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Sargassum Infauna Community Structure in the Florida Straits and Gulf Stream

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Thesis of Dayna S. Hunn

Submitted in Partial Fulfillment of the Requirements for the Degree of

Master of Science M.S. Marine Biology

Nova Southeastern University
Halmos College of Natural Sciences and Oceanography

December 2019

Approved:
Thesis Committee

Major Professor: David Kerstetter, Ph.D.

Committee Member: Christopher Blonar, Ph.D.

Committee Member: Amy Hirons, Ph.D.

Sargassum Infauna Community Structure of the Florida Straits and Gulf Stream

By

Dayna Hunn

Submitted to the Faculty of
Halmos College of Natural Sciences and Oceanography
in partial fulfillment of the requirements for
the degree of Master of Science with a specialty in:

Marine Biology

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Abstract

Community structure of *Sargassum*-associated organisms was examined from 11 sampling locations in the Florida Straits and Gulf Stream from May—September 2018 using a combination of modified shrimp trawls and dip nets. A total of 5413 organisms were collected from *Sargassum* habitat representing 14 species from 10 families. A core group of organisms (*Platynereis dumerilii*, *Litiopa melanostoma*, *Portunus sayi*, *Portunus spinimanus*, *Leander tenuicornis*, and *Latreutes fucorum*) were found throughout the entirety of the geographic range surveyed. This core community was not found to vary significantly with increasing distance to shore ($P=0.217$) and latitude ($P=0.217$), nor did it correlate with environmental variables such as salinity ($P=0.067$), and temperature ($P=0.193$). However, community structure was found to vary with clump size ($P=0.024$), with larger clumps harboring more speciose communities. The *Sargassum* community in the Florida Straits and Gulf Stream appears to provide habitat for a consistent core group of organisms. In turn, this stable group offers a sustainable food source for a variety of important, higher trophic level organisms that utilize *Sargassum* patches for a food source, shelter, and breeding purposes.

Keywords: *Sargassum*, community structure, stable, *Latreutes*, *Portunus*, invertebrate

Introduction

Free-floating aggregations of pelagic *Sargassum* are commonly found in nearshore and offshore waters throughout the North Atlantic Ocean, including the Caribbean Sea and the Gulf of Mexico. There are several species of *Sargassum*, but only two are completely holopelagic, meaning they spend their entire lifecycle on the surface of the water. *Sargassum fluitans* and *S. natans* (henceforth, simply *Sargassum*) can be identified by their yellow to golden color, highly branched thallus, leaf-like blades, and floating, gas-filled pneumatocysts. The two species vary slightly in appearance, with *S. natans* having a slender leaf structure with smooth stems and *S. fluitans* having a broader leaf and flexible thorns on the stipes. Multiple morphological forms with varying blade and float shape are known with both species (Laffoley et al., 2011).

Sargassum mats can vary from small, isolated patches to large patches and windrows that continue for several kilometers depending on certain mesoscale features such as current flow, storms, and wind. (Winge, 1923; Parr, 1939). Large patches are a result of low wind and areas where converging currents produce downwelling, resulting in massing of *Sargassum*. Windrows (colloquially called “weedlines”) occur due to Langmuir circulation (Langmuir, 1938).

The most well-known area in which *Sargassum* accumulates is the Sargasso Sea. The Sargasso Sea gets its name from the vast amount of *Sargassum* that collects and circulates in the western mid-Atlantic Ocean. The Sargasso Sea is unique in that it is completely defined by currents unlike other seas or bodies of water which are defined by landmasses. These defining currents include the North Atlantic Current in the northern region, the Canary Current in the eastern region, the North Atlantic Equatorial Current in the southern region, and the Gulf Stream in the western region.

History of *Sargassum* Studies

Christopher Columbus and his crew are credited with giving the Sargasso Sea its name. The word *Sargassum* is derived from the Portuguese word *salgazo*, meaning grapes. Likely they used this word due to the fact the floating pneumatocysts on the plants resembled small grapes (Weatheritt, 2006). Throughout his voyage in 1492, Columbus mentions *Sargassum* frequently, where his reports indicated that in some cases there would be little to no *Sargassum* and others would mention much larger mats. In one instance, he reported the sea was completely covered in

Sargassum and the crew feared the drifting *Sargassum* covered submerged reefs or rocks, not knowing the nearest coastline was miles away (Deacon, 1942).

Since Columbus, ship logs of captains from the western North Atlantic recorded similar opinions and concerns. By the 1800s, it was common belief among sailors that crossing these waters was dangerous due to the massive amount of *Sargassum* that could stall a ship in low wind conditions (Ryther, 1956). A log from a Danish ship reported that the biggest gathering of *Sargassum* he witnessed was so extensive that no open water could be seen and the *Sargassum* quickly regrouped after the ship drifted through, echoing Columbus's report.

By the mid 19th century, scientists debunked the belief that the Sargasso Sea was a dangerous area, and started to give more accurate distributions of *Sargassum*. One of the first scientists to study this was German scientist Otto Krummel. He used records from sea captains to assess the abundance of *Sargassum*. Based on his findings, he concluded that the Sargasso Sea covered an elliptical-shaped area from the middle of the Atlantic westward to the North American coast (Ryther, 1956; Krummel, 1891; Dickson, 1894). Winge (1923) expanded on this study by using samples collected from Danish expeditions as well as records from captains, and showed the previous distribution was much larger than what Krummel predicted. He placed the eastern boundary near the Azores and the southern boundary near the West Indies. The northern and western boundaries shifted seasonally due to changing weather conditions. The actual boundary of the Sargasso Sea was determined by Columbus O'Donnell Iselin, who determined the current system in the North Atlantic Ocean outlined the boundary of the Sargasso Sea. These currents enclose a giant eddy which slowly revolves in a clockwise motion, concentrating mats of floating *Sargassum* (Iselin, 1936).

By the 1930s, quantitative studies were conducted on *Sargassum* to gain further knowledge into the abundance, biology, and associated fauna. Parr (1939) was the first scientist to study the abundance of *Sargassum* in the Sargasso Sea. Throughout his expeditions, he traveled over 7000 miles and collected over 5000 pounds of *Sargassum*. He estimated there to be approximately 7 million tons of *Sargassum* in the Sargasso Sea. Today, the abundance of total *Sargassum* is still unknown due to its constant movement and widespread dispersal, but other estimations have the total biomass between 2 to 11 million tons (Butler et al., 1983; Luning 1990; South Atlantic Fishery Management Council, 2002; Wang and Hu, 2016).

Scientists have also debated the origin of *Sargassum*, with some suggesting that the patches derived from coastal plants that detached from the bottom and continued to float with the prevailing currents. However, today it is widely agreed upon that *Sargassum* is a completely pelagic species. Parr (1939) showed that species of vegetation torn from littoral bottoms were insignificant and that approximately 99% of the *Sargassum* found in the Sargasso Sea was composed of two species: *S. fluitans* and *S. natans*. He also determined that an insignificant amount of *Sargassum* was found below the surface. Woodcock (1950) extensively studied the extreme buoyancy of the *Sargassum* supporting Parr's results by showing that *Sargassum* is adapted to stay on the surface of the ocean rather than attached to substrate. Other evidence that supports a completely pelagic lifecycle is the fact that *Sargassum* lacks a basal holdfast, a structure of aquatic algae that serves to anchor the organism to the substrate.

