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

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Introduction

Abstract: *Climate change is an increasing threat to many ecosystems worldwide. Due to global warming, many species are under threat of extinction while others are forced into unusual patterns of migration. For example, the 'Round Scad' fish in the Philippines, which is a cheap source of protein in the diet of common citizens, is rapidly declining in both population and body size. In this project, we aim to develop a cheap, rapid, and sensitive method of monitoring the population dynamics of this fish in the wild. Recently, a new method called environmental DNA (eDNA) metabarcoding has been developed as a cost-effective way to monitor species richness and the presence of invasive species in marine ecosystems simply by detecting DNA released by dead tissues shed from organisms in the environment. Combined with the recent development of Nanopore MINion, a portable and cheap 3rd generation DNA sequencing technology, we hope to build a portable system of eDNA metabarcoding that can be used in the field 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 present our proposal here to examine the sensitivity of the system to detect two invasive fish species in our local Conesus Lake: the 'Rudd' and the 'Alewife'. If successful, the deployment of this method in the Philippines may contribute to acquiring important data for informing sustainable management and conservation strategies of marine species facing global climate change stress.*

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

Sampling

- We will first gather samples from various locations and depths from Conesus Lake to bring to the lab and analyze (**Figures 1 and 2**). This water should contain eDNA shed from the fish and other organisms in the marine environment which we want to analyze.

Figure 1. Conesus Lake, where we will be obtaining samples.

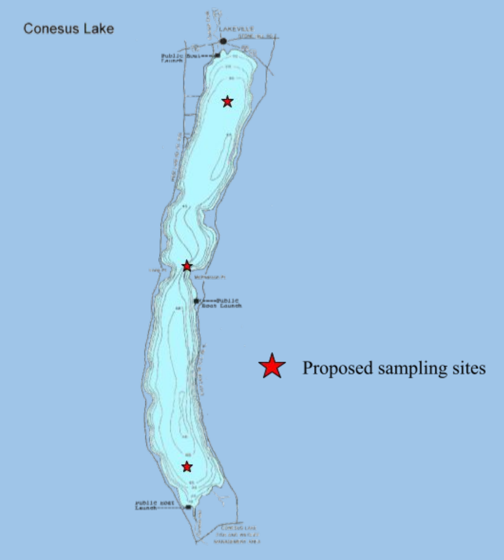

Figure 2. Proposed sampling sites on an overhead view of Conesus Lake (*NYS Dept. of Environmental Conservation*)

- We will use a filtration kit involving a filter cartridge and syringe to collect and concentrate the eDNA at the sampling site (**Figure 3a, b and c**; Miya et. al, 2022)

