

A DIET ANALYSIS OF WAHOO (*ACANTHOCYBIUM SOLANDRI*) FROM PELAGIC AND
HAWAIIAN NEARSHORE ECOSYSTEMS USING VISUAL AND DNA
METABARCODING TECHNIQUES

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ABSTRACT

Diet studies are an informative way to gather information on the ecology of a given organism, as well as the environment that organism inhabits. Wahoo (*Acanthocybium solandri*) is a globally popular commercial, sport, and recreational fish species but currently, detailed information is lacking on their diet composition. In the Central North Pacific we collected 233 stomachs from the offshore Hawaiian longline fishery, as well as 211 stomachs from the Hawaiian nearshore troll fishery from June to December 2014. Stomach contents can be difficult to identify when nearly digested, limiting the ability to identify prey items visually. To increase the taxonomic resolution of prey identifications, the CO1 region of the mtDNA genome was sequenced for individual prey items that could not be identified to species level visually. Clear spatial and temporal shifts in prey composition were observed in both fisheries. For nearshore-caught wahoo, juvenile pre-settlement reef species from various families (primarily *Heteropriacanthus cruentatus* (Priacanthidae) dominated the prey composition during the summer months, followed primarily by *Decapterus macarellus* (Carangidae), in the fall months. *Gempylus serpens* (Gempylidae), *Remora brachyptera* (Echeneidae), and *Katsuwonus pelamis* (Scombridae) were common prey taxa for wahoo collected from the offshore fishery. Clear spatial patterns were seen for two prey families. *Ranzania laevis* (Molidae) was a common prey item and was usually found in stomachs collected northeast of the Hawaiian Archipelago. Tetraodontiform reef fishes present in stomachs from the offshore fishery were *Melichthys niger* (Balistidae) and diodontids all known to have extended pelagic stages prior to reef settlement and were present in stomachs collected southwest of the Hawaiian Archipelago. The endoparasitic digenetic trematode *Hirudinella ventricosa* was observed in 98% of wahoo stomachs. The diet composition of wahoo was indicative of an opportunistic feeder and thus revealed dominant geographic and seasonal abundances of certain taxa from various ecosystems in the marine environment. Further, the addition of molecular barcoding to the traditional visual method of prey identifications allows for a more comprehensive range of the prey field of the predator to be elucidated.

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Appendix 3: Sequences identifications and percent similarities from the BOLD and GenBank databases. Sequence length and accession numbers from the GenBank output are also included. Records in bold were sequences used as internal validation.

BACKGROUND

Introduction

The sustainable management of fisheries resources requires in-depth knowledge of the life histories of the suite of species that characterizes the ecosystem in which the fishery operates. Trophic ecology is an integral branch of ecosystem studies, providing a key framework for understanding how the biological components in an ecosystem are connected. Diet studies are a standard method and the most direct way to investigate trophic ecology. In the new paradigm of ecosystem-based management, information concerning the connectedness of both target and non-target species on multi-trophic levels is fundamental to understanding and managing aquatic resources on an ecosystem level. Investigating the foraging habits of a predator is integral to understanding not only its trophic role in the environment, but also the trophic ecologies of its prey fields. Further, due to the expansive spatial ranges of migratory pelagic fishes, it is appropriate to understand regional differences in diet composition due to regional differences in prey resources.

The major advantage of diet studies is that they outline the basic structure of the ecosystem in terms of energy transfer. The degree to which organisms are feeding on other organisms or competing with other organisms for food resources is relative to the connectivity of the organisms in that ecosystem. In the framework of natural resource management, knowledge of the trophic structure of the aquatic environment informs our trophic role when we engage in activities that either directly (e.g., fishing, dredging) or indirectly (e.g., climate change, eutrophication) affect constituents in the aquatic environment. Because most pelagic fisheries target multiple top predator species in the marine ecosystem, careful examination of fishing

effects on the structure of the marine environment must be considered. Trophic level, along with growth rate and reproductive output, describes the productivity of a species relative to the other constituents of the ecosystem. A keen extension of the utility of predator-prey information is the development of ecosystem-level food web models like Ecopath (Polovina 1984) and Ecopath with Ecosim (Christensen and Walters 2004) which allow for the exploration of ecosystem structure (Kitchell et al. 1999), long-term fisheries management strategies (Howell et al. 2012), and ecosystem projections due to climate change and fishing (Woodworth-Jefcoats et al. 2013). These examples demonstrate the direct use of diet composition information to ecosystem assessment models.

