to the success of this project. Thanks to Martin Hazelton for valuable input into the development of the modified Hald model and Jonathan Marshall for his help with the publications. For stimulating discussion and the honour to be part of their group I would like to thank all members of the Enteric Zoonoses Modelling Group.

Thanks to all the people who helped me through the final steps of this thesis in various ways such as providing templates, de-bugging L<sup>A</sup>T<sub>E</sub>X and proof reading: Julie Collins-Emerson, Jonathan Marshall, Eve Pleydell, Deb Prattley, Daan Vink and Jacqui Benschop.

Thanks to my friends Jacqui Benschop (and her lovely family) and Eve Pleydell for giving me shelter and so many other things over the last years. Katie Owen for cheering me up over a coffee so many times. Petra Stübben, Jens Schwarz and Frederik for shared moments far away from the homeland and those early morning get-togethers watching the German soccer team play in championships. Thanks to all my other friends and family, most far away, for being there for me. To my parents-in-laws for all their support in our endeavours and visiting us in the final months of the thesis, providing me with time to fully immerse myself in those final steps. To my aunt and uncle Trude and Hartmut for caring so much about me, I couldn't wish for better god-parents to my children. To my cousin Ellen for the time we shared, with a promise to reply more often to my emails once this thesis is submitted. To my father, who did not live long enough, to meet my girls and share my happiness with me. Carina, Franzi, Kathrin, Soni, Brigitte, Susi, Kirsten and Janne it is great to have friends like you, even if we now live at different ends of this planet.

Most importantly thanks to my husband Uli for his support and love and keeping me from taking myself and life too seriously. You truly are the best thing that ever happened to me. And finally to my girls Lea and Stella, to the moon and back this is how much I love you!

# Nomenclature

AFLP	Amplified Fragment Length Polymorphism
AMOVA	Analysis of molecular variance
BA	Blood agar
BPW	Buffered Petone Water
CAC	Codex Alimentarius Commission
CI	Confidence interval
CC	Clonal complex
cfu	colony forming unit
CrI	(Bayesian) credible interval
CRISPR	Clustered regularly interspaced short palindromic repeats
DNA	Desoxyribonucleic acid
ELISA	Enzyme-linked immunosorbent assay
ERL	Enteric Reference Laboratory
ERIC	Enterobacterial repetitive intergenic consensus
ESR	Environmental Science and Research Ltd.
EU	European Union
EZDRG	Enteric Zoonosis Disease Research Group
FAO	World Agricultural Organisation
FAME	Fatty acid methyl ester
HACCP	Hazard Analysis and Critical Control Points
HL	Heat-labile (antigen)
HS	Heat-stable (antigen)
mCCDA	Modified Cefoperazone Charcoal Desoxycholate agar
MCMC	Markov Chain Monte Carlo
MEE	Multi locus enzyme electrophoresis
MLST	Multi locus sequence typing

MPRM	Modular process risk model
MRA	Microbial risk assessment
MST	Microbial source tracking
MST	Minimum spanning trees
NMD	National Microbiological Database
NZ	New Zealand
NZFSA	New Zealand Food Safety Authority
OIE	World Organisation for Animal Health
OR	Odds ratio
PCR	Polymerase chain reaction
PFGE	Pulsed field gel electrophoresis
PHS	Public Health Service
PSI	Proportional similarity index
QRA	Quantitative risk assessment
RA	Risk assessment
RAPD	Randomly amplified polymorphic DNA
rDNA	Ribosomal DNA
RE	Restriction enzyme
REA	Restriction endonuclease analysis
RFLP	Restriction fragment polymorphism
SD	Standard deviation
spp.	Species (multiple)
SPS	Sanitary and phytosanitary (agreement)
ST	Sequence type
SVR	Short variable region
US-NAS	United States National Academy of Science
WHO	World Health Organisation
WTO	World Trade Organisation

# Publications

**Mullner, P.**, Spencer S., Wilson D., Jones G., Noble A. D., Midwinter, A., Collins-Emerson, J., Carter, P., Hathaway, S., French, N. P. Assigning the source of human campylobacteriosis in New Zealand: A comparative genetic and epidemiological approach. *Infection, Genetics and Evolution* (9): 1311-1319 2009.

**Mullner, P.**, G. Jones, A. Noble, S. Spencer, S. Hathaway, and N. French. Source Attribution of Food Borne Zoonoses in New Zealand: A Modified Hald Model. *Risk Analysis*(7): 970-984 Jul 2009.