Sargassum Distribution

Sargassum can be found in varying size distributions in the North Atlantic Ocean, Caribbean Ocean, and Gulf of Mexico. It arrives throughout these regions seasonally by the loop system. Multiple studies have shown the continuity of the movement of *Sargassum* in the regions listed above by using satellite data to detect large slicks (Gower et al., 2006; Gower and King 2008). In the beginning of the year, it is detected in the northwestern region of the Gulf of Mexico. It expands and drifts east where it is caught by the Gulf Stream and advected into the western North Atlantic Ocean. In July *Sargassum* is detected in both the Gulf of Mexico and western Atlantic Ocean along the eastern boundary of the United States. *Sargassum* continues to travel with the Gulf Stream until approximately 45°W. Here, high pressure anomalies form, causing northern wind currents to push *Sargassum* south into the Caribbean Sea. Once it enters the Caribbean Sea, *Sargassum* is pushed west by ocean and atmospheric currents, then continues into the Gulf of Mexico or gets transported through the Florida Straits (Gower et al., 2006; Gower and King 2008; Gower and King, 2011; Frazier, 2014). An increasing amount of *Sargassum* becomes beached on shorelines in the Greater Caribbean region, including Mexico and the Atlantic coast of the United States (Gavio et al., 2015; Hu et al., 2016; Tussenbroek, 2017).

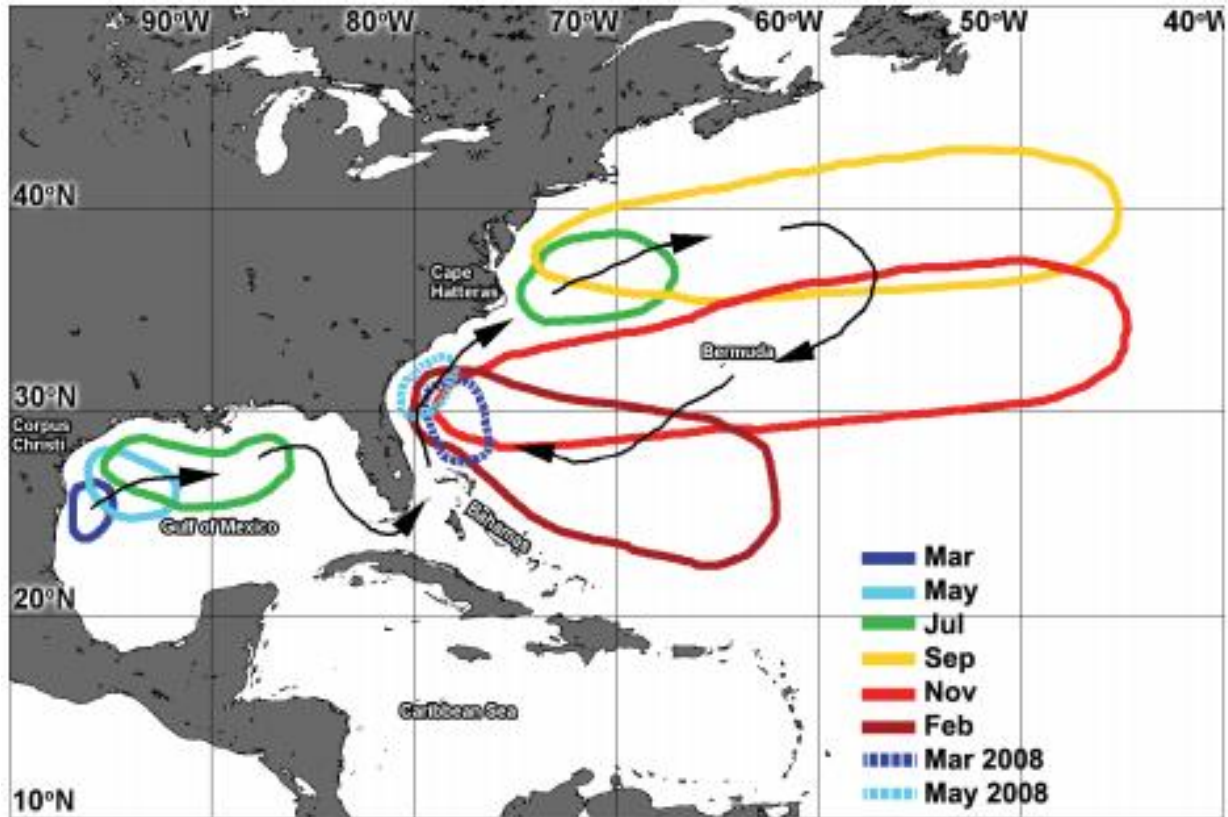


Figure 1: From Gower and King (2011) showing yearly distribution of *Sargassum* detected using satellite imagery. *Sargassum* is advected from a source area in the northwest Gulf of Mexico in the spring and transported into the Gulf Stream in the early summer. It then circulates with the prevailing currents in the fall and is moved south into the north Caribbean Sea in the winter.

Sargassum Community

The unique buoyancy adaptations of *Sargassum* and its wind-driven nature make it a major habitat for many organisms in areas of otherwise oligotrophic and shelter-poor waters in the open ocean. The *Sargassum* mats that occur throughout these pelagic regions provide substantial shelter and food for over 100 species of fish and over 145 invertebrate species, 10 of which are known to commonly inhabit such as the Sargassum shrimp, *Latreutes fucorum* and the Sargassumfish, *Histrion histrio* (Coston-Clements, 1991).

Sargassum-associated organisms can be categorized into four general groups: (1) sessile fauna, (2) mobile fauna, (3) clinging fauna, and (4) associated nektonic fauna (Martin, 2016; Fine, 1970). Sessile organisms are found permanently attached to the *Sargassum* and include bryozoans, hydroids, and tubeworms. The mobile fauna includes organisms such as polychaetes, nudibranchs, and snails that need a source of substrate on which to attach and move. For example, the polychaete *Platynereis dumerilli* secretes mucous tubes that entwine throughout the leaves and stipes of the *Sargassum* in which it can travel (Chambers and Garwood, 1992). Clinging fauna are found grasping to the *Sargassum*, including invertebrates such as shrimp or crabs, as well as vertebrates such as *H. histrio*. Many of these organisms possess unique adaptations and colorations to help them blend into the surrounding *Sargassum* (Weis, 1968). Associated nektonic fauna include organisms that can be found swimming or foraging near *Sargassum* aggregations, including fishes, sea turtles and even seabirds.

Apart from providing food and shelter, this *Sargassum* environment also acts as a nursery ground for many organisms. Four of seven sea turtle species use the *Sargassum* habitat in the western North Atlantic Ocean during their first few years of life, including loggerhead *Caretta caretta*, green *Chelonia mydas*, hawksbill *Eretmochelys imbricate*, and Kemp's ridley, *Lepidochelys kempii*. Both post-hatchlings and juvenile sea turtles exploit the habitat, using it as a source of shelter and food (Witherington et al., 2012). Various species of larval and juvenile fishes also benefit from inhabiting the *Sargassum*. Hoffmayer et al. (2005) collected over 18,000 pelagic larval and juvenile fishes in the northern Gulf of Mexico from in and around *Sargassum* habitats. These unique communities also attract predatory fishes and seabirds (Wells and Rooker, 2004a). Predatory fishes that commonly inhabit *Sargassum* include greater amberjack *Seriola dumerili*, yellowfin tuna *Thunnus albacares*, blackfin tuna *T. atlanticus*, and the common

dolphinfish *Coryphaena hippurus*, all of which are targeted by recreational and commercial fisheries (Casazza and Ross, 2008).

