

**THE EFFECTS OF HURRICANE HARVEY ON THE ABUNDANCE AND
BIODIVERSITY OF HYDROMEDUSAE IN GALVESTON BAY**

An Undergraduate Research Scholars Thesis

by

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TABLE OF CONTENTS

	Page
ABSTRACT.....	1
Literature Review.....	1
Thesis Statement.....	2
Theoretical Framework.....	2
Project Description.....	2
DEDICATION.....	3
ACKNOWLEDGMENTS.....	4
KEY WORDS.....	5
INTRODUCTION.....	6
1.1 HYDROZOAN LIFE CYCLE AND SEASONALITY.....	8
1.2 HURRICANE’S EFFECTS ON MARINE ENVIRONMENTS.....	10
1.3 THE STUDY SITE: GALVESTON BAY.....	12
1.4 RESEARCH AIMS.....	14
CHAPTERS	
I. METHODOLOGY.....	15
Medusa Collection, Isolation, and Photographs.....	15
DNA Extraction, Purification, and Analysis.....	15
Medusa Abundance and Correlation with Abiotic Factors.....	17
Comparison of Hurricane Year Abundances Versus Non-Hurricane Years.....	17
II. RESULTS.....	19
Seasonality of Hydromedusa.....	19
Relations between Hydromedusa and Abiotic Environmental Factors.....	21
Comparison between Previous Non-Hurricane Results and Hurricane Year Results.....	23
III. DISCUSSION.....	25

Seasonality of Hydromedusa	25
Relations between Hydromedusa and Abiotic Environmental Factors	25
CONCLUSION.....	27
WORKS CITED	28
APPENDIX.....	31

ABSTRACT

The Effects of Hurricane Harvey on the Biodiversity and Abundance of Hydromedusae in Galveston Bay

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Literature Review

Jellyfish of the Class Hydrozoa (hydromedusae), phylum Cnidaria are vastly understudied due to their size and simple morphology, even though they have a significant impact on the environment and fisheries industry. Hydromedusae were collected three times a week from March 2017 through February 2018 using plankton tow. In the laboratory, medusae were isolated from other planktonic organisms, counted, photographed, using a Leica microscope and identified to the lowest possible taxonomic level using morphology. Total DNA was then extracted and Polymerase Chain Reaction (PCR) was performed to amplify the 16S mitochondrial gene. Sequencing will be performed at Texas A&M University-Corpus Christi (TAMUCC). Once returned, the DNA sequence will be run through BLAST web application for species identification. Number of Hydromedusae collected during the sampling period will be compared with those collected before hurricane Harvey.

Thesis Statement

This project is targeted toward a) monitoring the biodiversity and abundance of hydromedusae in Galveston Bay after Hurricane Harvey, b) correlate their blooms with specific abiotic factors such as water temperature and salinity.

Theoretical Framework

This study is a part of a long-term monitoring process to better understand and map the biodiversity, blooms, and seasonal changes of jellyfish populations in the Galveston Bay.

Project Description

This project aims to monitor jellyfish abundance and biodiversity in Galveston Bay. Samples were taken three days/week from March 2017 to April 2018. Medusae were sorted in the laboratory, counted, photographed and barcoded for the mitochondrial 16S gene, to assess cryptic diversity. Abundance of medusae were correlated with abiotic factors. All data were then compared with similar datasets from previous years (specifically from September 2015 to April 2017) collected by former students in the Miglietta's Laboratory at Texas A&M University at Galveston. The final aim is to compare medusae patterns of diversity and abundance across years, and specifically look for the impact that major hurricane Harvey may have had on gelatinous zooplankton. This research is part of a long-term monitoring effect to:

1. Describe hydromedusae diversity in the Galveston Bay using morphological characteristics and the ~600bp fragment of the large ribosomal subunit of the mitochondrial RNA (lsu-rRNA, 16S).
2. Determine which abiotic factors correlate with their bloom, characterized by their seasonality in the Galveston Bay

3. Understand the effects of major hurricanes on biodiversity, abundance, and seasonality of medusae.

DEDICATION

I dedicate this to my family. I truly could not have done this without the constant support and reminder of not only my potential, but the faith you all had in me.

To my father, Anthony, who was always a phone call away no matter what the situation was. For being my rock through school and throughout my research. Who pushed me through when nothing was producing results and reminded me where I came from. You always remind me of the amount of potential I have, even when I don't know it myself.

To my aunt and uncle, Richard and Rena, for letting me stay with them for entire summer to continue my research. While also, answering my millions of questions about thesis papers way before I even had a title for my own.

To my grandfather, Mark, for teaching me what hard work truly is and the drive to push through to finish the job. To my late grandmother, Ann, for teaching me to be just as stubborn and strong will powered as she was, and a great female role model in a world full of boys.

To my mother and brother, Tracy and Cole, who were always there when I needed an escape and a laugh to push me through. Who never quite understood what I was talking about, but every time listened anyway and gave their full support.

I truly could not have done it without them as my support group.

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A big thank you to everyone in the Miglietta Lab, who helped teach me along the way and was never too busy to lend a helping hand. Also, a thank you go out to Dr. Quigg's Phytoplankton Dynamics Laboratory, the Marine Biology program, the Texas A&M University Corpus Christi Laboratory for sequencing of the samples, and to the Undergraduate Research Scholars Program for ensuring my success in pursuing research of my own.

I also want to extend my gratitude as publication supported in part by an Institutional Grant (NA14OAR4170102) to the Texas Sea Grant College Program from the National Sea Grant Office, National Oceanic and Atmospheric Administration, U.S. Department of Commerce. As well as, the Aggies Commit to Excellence Scholar (ACES) program for partially funding my research.

