

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.

**Epidemiological investigations of Shiga toxin-producing
Escherichia coli (STEC) O157 and STEC O26 in New
Zealand slaughter cattle, and the source attribution of
human illness**

A thesis presented in partial fulfilment of the requirements for the degree
of

Doctor of Philosophy
in
Veterinary Science

at Massey University, Palmerston North,
New Zealand.

Patricia Jaros

2014
(Submitted March 31, 2014)

*m*EpiLab, Hopkirk Research Institute
Institute of Veterinary, Animal and Biomedical Sciences
Massey University
Palmerston North, New Zealand

Abstract

Shiga toxin-producing *Escherichia coli* O157:H7 (STEC O157) and related non-O157 STEC strains are enteric pathogens of significant public health concern worldwide, including New Zealand, causing clinical diseases ranging from diarrhoea and bloody diarrhoea to the life-threatening haemolytic uraemic syndrome. Cattle are considered the principal hosts and have been shown to be a source of STEC infection for both foodborne and environmental outbreaks of human diarrhoeal disease overseas. A series of observational studies were conducted to gain knowledge on the epidemiology of STEC O157 and STEC O26 in New Zealand slaughter cattle and assess the relative importance of cattle as a source of domestically-acquired STEC infections in humans.

A repeated cross-sectional study conducted on four selected New Zealand beef slaughter plants provided detailed data on the prevalence and concentration of faecal shedding of STEC O157 and STEC O26 in 695 very young calves (4–7 days-old) and 895 adult cattle post-slaughter, identifying calves as more prevalent carriers of STEC. Findings of a subsequent cohort study, the first of its kind, provided evidence that for the 60 calves examined, transportation and lairage was not associated with increase of faecal shedding of *E. coli* O157 and O26 (STEC and non-STEC) but increase of cross-contamination of hides and carcasses post-slaughter.

In a national prospective case-control study, 113 STEC cases and 506 random controls were interviewed for risk factor evaluation. The study findings implicate that environmental and animal contact, but not food, as significant exposure pathways for sporadic STEC infections in humans in New Zealand, and suggest ruminants as the most important source of infection. The molecular analysis of bovine and human STEC O157 isolates provided evidence for the historical introduction of a subset of the globally-circulating STEC O157 strains into New Zealand and ongoing localised transmission of STEC between cattle and humans.

These findings will contribute to the development of a risk management strategy for STEC, similar to those already implemented for *Campylobacter*, *Salmonella*, and *Listeria*, which

pose a high risk to public health and New Zealand's access to international markets. Furthermore, risk factors identified in the case-control study will contribute to the design of public health interventions to reduce the incidence of STEC infections in New Zealand.

Acknowledgements

It was five years ago, April 2009, when I set sail to a long but adventurous journey, called a PhD. It was a life-changing journey loaded with numerous rewarding challenges, fulfilling experiences, and valuable friendships I have made. There are a number of people to whom I express my deep gratitude for their considerable help and contribution to this rather large research project and thesis.

First and foremost, to my excellent supervisors, Professor Nigel French, Dr Adrian Cookson, Dr Deborah Prattley, Dr Donald Campbell, and Dr Steve Hathaway, thank you for all your knowledge, inputs, and inspiring guidance during the study and writing of my thesis.

Thanks must go to the New Zealand beef industry, particularly the managers of the four beef slaughter plants, who consented to participate in the nationwide prevalence study, and their staff, who were equally helpful and accepted my presence during sampling without complaint. Special thanks must also go to the dairy farmers in the Waikato, who participated in the transport and lairage study and allowed me to sample their calves during the busy time of calving.

Angie Reynolds deserves special appreciation. I could not have asked for a better laboratory technician to help me with the processing of samples. Her assistance was so precious to me, especially during the weeks of intensive sampling for the transport and lairage study, when the laboratory workload was gigantic. Angie – you are a fabulous and hard-working technician with great organisational skills. Thanking you is not enough.

I am also indebted to several other ^mEpiLab staff members; Dr Anne Midwinter and Errol Kwan for providing valuable advice on microbiological and molecular laboratory techniques; and Sarah Moore, Rukshana Akhter, Dr Julie Collins-Emerson, Rebecca Pattison, and Lynn Rogers for providing their help in the laboratory when needed. I would also like to acknowledge Dr Jonathan Marshall for his contribution on the statistical analysis of data; Simon Verschaffelt for helping with any type of software- or computer-related issues, and

Christine Cunningham for dealing with all other administrative and contract-related issues of my research project.

