

Global patterns of diversity and phylogenetic community structure in free-living Nematodes: a metabarcoding meta-analysis

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Abstract

Identifying and understanding patterns of biological diversity is crucial at a time when even the most remote and pristine marine ecosystems are threatened by resource exploitation such as deep-seabed mining. Metabarcoding provides the means through which to perform comprehensive investigations of diversity by examining entire assemblages simultaneously. Nematodes commonly represent the most abundant infaunal metazoan group in marine soft sediments. In this meta-analysis, we compiled all publicly available metabarcoding datasets targeting the 18S rRNA v1-v2 region from sediment samples to conduct a global-scale examination of nematode Amplicon Sequence Variant (ASV) alpha diversity patterns, evolutionary distinctiveness (ED) and phylogenetic community structure at different depths and environments. We found that nematode ASV richness followed a parabolic trend, increasing from the intertidal to the shelf, reaching a maximum in the bathyal and decreasing in the abyssal zone. No depth- or environment-specific assemblages were identified as a large fraction of genera were shared. Contrastingly, the vast majority of ASVs were unique to each environment and/or depth zone; genetic diversity was thus highly localised. The intertidal and abyssal samples had the highest ED values, indicating that both a dynamic, fluctuating ecosystem, as well as a relatively stable yet very old one, can produce highly diversified assemblages. Overwhelmingly, nematode ASVs in all environments exhibited phylogenetic clustering, pointing to environmental filtering as the primary force defining community assembly rather than competitive interactions. This finding stresses the importance of habitat preservation for the maintenance of marine nematode diversity.

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