Until recently, relatively few studies have investigated the structure of the *Sargassum* community. Most studies have focused on differences in the fish community or how the community changes with broad geographic distances or season (Wells and Rooker, 2004a; Wells and Rooker, 2004b; Casazza and Ross, 2008; Rooker et al., 2006; Moser et al., 1998; Hoffmayer et al., 2005; Stoner and Greening, 1984; Huffard et al., 2014). For example, Moser et al. (1998) determined that the community structure of the *Sargassum* patches varies with patch size. They used remote operated vehicles (ROV) to determine if there was a change in abundance of fishes with differing patch sizes. They found only four taxa of fishes when no *Sargassum* was present, 12 under clumps, and 19 under larger mats showing that fish abundance increases with larger patch size. Moser et al. (1998) also suggested that species composition changes as the *Sargassum* mats drift closer to shore; for example, Wells and Rooker, 2004b found that juvenile amberjacks are rarely found on nearshore clumps. Furthermore, Huffard et al. (2014) determined that biological community structure changed with mat morphology. Larger mats held more large motile fish whereas smaller mats, broken up by storms or wind, held only smaller members of the community.

Even fewer studies have investigated the change in the community structure of the invertebrates that inhabit the *Sargassum*. Stoner and Greening (1984) investigated the change in geographic location in the *Sargassum* community, particularly the change between the Sargasso Sea and the Gulf Stream. They found a weak correlation between number of organisms and size of the clumps in both locations. Species composition was relatively stable over clump size however species richness increased with clump size. They related this to the fact that larger clumps can house more individuals. The more interesting finding of the Stoner and Greening (1984) study was the difference in community structure with geographic location, as *Sargassum* communities in the Gulf Stream showed lower species richness and less variable species composition than communities in the Sargasso Sea.

Sargassum Parasite Community

Another aspect of the *Sargassum* community that has been relatively unstudied is the parasitic fauna of the organisms that live in and around the *Sargassum*. The study of parasites

can significantly expand the understanding of an ecosystem. First, parasite diversity exceeds that of free-living species (Poulin and Morand, 2000). Second, parasites can shape how energy flows through an ecosystem by regulating the abundance of their hosts by either affecting the host pathologically or altering their behavior to make them more susceptible to predation (Lafferty and Morris 1996; Hudson et al., 2006). Parasites can also serve as biological tags which provide information on the host's long-term feeding history (Kabata, 1963).

Only a few studies have explicitly mentioned parasites of *Sargassum*-associated organisms such as *C. hippurus*, a common predator found near *Sargassum*. These studies mentioned the occurrence of gastric parasites, such as hemiurids in the genus *Dinurus* in *C. hippurus* (Carbonell et al., 1999; Brewton et al., 2016). Although only parasite occurrence was reported, information involving parasites provides further information on the feeding ecology of the *C. hippurus*. For example, the lifecycle of *Dinurus* sp. uses benthic gastropods as first intermediate hosts, and crustaceans or planktivorous fishes as the second intermediate host (Koie, 1979). The presence of these parasites indicates that *C. hippurus* had probably fed heavily on planktivorous fish or crustaceans which in turn had previously fed on gastropods.

Another organism previously examined for parasites in the *Sargassum* community is *Latreutes fucorum*, a species of shrimp commonly found in *Sargassum* throughout the Gulf of Mexico, western Atlantic Ocean, and Caribbean Sea. Martin et al. (2019) examined *L. fucorum* specimens from the Gulf of Mexico, Sargasso Sea and eastern Caribbean Sea and found a 6.7% infection rate with the bopyrid isopod, *Probopyrinella latreuticola*. Parasites in the family Bopyridae commonly infect decapods and are known to cause significant negative impacts on their host by preventing egg production, castrating female gonads, and feminizing males (Anderson, 1977; O'Brien and Van Wyk, 1985).

Parasite studies allow for a better understanding of the ecosystems in which they inhabit. It is known that the *Sargassum* community acts as a nursery ground for many species (Wells and Rooker, 2004a). Previous studies have shown that nursery habitats such as mangroves have relatively low parasite diversity and infection rates, which could be due to nursery habitats being structurally complex and larval transmission stages of some parasites becoming physically impeded in successfully locating and infecting the host (Welsh et al., 2004). Since the *Sargassum* community is considered a nursery to many organisms, the rate of parasitism should be comparable to other nursery habitats. A better understanding of the parasitic fauna of the

Sargassum community may therefore also provide valuable insights of the ecosystem and feeding ecology of the component organisms.

Significance of *Sargassum*

Sargassum is an important component in open water ecosystems in the North Atlantic Ocean, Gulf of Mexico, and Caribbean Ocean. It acts as a primary source of food, shelter, habitat, and nursery ground for various invertebrates and vertebrates at multiple trophic levels. Due to its importance, a fishery management plan was enacted in 2002 and designated *Sargassum* as essential fish habitat (South Atlantic Fishery Management Council, 2002). Besides *Sargassum*'s significant benefit in pelagic food webs, it also acts as a natural barrier against erosion on beaches when it washes ashore. As it decays, nutrients are transferred to the beach and plants in which they inhabit (Tussenbroek et al., 2017; Williams and Feagin, 2010).

Since 2011, *Sargassum* has gained unwanted international attention due to unprecedented massive blooms washing up on beaches throughout the Gulf of Mexico, East Coast of the United States, and the Caribbean Sea, as well as Brazilian and West African coasts (Gavio et al., 2015; Wang et al., 2019; Schell et al., 2015). Inundations of *Sargassum* have sporadically occurred throughout these locations in the past, but not as frequently and in such quantities as are currently being reported (Hu et al., 2016). These mass strandings have negative impacts and have caused financial disorder to tourism, aquaculture facilities, and numerous coastal fisheries in these areas (Milledge and Harvey, 2016). As previously mentioned, studies have been conducted on the distribution, abundance and growth of *Sargassum* but few studies have observed how this increase is affecting the communities that inhabit the *Sargassum*.

Even with the current unwanted, negative effects of *Sargassum* it is still crucial to study the organisms that inhabit it. The aim of this study was to examine members of the vertebrate and invertebrate community that inhabit *Sargassum* throughout the Florida Straits and Gulf Stream, a geographic area that lacks significant data on community composition. Building upon prior work, the project had two main components. The first component was to further describe the composition and structure of the *Sargassum*-associated communities, as well as community-level effects resulting from differences in environmental and oceanic factors such as latitude, distance to shore, clump size, salinity, and temperature. The second component examined the

parasitic fauna of certain *Sargassum*-associated organisms to obtain a better understanding of the *Sargassum* food web.

