PREDATORY FISH POPULATION DYNAMICS AND DIET IN A TRADITIONAL HAWAIIAN FISHPOND

A THESIS SUBMITTED TO THE GRADUATE DIVISION OF THE UNIVERSITY OF HAWAIʻI AT MĀNOA IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE OF

MASTER OF SCIENCE

IN

MARINE BIOLOGY

AUGUST 2018

By

Anela K. Akiona

Thesis Committee:

Erik C. Franklin, Chairperson
Brian N. Popp
Rob Toonen

Keywords: fishpond, population dynamics, diet, stable isotopes, barcoding

ABSTRACT

Overfishing and anthropogenic stressors have decimated Hawai‘i’s coastal fisheries. Traditional Hawaiian fishponds, or loko i‘a, are a low-impact and culturally significant food source in the face of climate change and increased concerns over food security. He‘eia fishpond, on the windward side of O‘ahu, is currently trying to raise herbivorous fish as a local and sustainable food source. It is therefore crucial to understand the population dynamics and diet of predatory fish to assess their potential impact on the food production species. A mark-recapture experiment (the Lincoln-Petersen closed population estimator with Chapman correction) was conducted to estimate the population of predatory fish in the pond, and visual, genetic barcoding, and stable isotope analyses were used to assess their diet. Catch-per-unit-effort data from community fishing days were also utilized to examine trends in the relative abundance of predator fishes. *Sphyraena barracuda* had the largest population in He‘eia fishpond at 189 individuals, follwed by *Caranx ignobilis* (89) and *C. melampygus* (19), which reflects trends in the CPUE from September 2016 – September 2017. Diets of the three species consisted mainly of nearshore, estuarine fishes and crustaceans. We did not find evidence that the predators consumed the herbivorous fishes typically raised as food, suggesting that they are either not specifically targeted by the dominant predators in the fisphond or are such low population sizes that they are not part of the predator’s diet. Based on these findings, we recommend maintaining current strategies for management of He‘eia Fishpond’s top predatory species.

ACKNOWLEDGMENTS

This work was supported by funding from the Hauʻoli Mau Loa Foundation, National Science Foundation Graduate Research Fellowship Program, Kamehameha Schools ʻImi Naʻauao Scholarship, Fernando Gabriel Leonida Memorial Scholarship Fund, and the Heʻeia NERR (NOAA-NOS-OCM-2017-2005226).

I am extremely grateful to my advisor, Dr. Erik Franklin, for his support, encouragement, and guidance throughout this project and my time at UH Mānoa. I am also grateful to my other committee members, Drs. Brian Popp and Rob Toonen, for their expertise and feedback. I would not have been able to complete such an ambitious project with my committe's support at every stage.

None of this would have been possible without the support of Paepae o Heʻeia. Thanks especially to Hiʻilei Kawelo, Keliʻi Kotubetey, Loea Morgan, and Kanaloa Bishop for their assistance in sample collection and coordination of volunteers for the tagging days. Many thanks to the fishers that volunteered for my project and who let me measure their fish at Lā Holoholo.

I am also very grateful to Maia Kapur, Zack Oyafuso, and Dr. Megsie Siple for their guidance and assistance with coding. Thanks as well to the Franklin Lab for all their support and feedback over the last two years.

Mahalo nui loa to my family for their constant love, support, and encouragement. Special thanks to my parents for assisting with every aspect of this project that they could, and for always supporting me in everything I do; aloha au iā ʻoe.

TABLE OF CONTENTS

FIGURE LEGENDS

TABLE LEGENDS

INTRODUCTION

The State of Hawai‘i, the most isolated archipelago on the planet, is home to nearly 1.43 million people. Because of this extreme isolation, the State imports nearly 90% of its food and energy resources from the mainland USA and other parts of the world (Keffer et al. 2009). The nearshore fisheries face not only overexploitation, but many anthropogenic stressors as well (Friedlander and DeMartini 2002).

Rising regional and global demand for fish and fishery products may fall short of wild fishery production capabilities. Aquaculture may be able to meet some of these demands while alleviating pressure on wild stocks (Naomasa et al. 2013). Local aquaculture production provides access to fresh seafood while avoiding high import costs and without diminishing freshness or quality. The local market in Hawai‘i exhibits favorable signs for increased aquaculture production. Hawaii consumers demonstrate an increasing demand for seafood with consumption rates that are double the national average (Loke et al. 2012).

The aquaculture industry in Hawai‘i is fast-growing and has been viewed as an important replacement for imported seafood. In 2010 it was a $30 million industry, doubling its value over the previous 10 years (USDA 2011). Aquaculture grew an additional 250% 2010 to $76 million in 2015 (USDA 2016). However, only 12% of the aquaculture farms in 2007 were classified as efficient (Kim et al. 2015), showing ample opportunity for additions to the aquaculture industry in Hawai‘i.

History of Hawaiian Fishponds

Traditional Hawaiian fishponds, or loko i‘a, are an example of ancient aquaculture that can provide a sustainable and pragmatic solution to sustainability challenges and biosecurity

concerns in the face of climate change. Since before the 13th century, loko iʻa served as a living food pantry that could be harvested from year round during food shortages or periods of poor fishing (Farber 1997, Sato and Lee 2007). Loko iʻa were typically built along the shore where a freshwater stream emptied into the ocean. The brackish water and shallow depths of these estuarine environments produced optimal conditions for the cultivation of algae (Apple and Kikuchi 1975, Kelly 1994). The combination of rich algae growth, along with the right species of herbivorous fish, gave Hawaiians a protein source that was 100 times more efficient than in the natural estuarine food chain (Kelly 1994).

Fishpond management focused on the cultivation of herbivorous fish such as (in order of importance): *Mugil cephalus* (mullet or ʻamaʻama), *Chanos chanos* (milkfish or awa), and *Polydactylus sexfilis* (threadfin or moi) (Vockeroth 1981). Occasionally predators entered the pond, but as long as their numbers were kept low they could not significantly impact the population of herbivores (Sato and Lee 2007).

Building a fishpond was a community undertaking—large loko iʻa required upwards of 10,000 men to complete construction (Kamakau 1976, Farber 1997); similarly, maintaining a fishpond required the help of many hands. However, Hawaiʻi's rapidly changing socioeconomic climate in the 1800's led to a decline in the number of operated fishponds. With the advent of more lucrative trades, such as sandalwood trading and whaling, the Great Māhele land division of 1848, and depopulation from diseases, loko iʻa maintenance declined (Farber 1997). Lower labor costs made it cheaper to import fish than to raise them, and short-term gains from ocean fishing became more enticing than the long-term investment of operating the loko iʻa (Farber 1997).

Out of 488 loko iʻa statewide, 178 were located on Oʻahu. Around 1900, fishponds accounted for almost 10% (682,484 pounds) of the fish caught in Hawaiʻi, of which 560,283 pounds were from Oʻahu alone (Cobb 1902). In 1994, only 6 were still operating commercially statewide, with a yield of just 31,639 pounds valued at $68,911 (Farber 1997). The Hawaiian Renaissance of the 1960s and 70s saw a renewed interest in loko iʻa, including at Heʻeia fishpond, located in Kāneʻohe Bay. A 1972 proposal to develop Heʻeia Fishpond into a boat harbor was met with strong protest (Farber 1997), and this community interest helped to lay the foundation for the pond's current restoration and the founding of Paepae o Heʻeia, the fishpond's managing organization.

Heʻeia Fishpond is one of only a handful of traditional Hawaiian fishponds that are still operational and working towards (or currently) commercially producing fish. Fishponds are grossly understudied even though they represent integrated multi-trophic aquaculture that is culturally significant, relatively low-cost, and low-impact. Estimates of loko iʻa yields vary from 175 to 275 pounds per acre per year (Wyban 1992, Farber 1997) up to 350 pounds per acre per year (Apple and Kikuchi 1975). This has the potential to provide a substantial amount of food to Hawaiʻi residents.

It will take several years before the native herbivores at Heʻeia Fishpond are ready to be harvested, but in the meantime it is important to understand how predators might be affecting their populations. This raises some questions about the population dynamics of the dominant predatory fish species in the loko iʻa: *Caranx melampygus* (ʻomilu), *C. ignobilis* (white papio), *Sphyraena barracuda* (kākū).

Approach

The objective of this thesis is to assess the population dynamics and dietary preferences of the three main predatory fish species in He‘eia Fishpond, with a focus on their interactions with and potential impact upon the herbivorous fish traditionally raised in these systems. The results could have implications for how the fishpond in managed, and has potential to be utilized by fishponds throughout Hawai‘i.

Chapter 1: Fishing for Science: Assessing predatory fish populations in He‘eia Fishpond directly and indirectly estimates the abundance of predatory fish in the pond using conventional mark-release-recapture methods and CPUE from community fishing events. Our findings indicate that the predatory fish population in He‘eia Fishpond is relatively low, when spread out over the pond’s 88 acres. We estimate the total population of the three dominant predatory fish to be less than 300 individuals, with evidence for seasonal changes in population numbers. This demonstrates that fishing effort may be best directed during warmer summer months, when fish catches are generally higher, although current management policies seem to be sufficient to keep population sizes low.

Chapter 2: Diets of the predatory fish of He‘eia Fishpond: Insights from stomach content and stable isotope analyses utilizes visual gut content techniques, genetic barcoding, and stable isotope analyses to determine whether the dominant fishpond predators are targeting the herbivorous fish traditionally raised and harvested for consumption. Genetic barcoding greatly improved the identification of prey taxa, many of which were greatly digested. The incorporation of bulk tissue stable isotope methods and Bayesian mixed modeling allowed for a more holistic picture of the predators’s dietary preferences, in addition to the ‘snapshot’ picture

provided by more traditional methods. We did not identify any of the herbivorous fish species of interest in any stomachs, which suggests that the predatory fish impact upon these species is minimal. This study has implications for the management of traditional Hawaiian fishponds around the State.

Chapter 1: Fishing for Science: Assessing predatory fish populations in He‘eia Fishpond

ABSTRACT

Mark-recapture and catch-per-unit-effort (CPUE) methods are fundamental tools of fisheries management. We used both methods to assess the population of predatory fish in He‘eia Fishpond, which is a traditional Hawaiian fishpond that is working towards producing herbivorous fish. CPUE (# fish/pole/hour) was calculated from monthly community fishing events that were held from September 2016 to September 2017. *Caranx ignobilis* was caught most frequently during these events, with overall catches appearing to be higher during warmer, summer months, although this relationship was not statistically significant. Additionally, a mark-recapture experiment was conducted in July 2017 to directly estimate the number of predatory fish in the pond. *Sphyraena barracuda* was the most abundant (190 individuals), followed by *C. ignobilis* (89), and *C. melampygus* (19). It is likely that the most abundant species changes throughout the year. All individiuals captured for all three species were smaller than mean length at maturity, indicating that the predatory fish populations are largely immature. Continued research and additional mark-recapture studies will greatly improve our understanding of the population dynamics of the dominant fishpond predators.

INTRODUCTION

Making unbaised abundance estimates is a critical part of successful fisheries management. Mark-recapture studies are used to make estimates of population size, survival and rectuitment, to learn about a population’s response to management protocols, and to validate

population indices used for long-term monitoring (Gwinn et al. 2011, Peterson et al. 2015, Ruetz et al. 2015). These methods have been used most successfully to estimate the abundance of terrestrial animals or of fishes in enclosed lakes, but they can be used for marine species in confined areas (Jennings et al. 2001). Mark-recapture methods for two sampling periods rely on marks being applied to a subset of the target population during the first sampling event, then using the ratio of marked to unmarked fish captured during the second sampling event to estimate abundance (Seber 1973).

One such model is the Lincoln-Petersen mark-recapture model with Chapman correction, which is unbiased at low sample sizes, particularly when the number of recaptures = 0 (Chapman 1951, Seber 1973). Capture probability (q) refers to the likelihood that a fish is captured during a sampling event, and we consider the case where sampling is conducted via hook-and-line fishing in a fishpond. This model has several assumptions that must be met (Pine et al. 2012):

(1) The population is closed both physically (i.e. no immgration or emigration) and demographically (i.e. no recruitment or mortality);

(2) q is the same for marked and unmarked fish;

(3) Marks are not lost or undetected;

(4) Marked fish mix randomly with the population when released; and

(5) Marking does not affect fish behavior or vulnerability.

Oftentimes, it is not possible to directly estimate fish populations, and therefore relative abundance is a widely used tool in fisheries stock assessment and management. An abundance index is used to monitor stock status for conservation to fine-tune population dynamics models (Geromont and Butterworth 2015, Tu et al. 2015). Since much of the data available is fishery-dependent, catch-per-unit-effor (CPUE) is calculated by accounting for various factors (such as

time) that are not constant between samples (Maunder and Punt 2004). While mark-recapture models provide direct estimates of population size, CPUE only demonstrates trends in catches which may or may not be related to population abundance (Stenseth 2002).

Traditional Hawaiian fishponds are estuarine environments enclosed by a rock wall, where herbivorous fish such as *Mugil cephalus*, *Chanos chanos*, and *Polydactylus sexfilis* were raised for consumption by the local community. In 1965, a large flood destroyed a 200 ft. portion of He‘eia Fishpond’s wall, allowing fish to transit freely in and out of the pond. The hole was repaired in 2015, but after 50 years of being open to the ocean, it is unclear how many predatory fish remain in the pond. As the fishpond managers work to cultivate the herbivorous fish, it is important to understand what local factors may be affecting their populations.

In the present study, we estimated the population sizes of the three dominant predatory species in He‘eia Fishpond using the Lincoln-Peterson model with Chapman correction. Our research objective is to provide meaningful scientific results to managers of Hawaiian fishponds that support sustainable food production through the utilization of mark-release-recapture methods and catch per unit effort (CPUE) data. These results will specifically benefit the community of fishers, seafood consumers, and caretakers of He‘eia Fishpond, with potential application to fishponds throughout the islands.

MATERIALS AND METHODS

Study site and species

This study was conducted at He‘eia Fishpond, an 88 acre traditional Hawaiian aquaculture system located in Kāne‘ohe Bay on the windard side of O‘ahu (21°26'8.33"N, 157°48'27.28"W). The 88 acre pond is surrounded by a 1.3 mile stone wall, or kuapā, built of

basalt boulders and filled with coral rubble. Built into the kuapā are mākāhā, or sluice gates, which control the flow of water and fish into and out of the pond (Farber 1997). Fishponds are traditionally built on shallow reef flats no more than 10-15 ft deep where algae, or limu, can easily grow. He‘eia Fishpond is a brackish water environment with freshwater input coming from nearby He‘eia stream and submarine groundwater discharge (Leta et al. 2016).

The study species were determined from previous hook-and-line catch records from the fishpond from December 2015 to January 2017. *Caranx ignobilis*, *C. melampygus*, and *Sphyraena barracuda* had the three highest catch numbers (Table 1.1). The next highest predatory species captured was *Lutjanus fulvus* (35 individuals).

Table 1.1. Catch number (n) and mean fork length (FL) and standard deviation (SD) of the top three species caught at Lā Holoholo and by Paepae o He‘eia staff from December 2015 to January 2017.

Species	n	Mean FL (mm) ± SD
Caranx ignobilis	276	280.3 ± 47.5
Caranx melampygus	249	303.8 ± 141.9
Sphyraena barracuda	78	349.3 ± 80.3

Catch-per-unit-effort

He‘eia Fishpond hosts a monthly fishing event where community members are allowed to fish for predatory fish inside and outside the pond using conventional hook-and-line methods. After a brief orientation, fishing started at approximately 9:30am and continued as late as 2:30pm. Fishers were allowed to use any type of bait and line setup they preferred and could fish from anywhere along the wall. While most fishing was done inside of the pond, fish were also allowed to be caught outside provided they adhered to State regulations. Any predatory fish caught inside the pond could be kept by the fisher or released outside of the pond.

We attended each of these events from September 2016 to September 2017 and collected data on the number of fishing poles per group, length of time fished, number of fish caught per group, fish species, fish length (to the nearest 0.1 mm), and fish weight (to the nearest g) when possible. When fish could not be weighed directly, body mass was calculated from available length-weight relationships for each species (Sudekum et al. 1991, Williams and Ma 2013). Number of poles and number of fish caught were consolidated by group because fishing participation often varied amongst group members (i.e. families with children), or there were more poles than there were group members. These data were used to calculate CPUE for each group and across fishing days in units of number fish per pole per hour, and weight of fish per pole per hour. Overall length and weight frequencies were also compared for each species, but there were insufficient data to make such comparisons between months. Using water temperature data from the University of Hawai‘i Project OTIS (Oceanographic Technological Innovations and Solutions), I used a linear model to determine if there was a significant relationship between montly mean water temperature and CPUE. All analyses were performed in R version 3.4.3 (R Development Core Team; www.r-project.org).

Mark-release-recapture

The tagging experiment was conducted over two different days set two weeks apart in July 2017. Each day had two shifts, morning and afternoon. Sampling days and shifts were chosen so that tidal and lunar cycles were as similar as possible across tagging and recapture. The fishpond was divided into four zones to ensure the entire pond was sampled; wall zones were fished from on the kuapā and the interior of the pond was fished from a boat (Fig. 1.1). Every zone had two fishers who were free to move anywhere within their zone during the

allotted time. Each fisher was equipped with a GPS unit to track his/her movements and allow identification of each fish capture location. Fishers all used the hook-and-line fishing method but with a variety of lures and bait. Any bait used was recorded in order to prevent bias in the diet analysis portion of this study.

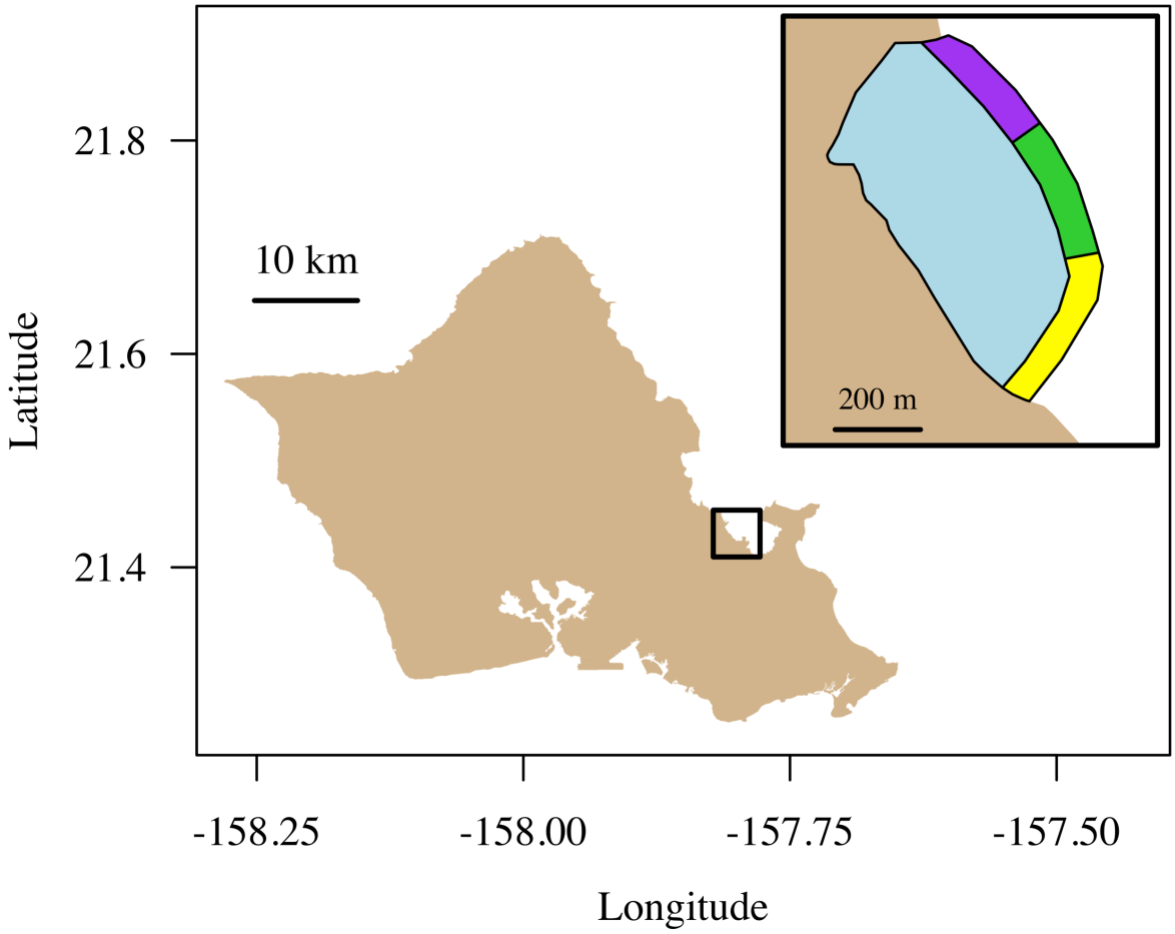


Figure 1.1. Map of sampling locations during the July 2017 tagging experiment at He'eia Fishpond. Zones: Wall 1 (orange), Wall 2 (green), Wall 3 (purple), and Pond (blue). Image from Google Earth.

