

Phylogenetics and biogeography of Australian subterranean Parabathynellidae



Brevisomabathynella leijsi (Parabathynellidae)

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DECLARATION

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Kym Abrams

*This thesis is dedicated to my parents,
Berenise and Rashaad*

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ABSTRACT

The putatively ancient subterranean crustacean family Parabathynellidae has been poorly studied, in part because of the problem of obtaining material from difficult to access subterranean habitats in which they live. Further, the systematics of the group has been complicated by their generally simplified morphology and isolated descriptions of new taxa in the absence of any phylogenetic framework. This thesis provides a comprehensive molecular systematics framework for Australian Parabathynellidae, which is used to explore phylogenetic relationships amongst parabathynellids, their diversity, some aspects of character evolution and their biogeographic history within Australia. In addition, taxonomic descriptions are provided for the first parabathynellid species from South Australia.

For the first data chapter molecular sequence data from the mitochondrial cytochrome c oxidase subunit 1 (*COI*) and *18S* rRNA genes were generated in order to examine phylogenetic relationships amongst Australian genera and assess the species diversity of this group within Australia. The resultant phylogenetic framework, in combination with an ancestral state reconstruction analysis, was used to explore the evolution of two key morphological characters previously used to define genera, and assess the oligomerization principle (i.e. serial appendage reduction over time), which is commonly invoked in crustacean systematics. The ancestral state reconstruction analysis was also used to determine whether there has been convergent evolution of appendage numbers during the evolution of Australian parabathynellids. Phylogenetic analyses revealed that species of each known genus, defined by traditional morphological methods, were monophyletic, suggesting that the commonly used generic characters are robust for defining distinct evolutionary lineages. These analyses also revealed a remarkable diversity of parabathynellids. Additionally, ancestral state reconstruction analysis provided evidence for multiple cases of convergent evolution for the two morphological characters evaluated and contradicted the conventional view of parabathynellid evolution, which assumes that more simplified taxa (i.e. those with fewer-segmented appendages and setae) are derived and more complex taxa are primitive.

The third chapter focuses on South Australia, where phylogenetic analyses revealed a previously unknown diversity of parabathynellids from South Australia, and a complex set of relationships with the New South Wales and Western Australian fauna. Additionally, the first parabathynellid genus from South Australia, *Arkaroolabathynella* gen. nov, is described and a key to and checklist of Australian parabathynellid genera is also provided.

The final data chapter used an expanded dataset to investigate the geographic distribution, history and evolutionary relationships of extant parabathynellids between subterranean bioregions in Australia. This study found evidence for significant regional biogeographic

structuring of parabathynellids at the genus and species levels, indicating a long and complex evolutionary history for these animals in Australia, likely shaped by fluctuating climates throughout the continent's development. The high incidence of regional endemism for parabathynellids is significant because it confirms the poor dispersal capability of these animals, which makes them particularly vulnerable to disturbance or destruction of their subterranean habitats.

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