Are we using eDNA metabarcoding to its full potential?

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In less than a decade, environmental DNA (eDNA) metabarcoding (the simultaneous identification of multiple taxa using DNA extracted from an environmental sample, like water) has rapidly come to the fore in biodiversity monitoring. Despite this rapid rise and widespread use, it is important to note that the field is still in its infancy. There is still much to learn, from how we define and use the term 'eDNA' (Pawlowski, Apothéloz-Perret-Gentil, & Altermatt, 2020; Rodriguez-Ezpeleta et al., 2021) to our understanding of how DNA from individual species originates, persists and is transported in the environment (Barnes & Turner, 2016). Nevertheless, the appeal to fisheries scientists and managers of using eDNA data is undoubtedly strong, and for many good reasons (Gilbey et al., 2021). Studying the marine environment and its biodiversity is logistically challenging and translating findings into robust conservation and management plans is often even more difficult. Yet, this is also crucial, as we attempt to move towards Ecosystem-Based Fisheries Management (Pikitch et al., 2004). We now know that eDNA metabarcoding offers a reliable and rapid snapshot of the biodiversity present in a sampled system, compares favourably with conventional sampling methods in terms of species detections and is cost-effective (McElroy et al., 2020). While there is now an obvious push towards investigating if eDNA can be used to accurately assess the relative abundance of species (Levi et al., 2019) in different environments/systems (the 'Holy Grail of eDNA', if you will!), is there more that eDNA data can do in aiding marine sustainability beyond describing richness and differences in species communities?

A paper published in this issue (D'Alessandro & Mariani, 2021) shows us that one novel way in which we can use eDNA metabarcoding data is to reconstruct marine food webs in multiple systems. Conventional methods for surveying marine food webs (e.g. stomach content analysis) are typically laborious, expensive and destructive/invasive, meaning that relatively few marine ecosystems are well-studied. As D'Alessandro and Mariani (2021) rightly affirm in their paper, we will be able to effectively respond to the impact on productivity and ecosystem services due to rapid change only if we are able to monitor such changes closely, efficiently and – above all – quickly. Environmental DNA metabarcoding might well be the right tool to facilitate this. Can we use eDNA metabarcoding to determine not just which species are present, but also estimate species interactions? Using previously published eDNA metabarcoding datasets, the authors attempt to reconstruct the trophic webs of different marine habitats: by combining the results with a thorough examination of the literature, the authors obtain estimates of the trophic relationships that fit within expectations in these habitats. The areas examined are tropical (Bahamas, Turks & Caicos and Jamaica, with an increasing degree of anthropogenic impact), cold temperate (New Zealand) and polar (Canadian Arctic).

Tropical trophic webs' complexity (number of nodes) was highest compared to the colder areas, and within the tropical locations, reflected the different levels of anthropogenic impact, with the highest number of nodes (34) in the Bahamas and the lowest (23) in Jamaica. Overall, results seem to be more encouraging/accurate for the tropical locations rather than the polar one. This is likely the result of the inherent knowledge gaps for the colder regions of the oceans, both in terms of biodiversity assessment and knowledge of their trophic ecology.

Although these overall trophic relationships presented in D'Alessandro and Mariani (2021) are simplified approximations, these inferences are importantly obtained within a short timescale and using pre-existing data. This study also highlights the importance of 'open science', whereby all associated data from the rapidly growing field of eDNA monitoring is made freely available and can be re-purposed to address novel questions. Moving forward, using such pre-existing and/or newly generated eDNA metabarcoding data for trophic ecology would require validation and optimisation (e.g. using dietary analysis) to more accurately infer potential ecological relationships. However, the authors' aim, with this pilot study, is to show us what can be achieved with the data we already have, if we think outside the box. Imagine the advantage of being able to sample seawater, metabarcode it, and produce a dataset which can simultaneously answer questions about species compositions and their interactions, and perhaps even, relative abundances within marine ecosystems. Monitoring of ecosystem and species diversities, and trophic level balance have been indicated amongst the most important objectives needed for the implementation of ecosystem-based fisheries management principles (Gislason, Sinclair, Sainsbury, & O'boyle, 2000), and for the 'balanced exploitation' of marine resources (Zhou et al., 2010), hence such approach could potentially be transformative to help achieve and maintain fisheries sustainability targets and ensure marine ecosystem functioning in the future.

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