BIO594 – Summary

Topic: Community ecology, eDNA, and microbial genomics

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This summary will provide an overview about two papers: Boussarie et al. 2018 (BO) and Sunagawa et al. 2015 (SU). BO describes the potential to increase sampling detection while minimizing sampling effort of assessing shark diversity by comparing eDNA metabarcoding with traditional baited remote underwater video station (BRUVS) and underwater visual census (UVC) survey methods. SU used the dataset from *Tara* Oceans, a unique mass sampling of oceanic water from multiple depths and environments globally, to characterize microbial genetic diversity. Both papers use metabarcoding techniques to answer very different questions. BO used metabarcoding to determine the presence or absence of sharks in New Caledonia and compared the results to other tedious methods. SU used metabarcoding to determine the microbiome of the ocean and how the changes are largely determined by temperature. To synthesize these papers, I will pose and address the following questions: (1) what are the advantages of using metabarcoding techniques in these papers and (2) what are the disadvantages of metabarcoding in these papers.

*What are the advantages of using metabarcoding techniques?*

In the BO paper, they conclude that eDNA approaches requires less sampling effort and a more sensitive detection of shark species when compared to BRUV and UVC detection. The authors suggest that eDNA samples are able to detect over a longer period of time, and a larger area, potentially increasing the detection of biodiversity. BRUVS and UVC are highly depended on personnel expertise and environmental conditions, such as visibility. Additionally, eDNA is a discreet, non-biased way of determining biodiversity, as it does not promote any behavioural responses that may bias presence or absences of a species. In the SU paper, metabarcoding is a necessity to analyse microbial communities over many samples. By utilizing a metabarcoding approach, the authors were able to characterize the ocean microbiome, determine the taxonomic breakdown, and functionality of the microbes from a wide array of samples. With this large data set of 68 global locations in epipelagic and mesopelagic waters, SU determined that the ocean microbiome is stratified by depth and is largely driven by differences in temperature.

*What are the disadvantages of using metabarcoding techniques?*

Although metabarcoding has been showcased to be a very powerful tool in community ecology, caveats are still present with these techniques. In relation to eDNA and the BO paper, the detection of a signal cannot provide any characteristics or history of that organism. The organism that provided that signal may be from a decaying individual from a nearby location, or potentially biased by human influences such as bait for fishing. Additionally, a negative signal may not necessarily mean that the organism is not present, as organisms have different rates of “shedding”, thus differing decay times of DNA that may not be detected using eDNA. Therefore, this type of data has to be carefully framed when presented to policy makers and management of marine protected areas.

For metabarcoding to be successful, a large database or library has to exist to identify the individuals of the community of interest. For example, SU utilized a pre-existing, publicly available ocean metagenomic and reference genomes to create their own *Tara Oceans* metagenomic dataset. With non-model organisms, such as marine invertebrates, this may be difficult to execute, as there are many species that have not been fully sequenced. Additionally, determining the genes of interest may be crucial when comparing orthologs. By being so reliant on reference databases, this may pose a challenge to using eDNA and metabarcoding without controls or references (i.e. BRUV and UVS surveys).

When using metabarcoding techniques, standardized protocols must be followed to ensure necessary quality control methods. BO was very explicit in the methods about how they followed strict sampling methods to reduce contamination while sampling and extracting the DNA. Additionally, negative controls were used during the extraction and PCR steps to ensure no contamination was present. As eDNA metabarcoding is becoming more popular, there has been an increase in literature to create global standardized protocols to reduce contamination and avoid sampling bias. Presently, eDNA can only be relatively used to represent presence or absence of a species, as the currently sampling methods cannot confirm metrics such as size, abundance, or age of the species of interest.

In summary, BO and SU used metabarcoding techniques to understand the community of unknown water samples. BO utilized an eDNA approach to determine the presence of shark species in New Caledonia and compared it to BRUV and UVC methods. SU used metabarcoding to uncover the global ocean’s microbiome and epipelagic and mesopelagic layers to understand the drivers behind marine microbial dynamics. eDNA metabarcoding is a useful tool for determining the community of a large sample and has much promise for biomonitoring techniques.