Exploiting Oysters as a biological eDNA sampling platform

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Background

Filter feeding organisms, specifically bivalves are some of the most successful organisms and are regularly found to be invasive within waterways globally. Their success can be attributed to this feeding behaviour and their ability to colonise most surfaces and rapidly grow. Due to this ability to colonise, they are some of the most prolific biofouling species for aquaculture farms; decreasing water flow, oxygen and in some cases, death of stock (Ba-Akdah, Satheesh & El-Sherbiny, 2020). However, while they may be an unwanted species, their ability to filter large quantities of water to capture phytoplankton and with it, shed DNA from surrounding taxa, allows these organisms to be a candidate for biological environmental DNA samplers. Environmental DNA (eDNA), is a rapidly developing environmental monitoring tool used for indirect species detection. eDNA utilises DNA shed in the environment to determine the presence of an organism(s) and has been shown to successfully compliment and replace direct monitoring methods. It is 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 and not degrade 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), and more recently biological samplers. Biological samplers are defined as organisms which can naturally accumulate DNA, most commonly due to their feeding habits. Bivalves offer the potential to significantly contribute to this field with their ability to near constantly filter water, and DNA, to be used in monitoring systems globally, as well as their presence in nearly every aquatic environment.

Objectives

Chapter 1

Determine the effect of time on the depletion of target organisms.

Identify specific organs where target taxa DNA accumulate within oysters

Chapter 2

Discover whether natural samplers outcompete traditional eDNA methods regarding specificity

Chapter 3

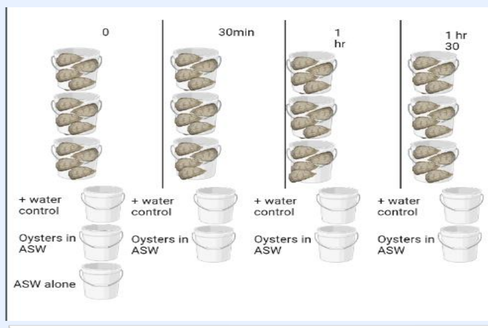
Identify whether depth has an affect on the identification of pathogens *in situ* using natural samplers.

Chapter 4

What effect does 'curing' have on the microbiome and metabolome influencing the desirability of oysters?

Design

1



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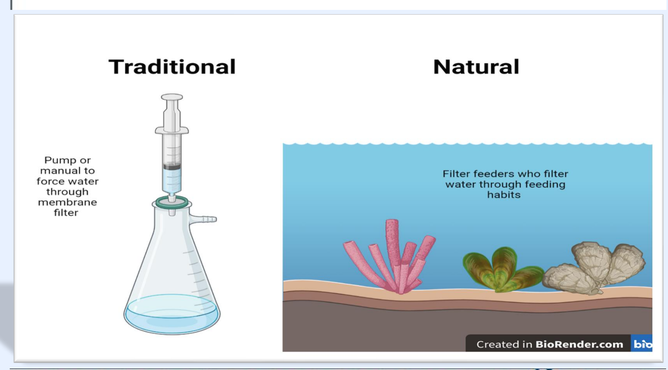

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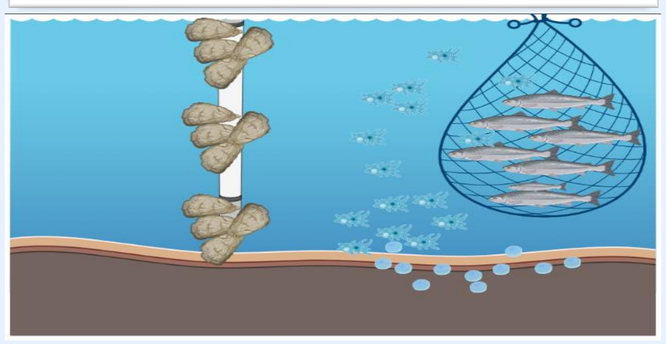

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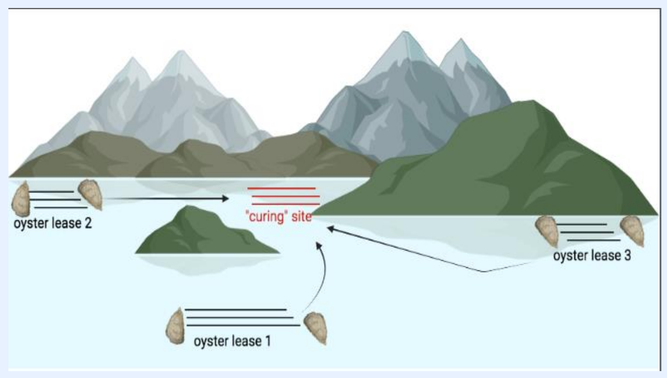

Hypotheses/Results

Chapter 1

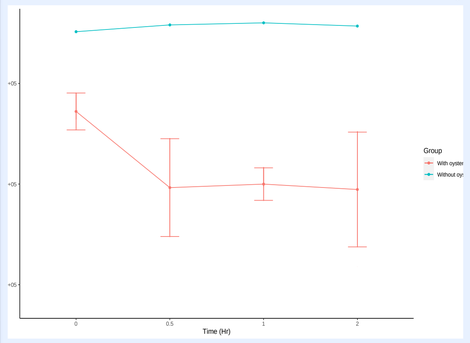

Figure 1: Quantity of E coli, normalized to Beta actin from the water column over 2 hours exposure