**Mullner P.**, Spencer S., Jones G., Noble A. D., Wilson D., Collins-Emerson, J., Midwinter, A., Carter, P., Hathaway, S., French, N. P. Attribution of campylobacteriosis in New Zealand: Approaches, results and outlook. *Proceedings of the 12th Symposium International Society for Veterinary Epidemiology and Economics*, Durban, South Africa: ISVEE 12, 432, 2009.

**Mullner, P.**, Benschop, J. Interdisciplinary research at the human and animal health interface: A personal perspective. *Proceedings of the 12th Symposium International Society for Veterinary Epidemiology and Economics*, Durban, South Africa: ISVEE 12, 125, 2009.

**Mullner, P.**, Collins-Emerson, J., Midwinter, A., Carter, P., Hathaway, S., French, N. P. Structured parallel studies of the molecular epidemiology of *Campylobacter jejuni* in environmental and food sources reveal insight into the importance and interconnection of different reservoirs. *Proceedings of the 12th Symposium International Society for Veterinary Epidemiology and Economics*, Durban, South Africa: ISVEE 12, 431, 2009.

**Mullner, P.**, Shadbolt, T., Spencer, S., Jones, G., Noble, A. D., Collins-Emerson, J., Midwinter, A., Carter, P., Campbell, D. M., Van der Logt, P., Lee, J., Hathaway, S., French, N. P. Enhanced surveillance to identify the origin of human campylobacteriosis in New Zealand: Conclusions drawn from an interdisciplinary sentinell surveillance site. *Proceedings of the 12th Symposium International Society for Veterinary Epidemiology and Economics*, Durban, South Africa: ISVEE 12, 379, 2009.

French, N.P., **Mullner P.**, Spencer S. Controlling campylobacteriosis in New Zealand: combining epidemiology and population genetics to trace the origin of human infections. *New Zealand Microbiological Society, Annual Conference 2008*, Christchurch, NZ.

G. McBride, P. van der Logt, R. Lake, N. French, A. Ball, **P. Mullner**, A. Elliott, A. Hunt and L. Oakley. Modelling initiatives for campylobacteriosis. *New Zealand Microbiological Society, Annual Conference 2008*, Christchurch, NZ.

French, N.P., **Mullner P.** Risk-based tools to inform decision making in food safety and public health - applications in Europe and New Zealand. *FOOD FRENZ, Annual Conference 2008*, Budapest, Hungary.

**Mullner P.**, Collins-Emerson, J., Midwinter, A., Spencer, S., French, N. Molecular and Modelling tools for *Campylobacter* Source Attribution. *Proceedings of the Epidemiology & Animal Health Management Branch of the NZVA*, 2008, Wellington, NZ.

**Mullner P.**, Pleydell, E., Shadbolt, T., Collins-Emerson, J., Midwinter, A., Spencer, S., French, N. Working at the human and animal health interface - a multidisciplinary team approach towards reducing New Zealand's campylobacteriosis problem. *Proceedings of the Epidemiology & Animal Health Management Branch of the NZVA*, 2008, Wellington, NZ.

French, N.P., Carter P., Collins-Emerson J., Midwinter A., **Mullner P.**, Wilson, D. Comparing 'source attribution' models for human campylobacteriosis. *Society for Veterinary Epidemiology and Preventive Medicine, Annual Conference 2008*, Liverpool, UK.

Lake, R., van der Logt, P., McBride, G., French, N., **Mullner, P.**, Andrew Elliott, Andrew Ball. Campylobacteriosis in New Zealand: modelling as a way forward. *NZ Science Review* 2007 Volume 64 (2) pp 37-41.

**Mullner P.** Source attribution of *C. jejuni* using molecular epidemiology. *New Zealand Institute of Food Science and Technology, Annual conference 2007*, Wellington, NZ.

**Mullner P**, Carter P, Midwinter A, Collins-Emerson J, Pattison R, French NP. Source attribution of *Campylobacter jejuni* using molecular epidemiology. *Proceedings of the Epidemiology & Animal Health Management Branch of the NZVA*, 69, 2007.

**Mullner, P.**, Carter, P., Cook, R., Tebje-Kelly, J., French, N. P. Strain Typing As A Valuable Tool For Quantitative Microbial Risk Assessment. *Proceedings 11th International Symposium ISVEE*, August 6-11, 2006, Cairns, Australia.

**Mullner, P.**, Carter, P., Midwinter, A., Collins-Emerson, J., French, N. P. Molecular epidemiology of *Campylobacter jejuni*: comparing Multilocus Sequence Types from humans and poultry. *Proceedings 11th International Symposium ISVEE*, August 6-11, 2006, Cairns, Australia.

