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# Birds in a tree: A journey through avian phylogeny, with particular emphasis on the birds of New Zealand

Gillian Claire Gibb 2010

A thesis presented in partial fulfilment of the requirements for the degree of Doctor of Philosophy in Genetics

> Allan Wilson Centre for Molecular Ecology and Evolution Institute of Molecular BioSciences Te Kura Putaiao Koiora-a-Ngota Massey University Palmerston North New Zealand

#### ABSTRACT

Two main themes to the avian research presented in this thesis are,

1. Deep resolution of birds generally, and

2. Investigation of specific aspects of the New Zealand avifauna.

More specifically, this thesis covers phylogeny, and predictions about palaeognaths, pigeons, pelecaniforms and passerines.

Significant progress is made in resolving the basal branches of Neoaves. This thesis examines whether the six-way basal Neoavian split of Cracraft (2001) is, in principle, resolvable. New mitochondrial genomes are added to improve taxon sampling, break up long branches, and allow testing of the prior assumptions of six Neoavian groups. This research shows the six-way split is resolvable, although more work is required for specific details. From a life-history perspective, it is interesting that the two bird-of-prey groups (falcons and buzzards) are very divergent, and may not be sister groups. Molecular dating supports major diversification of at least 12 Neoavian lineages in the Late Cretaceous. Additionally, novel avian mitochondrial gene orders are investigated and a hypothesis put forward suggesting gene conversion and stable intermediate forms allows an apparently rare event (gene rearrangement) to occur multiple times within Neoaves.

One of Cracraft's six groups, informally called the 'Conglomerati', is particularly difficult to resolve. The pigeons (Columbiformes) lie within the 'Conglomerati', and this chapter examines two aspects along the continuum of pigeon evolution. Firstly the large South Pacific fruit pigeon radiation is examined with mid-length mitochondrial sequences. This clade contains a third of all pigeon species, and has been very successful in island colonisation throughout South East Asia and the Pacific. Secondly, candidates for the closest relative of pigeons are tested using analysis of whole mitochondrial genomes. Highest support was found for the grouping of sandgrouse and pigeon, although they are clearly very divergent.

Also within the 'Conglomerati' is the traditional order Pelecaniformes, and their close allies the Ciconiiformes. These orders (the P&C) are part of an adaptive radiation of seabird water-carnivores, including loons, penguins, petrels and albatrosses. This group is separate from the large shorebird water-carnivore group; although both appear to have begun radiating abut 70 million years ago. The

tropicbird represents a separate, convergent life history and is not part of the Pelecaniformes, nor within the larger seabird water-carnivore group.

Resolution of the basal phylogeny of oscine passerines is important for interpreting the radiation of this group out of the Australasian region. Many endemic New Zealand oscine passerines belong to 'basal corvid' lineages, but have not previously been investigated with mitochondrial DNA. This chapter shows that many 'basal corvid' lineages are actually 'basal passerine' lineages, and there is a discrepancy between nuclear Rag-1 phylogenies (the most commonly used gene in passerine phylogenetics) and other phylogenies, including mitochondrial, that requires further investigation.

Taken as a whole, this thesis adds significantly to our understanding of the evolution of birds, and provides a foundation for future research, not only of phylogenetic relationships, but also of avian life history, long-term niche stability and macroevolution.

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### TABLE OF CONTENTS

Abstract	i
Acknowledgements	iii
LIST OF FIGURES	х
LIST OF TABLES	xi

## 1. Chapter One

Introduction	
1.1. STRUCTURE OF THE THESIS	1
1.2. BACKGROUND	3
1.2.1. Mitochondrial DNA – why is it useful for phylogeny?	3
1.2.2. Alignments	4
1.2.3. Model choice, rates across sites	4
1.2.4. Gene trees vs. species trees	5
1.2.5. Consilience of induction, generating hypotheses and testing	
predictions	5
<b>1.3.</b> What do we do when we know the tree of life?	6
1.3.1. Are the processes of microevolution sufficient to explain	
macroevolution?	6
1.3.2. Evolutionary-Stable Niche-Discontinuity (ESND)	7
1.4. CONTRIBUTIONS OF OTHERS TO THIS THESE PUBLICATIONS	8
1.5. References	9

### 2. Chapter Two

Vicars, tramps and the assembly of New Zealand avifauna – A review of molecular phylogenetic evidence.