On Day 1, fish were captured, tagged and released. Dart tags with unique number identfiers were provided by Pacific Islands Fisheries Group and are the same tags used in their Tag It Project (www.fishtoday.org/tagit). The first five fish captured in each zone were double

tagged to determine tag shedding rates. Length and weight measurements were taken for each fish, and all fish swam off immediately upon release. On Day 2, fish were captured, measured for length and weight, and sacrificed for the diet portion of this study. Fish were given unique identification numbers after capture and then immediately placed on ice to stop digestion, then frozen whole until analysis.

The mark-recapture abundance estimator ($\widehat{N}$) was calculated as (Chapman 1951)

$$\widehat{N} = \frac{(M+1)(n+1)}{(m+1)} - 1$$

where $M$is the number of fish captured, marked, and released on day 1; n is the number of marked and unmarked fish captured on day 2; and m is the number of marked fish captured on day 2 (i.e. recaptured). The Lincoln-Petersen model with Chapman modification is an unbiased estimator of the population size N when $(M + n) \geq N$, or is nearly unbiased when $m > 7$ (Krebs 1999).

RESULTS

Catch-per-unit-effort

Over the one-year sampling period, 298 predatory fish were caught over 2385.7 hours of fishing effort, of which 274 were kept by the fisher (Table 1.2). This resulted in a yield of 187.6 pounds of predatory fish being harvested from the fishpond. *Sphyraena barracuda* had the longest mean fork length, with the majority of individuals longer than 350 mm (Fig. 1.2). *Caranx ignobilis* and *C. melampygus* both had fork lengths around 300 mm. By weight, *C. melampygus* was the heaviest overall, although all three species had almost identical ranges for mass (Fig. 1.3). Monthly mean CPUE (# pounds/pole/hour) varied by almost 20-fold (Fig. 1.4),

with a similar pattern for weight. Warmer months appear to generally have a CPUE higher than the yearly average (Fig. 1.4), although no significant relationship was found between water temperature and CPUE for either number of fish or total fish weight. CPUE by species also varied throughout the year, but no clear pattern was observed (Fig. 1.5).

Table 1.2. Summary of information collected at Lā Holoholo from September 2016 to September 2017.

Date	Total # fish caught	Total # fish kept	Total lbs of fish kept	Total # poles	Total hours fished	Mean CPUE ± SD (# fish/pole/hr)	Mean CPUE ± SD (lbs/pole/hr)
Sep-16	46	37	40.2	46	210.9	0.21 ± 0.26	0.22 ± 0.28
Oct-16	11	6	2.3	31	123.5	0.07 ± 0.17	0.06 ± 0.19
Nov-16	6	6	2.2	108	415.9	0.01 ± 0.04	0.003 ± 0.02
Feb-17	19	18	2.9	38	139.1	0.12 ± 0.23	0.03 ± 0.06
Mar-17	3	4	3.7	52	189.3	0.04 ± 0.12	0.03 ± 0.14
Apr-17	35	30	13.6	54	230.1	0.10 ± 0.19	0.06 ± 0.11
May-17	26	26	21.6	42	180	0.18 ± 0.24	0.19 ± 0.32
Jun-17	31	31	28.7	42	191.2	0.21 ± 0.35	0.19 ± 0.33
Jul-17	20	17	11.8	42	201.4	0.08 ± 0.15	0.07 ± 0.16
Aug-17	40	40	26	56	260.6	0.16 ± 0.19	0.11 ± 0.20
Sep-17	60	59	34.8	55	243.7	0.18 ± 0.19	0.11 ± 0.13
Totals	298	274	187.6	566	2385.7	-	-

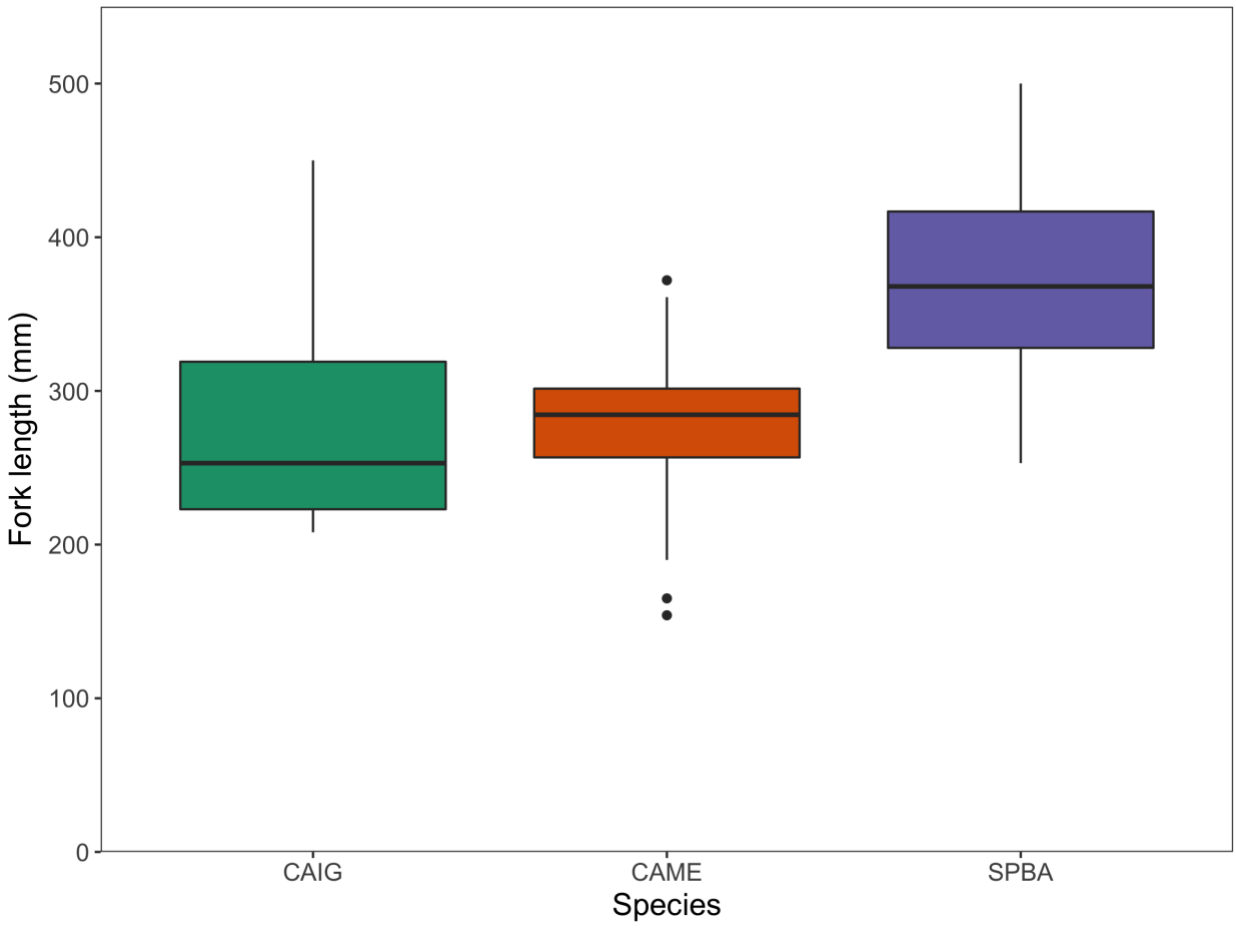


Figure 1.2. Boxplots of fork length (mm) for each species caught at Lā Holoholo. Species codes are: CAIG, *Caranx ignobilis*; CAME, *C. melampygus*; and SPBA, *Sphyraena barracuda.*

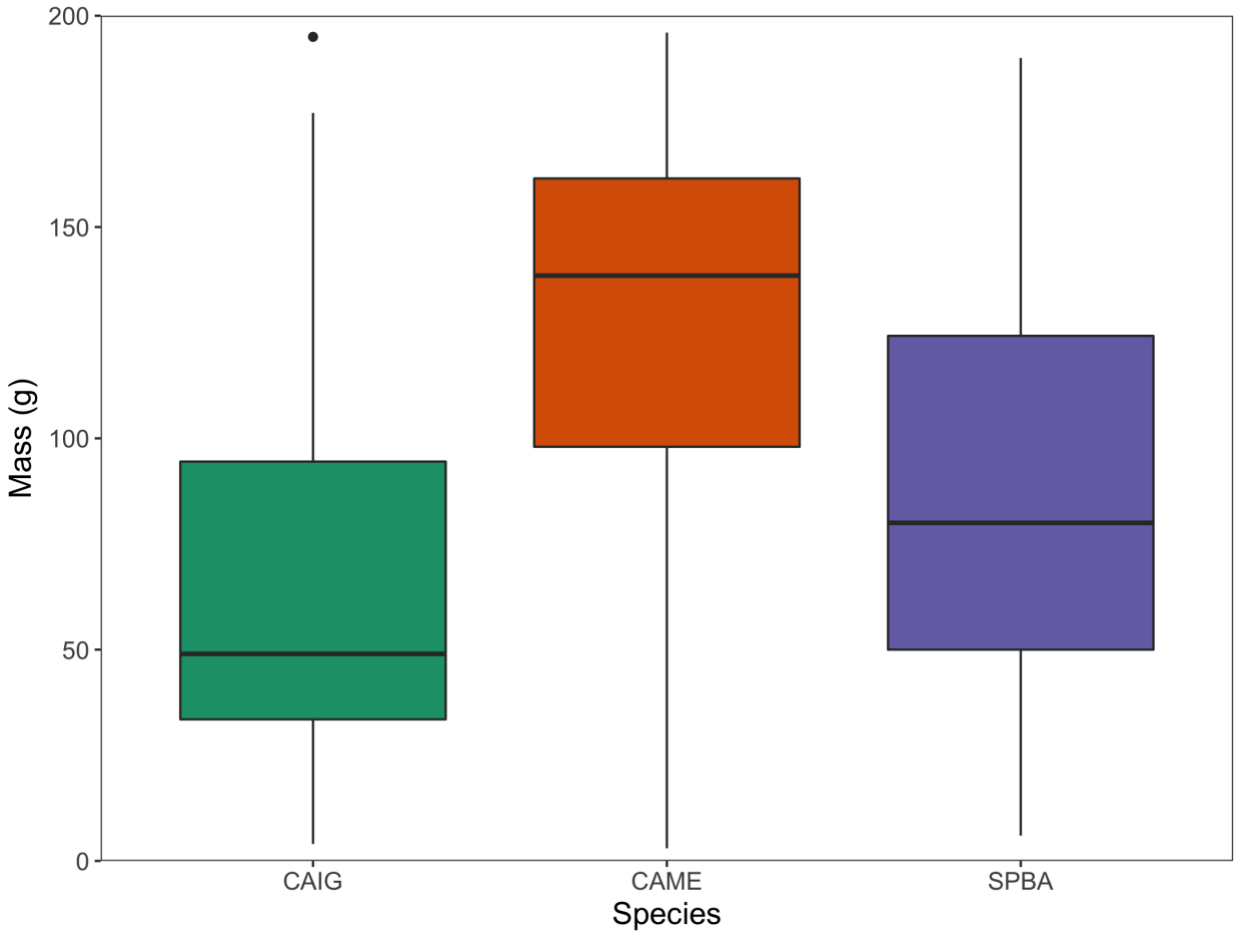


Figure 1.3. Boxplots of mass for each species caught Lā Holoholo. Species codes are: CAIG, *Caranx ignobilis*; CAME, *C. melampygus*; and SPBA, *Sphyraena barracuda*.

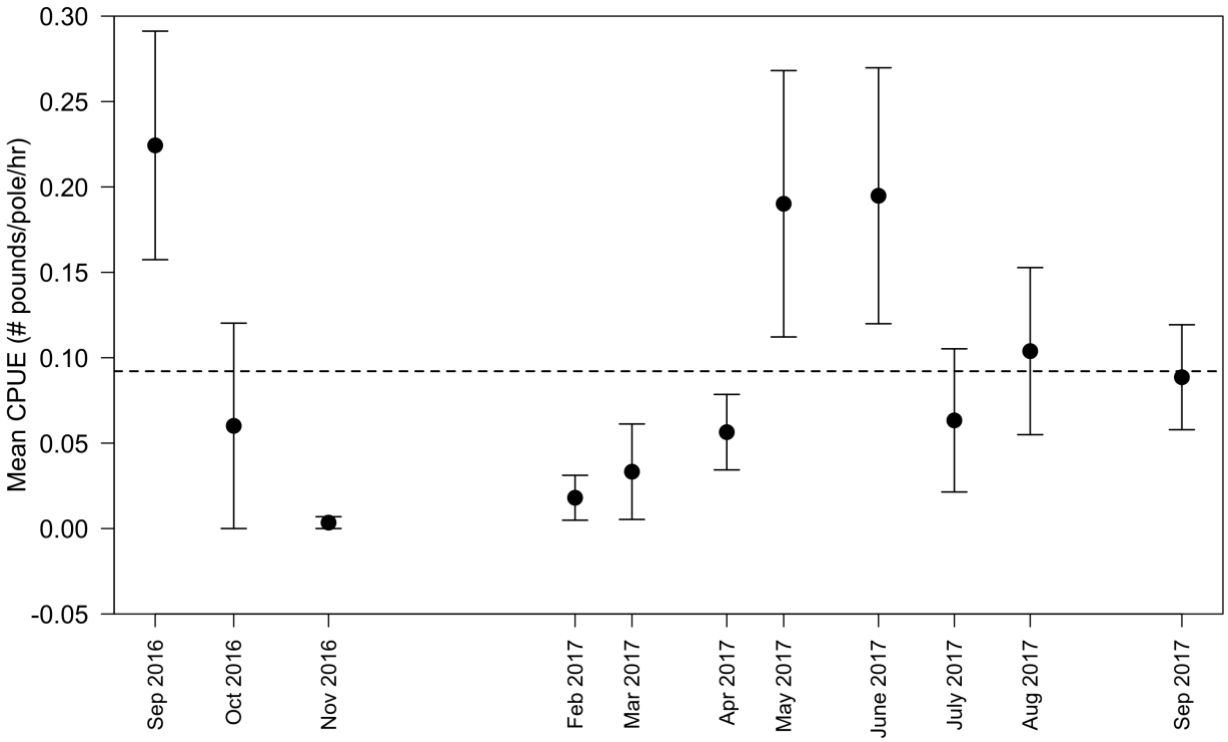


Figure 1.4. Monthly mean predatory fish CPUE (pounds of fish per pole per hour) for each Lā Holoholo with standard error bars shown. Dashed line represents the yearly mean CPUE of 0.09 pounds of fish per pole per hour.

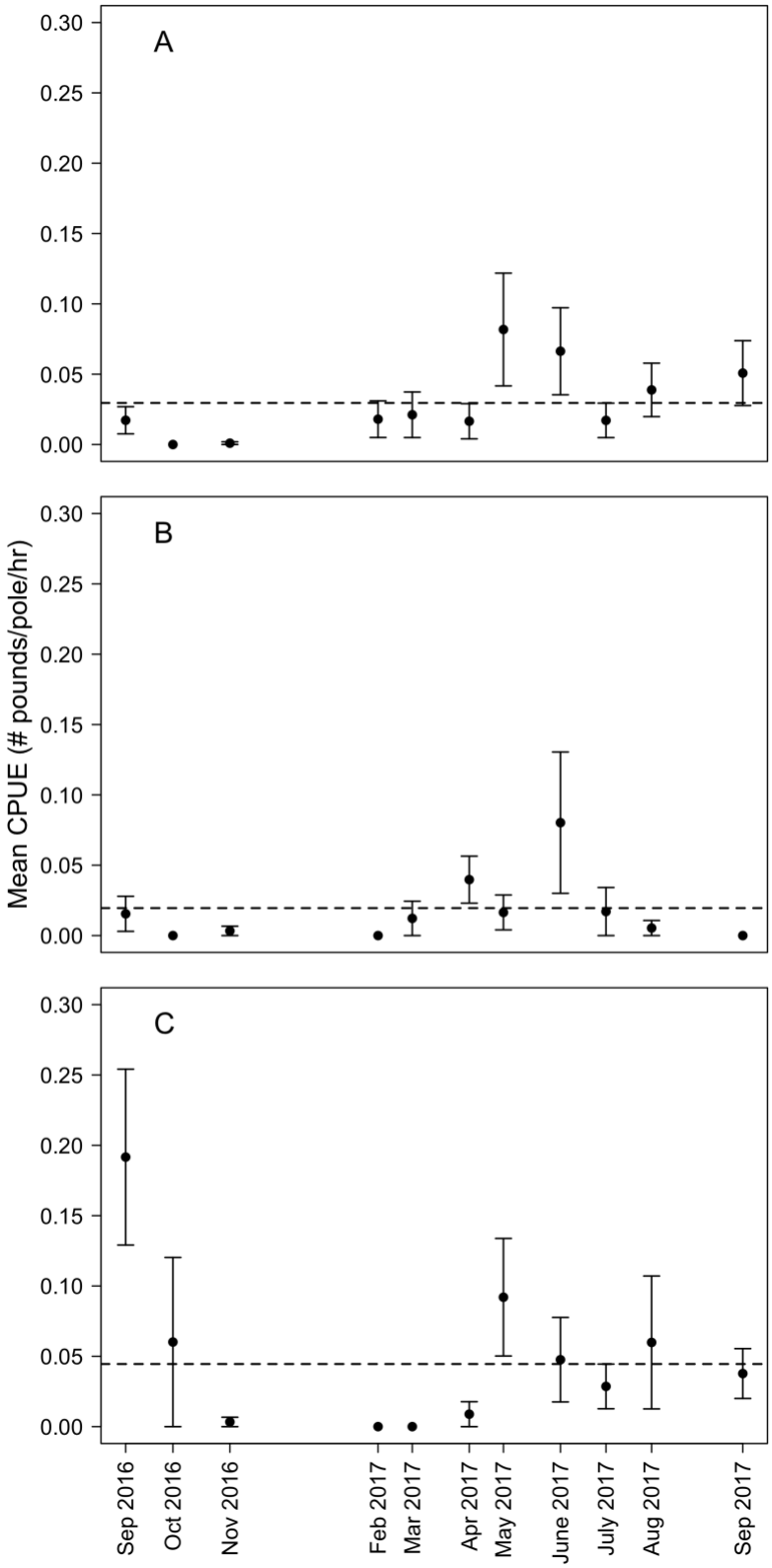


Figure 1.5. Monthly mean CPUE (pounds of fish per pole per hour) for each Lā Holoholo by species. A) *Caranx ignobilis*, B) *C. melampygus*, C) *Sphyraena barracuda*.

Mark-release-recapture

The majority of fish captured during the tagging experiment were *Sphyraena barracuda*, followed by *Caranx ignobilis* and *C. melampygus*; there were only recaptures for *S. barracuda* (Table 1.3). The Lincoln-Petersen model with Chapman correction estimates that there were less than 300 individuals for all three species combined when this study was conducted in July 2017. Most fish were caught in Wall 2, with the second highest number of catches inside the pond (Table 1.4). *Caranx ignobilis* was caught almost exclusively inside the pond, and *S. barracuda* were caught mostly in Wall 2 but had similar catches for the other three zones. Catch numbers of *C. melampygus* were much lower than the other two species. Mean length of each species captured during the tagging experiment was slightly larger than mean length from Lā Holoholo, but still spanned a similar size range (Table 1.5).

Table 1.3. Total numbers of fish marked on Day 1 (M), fish marked and unmarked caught on Day 2 (n), and fish recaptured on Day 2 (m) for each species across the entire fishpond. Estimates (N) given from the Lincoln-Petersen model with Chapman correction are rounded to the nearest integer.