I also thank my fellow students, colleagues and friends from the ^mEpiLab and EpiCentre, especially Barbara Binney, Hamid Irshad, Fang Fang, Kruno Bojanic, Zoë Grange, Anja Friedrich, Rima Shresta, Ben Phiri, Anou Dreyfus, Naomi Cogger, Jackie Benschop, and Charlotte Bolwell for their kind support throughout my study.

Jaimie Hunnam and Lesley Stringer, you were an inspiration for me. Thank you!

My sincere thanks also to people from other organisations for their collaboration and participation in different studies of this research project; the Food Microbiology and Safety Team from AgResearch (Ruakura, Hamilton, New Zealand), the Health Intelligence Team at the Institute of Environmental & Science Research Ltd (ESR) (Porirua, New Zealand), staff from UMR Research Ltd (Wellington, New Zealand), Muriel Dufour from the Enteric Reference Laboratory (ERL) (Upper Hutt, New Zealand), and Brent Gilpin from ESR (Christchurch, New Zealand).

I would also like to acknowledge the financial support of the Meat Industry Association of New Zealand (Inc) (Wellington, New Zealand) and the Ministry for Primary Industries (MPI) (Wellington, New Zealand), who generously funded this research project; Massey University for awarding me a Doctoral Scholarship, and the Institute of Veterinary, Animal and Biomedical Sciences for financial support to attend several national and international conferences.

Most of all I would like to express my special thanks and love to my parents in Switzerland and Bryce for continued moral support, encouragement and love throughout my PhD.

Declaration

Studies presented in this thesis are written in manuscript style prepared for publication in peer-reviewed journals, hence there is some repetition, particularly in the introductions and methodologies. Two chapters have been formatted in style required of the journals, to which they have been submitted. Co-authors of the papers have made their contributions to the research and/or manuscripts, however, my input was the greatest as I designed the studies, conducted all the fieldwork; entered and analysed all data, and wrote the manuscripts. Angie Reynolds, a designated laboratory technician from the ^mEpiLab, helped me with the processing of samples.

Nomenclature

A/E lesions	Attachment and effacement lesions
AIC	Akaike information criterion
AMOVA	Analysis of molecular variance
BPW	Buffered peptone water
CFU	Colony forming unit
CI	Confidence interval
CT-RMAC	Cefixime-tellurite rhamnose MacConkey agar
CT-SMAC	Cefixime-tellurite sorbitol MacConkey agar
DNA	Deoxyribonucleic acid
EHEC	Enterohaemorrhagic <i>Escherichia coli</i>
ERL	Enteric Reference Laboratory
ESR	Institute of Environmental Science & Research Ltd
HUS	Haemolytic uraemic syndrome
IMS	Immunomagnetic separation
MPN	Most probable number
OR	Odds ratio
PCR	Polymerase chain reaction
PFGE	Pulsed-field gel electrophoresis
rRNA	Ribosomal ribonucleic acid
SBI	Shiga toxin-encoding bacteriophage insertion
STEC	Shiga toxin-producing <i>Escherichia coli</i>
Stx	Shiga toxin
TSB	Tryptic (or tryptone) soy broth
UPGMA	Unweighted pair group method with arithmetic mean
US or USA	United States of America

Glossary –

New Zealand specific descriptions and terminology

Pastoral farming

New Zealand's beef and dairy production systems are pasture-based with year-round grazing (supplemented with hay, baleage, maize silage, or palm kernel during winter), outdoor housing, and seasonal calving in late winter/early spring (July/August to September/October). In 2013, 3.7 million beef cattle and 6.6 million dairy cattle (including bobby calves) were recorded [1].

Bobby calves

Bobbies are milk-fed calves, which are not reared for dairy replacement stock or the dairy beef market, but are slaughtered at 4–7 days of age and exported as veal to overseas markets (mainly the US).

Cattle slaughter system

Slaughter cattle in New Zealand comprise bobby calves and adult cattle. Adult slaughter cattle consist of dairy and beef animals, which are classified according to sex and maturity as bulls, steers, heifers, and cows [2]. Bulls are entire male cattle, compared to steers, which were castrated at a young age; heifers and cows are female cattle with ≤ 4 and >4 permanent incisors, respectively.