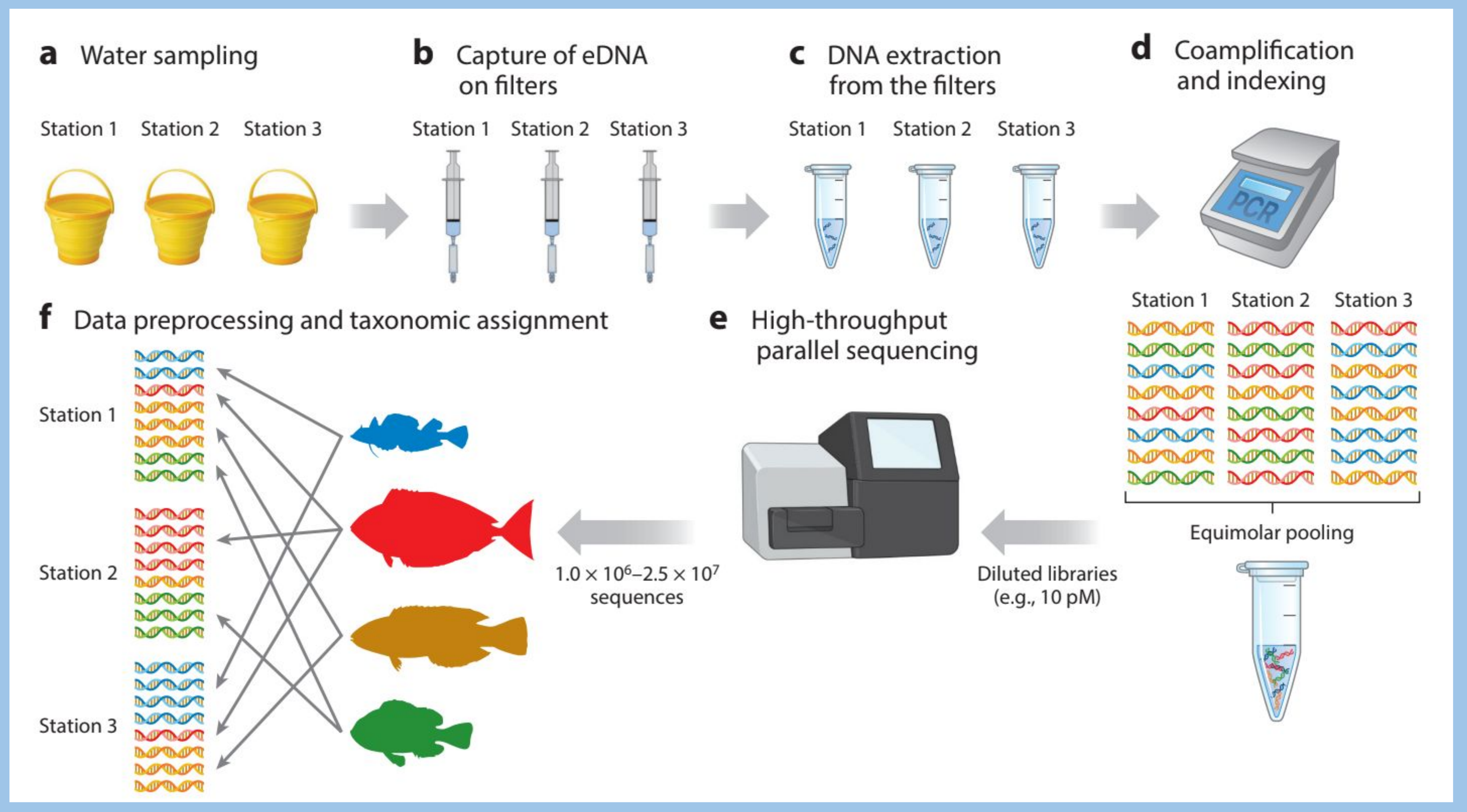

Figure 3. The eDNA metabarcoding workflow (Miya, 2022)

Sequencing

- We will run our samples through the Nanopore MinION (**Figure 3d and e; Figure 4**), 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
- If the *Alewife* and *Rudd* species (**Figures 5 and 6**, respectively) are present in our eDNA samples, then we would anticipate them to be identified in our BLAST analysis
- We will then analyze the spatial distribution patterns of the identified fish species, including *Alewife* and *Rudd*, throughout the different sampling locations in Conesus Lake

Methods Cont'd

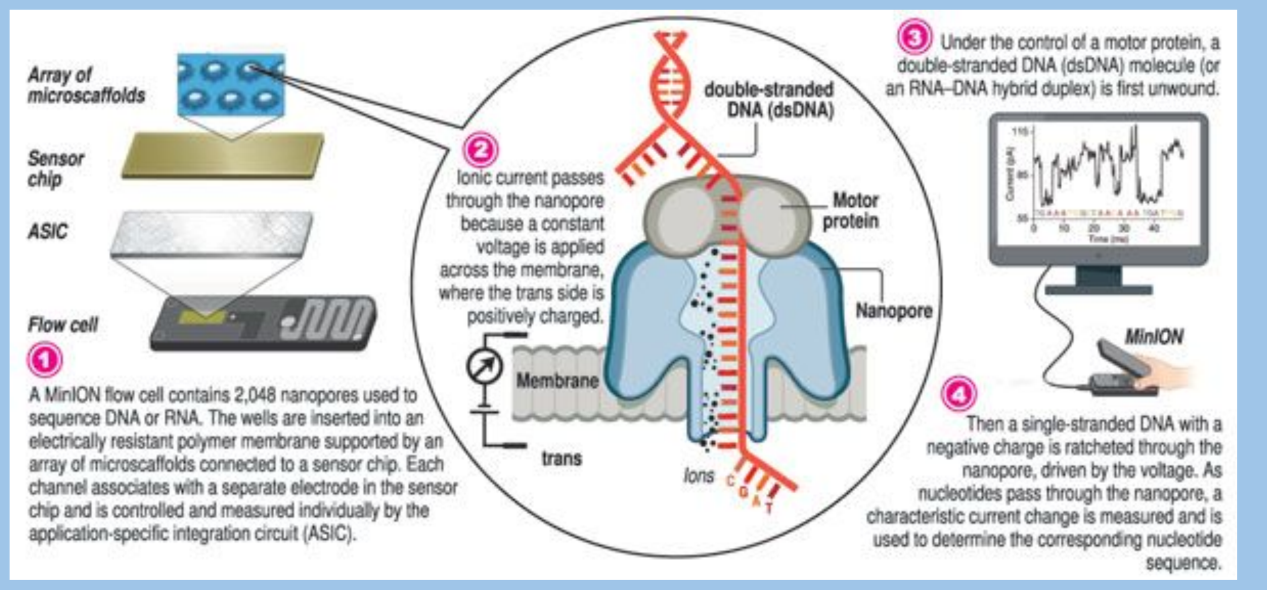

Figure 4. The principle of Nanopore MinION technology (Hettiarachchi and Ruqyyaha, 2022)

Anticipated Results

Our goal is to identify by BLAST analysis any detectable fish species from the sample sites including two invasive fish species in our local Conesus Lake: the *Rudd* and the *Alewife*, based on their genome sequences found in the current NCBI Database.

Figure 5. *Rudd* (average adult size 10 in)

Figure 6. Alewife (average adult size 5 inches)

Since the *Alewife* species have been a prominent invasive species in Conesus Lake for a couple decades, we will be able to examine shifts in dynamics such as the abundance and distribution as compared with previous years' data.

Limitations of the Study

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

References

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