

Possibilities and challenges for using morphological and molecular methods to unravel mysteries in the phylogeny of typical benthopelagic deep-sea calanoids

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Calanoid copepods constitute the most numerous organisms not only in the pelagic realm, but also in the benthic boundary layer, which gives them an important role in the turnover of organic matter in the benthopelagic habitat. Diversity within deep-sea benthopelagic calanoids is high and in some regions comparable to pelagic habitats. Most of the taxa occurring in the benthopelagial belong to the younger lineages within calanoids and their identification is often strongly impeded by the striking morphological diversity between different species of some taxonomic groups. Here we present first data on a combined taxonomic approach to investigate the phylogenetic relationships between different lineages of typical benthopelagic calanoids. We analyzed relationships between taxa by classical morphological methods and molecular genetics using a multiple-gene approach with nuclear and mitochondrial gene fragments. We discuss challenges in the single approaches and the interpretation that arise by the combined results.

Keywords: benthic boundary layer, deep sea, phylogeny calanoid copepods

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