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How can we track life in the ocean?

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Abstract

Have you ever tried to count all the different species in a pond? It's very hard, especially when you try to find all the tiny animals hiding among the weeds. Now, imagine if you wanted to count all the species in the sea! Scientists struggle to monitor life in the ocean, because it is so vast and deep. Yet we need to know exactly what's down there in order to protect it.

We wanted to use the bits of DNA that organisms leave behind in their environment to work out which species were present. This is called *environmental DNA (eDNA)*. We looked at interactions between different life forms in Monterey Bay, California. We also looked at how they responded to seasonal and environmental change.

We found that different species were present throughout the year. Warmer waters changed what was there. We also found that certain species (such as humpback whales – see Fig. 1) can be especially useful for telling us about the environment. Environmental DNA proved to be an exciting new method for tracking and protecting life in the ocean!

Introduction

Do you know that around a third of species living in the ocean might soon be extinct? This problem is called loss of *biodiversity* and is often caused by human activities such as overfishing. Scientists have been trying to keep track of biodiversity in the ocean for a long time, but it hasn't been easy!

Traditionally, scientists have used a method called visual assessment: for example, divers count the different species of fish they see when on a dive. This relies on a bit of luck and only counts what's there at that time. As the climate warms and *ecosystems* change, we urgently need a better way to track biodiversity. So how do we get a full picture of what lives in an ecosystem?

In recent years, scientists have been using environmental DNA (eDNA) to identify all the species present in an ecosystem. Wherever life forms are present, they leave DNA behind them. This includes everything from whales to tiny microbes. By taking samples from a habitat and seeing what DNA is there, we can see what lives in that habitat.

We wanted to see whether we could use eDNA to investigate:

1. The interactions between different groups of animals (known as *taxa* – sea lions are one such group, for example) at different levels of the food web.
2. How biodiversity within an ecosystem responds to environmental change over time.

Figure 1:
Humpback whales we spotted during our fieldwork in Monterey Bay National Marine Sanctuary.

Methods

We collected seawater samples from the Monterey Bay National Marine Sanctuary in California. We did this eight times between April 2015 and December 2016. We lowered a *rosette* with water collection bottles (Fig. 4) from our boat at a depth of between zero and one meter. We then filtered the water and flash froze the filters in liquid nitrogen to keep them at a chilly -80°C! At the same time, we recorded information such as water temperature and the amount of *chlorophyll*.

We then took our samples back to the lab and extracted the DNA. Each species has its own unique DNA "barcode". We used this to work out which species were present in the water. Each barcode contains a *conserved region* – this tells us broadly what it is, for example, a mammal or bacteria. There's also a *variable region* which we use to identify the species (Fig. 2).

We then grouped taxa into communities that had similar changes in numbers over time. This could be because of a predator-prey interaction. For example, when the numbers of copepods (a small type of crustacean) increased in winter, so did the numbers of Pacific jack mackerel (which eat them!). We used this to look at how biodiversity changed over the seasons and across different levels of the food web known as *trophic levels*.

