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Title: Metabarcoding analysis of zooplankton diversity: applications for monitoring regional and interannual variation of the pelagic assemblage of the NW Atlantic continental shelf

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Metabarcoding (i.e., large-scale taxonomic identification of a complex sample via the analysis of one or few orthologous DNA barcode regions) shows promise for analysis of biodiversity of marine zooplankton and detection of impacts of climate change. Metabarcoding relies on high throughput DNA sequencing (HTS) to yield millions of DNA sequences that can be analyzed to provide estimations of molecular operational taxonomic units (MOTUs) richness that may approximate taxon richness. We report preliminary results from metabarcoding analysis of the pelagic assemblage of the Northeast US continental shelf ecosystem, using samples from Ecosystem Monitoring Surveys (EcoMon) by the US NOAA Northeast Fisheries Science Center (NEFSC). Samples analyzed spanned three regions (Gulf of Maine, Georges Bank, and Mid-Atlantic Bight) and ten years (2003-2012). The genetic marker used was a hypervariable region (V9) of the nuclear small-subunit (18S) rRNA, which shows consistent patterns of divergence across invertebrate and vertebrate taxa and can reliably discriminate higher taxonomic groups (families and orders). Metabarcoding results were compared to NEFSC data from morphological (microscopic) species identification for a subsample of ~500 zooplankton specimens per sample. Since MOTUs cannot be matched to recognized taxonomic units unless there is a reference sequence for that taxon and gene, expanding the numbers of marine species for which sequences have been determined for identified specimens is critically important. With this caveat, metabarcoding approaches will become increasingly useful to characterize biodiversity of zooplankton assemblages for monitoring and ecosystem based management.

Keywords: zooplankton biodiversity, metabarcoding, environmental sequencing, Northwest Atlantic continental shelf

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