

Abstract

A cryptic species complex containing two members of the genus *Macrobrachium* Bate, 1868 (Crustacea: Decapoda: Palaemonidae) has been resolved using a combination of morphology and DNA-based taxonomy.

While the character set used in morphological analysis yielded limited differentiating data, by using mtDNA sequence distances from part of the cytochrome oxidase sub unit I (COI) gene, commonly known as the “DNA barcode”, it was possible to support the inference of a new species of *Macrobrachium*. Based on the COI sequence data, several species groups of *Macrobrachium* from Taiwan could be recognised including a distinct cluster of 16 individuals of the new species. Analysis of the COI sequence showed that the majority of species groups displayed high interspecific and low intraspecific variation with all forming clusters that concur with known taxonomic boundaries.

The morphological similarity of this new species to *M. latidactylus* is presented here with only the shape and proportions of the terminal part of the major periopod functioning to distinguish it from the new species.

This work highlights the importance of combining traditional morphology-based taxonomy with DNA sequence data to assist in the identification of cryptic species and delineation of the genus *Macrobrachium*, particularly in instances of morphologically similar or damaged material.