Species	M	n	m	N
Caranx ignobilis	8	9	0	89
Caranx melampygus	4	3	0	19
Sphyraena barracuda	21	51	5	190
Total	33	63	5	298

Table 1.4. Number of fish marked on Day 1 (M), number of fish marked and unmarked caught on Day 2 (n), and number of marked fish caught on Day 2 (m) by species for each zone. Species codes are: CAIG, *Caranx ignobilis*; CAME, *C. melampygus*; and SPBA, *Sphyraena barracuda.*

Zone	M			n			m			Total		
	CAIG	CAME	SPBA	CAIG	CAME	SPBA	CAIG	CAME	SPBA	CAIG	CAME	SPBA
Pond	5	1	4	7	1	11	0	0	1	12	2	15
Wall 1	1	2	1	0	2	15	0	0	0	1	4	16
Wall 2	0	1	8	0	0	21	0	0	4	0	1	29
Wall 3	2	0	8	2	0	4	0	0	0	4	0	12

Table 1.5. Sample size, mean fork length (FL), mass, and standard deviations (SD) for each species captured during the July 2017 mark-release-recapture experiment.

Species	n	Mean FL (mm) ± SD	Mass (g) ± SD
Caranx ignobilis	17	281.6 ± 80.1	439.9 ± 270.0
Caranx melampygus	7	341.7 ± 39.9	693.9 ± 265.2
Sphyraena barracuda	71	360.5 ± 52.6	310.2 ± 127.4

DISCUSSION

To my knowledge, this is the first in-depth study done on predatory fishes in Hawaiian fishponds, and the first study on these fishes in over 70 years (Hiatt 1947). While the mean length of each species were fairly similar between Lā Holoholo days and the mark-recapture experiment, there were individuals observed to be much smaller and larger than the mean size. This suggests that these fishes may have a minimum size where they enter the fishpond fishery, and a maximum size where they are no longer susceptible to capture. This is likely due to the method of fishing used, which could exclude individuals based on hook size. Minimum estimates of age at maturity are approximately 350 mm for *C. melampygus*, 600 mm for *C. ignobilis*, and 500 mm (males) to 660 mm (females) for *S. barracuda* (De Sylva 1963, Sudekum et al. 1991). All individuals captured were well under these sizes, suggesting that the populations of these predatory species are dominated by immature individuals.

Sphyraena barracuda were caught most frequently during the tagging experiment, but *Caranx ignobilis* and *C. melampygus* both outnumbered barracuda catches for Lā Holoholo. Given that the tagging only occurred in July, compared to a year of data for Lā Holoholo, it is unlikely that each species' population remains constant relative to one another. The differences in catches for each species could be due to environmental conditions, changes in fish behavior,

or it could be related to spawning season, which is roughly spring through fall for all three species (Sudekum et al. 1991, Kadison et al. 2010).

During the tagging experiment, most individuals were captured in zone Wall 2 or inside the Pond. Wall 2 includes the spot where the wall was destroyed by the 1965 flood, and during the 50-year period it was open the increased water flow through this area resulted in a deeper channel, which may attract the fish to this area. Inside the pond, most captures were near Egret Island, which is a small mangrove island in the northwest part of the pond. The increased nutrient input from the bird droppings may indirectly increase the numbers of prey fish, which could attract the predatory fish to this area.

The CPUE from the July Lā Holoholo appears small relative to June and August, which was right before the tagging experiment. There may have been some environmental factors that caused the predatory fish catches to decline, which also could have caused the mark-recapture catches to be lower than expected for that time of year. In previous years, July has had the highest number of catches at Lā Holoholo. While there was not a significant relationship between CPUE and water temperature, the p-value was just over 0.05 ($p = 0.058$), it is possible that with a longer time series this would become significant. However, many other factors that could influence fish catch such as tide and moon phase, were not held constant between each sampling and therefore could confound any potential relationship. The monthly CPUE could also have been influenced by events during the rest of the month such as outside fishing events, large tidal fluctuations, or flooding over the wall. There were no such events observed in between the two sampling days for the tagging experiment.

It is likely that catches for the mark-recapture experiment could have been improved if the fishing method and bait were the same for all fishers. Because these were volunteers and

each person had his/her own preferred fishing methods, this was not something that was feasible to coordinate. Additionally, the estimation would be much improved by the addition of a second round of tagging and another boat to sample inside the pond, but logistical constraints prevented this from happening. The estimates for the two Carangids are guidelines at best because there were no recaptures for these species.

This study provides the foundation for continued work on the predatory fish in He‘eia Fishpond. With the inclusion of the suggestions outlined above, future estimates can be made to directly track the predatory fish populations over time. I was unable to sample the herbivorous fish populations given the time constraints of this project, but any future studies on the predatory fishes would be greatly enhanced by the addition of herbivorous fish data. With the recent designation of He‘eia as a NERR (National Estuarine Research Reserve), there will surely be an increase in research at He‘eia Fishpond, which will greatly contribute to the aquaculture production of this system and in turn, the food security of the State.

Chapter 2: Diets of the predatory fish of He‘eia Fishpond: Insights from stomach content and stable isotope analyses

ABSTRACT

Knowledge of a predator’s diet is a crucial part of understanding its ecological role and predator-prey dynamics. In He‘eia Fishpond, it is common practice to remove predatory fish that could prey on the native species of herbivorous fish traditionally raised for food. Here we use a combination of visual gut content analysis and metabarcoding, in conjunction with bulk tissue stable isotope analysis, to determine whether these predatory fish feed on the native herbivores. Of the 11 juvenile *Caranx ignobilis* and 29 juvenile *Sphyraena barracuda* stomachs that contained food, none of them included any of the herbivore species that are being raised in the fishpond. The two species fed primarily on Portunid crabs, *Palaemon* shrimp, Gobiids, and Carangids. Taxonomic resolution was greatly improved by the use of the metabarcoding approach since most fish prey were too degraded to be visually identified. Trophic level calculations and isotopic niche breadth analyses indicate that *C. ignobilis* and *S. barracuda* occupy similar ecological niches in the fishpond, and stable isotope mixing models reveal that their long-term diet is not comprised of the anticipated prey fish found in the pond. While the native herbivores are observed regularly in the pond, their populations are likely too low to be a large portion of the predatory fish’s diets. These findings improve understanding of food web dynamics in Hawaiian fishponds, and highlight the need for continued research in these systems.

INTRODUCTION

Predator-prey interactions are one of the primary processes controlling change in animal populations (Symondson 2002). Detailed knowledge of a predator's diet is a key part of understanding its ecological function (Leray et al. 2015). Predator-prey interactions have traditionally been investigated through visual gut content analyses (Hyslop 1980). This method provides a "snapshot" of the individual's diet at the particular moment it was captured. Stomach content analysis is a direct method of investigating predator diet and feeding preferences, and provides valuable insight on prey species and trophic overlap (Orlov 2004, Sturdevant et al. 2012).

While visual stomach content analyses are useful, there are drawbacks to the method. One major limitation is that easily digested prey items can prevent high-resolution taxonomic identification (Baker et al. 2014, Leray et al. 2015). Furthermore, the degree of visual identification can be influenced by predator digestion rates, temperature, prey morphology, and time between animal capture and stomach processing (Folkvord 1993, Legler et al. 2010, Carreon-Martinez et al. 2011).

One of the most powerful tools available to characterize a predator's diet is PCR-based molecular analysis of gut contents (Symondson 2002). This method is a useful tool in characterizing the diet of predators through stomach content analysis (Leray et al. 2015, Oyafuso et al. 2016, Gimenez et al. 2017). Metabarcoding of a predator's gut contents improves the taxonomic resolution of prey identification and consequently allows for a better understanding of dietary preferences and food webs (Leray et al. 2013).

Carbon (C) and nitrogen (N) stable isotope techniques have been utilized in both aquatic and terrestrial systems as a complement to traditional stomach content analyses in order to

determine trophic position and to trace energy flows (Dale et al. 2011, Choy et al. 2012, Gimenez et al. 2017, McClain-Counts et al. 2017). This method is based on the principle that the ratio of nitrogen isotopes ($^{15}N/^{14}N$) is preferentially incorporated into consumer tissues at predictable rates relative to their prey, and can indicate the trophic level of the consumer over months to years, depending on growth dynamics and tissue turnover rates (Post 2002, Vanderklift and Ponsard 2003). Stable isotope analysis can be especially helpful in the cases where there are empty stomachs or unidentifiable prey. However, this method requires sampling across trophic levels, and it can be difficult logistically to fully capture the dietary breadth of a top predator.

Mixing models are a useful tool for estimating contributions of various food sources to the consumer's diet (McClain-Counts et al. 2017). MixSIAR is a Bayesian mixing model that allows for the inclusion of other potential food sources as well as informative priors (e.g. stomach contents) to estimate diet composition based on stable isotope data (Stock et al. 2018). Combining dietary reconstruction techniques can provide a more holistic picture of top predator diets and different insights into their dietary preferences (McClain-Counts et al. 2017).

He'eia Fishpond is a traditional Hawaiian aquaculture system that relies upon the growth of herbivorous fish such as striped mullet (*Mugil cephalus*), milkfish (*Chanos chanos*), and sixfinger threadfin (*Polydactylus sexfilis*) for food production. Once subject to extreme mangrove overgrowth, large flooding events, and high rates of sedimentation, the fishpond is now approaching a state where it can begin to produce fish once again. However, the dietary preferences of the top predators in these systems is poorly understood. Traditionally, it was common practice to actively remove these predators from the fishpond. According to previous

fishing events at He‘eia Fishpond, the dominant predatory fish are barracuda (*Sphyraena barracuda*), giant trevally (*Caranx ignobilis*), and bluefin trevally (*C. melampygus*).

A previous study found that *C. ignobilis* were predominantly piscivorous, feeding primarily on Scaridae, Labridae, Priacanthidae, and Carangidae, with some predation of crustaceans and cephalopods (Sudekum et al. 1991). *Caranx melampygus* was also predominantly piscivorous, with the most important taxa being Labridae, Mullidae, and Monacanthidae. Crustaceans were also found frequently in smaller *C. melampygus* stomachs (<350mm SL), with a shift to a more fish-based diet at larger sizes (Sudekum et al. 1991). A study on *S. barracuda* in the Equatorial Eastern Atlantic Ocean found that they mainly prey upon teleost fish species (mostly Clupeidae, Sphyraenidae, Carangidae, and Engraulidae), with some predation upon cephalopods and crustaceans (Akadje et al. 2013).

In the present study, we utilize visual diet analyses, metabarcoding of the mitochondrial *Cytochrome c Oxidase subunit I* gene (*COI*), and stable isotope analyses in order to characterize the dietary preferences of the three dominant predatory fish species in He‘eia Fishpond. Our primary goal was to determine whether these predators appear to be specifically targeting the traditional food production species, and thus attempt to determine whether they are likely to be greatly impacting the herbivorous fish populations.

MATERIALS AND METHODS

Study site and sample collection

Predatory fishes were collected from He‘eia Fishpond, an 88-acre brackish water pond in Kāne‘ohe, HI. The majority of samples were taken during a mark-release-recapture experiment conducted in July 2017 (see Chapter 1), but additional individuals were collected

opportunistically throughout the remainder of 2017. Fishes were collected using traditional hook-and-line fishing from fishing zones on the fishpond wall and interior (Fig. 1.1) with a variety of lures and bait. All bait was excluded from diet analyses. Upon collection, the whole fish was immediately placed in ice in order to halt the digestion process, then frozen whole until analysis.

Stomach content analyses

In the laboratory, fish were defrosted whole in water for 1 to 2 hours before processing. The weight and length of each fish were recorded, after which the stomach was removed. Whole stomach weight was recorded, the food bolus removed, and the weight of the cleaned stomach recorded. A qualitative estimate of stomach fullness was taken based on the volumetric fraction of the stomach containing food: 1 = empty or only containing bait, 2 = less than half full, 3 = more than half full.

Prey items were sorted and identified to the lowest possible taxon. The digestion state of the prey was classified similar to (Olson and Galvan-Magana 2002): 1 = intact with some or most of skin on, 2 = relatively intact with some soft parts digested, 3 = soft parts mostly digested, but skeleton or remains whole or mostly whole, 4 = individuals not identifiable, mostly hard parts remaining (e.g. bones, fish otoliths, cephalopod beaks). Each taxon per digestive state was weighed to the nearest 0.1g, and the number(s) of individual prey types were recorded. Length measurements were taken to the nearest 0.1mm: standard or total length (SL or TL) for fishes, TL or carapace length (CL) for crustaceans, and TL for other organisms. Approximate length (AP) was recorded for prey items that were less intact.

Pieces of muscle or mantle tissue from prey items that could not be identified from taxonomic keys were excised and stored in salt-saturated 20% DMSO. Scalpels and forceps were cleaned with 95% ethanol between excisions to prevent DNA cross-contamination of samples. When prey items were large enough, samples of muscle tissue were excised and frozen in Whirl-Paks for bulk stable isotope analysis (Letourneur et al. 2013). DNA was extracted via the hot sodium hydroxide and Tris method (HotSHOT; (Meeker et al. 2007). All prey fish were too degraded to be visually identified and therefore were only identified using genetic barcoding.

For prey item tissue samples, the *COI* region of the mitochondrial genome was amplified using primers FishF2 and FishR1 (Ward et al. 2005) for fish, or primers LCO1490 and HCO2198 (Folmer et al. 1994). Each 10µL reaction included: 3.85µL of nanopure H_2O, 5.0µL of BioMix Red (2X; Bioline; www.bioline.com), 0.1µL of each primer (10µM), and 1.0µL of DNA (5-50ng/µL). The thermocycling regime was as follows: 94°C for 4 min, 35 cycles consisting of 94°C for 1 min, 50°C for 30 s, and 72°C for 45s, and then a final extension period of 72°C for 10 min.

The PCR product was run on a 1.5% agarose gel and amplification success was defined as a single intense band around 700 bp. The post-PCR cleanup process consisted of 3.5µL of PCR product and 1µL ExoSAP-It (Affymetrix; www.affymetrix.com) heated to 37°C for 30 min and then 85°C for 15 min. All PCR product preparations were conducted in the ToBo Laboratory at the Hawai‘i Institute of Marine Biology, University of Hawai‘i. Cleaned PCR products were sent to the Advanced Studies in Genomic, Proteomics, and Bioinformatics Genomic Laboratory at the University of Hawai‘i for single-direction sequencing. Sequences were compared to BOLD (Ratnasingham and Hebert 2007) and GenBank (Benson et al. 2017) databases to determine taxonomic identity using a threshold of ≥ 97% nucleotide similarity. All

barcoded prey identifications and their nucleotide similarities to BOLD and GenBank databases are provided in Table A1 (Appendix).

The contribution of each prey item to the diet of *C. ignobilis*, *C. melampygus*, and *S. barracuda* was quantified with several metrics of dietary composition: importance as proportions of total prey weights (%W), numerical importance as proportions of total counts (%N), and frequency of occurrence as proportions of predator stomachs containing said prey item (%F). Individual metrics were also combined into a composite metric, the index of relative importance (IRI):

$$IRI = (\%N + \%W) \times \%F$$

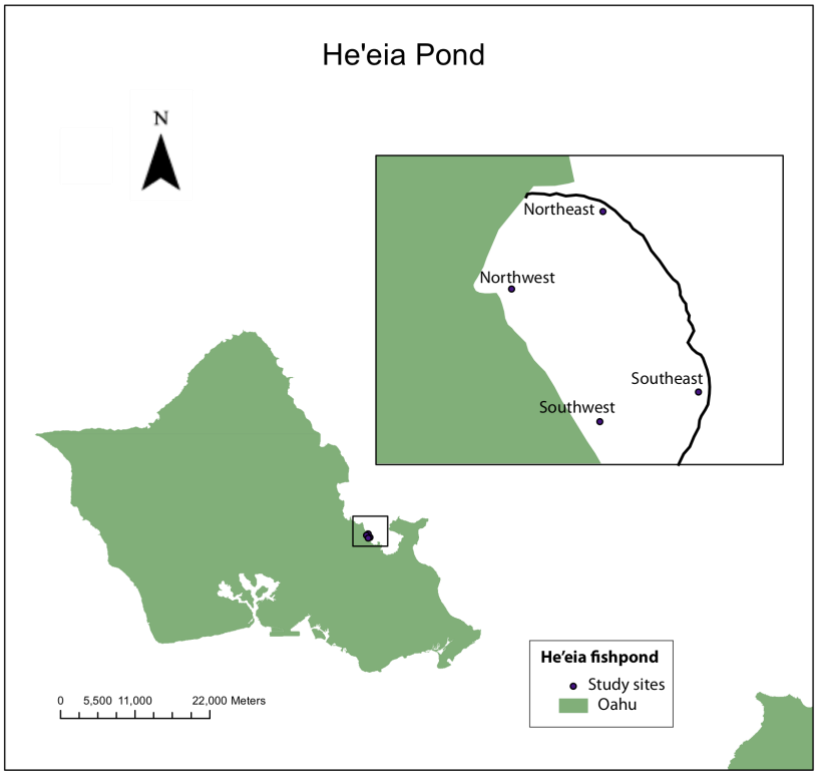
IRI values were expressed as a percentage (%IRI) to facilitate comparisons between prey taxon (Cortes 1997).

Estimates of asymptotic species richness with 95% confidence intervals were calculated using the 'chao1984' function from the 'SPECIES' package (Wang 2011) in the R statistical software version 3.4.3 (R Development Core Team; www.r-project.org) based on the methods described by (Chao 1984). Modified Costello diagrams (Costello 1990) plotting %W against %N were used to identify important prey items. Diagrams include the prey items by %W and %N. Prey points positioned closest to 100% by weight and 100% by count are considered the dominant prey taxa. All data analysis and statistics were performed using R version 3.4.3 (R Development Core Team; www.r-project.org).

Bulk tissue stable isotope analysis

A previous unpublished study conducted from 2010-2011 determined the stable isotope values of the base of the food chain in He‘eia Fishpond (pers. comm. M. Siple). Samples were collected from four locations within the pond (Fig. 2). Crabs, shrimp, microphytobenthos (MPB), phytoplankton, *Gracilaria salicornia*, and epiphytes were collected during the summer of 2011. MPB was collected by hand and separated from sediment using modified methods from (Melville and Connolly 2003). Sediments were run through a 53µm mesh and filtrate was then rinsed on a 5µm polycarbonate filter to remove bacteria and viruses. The rinsed material was spun in 15 mL colloidal silica (LUDOX AM 30, density = 1.21) at 10,000rpm for 10 minutes. Supernatant was rised again with filtered seawater on a GF/F filter and frozen until analysis.

Figure 2.2. Collection locations of stable isotope samples from 2010 to 2011. Groups collected were



crabs, shrimp, microphytobenthos (MPB), phytoplankton, *Gracilaria salicornia*, and epiphytes. Map courtesy Dr. Margaret Siple.

Phytoplankton were collected in water samples in light-sensitive bottles and filtered with GF/F filters. *G. salicornia* thalli were shaken in Whirl-Pak bags for 3 minutes to remove epiphytes, rinsed again, and frozen until analysis. Epiphyte samples were filtered through 500 µm mesh, then spun in colloidal silica to removed sediment and filtered on GF/F filters. Small invertebrates were removed with forceps under a dissecting microscope before freezing. Epiphytes, MPB, and phytoplankton were acidified using an aqueous solution of 9.0% SO_2 prior to being dried at 60°C and ground. Macroalgae were dried at 60°C, groud, and vapor acidified as described by (Brodie et al. 2011), then dried again before analysis.

Swimming crabs (*Thalamita crenata*) and glass shrimp (*Palaemon* sp.) were collected using seines and traps. Muscle tissue was dissected from chelae of crabs and from abdominal muscles of shrimp. Ten individual shrimp were used for one sample in order to ensure there was enough material for analysis. Samples were dried at 60°C and ground using a mortar and pestle.

Prey fish (*Mugil cephalus, Moolgarda engeli, Gambusia affinis,* and tilapia) were collected with nets from locations around the fishpond and frozen until analysis. These species were chosen based on what the fishpond managers suspected the predatory fish might be eating. In the lab, scales and skin of prey and predatory fish were removed and dorsal white muscle tissue dissected from each individual. Samples were freeze-dried at -88°C and ground to a fine powder with a mortar and pestle, the packaged into tin capsules for bulk tissue stable isotope analysis. The $\delta^{13}C$ and $\delta^{15}N$ values of all samples were determined with a carbon-nitrogen analyzer coupled with an isotope ratio mass spectrometer (ThermoFinnigan MAT Conflo IV/ThermoFinnigan Delta XP). Isotope values are reported as δ-values (as ‰) relative to Vienna PeeDee Belemnite (VPDB) and atmospheric N_2, respectively. Average accuracy and precision of all stable isotopic analyses determined by 10% replication of samples was < 0.2‰.

