# 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-CR<sub>d1</sub>, or HV- $MCR_{d1}$ ). 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



## 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.  $335 \,\mu m \, mesh)$
- 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-MCR<sub>d1</sub>)

## Morphological Analysis of *Panulirus argus* phyllosoma



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.

## Acknowledgments

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## **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

- size variability increases as developmental stage increases
- Genetic distance is not related to geographic distance
- The two different genetic lineages were found at all stations
- larvae collected closest to them





Stag	je 3		
20 Stag	30 je 4	40	50
20 Stag	30 je 5	40	50
20 Stag	30 je 6	40	50
20 Stag	30 je <b>7</b>	40	50
ہ 20 Stag	30 je 8	40	50
20 Stag	30 Je 9	40	50
20 Stage	30 e 10	40	50
20	30	40	50

**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.

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.

Some phyllosoma stages have a definite unimodal size classes (stages 5, 6, and 7), however Larger/older larvae are found closer to the center of the gyre, suggesting longer retention

Adults from Puerto Rico and Bermuda were not genetically more related to the phyllosoma