

{rokbox title=|Sample locations for Tara Oceans and Malaspina global expeditions :: Image: Authors| thumb=|images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-ieo-csic-assessing-patterns-metazoans-global-ocean-using-environmental-dna-geraldi-et-al-2024-thumb.jpg|} images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-ieo-csic-assessing-patterns-metazoans-global-ocean-using-environmental-dna-geraldi-et-al-2024.jpg{/rokbox}

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Caterina R. Giner, Santiago Hernández León, Ramiro Logares, Ramon Massana, Pablo Sánchez, Vladimir Bajic, Takashi Gojobori and Carlos M. Duarte, 2024.

[Assessing patterns of metazoans in the global ocean using environmental DNA](#)

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Abstract: Documenting large-scale patterns of animals in the ocean and determining the drivers of these patterns is needed for conservation efforts given the unprecedented rates of change occurring within marine ecosystems. We used existing datasets from two global expeditions, Tara Oceans and Malaspina, that circumnavigated the oceans and sampled down to 4000 m to assess metazoans from environmental DNA (eDNA) extracted from seawater. We describe patterns of taxonomic richness within metazoan phyla and orders based on metabarcoding and infer the relative abundance of phyla using metagenome datasets, and relate these data to environmental variables. Arthropods had the greatest taxonomic richness of metazoan phyla at the surface, while cnidarians had the greatest richness in pelagic zones. Half of the marine metazoan eDNA from metagenome datasets was from arthropods, followed by cnidarians and nematodes. We found that mean surface temperature and primary productivity were positively related to metazoan taxonomic richness. Our findings concur with existing knowledge that temperature and primary productivity are important drivers of taxonomic richness for specific taxa at the ocean's surface, but these correlations are less evident in the deep ocean. Massive sequencing of eDNA can improve understanding of animal distributions, particularly for the deep ocean where sampling is challenging.

Keywords: deep sea, diversity, global abundance, metabarcoding, metagenome, metazoan