Developing a Portable System of Environmental DNA (eDNA) Surveillance to Monitor Fish Population Dynamics in Conesus Lake and The Philippine Seas

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Introduction

Abstract: *Climate change is an increasing threat to many ecosystems worldwide. Therefore, many species are under threat of extinction, while others are forced into unusual patterns of migration. In this project, we aim to develop a cheap, rapid, and sensitive method of monitoring the population dynamics of fish. Recently, a new method called environmental DNA (eDNA) metabarcoding has been developed to monitor species richness and the presence of invasive species in ecosystems. Combined with PCR sequencing, we hope to build a portable system of eDNA metabarcoding to monitor 'Round Scad' population dynamics in the Philippine Seas, as well as detecting the presence of invasive species. As a 'proof of principle' study, we examine the sensitivity of the system to detect two invasive fish species in our local Conesus Lake: the 'Rudd' and the 'Alewife'.*

Long-term Significance

If successful, we anticipate that this 'proof of principle' study could be adapted for long term experimental investigation in the Philippines in order to provide empirical information critical to managing Round Scad and other marine fish facing similar environmental stressors.

Long-term Research Question

Does global climate stress cause changes in population dynamics in the migration patterns of *Round Scad* and other marine fish in the Philippine Seas?

Methods

Figure 1: Conesus Lake, Site 1

Figure 2: In-lab Filtration

Figure 3: Purelink Genomic DNA kit (*Thermo Fisher Scientific)*

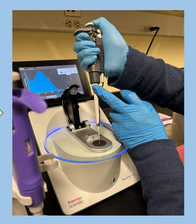

Figure 4: DNA Quantification with NanoDrop Microvolume Spectrophotometer

Figure 10: Sampling sites on an overhead view of Conesus Lake (*NYS Dept. of Environmental Conservation*)

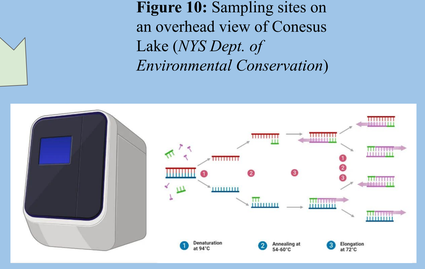

Figure 5: PCR amplification (*Karki, Prakriti, et al.*)

Figure 7: eDNA metabarcoding workflow (Guo, Mali, et al., 2022)

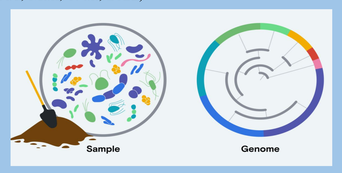

Figure 6: Metagenomics (*Element Biosciences)*

Figure 8: Portable Nanopore MinION Device (*Interprise)*

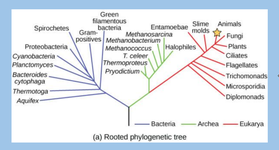

Figure 9: Species tree (*Phylogenetic Trees)*

Sampling

- We gathered samples from various locations on Conesus Lake and brought them to the lab to analyze (**Figure 10**). This water should contain eDNA shed from the fish and other organisms in the marine environment which we want to analyze.
- We used a filtration kit involving a filter cartridge and syringe to collect and concentrate the eDNA at the sampling site (**Figure 2**; Miya et. al, 2022)
- We quantified the DNA using the NanoDrop Microvolume Spectrophotometer (**Figures 4** and **11**)

Sequencing

- The universal primers that will be used for PCR sequencing are the Fish DNA Barcoding Primers, Fungal DNA Barcoding primers, Insect DNA Barcoding primers, Plant DNA Barcoding primers and Bacterial DNA Barcoding primers
- We will run our samples through the Nanopore MinION (**Figure 8**), which identifies the DNA sequences that are present in the sample
- We will use BLAST to interrogate an NCBI database in order to identify the species derived from the eDNA samples

Results

	Elution 1	Elution 2	Elution 3
Sample Number	Conc. (ng/μL)	Conc.(ng/μL)	Conc.(ng/μL)
1	9.9	1.6	2.6
2	5.2	1	0.9
3	11.8	3.1	1.3
4	6.5	1.1	0
5	7.1	1	2.2
6	6.2	0.8	0.5
7	6	2.9	2.4

Figure 11: Concentrations of our sample elutions

The use of universal PCR primers was a result of the little amount of DNA that we found present in our elutions (**Figure 11**). The NanoDrop Spectrophotometer indicated that there was not enough DNA present in order to use the MinIon.

Anticipated Results

We hope to yield data from the MinION that will present DNA sequences from an array of sequences spanning fish, fungus, plant, and bacterial species that we can identify through BLAST analysis using the NCBI database.

Limitations of the Study

The way we will conduct our experiment will allow us to identify species diversity, but not their abundance.

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Figure 12: Research Group at Site 2