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Ecology, epidemiology and evolution of enteric
microbes in fragmented populations of the endangered
takahe (*Porphyrio hochstetteri*)

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Abstract

Pathogenic diseases are increasingly recognised as a challenge to the conservation of wildlife. Complex host-pathogen relationships and transmission dynamics in wild populations can limit our understanding of how pathogens contribute to the decline and endangerment of wildlife. Endangered wildlife populations maintained in reserves present a unique opportunity to investigate wildlife host-microbe relationships in a controlled semi-natural environment where diversity, abundance and the movement of species are restricted. The aim of this study was to investigate the prevalence and molecular differentiation of enteric bacteria carried by endangered takahe (*Porphyrio hochstetteri*). Through the use of network analysis and molecular epidemiology, the study explored the effects of geographic isolation and translocation on the prevalence, transmission and evolution of *Campylobacter* and *Salmonella* spp. within fragmented populations of takahe.

Translocation and conservation management has created a dynamic network of takahe populations which vary in their likelihood to maintain and transmit pathogens. My study suggests that range expansion following a significant bottleneck and intensive conservation management of takahe has had unforeseen consequences on microbial diversity. The management of takahe in different environmental settings has influenced the carriage of *Campylobacter jejuni* and *Campylobacter coli*. A newly discovered rail-associated *Campylobacter* sp. *nova 1* was prevalent in all populations. However, more discriminatory whole genome analysis of isolates detected a significant biogeographic variation in *C. sp. nova 1* genotypes. Possible explanations for the observed pattern include the spatial expansion and isolation of hosts resulting in reduced gene flow of *Campylobacter* spp. and allopatric speciation, and the presence of heterogeneous environmental attributes or cross-species transmission of *Campylobacter* spp. from sympatric reservoir hosts. An assessment of vertebrate reservoirs in an island ecosystem indicated cross-species transmission of *Campylobacter* spp. was not likely to be a factor contributing to the maintenance and phylogeographical distribution of *Campylobacter* spp. in takahe.

This study was the first of its kind to explore microbial dynamics in a large proportion of a well-described but fragmented population of a wild bird. Results suggest historic and current management practices may be having unforeseen influences on enteric microbes, the consequences of which are unknown but could be detrimental to the health of translocated populations of takahe.

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Thesis structure and format

This thesis is presented as a series of seven chapters. Encompassed by a general introduction and discussion, five research chapters have been prepared and are presented as discrete papers for publication in peer reviewed journals.

Chapter one

General introduction introduces the concepts behind the research contained in this thesis by discussing and reviewing current literature on the principles of disease ecology and aspects of the epidemiology of infectious organisms in wildlife. The objectives of the study are summarised at the end of this chapter.

Chapter two

Network analysis of translocated takahe populations to identify disease surveillance targets has been published in the journal *Conservation Biology* (Grange et al. 2014).

Chapter three

Using a common commensal bacterium in endangered takahe (*Porphyrio hochstetteri*), as a model agent to explore pathogen dynamics in isolated wildlife populations is *in press* in the journal *Conservation Biology*.

Chapter four

Wildlife translocation and the evolution and population structure of a host associated commensal *Campylobacter* spp. is *under review* in the journal *Proceedings of the National Academy of Sciences (PNAS)* following publication of chapter 3.

Chapter five

Investigation of vertebrate reservoirs of *Campylobacter* spp. in an island ecosystem will be submitted to the *Journal of Animal Ecology* pending publication of chapters 3 and 4.

Chapter six

Location specific prevalence of *Salmonella* spp. in endangered takahe (*Porphyrio hochstetteri*) will be submitted to the Journal of Wildlife Disease.

Chapter seven

General discussion summarises the significant findings of this study. The relevance and implications of results are discussed and future research directions are suggested.

Chapter eight

Literature cited has been collated at the end of the thesis to reduce repetition. Literature is referred to in the format consistent with the format used for the journal Conservation Biology.