Trophic positions for each species were calculated with the following equation:

$$TP_{bulk} = \frac{\delta^{15}N_{consumer} - \delta^{15}N_{phytoplankton}}{3} + 1$$

where 3‰ is the assumed trophic enrichment factor (TEF), a value well within the range of reported variation (Vanderklift and Ponsard 2003). The average $\delta^{15}N_{phytoplankton}$ measured from the fishpond was 2.9. Since there were not samples of each taxa collected from every location, and since the δ^{15}N and δ^{13}C values did not seem to be clustered by location (Fig. 2.3), the locations were pooled for all comparisons. Bayesian mixing models were constructed to estimate the contribution of prey to consumer diets using the 'MixSIAR' package (Stock and Semmens 2016) in R statistical software version 3.4.3 (R Development Core Team; www.r-project.org). Microphytobenthos, *G. salicornia*, epiphytes, and phytoplankton were removed from this portion of the analysis to reduce the number of sources and help the model converge.

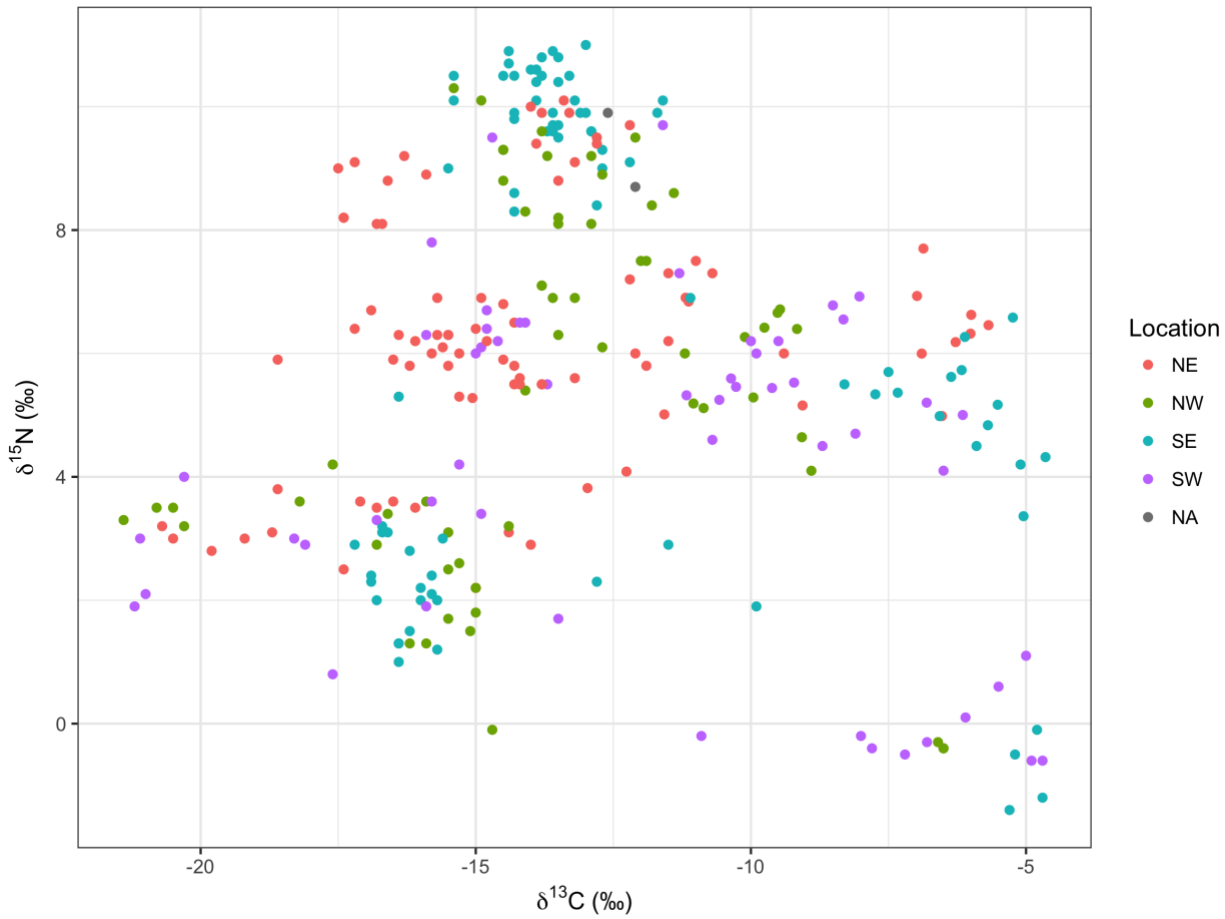


Figure 2.3. δ15N and δ13C values of all samples collected grouped by location. Locations refer to areas of the pond shown in Fig. 2.1 (Northeast (NE), Northwest (NW), Southeast (SE), and Southwest (SW)). Two S. barracuda captured opportunistically did not have a location reported and thus are listed as NA.

RESULTS

Stomach content analyses

A total of 73 stomachs of *Sphyraena barracuda*, *Caranx ignobilis*, and *C. melampygus* were sampled from He‘eia Fishpond, 42 of which contained food (Table 2.1). The percentage of empty stomachs varied greatly between species, with the greatest percentage occurring in *C. ignobilis* (91.7%), followed by *S. barracuda* (53.7%), and *C. melampygus* (28.5%).

Table 2.1. Summary table of predatory fish species examined for stomach contents in He'eia Fishpond. Most samples were captured during July 2017, with some opportunistic captures through the end of the year. Also included are the predator species codes, total number of stomachs examined (N) and number of those containing food, mean predator fork length (mm), and mean whole body mass (g) for all individuals examined.

Species	Species code	N	Stomachs with food	Fork length (mm)			Mean mass (g ± SD)
				Min.	Max.	Mean ± SD	
Caranx ignobilis	CAIG	12	11	162	433	314.6 ± 89.4	861.3 ± 613.0
Caranx melampygus	CAME	2	2	335	349	342.0 ± 9.9	870.0 ± 70.7
Sphyraena barracuda	SPBA	54	29	135	507	336.3 ± 59.1	294.6 ± 130.1

From these stomachs, 21 different prey types of varying taxonomic resolution were identified, including nine fish and two crustacean families (Table 2.3). Of the 21 different prey types, only one was found in all three species (*Palaemon sp.*). One species of goby was found in both *S. barracuda* and *C. melampygus*, but there were no additional similarities between *C. ignobilis* and *S. barracuda*. The utilization of genetic barcoding was crucial in identifying many prey items, particularly the fishes. Fish prey were often degraded beyond recognition (body condition 2.98 ± 0.93), and as such could not be identified to a high resolution with visual techniques alone. Approximately 70% of fish prey items were positively identified using the molecular approach.

The number of prey taxa identified in the stomach contents does not fall within the 95% confidence interval for species richness estimates, which indicates that sample sizes for *S. barracuda* and *C. ignobilis* were inadequate to fully describe the taxonomic breadth of their diet composition (Table 2.2). The data for *C. melampygus* were not included in the diet analyses due to low sample size (n = 2). A summary of the stomach contents from the two *C. melampygus* individuals with prey items is presented in Table 2.4.

Table 2.2. Asymptotic species richness estimates with 95% confidence intervals. The number of prey taxa identified in stomach contents is listed under N. Estimates of species richness ($\widehat{N}$), with standard error and 95% confidence interval bounds (Lower CI, Upper CI) were calculated based on methods from (Chao 1984).

Species	N	$\widehat{N}$	Standard error	Lower CI	Upper CI
Caranx ignobilis	6	9	1.9	8	19
Sphyraena barracuda	17	37	8.3	31	71

Table 2.3. Prey table for Caranx ignobilis (CAIG) and Sphyraena barracuda (SPBA). Included for each prey item are the percentage of the total number of prey (%N), the percentage of the total weight of the prey (%W), the percent frequency of occurrence (%F), and the percent index of relative importance (%IRI) for both predator species. Totals denote the total number and weight (g) of all prey items for each species.

	CAIG				SPBA			
	%N	%W	%F	%IRI	%N	%W	%F	%IRI
CRUSTACEANS								
Palaemonidae – *Palaemon sp.*	34.48	1.63	36.36	21.79	20.99	12.43	34.48	30.36
Portunidae – *Thalamita crenata*	10.34	13.61	18.18	7.23				
Unidentified crustacea	31.03	74.75	36.36	63.83				
FISH								
Albulidae – *Albula glossodonta*					1.23	0.89	3.45	0.19
Apogonidae – *Foa brachygramma*					4.94	2.65	6.90	1.38
Atherinidae – *Atherinomorus insularum*					1.23	1.62	3.45	0.26
Carangidae								
Caranx ignobilis	10.34	2.90	18.18	4.00				
Caranx melampygus	3.45	0.13	9.09	0.54				
Caranx sexfasciatus					1.23	0.03	3.45	0.12
Clupeidae – *Sardinella marquesensis*					1.23	4.58	3.45	0.53
Gobiidae								
Asterropteryx semipunctata					7.41	3.69	13.79	4.77
Oxyurichthys lonchotus					20.99	13.38	27.59	24.98
Psilogobius mainlandi					3.70	1.00	6.90	0.85
Mugilidae – *Osteomugil engeli*					3.70	38.51	6.90	7.67

Mullidae – *Mulloidichthys flavolineatus*					1.23	6.56	3.45	0.71
Synodontidae – *Saurida nebulosa*					1.23	0.02	3.45	0.11
Unidentified fish	10.34	6.99	9.09	2.62	12.35	12.25	34.48	22.34
MOLLUSKS					1.23	0.16	3.45	0.13
OTHER ORGANICS								
Algae					8.64	1.23	13.79	3.59
Unidentified organic material					4.94	0.61	13.79	2.02
ANTHROPOGENIC DEBRIS					3.70	0.38	6.90	0.67
Totals	42	58.26	-	-	240	135.36	-	-

Table 2.4. Summary of prey found in Caranx melampygus individuals as prey numbers and weights. A total of two C. melampygus individuals were examined, both of which contained prey.

Prey identification	Numbers(s)	Weights(s) (g)
Crustacea		
Palaemon sp.	65	3.96
Thalamita crenata	1	2.99
Unidentified crab	1	0.97
Teleostei		
Asterropteryx semipunctata	4	2.70
Psilogobius mainland	1	0.21
Unidentified fish	4	0.51
Unidentified organic material	1	0.15

Prey types were assigned to two broad categories: crustaceans and fishes. Since all individuals for each species were of a similar in size, a size class-specific analysis could not be counducted. Of the identified prey items, crustaceans, represented by glass shrimp (*Palaemon sp.*) and mangrove swimming crabs (*Thalamita crenata*) were the most important prey group for *C. ignobilis* (21.79% and 7.23%, respectively). *Palaemon sp.* was also important for *S. barracuda* (27.28%), along with the goby *oxyurichthys lonchotus* (22.44%, Table 2.3).

Palaemon sp. was the only crustacean prey found in any barracuda stomachs. Interestingly, the only fishes identified in *C. ignobilis* stomachs were other Carangids, including three instances of cannibalism. Both predators preyed most frequently upon *Palaemon sp.* (*C. ignobilis* 36.36%; *S. barracuda* 34.48%).

Numerical diet composition of *C. ignobilis* was dominated by *Palaemon sp.* (Fig. 2.4) but dominated gravimetrically by unidentified crabs (Fig. 2.4). Conversely, *Palaemon sp.* and the speartail mudgoby *Oxyurichthys lonchotus* had the same numerical importance (20.99%) for *S. barracuda* (Fig. 2.4). By weight, barracuda fed primarily on various unidentified fishes (26.55%) and secondarily on *Osteomugil engeli* (Fig. 2.4).

Costello diagrams illustrating the numeric and gravimetric importance of individual prey items indicate which prey items contributed the most to dissimilar diets between the predators (Fig. 2.5, 2.6). Australian mullet (*Osteomugil engeli*), speartail mudgoby (*Oxyurichthys lonchotus*), and unidentified fishes all emerge as predominant prey items for *S. barracuda* (Fig. 2.5). Conversely, unidentified crabs are clearly the most important food source for *C. ignobilis* (Fig. 2.5).

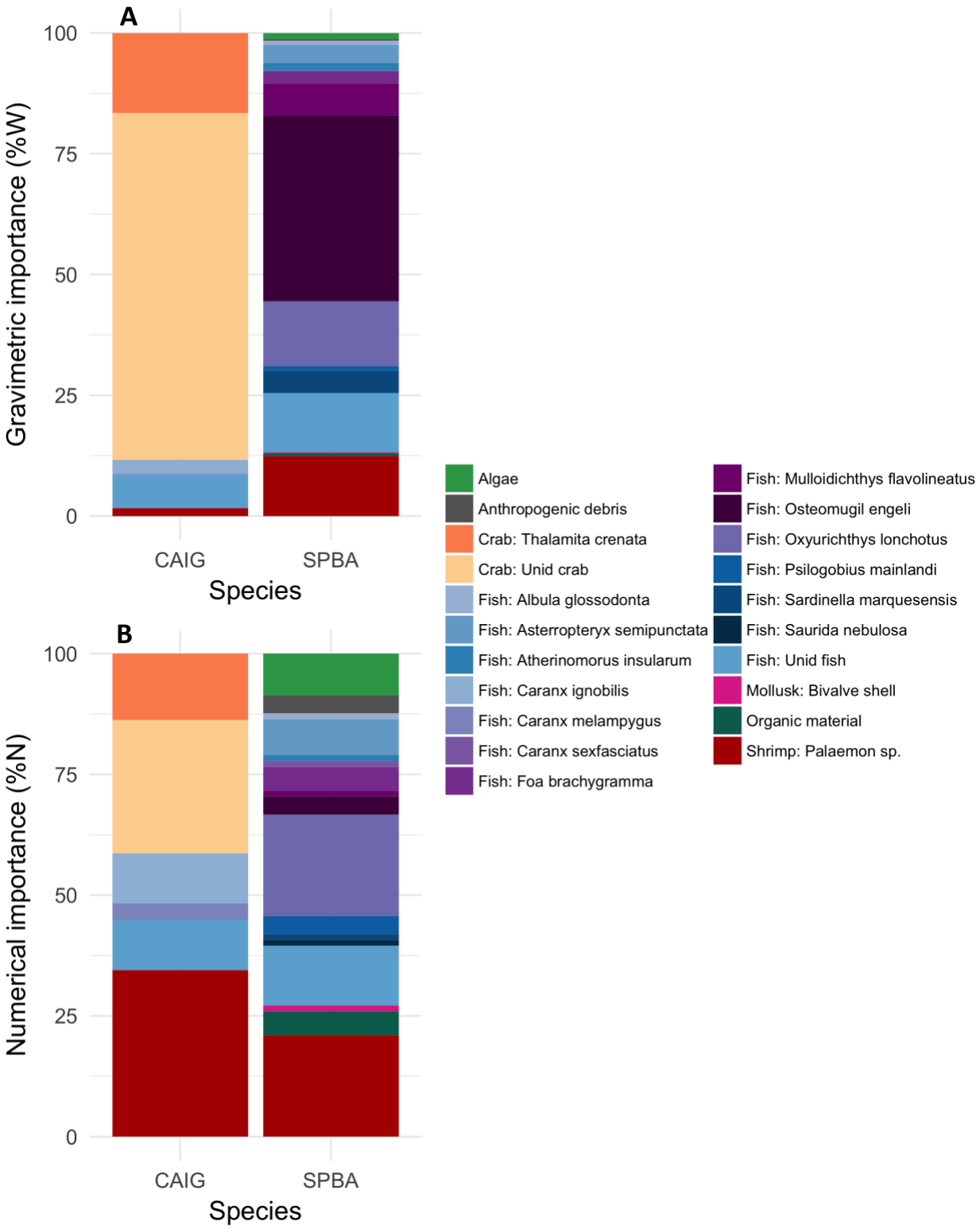


Figure 2.4. Stacked barplots of A) gravimetrically important prey (%N), and B) numerically important prey for *C. ignobilis* (CAIG, n = 11) and *S. barracuda* (SPBA, n = 29).

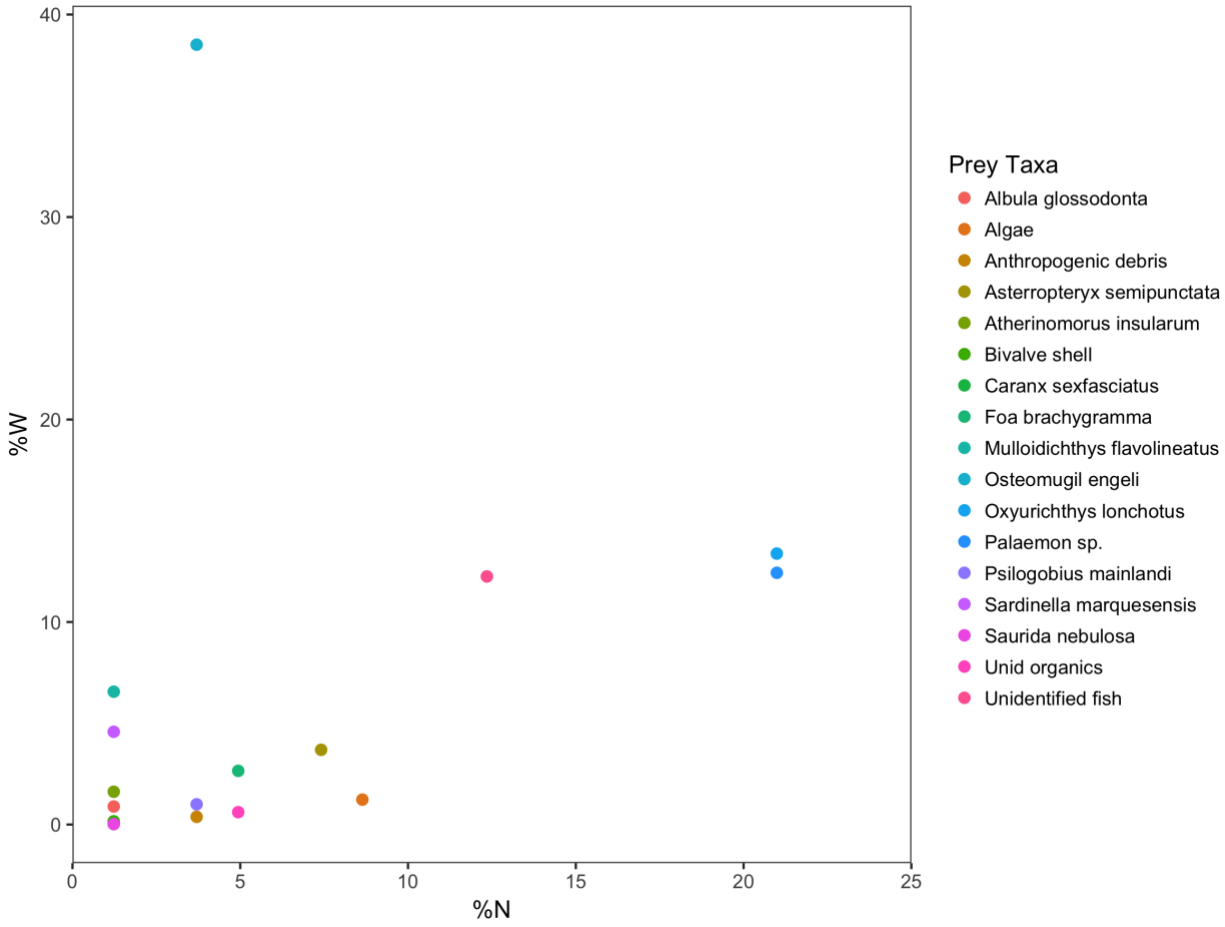


Figure 2.5. Modified Costello diagram showing the most important prey items in terms of prey biomass (%W) and numerical importance (%N) for *Sphyraena barracuda*.

