



Conference Abstract

Complexity matters: Evaluating the impact of bioinformatics parameters on eukaryotic MOTU delimitation and taxonomy assignment

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Abstract

Microbial metazoans (e.g. nematodes, copepods, tardigrades and other 'minor' animal phyla < 1mm in size) are ubiquitous and abundant across most ecosystems on earth. In marine sediment habitats, microbial metazoa exhibit high biodiversity but suffer from poor taxonomy and an ongoing lack of reference DNA sequences in public databases. Environmental DNA metabarcoding thus represents an increasingly critical tool for rapidly assessing the global biodiversity and phylogeographic patterns of such neglected metazoan groups. However, there are significant bioinformatics hurdles facing the study of microbial eukaryotes. Most software pipelines and databases have been designed and optimized for smaller (e.g. bacteria/archaea) or larger (e.g. vertebrate) taxa, and emphasize "standard" metabarcoding loci such as COI which are not useful for groups such as nematodes which lack universal COI primer binding regions. In addition, the sparsity of public reference barcodes for microbial metazoa often precludes accurate taxonomy assignments for unknown MOTUs in metabarcoding datasets. Here, I will present recent work focused on the refinement of bioinformatics workflows for microbial metazoan groups, including efforts to account for intragenomic variation observed in rRNA loci, discrepancies in results across OTU vs. ASV generation pipelines, and biases in sequence-based taxonomy assignment methods.

Keywords

metabarcoding, microbial metazoa, nematodes, 18S rRNA, bioinformatics, eDNA, marine habitats

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