Terry Ryan, Stuart MacDiarmid, Steve Hathaway, **Petra Mullner**, Neil Cox, Andrew Hill. A Quantitative Analysis of Foodborne Salmonellosis Exposure Pathways in New Zealand. *Proceedings of the International Conference on 'Priority Setting of Foodborne and Zoonotic Pathogens'*, MedVetNet and the US Food Safety Research Consortium, 19-21 July 2006, Berlin, Germany.



# Contents

<b>Preface</b>	<b>ii</b>
<b>Abstract</b>	<b>iv</b>
<b>Acknowledgements</b>	<b>vi</b>
<b>Nomenclature</b>	<b>viii</b>
<b>Publications</b>	<b>x</b>
<b>Contents</b>	<b>xviii</b>
<b>List of Tables</b>	<b>xxi</b>
<b>List of Figures</b>	<b>xxiii</b>
<b>1 Chapter 1</b>	<b>1</b>
1.1 Introduction . . . . .	1
1.2 The Manawatu Sentinel Surveillance Site . . . . .	4
1.3 The structure of this thesis . . . . .	6
<b>2 Chapter 2</b>	<b>7</b>
2.1 Summary . . . . .	7
2.2 Introduction . . . . .	8
2.3 Review of typing methods for <i>Campylobacter</i> spp. . . . .	9
2.3.1 Phenotyping . . . . .	10
2.3.2 Genotyping . . . . .	12
2.3.3 A comparison of phenotyping and genotyping . . . . .	21
2.4 MRA approaches . . . . .	22
2.4.1 Overview . . . . .	22
2.4.2 Different approaches to MRA . . . . .	25
2.4.3 Major <i>Campylobacter</i> risk assessments to date . . . . .	30
2.4.4 Source attribution approaches . . . . .	32
2.4.5 Strain variation and MRA approaches . . . . .	41



2.4.6	Suitable typing methods for <i>Campylobacter</i> risk research . . . . .	48
2.5	Conclusions . . . . .	53
2.6	Appendices . . . . .	54
<b>3</b>	<b>Chapter 3</b>	<b>55</b>
3.1	Summary . . . . .	55
3.2	Introduction . . . . .	56
3.3	Material and Methods . . . . .	57
3.3.1	Study population . . . . .	57
3.3.2	Case definition . . . . .	58
3.3.3	Case ascertainment . . . . .	58
3.3.4	Genotyping . . . . .	58
3.3.5	Epidemiological surveillance . . . . .	58
3.3.6	Data handling and statistical analysis . . . . .	59
3.4	Results . . . . .	60
3.4.1	Description of cases . . . . .	60
3.4.2	Incidence . . . . .	63
3.4.3	Distribution and source association of genotypes . . . . .	63
3.4.4	Risk factor analysis . . . . .	66
3.4.5	Spatio - temporal analysis . . . . .	67
3.5	Discussion . . . . .	72
3.6	Acknowledgements . . . . .	75
3.7	Appendices . . . . .	75
<b>4</b>	<b>Chapter 4</b>	<b>77</b>
4.1	Abstract . . . . .	77
4.2	Introduction . . . . .	78
4.3	Material and Methods . . . . .	79
4.3.1	<i>Campylobacter</i> isolates . . . . .	79
4.3.2	Bacterial culture and identification . . . . .	80
4.3.3	Sequence typing . . . . .	80
4.3.4	Statistical analysis of <i>Campylobacter</i> count data . . . . .	81
4.3.5	Statistical Analysis of ST distributions . . . . .	82
4.4	Results . . . . .	83
4.5	Discussion . . . . .	94
4.6	Acknowledgements . . . . .	97
4.7	Appendices . . . . .	97

