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854 Words

Community Ecology and eDNA

One of the more difficult parts of studying ecology is attempting to account for organisms that you can’t see such as microbes or elusive species. While methods such as growing cultures, wildlife cameras, and general observation are often used, these methods may only be providing a part of the picture. Through the use of eDNA, or environmental DNA, genomic and metagenomic techniques, two studies examining the diversity and richness of two organisms were able to compose a more complete picture to help understand the complex web of organisms in the oceans.

One study focused on understanding the structure and function of the oceans’ microbiome in comparison to the microbiome of the human gut. In this study they sequenced whole organisms and organized them to the phylum level. This is important since too high of a resolution would have made it difficult to find a pattern, so instead of species they grouped microbes based on phylum. They were able to identify a “functional core” in the genome of oceanic as well as the gut microbiome. In addition, they found that there was a lot of functional redundancy, which could help make this community resilient to changing climate and other anthropogenic stressors since if one phylum dies another will be there to replace it. While they examined a number of environmental variables such as dissolved oxygen, depth, salinity, temperature, nutrients, etc, they found that species richness was correlated with temperature (where it increases until 15 C where it significantly decreases) and depth (where organisms in the mesopelagic were significantly different from those in the epipelagic and DCM). While they collected samples from around the world, they unfortunately missed Indonesia and Australia, as well as the coral triangle.

The second study, which took place in New Caledonia, an island near Australia, compared a variety of methods to determine diversity of sharks in a given area. They compared the methods of eDNA, baited remote underwater video (BRUVs), and underwater visual census (UVCs) to barcode/detect a variety of shark species for the given area. They focused on identifying to the species level since, unlike the microbes, each shark species has uniquely evolved to serve a specific purpose. Unlike the microbes, when a shark species dies there isn’t a back-up species. Even if there is a similar species, this disappearance would still cause a significant shift in the ecosystem that would take time to rebalance. They found that the eDNA detected 44% more shark species than the traditional methods, which provides another tool for assessing the diversity and stability of an ecosystem. While eDNA is extremely useful for determining whether a species of shark is was present in the area, it unfortunately cannot give any other information other than presence. As a result, they concluded that this is helpful for uncovering an accurate measure of species diversity, but in order to gain the overall status and health of the species they need to continue using traditional methods. However, at least with the methods combined they should have a better idea of species range and what species they should be looking for. Another unfortunate issue with this study was they only collected data for 3 months. This is problematic since many marine mega-fauna tend to migrate seasonally. At which point they may be overestimating or underestimating the species diversity and richness for the area. With more consistent monitoring, we can start to understand and decode potential migration patterns for these larger pelagic animals. However, this too would be difficult since eDNA only lasts for a couple days. In addition, another issue with this study is they didn’t give specific environmental variables that they were examining and simply looked at disturbed vs non-disturbed areas. Especially since this area tends to be a hot spot for fishing (both shark fisheries and fish fisheries), they definitely could and should have included these variable into their analysis, along with temperature, which is a large issue in these areas since it damages the reef which could be problematic for the sharks. However, it is possible that for the purpose of this study they simply wanted to focus on if they could detect more species with fewer analyses/less sampling effort, which they did. For this reason, I feel that the next step should be integrating these environmental variables more in future studies.

I believe both studies provide evidence supporting the need for more eDNA analysis. While these studies focused on marine organisms, I am curious to know more about terrestrial and coastal ecosystems and how eDNA would be collected from these areas as well. While eDNA has been around for a couple decades, it’s value and popularity has begun to increase. With this type of analysis, along with current conventional methods, we can gain a more accurate analysis of ecosystems and the species that inhabit them. While it has many drawbacks, indicated in the paragraph above, it can accurately detect the presence of a species which could solve the issue of monitoring elusive species such as the blue whale and sharks, which like many species are hard to track.