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

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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 LaTeX 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

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