

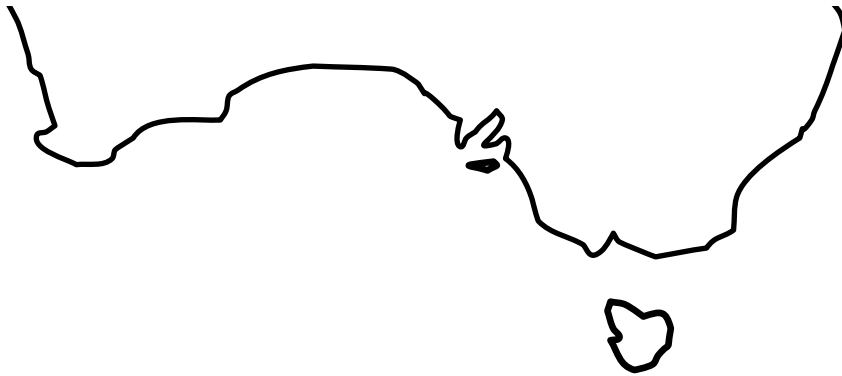
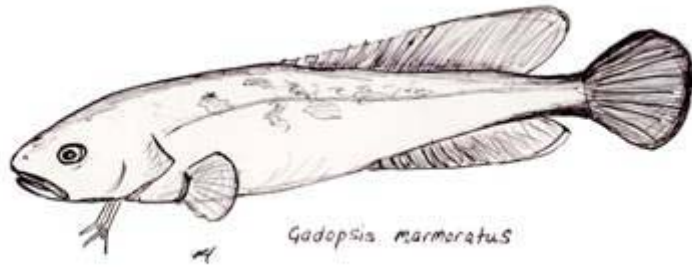
A Molecular Genetic Appraisal  
of Biodiversity and Conservation Units  
in Freshwater Fishes from Southern Australia

**Michael Hammer**

School of Earth and Environmental Sciences, The University of Adelaide  
&  
Evolutionary Biology Unit, South Australian Museum

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THE UNIVERSITY  
OF ADELAIDE  
AUSTRALIA

South Australian Museum





*Retropinna semoni s.l.*



*Nannoperca obscura*



*Nannoperca australis s.l.*



*Mogurnda adspersa*



*Philypnodon sp. (macrostomus complex)*



*Philypnodon grandiceps s.l.*



*Gadopsis marmoratus s.l.*

**Fishes from the lower River Murray, southern Australia (MH)**



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## SUMMARY

The freshwater fish fauna of southern Australia is characterised by low species richness and high endemism in groups displaying southern temperate, temperate-subtropical or temperate-tropical distributions. Comparatively few studies in Australia have incorporated modern molecular techniques to delineate species boundaries and define within-species conservation units. This is problematic because freshwater fishes are likely to show high levels of cryptic speciation and marked spatial sub-structure, and is information which is needed to conserve biological diversity and maintain the integrity of ecological communities and processes. The current study uses a ‘combined evidence’ approach, led principally by a set of nuclear genetic markers (allozymes), to assess species boundaries, spatial sub-structure and conservation units in obligate freshwater fishes from southern Australia.

A literature review (Chapter 2) concerns the nature and effects of fragmentation in freshwater environments. It considers the implications for freshwater fishes and the types of extrinsic and intrinsic characteristics, both natural and human accelerated, that might drive population fragmentation and divergence. This theoretical framework is then applied to a suite of six largely co-occurring species groups with contrasting biological characteristics, and derive hypotheses about expected levels of genetic divergence across and within different drainages.

### *Major findings*

Species of *Retropinna* (Chapter 3) are widespread and generally regarded as ‘common’ and mobile. Allozyme analyses revealed species-level and population-level sub-divisions, including five distinct species with contiguous ranges and no evidence of genetic exchange. Three occur along the eastern seaboard (including three instances of sympatry), another in coastal and inland southeastern Australia and Tasmania, and a fifth in the Lake Eyre Basin. There is no indication of a simple ‘*tasmanica*’ versus ‘*semoni*’ dichotomy, but instead a complex pattern involving discrete clusters for the Upper Murray plus Darling rivers, Lower Murray, Glenelg River and Tasmanian regions. These findings have implications for biodiversity, conservation and ecology. This chapter has been published in modified form (*Marine and Freshwater Research* 58, 327-341).

