Environmental DNA (eDNA) Project

Summary in plain English

1 Introduction

Since 2022, the Plymouth Ocean Science Voyage (POSV) is an annual event aboard the sail training tall ship Pelican of London (Figure 1). Around 24 students from Plymouth and the region come on board for a sail training adventure, personal development and experiential learning about environmental science, research procedure and sustainability. Showcasing state-of-the-art scientific instrumentation and technology is integral part of this voyage, and this year, we included environmental DNA (eDNA) sampling.

eDNA is the genetic material outside an organism, for example in the air, soil or water and includes DNA from cells, mucus, tissues, bodily fluids and excrement. It is a non-invasive method to assess biodiversity, ecosystem health, monitor threatened or invasive species, and evaluate water quality or aquaculture site compliance.

The aims of this small pilot study were to:

1) demonstrate how water sampling and molecular methods can be used to detect vertebrate biodiversity in marine environments,
2) contribute to an expanding data set of eDNA data in locations of scientific and conservation interest, including Plymouth Sound National Marine Park,
3) inform conservation organisations of presence or absence of species of interest, and
4) evaluate whether utilising eDNA metabarcoding as an educational tool adds value to ocean science education integrated into sail training.

Figure 1 Pelican of London under sail. © Pelican of London.

The project was funded by the marine conservation organisation Sea-Changers and by Challenging Habitat Outreach.

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2 Method overview

2.1 eDNA sampling and processing

During the 2025 POSV, two environmental DNA (eDNA) samples were collected, one off the entrance to Lulworth Cove, Dorset (21/09/25), and one in Cawsand Bay, Cornwall (01/10/25) (Figure 2). At each location, the datum depth was around 12 m. An inDepth sampling device (Figure 3), pre-programmed by Applied Genomics to sample for a full tidal cycle, was fitted with a new filter cartridge and attached to a harness. The assemblage was activated and lowered into the water column to 4 m depth and left to pump water across the filter overnight (12.25 hours). Following retrieval, DNA preservative was added to the filter cartridge, which was sealed, stored in the dark and shipped for DNA analysis to Applied Genomics.

