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The influence of space and time on the genetic architecture of rail species (Aves: Rallidae)

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Abstract

The main subject of this PhD research is the study of the underlying processes of evolutionary changes that lead to biological diversity. Such processes include those operating within and between populations (population divergence), as well as those operating among species (speciation), above the species level (e.g. genera and families) and the mechanisms that promote these divisions. Fundamental to these processes are the effects of genetic, demographic, geographical, ecological, behavioural and environmental factors on diversification. Rails (Aves: Rallidae) are used as an example to address central questions related to how these biological entities originated, when was that biological diversity generated, and why this biodiversity is distributed as it is. This thesis has been divided into four main chapters/papers for convenience to achieve this aim. In the first chapter, complete mitochondrial genomes and fossil data are used to provide a likely estimated time of rail ecology. I estimated that the origin and diversification of crown group Rallidae was during the Eocene about 40.5 (49–33) Mya with evidence of intrafamilial diversification from Late Eocene to Miocene time. This time is much older than currently available fossils assigned to Rallidae, but more direct evidence of fossils with reasonable taxonomy are likely to emerge. This estimated time implies that rail diversity originated deep in the avian tree supporting an inference of deep ancestry of terrestrial/walking habits among Neoaves. In addition, in the second chapter I used neutral molecular data (nuclear and mitochondrial gene fragments) to reveal the degree of historical biogeographic signal and net diversification in the current lineage distribution using the most complete species-level hypothesis for ralloids. This comprehensive intrafamilial molecular phylogeny allowed to infer spatial and ecological diversification in Rallidae associated with morphological innovation (frontal shield, body size and flightlessness) and the global retention of diversity in several lineages caused by dispersal, adaptation and exploitation of ecological opportunities. In the third and fourth chapters I explored historical patterns of diversification in a biogeographic context (in spatial and temporal scales) within a clade (*Porphyrio* but focused on the type species *Porphyrio porphyrio*) and a highly polymorphic species (*Gallirallus philippensis*). In the third chapter, a dated phylogeny and the tools of population genetics were used to gain insights into the congeneric relationships, diversification, and the history of expansion of one of the most peculiar clades within Rallidae. I found that the *Porphyrio* clade arose during the Mid-Miocene, apparently in Africa, with a single Long-Distance Dispersal (LDD) event occurring into the Americas and several other LDD events to the North-East around 10 Mya. *Porphyrio porphyrio* was not found to be a natural group with *P. melanotus* appearing in Australasia during the Pleistocene (600 kya). Dispersal, isolation, adaptation and selective pressure accounted for most of the variation found within this clade. On a finer scale, the fourth chapter explored genetic changes

within populations of the supertramp and great speciator *Gallirallus philippensis* using a mitochondrial DNA marker to recognise the genetic changes caused by founder events and provide important insights into the microevolutionary processes that drove the early stages of diversification. This study found that abrupt genetic changes of founder events are related to dispersal, colonisation, range expansion, gene flow, isolation and strong selection forces. The consequences of such processes for speciation and how they affected the population demography and evolutionary history of *Gallirallus philippensis* in the south western Pacific are discussed. These independent but linked studies within this thesis yield important clues to the evolutionary history that has shaped the diversity of rails. This research contributes to our understanding of Tertiary vertebrate evolution and establishes a bridge between macro- and micro-evolution.

Key words: Aves, biogeography, colonisation, dispersal, diversification, DNA, ecology, evolution, extinction, gene flow, isolation, phylogenetics, population genetics, Rallidae, speciation.

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Contributions of others to this thesis: So far three chapters from this thesis have been submitted for publication in peer-review journals and the last chapter is in preparation for submission. I carried out all the laboratory work, data analyses and writing of drafts. Co-authors for all the manuscripts provided various levels of advice and discussion on drafts. Some data used in Chapter 4 were provided by Leo Joseph at the Australian National Wildlife Collection (ANWC), Greg Adcock at the University of Canberra (UC), and Faye Lux and Julian Reid at the Australian National University (ANU).

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