Eel Biodiversity and Population Connectivity in the Sargasso Sea

Mareike Duffing Romero[1,2], Olivia Robson[1,3], Katarina Rolf [1,4], Sarah Stratton[1,5]

[1] Sea Education Association, Woods Hole , MA, [2]Humboldt State University, Arcata, CA, [3]University of Connecticut, Storrs, CT, [4]Carleton College, Northfield, MN, [5]Oberlin College, Oberlin, OH

Abstract

Eels play a major ecological role as predators and prey in coastal and marine food webs to help maintain other populations. Several species of eel migrate to the Sargasso Sea to spawn each year, yet little is known about eel biodiversity and abundance in the Sargasso Sea. We aimed to assess the biodiversity and population connectivity of eels by using the bandtooth conger eel, *Ariosoma balearicum,* as an indicator species and examining different environmental parameters. We collected a total of 262leptocephali covering 12 families and 15 species. Eel biodiversity was significantly greater at 50m depth than at the surface, but was not influenced by environmental parameters such as temperature, salinity, or chlorophyll-a concentration. The distribution of *A. balearicum* changed across geographic regions of the Sargasso Sea, with the highest concentrations in the Tropical Atlantic, and decreasing concentrations farther north. This research has helped contribute to a better understanding of economically and ecologically important eel species in the Sargasso Sea.

Introduction

- The Sargasso Sea is a spawning ground for many species of eel, including American, European eel and bandtooth conger.
- Leptocephali participate in diel vertical migration (DVM), the pattern of movement up to the epipelagic zone at night and back down into greater depths during the day
- No studies have measured eel diversity at the surface
- Bandtooth conger eels are a marine species that spawn in the Sargasso Sea before migrating to nursery grounds in rocky-sandy coastal areas
- Based on myomere (muscle band) counts, Miller (2002) suggests that there are two distinct *Ariosoma* populations in the Sargasso Sea.
- Population connectivity of bandtooth conger eels could explain eel population connectivity in the Sargasso Sea

Methods

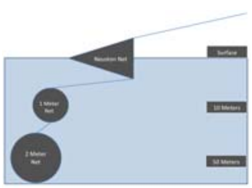

Figure 1: Diagram depicting the triple stacked net tow with the 2m net at 50m depth, the 1m net at 10m depth and the Neuston net at the surface

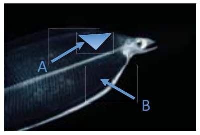

Figure 2: Eel larva with A) the proposed section of tissue that was excised from leptocephali samples for genetic analysis, and B) myomeres.

- Eel collection using a stacked net tow at surface, 10m, and 50m (Figure 1)
- Morphological ID, excised tissue samples, myomere counts (Figure 2)
- Genetic analysis of excised tissue samples using PCR, Geneious and TCS

Results and Discussion

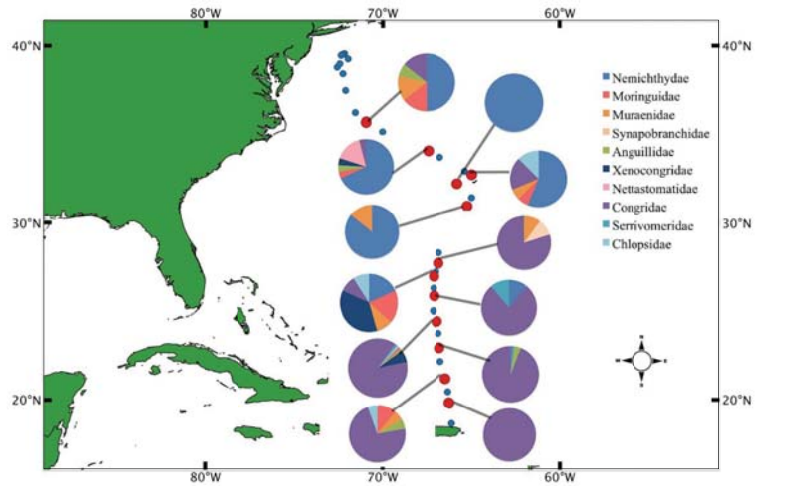

Figure 3: The cruise track from Puerto Rico to New York City. Each circle corresponds to a station where net tows occurred: eels were found at red circles, and not found at blue circles. The pie charts for each station represent the diversity of eels collected. There is significant geographic distribution of *A. balearicum* between sample sites, with the proportion of *A. balearicum* at each station decreasing with increasing latitude.

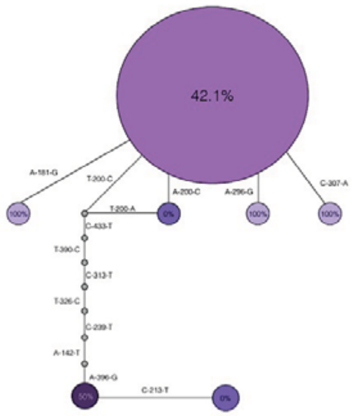

Figure 4: Haplotype network for *Ariosoma balearicum* using 16S ribosomal gene (TCS). The size of the oval corresponds to the amount of organisms sharing the same haplotype. Circles are colored based on the percent of the individuals within each haplotype that had a high myomere count.

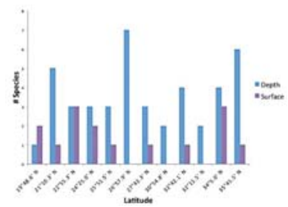

Figure 5: Leptocephali richness at the surface and at 50m depth. Abundance is not significantly different at depth than at the surface. There are significantly more species at depth than at the surface.

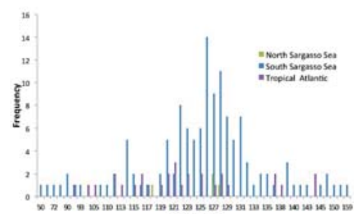

Figure 6: The frequency of *Ariosoma balearicum* with a given myomere count at each location sampled. Myomere counts were categorized into two groups: high (>127) and low (<127). There is a positive correlation between myomere count and length.

Policy Implications

- This is a key step to better understand effective management strategies for eels in the Sargasso Sea.
- We have more knowledge regarding the areas where the highest amount of biodiversity is maintained as well as the connectivity between populations of leptocephali.
- This information will allow policy makers to more effectively manage key areas within the Sargasso Sea.
- It provides a good basis for future SEA students hoping to further gather information on this subject.

Conclusions

- Leptocephali diversity was positively correlated with increasing depth and there is no significant correlation between eel biodiversity and environmental variance as originally predicted in our hypotheses.
- Currents did affect the distribution of leptocephali, as no eels were collected north of the Gulf Stream. However, our hypothesis that species richness would peak around the Subtropical Convergence Zone (STCZ), a frontal boundary between 25°N and 30°N, as found by Miller and McCleave (1994), was not supported by our data.
- Species richness and abundance did not change significantly between geographic regions, but species distribution did. We found a significant distribution of *A. balearicum*, with more samples found in the Tropical Atlantic and Southern Sargasso Sea than the North Sargasso, where it was replaced as the most abundant species by *Nemichthys scolopaceus*.
- There was more genetic variation than expected in the South Sargasso Sea, and significant variation between all sites, suggesting lots of different haplotypes but no pattern. However, we saw no significant geographic distribution based on myomere count. This could be because our sampling was not conducted in the same areas as Miller (2002).

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