Beef slaughter plant

In 2013, there were 55 beef slaughter plants actively processing adult cattle (and bobby calves) including slaughter and dressing and/or further processing of carcasses at primary industry level. Of those 55 beef plants, 42 were listed on the National Microbiological Database (NMD) as undertaking STEC-testing of beef as required for overseas market access.

Transportation and lairage of slaughter cattle

Adult cattle are usually transported as a mob in a livestock transporter from a farm to a slaughter plant where the animals are kept in separate holding pens in the lairage area until

slaughter. Adult cattle of the same mob are slaughtered consecutively as a line. In contrast, bobby calves are collected by a regional livestock transporter, picking-up calves from local dairy farms on a pre-determined route, and transported collectively to a slaughter plant where the calves are kept in large holding pens until slaughter. Bobby calves are slaughtered as large groups from different regions.

National Microbiological Database (NMD)

NMD is a mandatory food safety programme for New Zealand primary processors of meat, poultry, game and ratites, which receive live animals for slaughter, dressing or other processing to produce food suitable for human consumption [3]. The microbiological monitoring programme is controlled by the Ministry for Primary Industries (MPI, Wellington, New Zealand) and aims to minimise the incidence of foodborne pathogens. It ensures common microbiological standards for food sold on the domestic market and to meet the export requirements set by destination countries.

Human disease notification system

General practitioners/medical centres/hospitals notify cases of STEC infections to regional Public Health Units. Any notified case is then investigated by a Public Health Officer/Medical Officer, who completes a case report form and enters epidemiological data into a national surveillance database (EpiSurv) used for notified cases of communicable and other diseases. EpiSurv is held by the Institute of Environmental Science & Research Ltd (ESR). Most of STEC cases are confirmed by culture isolation of STEC from clinical specimen submitted to medical laboratories or the Enteric Reference Laboratory (ERL).

^mEpiLab

Unless stated otherwise, laboratory testing of samples and isolates used in studies presented in this thesis was conducted at the Molecular Epidemiology and Public Health Laboratory (^mEpiLab), which is located within the Hopkirk Research Institute at Massey University in Palmerston North, New Zealand.

List of Publications

Jaros P, *et al.* (2014) Geographic divergence of bovine and human Shiga toxin-producing *Escherichia coli* O157:H7 genotypes, New Zealand. *Emerging Infectious Diseases*, doi: 10.3201/eid2012.140281 (e-published ahead of print).

Jaros P, *et al.* (2014) Geographic divergence of bovine and human Shiga toxin-producing *Escherichia coli* O157:H7 genotypes in New Zealand. (Australasian Epidemiological Association (AEA) Annual Scientific Meeting, 8–10 Oct 2014; Auckland, New Zealand). *Australasian Epidemiologist*, Vol. 21 (3), p 65.

Jaros P, *et al.* (2014) International divergence of bovine and human Shiga toxin-producing *Escherichia coli* O157:H7 genotypes. (International Association for Food Protection (IAFP) 2014 Annual Meeting, 3–6 Aug 2014; Indianapolis, Indiana, USA). *Journal of Food Protection Suppl. A*, Vol. 77, p 161.

Jaros P, *et al.* (2014) Between- and within-island divergence of bovine and human Shiga toxin-producing *Escherichia coli* O157:H7 genotypes in New Zealand. In: *Proceedings of the Food Safety, Animal Welfare & Biosecurity Branch of the New Zealand Veterinary Association (NZVA)* (16–20 Jun 2014; Hamilton, New Zealand), pp 127-128.

Jaros P, *et al.* (2013) A prospective case-control and molecular epidemiological study of human cases of Shiga toxin-producing *Escherichia coli* in New Zealand. *BMC Infectious Diseases*, doi:10.1186/1471-2334-13-450.

Jaros P, *et al.* (2013) Source attribution for human cases of Shiga toxin-producing *Escherichia coli* in New Zealand. (IAFP 2013 Annual Meeting, 28–31 Jul 2013; Charlotte, North Carolina, USA). *Journal of Food Protection Suppl. A*, Vol. 76, p 58.

Jaros P, *et al.* (2013) Source attribution for human cases of Shiga toxin-producing *Escherichia coli* in New Zealand. In: *Proceedings of the Food Safety, Animal Welfare & Biosecurity Branch of NZVA* (3–4 Jul 2013; Palmerston North, New Zealand), p 11.

