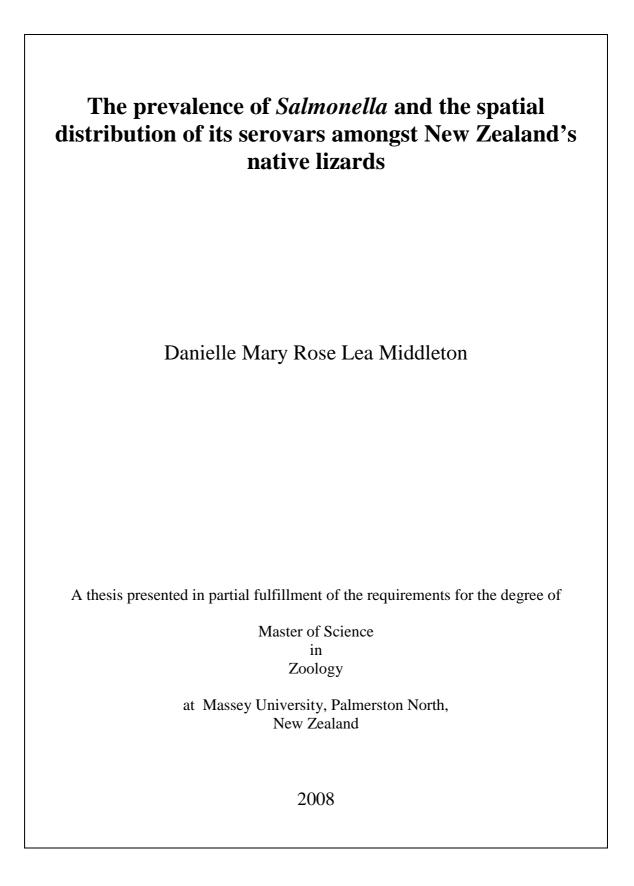
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<u>ii</u>_____

Abstract

This thesis considers the prevalence and spatial distribution of *Salmonella* serovars amongst wild endemic lizards on offshore islands around the coast of New Zealand. The mean test prevalence of faecal excretion of *Salmonella* was 4.7%. Skinks (*Scincidae*) were more likely (8.5%) to be carriers of *Salmonella* than geckos (1.6%). Each island was host to between one and three *Salmonella* serovars that were not found on any other islands in this study. Two exceptions were *Salmonella* Bousso and *Salmonella* Mana which were found on two islands within the same geographical area. Based on the findings of this study, different islands are likely to be hosts to different *Salmonella* serovars which could have implications for future translocations of native lizards.

I also assessed the prevalence and spatial distribution of faecal excretion of *Salmonella*, *Aeromonas* and *Hafnia alvei* within Mana Island. The prevalence of *Salmonella* on Mana Island was estimated at 5.8%. *Salmonella* was found predominantly in skinks (10.0%) and less often in geckos (4.1%). *H. alvei* was found at a prevalence of 1.9%. No *Aeromonas* species were cultured from any of the cloacal swabs, suggesting that the 95% confidence interval for the true prevalence is 0-3%. Each site sampled in this study was host to one or more unique serovar of *Salmonella* not found at any of the other sites. The results of this study indicate that *Salmonella* serovars may become established within populations of lizards and is not spread between them. This may be due to a lack of dispersal of lizards between sites, raising important considerations for the translocation of native lizards.

I investigated the prevalence of faecal excretion of *Salmonella*, *H. alvei* and *Aeromonas* by New Zealand native lizards from two captive populations. The mean prevalence of faecal excretion of *Salmonella* in the captive lizards sampled was 11.5%. There was a higher prevalence of *Salmonella* within captive population A (22.0%) than in population B (3.6%). No *Aeromonas* was cultured from any of the lizards. *H. alvei* was found at a prevalence of 5.2%. The prevalence of *Salmonella* and *H. alvei* was significantly higher in captive lizards than in wild populations. Captive lizards may, therefore, not be appropriate founders for new populations of wild lizards.

iv

Finally I assessed the different efficiencies of two media and two temperatures in isolating six *Salmonella* serovars from a reptilian source. All serovars grew equally well at 37°C and 27°C. For most serovars XLD agar was the more successful media than MacConkey agar but the success of different culture media depended on the serovar being cultured. Because lizards are frequently host to a wide range of *Salmonella* serovars, screening samples using multiple microbiological methods is likely to give the best chance of isolating all *Salmonella* serovars present.

Acknowledgements

Within this thesis I wanted to incorporate my passion for conservation, lizards and microbiology. This was to prove to be a daunting task. Not only because much of New Zealand's lizard fauna are maintained on offshore islands where access is restricted and difficult but also due to the multidisciplinary nature of the topic. So whilst it is accepted that a thesis has a single author this project would not have been possible without the help of a great many people who helped in a vast array of ways.