<b>5</b>	<b>Chapter 5</b>	<b>99</b>
5.1	Abstract . . . . .	99
5.2	Introduction . . . . .	100
5.3	The Bayesian risk attribution model by Hald et al. . . . .	101
5.4	A modified Hald model . . . . .	103
5.4.1	Modelling prevalence uncertainty . . . . .	103
5.4.2	Splitting data into different time periods . . . . .	105
5.4.3	Hierarchical model for bacterial parameters . . . . .	105
5.4.4	Exponential prior for source specific parameters . . . . .	106
5.4.5	Avoid food consumption weights . . . . .	106
5.4.6	Including potentially pathogenic subtypes . . . . .	107
5.5	Application of the modified Hald model . . . . .	107
5.5.1	Campylobacteriosis . . . . .	107
5.5.2	Salmonellosis . . . . .	118
5.6	Discussion . . . . .	123
5.6.1	Improving identifiability . . . . .	123
5.6.2	Choice of prior for $q_i$ and $a_j$ . . . . .	123
5.6.3	Introduction of uncertainty in prevalence matrix . . . . .	124
5.6.4	Novel approach to prevalence estimation . . . . .	124
5.6.5	Splitting data into different time periods . . . . .	125
5.6.6	Avoid food consumption weights . . . . .	125
5.6.7	Including potentially pathogenic subtypes . . . . .	126
5.6.8	Campylobacteriosis model . . . . .	127
5.6.9	Salmonellosis model . . . . .	128
5.7	Conclusions . . . . .	129
5.8	Acknowledgements . . . . .	129
5.9	Appendices . . . . .	129
<b>6</b>	<b>Chapter 6</b>	<b>131</b>
6.1	Summary . . . . .	131
6.2	Introduction . . . . .	131
6.2.1	Sources of data in New Zealand . . . . .	134
6.3	Material and Methods . . . . .	135
6.3.1	Human cases . . . . .	135
6.3.2	Animal food source prevalence . . . . .	135
6.3.3	Amount of food source consumed . . . . .	135
6.3.4	Analysis . . . . .	135
6.4	Descriptive analysis of data set: Human cases 2000 - 2004 . . . . .	136
6.4.1	Overview . . . . .	136
6.4.2	<i>Salmonella</i> serotypes occurring in human cases . . . . .	136

6.4.3	Serotype and travel status . . . . .	139
6.4.4	Serotype and outbreak status . . . . .	140
6.5	Descriptive analysis of data set - animal food sources 2002-2004 . . . . .	141
6.5.1	Overview . . . . .	141
6.5.2	Beef and veal . . . . .	145
6.5.3	Pork . . . . .	146
6.5.4	Lamb and mutton . . . . .	147
6.5.5	Chicken . . . . .	148
6.5.6	Eggs . . . . .	149
6.6	Descriptive analysis of data set - food consumption data . . . . .	150
6.7	Discussion . . . . .	151
6.8	Conclusions . . . . .	154
6.9	Acknowledgements . . . . .	154
6.10	Appendices . . . . .	154
<b>7</b>	<b>Chapter 7</b>	<b>155</b>
7.1	Abstract . . . . .	155
7.2	Introduction . . . . .	156
7.3	Methods . . . . .	157
7.3.1	Data . . . . .	157
7.3.2	Proportional similarity index . . . . .	158
7.3.3	Dutch model . . . . .	158
7.3.4	Modified Hald model . . . . .	159
7.3.5	Island model . . . . .	159
7.4	Results . . . . .	160
7.4.1	Proportional similarity index . . . . .	160
7.4.2	Dutch model . . . . .	160
7.4.3	Modified Hald model . . . . .	160
7.4.4	Island model . . . . .	160
7.4.5	Comparing the results from different approaches . . . . .	161
7.5	Discussion . . . . .	164
7.6	Acknowledgements . . . . .	167
7.7	Appendices . . . . .	168
<b>8</b>	<b>Chapter 8</b>	<b>169</b>
8.1	Summary . . . . .	169
8.2	Molecular epidemiology . . . . .	170
8.3	Source attribution modelling . . . . .	171
8.4	Interdisciplinarity . . . . .	172
8.5	Conclusions . . . . .	176

<b>A</b>	<b>Appendix A</b>	<b>177</b>
A.1	Summary . . . . .	177
A.2	Selected performance criteria for evaluation of typing systems . . . . .	177
A.2.1	Typeability . . . . .	177
A.2.2	Reproducibility . . . . .	177
A.2.3	Stability . . . . .	178
A.2.4	Discriminatory power . . . . .	178
<b>B</b>	<b>Appendix B</b>	<b>179</b>
B.1	Summary . . . . .	179
<b>C</b>	<b>Appendix C</b>	<b>183</b>
C.1	Summary . . . . .	183
C.2	Material and methods . . . . .	183
C.2.1	Summary . . . . .	183
C.2.2	Detailed methods . . . . .	183
C.3	Genotypes detected in human cases and poultry samples . . . . .	186
C.3.1	Summary . . . . .	186
<b>D</b>	<b>Appendix D</b>	<b>191</b>
D.1	Summary . . . . .	191
D.2	Bayesian statistics and simulation modelling . . . . .	191
D.3	Assignment of travel and outbreak association of cases . . . . .	195
D.3.1	Outbreak association . . . . .	195
D.3.2	Travel association . . . . .	195
D.4	'Other <i>Salmonella types</i> ' detected in human cases from 2002-2004 . . . .	196
<b>E</b>	<b>Appendix E</b>	<b>201</b>
E.1	Summary . . . . .	201
	<b>Bibliography</b>	<b>207</b>