Jaros P, *et al.* (2012) An analytical source attribution study on human cases of Shiga toxin-producing *Escherichia coli* in New Zealand. In: *Book of Abstracts of the Annual meeting of the New Zealand Microbiological Society (NZMS)* (26–29 Nov 2012; Dunedin, New Zealand), A2.5 (p 50).

Jaros P, *et al.* (2012) Molecular epidemiology: a tool for source attribution investigation of *Escherichia coli* O157:H7 infections in New Zealand. In: *Proceedings of the 13th International Symposium on Veterinary Epidemiology and Economics (ISVEE)* (20–24 Aug 2012; Maastricht, The Netherlands), p 452.

Jaros P, *et al.* (2012) Population dynamics of *E. coli* O157 and O26 – the effect of transport and lairage on faecal shedding and carcass contamination of very young calves in New Zealand. In: *Proceedings of the 8th International Symposium on Shiga Toxin (Verocytotoxin) Producing Escherichia coli Infections, VTEC 2012* (6–9 May 2012; Amsterdam, The Netherlands), pp 70-71.

Jaros P, *et al.* (2012) Molecular epidemiology of human and bovine *Escherichia coli* O157:H7 isolates in New Zealand. In: *Proceedings of the 8th International Symposium on Shiga Toxin (Verocytotoxin) Producing Escherichia coli Infections, VTEC 2012* (6–9 May 2012; Amsterdam, The Netherlands), p 99.

Jaros P, *et al.* (2011) Shedding of *Escherichia coli* O157:H7 and O26 STEC by slaughter cattle in New Zealand. In: *Book of Abstracts of the Annual meeting of NZMS* (23–25 Nov 2011; Palmerston North, New Zealand), p 86.

Jaros P, *et al.* (2010) Prevalence of faecal shedding of *E. coli* O157:H7 and non-O157 STEC in New Zealand slaughter cattle. In: *Book of Abstracts of the Annual meeting of NZMS* (30 Nov–3 Dec; Auckland, New Zealand), p 129.

Contents

Abstract	iii
Acknowledgements	v
Declaration	vii
Nomenclature	ix
Glossary	xi
List of Publications	xiii
List of Figures	xxiii
List of Tables.....	xxv
Preface	xxix
Chapter 1 Introduction.....	1
1.1 General background.....	1
1.2 STEC in New Zealand	2
1.3 Thesis aims and structure.....	3
Chapter 2 Literature review	7
2.1 Introduction.....	7
2.2 <i>Escherichia coli</i> – the organism	7
2.2.1 Discovery	7
2.2.2 Classification of <i>E. coli</i>	8
2.2.3 History of STEC (VTEC)	9
2.3 Epidemiology of STEC in humans	9
2.3.1 STEC O157.....	9

2.3.2	STEC O26	11
2.3.3	Annual incidence rates and seasonality of STEC.....	12
2.3.4	Transmission pathways and risk factors for STEC infection	14
2.3.5	Clinical disease.....	16
2.3.6	Infectious dose.....	17
2.3.7	Pathophysiology	18
2.3.8	Pathogenesis and bacterial virulence factors.....	20
2.4	Epidemiology of STEC in animals and environment.....	22
2.4.1	Cattle as reservoir.....	23
2.4.2	Colonisation and shedding pattern in cattle	24
2.4.3	Prevalence in cattle.....	26
2.4.4	Other animals	29
2.4.5	Environment.....	30
2.5	Laboratory methods for <i>E. coli</i> isolation.....	31
2.5.1	Enrichment	31
2.5.2	Culture	32
2.5.3	Immunomagnetic separation	33
2.6	Molecular typing methods of STEC	33
2.6.1	PCR	34
2.6.2	PFGE	34
2.6.3	SBI.....	37
2.6.4	Other typing methods	37
2.7	Animal processing and control of STEC contamination.....	38
2.7.1	Pre-harvest interventions and risk factors	38
2.7.2	Post-harvest interventions	40
2.7.3	Risk assessments	41
2.8	Epidemiology of STEC infections in humans in New Zealand	42