Chapter nine

Appendix contains all supplementary information organised by chapter

Table of Contents

1. General introduction	3
1.1. Wildlife disease ecology	3
1.1.1. Disease ecology concepts.....	3
1.1.2. Host pathogen relationships: from individuals to ecosystems	4
1.1.3. The host population.....	6
1.1.4. Multi-host pathogens and reservoir dynamics	7
1.2. Conservation of wildlife in the face of disease threats.....	9
1.2.1. Disease threats posed to and from wildlife	9
1.2.2. Anthropogenic management of threatened wildlife populations: translocations and sanctuaries as conservation tools	12
1.3. Epidemiological tools for species conservation	15
1.3.1. Risk assessments and disease surveillance	15
1.3.2. Pathogen ecology and epidemiology	18
1.4. Research focus.....	19
1.4.1. New Zealand conservation management	19
1.4.2. Takahe (<i>Porphyrio hochstetteri</i>).....	21
1.5. Microbes of interest to this study	24
1.5.1. <i>Campylobacter</i> species	24
1.5.2. <i>Salmonella</i> species	25
1.6. Objectives of the study.....	26
2. Network analysis of translocated takahe populations to identify disease surveillance targets.....	29
2.1. Abstract	29
2.2. Introduction	30
2.3. Methods.....	32
2.3.1. Data set.....	32
2.3.2. Network description and topology.....	33

2.3.3.	Network dynamics	34
2.4.	Results	35
2.4.1.	Network description and topology	35
2.4.2.	Network dynamics and node-level analysis	35
2.5.	Discussion	40
2.5.1.	Application of network analysis to takahe movements.....	40
2.5.2.	Identification of hubs, sinks, and sources	41
2.5.3.	Limitations	43
2.5.4.	Conservation implications and future directions.....	44
2.6.	Acknowledgments.....	46
2.7.	Supporting Information	46
3.	Using a common commensal bacterium in endangered takahe (<i>Porphyrio hochstetteri</i>), as a model to explore pathogen dynamics in isolated wildlife populations.....	51
3.1.	Abstract	51
3.2.	Introduction	52
3.3.	Materials and methods	53
3.3.1.	Study population	53
3.3.2.	Sample collection.....	53
3.3.3.	Microbiological culture and DNA extraction	54
3.3.4.	Molecular confirmation and speciation.....	54
3.3.5.	Prevalence of <i>Campylobacter</i> spp. in takahe	55
3.3.6.	Exploratory analysis of explanatory covariates	56
3.3.7.	Multiple correspondence analysis.....	58
3.3.8.	Multivariate logistic regression modelling.....	58
3.4.	Results	59
3.4.1.	Apparent prevalence of <i>Campylobacter</i> spp. in takahe.....	59
3.4.2.	Estimates of true prevalence using imperfect tests	60
3.4.3.	Analysis of explanatory covariates associated with the carriage of <i>Campylobacter</i> spp.	

3.5.	Discussion	64
3.6.	Acknowledgements	67
3.7.	Supporting information	68
4.	Wildlife translocation and the evolution and population structure of a host-associated commensal <i>Campylobacter</i> spp.	71
4.1.	Abstract	71
4.2.	Introduction	72
4.3.	Methods.....	74
4.3.1.	Sample collection and culture	74
4.3.2.	Selection of <i>C. sp. nova 1</i> for genomic sequencing	74
4.3.3.	Genomic DNA preparation and processing	74
4.3.4.	Genome assembly, curation and annotation.....	75
4.3.5.	Ribosomal multi locus sequence typing (rMLST) of <i>C. sp. nova 1</i>	75
4.3.6.	Core genome and rMLST tree construction.....	76
4.3.7.	Multivariate analysis of the relationship between location factors and genetic distance 77	
4.4.	Results	77
4.4.1.	<i>C. sp. nova 1</i> comparison to published <i>Campylobacter</i> spp.	77
4.4.2.	Genomic differentiation of <i>C. sp. nova 1</i> isolates.....	81
4.4.3.	Multivariate analysis of <i>C. sp. nova 1</i> rMLST allelic profiles.....	81
4.5.	Discussion	84
4.6.	Acknowledgements	88
4.7.	Supporting information	89
5.	Investigation of vertebrate reservoirs of <i>Campylobacter</i> spp. in an island ecosystem.....	93
5.1.	Abstract	93
5.2.	Introduction	94
5.3.	Methods.....	95
5.3.1.	Study site.....	95