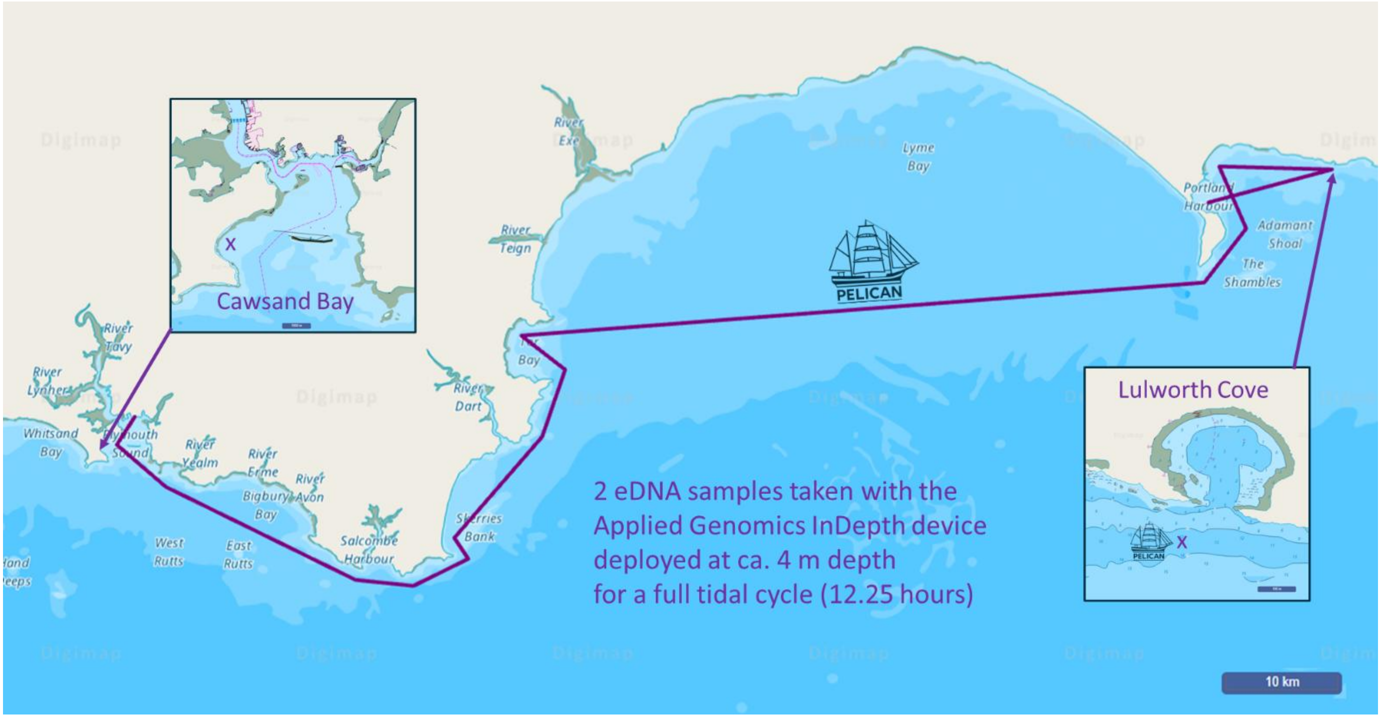


Figure 2 Voyage track from Plymouth to Weymouth in September during the Plymouth Ocean Science Voyage 2025. Samples for eDNA analysis were obtained at the anchoring location of Pelican off Lulworth Cove and in Cawsand Bay, Plymouth Sound.

The samples were analysed using a process called eDNA metabarcoding, using a vertebrate-targeted 16S rRNA metabarcoding marker, and involved the:

1) isolation and extraction of the DNA,
2) amplification of barcode genes using primers in polymerase chain reaction (PCR) to produce hundreds of thousands of DNA sequences
3) high-throughput DNA sequencing,
4) matching sequences to global reference databases (bioinformatics) that includes a range of quality control measures before species are assigned, and
5) ecological analysis using patterns.

Figure 3 The inDepth sampler contains a high-volume pump (top compartment) and enables the collection of eDNA on a filter cartridge housed in the protective cage (bottom compartment).

For this project, we targeted vertebrates only, which includes marine mammals and fish, as well as picking up signals from birds and land-based species entering the marine environment through recreational activities and run-off.

Quality control measures included a blank sample (a sub-sample of the eDNA preservative) exposed to the handling conditions on board during each deployment. DNA contained within the blank was eliminated from the data analysis.

As eDNA can detect rare or low-level signals, some assignments will be more certain than others. For this reason, the credibility of assignments was assessed using a Bayesian[1] credibility framework than integrated several parameters:

- taxonomic assignment confidence
- number of haplotypes[2] detected
- consistency across samples
- prior knowledge (e.g. regional occurrence)

This analysis classified each taxon as low, moderate or high credibility.

[1] Bayesian modelling is used to help answer research questions in complex systems, such as the human body or the environment. It incorporates prior knowledge and data to inform predictions arising from newly obtained data. A powerful advantage of Bayesian modelling is the ability to incorporate uncertainty and hence, estimate probability or credibility of the predictions it makes.

[2] A haplotype is a specific group of genes within an organism that are located on a single chromosome and that was inherited together from a single parent. Multiple haplotypes at one location indicate within-taxon diversity.

2.2 Auxiliary data

A remotely operated vehicle (ROV, by blueye robotics) was used to survey the seabed habitats. The eDNA sample off Lulworth Cove was taken from Pelican of London anchored in around 12 m depth. The ROV camera captured a barren, sandy seabed characterised by wave-formed ripples and little life. Among fragments of shells, a sole crab appeared. The water column contained dense marine snow (organic material, such as faecal matter, dead organisms and biofilms). This indicates a nutrient-rich, productive coastal system, that may have been damaged by destructive fishing practices (e.g. bottom trawling).

