BLUE ECONOMY
COOPERATIVE RESEARCH CENTRE

Exploiting Oysters as a natural eDNA sampling platform

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Background

Filter feeding organisms, such as bivalves, barnacles, sponges, and ascidians, are some of the most successful marine animals and are regularly found to be invasive within waterways globally. Further, they include some of the most prolific biofouling species on aquaculture farms, causing decreased water flow, oxygen, and in some cases, death of stock (Ba-Akdah, Satheesh & El-Sherbiny, 2020). Their suspension feeding behaviours allow for them to colonise most surfaces and grow quickly. In this project I will explore whether this feeding ability also allows these organisms to be a candidate for natural environmental DNA samplers. Environmental DNA (eDNA) is a rapidly developing environmental monitoring tool for indirect species detection. eDNA utilises DNA shed in the environment to determine the presence of organisms and has been shown to successfully compliment, or replace, direct monitoring methods. It is said to be a highly sensitive technique and can benefit biomonitoring by allowing for the identification of biodiversity and population assemblages (Taberlet, Bonin, Zinger, & Coissac, 2018; Taberlet, Coissac, Hajibabaei, & Rieseberg, 2012). Methods utilising eDNA to survey environmental samples must first concentrate the sample used for extraction. Several concentration methods are currently used across different environments, which are optimised for the target organism(s) and the specific research question. Different collection methods are used within the marine habitat ranging from using passive filter sampling (Bessey et al., 2021) to active filtering (Turner, Uy, & Everhart, 2015 2015; Walker et al., 2017; Walsh, Spear, Shannon, Krysan, & Vander Zanden, 2018). Another way to concentrate DNA is by using organisms which naturally accumulate DNA, most commonly due to their feeding habits, which allows for near constant filtration and accumulation of DNA within tissues. This results in increased transient times when compared with traditional filtering methods.

Objectives

Chapter 1

Determine the effect of time on the depletion of target organisms' DNA

Identify specific organs where target taxa DNA accumulates within oysters

Determine the effect of oyster size on depletion of organisms' DNA from the water column

Chapter 2

Discover whether natural samplers outcompete traditional eDNA methods

Chapter 3

Identify whether depth influences the identification of pathogens *in situ* using natural samplers.

Methods

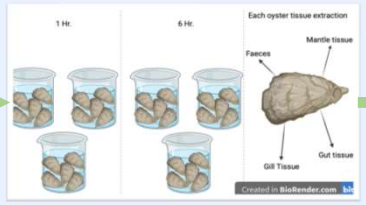

Figure 1: Time trial (1 & 6hr) post exposure to target organisms. Once completed, gills, mantle, faeces, gut and water samples will be collected

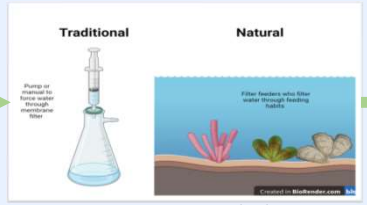

Figure 2: Traditional eDNA sampling alongside filter feeding organisms such as sponges, mussels and oysters used as natural samplers.

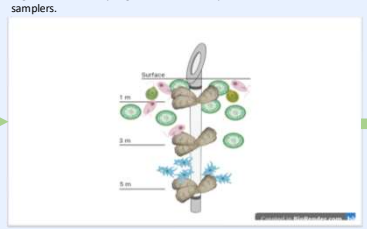

Figure 3: Oysters attached at 3 depths (1, 3 &5 m) from the surface *in situ* at specified aquaculture farms

Hypotheses

Chapter 1

Oysters will remove target pathogens from the water over time

Specific organs within the oyster will accumulate target pathogen DNA. This may be different based on each pathogen. Further, threshold values may be able to be determined.

Oyster size will influence the rate of removal from the water column. Additionally, optimised oyster size classes may affect the uptake of certain pathogens

Chapter 2

When compared to traditional sampling methods (Sterivex) taken at the same location as the deployment of oysters, natural samplers will provide similar, if not better, detection of target organisms.

Additionally, broader comparisons of entire communities from traditional sampling and natural sampling will provide similar species richness data.

Chapter 3

Optimised size-classed oysters deployed in situ at farms will detect pathogens at different depths. It is common knowledge that depth affects the dispersal of algal blooms and parasites; therefore, it is expected that targeting specific depths will increase the likelihood of detection using natural samplers.

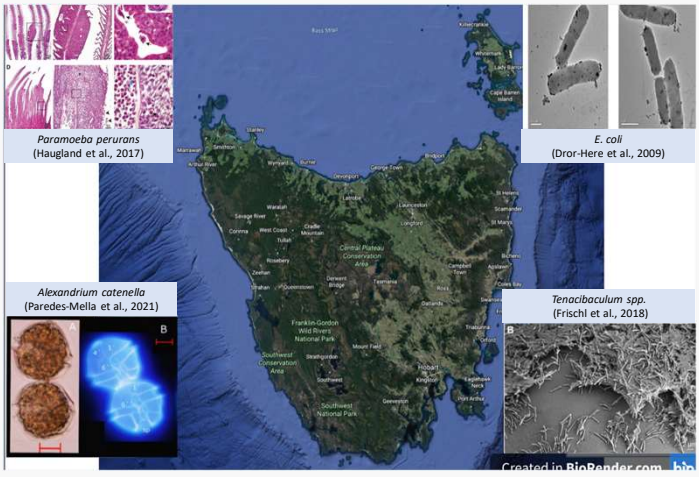

Figure 4: Target pathogens (sourced within Tasmania), which are all of concern for aquaculture farms globally, for the duration of the candidature. *Paramoeba perurans* (Top left) in a gill stain, responsible for Amoebic Gill Disease (AGD), one of the greatest pathogens, who's screening and treatment can account for 20% of salmon production *E. coli* (Top right), responsible for food poisoning if ingesting contaminated shellfish. *Alexandrium catenella* (Bottom left) responsible for Paralytic Shellfish Poisoning and mass fish die-off's. *Tenacibaculum spp*. (Bottom right) responsible for severe lesions and death among infected stock.

Applications

Exploiting bivalves, specifically oysters for eDNA collection, has large implications, not only for the aquaculture sector, but also the eDNA field more broadly. Due to their feeding habits, bivalves and other suspension feeders are constantly feeding and thus are always filtering the surrounding water, capturing DNA molecules shed from organisms. This constant filtering allows for longer transient times and accumulation of DNA within the tissues of natural samplers, in turn improving the potential to detect species within the aqueous environment, specifically those which are rare or sporadically distributed. Bivalves are found in nearly every aquatic environment allowing them to be an ideal candidate for biomonitoring in the world's waterways. These organisms can be exploited for the detection of rare or sporadically distributed species or detection in environments where traditional sampling is difficult (deep sea, turbid water).

Pathogen detection and treatment accounts for some of the largest costs for the aquaculture industry and, therefore, early detection of pathogens is important for the health of stock. Natural samplers as eDNA collection devices offer sensitive detection of target pathogens and limit the current invasive sampling stock. Further, natural samplers can aid in the determination of threshold values for harmful algal blooms which are heavily monitored due to their food health and safety. Although only a handful of pathogens will be tested in this candidature, it will develop methodologies to allow any pathogen to be tested through the application of specific assays.

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