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750-1000 Summary 5

Symbiosis

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Boussarie, G., Bakker, J., Wangensteen, O. S., Mariani, S., Bonnin, L., Juhel, J. B., ... & Vigliola, L. (2018). Environmental DNA illuminates the dark diversity of sharks. *Science advances*, *4*(5), eaap9661.

Sunagawa, S., Coelho, L. P., Chaffron, S., Kultima, J. R., Labadie, K., Salazar, G., ... & Cornejo-Castillo, F. M. (2015). Structure and function of the global ocean microbiome. *Science*, *348*(6237), 1261359.

Boussarie et al aim to address the gap in knowledge regarding whether megafauna populations are truly declining or if the population aren’t being detected by classic sample efforts. Populations of sharks can still be present in an environment, but not appear in great numbers in an ecological survey. Megafauna like larger shark species can be difficult to detect at all, and therefore hard to be confident in the estimates of population sizes. The lack of basic ecological data thus limits the potential for effective conservation management. There is a clear need for advanced ecological survey methods like environmental DNA due to the challenges of classic surveys for low-density, mobile species like sharks. Environmental DNA (eDNA) involves taking several liters for a water sample from a certain area in order to sequence the fragments of DNA in the water sample. This method is able to tell you what organisms were present in that area within a certain time frame, estimated between hours to days. Boussaire directly compared the biodiversity found in the eDNA samples with the underwater visual census (UVC) and the remote underwater video stations (BRUVS) survey methods in order to understand which method would provide the most accurate results.

This study found that sampling via eDNA was significantly more effective to detect shark species compared to traditional underwater visual censuses and videos recordings. Human presence is thought to heavily impact traditional survey methods, which was supported by the data presented by this research team. Shark species that were previously unobserved in human impacted areas were found in environmental DNA from the water samples in that area. eDNA samples that were barcoded with the COI gene suggest that previous techniques were overestimated the “dark diversity” of sharks in New Caledonia because the water samples showed an increase in number of shark species captured. However this method has potential drawbacks, like the overestimation of species richness if the water currents are carrying DNA samples to locations on the reefs that aren’t representative of that organism’s habitat. Environmental DNA differed in human impacted areas compared to the “wilderness” areas, but the UVC and BRUVS results did not. The authors suggest this could be an avoidance behavior from sharks not entering impacted areas. This conclusion has the potential to heavily influence management strategies and this measure could be used a proxy for address how human presence impacts the distribution of sharks. The authors sued rarefraction curves to show diversity of species seen compared to sampling efforts associated with each sampling survey. This metric showed that eDNA could mark a difference between “unseen diversity” and “dark diversity”. Based on this, the authors conclude that a few hundred eDNA samples could accurately depict an area’s diversity. Another drawback of using environmental DNA is that the dataset is only as reliable as the database in which sequenced samples are compared to. This study had trouble sequencing one of the sharks that were seen in visual surveys, so even if the DNA fragments were present in the water sample, sequencing was unable to detect it.

This paper highlights the potential advantages and caveats of using environmental DNA to sample an area. The more efforts in this field, the better the methods will become which will diminish the number of caveats associated with eDNA. The paper calls for an increase in the use of environmental DNA as a standard sampling method because of the high yield of biodiversity found in the water samples compared to traditional methods. As well as an urgent need for conservation efforts specifically targeted at elusive species and populations.

Using similar methods, Sunagawa et al sampled microbial communities from 68 locations across the world to create a novel database of marine viruses, prokaryotes, and picoeukaryotes. This massive effort to use metagenomics combined with environmental data to analyze locations well distributed across the globe provides novel information about the diversity and patterns of microbiome in a diverse location set. Sunagawa used similar data visualization methods to Boussarie, including rarefraction curves, bar, and pie charts to show the levels of biodiversity within all of the samples. Samples were preserved to identify morphology of each individual in the water sample to serve as a comparison like Boussarie had the BRUVS and UVC data. The research team sequenced the samples with the 16s RNA gene and mapped these OTUs, and results suggested that the metagenomes captured by this study had already been sequenced with 16s. The authors then found a negative correlation between temperature and species richness, and that dissimilarity between OTU samples increased with distance. The authors used PCA to display that depth was the main factor in stratification based on the 16s data. Additionally, with the subset of prokaryotic species, the authors showed that temperature was the main driver of stratification in the marine microbial community. Surprisingly, the authors found that around 70% of the organisms found in the marine ecosystems sampled are also found in the human gut.