

Dispersion and morphology of the Caribbean spiny lobster *Panulirus argus* phyllosoma



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Abstract

Because of the r-selected dispersal strategy of *Panulirus argus*, populations throughout the Caribbean have been shown to be highly connected. However, some of these populations contain two major genetic cohorts of *P. argus*. This study expands the area of study of *P. argus* from the Caribbean to Bermuda and the Sargasso Sea through collection and analysis of *P. argus* phyllosoma. Phyllosoma were sampled nightly along a sailing transect in the Sargasso Sea from San Juan, Puerto Rico, to St. George, Bermuda, to New York City, USA. Individuals captured in nightly tows were identified, staged, and sized. Additionally, genetic analysis was conducted on select individuals by analyzing single-nucleotide polymorphisms in the mitochondrial gene of the hypervariable domain of the control region (HV-CR₄₁ or HV-MCR₄₁). Results indicate that: 1) the abundance of phyllosoma, as well as number of unique stages sampled, is negatively correlated with latitude 2) there is substantial size variation within each larval stage, 3) individuals from both genetic lineages are present throughout the Sargasso Sea and Bermuda.

Introduction

Our aim was to study *Panulirus argus* larvae, called phyllosoma, in the Sargasso sea, in order to learn the following:

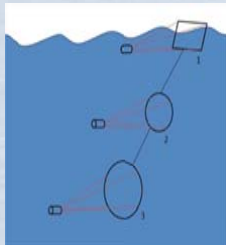
- ♦ If variation within phyllosoma developmental stages indicated discrete cohorts
- ♦ If the Bermudian population of *P. argus* phyllosoma is isolated from the Caribbean
- ♦ If genetic diversity of phyllosoma in the Sargasso Sea increases from South to North



Figure 1. *Panulirus argus* life cycle. https://doi.org/10.1007/978-1-4939-9888-8_12

Materials and methods

- Sailing transect from San Juan, Puerto Rico, to St. George's, Bermuda, to New York City, USA
 - Collected via:



1. **Surface-** Neuston net (1 m x 0.5 m, 335 µm mesh)
2. **10 m below surface-** 1 m ring plankton net (335 µm mesh)
3. **50 m below surface-** 2 m ring plankton net (335 µm mesh)

- Identified, staged on developmental scale (1-10 discrete stages), measured for size
- DNA barcoding using Mitochondrial Hypervariable Control Region (HV-MCR₄₁)

Morphological Analysis of *Panulirus argus* phyllosoma

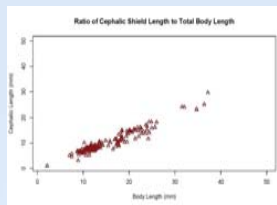


Figure 2. The ratio of body length to cephalic shield length in millimeters. The measurements show a strong linear correlation throughout the study, suggesting that independent of development or location, *Panulirus argus* phyllosoma develop with constant body proportions.

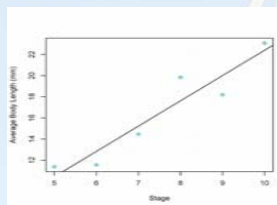


Figure 5. Average body size of each stage. A linear regression analysis shows a strong linear correlation between body size and stage, with an $R^2 = 0.8682$ and a p-value of .004

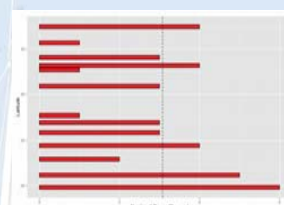


Figure 3. Number of developmental stages collected at each latitude. The dotted line at 3 indicates the average number of stages observed per station. There is no notable trend in richness of stages showing that most of the locations sampled likely had phyllosoma originating from the same amount of locations

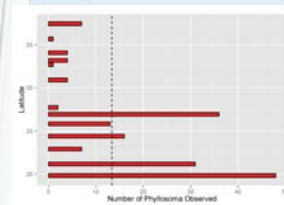


Figure 6. Abundance of phyllosoma collected across latitude. The dotted line at 13 indicates the average number of phyllosoma observed per station. There is a significant decreasing trend as latitude increases, suggesting that phyllosoma are either dispersing in the north, or that less phyllosoma are present overall farther north

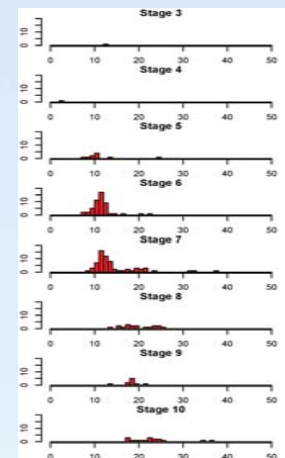


Figure 4. Histograms of sizes divided by the total body length. There was high amounts of variability in the number of phyllosoma collected of each stage, with stage 7 being the most frequently collected. Size generally showed a positive trend with further development, however multiple stages showed unimodal size classes around the same size.