Finally, thanks to the rest of my family and friends for their constant encouragement and patience along the way.

KEY WORDS

TAMUCC Texas A&M University at Corpus Christi

PCR Polymerase Chain Reaction

BLAST Basic Local Alignment Search Tool

INTRODUCTION

The term jellyfish is often used to describe the Cnidarian classes Cubozoa, Hydrozoa, and Scyphozoa and phylum Ctenophora. However, the majority of gelatinous zooplankton is composed of the Medusozoa group (Cubozoa, Hydrozoa, and Scyphozoa classes) (Collins *et al.*, 2002). There are general similarities but major life-cycle differences with the Medusozoa. The majority of the Medusozoa group alternate between a sessile, asexual polyp and a planktonic, sexually reproducing medusa (Hofmann *et al.*, 1996).

In the class Cubozoa, the larva planulae settles and develop into sessile polyp within a period of 2 days (Werner *et al.*, 1971). From this cubopolyp, a single sexual medusa, with a mouth and four tentacles is formed through metamorphosis (Werner *et al.*, 1971; Collins, 2002).

In the class Scyphozoans, the free-swimming planulae settle and develop into sessile and asexual reproducing polyps, similar to that of Cubozoan. However, a significant characteristic of this class, is the production of multiple juvenile medusae by metamorphosis and strobilation. Each polyp released on average of five juvenile medusae, formally known as ephyrae (Collins, 2002; Holst *et al.*, 2007). This ephyrae then matures into an adult medusa that can sexually reproduce. Medusae release gametes in the water column and fertilization is external. Larvae planula are so formed, closing the life cycle (Collins, 2002).

In the Class Hydrozoa, the larva planula settles and develop into a primary polyp, that will then form a full colony by means of asexual budding. Polyps release the medusa in the water column which in turn, when mature, will release the gametes. Within all the Cnidarian classes, hydrozoans possess the greatest variety of in life cycles, with some groups partially or entirely lacking the medusae stage.

Hydrozoan are also the most diverse and wide spread class of Phylum Cnidaria with about 3,800 nominal species, Scyphozoa and Cubozoa having 200 and 20 species respectively (Bouillon *et al.*, 2004).

All the medusozoans, including Hydrozoa medusae, display some aspect of seasonal population fluctuation. From an ecological perspective, all medusae are the top predators. They feed among zooplankton and prey mostly on small invertebrates and larva (including larvae). Medusa outbreak thus, pose a threat to fish stocks by competing for the same food source and by predation. An example of this issue was documented in East China Sea and Yellow Sea, where the decline of fisheries was associated with the increase of jellyfish blooms (Cheng *et al.*, 2004; Ge and He, 2004; Ding and Cheng, 2007; Dong *et al.*, 2010). Although, jellyfish can also be a source of energy for a variety of marine life who prey on them (Richardson *et al.*, 2001), only a few species are known to feed primarily on them (i.e. the leatherback turtle).

Without too many predators, jellyfish can quickly grow to a noticeably large population (Qiu, 2014). This leads to the concern of possible effects jellyfish blooms have on marine ecosystems as an increase in their frequency and population sizes has been recorded in several regions of the world's oceans (Condon *et al.*, 2013).

A validation of the hydromedusae investigation is the increasing concern of marine ecosystems degenerating and their response to natural disasters. Jellyfish have been shown to be “opportunistic” by quickly responding to environmental changes and thriving in environmental conditions that are detrimental to other species (Brodeur *et al.*, 2008). For example, increase of jellyfish populations has been recorded in areas with a high amount of nutrient runoff from agriculture and human activity (Qiu, 2014).

Although medusae of the class Hydrozoa are small compare to Scyphomedusae, they are extremely abundant, undergo seasonal blooms, that are at the moment unpredictable. (Miglietta *et al.*, 2008). Although speculation of increasing size and presence of blooms has been linked to abiotic and biotic factors within the ecosystem, the ecological factors that trigger medusae production by the polyps have not been studied intensely. Some of the abiotic factors identified as possible triggers are: temperature, salinity, lunar cycles, and productivity. However, they have been studied in a handful of species only (Boero *et al.*, 2008).

It is also not clear what is the effect of events such as hurricanes on biodiversity and bloom formation in Hydromedusae. Hurricane Harvey was a category 4 when it hit Corpus Christi, TX and was the first major hurricane to strike the Texas Coast since Ike in 2008 (US Department of Commerce, 2017). Harvey stalled over Southeast Texas for five days producing catastrophic flash and river flooding, with some Southeast Texas areas receiving over 40 inches of rain in 48 hours (US Department of Commerce, 2017). Hurricane Harvey offers an opportunity to see the effects of natural disasters on hydromedusae off the Texas coast by comparing continuous surveys of hydromedusa abundance, seasonality, and species richness before and after the hurricane.

1.1 Hydrozoan Life Cycle and Seasonality

The class Hydrozoa is the most diverse and widespread class of Cnidaria. However, due to their small size, seasonal occurrences, and difficulty to identify to species they are the least studied of the Cnidarian classes (Miglietta *et al.*, 2008). The average bell size for such medusae ranges from 1 to 50 mm, thus, making them difficult to identify at the genus or species level strictly based upon their morphological features (Boero and Bouillon, 1993; Miglietta *et al.*, 2008). Hydrozoans have a diverse and complex life cycle, but most contain a benthic and

planktonic phase. The majority can be characterized by the succession of these three main stages: planulae, polyps and medusae. Much similar to the scyphozoans and cubozoans. For most Hydrozoa species, the embryonic development of a lecithotrophic planula larva start the life cycle. This planula free-swims before settling on a substrate and metamorphosing into as a polyp. These polyps will then asexually reproduce forming colonies. Hydrozoan polyps produce medusae through the process of budding. This budding occurs generally laterally from the polyps (Collins, 2002; Boero *et al.*, 1992).

