

A genetic and morphological analysis of Atlantic Sargassum

Elizabeth F. Olson^{1,2} and Elizabeth M.B. Tonkin^{1,3}

¹Sea Education Association, Woods Hole, MA; ²Northeastern University, Boston MA; ³Colby College, Waterville ME

Abstract

During a five week cruise of the Sargasso Sea, three morphotypes of *Sargassum*, morphologically identified as *Sargassum fluitans III*, *Sargassum natans I*, and *Sargassum natans VIII*, were studied. SEA measured water temperature, phosphate concentration, current strength and direction, and wind speed and direction. None of these factors correlated with the change in the relative masses of the different *Sargassum* types. Satellite data gathered from NOAA shows that the current direction over a broader region does correlate with changes in *Sargassum* distribution, with *S. natans VIII* confined to areas south of the Sargasso Sea and *S. natans I* staying within the north Atlantic gyre. Genetic analysis of the mitochondrial gene cytochrome-oxidase I (COI) revealed very little variation between species. Out of a sequence of 552 nucleotides, only one was found to vary between species. This indicates that a different gene should be found to do a more robust analysis on potential speciation.

Introduction

- *Sargassum* is a brown macroalgae globally distributed in temperate and tropical waters
- *Sargassum natans* and *Sargassum fluitans* float freely and are never anchored to the sea floor
- Found floating as individual clumps or aggregated mats of various sizes
- Ecosystem engineer: provides a valuable habitat to
 - > 145 species of invertebrates
 - 100 species of fish
 - 10 endemic species
- Recently a rare variety of *Sargassum*, *S. natans VIII*, has been seen in the Caribbean
 - It has thick stems and broad leaves characteristic of *S. fluitans III*, but like *S. natans I* lacks thorns and has spherical floats (as opposed to oblong in *S. fluitans III*).
- This study examines the distribution and genetics of *Sargassum* in the North Atlantic.
- *S. natans I* and *S. fluitans III* are known to inhabit the Sargasso Sea but no factor has been shown to determine which species appears where in the Sea. Understanding distribution of *S. natans I* and *S. fluitans III* will help to clarify their roles in the ecosystem.
- *S. natans I*, *S. fluitans III*, and *S. natans VIII* were genetically analyzed in order to explore the genetic diversity within and across species and to determine how genetic sequence lines up with morphological appearance.



Image: *Sargassum natans*, Meyers Konversations-Lexikon

Methods

- Samples of *S. fluitans III*, *S. natans I*, and *Sargassum natans VIII* were collected during late April and May 2015 on a cruise from San Juan, PR to New York, NY via Bermuda. *Sargassum* was collected every day at noon and midnight using a Neuston net and morphologically identified.
- Satellite data of currents from NOAA's ocean current analysis real-time (OSCAR) project were also examined following the cruise, in order to look at a broader area of the Sargasso Sea.
- Samples for genetic analysis were collected at five stations along the cruise, as well as *S. natans VIII* samples collected March 2015 around the Lower Antilles. At each of the sampling stations ten specimens were collected of each species present.
- Five-centimeter fronds were cut from each individual and were thoroughly scraped clean of any epibionts and dried for 48 hours in silica gel. A DNeasy Plant Minikit (Qiagen, USA) was used for Deoxyribonucleic Acid (DNA) extraction and genomic DNA was cleaned using a PowerClean Pro DNA Clean-up Kit (MO BIO, USA). A brown algae-specific marker was used to amplify the cytochrome oxidase I (COI) gene.

Results

Species Composition by Mass (g) at Sample Stations

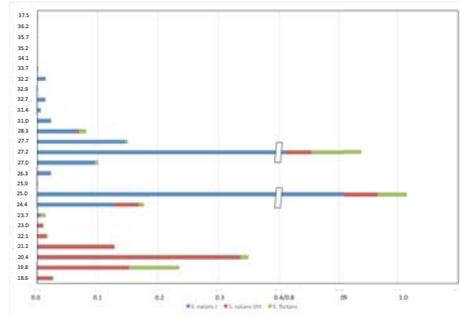


Figure 1: Species composition at sample stations (latitude) along the cruise track, along with the total mass (g) of the species at four stations. At the beginning of the cruise, *S. natans VIII* was observed in great abundance, declining while we went north. *S. fluitans III* began to appear in greater quantities, dominating at around 23° N, but *S. natans I* was observed with increasing amounts, dominating from 24°N northward. The total mass of the dominant species at each station declined gradually along the cruise track as we moved north.

