

## The taxonomy and biogeography of macrofaunal amphipod crustaceans, with a focus on the abyssal Pacific fauna relevant to the CCFZ: What can DNA tell us?

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The use of molecular tools as an aid in species identification of deep-sea taxa has been proven useful in the light of major challenges associated with this task, such as incomplete species descriptions, a high occurrence of taxa new to science and cryptic species, the small size of the organisms compared to those living in shallow waters and the tentative interpretation of both sexual dimorphism and intraspecific variability. Here I present the efficiency of the DNA barcoding method, i.e. the use of a standard genetic marker for species identification, used in two different approaches: the reverse taxonomy one, where morphological studies build upon the results of the initial molecular results, and the “blind” taxonomic approach where taxa are treated as Molecular Operational Units (MOTUs). First, DNA barcoding has been tested for a subset of Antarctic shallow-water and deep-sea lysianassoid amphipod species, and shown to be efficient for species assignments as well as for pinpointing species complexes and species new to science. Furthermore, this study sets a baseline for the use of threshold values to distinguish intraspecific variation and interspecific divergences in lysianassoid amphipods. Second, an integrative study combining genes and morphology identified nine previously overlooked species-level lineages within the assumed cosmopolitan and eurybathic deep-sea amphipod *Eurythenes gryllus*; several of these are being currently described with the reverse-taxonomy approach. This study demonstrates that abyssal diversity is higher than previously assumed and that geographical distributional patterns vary from restricted to widespread or bipolar for the distinct species-level clades. Molecular studies based on MOTUs are proposed for understudied and abundant amphipod families. In the past, comparative diversity studies have focused mainly on the better studied deep-sea groups or higher-level taxa, most likely leading to biased results. Hence, molecular approaches should be further explored with an aim to provide a rapid and cost-effective method for large-scale biodiversity studies, bearing in mind the recent advances in high-throughput sequencing techniques. Finally, molecular studies on deep-sea taxa do not only serve for rapid species assignments of specimens hard to identify but can provide information that is crucial to a better understanding of deep-sea ecosystems and their vulnerability to human-induced modifications, ranging from genetic connectivity and species’ distributions to general deep-sea biogeography and ecology as well as evolutionary histories and past colonization events of deep-sea taxa.