2.1. Abstract	11
2.2. INTRODUCTION	12
2.2.1. A Brief History Of New Zealand	14
2.2.2. Overview Of The New Zealand Avifauna	17
2.3. MOLECULAR VIEW OF THE NZ AVIFAUNA	20
2.3.1. Phylogeny of birds	20
2.3.2. Birds in New Zealand	22
2.4. DISCUSSION	40

2.4.1. Accumulation and Radiation	41
2.4.2. A Zealandian element?	44
2.4.3. Disharmony & Extinction	46
2.4.4. Dating diversification	48
2.5. CONCLUSION	51
2.6. ACKNOWLEDGEMENTS	52
2.7. References	52
2.8. Supplementary Material	71
2.8.1. Latin names of birds referred to in review	71
2.8.2. Peer reviewed molecular publications	72

## 3. Chapter Three

Mitochondrial Genomes and Avian Phylogeny: Complex Characters and Resolvability without Explosive Radiations

3.1. Abstract	85
<b>3.2.</b> INTRODUCTION	86
<b>3.3.</b> Materials and Methods	92
3.3.1. Phylogenetic Analysis	94
3.4. Results	96
3.4.1. Phylogenetic Analysis	99
3.5. DISCUSSION	104
<b>3.6.</b> ACKNOWLEDGMENTS	108
3.7. References	109

### 4. Chapter Four

Two aspects along the continuum of pigeon evolution: a South-Pacific radiation and the relationship of pigeons within Neoaves

4.1. Abstract	115
4.2. INTRODUCTION	116
4.2.1. A South East Asian/Pacific radiation of pigeons.	116
4.2.2. The closest relative of Pigeons.	117
4.2.3. Nuclear versus Mitochondrial DNA and the problem of introns in	
deep phylogeny	117
4.3. Methods	119
4.3.1. Taxon sampling	119

4.3.2. DNA extraction and PCR	119
4.3.3. Phylogenetic analyses	120
4.4. RESULTS	123
4.4.1. A South East Asian/Pacific radiation within Pigeons	123
4.4.2. Phylogenetic relationships of Pigeons within Neoaves	126
4.5. DISCUSSION	129
4.5.1. The Ducula–Ptilinopus radiation in a biogeographic context	129
4.5.2. Closest relative of Pigeons	132
4.6. ACKNOWLEDGEMENTS	133
4.7. References	133

# 5. Chapter Five

Beyond Phylogeny: Pelecaniform and Ciconiiform Birds, and Long-Term Niche Stability

5.1. ABSTRACT	139
5.2. INTRODUCTION	140
5.2.1. Consilience of Induction	140
5.2.2. History of the Pelecaniformes	141
5.3. Methods	144
5.3.1. Taxon Sampling, DNA Extraction, PCR and Sequencing	144
5.3.2. Species for Analysis	145
5.3.3. Alignment	146
5.3.4. Phylogenetic Analyses and Tree Building	146
5.3.5. Molecular Dating	147
5.4. RESULTS AND DISCUSSION	147
5.4.1. Details of New Mitochondrial Genomes and Gene Orders	147
5.4.2. Implications of Core Pelecaniform Gene Duplications for	
Phylogenetic Studies	148
5.4.3. Phylogenetic Analyses	150
5.4.4. Resolution of the Core Pelecaniforms	152
5.4.5. The Pelican is not a Pelecaniform	153
5.4.6. The predicted P&C Group	155
5.4.7. The Nature of the Tropicbird	156
5.4.8. Molecular Dating	157

5.4.9. Water-Carnivory in Neoaves, Adaptive Radiations and Niche	
Stability	158
5.5. Conclusion	160
5.6. Acknowledgements	161
5.7. References	161
5.8. APPENDIX 1	167
5.8.1. Predicting the probabilities of observing splits in a new dataset.	167

## 6. Chapter Six

New Zealand Passerines Help Resolve Basal Oscine Phylogeny.