The water depth within the Cove varies between 1 and 4 m. ROV footage shows a coarser whitish substrate with some boulders, both of which originated from erosion and rockfall of the chalk cliffs. Most surfaces are populated with a dense cover of diverse seaweeds (including kelp, various brown and red species, coralline seaweeds). The live ROV camera also showed several fish species.

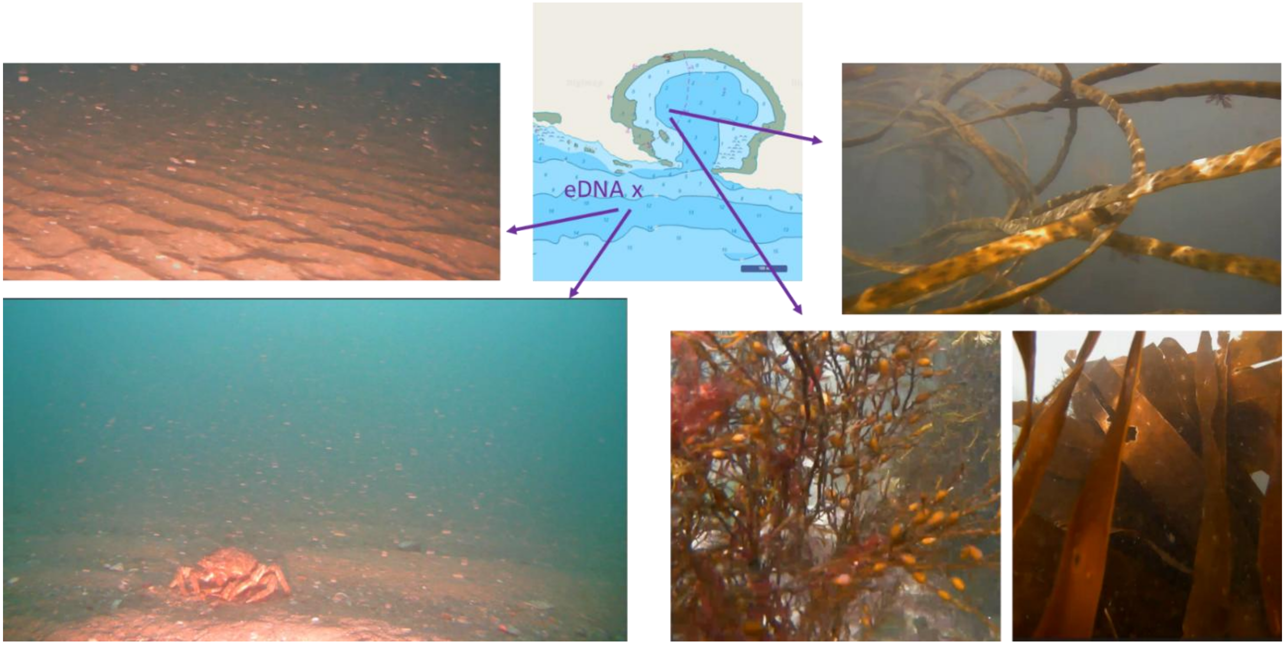


Figure 4 Images of the seabed off Lulworth cove (left), where the eDNA sample was taken, and within Lulworth Cove. Note the marine snow in the images on the left, visible as large, suspended particles illuminated by the ROV's lights. Coordinates: 50.60N, 2.25W.

Near the ship, an acoustic doppler current profiler (ADCP, ECO by Nortek) was deployed synchronously with the eDNA sampler (Figure 5 Left: underwater view of the ECO ADCP by Nortek ((c) Nortek). Right: results from overnight deployment, at around 7 m depth. Each blue dot represents a measurement, their distances from the centre indicate velocity measured in m/s and their positions on the compass rose provides their directions.Figure 5). The results at around 7 m depth show velocities between 0.0 and 0.6 m/s in predominantly west-north-westerly direction on the ebb tide and up to 0.5 m/s in east-south-easterly direction on the advancing tide. The direction of the current was aligned with the coastline. Although current measurements did not indicate water exchange with Lulworth Cove at that depth, Lulworth Cove receives freshwater inputs from a largely agricultural catchment in its northwest, and the tidal ebb is likely to release eDNA-containing water into the English Channel. The Cove is frequented by tourists and researchers for its setting and geology.