Materials and Methods

Field Collection

Samples were collected within U.S. waters in the Florida Straits and Gulf Stream on various marine vessels. The majority of the samples were collected aboard the M/V *OCEARCH* during a research cruise from 27 May to 18 June 2018. An initial visual survey was conducted to spot *Sargassum* patches. Once a *Sargassum* aggregation was sighted, a tender boat was deployed from the main vessel to obtain the sample. Once at the *Sargassum* patch, the size of the patch was estimated using a scale system developed specifically for *Sargassum* by USGS (Table 1), and a GPS location was recorded. An 8' shrimp otter trawl was modified by removing the weighted doors from either side and attaching extra flotation to the top so that the net would stay on the surface of the water. The net was towed behind the tender through the center of the mat just below the water surface for approximately 5-10 minutes or until the codend was filled. If *Sargassum* was too scattered to deploy the trawl, hand dipnets were used to sample isolated patches. The *Sargassum* sample was placed in a plastic storage tote and either transported back to the ship and worked up immediately or placed in a standard chest freezer at -20°C for later examination. The remaining samples were collected in locations in south east Florida opportunistically from different vessels using hand dip nets after Expedition Gulf Stream ended (Figure 3).

Laboratory Processing

Each sample was sorted by taking clumps of *Sargassum* and shaking them vigorously through fresh water to dislodge any entangled or embedded organisms. Preliminary work indicated that fresh water induced most of the organisms attached or clinging to the *Sargassum* to drop off, allowing them to be more easily collected. The shaken clump was then meticulously examined visually and picked over by hand to collect any organisms that still might be trapped in the *Sargassum* due to their cryptic coloration and small size. Fish were euthanized by cervical dislocation following IACUC protocol methods (Protocol 2018.06.DK7) and frozen in a Ziploc bag at -20°C until processing in the lab. All other organisms were removed from the *Sargassum*,

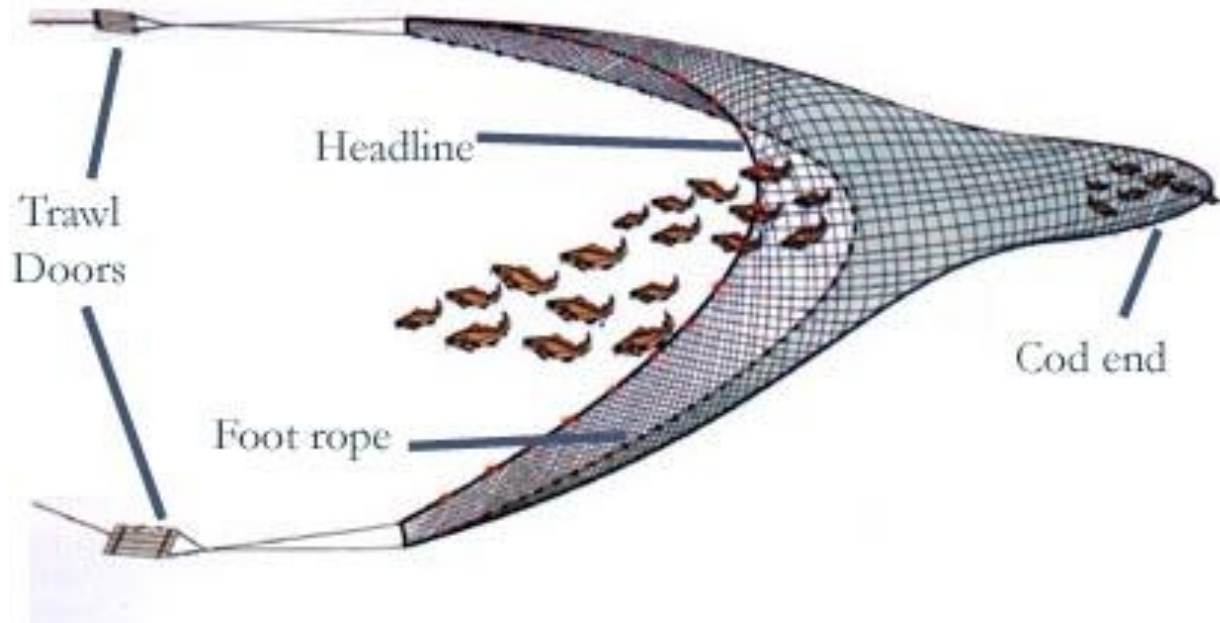


Figure 2: Diagram showing the 8' shrimp otter trawl used for collecting *Sargassum*. The trawl doors were removed and extra flotation was added to the headline to assure the net stayed in the upper level of the water column during deployment. During deployment, the net was pulled behind the tender vessel for 10 to 15 minute intervals or until the cod end was full of *Sargassum*. <https://www.memphisnet.net/product/4901/nets-trawl-complete>

preserved in 70% ethanol and placed in a -20°C freezer until further examination. Each organism was identified to species using the Bermuda Biological Station's "Identification Manual to the Pelagic *Sargassum* Fauna" (Morris and Mogelberg, 1973). Since so few fish were collected, parasitological dissections were only conducted on invertebrates (see below).

Invertebrate Processing

Invertebrate organisms collected included polychaetes, shrimps, crabs, isopods and snails. Random subsamples of 30 individuals of each species (when available) from each site were examined for parasites. None of these were found to harbor parasites. However, one species of shrimp, *Latreutes fucorum*, was infected by an ectoparasite located in the gill cavity beneath the carapace. Infected individuals were stored in 70% ethanol and sent to the National Museum of Natural History, Smithsonian Institution (USNM) for further identification.

Environmental variables

Environmental data such as surface temperature and salinity data were obtained during the Gulf Stream expedition. However, when collecting from the remaining sample sites environmental data was not collected due to equipment not being available. For these sites, estimated surface temperature and salinity data were downloaded from the publicly-available Gulf of Mexico 1/25 degree Hybrid Coordinate Model (HYCOM; www.hycom.org). Custom Matlab code was used to interpolate the HYCOM data from the surrounding grid to the exact location of the *Sargassum* sample using bilinear interpolation, or linear interpolation if the sample fell on the HYCOM grid (Cleveland, 2018). Distance to shore was estimated using Google Earth by dropping a point on each GPS location and dragging it to the closest shore line approximating the distance.