6.1. Abstract	169
<b>6.2.</b> INTRODUCTION	170
6.2.1. Oscine biogeography	170
6.2.2. Limitations of current deep oscine phylogenetic resolution	171
6.3. Methods	172
6.3.1. DNA extraction, PCR and sequencing of modern samples	172
6.3.2. Ancient DNA protocols	173
6.3.3. Alignment	174
6.3.4. Phylogenetic Analyses	177
6.4. RESULTS & DISCUSSION	177
6.4.1. Mitogenomic features	177
6.4.2. Phylogenetic analyses	178
6.4.3. Ancient DNA sequence verification	179
6.4.4. Phylogenetic analysis of the piopio with broader oscine sampling	180
6.5. FUTURE WORK	183
6.5.1. Dating Passeriformes	183
6.6. CONCLUSION	185
6.7. ACKNOWLEDGEMENTS	185
6.8. References	185
6.9. SUPPLEMENTARY MATERIAL	190

# 7. Chapter Seven

Thesis Summation	191
7.1. FUTURE DIRECTIONS: TO PHYLOGENY AND BEYOND	197
7.2. References	198

### 8. Appendix One

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### 9. Appendix Two

215

201

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# LIST OF FIGURES

FIGURE 1.1	Five models for the divergence of birds and placental mammals.	6
FIGURE 1.2	Evolutionarily-stable niche-discontinuity between two taxa.	7
FIGURE 2.1	New Zealand and neighbouring islands	15
FIGURE 2.2	Geological timescale	16
FIGURE 2.3	Phylogeny of birds based on multiple genes	21
FIGURE 2.4	Phylogeny of passerine diversity	35
FIGURE 2.5	The effect of taxon sampling on tree interpretation	45
FIGURE 3.1	Gene orders found in avian mitochondrial genome control regions	88
FIGURE 3.2	Comparison between $CR(1)$ and $CR(2)$ in Aracari (A) and Osprey (B)	97
FIGURE 3.3	Primers used to sequence duplicate tThr-CR gene order	98
FIGURE 3.4	Maximum Likelihood tree of 40 birds	100
FIGURE 3.5	Consensus network for 27 Neoavian birds	102
FIGURE 4.1	Phylogeny of pigeons with emphasis on the SE Asia/Pacific radiation	124
FIGURE 4.2	Bayesian rooted consensus tree of pigeons	123
FIGURE 4.3	Maximum likelihood tree of birds	127
FIGURE 5.1	Comparison of duplicated regions in the three core Pelecaniformes	148
FIGURE 5.2	Maximum likelihood tree from analysis using RAxML, with 31 taxa	150
FIGURE 5.3	Consensus network of the four analytical methods	151
FIGURE 5.4	Maximum likelihood tree from analyses using RAxML of 35 taxa	152
FIGURE 5.5	Maximum clade credibility chronogram of the 31 taxa dataset	158
FIGURE 6.1	Unrooted maximum likelihood analysis of mt genome dataset	178
FIGURE 6.2	Network of Bayesian analysis	180
FIGURE 6.3	Network of Bayesian analysis without Turnagra U51734	182
FIGURE 6.4	Consensus cladograms of passerine phylogeny	184
FIGURE S6.1	Piopio specimen Turnagra capensis	190
FIGURE 7.1	Network showing splits over 20% of RAxML bootstrap analysis	194

# LIST OF TABLES

TABLE 2.1	New Zealand native passerine diversity and endemicity	36
TABLE S2.1	Latin Names of Birds	71
TABLE S2.2	Peer reviewed publications reporting application of molecular data to New Zealand birds	72
TABLE 4.1	Accession numbers and mt genes included in analysis of pigeon phylogeny	120
TABLE 4.2	Accession numbers and species names for birds used in complete mt genome analyses	122
TABLE 4.3	Testing alternative hypotheses about pigeon relatives using the SH test	128
TABLE 5.1	Characters previously used to group pelecaniform families	143
TABLE 6.1	Genbank accessions of additional samples used in piopio	
	analyses	175