Phylogenetics, phylogeography and the evolutionary history of the chestnut-shouldered group of fairy-wrens (*Malurus* spp.)

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Submitted in fulfilment of the requirements of the degree of  
DOCTOR OF PHILOSOPHY  
March 2013
SYNOPSIS

The chestnut-shouldered fairy-wrens comprise a subgroup of four species in the genus *Malurus* (Passeriformes: Maluridae). Collectively, they are widespread across the Australian continent but phenotypic variation is strongly structured geographically in just one species, *M. lamberti*. Earlier phylogenetic analyses of this group have been limited to one or two individuals for each species and have not represented all currently recognized subspecies of *M. lamberti*. Historically, the taxonomy and nomenclature of the *M. lamberti* complex has been debated, in part because of morphological similarities among its subspecies and another member of the group, *M. amabilis*.

In the first data chapter of this thesis, I reconstructed the phylogeny of all four species of chestnut-shouldered fairy-wrens including all four subspecies of *M. lamberti* using a mitochondrial gene (ND2), five anonymous nuclear loci and three nuclear introns. Phylogenetic analysis of the mitochondrial ND2 gene nests *M. amabilis* within *M. lamberti* rendering the latter paraphyletic. Individual nuclear gene trees failed to reliably resolve each of the species boundaries or the phylogenetic relationships found in the mtDNA tree. When combined, a strongly supported overall topology was resolved supporting the monophyly of *M. lamberti* and its sister species relationships to *M. amabilis*. Current subspecies taxonomy of *M. lamberti* was not concordant with all evolutionary lineages of *M. lamberti*, nominotypical *M. l. lamberti* being the only subspecies recovered as a monophyletic group from mtDNA. *Malurus lamberti* is a relatively young species with strong geographically structured variation in plumage. *M. lamberti* ranges throughout the whole of Australia, from the
arid central deserts to some of the most humid coastal forests and heaths and four mainland subspecies are currently recognized: nominotypical *M. l. lamberti*; *M. l. assimilis*; *M. l. rogersi* and *M. l. dulcis*. Phylogeographic analysis provided a preliminary assessment of molecular differentiation and highlighted the important role of geographic barriers in Australia in promoting and maintaining population differentiation within a species. Although my topology did not support the recognition of the existing subspecies within *M. lamberti*, there is a substantial break between east (Clade L) and west of the Great Dividing Range (Clade A). AMOVA analyses of nuclear DNA detected significant genetic differentiation between the two mitochondrial clades and private alleles were observed in each. Further geographic structuring was evident within Clade A and the pattern was consistent with fragmentation caused by historical climate change and likely began developing in the Pleistocene. Populations of *M. l. assimilis* were not adversely affected by recent glaciations during this period and did not experience drastic population reductions. The results presented here are concordant with the multiple refugia hypothesis of Byrne (2008) in that suitable habitats were available in Australia during the Pleistocene and divergence of *M. l. assimilis* has built up through repeated cycles of contraction. The pattern of possible multiple refugia for subspecies *M. l. assimilis* raises the additional possibility that this widespread species may consist of numerous genetic groups that may warrant taxonomic recognition to capture the diversity within the subspecies.

Contact zones between subspecies provide important insights into the nature and process of speciation. In Chapter 5 I analysed genetic data from individuals spanning the inferred intergrade zone of *M. l. lambert* and *M. l. assimilis* in south-
east Queensland. This study found *M. l. lamberti* (eastern) and *M. l. assimilis* (western) have unique mitochondrial sequences that were deeply divergent and overlap in the intergrade zone proposed by Schodde (1982a). I found no evidence of population structure across the contact zone using microsatellites. However, nuclear sequences showed divergent *M. l. lamberti* and *M. l. assimilis* lineages and no haplotype sharing between the subspecies. A significant outcome from this research is the suggested division of *M. lamberti* into two species.
ACKNOWLEDGEMENTS

Many colleagues, friends and family have assisted me while working on this research. I wish to thank my dissertation supervisors, including Professor Jane Hughes, Dr Dan Schmidt, Dr Alicia Toon and Dr Leo Joseph who have provided support throughout the years and allowed me the freedom to follow my research interests and develop independently as a scientist. From my first meeting with Jane in third year of my undergraduate degree, I would like to specially thank for introducing me to the wonderful and sometimes frustrating world of genetics. For Jane’s encouragement, guidance and interest in my project over the years I am extremely grateful. From our first meeting, Leo Joseph, welcomed me to and made possible my path in the study of evolutionary genetics never doubting my ability to succeed despite a total lack of experience in the field. Leo Joseph assisted in many ways including helping acquire samples and financial support, field work, providing feedback on manuscripts and encouraging me to present my work at conferences. I would also like to thank Larissa Joseph for opening her home to me on numerous visits to Canberra. To Dan and Alicia, I thank you for your support, encouragement and provision of feedback to this dissertation.

I would also like to give special thanks to all the people in the Molecular Ecology Lab at Griffith University. In particular I would like to thank Kathryn Real who provided amazing assistance with microsatellites, lab techniques and computing support. To Olivier Baggiano, Andrew Bentley, Ana Dobson, Jemma Harris and Joel Huey, I thank you for the chats that kept my sanity during this process.
This work would not have been possible without the assistance of Alex Drew, Ian Mason, Alicia Toon (below) and the Australian National Wildlife Collection.

Field trips in the latter part of my PhD were a highlight and I will treasure the memories forever. The hard work and dedication of my fellow field trippers made possible interesting insights into a very discrete and hard to find small passerine.

This project would not have been possible without the constant support and help from my entire family. To my son, Jonathon, whom I owe endless hours of catching up, I thank you for your patience and understanding as I completed this project. From at times what felt like the sidelines I have watched you grow and mature into a wonderful young man. To my twin sister Diane and her husband Greg, I thank you.
both for your patience and understanding over the years as plans were made and cancelled at the last minute due to “deadlines” thrust upon me. You are both amazing people and I love you dearly. I would also like to thank my parents, Doug and Joan, for their constant and unwavering encouragement throughout. Finally to my close and dear friends, Susan, Lisa and Cate, thank you for the support throughout the years and your “you can do it “attitudes”.

Many thanks to the CodonCode Corporation for allowing me access to their program for the duration of my PhD. This allowed me the flexibility of working from home and to continue my most important role as a mother. This research was supported by a CSIRO Postgraduate Studentship, an Australian Postgraduate Award and CSIRO Ecosystem Sciences. I would like to give special thanks to the staff of the Australian National Wildlife Collection (Canberra), Western Australian Museum (Perth), Museum Victoria (Melbourne), Academy of Natural Sciences (Philadelphia) and the Australian Biological Tissue Collection (Adelaide) for tissue sub-samples from their collections.
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DECLARATION

The work described in this thesis is my own original work and no part has previously been submitted for a degree or diploma at any university and, to the best of my knowledge and belief, contains no material previously published or written by another person, except where due reference has been made in the text.

Alison McLean

08/03/2013