*Nannoperca obscura* (Chapter 4) is a small demersal fish with specialised habitat requirements. It is under threat of extinction, particularly in the western section of its range. Combined nuclear and matrilineal genetic data identified congruent within-species sub-structure, divided by patterns



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of distribution and biogeography. Four monophyletic mtDNA lineages, each distinct at multiple nuclear loci, indicate four Evolutionarily Significant Units (ESUs), namely (1) Lake Alexandrina in the Murray-Darling Basin (MDB), (2) Glenelg River, Millicent Coast River Basin and the outlying Mt Emu Creek, (3) Merri River and associated coastal streams, and (4) the eastern range section. Additional genetic and ecological data support multiple Management Units (MUs) within ESUs for individual or groups of river basins separated by marine barriers.

*Nannoperca australis* (Chapter 5) has a similar character to its aforementioned congener, except that it occurs across a much wider area. Although generally common, particular populations are threatened, especially in the MDB. Allozyme analyses of 57 populations confirm the presence of two divergent species, with an eastern species containing two ESUs: (1) Gippsland and Flinders Island, and (2) Ansons River in northeastern Tasmania. The western species shows sub-structure across its range, including a separation of MDB and coastal populations as two heterogeneous ESUs. The Lower Murray region (Mount Lofty Range streams and the Lower Lakes) harbours a remarkable level of between- and within-population diversity, underscoring its importance for conserving evolutionary potential.

*Mogurnda adspersa* (Chapter 6) has been presumed extinct in South Australia since the early 1970s and has also been assumed lost from the southern MDB. This chapter reports on the rediscovery of *M. adspersa* from a wetland near the terminus of the Lower Murray, some 2500 river kilometres from the nearest known population. The nature and basic ecology of this population is documented, but the combined effects of drought and water abstraction recently have led to the probable extirpation of the wild population. A combined allozyme and mtDNA dataset confirmed the 'nativeness' of the population as a distinct sub-population (and MU), with a moderate level of allele heterogeneity. This information provides a platform for captive breeding as a conservation measure.

The endemic genus *Philypnodon* (Chapter 7) contains two nominal species: *P. grandiceps* and the long recognised but only recently described *P. macrostomus*. The former is considered widespread and common (near ubiquitous), whereas the latter is more patchily distributed. Some tolerance to marine conditions is indicated, suggesting that there may be less sub-structure, but allozyme analyses of 269 individuals indicate the presence of multiple, species-level taxa within both described species. This obscures interpretations of existing ecological data. Although the presence of genetically-similar populations within and across some drainage divides indicates higher levels of gene flow, the pattern is complex and suggests historic genetic exchange between some but not other geographically-adjacent taxa.

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The freshwater blackfish genus *Gadopsis* (Chapter 8) has been a problem group for taxonomists, and it is unclear where the group is placed phylogenetically and how many species occur. Northern and southern forms on respective sides of the Great Dividing Range have been proposed, but with limited supporting evidence. Its dispersal ability (hence predicted genetic structure) is obscured by opposing life-history traits, including large body size (i.e. good swimming ability) *versus* habitat specialisation, demersal larvae and restricted home ranges. This chapter provides a genetic overview incorporating 61 locations across the range, and demonstrates unequivocally the presence of distinct northern and southern species of *G. marmoratus*. Moreover, distinct genetic discontinuities involving geographically abutting lineages indicate the likely presence of multiple ESUs within each species. A comparison of the allozyme data with previous mtDNA studies also identified two ESUs within *G. bispinosus*.

Overall, considerable complexity is demonstrated signalling the need for a review of how the southern Australian fish fauna should be viewed, studied and protected. The genetic data also provide insight into the interplay of intrinsic biological characters (e.g. dispersal ability, population ecology) with historic and contemporary extrinsic environmental factors (e.g. fragmentation, biogeographic processes). Comparisons between and within traditionally-defined species are problematic, however, owing to multiple species-level splits and other genetic divisions that may have matching biological counterparts. Together with other reports in the literature, the findings presented herein have significant conservation implications, particularly given the rapid pace of human-mediated change in some regions that house high species and genetic diversity and unique evolutionary components, notably southeastern Queensland (especially the Mary River) and the lower River Murray in South Australia. Other regions displaying high genetic substructure or divergent populations include the Clarence River and Lachlan River in New South Wales; Gippsland, Goulburn River, Glenelg River and Mt Emu Creek in Victoria, and the Macquarie River and Ansons River in Tasmania.

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## **DECLARATION**

This work contains no material which has been accepted for the award of any other degree or diploma in any university or other tertiary institution 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.

I give my consent to this copy of my thesis, when deposited in the University Library, being available for photocopy or loan, subject to the provisions of the *Copyright Act 1968*. No part of this thesis may be reproduced in part or in full without the prior written permission of the author.

**Signed:**

**Date:** 3rd September 2008

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