# List of Tables

2.1	Classification of different approaches to MRA. . . . .	26
2.2	Mean risk of infection for different strains of <i>Campylobacter</i> . . . . .	46
2.3	Ranking of four typing methods for <i>Campylobacter</i> spp. . . . .	53
3.1	Demographic characteristics of types and nontyped cases. . . . .	61
3.2	Frequency and source association of human <i>C. jejuni</i> genotypes. . . . .	64
3.3	Results of a multivariable case-case risk factor analysis. . . . .	66
4.1	Proportion of poultry samples positive. . . . .	85
4.2	Relative frequency of STs. . . . .	86
4.3	Multiple typed samples. . . . .	92
4.4	The proportional similarity index for each supplier. . . . .	93
5.1	Description of parameters of Hald model. . . . .	102
5.2	Description of different campylobacteriosis models. . . . .	112
5.3	Estimates for $a_j$ and $q_i$ and $\tau$ in campylobacteriosis model. . . . .	114
5.4	Data matrix for <i>Salmonella</i> prevalence estimation. . . . .	121
5.5	Prevalence estimates for <i>Salmonella</i> in beef. . . . .	122
6.1	Typing, outbreak and travel status of human salmonellosis cases. . . . .	136
6.2	Number of cases of <i>Salmonella</i> subtypes. . . . .	137
6.3	Percentage of cases of <i>Salmonella</i> serotypes with a history of travel. . . . .	139
6.4	Outbreak association of <i>Salmonella</i> serotypes 2000 - 2004. . . . .	140
6.5	Number of <i>Salmonella</i> serotypes isolated. . . . .	142
6.6	Prevalence estimates for <i>Salmonella</i> serotypes in beef and veal. . . . .	145
6.7	Prevalence estimates for <i>Salmonella</i> serotypes in pork. . . . .	146
6.8	Prevalence estimates for <i>Salmonella</i> serotypes in lamb and mutton. . . . .	147
6.9	Prevalence estimates for <i>Salmonella</i> serotypes in chicken. . . . .	148
6.10	Prevalence estimates for <i>Salmonella</i> serotypes in eggs. . . . .	149
6.11	Estimated food consumption in New Zealand 2002 - 2004. . . . .	150
7.1	Overview of samples collected in the Manawatu. . . . .	158
7.2	Comparison of proportional similarity indices. . . . .	161

C.1	Genotypes isolated from human cases and poultry samples. . . . .	187
D.1	Other <i>Salmonella</i> types. . . . .	196
E.1	Relative frequency of sequence types (ST). . . . .	201

# List of Figures

1.1	Campylobacteriosis rates in different countries (2004). . . . .	2
1.2	Number of notified campylobacteriosis cases in New Zealand 1997 - 2008. . . . .	5
2.1	The Risk Analysis Framework . . . . .	23
2.2	Minimum spanning tree . . . . .	37
2.3	Source attribution using STRUCTURE and the ISLAND model . . . . .	38
2.4	Consensus tree of <i>Campylobacter</i> isolates . . . . .	40
2.5	Framework for exposure assessment of <i>Campylobacter</i> spp. . . . .	47
3.1	Human samples from the Manawatu surveillance site . . . . .	62
3.2	The proportion of cases in each age category . . . . .	67
3.3	Smoothed temporal trends in human campylobacteriosis cases . . . . .	68
3.4	Relative risk surface for ST - 474. . . . .	69
3.5	Relative risk surface for non-poultry poultry strains. . . . .	70
3.6	Relative risk surface for other poultry strains. . . . .	71
4.1	Probability of contamination of poultry carcasses . . . . .	89
4.2	Level of contamination of poultry carcasses . . . . .	90
4.3	Population structure of <i>C. jejuni</i> in different poultry suppliers . . . . .	91
5.1	Plot of observed and expected campylobacteriosis cases . . . . .	109
5.2	Attribution results campylobacteriosis . . . . .	110
5.3	Sensitivity analysis for different campylobacteriosis models . . . . .	113
5.4	Attribution of salmonellosis cases . . . . .	120
6.1	Notified cases of salmonellosis in New Zealand. . . . .	133
6.2	Temporal trends of selected <i>Salmonella</i> serotypes . . . . .	138
6.3	Estimated median <i>Salmonella</i> prevalence in different food sources . . . . .	144
7.1	Comparison of attribution results . . . . .	162
7.2	Results from island model . . . . .	163
8.1	Framework of multidisciplinary approach . . . . .	175



B.1	Comparison of case numbers with notification data . . . . .	180
B.2	Relative frequency of human <i>C. jejuni</i> MLST genotypes . . . . .	181