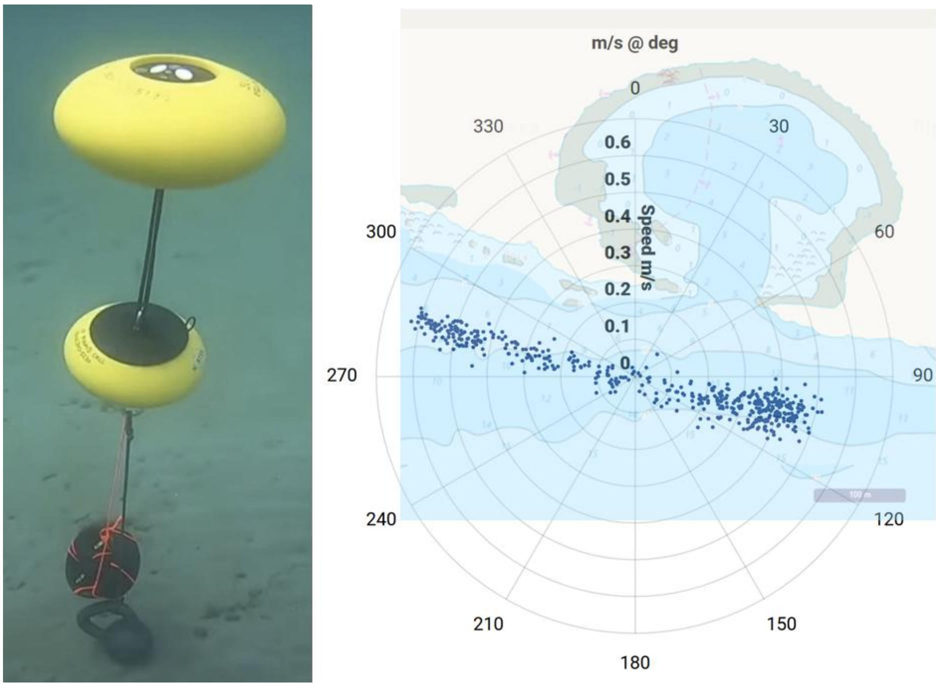
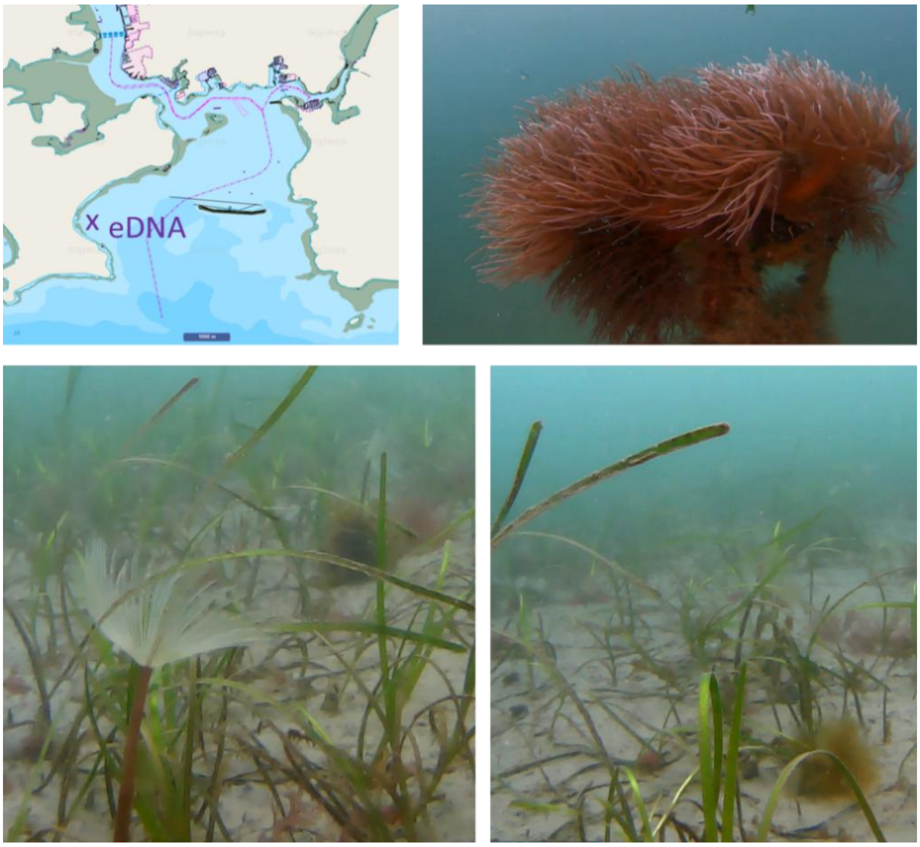