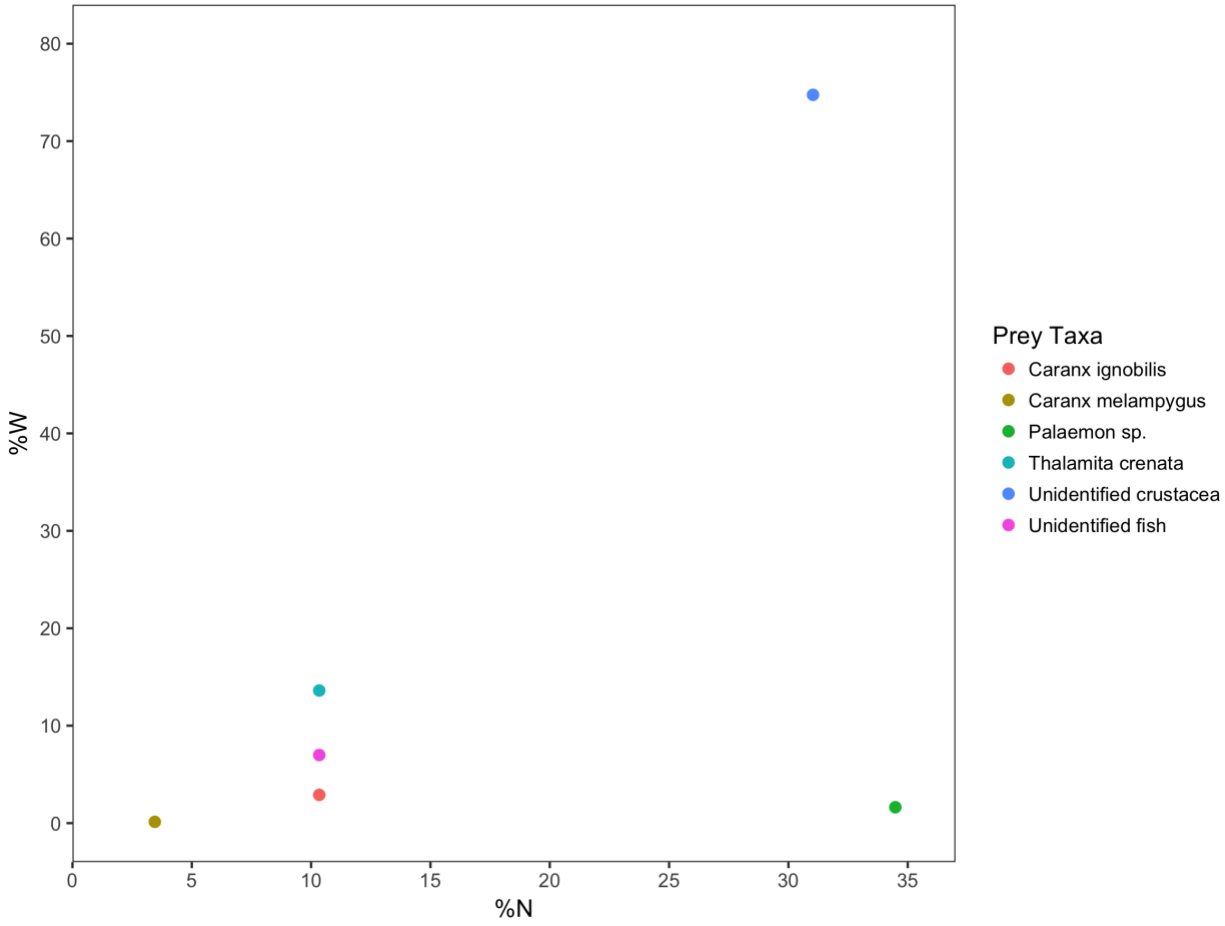


Figure 2.6. Modified Costello diagram showing the most important prey items in terms of prey biomass (%W) and numerical importance (%N) for *Caranx ignobilis*.

Bulk stable isotope analysis

White muscle tissue from 9 *C. ignobilis* and 59 *S. barracuda* collected from He'eia Fishpond were analyzed for bulk carbon and nitrogen isotopic compositions. These fishes were all individuals analyzed for stomach content analyses. Trophic position of both predators was nearly identical (Table 2.5). This is reflected in Figure 2.8, showing both *C. ignobilis* and *S. barracuda* having the highest values of $\delta^{15}N$ of all species and very similar dietary niche breadths (Fig. 2.9).

The Bayesian mixing model identified the non-native Australian mullet *Osteomugil engeli* as the main contributor to *S. barracuda* diets and second largest contributor to *C. ignobilis* diets (62.8% and 53.2% median prey contribution, respectively). *Palaemon sp.* was estimated to be most important for *C. ignobilis* (53.2%), and second most important for *S. barracuda* (36.2%) (Fig. 2.10). The mangrove swimming crab *Thalamita crenata* was also a minor contributor for (*C. ignobilis* 3.7%).

Table 2.5. Mean and standard deviation (SD) of Caranx ignobilis and Sphyraena barracuda bulk $\delta^{15}N$ and $\delta^{13}C$. Trophic position estimates for all individuals combined provided.

Species	$\delta^{13}C$	SD	$\delta^{15}N$	SD	Trophic position
Caranx ignobilis	-12.62	1.13	9.23	0.75	3.2
Sphyraena barracuda	-13.66	0.83	9.63	0.84	3.1

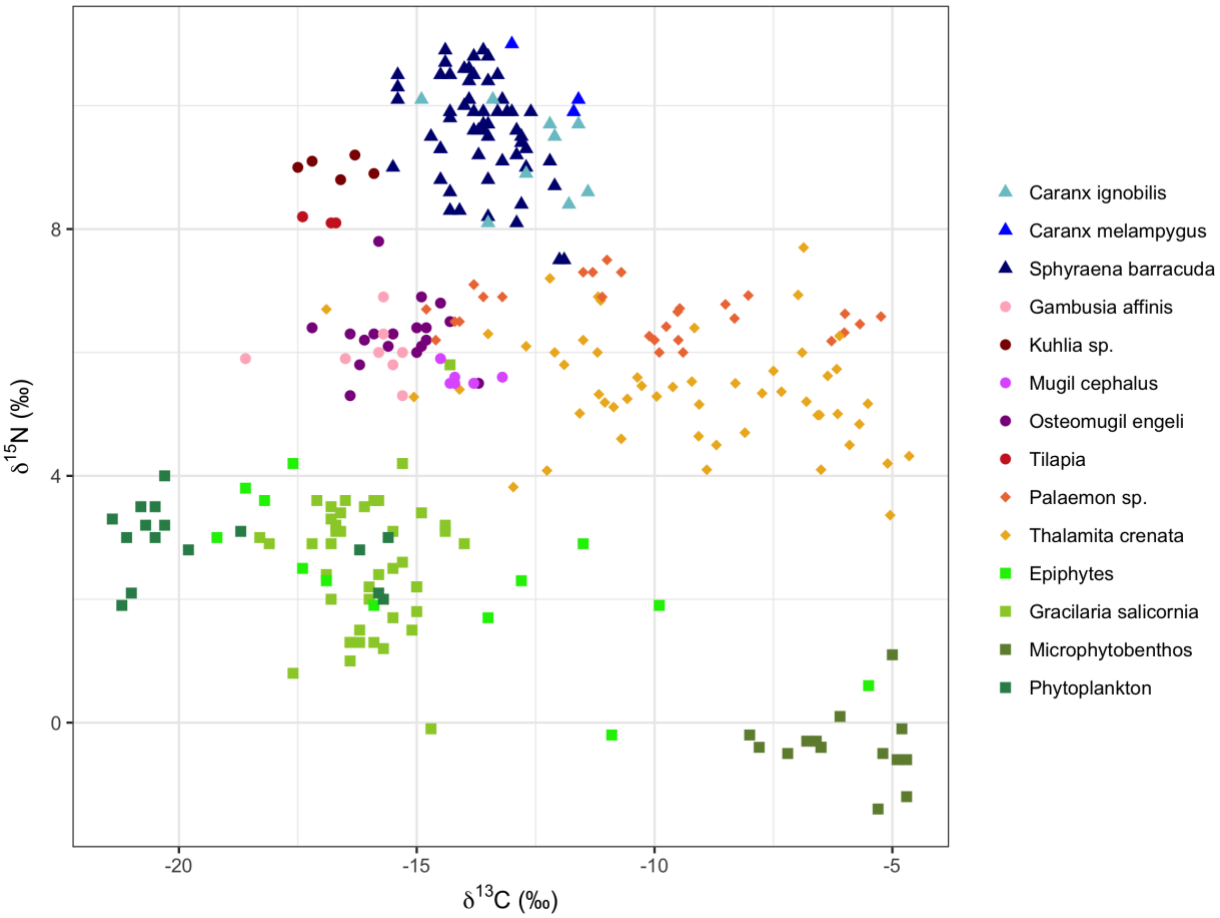


Figure 2.8. δ15N and δ13C values of all samples collected. Colors indicate taxa collected from He'eia Fishpond during 2010, 2011, and 2017.

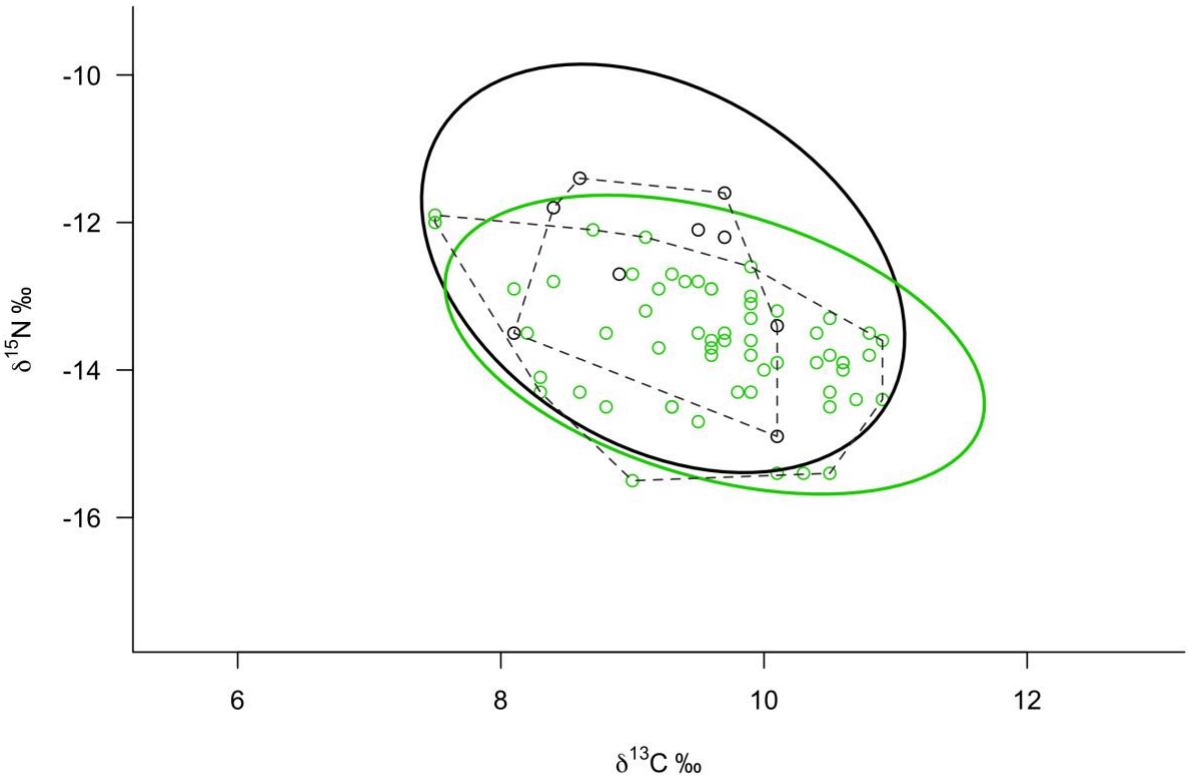


Figure 2.9. Isotopic niche breadth similarity of Caranx ignobilis (black ellipse) and Sphyraena barracuda (green ellipse) in He'eia Fishpond. Plot was created using package 'SIBER' in R Statistical Software (Jackson et al. 2011).

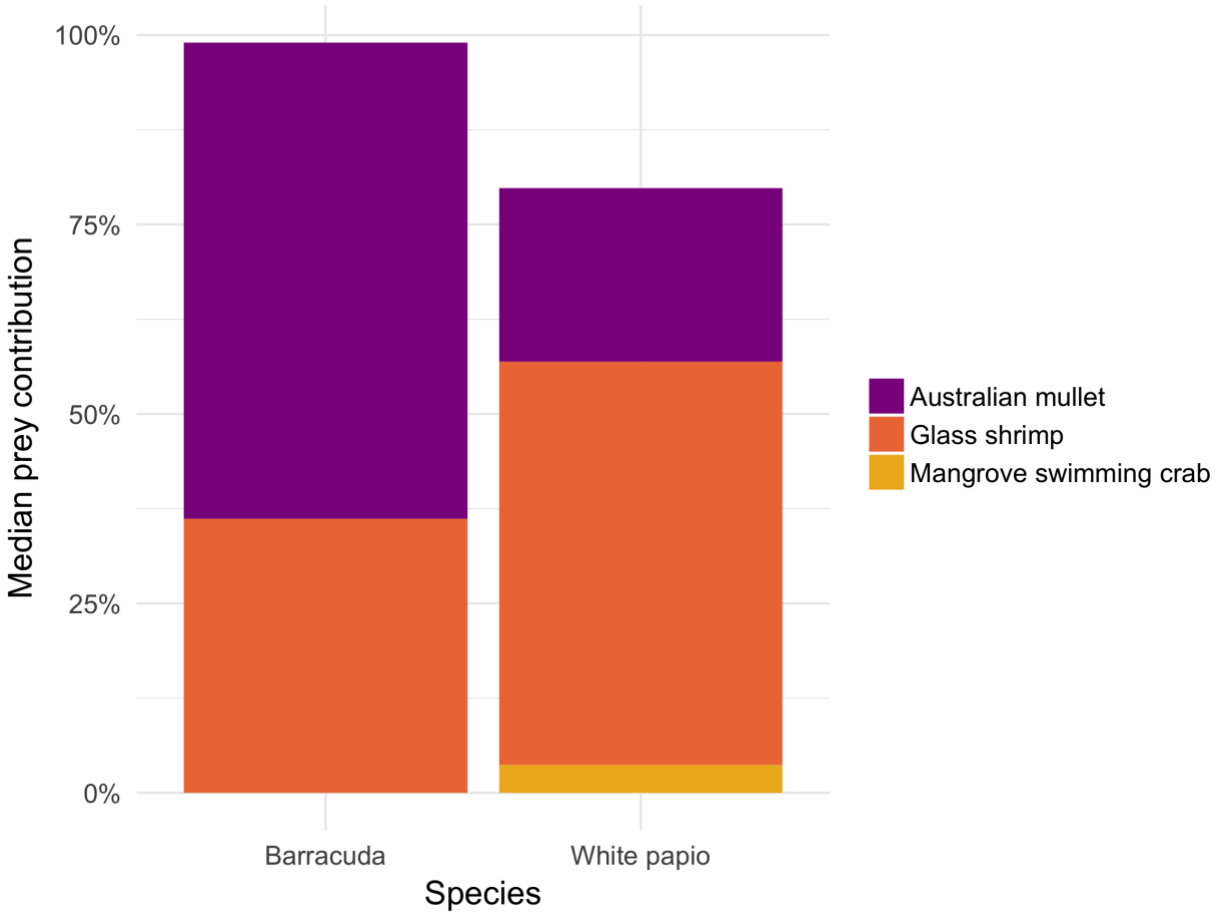


Figure 2.10. Estimated median contibution of prey taxa to the diet of *Caranx ignobilis* (white papio) and *Sphyraena barracuda*(barracuda) in He'eia Fishpond. Estimates was calculated using informative Bayesian mixing models in the 'MixSIAR' package in R statistical software (Stock and Semmens 2016).

DISCUSSION

To our knowledge, this is the first characterization of the diet of predatory species in a Hawaiian fishpond. Overall, the results obtained in the present study are similar to the studies performed elsewhere on these species, indicating that they feed broadly on crustaceans and fishes (Blaber and Cyrus 1983, Sudekum et al. 1991, Brewer et al. 1995, Smith and Parrish 2002, Akadje et al. 2013). All predatory fish examined in this study were juveniles (De Sylva 1963,

Sudekum et al. 1991), which is representative of the overall predatory fish population in the fishpond (see Ch. 1).

There were stark differences between the diets of *Caranx ignobilis* and *Sphyraena barracuda*. Barracuda fed almost exclusively on fish, whereas *C. ignobilis* fed primarly on crustaceans. It is likely the high %IRI of *Palaemon sp.* for barracuda is the result of a few individuals which had eaten 20 or more glass shrimp, which greatly contributed to the high %N. Most of the fish found in *C. ignobilis* and *C. melampygus* were unidentifiable, but a previous study found that they both also feed on Gobiods (Smith and Parrish 2002).

The most striking finding was that there were no instances of predation upon *Mugil cephalus*, *Chanos chanos*, or *Polydactylus sexfilis*, the primary species raised in Hawaiian fishponds. While genetic barcoding helped identify prey items in advanced digestion stages, some fish remained unidentified and may include the three herbivorous fish species. However, by incorporating Bayesian mixing models of bulk stable isotopes, we were able to show that it is very unlikely that *Mugil cephalus* comprises a large part of the diet of *Caranx ignobilis, C. melampygus*, or *Sphyraena barracuda* (Fig. 2.10). Given the logistical difficulties of capturing large herbivores such as *Chanos chanos* and *Polydactylus sexfilis*, it was only possible to obtain juvenile *Mugil cephalus*, which school in the outer edges of the fishpond, for bulk tissue stable isotope analysis.

Interestingly, the anticipated prey fish were shown to contribute very little, if at all, to the predators' overall $\delta^{15}N$ values. Ghost shrimp and mangrove swimming crabs were estimated to contribute greatly to all three species' diets, with barracuda also feeding on Australian mullet. Australian mullet is a non-native fish that directly competes with the native striped mullet *Mugil cephalus*. While predation by barracuda on Australian mullet could be beneficial for the native

mullet population, it is unlikely that there is no predation upon *Mugil cephalus*, which has been observed in the pond. What is likely happening is that the native herbivore populations are too low to greatly contribute to the predators' diet. Sampling of the Gobiids and other fish taxa that were found in the stomachs would greatly improve the ability of the model to determine which prey contribute to the predatory species' isotopic composition. Additionally, the samples that formed the base of the isotopic food web were collected in 2010 and 2011. It would be useful to resample those materials, including fish samples from locations that span the entirety of the pond, so that location can be included as a factor in the mixing model.

A previous study in Kāneʻohe Bay analyzed the trophic position of the brown stingray, *Dasyatis lata*, finding that they occupy a trophic position of 3.3-3.6, depending on disk width size (Dale et al. 2011). This is similar to this study's estimated trophic positions of *C. ignobilis*, *C. melampygus*, and *S. barracuda*, although slightly different values were used for the average nitrogen isotopic value at the base of the food web (3.3‰ vs. 2.9‰ used in this study) and the trophic enrichment factor (2.7‰ vs. 3‰ used in this study).

While this study provides a first look at the dietary preferences of the dominant predatory fish in Heʻeia Fishpond, the sample size was insufficient to characterize the full breadth of prey species (Table 2.2). This is largely due to a high index of vacuity and sampling challenges outlined in Ch. 1. Sampling occurred mainly during July 2017, which prevents any determination of temporal changes in dietary preferences or feeding success (Ley and Halliday 2007). Furthermore, these species have been found to primarily hunt at night, with some feeding during the day (Varghese et al. 2014). This likely impacted not only the sampling success of this study as well as the vacuity index and the amount of prey items present. Many of the prey items could not be identified visually or genetically, which would potentially be masking predation

upon the three herbivorous fish species. Collecting samples at night may provide more intact prey items and increase the number of prey species identified.

This study provides the first characterization of predatory fish diets in traditional Hawaiian fishponds. Our findings that these predators do not prey primarily upon the traditional food production species has implications for fishponds throughout the State of Hawai‘i. *Caranx ignobilis*, *C. melampygus*, and *S. barracuda* generally feed on a variety of fishes and crustaceans that are primarily demersal. Based on our results, we recommend maintaining current strategies for management of He‘eia Fishpond’s top predatory species. Further research on these species to fill in data gaps will help to fully characterize their dietary preferences.

LITERATURE CITED

Akadje, C., M. Diaby, F. Le Loc'h, J. K. Konan, and K. N'da. 2013. Diet of the barracuda Sphyraena guachancho in Cote d'Ivoire (Equatorial Eastern Atlantic Ocean). Cybium **37**:285-293.

Apple, R. A., and W. K. Kikuchi. 1975. Ancient Hawai‘i Shore Zone Fishponds: An Evaluation of Survivors for Historic Preservation. U.S. Department of the Interior, Honolulu.

Baker, R., A. Buckland, and M. Sheaves. 2014. Fish gut content analysis: robust measures of diet composition. Fish and Fisheries **15**:170-177.

Benson, D. A., M. Cavanaugh, K. Clark, I. Karsch-Mizrachi, D. J. Lipman, J. Ostell, and E. W. Sayers. 2017. GenBank. Nucleic Acids Research **45**:D37-D42.