2.8.1	Epidemiological facts.....	42
2.8.2	Under-reporting.....	44
2.9	Epidemiology of STEC in New Zealand cattle	44
2.10	Economic costs of STEC in New Zealand	45
2.10.1	Meat industry	45
2.10.2	Public health.....	46
2.11	Conclusions.....	46
Chapter 3	A repeated cross-sectional study investigating the prevalence of faecal shedding of Shiga toxin-producing <i>Escherichia coli</i> O157 and O26 in very young calves and adult cattle at slaughter in New Zealand	49
3.1	Abstract.....	49
3.2	Introduction.....	51
3.3	Materials and methods	52
3.3.1	Sample size calculations	52
3.3.2	Sample collection.....	53
3.3.3	Laboratory methods	54
3.3.4	Data management and statistical analysis.....	60
3.4	Results.....	62
3.4.1	Animal data.....	62
3.4.2	Prevalence of <i>E. coli</i> (STEC and non-STEC) in animals	66
3.4.3	Test performance of real-time PCR and culture isolation	68
3.4.4	Characterisation of confirmed isolates.....	69
3.4.5	Concentrations of <i>E. coli</i> and STEC in faecal samples	72
3.4.6	Prevalence of STEC in animals	75
3.4.7	Prevalence of <i>E. coli</i> and STEC between farm types	76
3.4.8	Spatial distribution of <i>E. coli</i> and STEC.....	78
3.4.9	Seasonality of <i>E. coli</i> and STEC.....	83

3.4.10 Risk factors for faecal shedding of <i>E. coli</i> (STEC and non-STEC) at slaughter	84
3.5 Discussion	89
3.5.1 Prevalence of STEC O157 and STEC O26 in animals and farms.....	90
3.5.2 Diagnostic methods	93
3.5.3 <i>E. coli</i> concentrations	96
3.5.4 Spatial and temporal findings.....	97
3.5.5 Risk factors for faecal shedding of <i>E. coli</i> (STEC and non-STEC).....	98
3.6 Conclusions.....	100
3.7 Acknowledgements	100
Chapter 4 Population dynamics of <i>Escherichia coli</i> O157 and O26 – the effect of transportation and lairage on faecal shedding and carcass contamination of very young calves in New Zealand.....	103
4.1 Abstract	103
4.2 Introduction	104
4.3 Materials and methods	106
4.3.1 Pre-selection, pre-testing and classification of farms.....	106
4.3.2 Sample size calculations.....	108
4.3.3 Animal selection and description of transportation and lairage	109
4.3.4 Sample collection	109
4.3.5 Financial restrictions	110
4.3.6 Data recording	111
4.3.7 Laboratory methods.....	111
4.3.8 Ethical approval.....	118
4.3.9 Data management and statistical analysis	118
4.4 Results	120
4.4.1 Data from pre-testing.....	120
4.4.2 Number of animals and samples collected	121

4.4.3	Real-time PCR and culture isolation.....	122
4.4.4	Characterisation of confirmed isolates.....	124
4.4.5	Risk factors	128
4.4.6	Genotype diversity of isolates.....	129
4.4.7	Counts and concentrations of <i>E. coli</i> in faecal and carcass samples	133
4.5	Discussion.....	136
4.5.1	Effect of transportation and lairage on faecal shedding.....	136
4.5.2	Effect of transportation and lairage on hide contamination.....	138
4.5.3	Carcass contamination at pre- and post-intervention.....	139
4.5.4	Counts and concentrations of <i>E. coli</i>	140
4.5.5	Dynamic changes of <i>E. coli</i> prevalence and indications of different epidemiology between <i>E. coli</i> serotypes.....	142
4.6	Conclusions.....	143
4.7	Acknowledgements.....	143
Chapter 5	A prospective case-control and molecular epidemiological study of human cases of Shiga toxin-producing <i>Escherichia coli</i> in New Zealand.....	145
5.1	Abstract.....	145
5.2	Introduction.....	146
5.3	Methods	147
5.3.1	Study design, definition of cases and controls.....	147
5.3.2	Questionnaire	148
5.3.3	Sample sizes of cases and controls	149
5.3.4	STEC isolates of study cases	149
5.3.5	Ethical approval	149
5.3.6	Data management and statistical analysis.....	150
5.4	Results.....	153
5.4.1	Study population, spatial and temporal epidemiology.....	153