Figure 5 Left: underwater view of the ECO ADCP by Nortek ((c) Nortek). Right: results from overnight deployment, at around 7 m depth. Each blue dot represents a measurement, their distances from the centre indicate velocity measured in m/s and their positions on the compass rose provides their directions.

The ROV survey of the seabed near the eDNA sampling location in Cawsand Bay revealed a substrate of silty sand, sparsely covered by a 'recovering' seagrass meadow, algae and benthic animals, such as tubeworms. A few small fish were also present.



Cawsand bay receives freshwater runoff from two small village in an agricultural setting and is located on the southern fringe of Plymouth Sound, a large conurbation. Unfortunately, no current measurements were undertaken here for logistical reasons.

Figure 6 The Cawsand Bay seabed survey shows a recovering seagrass meadow.

Coordinates: 50.33 N, 4.20 W.

3 eDNA results and interpretation

The taxonomic assignments were dominated by marine fish in both samples, while other chordates (amphibians, birds and mammals) were also present.

The total number of marine taxa detected in Cawsand Bay was 35, of which 17 were assigned moderate or high credibility. Also present was DNA of the common toad, moorhen, Canada goose and dog, which indicate the influence of freshwater runoff, coastal bird populations and recreational activities. Although interesting from a sensitivity angle, they are excluded from this discussion.

At the location off Lulworth Cove, the total taxa count was 61, with 25 assigned moderate or high credibility (Table 1, Table 2). Species with multiple (>2) haplotypes and hence have within-taxon diversity in the sample, are shown in Figure 7.

Table 1 Species determined with a high credibility score using eDNA analysis at two locations, off Lulworth Cove and in Cawsand Bay. The numerical value in the location columns provides the number of haplotypes. Blue font indicates key species (see below).

Common name	Scientific name	Lulworth	Cawsand
Conger eel	*Conger conger*	5	6
European sardine	*Sardina pilchardus*	6	-
Fivebeard rockling	*Ciliata Mustela*	4	-
Leopard-spotted Goby	*Thorogobius ephippiatus*	4	-
Smooth sandeel	*Gymnammodytes semisquamatus*	3	-

