Diversity and Phylogenetics in Marine Siboglinid Worms

William Hatleberg, 2011

Siboglinids are a highly specialized group of annelid worms that completely lack a digestive system. Instead siboglinids rely on symbiotic bacteria that are capable of sequestering chemical energy from the environment, much like a plant can make energy from the sun. For many years, siboglinids were thought to be an obscure group of worms of little ecological importance until deep-sea explorers discovered many new siboglinid species, including the prominent ecosystem engineers found on the Pacific hydrothermal vents.

We currently recognize four main lineages of siboglinid worms: the frenulates, the vestimentiferans, Osedax, and the moniliferans. The most well known species of siboglinid worms are the vestimentiferans, which are large (1-2 m long) deep-sea worms found at hydrothermal vent and hydrocarbon seep environments. In contrast, very little is known about the moniliferan, Osedax or frenulate species. This is especially surprising for the frenulates, because they are the most diverse (~140 described species), widespread, and accessible group of siboglinid worms. In fact, frenulates are likely the most common marine endosymbiotic organisms in the world, inhabiting muddy environments from shallow water to the deep-sea, yet very little research has been conducted on them to date. Osedax worms are equally fascinating and are the most recently discovered lineage. These worms were only discovered in 2002, when exploration of the deep-sea uncovered the bizarre ecosystems that form around the carcass of a dead whale. Osedax can only be found on the bones of dead whales, where they are capable of extracting the energy buried deep inside the bone as they digest it.

Last summer, with the help of a Doherty Coastal Studies Research Fellowship, I was able to begin a preliminary examination of siboglinid phylogeny, which revealed a basal polytomy among the major siboglinid lineages. This means that there is little evidence as to which lineage is the ancestral group of siboglinids and which lineages are derived. Because little is still known about the evolutionary history of siboglinids, my project this summer has been to continue to understand how the siboglinid host species are related, which will ultimately allow us to understand how this unique symbiosis evolved and how it can be maintained in these remarkable worms.

To make more complete evolutionary tree, one of our goals was to obtain samples representing all of the main taxonomic lineages, as well as the samples representing the different metabolic modes of the hosts and symbionts. Since last summer, I have been able to go with Professor Thornhill to the Gulf of Mexico to collect vestimentiferan worms from the cold seeps, which occur deeper than 1500 ft below the surface using a deep-sea submersible. Additionally, earlier this summer this fellowship allowed me to go with Professor Thornhill again to collect species from the frenulate lineage in the coastal waters and fjords in Norway. The samples that we obtained on these research cruises have been essential in filling out our evolutionary trees. By adding more species to our tree, we have been able to reduce some of the ambiguity of last summers analyses, as well as characterizing some previously understudied species.

From my analyses this summer, we have been able to draw up two possible evolutionary scenarios for siboglinid evolution: one in which Osedax species are the ancestral group and one where the frenulates are the most ancient lineage. However, the most striking results from our newest evolutionary trees are the complex evolutionary history of frenulate lineages. While the frenulates are the most abundant and morphologically diverse of the siboglinid lineages, they are also the least studied. Previous methods of frenulate identification were limited to morphological characteristics, such as the number of pinnules, however, evolutionary trees based on molecular techniques have challenged these previous methods of frenulate identification. This suggests that there is a complex internal evolutionary structure among frenulate taxa that is not supported by morphological comparisons alone. A powerful example of this inference is the evolutionary distance between species that had been placed in the same genus based on morphological characteristics. Therefore, the results of this research have teased apart the specific relationships among the frenulate taxa, as well as the deeper evolutionary relationships of the siboglinid lineages. We are currently preparing this work for publication in the journal of Molecular Phylogenetics and Evolution, and plan on applying our knowledge of siboglinid host phylogeny to a more functional understanding of the evolution of hemoglobin in these highly specialized annelid worms.

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Funded by the Doherty Coastal Studies Research Fellowship