Jellyfish population survey and sampling techniques

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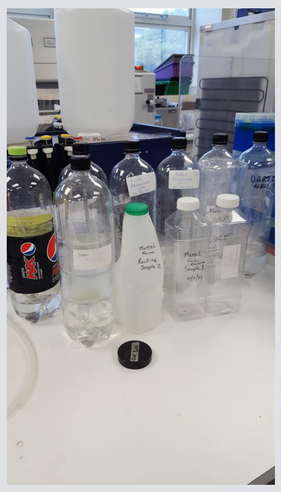
Abstract

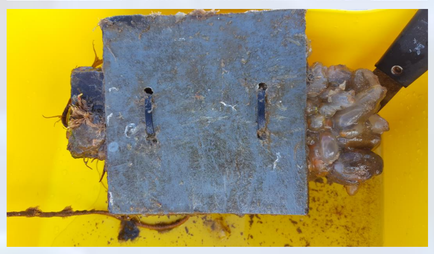
It is difficult to predict when, where and which species of jellyfish will bloom, partly because we lack tools to easily study these animals and partly because little is known about jellyfish populations in any given location. Jellyfish do leave a molecular trace in the water - they shed mucus and stinging cells, both of which contain DNA fragments. This research aims to develop new molecular tools / techniques to detect this residue from jellyfish populations in SW England. Three connected research methods are employed: settlement plates in marinas; mapping citizen science jellyfish sightings data; and the collection and analysis of water samples. Study of settlement plates and Jellyfish sightings data facilitates the targeted collection of water and jellyfish. From these targeted samples, new molecular tools/techniques are being developed. This study also generates new information about the jellyfish populations in the SW, providing baseline data for temporal studies, against which climate change and ecosystem degradation can be studied. .

Methods

Seawater was collected using commonly available bottles, treated with Milton sterilisation solution, to test suitability for citizen scientist involvement. Surface seawater samples were filtered through 0.45µm filters and DNA was isolated from the filters.



Each settlement (SETL) plate is a 14cm x 14cm PVC square, tied to an airbrick and suspended 1m below the water surface on floating pontoons in local marinas[1]. SETL plates were photographed quarterly, scraped into sterile containers and DNA was extracted from homogenised scrapings.



SETL plate scrapes were homogenised in a blender and a 1.5ml sample was frozen in a microcentrifuge tube

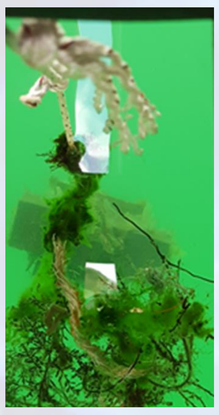
Following a Literature review, the most common method for extracting DNA from environmental samples for metabarcoding analysis – the Qiagen DNeasy Blood and Tissue Kit - was chosen. Thus, water filter and homogenised SETL plate samples were processed using spin columns to purify the DNA, preceded by lysis at 56°C in a proprietary lysis buffer (contains guanidine hydrochloride) with Proteinase K added.

- eDNA concentration and purity was measured on a Nanodrop ND1000.
- DNA was prepared for Illumina paired-end sequencing by PCR, using primers with Illumina adapters incorporated.
- Two universal primer sets were used, targeting CO1 and 18S to maximise the eukaryotic fraction of marine diversity detected.
- The primer pairs used were:
  mlCOIintF: 5'- GGWACWGGWTGAACWGTWTAYCCYCC - 3' and
  LoboR1: 5' - TAAACYTCWGGRTGWCCRAARAAYCA - 3' for CO1[2,3]
  and
  V4_18SNext.For: 5'-CCAGCASCYGCGGTAATTCC -3' and
  V4_18SNext.Rev: 5' - ACTTTCGTTCTTGATYRATGA – 3' for 18S[4].

Jellyfish observations and citizen science: most sightings were collected via a Facebook page but the research team and volunteers surveyed local beaches for strandings and undertook snorkel and kayaking surveys. Local water users reported sightings direct to the researchers.

Results

SETL plates, bricks and ropes all became colonised by a variety of organisms

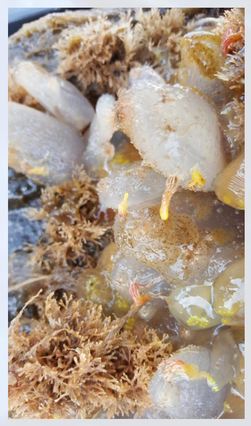


Torquay marina summer SETL plate A1
28/8/19

Torquay marina winter SETL plate A1
07/12/19

Torquay marina SETL plate detail

15/06/19



28/08/19

Jellyfish sighting results 2019-2020

	2019										2020												sightings
	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec	
Barrel																							108
Blue																							46
Compass																							91
Crystal																							61
Moon																							22
PMOW																							40

(Darker colours = larger numbers/sighting (red>100indivduals in one sighting; PMOW=Portuguese Man O'War))

Very few sightings were obtained during any of the various Covid Lockdowns, making comparisons between years unreliable.

Conclusions

- A pattern is emerging which shows barrel jellyfish being observed earliest in the year, beginning in March/April, followed by blue, compass, moon and crystal in May/June. The occasional Portuguese Man O'War was also sighted in the autumn and winter. More data needs to be collected long term.
- NGS data from seawater samples has yet to be obtained (PCRs are still being carried out) but should reveal the most common organisms present in our local waters which could possibly include the jellyfish. Access to our marina sites was restricted during the lockdowns, but a local mussel farm continued to collect water samples for us from their site in Torbay.
- Jellyfish polyps were not observed on the SETL plates, possibly they were not low enough in the water, however a plethora of other marine life colonised the plates and we look forward to the eDNA sequencing results to see if that data correlates with the observed organisms (e.g. hydroids, ascidians, ophiuroids and nudibranchs).

References

1. Van Walraven, L. *et al*. Where are the polyps? Molecular identification, distribution and population differentiation of Aurelia aurita jellyfish polyps in the southern North Sea area. *Mar. Biol*. 163:172 (2016)
2. Leray, M. & Knowlton, N. DNA barcoding and metabarcoding of standardized samples reveal patterns of marine benthic diversity. *Proc Natl Acad Sci USA* 112, 2076–2081 (2015).
3. Lobo, J. *et al*. Enhanced primers for amplification of DNA barcodes from a broad range of marine metazoans. *BMC Ecol*. 13, 34, https://doi.org/10.1186/1472-6785-13-34 (2013)
4. Stoeck T, Bass D, Nebel M *et al*. Multiple marker parallel tag environmental DNA sequencing reveals a highly complex eukaryotic community in marine anoxic water. *Mol Ecol.* 19: 21–31 (2010)