Medusae are released seasonally, but the nature of the trigger is unknown for most species (Bueno and Bouillon, 1993; Coma *et al.*, 2000). This lack of knowledge on how the benthic polyps respond to different environmental triggers or cues make it nearly impossible to map the blooms of these organisms, and the intensity of them.

In tropical waters, upwelling has been correlated to hydromedusae blooms. Often associated with upwellings is the increase in phytoplankton productivity (Miglietta *et al.*, 2008). This similar relationship was seen in the East China Sea, in correspondence to eutrophication of red tides. The eutrophication leads to a high biomass of phytoplankton, which can support a large biomass of zooplankton, such as dinoflagellates. This increase in biomass creates a dense population growth leading a decrease in dissolved oxygen levels. The combination of both the hypoxic conditions and increase abundance of zooplankton was correlated with an increased in jellyfish abundance and blooms (Dong *et al.*, 2010). In contradiction, recent studies have not found a strong correlation linking the medusa blooms and phytoplankton blooms (Xu *et al.*, 2013).

Recent studies also account for a combination of abiotic factors such as: salinity, temperature, dissolved oxygen, and water turbidity to be initial triggers in hydromedusae blooms

but, again, focus on single species rather than the whole class (Nowaczyk et al., 2016; Wintzer et al., 2013).

1.2 Hurricane's Effects on Marine Habitats

Hurricane's cause a multitude of alterations in an environment from the time it starts forming until the last rainfall. These alterations include changes in salinity, nutrient loading, turbidity, and mortalities of marine and terrestrial organisms and habitats (Tilman *et al.*, 1994; Tabb & Jones, 1962).

Water quality after a hurricane is significant in its increase of turbidity, nutrient loading, and dissolved amounts of organic carbon (Tilman *et al.*, 1994). The high turbidity is caused by the suspension of sediments in the water column, along with the combination of post-storm plankton blooms. Immediately after a hurricane, the turbidity is at such a high rate that it drops the dissolved oxygen levels to rates of almost zero in areas near-shore (Tilman *et al.*, 1994). This causes problems for the marine organisms in these areas, resulting in unusual behavior in order to obtain oxygen. Also, once dissolved oxygen levels start to rise back to normal levels due to the dissolved inorganic nitrogen and organic nutrient concentrations being above average, this triggered a phytoplankton bloom to occur (Tilman *et al.*, 1994).

Salinity changes are a common occurrence with hurricanes, due to the addition of tremendous amounts of rainfall produced by the storm. This excess rain can lower surface salinities to a range as low as 0-10 parts per thousands. Bays and waterways can also be affected, but with higher-than-normal salinity levels. This is dependent upon the movement of the storm and how the waters move because of it. It may cause a flow of higher salinity water to move in regions of enclosed bays and other freshwater waterways; therefore, creating an increase in

salinity in commonly freshwater regions. Although, salinity can vary drastically and widespread, these changes are only temporary in result of the hurricane (Tabb & Jones, 1962).

Hurricanes are equipped with a particularly destructive force that is detrimental to marine environments, especially shallow-water habitats, as a direct action of the storm (Tilman *et al.*, 1994; Tabb & Jones, 1962). Mortalities occurring from hurricanes, usually take place in two waves: the initial, direct action and the oxygen depletion of marine waters that occurs after the storm. The first wave, results in dead organisms from the power of the storm, including being carried by the storm tides and even mangled due to the strength it holds. This wave can be responsible for the deaths of larger vertebrate fish, such as: Crevalle jacks (*Caranx hippos*), snook (*Centropomus undecimalis*), sheepshead (*Archosargus probatocephalus*), and southern stingrays (*Dasyatis americana*) (Tabb & Jones, 1962). The second wave, is most prevalent, because of the high turbulence leading to suffocation of marine organisms. Oxygen depletion is the main cause of the massive amounts of fish deaths after a hurricane. This is often exhibited in smaller fish species such as: clown gobies (*Microgobius gulosus*), gaftopsail catfish (*Bagre marinus*), speckled worm eels (*Myrophis punctatus*), and blackcheek tonguefish (*Symphurus plagiusa*) (Tabb & Jones, 1962).

The impact of natural disasters (of large scale, high intensity, but low frequency) on invertebrate species is the least understood in comparison to any other animal taxa. Nonetheless, disasters, such as hurricanes, play a critical role in shaping ecosystems that are currently in action and those to come later (Willig & Camilo, 1991). Hurricanes have the capacity to severely alter the ecosystems in which they hit (Mallin *et al.*, 1999).

Hurricane Hugo, that severely hit Puerto Rico, had a dramatic effect on the Luquillo Experimental Forest's invertebrate fauna. All taxa suffered population reductions to be less than

25 percent of their original densities. Some species were absent all around after the hurricane had struck, and most were no longer distributed in a clumped spatial formation (Willig & Camilo, 1991).

Although hardbottom communities are usually only moderately affected by hurricanes, sponges are among the most heavily affected component of these communities. The reason being is mainly due to the storm's deposition of fine, silty sediment along the ocean floor. This sediment smothers most of the sponges and results in their deaths. However, this sediment loading did show no significance on the thriving abilities of stony corals, sea plumes, algae, or seagrass in that same area of study (Tilman *et al.*, 1994). The effect of hurricanes on bloom, seasonality, and biodiversity of medusae of the class Hydrozoa is very understudied.