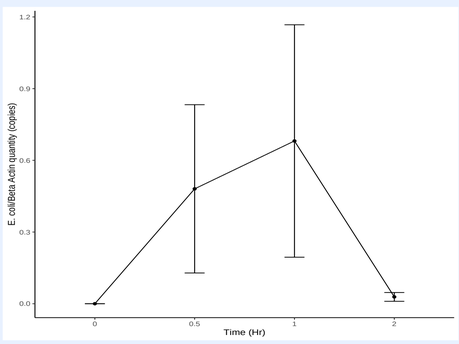

Figure 2: Quantity of E coli, normalized to Beta actin detected within the gill of oysters over 2 hours of exposure

Chapter 2

When directly 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 metazoan communities.

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

Chapter 3

Oysters deployed *in situ* at salmon aquaculture farms will detect pathogens, specifically, *Neoparamoeba perurans*, at various depths. It is common knowledge that depth affects the dispersal of algal blooms and parasites, therefore it is expected that targeting these depths will increase the likelihood of detection using natural samplers.

Chapter 4

Moving oysters from a grow-out lease to a "curing" site influences their perceived desirability. The oyster metabolome will reflect these changes based on a number of environmental factors. This data can be utilised to determine the best sites for curing prior to harvest, successfully influencing the "merroir" effect within oysters. Additionally, specific metabolites can be isolated to determine the greatest metabolites for desirability of a given oyster.

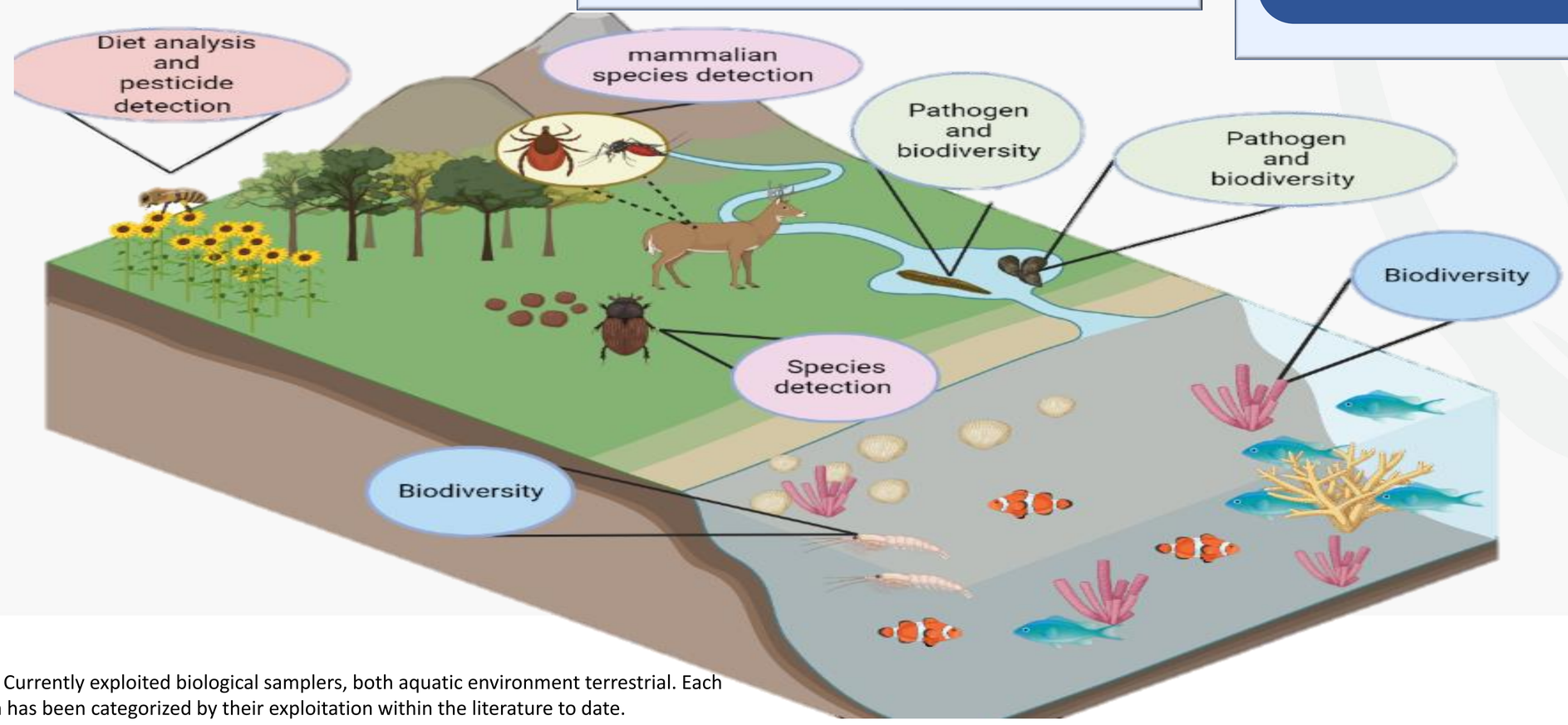

Figure 3: Currently exploited biological samplers, both aquatic environment terrestrial. Each organism has been categorized by their exploitation within the literature to date.

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