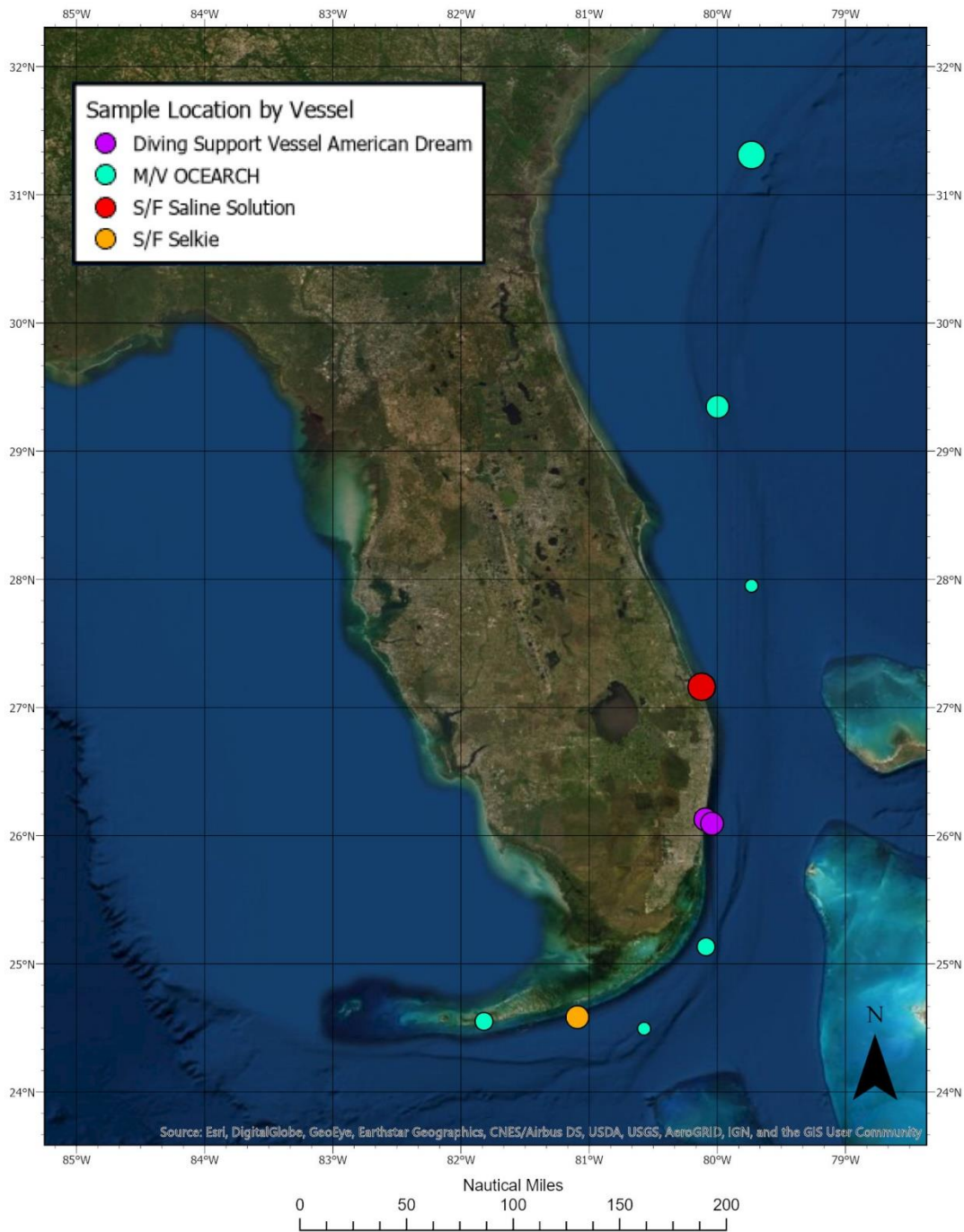


Figure 3: Map of sampling locations and corresponding vessel from which each sample was obtained. Pink dots represent samples collected from diving support vessel M/V *American Dream*, blue dots represent samples collected from M/V *OCEARCH*, the yellow dot represents a sample collected from S/F *Selkie*, and the red dots represents samples collected from a S/F *Saline Solution*. The size of the dot represents the size of the clump during collection – the bigger the dot the larger the clump.

Table 1: *Sargassum* score sheet derived from a score sheet created by members of the Fish and Wildlife Research Unit, USGS, and Department of Wildlife Ecology and Conservation at the College of Agricultural and Life Sciences used to classify *Sargassum* clump size. A value closer to 1 represents a smaller, less-defined patch whereas a number closer to 6 represents a larger, well-defined patch.

Sargassum Score Sheet

<i>Sargassum</i> score	Description
1	No <i>Sargassum</i> present
2	Single to few clumps of <i>Sargassum</i>
3	Lightly scattered clumps of <i>Sargassum</i>
4	Dense scattered clumps of <i>Sargassum</i>
5	Thin parallel windrows of <i>Sargassum</i>
6	Thick convergence line of <i>Sargassum</i>

Table 2: Number of species sampled from each vessel (R/V *OCEARCH*, S/F *Selkie*, S/F *American Dream*, and S/F *Saline Solution*). The taxon and family of each species is also given.

Taxon	Family	Species	<i>OCEARCH</i>	<i>Selkie</i>	<i>American Dream</i>	<i>Saline Solution</i>
Phyllodocida	Nereididae	<i>Platynereis dumerilii</i>	419	224	336	224
Mollusca	Litiopidae	<i>Litiopa melanostoma</i>	78	146	240	474
Decapoda	Portunidae	<i>Portunus sayi</i>	209	23	38	46
		<i>Portunus spinimanus</i>	8	0	0	1
	Palaemonidae	<i>Leander tenuicornis</i>	197	42	75	111
	Hippolytidae	<i>Latreutes fucorum</i>	1107	487	286	37
Perciformes	Carangidae	<i>Carangoides bartholomaei</i>	1	0	0	0
		<i>Carangoides ruber</i>	0	0	1	0
	Pomacentridae	<i>Abudefduf saxatilis</i>	1	0	0	5
	Lobotidae	<i>Lobotes surinamensis</i>	1	0	0	0
Tetradontiformes	Monacanthidae	<i>Stephanolepis hispidus</i>	18	0	2	1
Lophiiformes	Antennariidae	<i>Histrion histrio</i>	1	0	0	1

Statistical Analysis

Multivariate analyses: Community Species Composition

The multivariate analytical approach with the Bray-Curtis similarity index recommended by Clark and Gorley (2006) was used to compare the biological communities in each sample based on the relative abundance of each species. First, abundance data were square root transformed to decrease the analytical impact of species with consistently high abundances across all samples. Transformed abundance data were then used to calculate pairwise Bray-Curtis similarity indices for all pairs of samples, yielding a triangular matrix of pairwise community similarity indices that were used for the basis for subsequent analyses. The Bray-Curtis index ranges from 0% to 100%: values approaching 100% indicate that two samples are identical in terms of both species composition and the relative abundance of those species; values approaching 0% indicate that the samples share few to no species.

A one-way analysis of similarity (ANOSIM) was used to test for differences in biological community among samples for *Sargassum* clump size, which was used here as categorical factors taking values from 1 to 6 (see Table 1). A one-way ANOSIM can be considered the multivariate analogue to classical ANOVA (Clark and Gorley, 2006). To test for differences due to distance among samples, decimal degree geographic coordinates were used to establish a Euclidean distance matrix, which were then compared to the biological similarity matrix using the RELATE function. The same approach was also used to test for effects of both (a) distance to shore and (b) environmental variables (normalized data on temperature and salinity from each sampling location) by establishing a Euclidean distance matrix based on distance to shore values and using the RELATE function to explore possible correlations with biological community.

Preliminary data exploration suggested that a subset of the biological community co-occurred in all samples. To further explore this possibility, the Bray-Curtis similarity matrix was analyzed via average-link cluster analysis using the CLUSTER routine, with a similarity profile (SIMPROF) test to identify statistically significant clusters of co-occurring taxa. Abundance patterns were graphically depicted using a shade plot, which provides a simple visual representation of abundances of species from each sample site; taxa were clustered per the results of the SIMPROF test described above.

Multi-dimensional scaling (MDS) was used to visualize among-sample Bray-Curtis similarities. MDS uses the entries given by the resemblance matrix as actual distances so that the

proximity of two data points on the plot is positively correlated to the similarity of their biological communities. (Clark and Gorley, 2006). v. 7.0.10; PRIMER-e, Quest Research Limited was used for all multivariate analyses.