1.3 The Study Site: Galveston Bay

Galveston Bay is located on the southeast Texas coast, along the Gulf of Mexico. The estuarine system is composed of five different bay systems: Upper and Lower Galveston Bays, Trinity Bay, East Bay and West Bay. One of the major characteristics of Galveston's bay system is its series of dredged channels including Intracoastal Waterway, the Houston Ship Channel, the Texas City Channel, Dike, and other small channels. Trinity River accounts for the majority of the freshwater flow into the northwestern part of Upper Galveston Bay. Additional freshwater is brought in via Intracoastal Waterway and numerous bayous to regions across the Bay (Copeland & Bechtel; 1971).

Out of all the bays on the Texas coast, one of the largest and most important estuarine system, both economically and ecologically, is the Galveston Bay complex (Currington *et al.*, 1966; Masch and Espey, 1967). This is account for the quantity and quality of the vastly array of habitats available to provide nursery grounds. It was estimated over 80% of the poundage taken

as fishery products in the Gulf of Mexico was founded in these nursery grounds of Galveston Bay (Currington *et al.*, 1966). A popular economically important species founded in this region would be the red drum, *Scianops acellatus*. Red drum typically spawns early in the fall season, and their planktonic larvae are gathered into the bay by the water currents, where they will settle until they are large enough to return to the open water (Stunz *et al.*, 2002). The larval stage of these fish, like most fishes, has the highest mortality rates due to predation, starvation, and environmental varying factors, as a result of being vulnerable (Perez & Fuiman, 2015).

Hydromedusae have been reported to alter planktonic communities such as: zooplankton, ichthyoplankton, and protistan, based upon their carnivorous diet (Wintzer *et al.*, 2013; Yilmaz, 2015). As a result, a hydromedusae jellyfish bloom could be a hazard to the economically value fish populations within the bay by outcompeting them for food, and prey on them, as well (Richardson, et al., 2009). For this reason, it is important for fisheries to gather information and study the factors of hydromedusae in Galveston bay such as: abundance, seasonality, and diversity. This will allow for the understanding and managing of the marine ecosystem in which both are a significant part of. In addition to that, knowing how hydromedusae react and change after a natural disaster, such as Hurricane Harvey, can also provide insight on how the fisheries management may also be altered, as a result.

Very few studies have been conducted on Hydrozoa in Galveston Bay. The most recent was in 1973 by Defenbaugh and Hopkins, but strictly focused on the polyp stage rather than the medusa. This survey provided the only check list of Galveston Bay Hydrozoa, as it was the first study of its kind within the region (Defenbaugh & Hopkins, 1973). Since then, no updates have been made, nor the addition of any information of the medusa stage (any morphological

identification keys) for the corresponding species of the polyps originally found by Defenbaugh and Hopkins.

1.4 Research Aims

This project aims to monitor jellyfish abundance and biodiversity of medusa of the class Hydrozoa (phylum Cnidaria) in the Galveston Bay for a year cycle. This aim of this research is part of a long-term monitoring project to:

1. Describe hydromedusae diversity in the Galveston Bay using morphological characteristics and a molecular approach.
2. During a one-year cycle, medusa are collected, each hydromedusa is photographed and recorded, and barcoded using the mitochondrial 16S gene. Characterize the seasonal cycles of the hydromedusa in the Galveston Bay, and investigate correlation between their peaks and abiotic factors such as temperature and salinity.

Recent studies indicated warmer temperatures accounting for a higher density of medusa of their specific hydrozoan species (Wintzer *et al.*, 2013). If temperature is the driving force behind medusae budding, it can be expected there will be more blooms and overall a larger total of hydromedusae in Spring and Summer, compared to Fall and Winter.

3. Compare the data from this research project with historical data collected by the Miglietta lab during a 2-year cycle to assess the impact of hurricane Harvey on density and biodiversity of hydromedusae

CHAPTER I

METHODOLOGY

Medusa Collection, Isolation and Photographs

Hydromedusae were collected two to three times a week from September 2017 to April 2018. This was performed within the boat basin at Texas A&M University at Galveston campus on Pelican Island (29°18'47.0"N 94°48'59.8"W). The planktonic samples were collected using a 100-micron net, 90 cm long, with a 30 cm mouth, a collecting bottle attached to the end. Two tows were taken per sample day. Each tow consisted of towing the net six times alongside the dock for a total of 156 m, at a constant, steady rate. The plankton net was kept just below the water's surface to allow as much water as possible to pass through the net. This also ensured the consistency of water volume sampled to be approximately the same throughout the study. The plankton samples from each of the two tows were combined and considered as a single daily sample.

The sample was then taken to the laboratory and examined under a Leica M80 Stereomicroscope. The individual hydromedusae were isolated from the sample using a pipette. Each isolated hydromedusa was anesthetized using menthol crystals and photographed using a Leica MC170 HD camera mounted onto the stereoscope. These photographs were analyzed using the Leica Application software. The number of species and total hydromedusae present in each sample was recorded, in addition to the photos taken.

DNA Extraction, Purification, and Analysis

Genomic DNA was extracted from the hydromedusae using standard extraction protocol (Miglietta *et al.*, 2008; Zietara *et al.*, 2000). The protocol is as follows: 1 jellyfish, 8 μ L distilled

water, and 1 μ L PCR buffer, incubated at 90°C for 10 minutes, addition of 1 μ L Proteinkinase, incubated at 55 °C for 30 minutes followed by 90 °C for 10 minutes. Upon the extraction of the DNA, the ~600bp fragment of the large ribosomal subunit of the mitochondrial RNA (lsu-rRNA, 16S) was amplified using primers SHA (5' ACGGAATGAACTCAAATCATG T-3') and SHB (5'-TCGACTGTTTACCAAAAACA TA-3') (Miglietta *et al.*, 2008). The PCR mix was prepared as follows: 12.5 μ L of Green GoTaq PCR primer, 11 μ L of nucleus free water, 0.5 μ L of primers SHA and SHB, and 0.5 μ L of extracted DNA. The PCR amplification was implemented with the following conditions: 1 min at 94°C, 35 cycles of 94°C for 15 s, 50°C for 1:30 min and 72°C for 2:30 min, and finally an extension at 72°C for 5 min.

