Does the Presence of a Venom Apparatus Affect the Diets of Venomous and Nonvenomous Terebridae?

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ABSTRACT

Terebridae are an interesting group of carnivorous snails, yet, not much is known about the diets that would allow terebridae to survive, flourish, and adapt to their surroundings. In this experiment, we dissected the guts of two species of Terebridae, *Hastula hectica* (venomous) and *Myurella affinis* (nonvenomous), to see if the presence of a venom apparatus affects the diets of the snails. We conjecture that there *will* be a difference in the diet content of the terebridae with a venom apparatus and the diet content of the terebridae without a venom apparatus. To do this, the guts of three of the venomous and three of the nonvenomous terebridae that were previously collected, were dissected, DNA was extracted and the COI gene was sequenced. Gut content was not found after the analysis. Unfortunately, the protocol did not allow for the determination of any prey content, but it did help to confirm the taxonomy of the species of snails used.

Fig A. *Hastula hectica*

Fig B. *Myurella affinis*

INTRODUCTION

The superfamily Conoidea contains marine snail species that are both venomous and nonvenomous, yet both of these species are able to survive. This superfamily includes cone snails, terebrids, and turrids. The peptide toxins produced by certain terebridae, teretoxins, are promising bioactive biomedical compounds. They can range from carnivores, that hunt fish, polychaetes or worms, and other snails, to detritivores, that scavenge for dead fish or other organic debris. Terebrid snails with a venom apparatus have a hollowed out radula which is used to inject venom into prey, similar to a hypodermic needle. The fact that some species of Conoidea have toxins while others do not is an important evolutionary development. By studying this evolutionary divergence we are better able to understand the separation of species in the Conoidea family and possibly trace when toxins became necessary for these snails to survive.

Fig C. Kavieng, Papua New Guinea

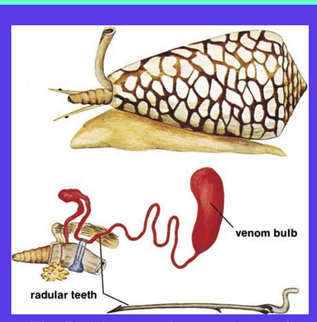

Fig D. Venom Apparatus of Terebrid Snails, *Radula*

METHODS

Dissect Gut Content

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DNA Extraction

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Phenol-Chloroform

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Amplify DNA (PCR)

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LCO1490 and HCO2198 Primers

↓

Sequencing

↓

Illumina MiSeq. Platform

↓

Analysis

DATA

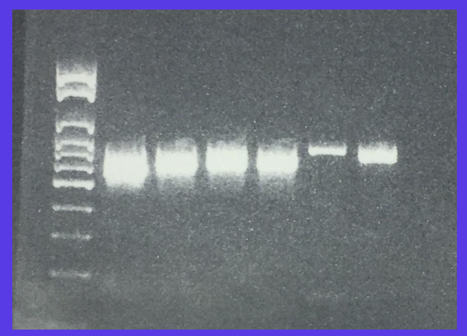

Fig E. Gel showing bands of amplified DNA.

RESULTS

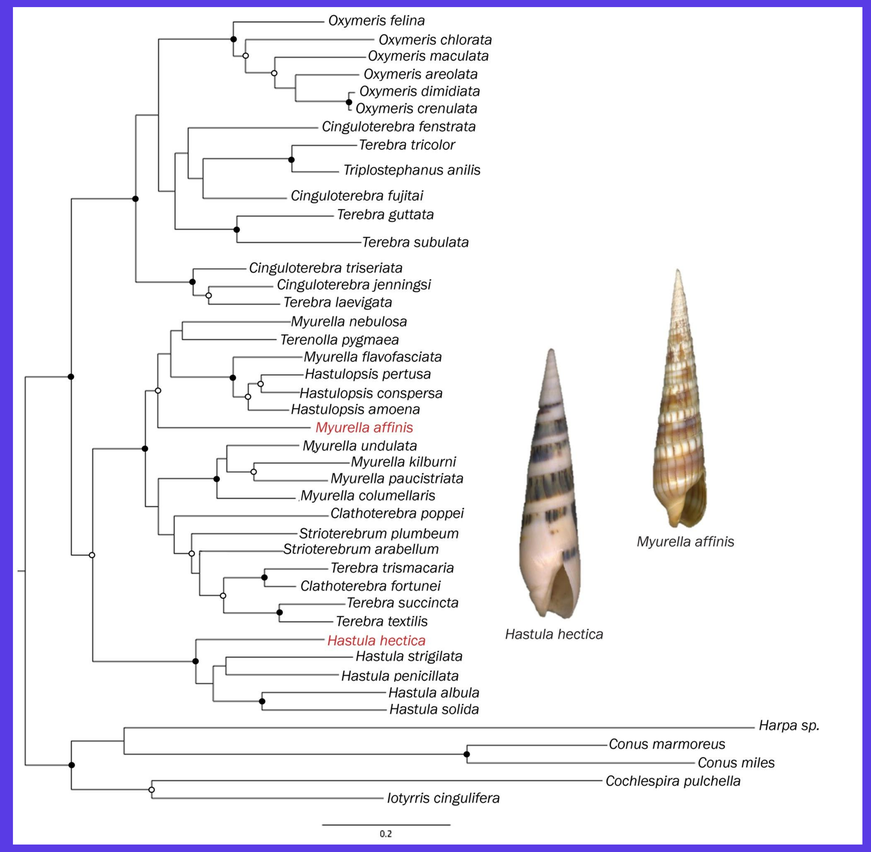

Fig F. Phylogenetic tree of Terebridae. *H. hectica* and *M. affinis* are colored in red

DISCUSSION

After running our samples on the MiSeq, we were only able to obtain sequences for 4 out of the 6 originally sequenced. Our sequences unfortunately did not reveal any polychaete DNA, therefore we could not determine the prey of *H. hectica* and *M. affinis*. We were able to confirm our species of terebridae that were identified previously solely based on their phenotype, not genotype. In this case it is possible that the metabarcoding gene used, the 658 base pair COI, was degraded during the digestion of the polychaetes, so no intact DNA was left to be identified. To further improve our experiment another primer such as a mini barcoding gene could be used to identify the sequence regions since COI, the “universal primer” is too large for sequencing degraded DNA (Leray et al., 2013).

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