5.3.2.	Study populations.....	96
5.3.3.	Sample collection.....	97
5.3.4.	Microbiological culture, molecular confirmation and speciation	97
5.3.5.	rMLST analysis.....	98
5.3.6.	<i>In silico</i> PCR of the C4-dicarboxylate trans-membrane transport gene.....	98
5.4.	Results	98
5.4.1.	Prevalence of <i>Campylobacter</i> spp. in vertebrate communities	98
5.4.2.	Comparative genomics of <i>Campylobacter</i> spp.	99
5.1.	Discussion	103
5.2.	Acknowledgements	107
5.3.	Animal ethics and permits.....	107
5.4.	Supplementary information.....	107
6.	Location specific prevalence of <i>Salmonella</i> spp. in endangered takahe (<i>Porphyrio hochstetteri</i>)	111
6.1.	Abstract	111
6.2.	Introduction	112
6.3.	Methods.....	113
6.4.	Results	114
6.5.	Discussion	115
6.6.	Acknowledgements	117
7.	General Discussion	121
7.1.	Microbial dynamics in translocated takahe (<i>Porphyrio hochstetteri</i>).....	121
7.2.	Disease risks associated with translocations	123
7.3.	Advancing tools for epidemiological investigations of wildlife	126
7.4.	Implications for conservation management	127
7.5.	Future research directions	129
7.6.	Concluding remarks	131
8.	Literature Cited.....	135

9. Appendix	161
9.2. Chapter 2 supplementary information.....	161
9.3. Chapter 3 supplementary information.....	167
9.4. Chapter 4 supplementary information.....	179
9.5. Chapter 5 supplementary information.....	184

List of tables and figures

Tables

Table 2-1	Takahe network measures	36
Table 2-2	Network key locations.....	38
Table 3-1	Takahe sampling effort and variables.....	57
Table 3-2	Multivariate models for <i>Campylobacter</i> spp. carriage in takahe	63
Table 4-1	<i>Campylobacter</i> sp. <i>nova</i> 1 PERMANOVA models.....	82
Table 5-1	List of hosts and <i>Campylobacter</i> spp. prevalence on Maud island.....	100
Table 5-2	rMLST allelic profiles of <i>Campylobacter</i> spp. on Maud Island	102
Table 6-1	Apparent prevalence of <i>Salmonella</i> spp. in takahe populations.....	114
Table 6-2	True prevalence of <i>Salmonella</i> spp. in takahe by sample type.....	115

Figures

Figure 1-1	Theoretical hypotheses for the modes of speciation.....	5
Figure 1-2	Pathogen transmission dynamics between native and introduced populations.....	15
Figure 1-3	Takahe.....	21
Figure 1-4	Map of takahe distribution in New Zealand	23
Figure 2-1	Takahe translocation networks	37
Figure 2-2	Relationship between in degree and out degree network measures	39
Figure 3-1	Apparent and true prevalence of <i>Campylobacter</i> spp. in takahe.....	60
Figure 3-2	Venn diagram of <i>Campylobacter</i> spp. carriage in takahe.....	61
Figure 4-1	Map of sampling locations.....	78
Figure 4-2	Takahe <i>Campylobacter</i> spp. rMLST tree.....	79
Figure 4-3	Takahe <i>Campylobacter</i> sp. <i>nova</i> 1 core and rMLST trees.....	80
Figure 4-4	Takahe <i>Campylobacter</i> sp. <i>nova</i> 1 F_{ST} tree.....	83
Figure 4-5	Schematic of hypotheses for <i>Campylobacter</i> sp. <i>nova</i> 1 genotypes in takahe.....	86
Figure 5-1	Maud island <i>Campylobacter</i> spp. rMLST tree and distance matrix.....	101