The PCR product was run through a 1% agarose gel stained with Sybersafe at 110V for 15 minutes to determine the presence or absence of DNA. After conformation of DNA amplification, DNA was purified using exoSAP-it digestion (Affrimetrix). The purification process was performed by following manufacturer protocol, as listed: 10 μ L of the PCR product mixed with 2 μ L of ExoSAP-IT reagent, incubated at 37°C for 15 minutes, thus degrading the remaining primers and nucleotides, and then incubated at 80°C for 15 minutes to inactivate the ExoSAP-IT reagent. Purified DNA samples have been prepared and will be sent to the Genomic Core Facility at Texas A&M University-Corpus Christi for sequencing.

Upon the DNA sequence returning, the Geneious software will be used for sequence clean up. Following clean up, species identification will be performed by running the sequences through the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST). Within BLAST, for each sequence the parameters of E-value, query percentage, and identity will be evaluated for its most significant BLAST hit.

The methods described will take place in Maria Pia Miglietta's laboratory with initial assistance of herself. Texas A&M University Corpus Christi genomic core facility will be utilized for the 16S gene sequencing of the hydromedusae. Finally, the library database will be used along with Google Scholar for background material needed for introductory purposes.

Medusa abundance and correlation with abiotic factors

Daily water temperatures (°C) and salinity (ppt) levels of Galveston Bay were obtained for each sampling day. The water temperatures were collected from the National Oceanic and Atmospheric Administration Tides & Currents website. The salinity values were obtained from the Dr. Quigg's Phytoplankton Dynamics Laboratory at Texas A&M University at Galveston, as well. These abiotic factors were analyzed together in correlation with the daily jellyfish totals collected throughout the year cycle.

The relative abundance of medusa was plotted against the dates of collection to identify any blooms formed. A "bloom" was determined to be any day with a total medusa count equal at least 1 standard deviation above the mean daily abundance (Miglietta *et al.*, 2008). Each set of data was also compartmentalized into the four different seasons to be further analyzed. Fall was considered to be the months of October, November, and December. Winter was categorized as January, February, and March. Spring's months were April, May, and June. Finally, Summer included the months of July, August, and September.

Comparison of Hurricane Year Abundances Versus Non-Hurricane Years

The relative abundance values, maximum daily totals, seasonal daily averages and total number of bloom counts of the sample year March 2017 through February 2018 were compared to 2-years of previous data from this long-term survey. These studies were performed from August 2015 through September 2016 and from October 2016 to February 2017 by students in

Miglietta's lab. The values gathered from the non-hurricane effected years were compared against that of the set that was affected by hurricane Harvey. The differences, and similarities were recorded in a table, in order to better understand the effects this disaster had or did not have on the hydromedusa community in Galveston Bay.

CHAPTER II

RESULTS

Seasonality of Hydromedusa

Hydromedusae were collected over 71 sampling days in 12 months (March 2017 through February 2018). There were 8 sampling days in March, 11 in April, 6 in May, 8 in June, 10 in July, 4 in August, 8 in September, 4 in October, 7 in November, 1 in December, and 2 in January and February. This averaged to just below 6 sampling days per month. The lower numbers in December through February were due to a combination between holiday break and inclement weather.

Over these 71 days a total number of 2385 individual medusae were isolated. Figure 1 represents the total medusa abundance collected for each sampling day. The total number of hydromedusae collected per sampling day ranged from 0 individuals to 355. This maximum daily abundance value of 355 individuals occurred on September 27, 2017. Overall, there was a daily average of 33.59 medusa collected over the sampling period, with a standard deviation of 49.00. The minimum abundance for a bloom was calculated to be 82 medusae (average plus one standard deviation), represented in Figure 1 by a dashed line. There were 7 days with the medusa abundance greater than 82. Thus, there were 7 blooms generated over the 12-month period. Of these 7 blooms, 2 were in the spring, 2 in the summer, and 3 in the fall.