Univariate analyses: Community Species Richness, Total Abundance and Species Evenness

Species richness (S), total abundance (N), community evenness (J') for each sample site were all generated in PRIMER using the DIVERSE routine. These data were then analyzed in JMP (v. 12.1.0; SAS Institute Inc.) using one-way analysis of variance (ANOVA) to test for the effect of latitude, clump size, distance to shore, temperature, and salinity individually. In JMP a one-way analysis of variance (ANOVA) tested for the effect of latitude, clump size, distance to shore, temperature, and salinity with species richness (S), total abundance (N), and community evenness (J'). Species richness is the number of species within a given sample. Species richness was tested against latitude, distance to shore, clump size, salinity, and temperature.

Parasite Analyses

The prevalence of parasite species documented was determined by dividing the number of infected individuals by the total number of individuals in each sample, per Bush et al. (1997).

Results

Multivariate Data: Community Species Composition

A total of 5413 organisms were collected from *Sargassum* habitat representing 14 species from 10 families at 11 sampling locations. Total community data is shown in Table 2.

Analysis of similarity (ANOSIM) was used to test for differences in the biological community among sampling sites across samples for clump size. R values close to 1 indicate high separation whereas R values close to 0 indicate no separation. Results showed a significant difference for *Sargassum* clump size (R=0.384, P=0.024).

The RELATE function was used to test for differences in the biological community with latitude among sample sites. No significant differences were found with latitude and biological community ($\rho=0.023$, P=0.193). Differences in distance to shore with the biological community was also investigated however, no significant differences were found ($\rho =0.112$, P=0.217).

Temperature and salinity were tested against the biological community to see if there were any significant differences. The RELATE function yielded no significant results with salinity ($\rho = 0.247$, $P = 0.067$) and temperature ($\rho = 0.124$, $P = 0.193$).

A shade plot (Figure 5) was produced to show variation between *Sargassum* species and sample sites. Clustering analysis revealed the existence of a core group of co-occurring taxa across all sample sites. These include: *L. tenuicornis*, *P. sayi*, *L. melanostoma*, *P. dumerilii*, and *L. fucorum*. The other organisms, *C. ruber*, *S. hispidus*, *A. saxatilis*, *C. bartholomaei*, *P. spinimanus*, *H. histrio*, and *L. surinamensis* were found less frequently and were not statistically included in the core group.

Ordination via MDS mapped the similarities among the sample sites in their biological communities (Figure 4).

Univariate Data: Community Species Richness, Total Abundance and Species Evenness

No significant effect was detected for latitude ($P = 0.206$, $R^2 = 0.521$, $DF = (5,5)$, $F\text{-ratio} = 1.088$), distance to shore ($P = 0.219$, $R^2 = 0.521$, $DF = (5,5)$, $F\text{-ratio} = 1.088$), clump size ($P = 0.472$, $R^2 = 0.521$, $DF = (5,5)$, $F\text{-ratio} = 1.088$), salinity ($P = 0.506$, $R^2 = 0.521$, $DF = (5,5)$, $F\text{-ratio} = 1.088$), or temperature ($P = 0.811$, $R^2 = 0.521$, $DF = (5,5)$, $F\text{-ratio} = 1.088$) with species richness. Total abundance is the number of individuals per species. Results showed there was a positive correlation between clump size and abundance ($P = 0.019$, $R^2 = 0.861$, $DF (5,5)$, $F\text{-ratio} = 6.234$); however, there was no significant correlation with latitude ($P = 0.194$, $R^2 = 0.861$, $DF (5,5)$, $F\text{-ratio} = 6.234$), distance to shore ($P = 0.413$, $R^2 = 0.861$, $DF (5,5)$, $F\text{-ratio} = 6.234$), salinity ($P = 0.834$, $R^2 = 0.861$, $DF (5,5)$, $F\text{-ratio} = 6.234$), or temperature ($P = 0.988$, $R^2 = 0.861$, $DF (5,5)$, $F\text{-ratio} = 6.234$). Species evenness (J') refers to how close in abundance each species is in a community. There was a significant effect for distance to shore ($P = 0.03$, $R^2 = 0.822$, $DF (5,5)$, $F\text{-ratio} = 4.635$) latitude ($P = 0.04$, $R^2 = 0.822$, $DF (5,5)$, $F\text{-ratio} = 4.635$), and temperature ($P = 0.009$, $R^2 = 0.822$, $DF (5,5)$, $F\text{-ratio} = 4.635$), but no significant effect for clump size ($P = 0.85$, $R^2 = 0.822$, $DF (5,5)$, $F\text{-ratio} = 4.635$) or salinity ($P = 0.10$, $R^2 = 0.822$, $DF (5,5)$, $F\text{-ratio} = 4.635$).

Parasite Results

Few parasites were recovered during this study, precluding detailed statistical analysis of this component of the community. As stated previously, parasite dissections were only conducted

on invertebrate species. *L. fucorum* was the only species found to be parasitized. The parasite species was identified as the isopod *Probopyrinella latreuticola*. Parasitized individuals had a single parasite on the external surface on one side of the carapace. The prevalence rate of *P. latreuticola* on *L. fucorum* was 9.1%.

Discussion

This study provided insight on the *Sargassum* community structure in the Florida Straits and Gulf Stream. The community remained relatively stable given the inherently dynamic nature of the *Sargassum* substrate. A core group of co-occurring species occurred throughout the entirety of the samples collected (see Figure 4) which spanned from 24° to 29°N. This core group consisted of five invertebrate species whereas the visiting group, or organisms that occurred less frequently, consisted of mostly fish species (see Table 1). Each core species was present at every sample site. All organisms identified have been documented as being associated with *Sargassum* (e.g., Coston-Clements et al., 1991); however, this is the first study to investigate the species composition and structure of the *Sargassum* habitat in the Florida Straits and Gulf Stream.

Sargassum studies have been conducted in the Gulf of Mexico, Caribbean Sea, western North Atlantic, and Sargasso Sea (Huffard et al., 2014; Borton et al., 1977; Wells and Rooker, 2004; Witherington et al., 2012; Moser and Lee, 2012; Fine, 1970; Casazza and Ross, 2008; Stoner, 1983). These prior studies have shown that the floating mats of *Sargassum* found throughout these areas act as a nursery ground, temporary refuge, and food source for numerous organisms in an environment that is otherwise lacking in productivity and physical structure. Our study complements these findings and shows that the *Sargassum* patches in the Florida Straits and Gulf Stream offer a steady food source for associated and foraging organisms. Many organisms utilize the Gulf Stream as a nursery ground, transient pathway, or opportunistic food source. For example, at least four species of sea turtles are known to utilize the *Sargassum* habitat during their early life stages. Witherington et al. (2012) examined diet contents of juvenile sea turtles and found that most their diet consisted of organisms associated with *Sargassum*. Of the species identified as a food source for the sea turtles they sampled, three (*L. melanostoma*, *P. sayi*, and *S. hispidus*) were commonly found in our samples.

