

An Update on the Molecular Phylogeny of Decapoda

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The tremendous morphological diversity of decapods is fascinating, but it is also a major hurdle for phylogenetic reconstructions due to challenges in acquiring and coding for sufficient homologous characters. The use of molecular markers has become integral in helping to resolve the question. Over the past decade, our group has developed a number of new nuclear gene markers for decapod phylogenetics and achieved good resolutions in gene tree topologies. Over the years, we have attained a wide taxon sampling across the decapod infraorders. Here, we present an updated molecular phylogeny of Decapoda based on sequences from two mitochondrial rRNA and five nuclear protein-coding genes, using more than 500 species from >150 families, representing over 80% of the 190 decapod families. Statistical support for most of the nodes is strong at infraordinal level, and the monophyly of the Dendrobranchiata and Pleocyemata, and all pleocyemate infraorders is confirmed; with the surprise that Procarididea is nested within Caridea. However, relationships within the highly diverse Brachyura and Caridea remain largely unresolved, probably due to relatively lower taxonomic sampling. These two taxa constitute more than 70% of all decapod species, with a large number of families and genera known. We continue to explore the utility of additional markers in resolving these two groups. Together with effort in expanding taxon coverage, we believe we could attain a consensus on the decapod tree of life in the near future.

[This work was supported by a research grant (41476146) from the National Natural Science Foundation of China.]

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