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Title: Name that Species: The Need for Reference DNA Barcode Databases for Analysis of Zooplankton Diversity using Barcoding and Metabarcoding

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Integrative morphological and molecular approaches to understanding zooplankton diversity require accurate identification of species by taxonomic experts, in parallel with determination of an appropriate molecular marker from identified specimens. After more than two decades, the barcode region of the mitochondrial cytochrome c oxidase I (COI) gene has been sequenced for some members of all major groups of marine zooplankton. A fraction of these sequences are “gold standard” barcodes (i.e., DNA sequences for specimens identified by expert taxonomists, with voucher specimens, and ideally photographs) that allow identification of known species, discovery of new species, and detection of cryptic species. The mitochondrial 16S rRNA gene has been used for similar purposes, especially for cnidarians. Portions of nuclear small- (18S) and large-subunit (24S) rRNA genes have provided group-specific markers (genera, families, or orders). More recently, high-throughput DNA sequencing (HTS) technologies have allowed the development of metabarcoding (i.e., large-scale taxonomic identification of complex samples via analysis of one or more DNA barcode regions). The millions of DNA sequences produced in parallel by metabarcoding can be analyzed to discriminate molecular operational taxonomic units (MOTUs), which may be used to approximate species richness. However, neither DNA barcodes nor MOTUs can be matched to species or other recognized taxonomic units unless there is a reference sequence for that taxon and gene. Geographically- and taxonomically-comprehensive reference barcode databases are critically needed to ensure that barcoding and metabarcoding analyses can discriminate, identify, and name recognized taxonomic units – ideally species – in assessing of zooplankton biodiversity and shifting patterns associated with environmental variability and climate change.

Keywords: DNA Barcode, Metabarcoding, Biodiversity

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