Population Genetics, Biogeography and Ecological Interactions of the New Zealand Bellbird (*Anthornis melanura*) and their Avian Malaria Parasites

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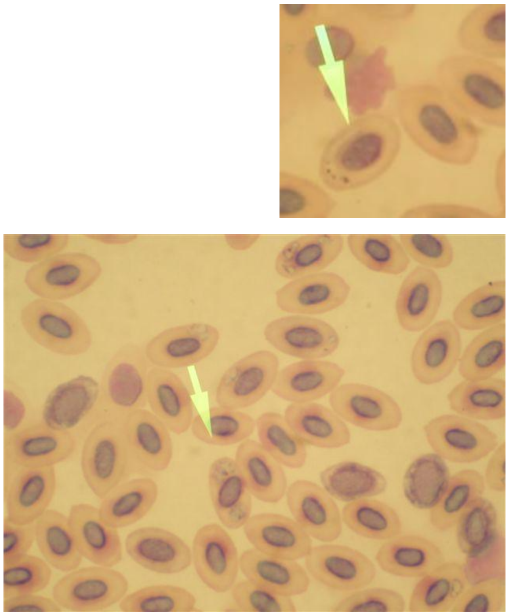
Adult female New Zealand bellbird
(Photo: Jordi Segers)



Giemsa-stained blood smears from a bellbird at Tawharanui Regional Park infected with intracellular *Plasmodium* sp. (arrows in upper and lower photos)
(Photos: Gribbles Veterinary)

Singing adult male New Zealand bellbird
(Photo: Rob Cross)

Three adult male bellbirds at a sugar water feeder on Tiritiri Matangi (Photo: Jordi Segers)

Abstract

Habitat loss and redistribution of species has lead to population declines and loss of genetic diversity with serious implications to species survival on ecological and evolutionary scales. While there is no doubt that rapidly dwindling endangered populations require our immediate attention, studies on common species are equally important. The purpose of this thesis is to investigate the genetic connectivity, biogeographical relationships and host-parasite interactions of a common and widely distributed bird species, mainly because we want common species to remain common. Furthermore, I illustrate how studies such as this provide invaluable comparisons for sympatric endangered species.

In this thesis, patterns of genetic variation of the New Zealand bellbird (*Anthornis melanura*) are delineated to assess their re-colonization potential among fragmented landscapes. Using a phylogeographic perspective I show how dispersal ability and secondary contact among isolated population fragments shape the evolutionary trajectory of a species. I also determine the biogeographical relationships between the bellbird host and its malaria parasites with key emphasis on host-parasite specificity. Finally, immunological trade-offs are investigated in disease epidemiology by examining host factors that influence malaria prevalence.

I show that an immense capacity for dispersal has prevented divergence and shaped the high levels of genetic diversity and connectivity in bellbirds today. However, substantial genetic differentiation among subpopulations reflects recent habitat fragmentation. Based on these findings I conclude that continued habitat loss can lead to further reductions in gene flow, despite dispersal. Though restricted to northern populations, I provide evidence that the most abundant avian malaria lineage infecting bellbirds is likely an endemic *Plasmodium* (*Novyella*). This parasite exhibits bimodal seasonality and male-biased infections, but these relationships vary among subpopulations. Malaria prevalence appears to be governed by food availability and territory stability, thus habitat disturbance has repercussions to immune phenotype.

With this thesis I advocate a re-thinking of conservation strategies toward spatial planning that enables ‘natural’ secondary contact among habitat fragments. Translocation is not necessary for all species. In addition to being the first study on seasonal and host factors affecting malaria patterns in the Southern Hemisphere, this thesis makes major contributions to science by elucidating some ecological relationships that underpin the evolution of immunity.

Acknowledgments

First and foremost, I would like to dedicate this thesis to my mother, Diane Sylvester, in memoriam. Her intelligence and free-spirit are the true inspiration behind the undertaking of this thesis.

I could not have done this thesis without the never failing support of my main supervisor Dr. Dianne Brunton (Director of the Ecology and Conservation Group, Institute of Natural Sciences, Albany Campus, Massey University, New Zealand). Dianne is an extraordinary person able to field various students, and somehow keep us happy while demanding the best from us. These traits are a rare combination in an individual, let alone a PhD supervisor (as a quick perusal of PhD Comics.com will illustrate) and I feel very lucky and privileged to have worked under her.

