



Conference Abstract

Addressing the "Paradox of the Plankton": Using Metabarcoding to Explore Zooplankton Diversity Patterns Across Chemical Conditions in the Salish Sea

Haila K. Schultz[‡], Carol A Stepien[‡], Julie E. Keister[‡], Emily L. Norton[§], Sean M. McAllister^{§,1}, Beth Slikas^{§,1}

[‡] School of Oceanography, University of Washington, Seattle, United States of America

[§] Cooperative Institute for Climate, Ocean, and Ecosystem Studies (CICOES), Seattle, United States of America

¹ Pacific Marine Environmental Laboratory, National Oceanic and Atmospheric Administration, Seattle, United States of America

Corresponding author: Haila K. Schultz (schulh2@uw.edu)

Received: 23 Feb 2021 | Published: 04 Mar 2021

Citation: Schultz HK, Stepien CA, Keister JE, Norton EL, McAllister SM, Slikas B (2021) Addressing the "Paradox of the Plankton": Using Metabarcoding to Explore Zooplankton Diversity Patterns Across Chemical Conditions in the Salish Sea. ARPHA Conference Abstracts 4: e64847. <https://doi.org/10.3897/aca.4.e64847>

Abstract

Traditional taxonomic analysis of zooplankton is time consuming, expensive, and unable to resolve the true species diversity of a community due to a lack of diagnostic morphological characters for many taxa. This is especially true for early life stages, undescribed, and cryptic species. This limitation has led to a dramatic under-estimation of the incredible diversity of life that inhabits the ocean, hindering our understanding of the environmental conditions that structure communities. Multi-gene metabarcode high-throughput sequencing (HTS) analyses entailing field sampling and bioinformatics offer new means to rapidly and accurately characterize the species identities, diversity, and composition of entire communities. We use multiple diagnostic Illumina MiSeq HTS metabarcode assays (for mitochondrial COI, 16SRNA, and 12SRNA gene regions) and a custom bioinformatics pipeline to analyze communities of invertebrates and fishes from zooplankton net tows collected concurrently with environmental chemistry data across Puget Sound in the southern Salish Sea. We compare results among sites for spring and autumn seasons, as

a prelude to multi-year analyses. Findings show considerable divergence in species composition and diversity among sites and season, reflecting differences in salinity, pH, and proximity to the ocean. This approach has great potential for wide-spread use in monitoring programs to assess the diversity of marine plankton communities in conjunction with changing conditions, including ocean acidification, hypoxia, and global temperature rise.

Keywords

Zooplankton, Ichthyoplankton, Metabarcoding, Puget Sound, Salish Sea

Presenting author

Haila K. Schultz

Presented at

1st DNAQUA International Conference (March 9-11, 2021)