5.4.2	Risk factors.....	156
5.4.3	Population attributable fractions	160
5.4.4	Molecular analysis of <i>E. coli</i> O157:H7 isolates	162
5.5	Discussion	166
5.5.1	New Zealand – an agricultural country	166
5.5.2	Spatial and temporal epidemiology.....	167
5.5.3	Risk factors.....	168
5.5.4	Molecular epidemiology of <i>E. coli</i> O157:H7	170
5.5.5	Sources of bias.....	171
5.6	Conclusions	172
5.7	Acknowledgements.....	172

Chapter 6 Geographic divergence of bovine and human Shiga toxin-producing *Escherichia coli* O157:H7 genotypes in New Zealand.....175

6.1	Abstract	175
6.2	Introduction	175
6.3	Materials and methods	176
6.3.1	Human isolates and data.....	176
6.3.2	Bovine faecal isolates and data	177
6.3.3	Bovine meat isolates and data	177
6.3.4	PCRs for detection of virulence genes	177
6.3.5	Molecular typing methods.....	178
6.3.6	Ethical approval.....	178
6.3.7	Data management and statistical analysis	179
6.4	Results	180
6.4.1	Genotype diversity	180
6.4.2	Between-island comparisons.....	182

6.4.3	Within-island comparisons	183
6.4.4	International comparison	187
6.5	Discussion.....	188
6.5.1	Between-island divergence	189
6.5.2	Regional divergence.....	189
6.5.3	International divergence.....	190
6.6	Conclusions.....	191
6.7	Acknowledgments	191
Chapter 7	General discussion	193
7.1	Prevalence of STEC in New Zealand cattle (Chapter 3)	193
7.1.1	Calves – a major source of STEC	194
7.1.2	Farm level prevalence	195
7.1.3	Seasonality	195
7.2	Carcass contaminations with <i>E. coli</i> at calf processing (Chapter 4).....	196
7.2.1	Contamination of hides and carcasses at pre-intervention.....	196
7.2.2	Contamination at post-intervention.....	197
7.2.3	<i>E. coli</i> genotypes	197
7.3	Source and exposure pathways of STEC infections in humans (Chapter 5)	198
7.3.1	Risk factors	198
7.3.2	Seasonality	199
7.3.3	Molecular findings	200
7.4	Transmission of STEC O157 between cattle and humans (Chapter 6)	200
7.4.1	Selection of isolates	201
7.4.2	Between-island divergence	202
7.4.3	Regional divergence.....	202
7.4.4	International divergence.....	203

7.5 Implications of research	203
7.6 Areas for further research.....	203
7.7 Concluding statement.....	204
Bibliography	207
Appendices.....	245

List of Figures

1.1: General outline of PhD research	4
2.1: Possible routes of STEC contamination of environment, animal products, and food and produce, and transmission pathways of STEC infection in humans	15
2.2: Pathophysiology of STEC infection in humans	19
2.3: STEC notifications in New Zealand by year.....	42
3.1: Map of New Zealand showing distribution of farms of origin of calves and adult cattle sampled in a prevalence study on faecal shedding of STEC	64
3.2: Age distribution of adult cattle in a prevalence study on faecal shedding of STEC.....	65
3.3: Agarose gel electrophoresis showing PCR amplicons of DNA from <i>E. coli</i> isolates.....	70
3.4: Map of New Zealand with bivariate kernel density plots showing estimates of relative risks of calves and adult cattle being tested real-time PCR-positive for all <i>E. coli</i> O157 and O26 (STEC and non-STEC).....	81
3.5: Map of New Zealand showing distribution of animals from which STEC isolates were recovered.....	82
3.6: Seasonal prevalence of <i>E. coli</i> and STEC in calves at slaughter, stratified by serogroups O157 and O26	83
3.7: Seasonal prevalence of <i>E. coli</i> and STEC in adult cattle at slaughter, stratified by serogroups O157 and O26.....	84
4.1: Study scheme with pre-testing of dairy farms in three locations in the Waikato region in the North Island of New Zealand to investigate the effect of transportation and lairage on faecal carriage and carcass contamination with <i>E. coli</i> O157 and O26 in very young calves.....	107
4.2: Agarose gel electrophoresis showing PCR amplicons of DNA from <i>E. coli</i> isolates...	125
4.3: Diversity of PFGE profiles of <i>E. coli</i> O157 isolates recovered at multiple sampling sites from very young calves at pre-slaughter and post-slaughter	131
4.4: Diversity of PFGE profiles of <i>E. coli</i> O26 isolates recovered at multiple sampling sites from very young calves at pre-slaughter and post-slaughter	132
5.1: Age and spatial distribution of STEC cases and controls across New Zealand.....	154
5.2: Temporal distribution of sporadic STEC cases from July 2011 to July 2012.	155

