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# Morphology and molecular phylogeny of *Macrobrachium snpurii,* a new species of the genus *Macrobrachium* Bate, 1868 from Kerala, India

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## Abstract

*Macrobrachium snpurii* **sp. nov.**, collected from the Karamana River, in the lower reaches of Western Ghats, is described and illustrated. DNA barcoding using Cytochrome B gene sequences has elucidated the taxonomic status of the new species and the NJ tree reveals that *M. snpurii* **sp. nov.**, is phylogenetically close to *M. idella idella*. However, morphometric and meristic features of the species share certain characters with *M. idella idella, M. patheinense* and *M. tratense,* while it diverges remarkably from these three species in distinctive diagnostic characters: rostral formula 12–14/4 with 2 postorbital teeth; carapace smooth with distal end of rostrum directed upwards; chelae with 2 proximal denticles both in the movable and immovable fingers. A wide gap present in the distal part of the chelae, when fingers are closed. Movable finger, longer than the immovable and distal end of fingers inwardly hook-like; palm more pigmented than fingers and telson extends beyond the level of the outer lateral spine of uropodal exopod. A pair of plumose setae is present between the inner pair of movable spines of telson.

**Key words:** Taxonomy, new species, molecular phylogeny, Caridea, Palaemonidae, *Macrobrachium*, Cytochrome b, Kerala, India

## Introduction

The species of the genus *Macrobrachium* Bate, 1868 normally occur in freshwater but some may also be found in brackish and even salt water (Riek, 1951). During a survey of the Palaemonid prawns along the South-west coast of India, the present authors collected several species from the Karamana River (>20 m Mean Sea Level) in the lower reaches of the Western Ghats, a global biodiversity hotspot. Among these, 4 specimens showed morphometric and meristic features that did not synchronize with any other known species of *Macrobrachium*, hence described as a new species, herein**.**

According to Dayrat (2005) ‘delineating species boundaries correctly and also identifying species are crucial to the discovery of life’s diversity because it determines whether different individual organisms are members of the same entity or not’. The identification of species depends on the information generated by taxonomists whose work cannot cover all the taxa. However the ‘DNA Barcode of Life’ resolves this crisis by the standardized, rapid and inexpensive species identification methodology accessible to non-specialists or non-taxonomists also. Moreover the micro evolutionary divergence between closely related species is essential for comparison of the physiological traits between them. The ideal DNA-based identification system employs a single gene for the placement of any organism in the full taxonomic hierarchy from Kingdom to species. The use of DNA sequence has the added advantage that it allows the creation of a phylogeny that enables the testing of a systematic hypothesis for independent assessment of morphological evolution and sequences of cytochrome b (CytB) is the most popular methodology in phylogenetics (Kartavtsev and Lee, 2006). Hence, along with the conventional taxonomic account of the species, we analyzed the CytB gene sequences of *M. snpurii* **sp. nov.**, to corroborate the uniqueness of the species.

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