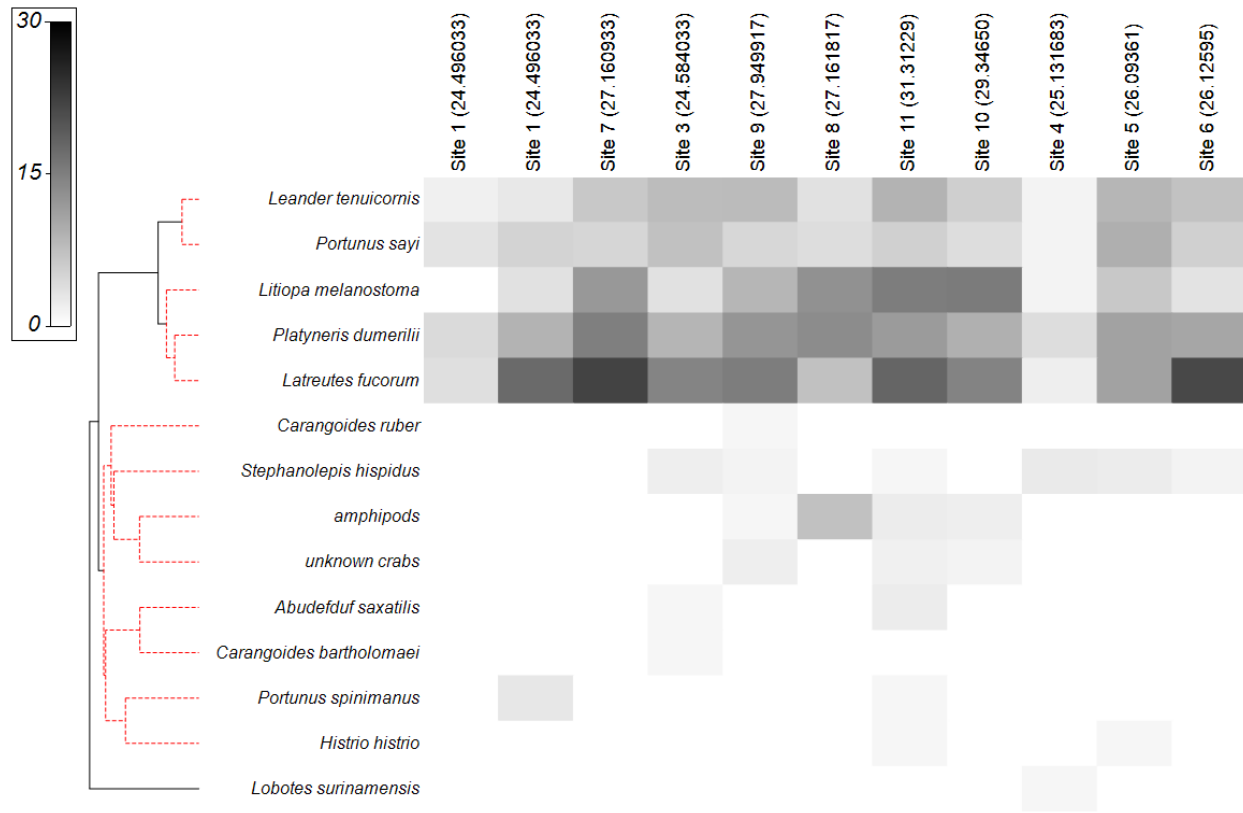


Figure 4: Shade plot illustrates the relative abundances of the taxa associated with *Sargassum* (all abundance data square root transformed). The first five taxa listed are identified via hierarchical clustering as a core group of co-occurring organisms dominating all samples. Sample sites are arranged left to right by increasing latitude.

Besides sea turtles, there are other organisms who use the *Sargassum* communities in the Gulf Stream. Large predatory fishes such as dolphinfish, billfishes, and tunas have been documented actively predating on organisms found under or around *Sargassum* patches or have pieces of *Sargassum* in their stomach contents (Manooch et al., 1984; Rudershausen et al., 2010; Luckhurst, 2015). Fish are known to congregate under and around physical structure, especially in the pelagic environment because it acts as a source of shelter from predation (Gooding and Magnuson, 1967). The stability and presence of the core group of invertebrates in the *Sargassum* community in the Florida Straits and Gulf Stream provide a constant source of food for the smaller trophic level organisms that use this habitat for protection such as *S. hispidus*, the most common species collected during our study. Casazza (2008) examined stomach contents of fishes collected under *Sargassum* mats and found that the lower trophic level fishes fed primarily on endemic *Sargassum* species such as *L. fucorum* and *L. tenuicornis*, all species found in our samples. Since there is a substantial food supply for the lower trophic level organisms, the higher trophic level organisms such as the fishes listed previously can use the *Sargassum* communities in the Florida Straits and Gulf Stream as a foraging ground. The occurrence of a constant core group of organisms throughout our sample sites suggests that reproduction could occur offshore within the *Sargassum* habitat. For example, egg-bearing female individuals of *P. sayi* and *L. tenuicornis* were observed throughout the sample sites. Since this concept was not investigated throughout this project, more research is needed to fully understand the reproductive success and recruitment of these commonly occurring *Sargassum*-associated organisms.

Sargassum Species Abundance

Even though the community structure stayed relatively stable throughout the sampling locations, total species abundance had a significant positive correlation with *Sargassum* clump size which is intuitive considering larger *Sargassum* clumps create larger areas of habitat for organisms to live in and around and these findings agree with other similar studies (Fine, 1970; Butler et al., 1983; Stoner and Greening, 1984, Settle 1993; Wells and Rooker, 2004b).