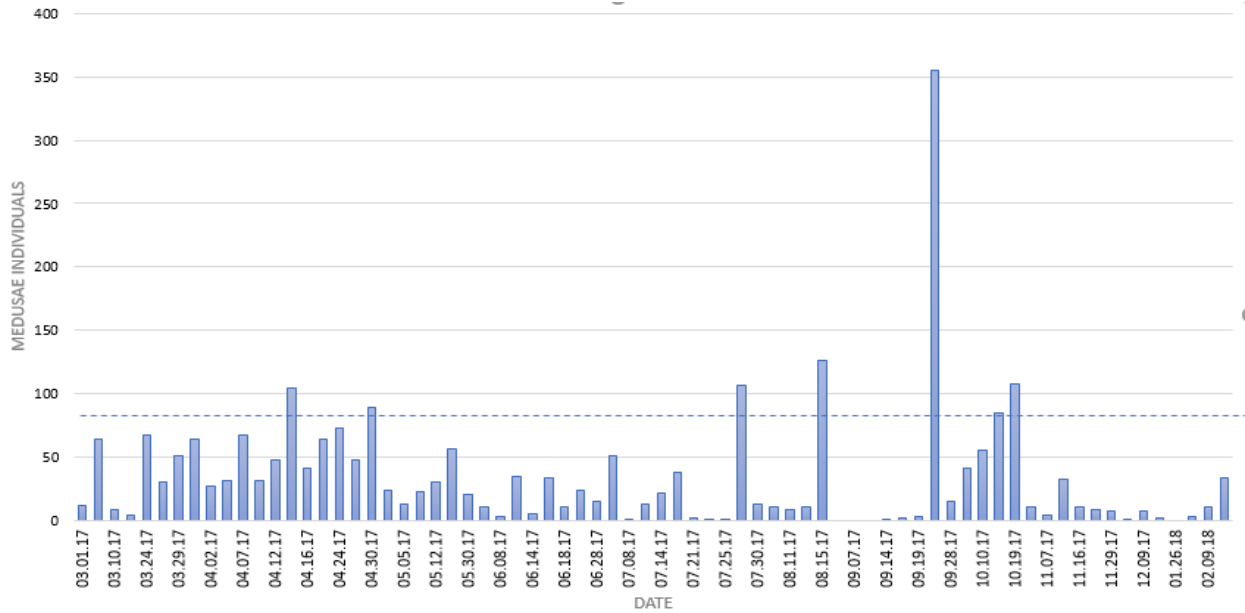


Figure 1. *Hydromedusa* abundance per sampling day. The dashed line represents one standard deviation above the mean abundance; any abundance above the line is considered a bloom

Figure 2 represents the seasonal break down of the 2385 medusae collected. 923 medusae were collected within the 25 sampling days in Spring. This produces a daily average of 36.92 medusa between the summer months. For the summer, 778 were collected within 22 sampling days, resulting in a daily average of 35.36. Fall had a daily average of 30.75 with 369 medusae collected in 12 sampling days. Finally, winter had a daily average of 26.25 with 315 medusae in 12 sampling days. These seasonal, daily medusa averages are represented in Figure 3 for visualization purposes.

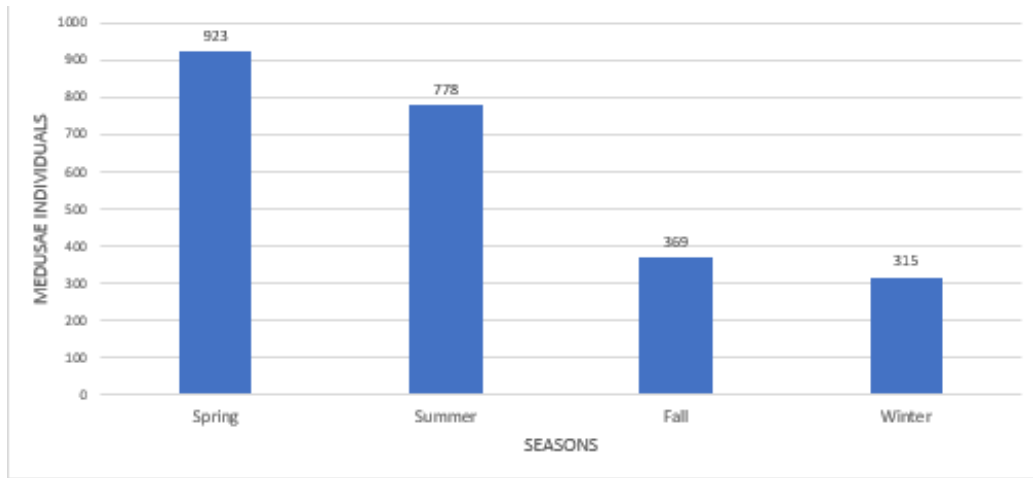


Figure 2. Seasonal breakdown of total hydromedusa abundance throughout the year cycle.

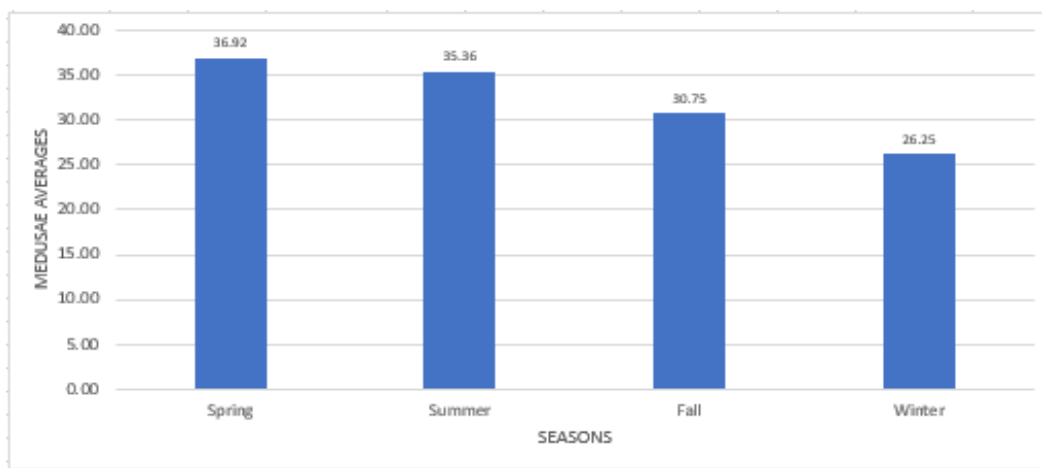


Figure 3. Seasonal breakdown of total hydromedusa abundance throughout the year cycle.

Relations Between Hydromedusa and Abiotic Environmental Factors

The relationship between abundance, water temperature and salinity for each sampling day is shown in Figure 4. The water temperature data (obtained from NOAA Tides & Currents) showed no unordinary, or dramatic changes. The temperature peaked at 31.28^oC on 2 sampling days (August 12th and 18th of 2017) and showed a low of 10.78^oC on January 24th, 2018. As

expected, the trend in water temperature depicts the highest temperatures in the summer months and the lowest in the winter months.