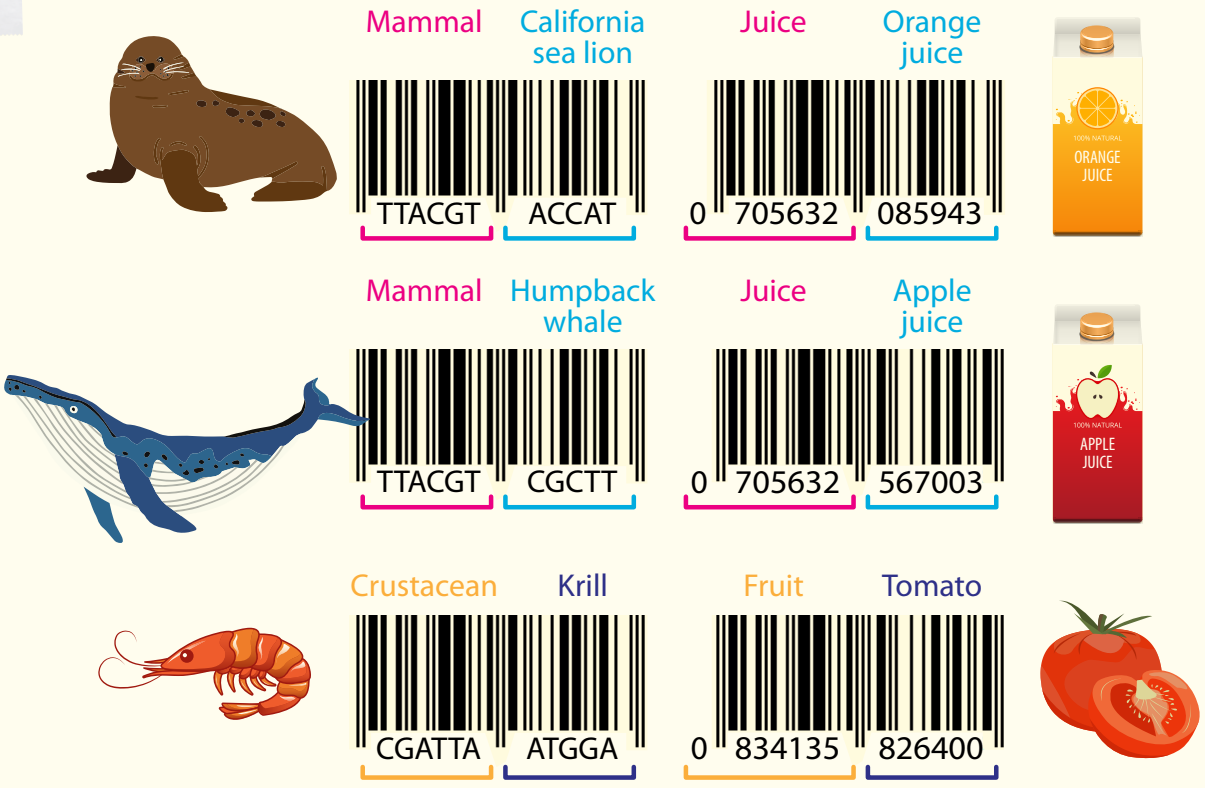


Figure 2:
We catalog species' DNA with barcodes using the same principle as with items in a grocery store. The first part of the "barcode" (called the conserved region) shows the "type" e.g. marine mammal, or juice carton. The second part of the barcode (called the variable region) shows the exact species e.g. California sea lion vs. humpback whale or orange vs. apple juice. Notice how different "types" have different conserved regions - e.g. marine mammals vs. crustacea; juice cartons vs. fruit.

We looked for four conserved regions in our samples, targeting all types of marine life. By doing this, we made sure we identified the greatest amount of biodiversity.

Results

We identified 348 different marine animal, plant, and microbial taxa in our samples. We found six different communities that increased during specific seasons. The autumn and winter communities were most sensitive to environmental changes (Fig. 3).

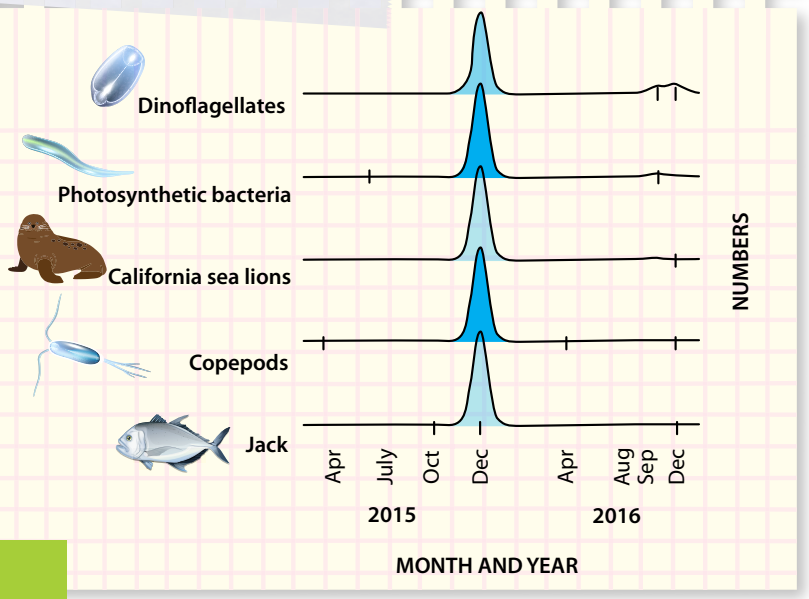
- The winter community was influenced by chlorophyll levels. When chlorophyll levels were higher, this community changed.
- The autumn community was influenced when the water temperature was higher than usual (14°C and above). There were more *phytoplankton* when it was warmer. Phytoplankton produce oxygen but some species can cause harmful *algal blooms*.

There were also interactions between taxa from different levels of the food web:

- We found strong links between the California sea lion (a top predator) and the Pacific jack mackerel (its prey). The numbers of each of these animals had a strong effect on the other.
- Humpback whales (a top predator) were the most highly connected taxa. This meant they influenced and are influenced by lots of other animal groups. They were also the most sensitive to temperature change.

We also detected unusually warm waters during an *El Niño* event in autumn 2015 and 2016. This caused further changes in biodiversity between the years.

Figure 3:
The numbers of some of the winter community taxa over time.



