



## Phylum Tardigrada: A re-evaluation of the Parachela

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### Abstract

We assessed the available morphological evidence to see if this corroborates the paraphyly in the Parachela (Tardigrada) as suggested by recent molecular data. We reconcile molecular phylogenetics with alpha morphology, focusing on claw and apophysis for the insertion of the stylet muscles (AISM). We combine molecular and morphological evidence to define six new taxa within the Parachela Schuster et al 1980. These include two new families of Isohypsibiidae **fam. nov.** and Ramazzottidae **fam. nov.** along with four new superfamilies of Eohypsibioidea **superfam. nov.**, Hypsibioidea **superfam. nov.**, Isohypsibioidea **superfam. nov.**, and Macrobiotidea **superfam. nov.**

**Key words:** Tardigrade, Eohypsibioidea **superfam. nov.**, Hypsibioidea **superfam. nov.**, Isohypsibioidea **superfam. nov.**, Macrobiotidea **superfam. nov.**, Isohypsibiidae **fam. nov.**, Ramazzottidae **fam. nov.**, Morphology, Molecular, Systematics

### Introduction

Familial level taxa that have separated into distinct lineages over many millions of years are usually clearly identifiable via a unique suite of morphological characters. In some groups, particularly the “lesser-known” or “minor” phyla, basic morphology may be so strongly conserved that deep divergences are often difficult to detect or resolve. The application of genetic techniques has frequently uncovered unexpected diversity in such groups. For example, while 13 Australian species were recognised previously within the phylum Onychophora Grube, 1853 (Reid 1996), allozyme electrophoresis has identified deep cryptic divergences within these recognised groups (Brisco and Tait 1995), leading to the description of 22 new genera and 41 new species (Reid 1996). Onychophora are relatively large, usually between 50 and 200 mm long, with an average of *ca.* 50 mm, (C.J. Sands, personal obs.), and possess many characters that are clearly visible without the aid of a microscope. As the complexity and size of the animals within a taxonomic group diminishes the number of available characters usually becomes restricted and the ability to detect subtle morphological variation technologically limited. So, while recent molecular work has indicated cryptic lineages in the phylum Tardigrada Spallanzani, 1776 (e.g. Kiehl *et al.* 2007; Sands *et al.* 2008a, b, Jørgensen *et al.* 2010) there are relatively few morphological features to corroborate such morpho-crypsis.

In this paper we discuss the current systematics of the phylum Tardigrada in light of the growing body of molecular phylogenetic evidence. We argue that despite a lack of clear morphological apomorphies, there is sufficient evidence for a considerable re-arrangement of currently accepted systematics. The re-arrangement we propose results in the establishment of four superfamilies corroborated by both alpha taxonomy and molecular analyses.

Dedication: In memoriam Prudence de Villiers, friend of the first author, who died whilst this paper was in review.