The salinity data (obtained by Dr. Quigg’s Phytoplankton Dynamics Laboratory at Texas A&M University at Galveston) showed only one area of drastic change in the levels of salinity and that was in the early part of September, right after hurricane Harvey hit Galveston, Texas. Salinity started to increase steadily again and by mid-September the levels were fairly steady again, but did not reach normal levels, again, until the beginning of November.

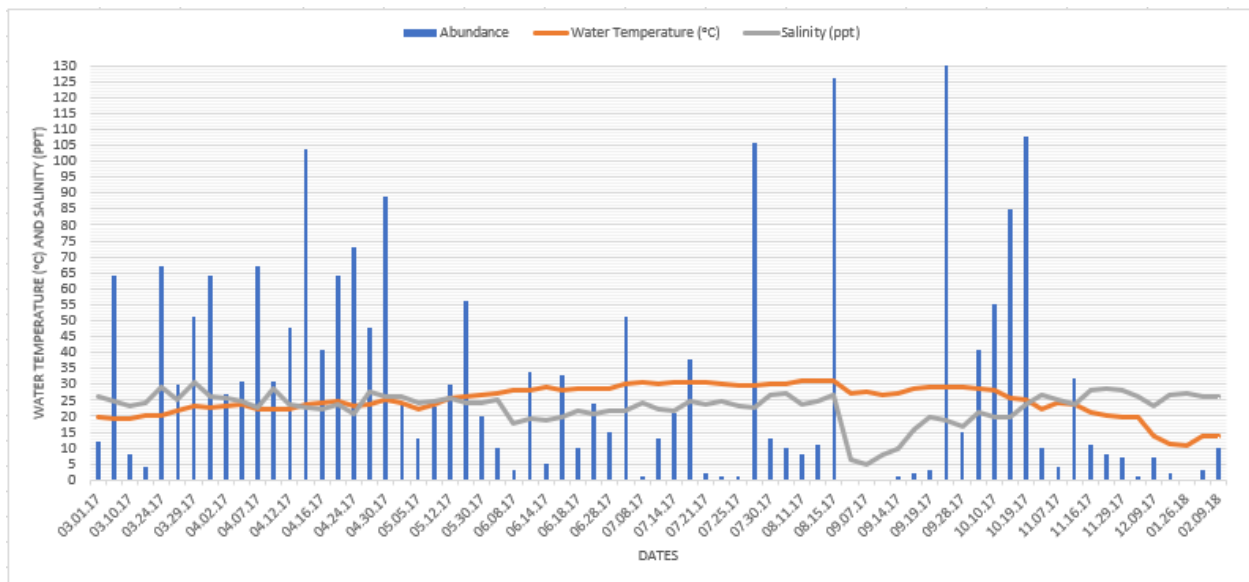


Figure 4. Daily water temperatures (oC) and salinity (ppt) against the daily medusa abundance. Note on sample day: 09.27.17 true abundance value is 355 medusae, due to scale it was altered.

Appendix I is a numerical log of sample dates, abundance values, salinity, and daily water temperatures for the study year. Correlation between hydromedusa abundance and both abiotic factors-salinity and temperature, was tested. Correlation between number of medusa per day and salinity was 0.0389, and between the number of medusa per day and temperature was 0.1303.

Comparison Between Previous Non-Hurricane Results and Hurricane Year Results

Table 1 shows a comparison between results gathered during 3 sampling cycle. Sample cycles (2 pre-Harvey and 1 after Harvey). Sample cycle September 2015 through September 2016 had a total abundance of 1321 medusae over a total of 191 sampling days, resulting in an average of 7 medusae per day. It had a maximum abundance occur in April totaling 104 individuals. Due to this peak the standard deviation was a value of 12. The standard deviation in addition to the daily average, set the value for bloom count at 19. This sampling cycle had a total of 19 blooms, or days the abundance was greater than 19 individuals.

Sample cycle October 2016- February 2017 had a total abundance of 750 medusae over a total of 36 sample days, resulting in an average of 20.8 medusae per day. It had its maximum abundance of 51 individuals in November. This set the standard deviation at a value of 13.3, thus the bloom value at 34.1 medusae/day. During this cycle, a total of 6 blooms occurred.

During the sample cycle March 2017- February 2018, a hurricane occurred on August 25th through August 29th. This sample cycle had a total abundance of 2385 medusae over a total of 71 days. Resulting in a daily abundance average of 33.6 individuals. It had a maximum abundance total of 355 medusae occurring in the month of September. This high peak, set the deviation value at 49.0, resulting for a bloom value of 82.6 medusae. The total number of blooms occurring during this cycle was 7.

Table 1: Comparison of previous sampling cycles to this study's. Including multiple factors such as: total abundance, total amount of sampling days, number of months, average sampling days per month, daily medusa average, standard deviation, bloom indexes, number of blooms, maximum medusa count, and month of peak in medusae.

			Hurricane year
Sampling cycle	Sept. 2015- Sept. 2016	Oct. 2016-Feb. 2017	Mar. 2017- Feb 2018
Total abundance	1321	750	2385
Total number of sample days	191	36	71
Number of months sampled	13	5	12
Average days per month	14.7	9	5.9
Daily medusa average	7	20.8	33.6
Standard deviation	12	13.3	49
Bloom index	19	34.1	82.6
Total number of blooms	19	6	7
Maximum daily medusa count	104	51	355
Month maximum occurred	April	November	September

CHAPTER III

DISCUSSION

Effects of Temperature and Salinity on Abundance

In this investigation, statistical analysis was performed in order to determine the correlation of both water temperature and salinity to the abundance values of hydromedusae within the sampling period. No significant correlation between the abundance of medusa to either water temperature (0.1303) nor salinity (0.0389). However, the overall number of Hydromedusae collected was greatest in the spring (923) and summer (778) months, with generally higher water temperatures, in comparison to that of the fall (369) and winter (315), which had much colder temperatures. The salinity, other than after the hurricane, was constant throughout the year in the Galveston Bay.

