

# Phylogenetics and Evolutionary Dynamics of *Tetratheca* (Elaeocarpaceae)



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# Abstract

*Tetratheca* Sm. (Elaeocarpaceae) is an endemic Australian genus of small shrubs distributed mainly across the southern part of the continent. Most species are narrowly endemic or highly disjunct: very few are widespread. Adequate conservation planning relies on comprehensive knowledge of the evolutionary history of the taxa, strength and direction of current gene flow and connectivity between populations, and the occurrence of local adaptation or drift.

In this study I investigated species distribution patterns and processes driving speciation in the Australian endemic genus *Tetratheca* at a variety of taxonomic, geographic and temporal scales. Evolutionary processes were explored using a hierarchy of molecular approaches: phylogenetic reconstruction, comparative phylogeography and population genetics.

Phylogenetic analyses of plastid and nuclear DNA sequence data for over 85% of the known species confirmed that *Tetratheca* is monophyletic, with several lineages in Western Australia and only two in the eastern states of the continent. Resolution within some lineages was poor and there were minor points of conflict between phylogenies, implying a role for incomplete lineage sorting (ILS) or hybridisation in the evolution of the genus.

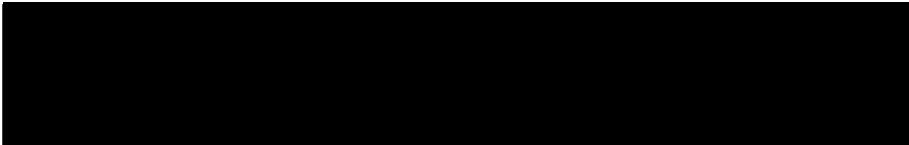
Phylogeographic and population genetic analyses using data from a range of chloroplast and novel nuclear microsatellite loci was undertaken on the *Tetratheca pilosa* and *T. ciliata*-*T. stenocarpa* species complexes. The results helped to clarify phylogenetic ambiguities, and support the hypothesis that ILS is more influential than hybridisation in explaining phylogenetic incongruence in the studied taxa.

The present study shows that in the case of *Tetratheca*, a recently derived and rapidly evolving component of the Australian flora, patterns of genetic diversity at the micro-evolutionary scale can help with interpretation of macroevolutionary processes in the genus. It thereby confirms that comparative studies of a range of species, applied at a variety of hierarchical scales, can be particularly useful for understanding evolutionary processes and genetic diversity of any single species.

# Declaration

I certify that the substance of this thesis has not already been submitted for any degree and is not currently being submitted for any other degree or qualification.

I certify that any help received in preparing this thesis and sources used, have been acknowledged in this thesis.



Hannah McPherson

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