Blaber, S. J. M., and D. P. Cyrus. 1983. THE BIOLOGY OF CARANGIDAE (TELEOSTEI) IN NATAL ESTUARIES. Journal of Fish Biology **22**:173-188.

Brewer, D. T., S. J. M. Blaber, J. P. Salini, and M. J. Farmer. 1995. FEEDING ECOLOGY OF PREDATORY FISHES FROM GROOTE-EYLANDT IN THE GULF OF CARPENTARIA, AUSTRALIA, WITH SPECIAL REFERENCE TO PREDATION ON PENAEID PRAWNS. Estuarine Coastal and Shelf Science **40**:577-600.

Brodie, C. R., J. S. L. Casford, J. M. Lloyd, M. J. Leng, T. H. E. Heaton, C. P. Kendrick, and Y. Q. Zong. 2011. Evidence for bias in C/N, delta C-13 and delta N-15 values of bulk organic matter, and on environmental interpretation, from a lake sedimentary sequence by pre-analysis acid treatment methods. Quaternary Science Reviews **30**:3076-3087.

Carreon-Martinez, L., T. B. Johnson, S. A. Ludsin, and D. D. Heath. 2011. Utilization of stomach content DNA to determine diet diversity in piscivorous fishes. Journal of Fish Biology **78**:1170-1182.

Chao, A. 1984. NONPARAMETRIC-ESTIMATION OF THE NUMBER OF CLASSES IN A POPULATION. Scandinavian Journal of Statistics **11**:265-270.

Chapman, D. G. 1951. Some properties of the hypergeometric distribution with applications to zoological sample censuses. University of California Press, Berkeley, CA.

Choy, C. A., P. C. Davison, J. C. Drazen, A. Flynn, E. J. Gier, J. C. Hoffman, J. P. McClain-Counts, T. W. Miller, B. N. Popp, S. W. Ross, and T. T. Sutton. 2012. Global Trophic Position Comparison of Two Dominant Mesopelagic Fish Families (Myctophidae, Stomiidae) Using Amino Acid Nitrogen Isotopic Analyses. Plos One **7**.

Cobb, J. N. 1902. Commercial Fisheries of the Hawaiian Islands. Washington, D.C.

Cortes, E. 1997. A critical review of methods of studying fish feeding based on analysis of stomach contents: Application to elasmobranch fishes. Canadian Journal of Fisheries and Aquatic Sciences **54**:726-738.

Costello, M. J. 1990. PREDATOR FEEDING STRATEGY AND PREY IMPORTANCE - A NEW GRAPHICAL ANALYSIS. Journal of Fish Biology **36**:261-263.

Dale, J. J., C. G. Meyer, and C. E. Clark. 2011. The Ecology of Coral Reef Top Predators in the Papahānaumokuākea Marine National Monument. Journal of Marine Biology **2011**:1-14.

De Sylva, D. P. 1963. Systematics and Life History of the Great Barracuda, Sphyraena barracuda (Walbaum). University of Miami Press.

Farber, J. M. 1997. Ancient Hawaiian Fishponds: Can Restoration Succeed on Molokaʻi? Neptune House Publications, Encinitas, CA.

Folkvord, A. 1993. PREY RECOGNITION IN STOMACHS OF CANNIBALISTIC JUVENILE COD (GADUS-MORHUA L). Sarsia **78**:97-100.

Folmer, O., M. Black, W. Hoeh, R. Lutz, and R. Vrijenhoek. 1994. DNA primers for amplification of mitochondrial cytochrome c oxidase subunit I from diverse metazoan invertebrates. Molecular Marine Biology and Biotechnology **3**:294-299.

Friedlander, A. M., and E. E. DeMartini. 2002. Contrasts in density, size, and biomass of reef fishes between the northwestern and the main Hawaiian islands: the effects of fishing down apex predators. Marine Ecology Progress Series **230**:253-264.

Geromont, H. F., and D. S. Butterworth. 2015. Generic management procedures for data-poor fisheries: forecasting with few data. Ices Journal of Marine Science **72**:251-261.

Gimenez, J., A. Marcalo, F. Ramirez, P. Verborgh, P. Gauffier, R. Esteban, L. Nicolau, E. Gonzalez-Ortegon, F. Baldo, C. Vilas, J. Vingada, M. G. Forero, and R. de Stephanis. 2017. Diet of bottlenose dolphins (Tursiops truncatus) from the Gulf of Cadiz: Insights from stomach content and stable isotope analyses. Plos One **12**:14.

Gwinn, D. C., P. Brown, J. C. Tetzlaff, and M. S. Allen. 2011. Evaluating mark-recapture sampling designs for fish in an open riverine system. Marine and Freshwater Research **62**:835-840.

Hiatt, R. W. 1947. Food-chains and the food cycle in Hawaiian fish ponds, Albany, etc.

Hyslop, E. J. 1980. STOMACH CONTENTS ANALYSIS - A REVIEW OF METHODS AND THEIR APPLICATION. Journal of Fish Biology **17**:411-429.

Jackson, A. L., R. Inger, A. C. Parnell, and S. Bearhop. 2011. Comparing isotopic niche widths among and within communities: SIBER - Stable Isotope Bayesian Ellipses in R. Journal of Animal Ecology **80**:595-602.

Jennings, S., M. J. Kaiser, and J. D. Reynolds. 2001. Marine Fisheries Ecology. Blackwell Science Ltd, Oxford, UK.

Kadison, E., E. K. D'Alessandro, G. O. Davis, and P. B. Hood. 2010. AGE, GROWTH, AND REPRODUCTIVE PATTERNS OF THE GREAT BARRACUDA, SPHYRAENA BARRACUDA, FROM THE FLORIDA KEYS. Bulletin of Marine Science **86**:773-784.

Kamakau, S. M. 1976. The works of the People of Old, Na Hana a ka Poʻe Kahiko. Bishop Museum Press, Honolulu.

Keffer, V. I., S. Q. Turn, C. M. Kinoshita, and D. E. Evans. 2009. Ethanol technical potential in Hawaii based on sugarcane, banagrass, Eucalyptus, and Leucaena. Biomass & Bioenergy **33**:247-254.

Kelly, M. 1994. The Impact of Missionaries and Other Foreigners on Hawaiians and their Culture.*in* U. Hasager and J. Friedman, editors. Hawai'i: Return to Nationhood. International Work Group for Indigenous Affairs (IWGIA), Copenhagen, Denmark.

Kim, K., K. Burnett, and J. Ghimire. 2015. Assessing the potential for food and energy self-sufficiency on the island of Kauai, Hawaii. Food Policy **54**:44-51.

Krebs, C. J. 1999. Ecological Methodology. Second edition. Addison-Welsey Educational Publishing, Menlo Park, CA.

Legler, N. D., T. B. Johnson, D. D. Heath, and S. A. Ludsin. 2010. Water Temperature and Prey Size Effects on the Rate of Digestion of Larval and Early Juvenile Fish. Transactions of the American Fisheries Society **139**:868-875.

Leray, M., C. P. Meyer, and S. C. Mills. 2015. Metabarcoding dietary analysis of coral dwelling predatory fish demonstrates the minor contribution of coral mutualists to their highly partitioned, generalist diet. Peerj **3**:19.

Leray, M., J. Y. Yang, C. P. Meyer, S. C. Mills, N. Agudelo, V. Ranwez, J. T. Boehm, and R. J. Machida. 2013. A new versatile primer set targeting a short fragment of the mitochondrial COI region for metabarcoding metazoan diversity: application for characterizing coral reef fish gut contents. Frontiers in Zoology **10**:14.

Leta, O. T., A. I. El-Kadi, H. Dulai, and K. A. Ghazal. 2016. Assessment of climate change impacts on water balance components of Heeia watershed in Hawaii. Journal of Hydrology-Regional Studies **8**:182-197.

Letourneur, Y., T. L. de Loma, P. Richard, M. L. Harmelin-Vivien, P. Cresson, D. Banaru, M. F. Fontaine, T. Gref, and S. Planes. 2013. Identifying carbon sources and trophic position of coral reef fishes using diet and stable isotope (delta N-15 and delta C-13) analyses in two contrasted bays in Moorea, French Polynesia. Coral Reefs **32**:1091-1102.

Ley, J. A., and I. A. Halliday. 2007. Diel variation in mangrove fish abundances and trophic guilds of northeastern Australian estuaries with a proposed trophodynamic model. Bulletin of Marine Science **80**:681-720.

Loke, M. W., C. Geslani, B. Takenaka, and P. Leung. 2012. Seafood consumption and supply sources in Hawaii, 2000-2009. Marine Fisheries Review **74**:44-51.

Maunder, M. N., and A. E. Punt. 2004. Standardizing catch and effort data: a review of recent approaches. Fisheries Research **70**:141-159.

McClain-Counts, J. P., A. W. J. Demopoulos, and S. W. Ross. 2017. Trophic structure of mesopelagic fishes in the Gulf of Mexico revealed by gut content and stable isotope analyses. Marine Ecology-an Evolutionary Perspective **38**:23.

Meeker, N. D., S. A. Hutchinson, L. Ho, and N. S. Trede. 2007. Method for isolation of PCR-ready genomic DNA from zebrafish tissues. BioTechniques **43**:610-614.

Melville, A. J., and R. M. Connolly. 2003. Spatial analysis of stable isotope data to determine primary sources of nutrition for fish. Oecologia **136**:499-507.

Naomasa, E., S. Arita, C. Tamaru, and P. Leung. 2013. ASSESSING HAWAII'S AQUACULTURE FARM AND INDUSTRY PERFORMANCE. Aquaculture Economics & Management **17**:184-207.

Olson, R. J., and F. Galvan-Magana. 2002. Food habits and consumption rates of common dolphinfish (Coryphaena hippurus) in the eastern Pacific Ocean. Fishery Bulletin **100**:279-298.

Orlov, A. M. 2004. Trophic interrelations in predatory fishes of Pacific waters circumambient the northern Kuril Islands and southeastern Kamchatka. Hydrobiological Journal **40**:106-124.

Oyafuso, Z. S., R. J. Toonen, and E. C. Franklin. 2016. Temporal and spatial trends in prey composition of wahoo Acanthocybium solandri: a diet analysis from the central North Pacific Ocean using visual and DNA bar-coding techniques. Journal of Fish Biology **88**:1501-1523.

Peterson, J. T., P. D. Scheerer, and S. Clements. 2015. An Evaluation of the Efficiency of Minnow Traps for Estimating the Abundance of Minnows in Desert Spring Systems. North American Journal of Fisheries Management **35**:491-502.

Pine, W. E., J. E. Hightower, L. G. Coggins, M. V. Lauretta, and K. H. Pollock. 2012. Design and analysis of tagging studies. Pages 521-572 *in* A. V. Zale, D. L. Parrish, and T. M. Sutton, editors. Fisheries Techniques. American Fisheries Society, Bethesda, MD.

Post, D. M. 2002. Using stable isotopes to estimate trophic position: Models, methods, and assumptions. Ecology **83**:703-718.

Ratnasingham, S., and P. D. N. Hebert. 2007. BOLD: The Barcode of Life Data System (www.barcodinglife.org). Molecular Ecology Notes **7**:355-364.

Ruetz, C. R., B. S. Harris, J. N. McNair, and J. J. Homola. 2015. Removal and Mark-Recapture Methods for Estimating Abundance: Empirical and Simulation Results for Mottled Sculpin in Streams. North American Journal of Fisheries Management **35**:62-74.

Sato, V. T., and C.-S. Lee. 2007. Keeper of Mōliʻi Pond: An Informal Account of George Uyemura and His Amazing Hawaiian Fishpond. The Oceanic Institute, Waimanalo.

Seber, G. A. F. 1973. The estimation of animal abundance and related parameters. Charles Griffin & Company Ltd, London.

Smith, G. C., and J. D. Parrish. 2002. Estuaries as nurseries for the jacks Caranx ignobilis and Caranx melampygus (Carangidae) in Hawaii. Estuarine Coastal and Shelf Science **55**:347-359.

Stenseth, N. C. 2002. Analysis and management of animal populations - Modeling, estimation, and decision making. Science **298**:367-368.

Stock, B. C., A. L. Jackson, E. J. Ward, A. C. Parnell, D. L. Phillips, and B. X. Semmens. 2018. Analyzing mixing model systems using a new generation of Bayesian tracer mixing models. PeerJ Preprints.

Stock, B. C., and B. X. Semmens. 2016. MixSIAR GUI User Manual.

Sturdevant, M. V., J. A. Orsi, and E. A. Fergusson. 2012. Diets and Trophic Linkages of Epipelagic Fish Predators in Coastal Southeast Alaska during a Period of Warm and Cold Climate Years, 1997-2011. Marine and Coastal Fisheries **4**:526-545.

Sudekum, A. E., J. D. Parrish, R. L. Radtke, and S. Ralston. 1991. LIFE-HISTORY AND ECOLOGY OF LARGE JACKS IN UNDISTURBED, SHALLOW, OCEANIC COMMUNITIES. Fishery Bulletin **89**:493-513.

Symondson, W. O. C. 2002. Molecular identification of prey in predator diets. Molecular Ecology **11**:627-641.

Tu, C. Y., Y. J. Tian, and C. H. Hsieh. 2015. Effects of climate on temporal variation in the abundance and distribution of the demersal fish assemblage in the Tsushima Warm Current region of the Japan Sea. Fisheries Oceanography **24**:177-189.

USDA. 2016. Hawaii Aquaculture. United States Department of Agriculture, Honolulu, HI.

USDA, N. 2011. Hawaii farm facts. USDS, NASS, Hawaii Field Office, Honolulu.

Vanderklift, M. A., and S. Ponsard. 2003. Sources of variation in consumer-diet delta(15)N enrichment: a meta-analysis. Oecologia **136**:169-182.

Varghese, S. P., V. S. Somvanshi, and R. S. Dalvi. 2014. Diet composition, feeding niche partitioning and trophic organisation of large pelagic predatory fishes in the eastern Arabian Sea. Hydrobiologia **736**:99-114.

Vockeroth, D. 1981. The Hawaiian Fishpond (Loko Kuapa); Past and Present.

Wang, J. P. 2011. SPECIES: An R Package for Species Richness Estimation. Journal of Statistical Software **40**:1-15.

Ward, R. D., T. S. Zemlak, B. H. Innes, P. R. Last, and P. D. N. Hebert. 2005. DNA barcoding Australia's fish species. Philosophical Transactions of the Royal Society B-Biological Sciences **360**:1847-1857.

Williams, I., and H. Ma. 2013. Estimating Catch Weight of Reef Fish Species Using Estimation and Intercept Data from the Hawaii Marine Recreational Fishing Survey. H-13-04, Pacific Islands Fisheries Science Center, National Marine Fisheries Service, NOAA, Honolulu, HI.

Wyban, C. A. 1992. Tide and Current: Fishponds of Hawai‘i. University of Hawaii Press, Honolulu.

APPENDIX

Table A1. Stable isotope values for all prey taxa collected in He‘eia Fishpond from 2010-2017. Data from 2010 and 2011 provided by Megsie Siple.

Species	Year	d15N (‰)	d13C (‰)
Gracilaria salicornia	2010	2.2	-15.0
Gracilaria salicornia	2010	2.9	-14.0
Gracilaria salicornia	2010	5.8	-14.3
Gracilaria salicornia	2010	3.1	-14.4
Gracilaria salicornia	2010	9.4	-13.9
Gracilaria salicornia	2010	1.3	-16.2
Gracilaria salicornia	2010	-0.1	-14.7
Gracilaria salicornia	2010	1.7	-15.5
Gracilaria salicornia	2010	1.5	-15.1
Gracilaria salicornia	2010	1.8	-15.0
Gracilaria salicornia	2010	2.5	-15.5
Gracilaria salicornia	2010	1.3	-15.9
Gracilaria salicornia	2010	3.1	-15.5
Gracilaria salicornia	2010	2.2	-15.0
Gracilaria salicornia	2010	2.6	-15.3
Gracilaria salicornia	2010	1.5	-16.2
Gracilaria salicornia	2010	1.0	-16.4
Gracilaria salicornia	2010	2.4	-16.9
Gracilaria salicornia	2010	1.3	-16.4
Gracilaria salicornia	2010	2.2	-16.0
Gracilaria salicornia	2010	2.4	-15.8
Gracilaria salicornia	2010	1.3	-16.4
Gracilaria salicornia	2010	1.2	-15.7
Gracilaria salicornia	2010	2.0	-16.8
Gracilaria salicornia	2010	2.0	-16.0
Gracilaria salicornia	2010	2.9	-18.1
Gracilaria salicornia	2010	3.0	-18.3
Gracilaria salicornia	2010	0.8	-17.6
Microphytobenthos	2010	-0.4	-6.5
Microphytobenthos	2010	-0.3	-6.6
Microphytobenthos	2010	-0.4	-6.5
Microphytobenthos	2010	-0.5	-5.2
Microphytobenthos	2010	-0.3	-6.8
Microphytobenthos	2010	-0.5	-7.2

Microphytobenthos	2010	-0.4	-7.8
Microphytobenthos	2010	-0.2	-8.0
Palaemon sp.	2010	6.5	-5.7
Palaemon sp.	2010	6.3	-6.0
Palaemon sp.	2010	6.6	-6.0
Palaemon sp.	2010	6.2	-6.3
Palaemon sp.	2010	6.7	-9.5
Palaemon sp.	2010	6.3	-10.1
Palaemon sp.	2010	6.7	-9.5
Palaemon sp.	2010	6.4	-9.8
Palaemon sp.	2010	6.6	-5.2
Palaemon sp.	2010	6.6	-8.3
Palaemon sp.	2010	6.8	-8.5
Palaemon sp.	2010	6.9	-8.0
Thalamita crenata	2010	3.8	-13.0
Thalamita crenata	2010	4.1	-12.3
Thalamita crenata	2010	5.2	-9.1
Thalamita crenata	2010	5.0	-11.6
Thalamita crenata	2010	6.8	-11.1
Thalamita crenata	2010	6.9	-11.2
Thalamita crenata	2010	6.9	-7.0
Thalamita crenata	2010	7.7	-6.9
Thalamita crenata	2010	6.0	-6.9
Thalamita crenata	2010	5.3	-15.1
Thalamita crenata	2010	5.0	-6.5
Thalamita crenata	2010	6.4	-9.2
Thalamita crenata	2010	5.3	-10.0
Thalamita crenata	2010	4.6	-9.1
Thalamita crenata	2010	4.1	-8.9
Thalamita crenata	2010	5.2	-11.0
Thalamita crenata	2010	5.1	-10.9
Thalamita crenata	2010	3.4	-5.0
Thalamita crenata	2010	4.3	-4.6
Thalamita crenata	2010	5.7	-6.2
Thalamita crenata	2010	6.3	-6.1
Thalamita crenata	2010	5.6	-6.4
Thalamita crenata	2010	5.0	-6.6
Thalamita crenata	2010	5.3	-7.7
Thalamita crenata	2010	5.2	-5.5
Thalamita crenata	2010	4.8	-5.7

Thalamita crenata	2010	5.4	-7.3
Thalamita crenata	2010	5.2	-6.8
Thalamita crenata	2010	5.0	-6.1
Thalamita crenata	2010	5.4	-9.6
Thalamita crenata	2010	5.3	-11.2
Thalamita crenata	2010	5.5	-9.2
Thalamita crenata	2010	5.2	-10.6
Thalamita crenata	2010	5.5	-10.3
Thalamita crenata	2010	5.6	-10.4
Epiphytes	2011	2.5	-17.4
Epiphytes	2011	3.8	-18.6
Epiphytes	2011	3.0	-19.2
Epiphytes	2011	3.6	-18.2
Epiphytes	2011	4.2	-17.6
Epiphytes	2011	2.9	-11.5
Epiphytes	2011	2.3	-16.9
Epiphytes	2011	2.3	-12.8
Epiphytes	2011	1.9	-9.9
Epiphytes	2011	0.6	-5.5
Epiphytes	2011	1.9	-15.9
Epiphytes	2011	-0.2	-10.9
Epiphytes	2011	1.7	-13.5
Gracilaria salicornia	2011	3.5	-16.1
Gracilaria salicornia	2011	3.6	-17.1
Gracilaria salicornia	2011	3.6	-16.5
Gracilaria salicornia	2011	3.5	-16.8
Gracilaria salicornia	2011	3.6	-15.9
Gracilaria salicornia	2011	3.4	-16.6
Gracilaria salicornia	2011	2.9	-16.8
Gracilaria salicornia	2011	3.2	-14.4
Gracilaria salicornia	2011	3.2	-16.7
Gracilaria salicornia	2011	2.9	-17.2
Gracilaria salicornia	2011	3.1	-16.6
Gracilaria salicornia	2011	3.1	-16.7
Gracilaria salicornia	2011	4.2	-15.3
Gracilaria salicornia	2011	3.3	-16.8
Gracilaria salicornia	2011	3.6	-15.8
Gracilaria salicornia	2011	3.4	-14.9
Microphytobenthos	2011	-1.4	-5.3
Microphytobenthos	2011	-1.2	-4.7