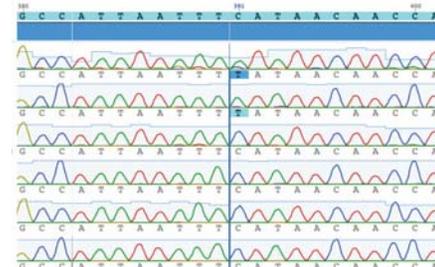


Figure 3: Selected section of COI gene shown with chromatograms for forward and reverse sequences for an example of each variety. The difference between the *S. fluitans III* and *S. natans I* species are distinguishable in this section. COI sequences did not contain significant differences between *S. natans I*, and *S. natans VIII*, with a single nucleotide between *S. fluitans III* and *S. natans I* varieties. The single nucleotide difference seen between *S. fluitans III* and *S. natans I* was not consistent, as one sample of *S. fluitans III* had the difference and one sample of *S. natans I* did not. This may indicate that COI is not an appropriate genetic marker for *Sargassum*.

5-Day Interval Ocean Surface Currents (meter/sec)

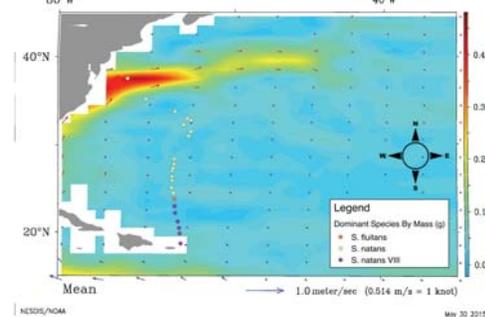


Figure 2: Sample stations from the cruise track overlaying satellite data of the five day average of current speed and direction centered on April 27, 2015. Current magnitude and direction are indicated by arrows on the map, red arrows are westward currents and blue arrows are eastward currents. Current magnitude is also represented by the heat map, where warmer colors indicate higher current speeds. Current data from NOAA's ocean current analysis real-time (OSCAR). A correlation was found between sea surface current magnitude and the distribution of *Sargassum*. It appears that the shift in surface current direction from westerly to easterly around 25° N is accompanied by a shift in dominant species of *Sargassum* (by mass).

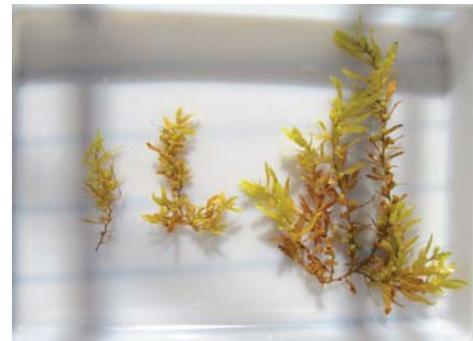


Figure 4: Fragments of *S. natans I*, *S. fluitans III*, and *S. natans VIII*. *S. natans I* has narrow blades and spherical floats with apical processes. *S. fluitans III* has broad blades, oblong floats that lack apical processes, and small "thorns" on its stem. *S. natans VIII* lacks thorns and has the broad blades of *S. fluitans III* but has spherical floats without apical processes. Image: Amy Siuda.

Policy Implications

- The apparent transition zone between *S. natans I* and *S. natans VIII* is an important discovery in determining how *Sargassum* is distributed, as it is evidence that the *Sargassum* is being carried into the Sargasso Sea from different origins. This indicates that the *Sargassum natans VIII* causing the *Sargassum* inundation is not originating from the Sargasso Sea, and thus any attempts to prevent further inundations must focus elsewhere to find the source of the *Sargassum*.



Caribbean *Sargassum* inundation. Image: George Smith.

Conclusions

- Distribution of *Sargassum* varies with the overall current direction. This may mean that different *Sargassum* types originate in different areas of the sea, and then are distributed to new locations by the currents.
- 90% of the *Sargassum* observed during a recent research cruise in the Caribbean was *S. natans VIII*, a species previously thought to be rare. Given our results, *S. natans VIII* is likely transported by westerly currents from its origin, which could be either in the Caribbean or east of South American coastlines.
- COI sequences did not contain significant differences between *S. natans I* and *S. natans VIII*, with a single nucleotide between *S. fluitans III* and *S. natans I* varieties. This supports our morphological identification of the species of *Sargassum*, but does not give any insight into intraspecific variation and very little insight into interspecific variation. According to the COI marker, all three varieties of *Sargassum* collected, including the two different varieties of *S. natans* and *S. fluitans III*, were almost genetically identical. For future studies on Atlantic species of *Sargassum*, a better marker is needed for distinguishing species and for use as a barcode.

Acknowledgements

Poster Template © Colin Purrington. Olson and Tonkin would like to thank Sea Education Association for providing the opportunity to perform the following research. We would also like to acknowledge Linda Amaral-Zettler for her mentoring, and Amy Siuda for her help with morphological identities and guidance with this project. Thanks to the crew of the SSV Corwith Cramer for their help with data collection.