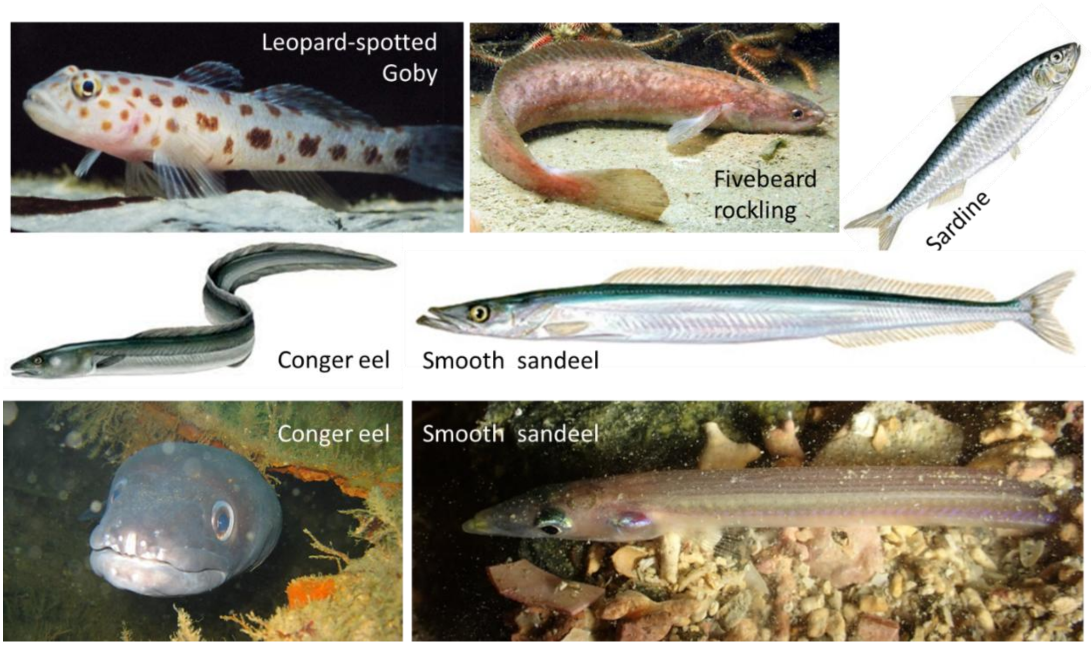


Figure 7 Species detected with high credibility off Lulworth Cove (all) and Cawsand Bay (Conger eel only) using eDNA samples.

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Among these tables, the conger eel, sardine, hake, sand smelt, sandeel and several wrasse species are of particular interest, as they are key food-web species within the coastal marine and ecosystem and/or commercially valuable species. Of these key species, nine were present at Lulworth and five at Cawsand (Table 1, Table 2). Haddock, present at Lulworth, has Vulnerable IUCN Red List[3] status.

Table 2 Species or genera determined with a moderate credibility score using eDNA analysis at two locations, off Lulworth Cove and in Cawsand Bay. 'NA' in the common name column denotes determination at genus level, as indicated in the scientific name column, with no common name assigned. The numerical value in the location columns provides the number of haplotypes. Blue font indicates key species (see below).

Common name	Scientific name	Lulworth	Cawsand
Atlantic herring	Clupea harengus	-	2
Atlantic mackerel	Scomber scombrus	1	-
Baillon's wrasse	Symphodus bailloni	1	-
Black goby	Gobius niger	1	-
Common goby	Pomatoschistus microps	-	1
Connemarra clingfish	Lepadogaster candolii	2	-
Corkwing wrasse	Symphodus melops	1	2
Crystal goby	Crystallogobius linearis	1	-
Cuckoo wrasse	Labrus mixtus	1	-
Dragonet	Callionymus lyra	1	1
European hake	Merluccius merluccius	-	2
European seabass	Dicentrarchus labrax	1	1
European sprat	Sprattus sprattus	1	2
Golden grey mullet	Chelon auratus	1	1
Goldsinny wrasse	Ctenolabrus rupestris	1	-
Haddock	Melanogrammus aeglefinus	-	1
Montagu's blenny	Coryphoblennius galerita	1	-
NA	Labrus sp. (genus)	2	1
NA	Trisopterus luscus (genus)	1	1
NA	Taurulus bubalis (genus)	-	1
Painted goby	Pomatoschistus pictus	-	2
Poor cod	Trisopterus minutus	1	-
Sand smelt	Atherina presbyter	2	1
Shanny	Lipophrys pholis	-	1
Striped red mullet	Mullus surmuletus	2	1
Tompot blenny	Parablennius gattorugine	1	-
Blonde ray	Raja brachyura	1	1

[3] The IUCN Red List is an indicator of the worlds biodiversity and pressures acting on species. It includes non-threatened and threatened species in the categories Data Deficient, Least Concern, Near Threatened, Vulnerable, Endangered, Critically Endangered, Extinct in the Wild and Extinct, as well as Not Evaluated. More at https://www.iucnredlist.org/.

Three Elasmobranchii[4], namely *Raja sp*., the Spotted ray (*Raja montagui*) and the Blonde ray (*Raja brachyura*), were detected at Lulworth, the latter also at Cawsand with moderate credibility. Although these are not yet evaluated by the IUCN, they are of conservation concern in British waters, as they are slow to mature to reproductive age and are threatened as bycatch, by unsustainable fishing and by fishing practices that destroy habitat, such as bottom trawling.