Apart from winter 2015, when else did the numbers of dinoflagellates increase?

Discussion

Our results are important for all marine ecosystems in the world. Our study was the first to show that we can use eDNA to investigate changes in biodiversity within a whole ecosystem. Using eDNA we were able to gain a full picture of marine biodiversity over time – from microbes to mammals!

Other studies have shown that eDNA can help to identify species that *look* the same as other species (but are in fact different!). This may not have been possible using traditional biodiversity assessments. In our study, we were also able to identify new interactions between taxa and their environment.

Using eDNA we identified highly connected taxa such as humpback whales. These species had lots of interactions with other species and were the most sensitive to environmental change. They could act as early indicators of ecosystem change following events such as El Niño or human disturbances. We can protect biodiversity by monitoring these species in long-term programs (such as the Marine Biodiversity Observation Network – MBON).

Conclusion

Biodiversity in our oceans continues to change as the climate warms. Using eDNA we can work out which species live in an area without ever having to see or disturb them. By simply sampling the water we can detect the presence of a rare species. By showing that they are present, we can push for their protection!

But what can you do to help protect our oceans?

- Organize a 'beach clean-up' to clear plastic waste from your local beach.
- Use alternatives to plastic, like paper, wood, and glass products.
- Don't dump harmful substances down your drain, e.g. oil and cleaning chemicals. These end up in our oceans and damage marine life.
- Never release aquarium pets into the sea. They can harm other species.

Check your understanding

1. Human activities such as fishing can cause loss of biodiversity. Can you think of any other ways in which humans threaten life in the ocean?
2. What is the difference between a conserved and a variable region of DNA?
3. We found strong interactions between California sea lions and Pacific jack mackerel – why might this be?
4. Why could it be especially useful to monitor species such as humpback whales?
5. Why is it important to protect marine biodiversity?

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Marine Biodiversity Observation Network (MBON)
https://ioos.noaa.gov/project/bio-data/

Glossary of Key Terms

Algal blooms – a sudden growth of algae in a marine or freshwater environment. They usually color the water either green, brown, or red. Overgrowth of algae can be caused by chemicals from farming entering the water and rising ocean temperatures, among other things. A lot of algae can lead to lower oxygen levels in the water, harming marine life.

Biodiversity – the number of different living things in an area and how balanced their numbers are. This includes how many different types of organisms there are within and between species. Generally, the more biodiverse an ecosystem is, the healthier it is.

Chlorophyll – the green pigment in plants, algae, and cyanobacteria. High chlorophyll measurements can indicate algal blooms in the marine environment. (See *algal blooms.*)

Conserved region – a part of DNA that is identical or very similar in different species (see Fig. 3) of the same type.

Ecosystem – a community of interacting organisms and their non-living environment. For example, a coral reef ecosystem is made up of corals, non-living rock structures, and the species which live in or around them.

El Niño – a climatic change, characterized by unusually warm, nutrient-poor water, typically in late December.

Environmental DNA (eDNA) – the genetic material left behind in the environment (for example, in seawater) by an organism when it sheds skin, mucus, or produces waste.

Phytoplankton – microscopic plants that live in the sea. Phytoplankton are important photosynthesizers (plants that take in carbon dioxide and produce oxygen) – approximately half of the oxygen in every breath you take comes from phytoplankton! However, some species can cause harmful algal blooms (see *algal blooms*).

Rosette – a piece of equipment containing a circular array of sampling bottles to collect seawater (Fig. 4). Sensors can be attached to measure how salty the water is, its temperature, and its depth.

Taxa – the members of any particular taxonomic group. Taxonomy is a way of classifying animals into groups based on shared characteristics. For example, a particular family such as the Hominidae (the "great apes") contains *Homo sapiens* (us), *Pongo* (orangutans), and others. Taxa can be as narrow as a certain species or as broad as a whole group of animals, e.g. mammals.

Trophic level – a level in a food web defined by the method of obtaining food. For example, an autotroph produces its own food, whereas a herbivore eats plant material.

Variable region – a part of DNA that is different between different species and can be used to identify that specific animal (Fig. 3).

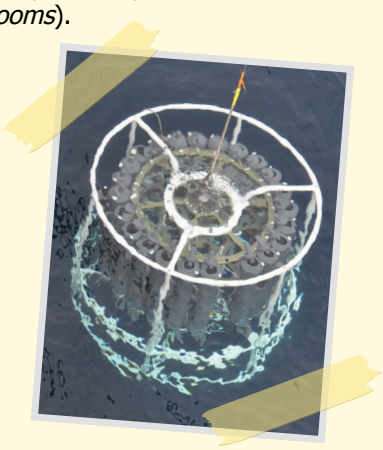

Figure 4:
The rosette we used to collect samples of seawater.

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