# Evolution of diversity: analysis of species and speciation in *Hemiandrus* ground wētā

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In loving memory of my grandad,
Bruce Smith

"The important thing is not to stop questioning. Curiosity has its own reason for existing. One cannot help but be in awe when he contemplates the mysteries of eternity, of life, of the marvellous structure of reality. It is enough if one tries merely to comprehend a little of this mystery every day. Never lose a holy curiosity."

- Albert Einstein

# Abstract

Patterns of biodiversity and endemism in New Zealand are explored, with a focus on the ground wētā genus *Hemiandrus*. I first investigated factors that determined regional levels of endemism using a generalised linear model based on analysis of 2322 species of endemic New Zealand invertebrates. I found that widespread species are uncommon in New Zealand and most invertebrates occupied few regions. Number of endemic species per region was positively correlated with total number of species and size of the region 3 million years ago. Within one clade of *Hemiandrus* I found that North and South Islands differed in how they were occupied: South Island had many species with small non-overlapping ranges, whereas North Island was largely dominated by a single species. This is likely due to differences in age of different parts of New Zealand, yet this pattern was absent in another clade of ground wētā species, showing that properties of species themselves also have a large impact on species ranges and speciation.

I applied several strategies to the *Hemiandrus maculifrons* species complex to test putative species boundaries (chapter 3). I compared morphological methods (Gaps in Continuous Characters across Geography (GCCG)) and genetic methods (Bayesian Species Delimitation, Rosenberg's P(AB), P(Randomly Distinct), P ID(Liberal)). Some of these strategies indicated that all or nearly all mtDNA clades tested represented separate species, while others indicated that no clades were likely to be distinct species. I concluded that *H. maculifrons* comprises three species (plus an under-sampled microendemic species, chapter 4); a conclusion that is discordant with the results of the "species delimitation" methods but consistent with other genetic, morphological and distributional data.

Since the genus *Hemiandrus* was thought to comprise only nine named species but dozens of alleged species, I tested whether the purported diversity accurately reflected biological diversity in the genus or whether it was exaggerated due to speculative classification (chapter 5). To do this, I applied traditional techniques to search for qualitative or quantitative differences between individuals using a model where species are separately evolving lineages that form separate genotypic clusters with no or few intermediates when in contact (Mallet 1995). Most proposed operational taxonomic units were supported, but some names appear to be synonymies while others appear to encompass more diversity than previously recognised. I concluded that *Hemiandrus* comprises at least 25 species, but as specimens representing all tag-names[1]

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[1] A tag-name is an informal name that indicates an entity that may be a separate species, monophyletic group or separate interbreeding population of uncertain taxonomic rank (Leschen *et al*. 2009).

were not available, additional diversity may exist within *Hemiandrus* than recognised here.

Phylogenetic analysis of mtDNA sequences identified two major clades within New Zealand *Hemiandrus*. Using nuclear markers and morphological traits I found strong support for these two clades. Derived shared traits were identified that can determine to which clade each species belongs. Concordance between genetic markers (four loci) and morphology resolved evolutionary relationships from which I propose dividing the group into two separate genera.

# Preface

The overall aim of this research project, "Evolution of diversity: analysis of species and speciation in *Hemiandrus* ground wētā", was to examine patterns of biodiversity and endemism in New Zealand, focusing particularly on the genus *Hemiandrus* (ground wētā). This genus has been suggested to comprise high species diversity and many taxa with restricted ranges, but diversity within this genus is largely unquantified.

In chapter one I explore the patterns and drivers of microendemism in New Zealand invertebrates. The finding that widespread species are uncommon in New Zealand and most invertebrates occupied few regions led me to question why a single ground wētā species, *H. maculifrons*, is found so extensively throughout both main islands of New Zealand (chapter 3). I explored this using multiple lines of evidence, including nuclear markers developed in chapter 2 with the help of Eddie Dowle, who sequenced multiple anostostomatid mtDNA genomes for her PhD thesis (2013). My results from chapter 3 suggest that *H. maculifrons* comprises multiple species and these are described in chapter 4 along with two morphologically similar species.

In chapter 5 I assess the overall purported species diversity within *Hemiandrus*. I first examined specimens collected during extensive field work and from assorted collections, in order to gain an understanding of morphological variation within the genus. Based on this background knowledge I was then able to match specimens to tag-names. Most tag-names do reflect biological diversity, although some appear to be synonymies, while others may comprise several species. Two of these tag-named species are described in chapter 6: Taylor Smith, B. L., Morgan-Richards, M., & Trewick, S. A. (2013). New Zealand ground wētā (Anostostomatidae: *Hemiandrus*): descriptions of two species with notes on their biology. *New Zealand Journal of Zoology, 40*(4), 314-329).

In chapter 7 I show that the high species diversity within *Hemiandrus* compared to other New Zealand anostostomatid genera may be partially explained by ground wētā comprising multiple morphologically and genetically distinct genera.

These chapters are intended for publication and so references are presented at the end of each chapter.

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