Abstract 2109

The Prevalence of Angiostrongylus cantonensis in Molluscs found on the University of Hawai'i - West O'ahu campus, a Preliminary Study

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Keywords: Angiostrongsylus cantonensis, Rat lungworm, Molluscs, Hawai'i

Angiostrongylus cantonensis, is a parasitic nematode that thrives in subtropical and tropical environments, like Hawai'i, where conditions lead to its pervasiveness in its definitive hosts: rodents, and in its intermediate hosts: molluscs. The incidental infection of human hosts can lead to Rat Lungworm (RLW) disease. Symptoms of infection include vomiting, nausea, abdominal pain, headaches, and other neurological symptoms that can occur over a one-to-four-week period. If not caught soon enough, these parasites can travel through a person's central nervous system and to the brain eventually leading to eosinophilic meningitis. Since the early 2000's to now, there has been an increase in diagnosed cases of RLW disease in humans, primarily in Hawai'i. The main goal of this study was to detect if A. cantonensis in molluscs were prevalent on the grounds of the University of Hawai'i-West O'ahu (UHWO) campus. In the Summer of 2023, two species of molluscs, Lissachatina fulica (n=6) and Veronicella cubensis (n=9), were collected on the UHWO campus. Genomic DNA was extracted from tissue at the foot of both molluscs. Using conventional PCR and gel electrophoresis, we were able to examine these molluscs for A. cantonensis. Of the six snails tested, none showed evidence of having A. cantonensis DNA and of the nine slugs tested, only one showed there was a possibility of having A. cantonensis DNA. Our findings indicate that the UHWO campus may have molluscs that could potentially be infected with A. cantonensis. Further studies with more sampling, species types, and increased sample sizes will be measured. As well as the refining of our extraction methods and sequencing of any of our PCR samples that show unexpected bands during our gel electrophoresis will have to be done.

This work was supported by INBRE Hawai'i.

106651, https://doi.org/10.1016/j.jbc.2024.106651

Abstract 2127

Using Metagenomics to Explore Biodiversity in Local Ponds

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Keywords: metagenomics, pond ecosystem, biodiversity

The microbiome is a group of microorganisms living in a particular environment. Microorganisms living in ponds play an important role in the health and balance of these ecosystems. This study aimed to understand how microorganisms vary in different local ponds using metagenomics. Water samples were collected from local ponds around Jackson, Tennessee, to be examined for the presence of microorganisms. DNA was extracted using a standard ethanol precipitation protocol followed by clean-up with a ZymoBIOMICS genomic DNA mini kit. The whole genome DNA was then amplified using the Nanopore Polymerase Chain Reaction (PCR) Barcoding kit due to low DNA yield and to allow multiplexing during DNA sequencing. This process involves fragmentation of the genomic DNA and addition of a linker oligonucleotide using an engineered transposase followed by amplification of the DNA with specific primers containing a unique barcode. All amplified genomic DNA samples were cleaned using MagBeads, prepped for the Genomic libraries, and ran on the Nanopore MinION Mk1c DNA sequencer. DNA reads were analyzed using the Epi2Me What's in My Pot workflow to identify specific microorganisms using standard sequence alignment to NCBI reference sequences. Initial findings showed that the microorganisms differed significantly from pond-to-pond. Each pond had its own unique mix of microorganisms, and some ponds had more diverse microorganisms than others. Various types of bacteria, archaea, and fungi were found, but their abundance and distribution varied across ponds. Environmental factors that were documented to influence diversity of microorganisms were also studied. These factors, including acidity of the water and oxygen levels, seemed to affect the types of microorganisms present. Some connections between specific microorganisms and these environmental factors suggests that they work together in the pond ecosystem. Understanding these differences can contribute to effective management and conservation of local ponds. Further research on how the microorganisms change over time, as well as studying other environmental factors and how the microorganisms function in the ponds. This information can help monitor water quality, protect the environment, and manage ponds more effectively.

This work is supported by an HBCU-UP Implementation Project grant from the National Science Foundation EES 2011938.

106652, https://doi.org/10.1016/j.jbc.2024.106652