Title: Environmental sequencing and metagenetic analysis of zooplankton diversity: applications for monitoring seasonal and regional variation of the pelagic assemblage of the NW Atlantic continental shelf.

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Environmental sequencing and metagenetic analysis (i.e., the large-scale analysis of taxon richness via the analysis of homologous genes) was used to characterize temporal and spatial patterns of zooplankton biodiversity of the Northeast US continental shelf ecosystem. The genetic marker used was a portion of the nuclear small-subunit (18S) rRNA, which shows consistent patterns of divergence across invertebrate and vertebrate taxa and reliable amplification with consensus primers. The ~325 bp region analyzed discriminated most species, genera, families, and higher taxonomic groups, with accurate classification of novel sequences. Preliminary results are shown for comparative analysis of zooplankton samples collected during Spring 2012 from the Gulf of Maine and Mid-Atlantic Bight as part of the Ecosystem Monitoring (EcoMon) Surveys by the US NOAA-NMFS Northeast Fisheries Science Center (NEFSC). Metagenetic analysis of biodiversity was compared to taxonomic analysis carried out by NEFSC, with morphological (microscopic) species identification for a subsample of ~500 zooplankton specimens per sample. Zooplankton diversity was analyzed in relation to environmental parameters and expected biogeographical patterns (e.g., Gulf of Maine is the southern boundary for many boreal species). The taxonomic complexity of marine zooplankton assemblages makes metagenetic approaches particularly useful to characterize temporal and spatial patterns of variation. Environmental sequencing and metagenetic analysis can provide accurate, high-resolution, and rapid biodiversity assessments for monitoring and ecosystem based management.

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

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