To everyone who has contributed to this thesis by: answering my questions; asking me questions; setting me on the right path and occasionally the wrong path; sitting beside me and understanding; making me laugh (and cry); allowing me into your homes and lives and imparting your wisdom, thank-you. You have all contributed towards making this thesis what it is.

This thesis would not have been possible without the excellent assistance I received from a great many volunteers in the field. Together we have suffered in the heat and shivered till 3am in howling winds and driving rain when all the lizards seemed to be MIA. You all know who you are and thanks for making what could have been some very cold depressing nights more bearable.

A special thank you must go to my family as they have been the longest suffering of anyone involved in this project – which actually began long before I started university. Thank you for all your unconditional love and support; for instilling in me an interest in nature and conservation; for listening to all the ecology related conversations with interest and encouragement. I love you all. My mum requires special mention for her hands on help in this project. Not only was she one of my many field assistants but she has also spent a vast number of hours editing, entering data and offering stylistic advice, however, more important than any of that she has been there with soft words and a cup of tea when I needed it most. Thank you very much to my uncle Darryl for the long hours he has put in to finding missing commas and full stops within this thesis. I know that he gave up many weekends to ensure that this thesis was grammatically correct. I gratefully acknowledge my supervisors Ed Minot and Brett Gartrell for their friendship; many hours of editing and advice and the invaluable weekly meetings. I also thank Hamish Mack for his help with the microbiological aspects of this project, for helping to make the long hours in the lab more bearable with his entertaining stories and the odd joke, but most of all for not complaining when I filled up all the incubators with my samples.

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This thesis is dedicated to my late grandmother who did not get to see this thesis in its completion, but whose love and support was a driving force behind it. Her spirit lives on through my desire for a sustainable future.

Preface

This thesis has been written as a series of self-contained chapters, which will form the basis of a number of papers to be submitted to peer-reviewed scientific journals. Each chapter is therefore written as a fully referenced self-contained paper, and investigates specific components of the spatial distribution and prevalence of *Salmonella* amongst New Zealand endemic lizards. Because of this, there is some overlap between chapters, but essentially they each provide new information towards different components of the spatial distribution and prevalence of *Salmonella*.

I conducted the fieldwork, statistical analyses and have written each chapter. My supervisors have contributed throughout the thesis with help during the fieldwork, analysis, and write-up stages of the study.

Contents

Abstract	iii
Acknowledgements	v
Preface	vii
Contents	viii
List of Figures	xiii
List of Tables	xiv

Chapter One: General Introduction

1.1 Introduction	3
1.2 Importance of lizard conservation in New Zealand	5
1.3 Conservation status and ecology of New Zealand native lizards	6
1.4 Human impacts	10
1.5 Translocation as a conservation tool	11
1.6 Salmonella	13
1.6.1 Salmonella characteristics	14
1.6.2 Salmonella prevalence and disease in reptiles	17
1.6.3 Disease outbreaks of Salmonella in other wildlife	19
1.6.4 Reptile-associated salmonellosis in humans	20
1.6.5 Salmonella culture techniques	21
1.6.5.1 Isolation media	21
1.6.5.2 Effects of isolation temperature	22
1.7 Hafnia alvei	
1.7.1 Characteristics of Hafnia alvei	23
1.7.2 Hafnia alvei disease amongst reptiles	23

1.7.3 Hafnia alvei disease amongst other wildlife	24
1.7.4 Human cases of <i>Hafnia alvei</i>	25
1.8 Aeromonas	
1.8.1 Characteristics of Aeromonas	25
1.8.2 Aeromonas disease in reptiles	25
1.8.3 Aeromonas in other wildlife	26
1.8.4 Aeromonas in humans	27
1.8.5 Microbiological isolation of Aeromonas	27
1.9 Study sites	28
1.9.1 Korapuki Island	28
1.9.2 Mana Island	29
1.9.3 Matiu/Somes Island	29
1.9.4 Maud Island (Te Hoiere)	30
1.9.5 Motuopao Island	31
1.9.6 Cuvier Island (Repanga)	31
1.9.7 Little Barrier Island (Hauturu)	32
1.9.8 Stephens Island (Takapourewa)	32
1.10 Thesis aims and organisation	36
References	

Abstract	49
2.1 Introduction	50
2.2 Materials and Methods	
2.2.1 Study sites	53
2.2.2 Field methods	54
2.2.3 Laboratory isolation of Salmonella	56
2.2.4 Statistical analysis	57
2.3 Results	
2.4 Discussion	
References	

