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TITLE: Comparison of morphological and next generation DNA sequencing methods for assessing zooplankton assemblages

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ABSTRACT:

Morphological taxonomic methods are currently insufficient to satisfy the rising demand for taxonomic information and rapid sample turnover required to support conservation and resource management efforts. Next generation DNA sequencing (NGS) is capable of rapidly producing taxonomic assessments for a broad diversity of organisms present in environmental samples. To achieve taxonomic coverage of similar breadth, multiple morphologists who tend to specialize by taxonomic group would be required. Unfortunately, both morphological and molecular approaches are subject to various methodological biases. Accurate assessment (both taxonomic composition and abundances) of marine zooplankton assemblages is a critical component of effective ecosystem-based conservation and resource management efforts. To address this need and determine the extent of agreement between methods, morphological data was compared to 454 NGS results for zooplankton assemblages collected in plankton net tows from northern Monterey Bay, California. Results indicate areas of agreement between data sets, but also characterize biases specific to each method. Morphological analyses provided life history stage and biomass information for many zooplankton taxa. The NGS data included 313 bp from the 3' end of the mitochondrial cytochrome-c-oxidase subunit-I (COI; 3234 OTUs) region and 365 bp from the 5' end of the large subunit of the nuclear ribosomal RNA (28S; 1669 OTUs). Results of NGS analysis corroborated the presence of 40 of the 61 morphologically identified genera and species. For some organisms, NGS provided finer taxonomic resolution where morphological data or knowledge was limited. Correlations between biomass and NGS percent sequence abundances were significant for some, but not all taxa, and were gene-specific in some cases (i.e., COI?Diplostraca, Polychaeta, Callianassidae, Clausocalanidae, Oncaeidae, Podonidae, Evadne, Neotrypaea, Oncaea, Podon, Psuedocalanus; 28S?Euphausiacea, Euphausiidae, Oncaeidae, Oncaea). Despite various methodological biases, both data sets were in agreement with respect to alpha diversity indices generated for zooplankton assemblages collected at four sampling stations. These results suggest that a partnership between morphological and molecular methods represents a powerful tool, that when used appropriately, can effectively extend taxonomic assessment capabilities to better address present needs.

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