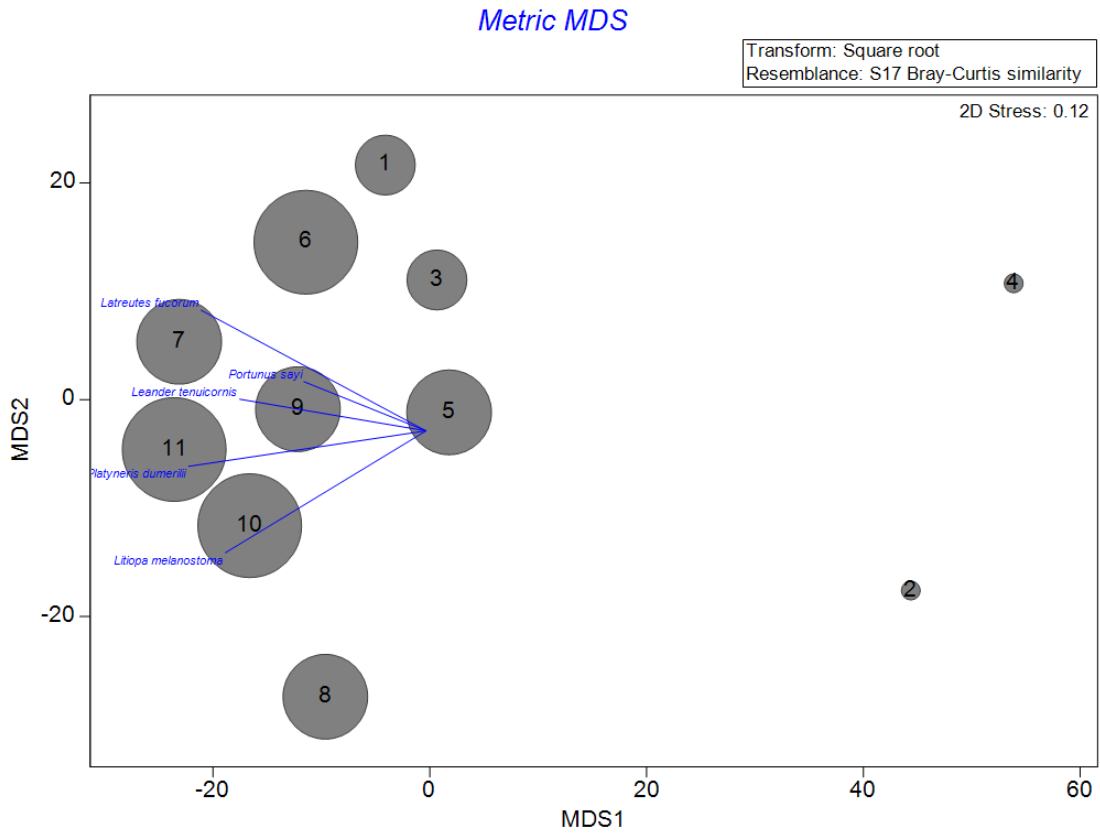


Figure 5: Metric multi-dimensional scaling ordination showing the relationship between the *Sargassum* community and sample sites. Each sample site is indicated by a circle whose diameter is proportional to clump size; label proximity implies similarity of biological communities, based on square root transformed Bray-Curtis similarity indices. Pearson Correlation vectors are shown with straight blue lines.

Sargassum Species Richness

The species richness of the *Sargassum* community was not significantly affected by any of the environmental factors tested (Table 5). Given the fact that the *Sargassum* environment is ever-changing due to variable wind and current conditions species richness would be expected to change. However, the present study has shown a distinct core group of species inhabiting *Sargassum* throughout our sampling locations. A similar study collected samples of *Sargassum* in the northern Gulf Stream and Sargasso Sea and found that the macrofauna was strongly influenced by the location of sampling. Samples collected in the Gulf Stream were dominated by *L. fucorum*, which coincides with the results found in this study. Samples found in the Sargasso Sea were dominated by *L. melanostoma* (Stoner and Greening, 1984). Other studies have investigated the *Sargassum* community structure in the Gulf Stream (e.g., Huffard et al., 2014; Casazza and Ross, 2008; Martin, 2016; Fine, 1970), but no study has investigated the community from the locations where we collected from. Besides the core group of species, other species found include: unidentified amphipods, unidentified juvenile crabs, *P. spinimanus* (a crab commonly found on benthic substrate), and six other teleost fishes. As mentioned earlier, organisms use structure in the open ocean as a temporary refuge or food source. *Sargassum* habitat has been shown to deter predation (Brooks, 2007). The fact that the less frequent species did not occur throughout the entirety of the sampling locations suggests that they used the *Sargassum* patches as a temporary shelter rather than a permanent habitat.

Most of the visiting group collected during this study were juvenile fishes. Wells and Rooker (2004b) determined that over 95% of the species collected in the northwestern Gulf of Mexico *Sargassum* mats were in the early life stages. They also showed that different species have differing relationships with the *Sargassum* habitat ranging from essential to facultative needs meaning some stay for a short period whereas others stay for an extended amount of time like *H. histrio* who have adapted unique coloration and appendages for living in *Sargassum*. They found that more mobile species like *A. saxatilis* and *C. crysos* exploit the *Sargassum* community for prey and protection from predators. These findings echo those of this study, further highlighting that pelagic *Sargassum* not only serves as a nursery habitat but likely also influences the recruitment of several species.

Individual Species Composition

Each species was investigated individually to determine if latitude, clump size, distance to shore, temperature, or salinity affected the composition. The only species that was significantly affected by any of the above factors was *L. melanostoma*. Both clump size and temperature had a positive correlation suggesting there were significantly more individuals of *L. melanostoma* in areas with larger clump sizes and higher temperatures. Stoner and Greening (1984) showed *L. melanostoma* is historically known to be more common in the Sargasso Sea where the water is colder than in the Gulf Stream. It is important to note the potential sampling biases for *L. melanostoma*. During the sampling events on the M/V *OCEARCH*, samples were sorted on the deck. This made sorting more difficult due to the constant movement of the ship. Some individuals of *L. melanostoma* might have been missed due to their extremely small size and coloration.

Parasite Community

The only invertebrate species found to be infected with parasites was *L. fucorum*. Parasites found on *L. fucorum* were sent to the National Museum of Natural History, Smithsonian Institution (USNM) and identified definitively as *Probopyrinella latreuticola*. At present, there are two species of *Probopyrinella* that have been described infesting species of *Latreutes*: *P. latreuticola* from *L. fucorum* and *P. heardi* from *L. parvulus*. Adkison (1984) listed six characters that putatively separate the two *Probopyrinella* species and Thoma & Heard (2009) added an additional four diagnostic characters (Table 1). During the course of the present study, a dozen pairs of *Probopyrinella* from *L. fucorum* were examined in detail; they showed considerable variation and all the character states described and illustrated for *P. heardi* (Adkison, 1984; Thoma & Heard, 2009) occurred in at least some of these specimens from *L. fucorum*. It was later realized that neither Adkison (1984) nor Thoma & Heard (2009) ever stated that they examined any parasites of *L. fucorum* and based their conclusion that two species of *Probyrinella* existed on the incomplete and sometimes erroneous descriptions of *P. latreuticola* by Richardson (1905) and Markham (1977). Although Adkison (1984) stated that he was giving “an amended generic diagnosis for *Probopyrinella* based on study of *P. heardi*, *P. latreuticola* and previous generic diagnoses,” nowhere in his paper did he state that he directly examined any specimens of *P. latreuticola*. In fact, most of the character states given or implied for *P.*

latreuticola clearly come from the incomplete redescription of that species by Markham (1977). Likewise, Thoma & Heard (2009), while providing keys based on the characters used to separate the two species of *Probopyrinella*, merely recycled figures of the two species from Richardson (1905), Markham (1977), and Adkison (1984), several of which are in error. Based on our examination of the new materials and comparison with the literature, we conclude that *P. heardi* and *P. latreuticola* are synonymous.

The prevalence of *P. latreuticola* on *P. heardi* was 9.08% which is considerably low. Nursery habitats such as mangroves or estuaries have been shown to have lower infection rates of parasites with their host organisms due to nursery habitats being structurally complex and larval transmission stages of some parasites becoming physically impeded in successfully locating and infecting the host (Welsh et al., 2004). Our study supports this idea since *Sargassum* is similarly a nursery habitat for many organisms and structurally complex.

Conclusion

There is significant evidence showing *Sargassum* is an important ecosystem for numerous organisms at multiple trophic levels. This study shows the *Sargassum*-associated communities in the Florida Straits and Gulf Stream are surprisingly stable, featuring a core group of co-occurring organisms that inhabit the mats regardless of latitudinal gradient, differing distances from shore, variable clump sizes, and varying oceanic parameters. This community stability likely enhances the value of *Sargassum* habitat as a reliable source of food in addition to shelter. Future research should include sampling from the remaining portion of the Gulf Stream to see if there is any variability with the community structure as well as a seasonal component. Though more research is needed, this study gives a baseline understanding of the core community structure of the *Sargassum* community in the Gulf Stream.

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