Chapter Two: Salmonella enterica in lizards of New Zealand's offshore islands

Chapter Three: A survey of potential pathogens in New Zealand native lizards

from Mana Island, New Zealand

Abstract	77
3.1 Introduction	
3.1.1 Mana (Te Mana o Kupe ki Aotearoa) Island	79
3.1.2 Salmonella	81
3.1.3 Hafnia alvei	82
3.1.4 Aeromonas	82
3.2 Materials and Methods	
3.2.1 Field methods	83
3.2.2 Laboratory methods	86
3.2.3 Statistical analysis	86
3.3 Results	

3.3.1 Salmonella	87
3.3.2 Hafnia alvei	89
3.3.3 Aeromonas	89
3.4 Discussion	
References	94

xi

Chapter Four: Disease prevalence amongst endemic lizards at captive breeding facilities 99 Abstract 4.1 Introduction 100 4.2 Materials and Methods 102 4.2.1 Statistical analysis 105 4.3 Results 105 4.3.1 Salmonella 105 4.3.2 Aeromonas 108 4.3.3 Hafnia alvei 108 4.4 Discussion 109 References 116

Chapter Five: Microbiological isolation of Salmonella from New Zealand

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Abstract	121
5.1 Introduction	122
5.2 Methods	
5.2.1 Survey	124

	5.2.2 Experiment	124
	5.2.3 Statistical analysis	125
5.3 Re	esults	125
	5.3.1 Survey	125
	5.3.2 Experiment	127
5.4 Di	scussion	129
Refere	References	
Chap	ter Six: Summary and Recommendations	137
Refere	ences	144
Apper	ndices	
Apper	ndix 1	149
Apper	ndix 2	150

151

152

- Appendix 3
- Appendix 4

List of Figures

1.1	Maud Island	4
1.2	Robust skink (C. alani) registered as Vu by the IUCN red list	6
1.3	North Island and upper South Island showing location of islands surveyed	in this
study		35
2.1	Location of study sites throughout the North Island and upper South Island	d of
New Z	Jealand	54
2.2	Obtaining an SVL measurement	55
2.3	O. smithi and O. suteri caught in a pitfall trap using dead fish as bait	67
3.1	View across the valley on Mana Island	79
3.2	Cloacal sampling a common gecko (H. maculatus)	84
3.3	Aerial map of Mana Island showing location of sites surveyed (adapted fro	om
Google	e Earth)	85
4.1	Weighing a common gecko (Hoplodactylus maculatus)	103
4.2	Minitip swabs used for obtaining cloacal samples	103
4.3	Naultinus elegans one of the only species found positive for Salmonella in	this
study		107
5.1	Boxplot of CFUs for reptile-associated Salmonella serovars grown on XLI	D and
MacCo	onkey agar	128
5.2	Mean CFU's grown each day for six reptile-associated Salmonella serovar	rs 129

List of Tables

1.1	Habitat and distribution of Gekkonidae species found wild in New Zealand	18
1.2	Habitat and distribution of <i>Scincidae</i> species found wild in New Zealand.	9
1.3	Six subspecies of Salmonella enterica can be designated by names or l	Roman
numera	als	15
1.4	Islands on which lizards were sampled for Salmonella in this study	28
1.5	The distribution of lizards on New Zealand's offshore islands and the original	in and
date th	e founder population was translocated	33
1.6	Presence of lizards on New Zealand offshore islands included in this stud	dy that
do not	have a history of lizard translocations	34
2.1	Islands on which lizards were sampled for Salmonella in this study and dat	tes of
survey		53
2.2	The history of lizard translocations to islands investigated in this study	56
2.3	Prevalence of Salmonella serovars found on New Zealand offshore islands	and
the true	e prevalence range at the 95% confidence interval	61
2.4	Prevalence of Salmonella serovars found in New Zealand endemic lizard s	pecies
and the	e true prevalence range at the 95% confidence interval	63
2.5	Numbers of lizard translocations to study sites and the corresponding num	ber of
Salmor	nella serovars found on the island	64
3.1	Source of lizard translocations to Mana Island	81
3.2	Distribution of Salmonella serovars amongst native lizards on Mana Island	l, New
Zealan	d	88
4.1:	Lizard species sampled in population A and the percentage prevalence of <i>I</i>	H.
<i>alvei</i> a	nd Salmonella within species	106
4.2	: Lizard species sampled in population B and the percentage prevalence of	<i>H</i> .
<i>alvei</i> a	nd Salmonella within species	106

5.1	Number of samples found to be positive when tested using each of	the four
microb	biological methods	126
5.2	Mean CFUs for six reptile-associated Salmonella serovars	127
5.3	Mean CFUs growth at 27°C and 37°C	128