Microphytobenthos	2011	-0.1	-4.8
Microphytobenthos	2011	-0.6	-4.7
Microphytobenthos	2011	1.1	-5.0
Microphytobenthos	2011	0.1	-6.1
Microphytobenthos	2011	-0.6	-4.9
Palaemon sp.	2011	7.5	-11.0
Palaemon sp.	2011	7.3	-11.5
Palaemon sp.	2011	6.0	-9.4
Palaemon sp.	2011	7.3	-10.7
Palaemon sp.	2011	7.1	-13.8
Palaemon sp.	2011	6.9	-13.2
Palaemon sp.	2011	7.1	-13.8
Palaemon sp.	2011	6.9	-13.6
Palaemon sp.	2011	6.9	-11.1
Palaemon sp.	2011	6.2	-10.0
Palaemon sp.	2011	6.0	-9.9
Palaemon sp.	2011	7.3	-11.3
Palaemon sp.	2011	6.2	-9.5
Phytoplankton	2011	3.2	-20.7
Phytoplankton	2011	2.8	-19.8
Phytoplankton	2011	3.0	-20.5
Phytoplankton	2011	3.1	-18.7
Phytoplankton	2011	3.5	-20.5
Phytoplankton	2011	3.2	-20.3
Phytoplankton	2011	3.3	-21.4
Phytoplankton	2011	3.5	-20.8
Phytoplankton	2011	2.8	-16.2
Phytoplankton	2011	3.0	-15.6
Phytoplankton	2011	2.0	-15.7
Phytoplankton	2011	2.1	-15.8
Phytoplankton	2011	4.0	-20.3
Phytoplankton	2011	2.1	-21.0
Phytoplankton	2011	3.0	-21.1
Phytoplankton	2011	1.9	-21.2
Thalamita crenata	2011	5.8	-11.9
Thalamita crenata	2011	6.2	-11.5
Thalamita crenata	2011	7.2	-12.2
Thalamita crenata	2011	6.0	-12.1
Thalamita crenata	2011	6.1	-12.7
Thalamita crenata	2011	6.3	-13.5

Thalamita crenata	2011	6.0	-11.2
Thalamita crenata	2011	5.4	-14.1
Thalamita crenata	2011	5.5	-8.3
Thalamita crenata	2011	5.7	-7.5
Thalamita crenata	2011	4.5	-5.9
Thalamita crenata	2011	4.2	-5.1
Thalamita crenata	2011	4.6	-10.7
Thalamita crenata	2011	4.1	-6.5
Thalamita crenata	2011	4.5	-8.7
Thalamita crenata	2011	4.7	-8.1
Sphyraena barracuda	2017	9.3	-12.7
Sphyraena barracuda	2017	9.6	-12.9
Sphyraena barracuda	2017	9.1	-12.2
Sphyraena barracuda	2017	10.8	-13.5
Sphyraena barracuda	2017	10.5	-13.8
Sphyraena barracuda	2017	10.1	-13.9
Sphyraena barracuda	2017	9.6	-13.6
Sphyraena barracuda	2017	9.5	-13.5
Sphyraena barracuda	2017	9.9	-13.1
Sphyraena barracuda	2017	9.0	-15.5
Sphyraena barracuda	2017	9.6	-12.9
Sphyraena barracuda	2017	9.7	-13.5
Sphyraena barracuda	2017	8.3	-14.3
Sphyraena barracuda	2017	10.1	-13.2
Osteomugil engeli	2017	5.3	-16.4
Sphyraena barracuda	2017	9.9	-13.0
Sphyraena barracuda	2017	10.8	-13.8
Sphyraena barracuda	2017	10.5	-14.3
Sphyraena barracuda	2017	10.5	-15.4
Sphyraena barracuda	2017	8.6	-14.3
Sphyraena barracuda	2017	9.6	-13.7
Sphyraena barracuda	2017	9.7	-13.6
Sphyraena barracuda	2017	10.6	-13.9
Caranx melampygus	2017	11.0	-13.0
Sphyraena barracuda	2017	10.4	-13.9
Sphyraena barracuda	2017	10.5	-14.5
Sphyraena barracuda	2017	9.8	-14.3
Sphyraena barracuda	2017	9.9	-14.3
Sphyraena barracuda	2017	10.4	-13.5
Sphyraena barracuda	2017	10.1	-15.4

Sphyraena barracuda	2017	10.6	-14.0
Sphyraena barracuda	2017	9.0	-12.7
Sphyraena barracuda	2017	10.7	-14.4
Sphyraena barracuda	2017	10.5	-13.3
Sphyraena barracuda	2017	8.4	-12.8
Sphyraena barracuda	2017	9.9	-13.6
Sphyraena barracuda	2017	10.9	-13.6
Sphyraena barracuda	2017	10.6	-13.9
Sphyraena barracuda	2017	10.0	-14.0
Sphyraena barracuda	2017	9.9	-13.8
Sphyraena barracuda	2017	9.9	-13.3
Caranx ignobilis	2017	10.1	-13.4
Caranx ignobilis	2017	9.7	-12.2
Sphyraena barracuda	2017	9.5	-14.7
Caranx ignobilis	2017	9.7	-11.6
Sphyraena barracuda	2017	9.6	-13.8
Sphyraena barracuda	2017	8.2	-13.5
Caranx ignobilis	2017	10.1	-14.9
Sphyraena barracuda	2017	10.3	-15.4
Sphyraena barracuda	2017	8.3	-14.1
Sphyraena barracuda	2017	9.4	-12.8
Sphyraena barracuda	2017	9.5	-12.8
Sphyraena barracuda	2017	8.1	-12.9
Caranx ignobilis	2017	9.5	-12.1
Sphyraena barracuda	2017	9.9	-12.6
Caranx melampygus	2017	9.9	-11.7
Caranx melampygus	2017	10.1	-11.6
Sphyraena barracuda	2017	10.9	-14.4
Sphyraena barracuda	2017	7.5	-12.0
Sphyraena barracuda	2017	7.5	-11.9
Caranx ignobilis	2017	8.6	-11.4
Sphyraena barracuda	2017	8.8	-14.5
Sphyraena barracuda	2017	9.3	-14.5
Sphyraena barracuda	2017	9.3	-14.5
Caranx ignobilis	2017	8.4	-11.8
Caranx ignobilis	2017	8.9	-12.7
Sphyraena barracuda	2017	9.2	-13.7
Caranx ignobilis	2017	8.1	-13.5
Sphyraena barracuda	2017	9.2	-12.9
Sphyraena barracuda	2017	9.1	-13.2

Sphyraena barracuda	2017	8.8	-13.5
Sphyraena barracuda	2017	8.7	-12.1
Osteomugil engeli	2017	6.4	-17.2
Osteomugil engeli	2017	6.3	-16.4
Osteomugil engeli	2017	6.3	-15.5
Osteomugil engeli	2017	6.3	-15.5
Osteomugil engeli	2017	5.8	-16.2
Osteomugil engeli	2017	6.1	-15.6
Osteomugil engeli	2017	6.2	-16.1
Osteomugil engeli	2017	6.3	-15.9
Osteomugil engeli	2017	6.1	-14.9
Osteomugil engeli	2017	5.5	-13.7
Osteomugil engeli	2017	6.0	-15.0
Osteomugil engeli	2017	7.8	-15.8
Osteomugil engeli	2017	6.4	-14.8
Osteomugil engeli	2017	6.9	-14.9
Osteomugil engeli	2017	6.5	-14.3
Osteomugil engeli	2017	6.2	-14.8
Osteomugil engeli	2017	6.4	-15.0
Osteomugil engeli	2017	6.8	-14.5
Thalamita crenata	2017	6.7	-16.9
Kuhlia sp.	2017	8.8	-16.6
Kuhlia sp.	2017	9.0	-17.5
Kuhlia sp.	2017	8.9	-15.9
Kuhlia sp.	2017	9.2	-16.3
Kuhlia sp.	2017	9.1	-17.2
Gambusia affinis	2017	5.9	-16.5
Gambusia affinis	2017	5.9	-18.6
Gambusia affinis	2017	6.0	-15.3
Gambusia affinis	2017	6.9	-15.7
Gambusia affinis	2017	5.3	-15.3
Gambusia affinis	2017	6.0	-15.8
Gambusia affinis	2017	5.8	-15.5
Gambusia affinis	2017	6.3	-15.7
Mugil cephalus	2017	5.6	-14.2
Mugil cephalus	2017	5.5	-14.2
Mugil cephalus	2017	5.5	-13.8
Mugil cephalus	2017	5.5	-13.8
Mugil cephalus	2017	5.9	-14.5
Mugil cephalus	2017	5.6	-13.2

Mugil cephalus	2017	5.5	-14.3
Palaemon sp.	2017	6.5	-14.1
Palaemon sp.	2017	6.7	-14.8
Palaemon sp.	2017	6.2	-14.6
Palaemon sp.	2017	6.5	-14.2
Tilapia	2017	8.1	-16.8
Tilapia	2017	8.2	-17.4
Tilapia	2017	8.2	-17.4
Tilapia	2017	8.1	-16.7

Table A2. Sequence identifications, length, and percent similarities from the BOLD and GenBank (with ACCN) databases.

Species identification (BOLD)	% similarity (BOLD)	Species identification (GenBank)	% similarity (GenBank)	ACCN (GenBank)	Sequence length
Saurida nebulosa	99.46	*Halichoeres biocellatus*	85	KU944629	591
Oxyurichthys lonchotus	99.28	*Oxyurichthys petersi*	87.6	KY176548	588
Oxyurichthys lonchotus	99.35	*Oxyurichthys petersi*	88.4	KY176548	630
Oxyurichthys lonchotus	99.47	*Oxyurichthys petersi*	88.7	KY176548	585
Oxyurichthys lonchotus	99.47	*Oxyurichthys petersi*	88.7	KY176548	586
Oxyurichthys lonchotus	99.47	*Oxyurichthys petersi*	88.7	KY176548	589
Oxyurichthys lonchotus	99.47	*Oxyurichthys petersi*	88.7	KY176548	587
Oxyurichthys lonchotus	99.47	*Oxyurichthys petersi*	88.7	KY176548	587
Oxyurichthys lonchotus	99.47	*Oxyurichthys petersi*	88.7	KY176548	588
Oxyurichthys lonchotus	99.47	*Oxyurichthys petersi*	88.7	KY176548	588
Oxyurichthys lonchotus	99.47	*Oxyurichthys petersi*	88.7	KY176548	575
Oxyurichthys lonchotus	99.47	*Oxyurichthys petersi*	88.7	KY176548	579
Oxyurichthys lonchotus	99.47	*Oxyurichthys petersi*	88.7	KY176548	586
Oxyurichthys lonchotus	99.29	*Oxyurichthys petersi*	88.8	KY176548	587
Oxyurichthys lonchotus	99.64	*Oxyurichthys petersi*	88.9	KY176548	588
Oxyurichthys lonchotus	99.35	*Oxyurichthys petersi*	89.1	KY176548	631
Oxyurichthys lonchotus	99.35	*Oxyurichthys petersi*	89.1	KY176548	631
Oxyurichthys lonchotus	99.47	*Oxyurichthys petersi*	89.1	KY176548	575
Psilogobius mainlandi	99.07	*Gobiidae sp.*	92.3	MG816687	554
Psilogobius mainlandi	100	*Gobiidae sp.*	93.3	KY675582	587

No match		*Mulloidichthys flavolineatus*	97	KU944161	589
Osteomugil engeli	99.32	*Osteomugil engeli*	98.4	MG816711	448
Psilogobius mainlandi	99.42	*Psilogobius mainlandi*	98.7	MG816721	520
Mulloidichthys flavolineatus	100	*Mulloidichthys flavolineatus*	99.2	KY371760	543
Asterropteryx semipunctata	100	*Asterropteryx semipunctata*	99.2	KR059871	633
Caranx sexfasciatus	100	*Caranx sexfasciatus*	99.2	HQ560966	643
Thalamita crenata	99.46	*Thalamita crenata*	99.2	JX398104	570
Asterropteryx semipunctata	99.83	*Asterropteryx semipunctata*	99.3	KR059871	589
Asterropteryx semipunctata	100	*Asterropteryx semipunctata*	99.4	KR059871	630
Asterropteryx semipunctata	100	*Asterropteryx semipunctata*	99.4	KR059871	631
Psilogobius mainlandi	99.81	*Psilogobius mainlandi*	99.4	MG816721	556
Thalamita crenata	99.83	*Thalamita crenata*	99.4	JX398104	587
Foa brachygramma	99.52	*Foa brachygramma*	99.5	MG816687	631
Caranx ignobilis	100	*Caranx ignobilis*	99.5	KF649842	623
Foa brachygramma	99.51	*Foa brachygramma*	99.5	MG816687	632
No match		*Osteomugil engeli*	99.6	JQ431913	590
Caranx melampygus	100	*Caranx melampygus*	99.6	KY371310	480
Thalamita crenata	99.81	*Thalamita crenata*	99.6	KT365763	538
Caranx ignobilis	100	*Caranx ignobilis*	99.7	FJ347936	635
Asterropteryx semipunctata	100	*Asterropteryx semipunctata*	99.8	KR059871	630
Albula glossodonta	99.84	*Albula glossodonta*	99.8	JQ431400	631
Asterropteryx semipunctata	100	*Asterropteryx semipunctata*	99.8	KR059871	578
Osteomugil engeli	99.82	*Osteomugil engeli*	99.8	JQ060502	574
Asterropteryx semipunctata	100	*Asterropteryx semipunctata*	99.8	KR059871	632

Asterropteryx semipunctata	100	*Asterropteryx semipunctata*	99.8	KR059871	630
Foa brachygramma	99.84	*Foa brachygramma*	99.8	KJ967855	634
Caranx ignobilis	100	*Caranx ignobilis*	99.8	KU943739	588
Foa brachygramma	99.84	*Foa brachygramma*	99.8	MG816687	636
Thalamita crenata	100	*Thalamita crenata*	99.8	JX398104	589
Atherinomorus insularum	100	*Atherinomorus insularum*	100	MG816654	633
Sardinella marquesensis	100	*Sardinella marquesensis*	100	MG816723	587
Asterropteryx semipunctata	100	*Asterropteryx semipunctata*	100	KR059872	577
Asterropteryx semipunctata	100	*Asterropteryx semipunctata*	100	KR059872	581
Thalamita crenata	99.66	*Thalamita crenata*	100	KT365763	599
Thalamita crenata	100	*Thalamita crenata*	100	JX398104	583

Table A3. Fork length (mm), total length (mm), weight (g), and stomach fullness (g) of all fish utilized for diet analyses.

Capture date	Capture time	Predator ID	Tag 1	Tag 2	Species	Fork length (mm)	Total length (mm)	Weight (g)	Stomach mass - full (g)	Stomach mass - empty (g)	Fullness coefficient
7/29/17	15:30	LD01			*Caranx melampygus*	349	415	920	17.91	8.88	3
7/29/17	17:50	LD02			*Sphyraena barracuda*	332	371	263.14	1.69	1.19	1
7/29/17	9:10	DA06			*Sphyraena barracuda*	296	346	204.8	12.72	1.05	3
7/29/17	9:15	DA07			*Sphyraena barracuda*	272	308	162.25	18.66	1.21	3
7/29/17	8:15	AA01			*Sphyraena barracuda*	355	396	299.66	4.74	1.67	2
7/29/17	8:25	DA01			*Sphyraena barracuda*	327	369	240.95	2.55	1.83	1
7/29/17	10:00	DA12			*Sphyraena barracuda*	320	282	166.5	1.25	0.93	1
7/29/17	10:40	DA15			*Sphyraena barracuda*	298	333	204.92	8.99	1.31	3
7/29/17	9:43	DA09			*Sphyraena barracuda*	280	321	166.35	1.24	0.95	1
8/11/17	2:30	KB01			*Caranx ignobilis*	401	480	1520	25.33	20.65	2
7/29/17	15:22	AA04			*Sphyraena barracuda*	507	554	800	5.14	3.98	2
7/29/17	16:07	AA18			*Sphyraena barracuda*	379	434	347.86	2.57	1.81	2
7/29/17	16:18	AA09			*Sphyraena barracuda*	350	403	343.85	4.41	2.16	2
7/29/17	16:24	AA11			*Sphyraena barracuda*	330	383	269.37	2.10	1.57	2
7/29/17	16:21	AA10			*Sphyraena barracuda*	308	350	198.38	1.33	1.08	1
7/29/17	8:20	LT01			*Sphyraena barracuda*	292	331	184.2	1.28	0.92	1
7/29/17	16:37	AA13			*Sphyraena barracuda*	318	365	258.01	1.73	1.33	1
7/29/17	16:39	AA14			*Sphyraena barracuda*	345	389	289.63	9.11	1.70	1
7/29/17	10:30	AA03			*Sphyraena barracuda*	352	394	313.18	1.72	1.24	1
7/29/17	9:40	LT02			*Sphyraena barracuda*	135	162	49.49	0.62	0.45	2
7/29/17	10:25	DA13			*Sphyraena barracuda*	282	321	182.39	2.81	1.31	2
7/29/17	15:46	AA06			*Sphyraena barracuda*	421	462	466.04	3.10	2.45	2

7/29/17	8:53	DA03			*Sphyraena barracuda*	317	361	221.11	6.63	2.03	3
7/29/17	9:48	DA10			*Sphyraena barracuda*	326	362	241.6	7.43	1.83	3
7/29/17	9:23	DA08			*Sphyraena barracuda*	343	380	268.16	14.24	2.37	2
7/29/17	9:05	DA05			*Sphyraena barracuda*	261	302	139.43	8.10	0.89	2
7/29/17	15:53	AA07			*Sphyraena barracuda*	438	514	536.22	10.95	3.49	1
7/29/17	15:29	AA05			*Sphyraena barracuda*	380	441	413.59	4.19	2.61	2
7/29/17	8:12	LM03			*Sphyraena barracuda*	302	337	212.27	5.32	1.53	3
7/29/17	8:52	LM06			*Caranx ignobilis*	243	284	286.96	6.76	2.56	3
7/29/17	10:24	LM08			*Caranx ignobilis*	162	196	102.33	2.33	0.98	3
7/29/17	16:12	KK05			*Caranx ignobilis*	212	250	206.88	2.43	2.35	2
7/29/17	10:43	LM09			*Sphyraena barracuda*	300	348	198.05	3.37	1.47	2
7/29/17	7:56	LM01			*Sphyraena barracuda*	301	344	228.14	1.46	1.24	1
7/29/17	8:30	LM05			*Caranx ignobilis*	252	311	414.82	4.89	4.41	2
7/29/17	8:18	LM04			*Sphyraena barracuda*	305	345	225.39	1.53	1.19	1
7/29/17	16:20	KK06			*Sphyraena barracuda*	213	252	218.48	2.86	2.00	2
7/29/17	16:54	KK09			*Sphyraena barracuda*	334	375	283.02	3.77	1.61	2
7/29/17	16:28	KK07			*Sphyraena barracuda*	316	354	239.92	2.82	1.59	2
7/29/17	15:10	KK01			*Sphyraena barracuda*	295	341	185.53	1.94	1.35	2
7/29/17	16:08	KK04			*Sphyraena barracuda*	384	428	433.26	5.73	2.40	3
7/29/17		NT01			*Sphyraena barracuda*	346	394	280.58	2.15	1.76	2
7/29/17	16:04	KK03	A7142	A7143	*Sphyraena barracuda*	332	374	263.6	5.23	1.85	3
7/29/17	18:37	KK08			*Sphyraena barracuda*	307	348	231.27	1.38	1.11	1
7/29/17	9:50	LM07			*Sphyraena barracuda*	369	406	373.63	8.68	2.92	3
7/29/17	8:05	LM02			*Caranx ignobilis*	275	332	473.34	5.83	4.79	2
7/29/17	16:10	AA08			*Sphyraena barracuda*	440	489	560.5	22.23	4.71	1
7/29/17	17:28	ER02			*Sphyraena barracuda*	431	484	552.44	32.86	4.49	3
7/29/17	17:07	AA15			*Sphyraena barracuda*	386	457	458.22	28.36	3.33	3

7/29/17	16:26	AA12			*Sphyraena barracuda*	364	407	350.83	4.43	3.00	2
7/29/17	16:01	ER01			*Sphyraena barracuda*	355	399	328.58	1.99	1.77	1
7/29/17	9:27	AA02			*Sphyraena barracuda*	325	380	284.55	4.05	1.84	2
7/29/17	10:03	DA11			*Sphyraena barracuda*	296	337	187.88	4.66	1.78	3
7/29/17	10:30	DA14			*Sphyraena barracuda*	330	371	244.34	8.33	1.71	3
7/29/17	9:00	DA04			*Sphyraena barracuda*	311	351	219.38	13.79	1.75	2
7/29/17	19:00	ER04			*Caranx ignobilis*	405	481	1580	43.70	26.82	3
7/29/17	16:59	KK10			*Caranx ignobilis*	275	335	451.58	7.59	7.35	2
7/29/17	15:12	KK02			*Caranx ignobilis*	395	477	1460	23.01	22.86	1
9/30/17		KP01			*Sphyraena barracuda*	353	391	280.89	2.50	1.93	2
7/29/17	18:06	AA16			*Sphyraena barracuda*	330	383	266.33	1.99	1.57	2
7/29/17	8:50	DA02			*Caranx melampygus*	335	392	820	17.99	8.69	3
7/29/17	18:31	AA17			*Sphyraena barracuda*	339	375	259.8	3.05	1.73	2
7/29/17	19:05	ER03			*Sphyraena barracuda*	389	435	379.32	3.48	2.67	2
7/29/17	16:30	AA20	A7128	A7129	*Sphyraena barracuda*	443	486	491.13	7.85	4.23	2
7/29/17	16:05	AA19			*Sphyraena barracuda*	398	451	441.27	4.67	3.99	2
12/18/17		KB02			*Caranx ignobilis*	433	518	1780	51.51	25.78	3
12/18/17		KB03			*Caranx ignobilis*	333	396	840	20.94	13.16	3
12/18/17		KB04			*Caranx ignobilis*	389	466	1220	28.84	19.36	2

Table A4. Prey taxa, digestion state, length (mm), weight (g), and total weight (g) of all prey items found.