5.3: Relative risk estimates of sporadic STEC infection across New Zealand and cattle density from 2011.....	156
5.4: Comparison of PFGE profiles from 97 human <i>E. coli</i> O157:H7 isolates	163
5.5: Multi-dimensional scaling plots showing the genotypic clustering of <i>E. coli</i> O157:H7 human isolates and SBI types; age categories; and island of residence	165
6.1: Proportional distributions of predominant SBI types of 363 human STEC O157:H7 isolates from clinical cases in New Zealand occurring between 2008 and 2011	182
6.2: NeighborNet trees showing population differentiation of STEC O157:H7 isolates from human cases and bovine meat samples from different regions in the North Island and the South Island of New Zealand	184
6.3: Multi-dimensional scaling plots showing the genotypic clustering of human STEC O157:H7 isolates originating from the North Island and the South Island of New Zealand	186
6.4: Proportional distributions of SBI types of STEC O157:H7 isolates sourced from cattle and human in New Zealand, Australia, and the United States	187
6.5: NeighborNet tree showing the geographic divergence of bovine and human STEC O157:H7 isolates sourced from New Zealand, Australia, and the United States.....	188

List of Tables

2.1: Annual incidence rates of confirmed STEC infections listed by countries	13
2.2: A summary of main virulence factors of STEC including their genomic location, bacterial structure, and functions in the pathogenesis of STEC infections.....	20
3.1: Statistical sample size estimations for New Zealand calves and adult cattle considering variable prevalence estimates.....	53
3.2: Nucleotide sequences of forward and reverse primers used for the detection of specific target genes of <i>E. coli</i> in faecal samples collected from New Zealand slaughter cattle .	55
3.3: Number of faecal swab samples collected post-slaughter from calves and adult cattle at four large cattle slaughter plants in New Zealand from July 2009 to June 2011, stratified by island of New Zealand, slaughter plant, and type of missing data.....	63
3.4: Prevalences of <i>E. coli</i> O157 and O26 in recto-anal faecal swab samples collected from calves and adult cattle at slaughter.....	66
3.5: Prevalences of <i>E. coli</i> O157 and O26 in recto-anal faecal swab samples from calves and adult cattle as tested by real-time PCR; the recovery rates of isolates by culture isolation methods; and prevalence estimates of <i>E. coli</i> O157 and O26 adjusted for test sensitivity and specificity of real-time PCR and culture methods used	67
3.6: Prior and posterior probability estimates of sensitivity and specificity of real-time PCR and culture methods used to test recto-anal faecal swabs from calves and adult cattle for the prevalence of all <i>E. coli</i> O157 and O26	68
3.7: Prior and posterior probability estimates of sensitivity and specificity of real-time PCR and direct culture plating methods calculated on a subset of recto-anal faecal samples from calves and adult cattle tested for the prevalence of <i>E. coli</i> O157.....	69
3.8: Characteristics of <i>E. coli</i> O157 and O26 isolates retrieved from faecal samples collected from New Zealand slaughter cattle, stratified by sampled animal group and serogroups	71
3.9: Minimum, maximum, and quartiles for counts of fermenting and non-fermenting colonies on direct culture plates inoculated with recto-anal faecal samples collected from calves and adult cattle at slaughter.....	73