Comparison Between the Different Sampling Cycles

When comparing the pre-hurricane sample cycles to this sample cycle, there were noticeably different results. The hurricane cycle had a significant higher amount of hydromedusa collected than the other two cycles. In comparison to the September 2015 through September 2016 cycle there were 2.69 times as many sampling days than this March 2017 through February 2018 cycle; however, in this cycle there were almost twice as many medusae collected throughout. This lead to the daily abundance to be greater than the other two cycles, as well. Also, another distinguished difference was the maximum daily abundance each cycle experienced. The larger of the two non-hurricane cycles was 104 individuals, while this cycle had five days with totals that were equal to or greater than that, with a maximum of 355

individuals in a single day. The number of blooms was in the middle of the two non-hurricane cycles, but this was due to the large value calculated for the bloom index. The previous cycles had bloom indexes of 19 individuals and 34.1, while the hurricane cycle bloom index was 82.6 individuals. If the index would have been as low as previous years, there would have been several more 'blooms' calculated throughout the 12-month period. In conclusion a significant higher number of medusa were collected during the last cycle (2017-2018) when compared with previous, pre-Harvey sampling cycles (2015-2016).

CONCLUSION

The hydromedusa of Galveston Bay were collected and identified through morphological and molecular techniques over a 12 month cycle to assess the abundance and biodiversity of the species present. The hydromedusa abundance was compared to abiotic factors such as: temperature and salinity. These produced no significant correlation between them in this model.

This study represents the first look into the hydromedusa community, after a significant natural disaster, in Galveston Bay which play the role of top predator in the marine food web. Continuation of this study and long-term monitoring are necessary to understand the seasonality and diversity of hydromedusa in Galveston Bay. In this sampling cycle, only temperature and salinity were analyzed for environmental parameters. A wider variety of parameters should be performed as some not tested may be involved in triggering medusa blooms or adhere with another parameter to do so. Further analysis will also be performed to test the potential correlations between the bloom frequency and intensity to that of the environment.

Due to this being part of a long-term study, the continuation of comparison of aspects such as: overall abundance, number of blooms, species richness, and seasonality of the medusa, between the years will be performed in the future. This could help determine the changes, if present, of this community and the driving factors behind such changes. If the dynamics between Hydromedusae and the Galveston Bay environment are successfully monitored over an extended period of time, valuable information about the driving effects of abiotic factors could be better understood and predicted.

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APPENDIX I

Sampling cycle results, including sample dates, medusa abundance, water temperature (°C) and salinity (ppt).

Sampling Days	Medusa Abundance	Water Temperature (°C)	Salinity (Ppt)
03.01.17	12	19.72	26.14
03.08.17	64	19.22	24.63
03.10.17	8	19.11	23.02
03.22.17	4	20.22	24.31
03.24.17	67	20.22	29.04
03.26.17	30	21.78	25.19
03.29.17	51	23.00	30.41
03.31.17	64	22.89	26.31
04.02.17	27	23.22	25.94
04.05.17	31	23.50	24.46
04.07.17	67	22.39	22.67
04.09.17	31	22.28	28.76
04.12.17	48	22.28	23.73
04.14.17	104	23.50	22.78
04.16.17	41	24.22	22.25
04.19.17	64	24.61	23.61
04.24.17	73	23.11	20.83
04.27.17	48	23.72	27.6
04.30.17	89	25.22	26
05.03.17	24	24.22	26.03
05.05.17	13	22.39	24.08
05.08.17	23	23.72	24.56
05.12.17	30	25.50	25.88
05.14.17	56	26.22	24.14
05.30.17	20	26.78	24
06.02.17	10	27.22	25.02
06.08.17	3	28.28	18
06.11.17	34	28.39	19.35
06.14.17	5	29.00	18.85
06.17.17	33	28.28	19.91
06.18.17	10	28.72	21.95
06.27.17	24	28.89	20.69
06.28.17	15	28.50	21.63
07.05.17	51	30.39	21.5

07.08.17	1	30.89	24.28
07.11.17	13	30.00	22.35
07.14.17	21	30.72	21.5
07.16.17	38	30.72	24.56
07.21.17	2	30.61	23.47
07.24.17	1	30.22	24.52
07.25.17	1	29.89	23.11
07.26.17	106	29.50	22.81
07.30.17	13	30.11	26.89
08.08.17	10	30.28	27.3
08.11.17	8	31.22	23.8
08.12.17	11	31.28	24.85
08.15.17	126	31.28	26.53
09.02.17	0	27.22	6.2
09.07.17	0	27.50	5
09.12.17	0	26.50	8
09.14.17	1	27.28	9.82
09.17.17	2	28.61	15.76
09.19.17	3	29.11	19.67
09.27.17	355	29.22	18.95
09.28.17	15	29.39	17
10.03.17	41	28.89	21.22
10.10.17	55	28.39	19.61
10.17.17	85	25.50	19.85
10.19.17	108	25.11	23.85
11.02.17	10	22.28	26.91
11.07.17	4	24.28	25.24
11.09.17	32	23.61	23.82
11.16.17	11	21.39	28
11.22.17	8	20.28	28.79
11.29.17	7	19.61	28.21
11.30.17	1	19.72	26.1
12.09.17	7	14.00	23.2
01.24.18	2	11.11	26.5
01.26.18	0	10.78	27.08
02.02.18	3	13.61	26
02.09.18	10	13.61	26