

**Examining the patterns and processes of speciation and species
diversity in Australian *Gehyra* gecko lizards**

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“The footsteps of Nature are to be trac'd, not only in her *ordinary course*, but when she seems to be put to her shifts, to make many *doublings* and *turnings*, and to use some kind of art in endeavouring to avoid our discovery.”

— Robert Hooke, *Micrographia* (1665, reprint 2008), 17.

Declaration

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Abstract

Understanding the process of speciation and the nature of relationships between species is one of the fundamental aims of evolutionary biology. These processes are integral to the study of species delimitation and taxonomy, phylogenetic reconstruction and evolutionary history and the study of speciation processes. Under this premise I evaluate a recently evolved and taxonomically challenging group– the *Gehyra* geckos of Australia, to gain a better understanding of how the process of speciation and species relationships have developed in this genus.

My research has three main aims:

1) *Explore the adequacy of current taxonomy in accounting for species diversity in the group and improve it where necessary: Gehyra* have proven taxonomically troublesome historically, with extensive and geographically complex arrangements of genetic diversity apparently not associated with patterns of morphological diversity. I explored species delimitation and the taxonomic status of lineages within the arid-adapted *Gehyra variegata* species complex using multi-locus (mtDNA, nuclear loci, karyotypes) genetic, distribution and morphological data, generating the first comprehensive phylogenetic framework for the genus. I describe one new species and identify an additional five putative species. I support previously hypothesized high levels of cryptic diversity in the group and present a concentrated effort in taxonomically resolving the genus.

2) *Evaluate previously proposed evolutionary scenarios for the diversification of the Australian Gehyra and propose a comprehensive evolutionary history of the group:* Using a multi-locus dataset (one mtDNA locus, six nuclear loci), I generated a calibrated

species tree of the group, which showed support for a late-Eocene to mid Miocene introduction of the genus to Australia from Asia and for the division of the Australian *Gehyra* into a tropically-adapted *Gehyra australis* species complex and a generally arid-adapted *Gehyra variegata* species complex containing morphologically transitional species in the Kimberley region. My analyses did not support a previously suggested model of chromosomally driven speciation in Australian *Gehyra* and assert that diversification of both species complexes occurred simultaneously from the late Miocene through to the present.

I undertook a quantitative evaluation of gene tree discordance in *Gehyra*, showing a high degree of discordance between genes for the group, further supporting the recent diversification of the group.

3) *Examine possible processes of speciation in Australian Gehyra*: I investigated a case study in which a geographically constrained, distinct population of *Gehyra* was shown to be morphologically and ecologically distinct but genetically indistinguishable from a comparatively widespread, geographically parapatric species. This indicates a scenario of emergent, ecological speciation and presents a model system in which the process of ecological speciation could be observed. It also contrasts previous studies highlighting allopatric speciation driving the Australian *Gehyra* radiation, showing ecological speciation may play an important role.

In carrying out these studies, I have both explored the use of emergent methods for delimiting species and evaluating relationships between species, and significantly increased our understanding of the Australian *Gehyra* radiation. This body of work represents an ideal framework for rapid and effective evaluation of novel *Gehyra* species

and will greatly assist in discovering and documenting the diversity of this problematic radiation in the future.

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Notes on chapter styles

Chapter 1 is published in the journal *Zootaxa* and thus follows that journal format precisely. Chapter 2 is intended for submission in the journal *Molecular Phylogenetics and Evolution* and is thus formatted in the style prescribed by that journal. Chapter 3 is intended for submission in the journal *Systematic Biology* and thus follows that journal's style precisely. Chapter 4 is published in the *Journal of Evolutionary Biology* and thus follows that journal's style precisely.

A statement declaring co-author contributions prefaces each chapter submitted or intended for publication.

The format of this thesis complies with that outlined in “Specifications for Thesis 2011” provided by the University of Adelaide Graduate Centre:

http://www.adelaide.edu.au/graduatecentre/pdf/specifications_thesis_2011.pdf