3.10: Minimum, maximum and quartiles for estimated concentrations of all <i>E. coli</i> O157 and O26 in recto-anal swab samples collected from calves and adult cattle at slaughter, stratified by detection method	74
3.11: Minimum, maximum and quartiles for estimated concentrations of all STEC in recto-anal swab samples collected from calves and adult cattle at slaughter, stratified by detection method.....	75
3.12: Prevalence estimates of STEC O157 and STEC O26, and overall STEC prevalence in recto-anal faecal swab samples from calves and adult cattle collected at slaughter	75
3.13: Prevalence of all <i>E. coli</i> O157 and O26 and all STEC O157 and STEC O26 among beef and dairy farms of which animals were faecal sampled at slaughter plants.....	77
3.14: Real-time PCR prevalence of all <i>E. coli</i> O157 and O26 and prevalence of STEC O157 and STEC O26 in faecal samples collected from slaughter cattle in the North Island and the South Island of New Zealand	79
3.15: Results of multivariate logistic regression analysis for a calf being tested real-time PCR-positive for <i>E. coli</i> O157.....	86
3.16: Results of multivariate logistic regression analysis for a calf being tested real-time PCR-positive for <i>E. coli</i> O26.....	87
3.17: Results of multivariate logistic regression analysis for an adult cattle being tested real-time PCR-positive for <i>E. coli</i> O157.....	88
3.18: Results of multivariate logistic regression analysis for an adult cattle being tested real-time PCR-positive for <i>E. coli</i> O26.....	89
4.1: Example estimates of power for cluster sampling on selected farms, considering design effect and intra-cluster correlation for a sample size of 10 animals per farm	108
4.2: Nucleotide sequences of forward and reverse primers used for the detection of specific target genes of <i>E. coli</i> to investigate the effect of transportation and lairage on the faecal carriage and carcass contamination with <i>E. coli</i> O157 and O26 in very young calves.....	112
4.3: Recto-anal faecal swab samples collected from calves on eight pre-selected dairy farms in three locations in the Waikato region and screened for the presence of <i>E. coli</i> O157 and O26 by real-time PCR.....	120
4.4: Total number of animals and samples collected at pre- and post-slaughter during three separate runs to investigate the effect of transportation and lairage on the faecal shedding and contamination of carcasses with <i>E. coli</i> O157 and O26 in very young calves	121

4.5:	Results of real-time PCR and culture confirmed isolation of <i>E. coli</i> O157 and O26 from pre- and post-slaughter samples collected from very young calves in a transport and lairage study	122
4.6:	Results of real-time PCR and culture confirmed isolation of <i>E. coli</i> O157 and O26 from pre- and post-slaughter samples collected from very young calves during three separate runs in a transport and lairage study, stratified by risk type of farm	123
4.7:	Characteristics of <i>E. coli</i> O157 and O26 isolates collected from multiple samples from very young calves at pre-slaughter and post-slaughter	126
4.8:	Results of multivariate logistic regression analysis for a calf being real-time PCR-positive for <i>E. coli</i> O157 in faeces on-plant after transportation and lairage	128
4.9:	Results of multivariate logistic regression analysis for a calf being real-time PCR-positive for <i>E. coli</i> O26 in faeces on-plant after transportation and lairage	129
4.10:	Simpson's index values showing the diversity of PFGE profiles of <i>E. coli</i> O157 and O26 isolates recovered from faeces from very young calves on-farm and after transportation to and lairage on-plant, and from carcasses at the slaughter plant.....	129
4.11:	Minimum, maximum, and quartiles for counts of fermenting and non-fermenting colonies in recto-anal faecal samples at pre-slaughter and carcass swab samples at post-slaughter from very young calves, using direct culture plating	134
4.12:	Minimum, maximum and quartiles for estimated concentrations of <i>E. coli</i> O157 and O26 in recto-anal faecal samples collected from very young calves on-farm and on-plant at pre-slaughter, and in carcass swab samples at post-slaughter, stratified by detection method.....	135
5.1:	Multivariate logistic regression model showing risk factors for sporadic cases of STEC infections in New Zealand in a prospective case-control study.....	157
5.2:	Multivariate logistic regression model showing risk factors for sporadic cases of STEC infections in New Zealand based on phone interviews.....	159
5.3:	Population attributable fractions of identified risk factors.....	161
5.4:	Number of SBI types in STEC O157:H7 isolates shown for statistically significant exposure variables considered in the multivariate logistic regression analysis of the case-control study.....	164
5.5:	PERMANOVA analysis of STEC O157:H7 isolates	166
6.1:	Virulence profiles and SBI types of STEC O157:H7 isolates collected from human cases and faecal samples of slaughter cattle in New Zealand between 2008 and 2011.....	181

6.2: Frequency distribution of predominant SBI genotypes of STEC O157:H7 isolates collected from human cases, bovine faeces and bovine meat samples, stratified by island of New Zealand 183

Preface

“Learn from yesterday, live for today, hope for tomorrow.
The important thing is not to stop questioning.”

Albert Einstein