Genetic Analysis of *Panulirus argus*

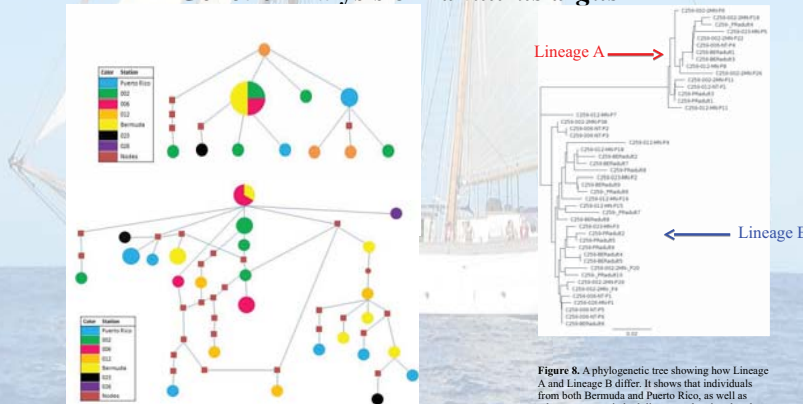


Figure 7. Shows the Haplotype tree for Lineage A (top) and Lineage B (bottom). They show the relatedness with comparison to station as well as which stations share haplotypes. The tree shows that there are examples of each station in each lineage and that no one station precedes the others. Most stations tend to share haplotypes solely with themselves. Only Bermuda and station 006 are shown to share a haplotype. This occurs in both lineages, providing another example of how mixed they are.

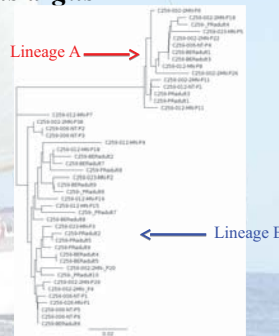


Figure 8. A phylogenetic tree showing how Lineage A and Lineage B differ. It shows that individuals from both Bermuda and Puerto Rico, as well as other stages, are in both lineages, showing that they are intermixing.

Acknowledgments

This work would not have been possible without the resources, manpower, and support of the Sea Education Association (SEA). In particular, the mentorship of Dr. Eric Zetler, Dr. Amy Sunda, and Dr. Linda Amaral-Zetler was invaluable for the success of this project. We thank Dr. Annette Govindarajan for guidance with single nucleotide polymorphism analysis, and Dr. Laura Cooney for guidance of fieldwork, sample preparation, and general guidance for this project.

Additionally, data collection would not have been possible without the tireless work of the crew of the *SVV Corwith Crane*, who worked around the clock to ensure that data was collected effectively and nightly throughout the sailing voyage. Lastly, from preparation, to data collection, to analysis, support by the SEA class C-259 has been an indispensable resource.

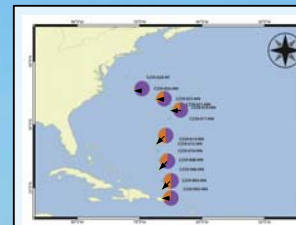


Figure 9. A map of our research stations. Yellow sites had individuals that were genetically analyzed. Shows Lineage A in Orange and Lineage B in Purple. Lineage B seems to be more frequent, especially north of Bermuda. The fact that both exist across the entire Sargasso Sea has never been documented before and shows that, while they are mixing, they are staying separate.

Policy Impacts

The discovery of the presence of lineage A and lineage B in the Sargasso Sea and Bermuda is an important point in understanding the connectivity of Bermuda to the Caribbean. Both of these lineages are present in Bermuda, though it is unclear how connected they may be to each other. This is foundational to the creation and upkeep of a sustainable Bermuda fishery, since these separate lineages may need to be managed differently. Additionally, our research gains insight into the understanding of *Panulirus argus* phyllosomal development, an important key to future research.

Conclusions

- Some phyllosoma stages have a definite unimodal size classes (stages 5, 6, and 7), however size variability increases as developmental stage increases
- Larger/older larvae are found closer to the center of the gyre, suggesting longer retention
- Genetic distance is not related to geographic distance
- The two different genetic lineages were found at all stations
- Adults from Puerto Rico and Bermuda were not genetically more related to the phyllosoma larvae collected closest to them