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Conference Abstract

Environmental DNA diffusion of reef fishes along a distance gradient from four isolated islands of the Western Indian Ocean

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Abstract

Islands have traditionally served as model systems to study ecological and evolutionary processes (Warren et al. 2015) and could also represent a relevant system to study environmental DNA (eDNA). Isolated island reefs that are affected by climatic threats would particularly benefit from cost- and time-efficient biodiversity surveys to set priorities for their conservation. Among time efficiency methods, eDNA has emerged as a novel molecular metabarcoding technique to detect biodiversity from simple environmental samples even in remote marine environments. However, eDNA monitoring techniques for marine environments are at a developmental phase, with a few remaining unknowns related to DNA residence time and movement. In particular, the redistribution of eDNA, via

ocean currents, could blur the composition signal and its association with local environmental conditions (Goldberg et al. 2016). Here, we investigated the detection variation of eDNA along a distance gradient across four islands in the French Scattered Islands. We collected 30 L of surface water per filter at an increasing distance from the islands reefs (0m, 250m, 500m, 750m). Using a metabarcoding protocol, we used the teleo primers to target a fraction of 12S mitochondrial DNA to detect Actinopterygii and Elasmobranchii. We then applied a sequence clustering approach to generate Molecular Taxonomic Units (MOTUs), which were assigned to a taxonomic group using a reference database. By assigning eDNA sequences to species using a public reference database, we classified species according to their preferred habitat types between benthic/demersal and pelagic. Our results show no significant relationship between distance and MOTUs richness for both habitat types. By using a Joint Species Distribution Modelling approach (JSDM, Hierarchical Modelling of Species Communities), we retained the multidimensional information captured by eDNA and detect species- and family-specific responses to distance (Fig. 1). We showed that benthic MOTUs were found in closer proximity to the reef, while typical pelagic MOTUs were found at greater distances from the reef. Hence, MOTU-level analyses coupled with JSDM were more informative that when aggregating it into coarser richness. Altogether, our eDNA distance sampling gradient detected an ecological signal of habitat selection by fish species, which suggest that eDNA could help understand the behavior of species and their distribution in marine environments at a fine spatial scale.
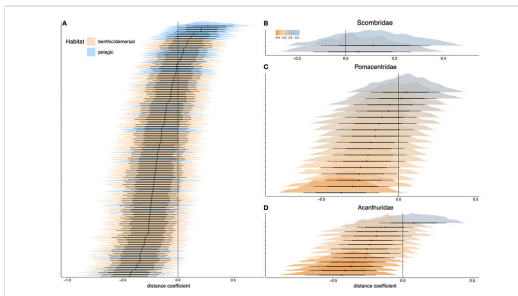

Figure 1. doi

Effect of distance on occurrence probability of MOTUs detected by eDNA. MOTUs occurrence probability was modelled using Hierarchical Modelling of Species Communities statistical framework, enabling us to estimate a separate distance coefficient for each species. (A) Overall effect of distance for all 143 MOTUs, (B) a subset of pelagic MOTUs from the family Scombridae, (C) mixed habitat MOTUs from the family Pomacentridae, and (D) benthic/demersal MOTUs from the family Acanthuridae. In (A) species coefficient estimates are coloured by pelagic (blue) and benthic/demersal habitat type (orange), in (B-D) colour represents the effect of distance. A total of 1000 posterior estimates were calculated for each MOTUs. Each line represents an MOTUs with coloured histograms showing the 95% confidence intervals of parameter posterior estimates. Points represent the median of the posterior estimates and thick solid lines and thin solid lines represent the 60% and 80% confidence intervals, respectively. The vertical line represents the reference point to determine coefficients significance.

Keywords

biodiversity, biomonitoring, environmental DNA, diffusion, spatial extent, island, coral reef

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