Predator ID	Species	Prey taxa	Prey group	Digestion state	Weight (g)	Length (mm)	Length type	Total count	Total weight (g)	Bait
LD01	*Caranx melampygus*	*Thalamita crenata*	Crab	2	2.99	25	Carapace	1	2.99	N
LD01	*Caranx melampygus*	*Palaemon sp.*	Shrimp	2	0.06	18	Total	5	0.33	N
LD01	*Caranx melampygus*	*Palaemon sp.*	Shrimp	3	0.10	22	Total	6	0.47	N
LD01	*Caranx melampygus*	*Palaemon sp.*	Shrimp	4	0.05	18	Total	23	0.9	N
LD01	*Caranx melampygus*	*Asterropteryx semipunctata*	Fish	3	0.22	23	Approximate	1	0.22	N
LD01	*Caranx melampygus*	Unidentified organics	Organic material	3	0.15	25	Approximate	1	0.15	N
DA06	*Sphyraena barracuda*	*Palaemon sp.*	Shrimp	4	0.08	21	Total	4	0.29	N
DA06	*Sphyraena barracuda*	*Asterropteryx semipunctata*	Fish	4	0.39	33	Approximate	1	0.39	N
DA06	*Sphyraena barracuda*	Unidentified fish	Fish	3	8.20	57	Approximate	1	8.2	N
DA07	*Sphyraena barracuda*	*Mulloidichthys flavolineatus*	Fish	2	5.82	73	Approximate	1	5.82	Y
DA07	*Sphyraena barracuda*	*Palaemon sp.*	Shrimp	4	0.09	11	Total	20	1.62	N
AA01	*Sphyraena barracuda*	Unidentified organics	Organic material	4	0.16	34	Approximate	1	0.16	N
AA01	*Sphyraena barracuda*	Unidentified fish	Fish	3	0.26	30	Approximate	1	0.26	N
DA15	*Sphyraena barracuda*	*Mulloidichthys flavolineatus*	Fish	3	5.99	53	Approximate	1	5.99	N
KB01	*Caranx ignobilis*	*Thalamita crenata*	Crab	4	0.61	35	Approximate	1	0.61	N
KB01	*Caranx ignobilis*	Unidentified crab	Crab	4	1.03	42	Approximate	1	1.03	N
AA14	*Sphyraena barracuda*	*Australian mullet*	Fish	1	7.05	43	Approximate	1	7.05	Y
LT02	*Sphyraena barracuda*	*Palaemon sp.*	Shrimp	4	0.03	5	Approximate	2	0.06	N
DA13	*Sphyraena barracuda*	*Palaemon sp.*	Shrimp	3	0.09	25	Total	1	0.09	N
DA13	*Sphyraena barracuda*	*Foa brachygramma*	Fish	4	0.18	10	Approximate	1	0.18	N

DA13	*Sphyraena barracuda*	*Foa brachygramma*	Fish	4	0.08	16	Approximate	1	0.08	N
DA03	*Sphyraena barracuda*	Unidentified fish	Fish	2	0.55	29	Approximate	1	0.55	N
DA03	*Sphyraena barracuda*	*Oxyurichthys lonchotus*	Fish	2	0.56	28	Approximate	1	0.56	N
DA03	*Sphyraena barracuda*	*Oxyurichthys lonchotus*	Fish	3	0.15	17	Approximate	1	0.15	N
DA03	*Sphyraena barracuda*	*Asterropteryx semipunctata*	Fish	3	0.08	13	Approximate	1	0.08	N
DA03	*Sphyraena barracuda*	*Asterropteryx semipunctata*	Fish	3	0.07	12	Approximate	1	0.07	N
DA03	*Sphyraena barracuda*	*Asterropteryx semipunctata*	Fish	4	0.03	9	Approximate	1	0.03	N
DA03	*Sphyraena barracuda*	*Palaemon sp.*	Shrimp	2	0.13	20	Total	8	0.77	N
DA03	*Sphyraena barracuda*	*Palaemon sp.*	Shrimp	3	0.05	18	Approximate	6	0.29	N
DA10	*Sphyraena barracuda*	*Sardinella marquesensis*	Fish	2	4.18	59	Approximate	1	4.18	N
DA08	*Sphyraena barracuda*	Unidentified fish	Fish	2	1.13	41	Total	1	1.13	N
DA08	*Sphyraena barracuda*	*Psilogobius mainlandi*	Fish	2	0.33	34	Total	1	0.33	N
DA08	*Sphyraena barracuda*	*Psilogobius mainlandi*	Fish	2	0.16	22	Total	1	0.16	N
DA08	*Sphyraena barracuda*	*Palaemon sp.*	Shrimp	1	0.21	22	Total	1	0.21	N
DA08	*Sphyraena barracuda*	*Palaemon sp.*	Shrimp	2	0.03	16	Total	33	2.91	N
DA05	*Sphyraena barracuda*	*Foa brachygramma*	Fish	2	1.38	25	Approximate	1	1.38	N
DA05	*Sphyraena barracuda*	*Foa brachygramma*	Fish	3	0.78	28	Approximate	1	0.78	N
AA07	*Sphyraena barracuda*	*Australian mullet*	Fish	1	6.68	73	Approximate	1	6.68	Y
LM03	*Sphyraena barracuda*	*Oxyurichthys lonchotus*	Fish	2	2.20	70	Total	1	2.20	N
LM03	*Sphyraena barracuda*	*Oxyurichthys lonchotus*	Fish	4	0.21	23	Approximate	1	0.21	N
LM03	*Sphyraena barracuda*	*Oxyurichthys lonchotus*	Fish	4	0.07	11	Approximate	1	0.07	N
LM06	*Caranx ignobilis*	Unidentified fish	Fish	3	0.41	35	Standard	1	0.41	N
LM06	*Caranx ignobilis*	Unidentified fish	Fish	2	1.89	75	Total	1	1.89	N
LM06	*Caranx ignobilis*	Unidentified fish	Fish	3	0.45	42	Standard	1	0.45	N
LM06	*Caranx ignobilis*	*Caranx melampygus*	Fish	4	0.05	15	Approximate	1	0.05	N
LM06	*Caranx ignobilis*	*Palaemon sp.*	Shrimp	2	0.08	21	Total	1	0.08	N
LM06	*Caranx ignobilis*	*Palaemon sp.*	Shrimp	2	0.08	21	Total	1	0.08	N

LM06	*Caranx ignobilis*	*Palaemon sp.*	Shrimp	2	0.09	20	Total	1	0.09	N
LM06	*Caranx ignobilis*	*Palaemon sp.*	Shrimp	3	0.04	16	Total	1	0.04	N
LM06	*Caranx ignobilis*	*Palaemon sp.*	Shrimp	3	0.08	22	Total	1	0.08	N
LM06	*Caranx ignobilis*	*Palaemon sp.*	Shrimp	4	0.02	7	Approximate	1	0.02	N
LM06	*Caranx ignobilis*	*Palaemon sp.*	Shrimp	4	0.02	10	Approximate	1	0.02	N
LM08	*Caranx ignobilis*	*Caranx ignobilis*	Fish	2	1.04	47	Total	1	1.04	N
KK05	*Caranx ignobilis*	*Palaemon sp.*	Shrimp	4	0.01	6	Approximate	1	0.01	N
LM09	*Sphyraena barracuda*	Otolith	Fish	4				1	NA	N
LM09	*Sphyraena barracuda*	*Oxyurichthys lonchotus*	Fish	4	0.23	40	Approximate	1	0.23	N
LM09	*Sphyraena barracuda*	*Palaemon sp.*	Shrimp	2	0.11	24	Total	1	0.11	N
LM09	*Sphyraena barracuda*	*Palaemon sp.*	Shrimp	4	0.05	16	Approximate	4	0.35	N
LM05	*Caranx ignobilis*	*Palaemon sp.*	Shrimp	4	0.02	7	Approximate	2	0.06	N
KK06	*Sphyraena barracuda*	*Caranx sexfasciatus*	Fish	4	0.03	23	Approximate	1	0.03	N
KK09	*Sphyraena barracuda*	Algae	Algae	2	0.31	67	Total	1	0.31	N
KK09	*Sphyraena barracuda*	*Oxyurichthys lonchotus*	Fish	4	0.03	10	Total	1	0.03	N
KK09	*Sphyraena barracuda*	*Oxyurichthys lonchotus*	Fish	4	0.06	15	Total	1	0.06	N
KK09	*Sphyraena barracuda*	*Oxyurichthys lonchotus*	Fish	4	0.01	14	Total	1	0.01	N
KK09	*Sphyraena barracuda*	Otolith	Fish	4				2	NA	N
KK07	*Sphyraena barracuda*	Unidentified fish	Fish	2	0.07	12	Approximate	1	0.07	N
KK07	*Sphyraena barracuda*	*Oxyurichthys lonchotus*	Fish	4	0.05	18	Total	1	0.05	N
KK01	*Sphyraena barracuda*	*Palaemon sp.*	Shrimp	4	0.02	8	Approximate	1	0.02	N
KK01	*Sphyraena barracuda*	Unidentified organics	Organic material	3	0.07	25	Total	1	0.07	N
KK04	*Sphyraena barracuda*	*Oxyurichthys lonchotus*	Fish	3	0.33	28	Approximate	1	0.33	N
KK04	*Sphyraena barracuda*	*Oxyurichthys lonchotus*	Fish	3	0.94	45	Approximate	1	0.94	N
KK04	*Sphyraena barracuda*	Unidentified fish	Fish	3	0.64	42	Approximate	1	0.64	N
KK04	*Sphyraena barracuda*	Algae	Algae	2	0.16	25	Total	1	0.16	N

KK04	*Sphyraena barracuda*	Algae	Algae	2	0.18	23	Total	1	0.18	N
NT01	*Sphyraena barracuda*	Unidentified fish	Fish	3	0.18	21	Approximate	1	0.18	N
KK03	*Sphyraena barracuda*	*Oxyurichthys lonchotus*	Fish	2	1.91	62	Total	1	1.91	N
KK03	*Sphyraena barracuda*	*Oxyurichthys lonchotus*	Fish	3	0.78	30	Approximate	1	0.78	N
KK03	*Sphyraena barracuda*	Algae	Algae	2	0.07	30	Total	1	0.07	N
KK03	*Sphyraena barracuda*	Algae	Algae	2	0.04	18	Total	1	0.04	N
LM07	*Sphyraena barracuda*	*Oxyurichthys lonchotus*	Fish	2	2.36	78	Total	1	2.36	N
LM07	*Sphyraena barracuda*	*Oxyurichthys lonchotus*	Fish	2	2.10	67	Total	1	2.10	N
LM07	*Sphyraena barracuda*	*Oxyurichthys lonchotus*	Fish	4	0.23	36	Approximate	1	0.23	N
LM02	*Caranx ignobilis*	*Caranx ignobilis*	Fish	4	0.05	10	Approximate	1	0.05	N
LM02	*Caranx ignobilis*	*Caranx ignobilis*	Fish	4	0.05	18	Approximate	1	0.05	N
AA08	*Sphyraena barracuda*	Gobiid	Fish	1	8.04	90	Total	1	8.04	Y
AA08	*Sphyraena barracuda*	Gobiid	Fish	1	7.98	89	Total	1	7.98	Y
ER02	*Sphyraena barracuda*	*Mulloidichthys flavolineatus*	Fish	1	7.88	74	Approximate	1	7.88	Y
ER02	*Sphyraena barracuda*	*Osteomugil engeli*	Fish	1	14.61	67	Approximate	1	14.61	N
ER02	*Sphyraena barracuda*	Unidentified organics	Organic material	4	0.10	10	Approximate	1	0.10	N
ER02	*Sphyraena barracuda*	*Mulloidichthys flavolineatus*	Fish	1	0.61	40	Approximate	1	0.61	Y
AA15	*Sphyraena barracuda*	*Osteomugil engeli*	Fish	2	13.06	62	Approximate	1	13.06	N
AA15	*Sphyraena barracuda*	*Osteomugil engeli*	Fish	1	7.49	87	Total	1	7.49	N
AA15	*Sphyraena barracuda*	*Saurida nebulosa*	Fish	4	0.02	21	Approximate	1	0.02	N
AA12	*Sphyraena barracuda*	*Albula glossodonta*	Fish	4	0.81	48	Approximate	1	0.81	N
AA12	*Sphyraena barracuda*	Unidentified organics	Organic material	4	0.23	17	Approximate	1	0.23	N
AA02	*Sphyraena barracuda*	*Atherinomorus insularum*	Fish	3	1.48	57	Approximate	1	1.48	N
AA02	*Sphyraena barracuda*	Anthropogenic debris	Anthropogenic debris	0	0.21	16L x 15W		1	0.21	N

DA11	*Sphyraena barracuda*	*Asterropteryx semipunctata*	Fish	3	2.54	60	Approximate	1	2.54	N
DA14	*Sphyraena barracuda*	*Palaemon sp.*	Shrimp	2	0.05	19	Total	12	1.01	N
DA14	*Sphyraena barracuda*	*Palaemon sp.*	Shrimp	3	0.08	21	Total	35	2.65	N
DA14	*Sphyraena barracuda*	*Palaemon sp.*	Shrimp	4	0.04	17	Total	14	0.45	N
DA14	*Sphyraena barracuda*	Algae	Algae	1	0.17	28	Longest	5	0.17	N
DA14	*Sphyraena barracuda*	Algae	Algae	3	0.19	22	Longest	9	0.19	N
DA14	*Sphyraena barracuda*	*Asterropteryx semipunctata*	Fish	3	0.26	33	Total	1	0.26	N
DA04	*Sphyraena barracuda*	*Psilogobius mainlandi*	Fish	2	0.42	33	Total	1	0.42	N
DA04	*Sphyraena barracuda*	Unidentified fish	Fish	3	0.09	24	Total	1	0.09	N
DA04	*Sphyraena barracuda*	*Palaemon sp.*	Shrimp	2	0.12	21	Total	6	0.47	N
DA04	*Sphyraena barracuda*	*Palaemon sp.*	Shrimp	4	0.04	18	Total	1	0.04	N
DA04	*Sphyraena barracuda*	*Palaemon sp.*	Shrimp	4	0.01	9	Approximate	1	0.01	N
ER04	*Caranx ignobilis*	*Thalamita crenata*	Crab	2	2.00	21	Shell width	1	2.00	N
ER04	*Caranx ignobilis*	*Thalamita crenata*	Crab	3	1.16	19	Shell width	1	1.16	N
ER04	*Caranx ignobilis*	Unidentified crab	Crab	3	3.34	24	Shell width	1	3.34	N
ER04	*Caranx ignobilis*	Unidentified crab	Crab	3	1.27	21	Shell width	1	1.27	N
ER04	*Caranx ignobilis*	Unidentified crab	Crab	4	1.07	17	Shell width	1	1.07	N
ER04	*Caranx ignobilis*	*Thalamita crenata*	Crab	4	0.37	12	Shell width	1	2.74	N
KK10	*Caranx ignobilis*	*Palaemon sp.*	Shrimp	2	0.16	21	Total	1	0.16	N
DA02	*Caranx melampygus*	*Asterropteryx semipunctata*	Fish	1	1.19	46	Total	1	1.19	N
DA02	*Caranx melampygus*	*Asterropteryx semipunctata*	Fish	1	1.15	45	Total	1	1.15	N
DA02	*Caranx melampygus*	Unidentified fish	Fish	3	0.21	30	Approximate	1	0.21	N
DA02	*Caranx melampygus*	Unidentified fish	Fish	3	0.07	22	Approximate	1	0.07	N
DA02	*Caranx melampygus*	*Asterropteryx semipunctata*	Fish	3	0.14	17	Approximate	1	0.14	N
DA02	*Caranx melampygus*	*Psilogobius mainlandi*	Fish	4	0.21	33	Approximate	1	0.21	N
DA02	*Caranx melampygus*	Unidentified fish	Fish	4	0.16	27	Approximate	1	0.16	N
DA02	*Caranx melampygus*	Unidentified fish	Fish	4	0.07	14	Approximate	1	0.07	N

DA02	*Caranx melampygus*	*Thalamita crenata*	Crab	1	0.97	10	Shell width	1	0.97	N
DA02	*Caranx melampygus*	*Palaemon sp.*	Shrimp	2	0.10	22	Total	11	0.82	N
DA02	*Caranx melampygus*	*Palaemon sp.*	Shrimp	3	0.28	29	Total	13	1.07	N
DA02	*Caranx melampygus*	*Palaemon sp.*	Shrimp	4	0.05	21	Total	7	0.37	N
AA17	*Sphyraena barracuda*	Unidentified fish	Fish	4	0.02	17	Approximate	1	0.02	N
AA17	*Sphyraena barracuda*	Unidentified fish	Fish	4	0.04	16	Approximate	1	0.04	N
ER03	*Sphyraena barracuda*	Bivalve shell	Mollusk	4	0.15	10	Total	1	0.15	N
ER03	*Sphyraena barracuda*	Otoliths	Fish	4				4	NA	N
ER03	*Sphyraena barracuda*	Anthropogenic debris	Anthropogenic debris	4	0.06	8	Total	1	0.06	N
ER03	*Sphyraena barracuda*	Anthropogenic debris	Anthropogenic debris	4	0.08	8	Total	1	0.08	N
KB02	*Caranx ignobilis*	Unidentified crab	Crab	2	7.43	28	Carapace	1	7.43	N
KB02	*Caranx ignobilis*	Unidentified crab	Crab	3	5.42	25	Carapace	1	5.42	N
KB02	*Caranx ignobilis*	Unidentified crab	Crab	3	5.09	13	Approximate	1	5.09	N
KB02	*Caranx ignobilis*	Unidentified crab	Crab	3	3.58	13	Approximate	1	3.58	N
KB02	*Caranx ignobilis*	Crab mush	Crab	4	2.34	NA	NA	NA	2.34	N
KB03	*Caranx ignobilis*	Unidentified crab	Crab	3	3.80	NA	NA	6	3.80	N
KB03	*Caranx ignobilis*	Unidentified crab	Crab	4	2.72	NA	NA	1	2.72	N
KB03	*Caranx ignobilis*	Crab mush	Crab	4	1.00	NA	NA	1	1.00	N
KB04	*Caranx ignobilis*	Unidentified crab	Crab	3	5.27	NA	NA	3	5.27	N
KB04	*Caranx ignobilis*	Unidentified crab	Crab	4	3.81	NA	NA	1	3.81	N