Most other species already assessed by IUCN are classed of Least Concern, including commercial species, such as anchovy, sardine, herring, pollack and whiting.

Among the other species detected with low credibility, the short-snouted seahorse (Figure 9) is worth mentioning. The presence of the short-snouted seahorse at the anchoring location off Lulworth Cove is unlikely, given the condition of the seabed (Figure 4). Rather, eDNA of this species was most likely transported to the sampling location by the tide from a near-shore environment featuring seagrass or macrophytes (large algae), such as inside Lulworth Cove. No seahorses were detected at the recovering seagrass meadow in Cawsand (Figure 6), although this relatively rare species has been observed in Plymouth Sound by the Ocean Conservation Trust before.

Figure 8 Short-snouted seahorse holding onto seaweed.

The full table of results and the summary report by Applied Genomics are available for public access at https://challenginghabitat.com/projects/#eDNA.

4 Outcomes

This, predominantly educational, eDNA exercise provides food for thoughts that can only be tentatively called 'preliminary conclusions', as they would have to be ascertained through further studies:

- eDNA suggests that the diversity and health of the ecosystem at Lulworth is better than in Cawsand Bay. Lulworth most likely benefits from the proximity of richly diverse, shallow habitats, that are protected from commercial fishing activities and act as nursing grounds for marine life that may spill over into the coastal zone food web. Invertebrate diversity would be an important parameter to obtain a more complete understanding of the ecosystem health.
- Given that there is evidence of habitat destruction in the sea south of Lulworth Cove, the presence of rays and other key species in this location is reassuring in the sense that, were

[4] Elasmobranchii are cartilaginous fish, including sharks, rays, skates and sawfish.

habitat recovery made possible by conservation measures, such as the cessation of bottom trawling, rapid recovery of the food web and ecosystem are likely outcomes.
- Cawsand Bay seagrass meadows are 'recovering' after years of damage from fishing, mooring and anchor chains. This part of the seagrass meadow surveyed with the ROV was relatively deep (12 m), whereas seagrass may thrive better in somewhat shallower waters (~6 m). Monitoring and conservation efforts of the Ocean Conservation Trust are ongoing and part of the seagrass bed is now a voluntary 'no anchor zone'. This location may be affected by additional challenges, such as recreational, commercial and naval ship movements, run-off from a large urban area and industry, as well as agrochemicals and metal contamination related to metal mining in the Tamar, Tavy and Plym catchments. Many factors may explain the lower diversity at this location.

We have achieved the original aims of this project:

1) Schools and conservation organisations attended a webinar, during which the method and key findings were explained and a lively Q&A session testified to the interest among participating students. Therefore, in an educational sense, the project demonstrated that water sampling and molecular methods can be used to detect biodiversity in marine environments.
2) The full eDNA data is publicly available and various organisations (Shark Trust, OCT, PSNMP, colleges) have been made aware of its location. Hence, these samples contribute to the available data set of eDNA data in locations of scientific and conservation interest.
3) The Shark Trust UK has confirmed their interest in the presence of diverse ray species and will use this to inform areas to focus on for tagging species. In time, I hope to gather more feedback from other organisations.
4) A-level Biology teachers and their classes attending the webinar integrated the eDNA topic into the relevant curriculum, bringing it to life. The teachers, we liaise with for this voyage, appreciated our showcasing state-of-the-art technology and clearly value the inclusion of eDNA metabarcoding to the ocean science programme on Pelican.

5 Acknowledgements

I thank Sea Changers for part-funding the eDNA sampling and analysis and Nortek Group for their continued support by loaning the current meter free of charge for our educational mission on Pelican of London. Crew and volunteers on Pelican of London deserve a special mention for their support with instrument deployment and science projects on board. Finally, many thanks to Sebastian Mynott of Applied Genomics, who brought eDNA to life in a webinar, explaining this state-of-the-art technology, not only to participants on the voyage, but also to the biology A-level students at collaborating schools.

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