



Conference Abstract

Circumglobal distribution of fish environmental DNA in coral reefs

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Abstract

Coral reefs host the highest fish diversity on Earth despite covering less than 0.1% of the ocean's seafloor. At the same time they are also extremely threatened. Data syntheses over decades of surveys estimate the total number of coral reef fishes to vary from 2,400 to 8,000 species distributed among roughly 100 families. But this diversity remains largely unknown.

Here, we investigated how environmental DNA (eDNA) could describe the distribution of fish diversity in coral reefs. We generated 504,457,267 raw 12S ribosomal DNA (rDNA) sequence reads from 251 samples (2,693 PCR replicates) collected at 25 sites in 145 stations covering five regions across the Indian, Pacific and Atlantic Oceans. Bioinformatic analysis clustered these sequences into 2,160 molecular operational taxonomic units (MOTUs) corresponding to distinct species (Marques 2020) We compared our results, with visual census surveys from Reef Life Survey, on 2,813 transects in tropical regions.

Our outcomes demonstrate the capacity of eDNA metabarcoding from water samples to reconstruct well-known biogeographic patterns of fish diversity on coral reefs, such as species richness gradients towards the coral triangle, and family proportion stability across sites (Bellwood and Hughes 2001). Additionally, eDNA survey data documented a higher fish species (16%) and family (50%) diversity than estimates obtained with underwater visual surveys carried out on 20 times more sites. MOTU richness per family retrieved with eDNA closely matched fish species richness within families recorded in visual census data. However, eDNA revealed higher richness of reef-associated species and species from adjacent habitats, of cryptobenthic or nocturnal species, but also of pelagic and wide-ranging species. eDNA survey data showed that fish diversity is characterized by spatially heterogeneous species assemblages among regions, with more dissimilarity among adjacent coral reefs than detected with visual survey data. Unlike visual surveys, eDNA metabarcoding revealed the same prevalence of rarity as expected under the neutral theory of biodiversity, suggesting the predominance of random processes and ecological equivalence within trophic groups at large scale to explain fish biodiversity patterns on coral reefs. Our study demonstrates how sequencing eDNA from water provides a rapid and effective approach to characterize and assess coral reef diversity across large spatial scales, thereby also uncovering hidden biodiversity patterns.

Keywords

MOTUs, Coral reefs, eDNA biodiversity assessment, marine fish

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