The first 'field ecology' phase of my PhD thesis was spent at Massey University where in addition to conversations with Dr. Dianne Brunton. I am grateful to Dr. Rosemary Barraclough, Dr. Weihong Ji and Dr. Kevin Parker for helpful and incredibly knowledgeable discussions in the earlier phase of my thesis. For the second 'genetics laboratory' phase, Dr. Pete Ritchie welcomed me into his genetics lab at the School of Biological Sciences (SBS), Victoria University of Wellington, Kelburn Campus, Wellington, New Zealand. Dr. Ritchie was well equipped with the generosity, grace and patience required to accept a completely green-to-population-genetics PhD student into his lab. I am forever indebted that he took me in. Pete was an integral part of this thesis, I was very inspired by the work done and expertise within Pete's lab group and learned so much from our weekly Population Genetics Lab Group Meetings.

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Ludbrook and Eva Krause who helped capture bellbirds at Tawharanui. At the Poor Knights Islands Michael Anderson and Yuri Shanas were crucial to fieldwork and in making that trip an incredible adventure. Additionally, I want to give special thanks to Ngati Wai Iwi Trust Board and particularly to Clive Stone for meeting with me and giving us the permission to visit and conduct my research within their *wāhi tapu*. Dr. Graeme Elliott of the New Zealand Department of Conservation (DoC) generously collected blood samples from the Auckland Islands. All blood collection from birds was performed under DoC permit, Auckland Regional Council (ARC) and Massey University Animal Ethics Committee (MUAEC).

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Thesis Structure and Format

I have written this thesis as a collection of five scientific papers for publication in peer reviewed journals. An introductory chapter (Chapter One) precedes the five data chapters and is written for a general science audience that provides some background on the theory and analytical components of my thesis. This format has meant that some of the Introduction is repeated in the various Introductions throughout the thesis, but this is necessary for the reader to have a complete overview of the thesis. Chapter Seven is a synthesis that summarizes my findings and outlines my contributions to science and future research.

Chapters Two to Six are data chapters that each stand as independent scientific papers. Within the text of these five data chapters, I used the plural first person because my supervisors are on these papers as co-authors. However, the study design, fieldwork, laboratory work and all statistical analyses and writing were performed by me with only supervisorial input from co-authors. During the process of my first population genetics chapter, Chapter Two, I presented my work at several stages to Dr. Pete Ritchie's Population Genetics Discussion Group at Victoria University of Wellington (VUW) in order to receive feedback. After this first chapter, I had amassed a foundation of programs, analyses and genetic theory required to perform a thesis in population genetics. I submitted Chapter Two for publication in *Conservation Genetics* and it is currently in review. I invited Dr. Sebastien Rioux-Paquette, a post-doctorate researcher in Dr. Pete Ritchie's lab at VUW the time to be a co-author on the journal article for Chapter Three, which will be submitted to *Molecular Ecology*. Dr. Rioux-Paquette specifically suggested the 'mixed-stock' analysis and I was introduced to population computer simulations through exposure to his concurrent work. However, I independently researched, learned and decided upon the programs and analyses used in this thesis. Once this manuscript (Chapter Three) was completely written to a high standard, I circulated it to my supervisors and Sebastien, my soon to be co-authors. The remaining chapters are independent works, which have received commentary from my supervisors and other PhD students. Chapter Four will be submitted to *Journal of Biogeography* within the coming months. Chapter Five has been accepted by *Parasitology* (please refer to Appendix F for a copy of that submission) and Chapter Six has been submitted to *Journal of Animal Ecology* recently. There are two papers sketched out in the Appendix D and E on bellbird morphological congruence with genotype and bellbird breeding biology, respectively. These papers will be written and submitted to peer-reviewed journals after thesis submission.

I have retained the Abstract, Keywords and Acknowledgments sections within each of the five data chapters so that the 'collection of scientific papers' format is consistent throughout. Additionally, I feel that each individual Abstract facilitates the reader of this thesis in that they provide specific summaries of the material about to be read. Similarly, the Acknowledgments sections, though repetitive at times, allow for each data chapter to exist as a separate paper without the reader having to search back to the beginning for contributions.

The purpose of the Appendices section in this thesis is twofold. First, the Appendices provide specific information that supplement analyses within each data chapter. In these cases, the appropriate Table or Figure in the Appendix is specified, e.g., Table D.3 means the third table in Appendix D. In this manner, tables and figures that might disrupt the flow of the text but provide supportive information are accessible. Second, I have used the Appendices to disseminate information or data that is not directly referred to in my thesis. In these cases, the items within each Appendix is thought to be informative for future researchers, e.g., DNA sequences, observations in the field and breeding biology and habitat information. All Literature Cited sections in this thesis are consistent with the format used for *Conservation Genetics* and journal title abbreviations follow the International Standard Serial Number (ISSN) list of title word abbreviations, see /www.csa.com/ids70/serials_source_list.php?db=biolclust-set-c.

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