Hawaiian Pelagic Fisheries

The Hawaii longline fishery comprises the majority of the landings of pelagic fishes in Hawaii, primarily targeting bigeye tuna (*Thunnus obesus*), yellowfin tuna (*Thunnus albacares*), and swordfish (*Xiphias gladius*). A plethora of bycatch species is also considered commercially significant including: billfishes (Istiophoridae), wahoo (*Acanthocybium solandri*), moonfish (*Lampris* spp.), sickle pomfret (*Taractichthys steindachneri*), mahimahi (*Coryphaena hippurus*), and escolar (*Lepidocybium flavobrunneum*) (Allen and Gough 2007). The modern longline fishery operation consists of a main line supported by a series of floats resulting in drooping sags from which branch lines are suspended, with each branch line ending with a baited hook (Boggs and Ito 1993). The multimillion-dollar fishery has been in operation for nearly a century and provides a fresh source of fishes for local businesses in Hawaii, as well as US domestic and foreign markets (Cai et al. 2005). The domain of the fishery encompasses the tropical and subtropical Central North Pacific from 4 – 33 °N and 140 – 168 °W (Figure 1). Scads, sardines, herring, and Pacific saury are common bait types used on these vessels (Boggs and Ito 1993).

The troll fishery is smaller in fleet and commercial value relative to the longline fishery, whose participants consist of a variety of fully recreational and subsistence to part- and full-time commercial fishers. Recreational and subsistence fishers will occasionally also sell some of their catch, thus there is some flexibility in the identities of the resource users. Big game fish species are caught with artificial lures or baited hooks dragged behind a moving vessel. This fishery usually targets yellowfin tuna, skipjack tuna (*Katsuwonus pelamis*), billfishes, mahimahi, and wahoo and usually operates within 20 nautical miles offshore (Boggs and Ito 1993). The Fishing Aggregation Device system implemented by the State of Hawaii in the 1970s has increased the efficiency of the fishery (Matsumoto 1981).

Wahoo Life History

Wahoo is a popular big game and commercial fish species globally and a common incidental catch species in the Hawaii longline fishery. A member of Scombridae, the family that includes tunas, mackerels, and bonitos, wahoo is apparently unique amongst large pelagic fishes in that it consist of one globally panmictic genetic population (Theisen et al. 2008). Wahoo is one of the fastest growing pelagic fishes reaching sexual maturity after approximately one year with an estimated length at 50% sexual maturity (L_{50}) of 1046 mm (Zischke et al. 2013a, 2013b). Wahoo usually spend > 97% of its time inhabiting the upper epipelagic zone in the warm mixed layer, i.e., the upper 50 – 100 m of the water column (Iversen and Yoshida 1957; Sepulveda et al. 2011).

Wahoo is generally described as an opportunistic feeder, consuming seasonally and geographically abundant fishes and squids (e.g., Manooch et al. 1983; Frank et al. 2007; Malone et al. 2011). The lack of gill rakers is thought to be the reason crustaceans are not a considerable portion of the diet, relative to other pelagic fishes (Magnuson and Heitz 1971). Gill rakers act as

filters, trapping smaller prey items as water passes into the buccal cavity and out through the gills, and the diminishment of the gill rakers in wahoo may be an evolutionary trait due to dietary preferences. There is a lack of detailed information on the diet composition of wahoo in the Central North Pacific where it is caught in the pelagic longline as well as the coastal Hawaiian troll fisheries.

Visual Surveys and Molecular Barcoding in Diet Analyses

Trophic predator-prey interactions have traditionally been examined through visual surveying of stomach contents (Hyslop 1980). The main limitation of this time-consuming approach is that partially and easily digested prey items obstruct high-resolution identifications of prey items. Further, the degree to which prey items can be identified is dependent on many factors, including: digestion rate of predators, handling time between capture and stomach content analysis, temperature, morphology and bulk composition of prey, and the availability of appropriate taxonomic keys. Thus, the utilization of rapid, accurate methods to identify prey items is integral to understanding the complexities of trophic interactions in marine fish communities.

DNA Metabarcoding—the use of a specific region of the genome to infer species identity—is a classic molecular genetics application for identifying organisms at fine taxonomic resolutions (Hebert et al. 2003a). The cytochrome c oxidase subunit 1 (CO1) gene (600-700 bp) in the mitochondrial genome is present in a wide range of organisms and has been attributed as a reliable gene region for species identification (Hebert et al. 2003a; Hebert et al. 2003b). The first universal CO1 primer set was designed by Folmer et al. (1994), and was used to amplify 11 phyla of invertebrates. Hebert et al. (2003a; 2003b) supported the use of the primers designed by Folmer et al. (1994) to distinguish among 200 species of lepidoterans as well as individuals

representing different phyla. Machida et al. (2009) used these universal CO1 primers to identify 189 species from mesozooplankton samples in Micronesia, indicating the power of barcoding to identify a diverse range of potential fish prey items. Ward et al. (2005) designed a specific CO1 primer set to accurately identify 207 species of fishes.

DNA barcoding is a powerful and efficient way of identifying organisms with high taxonomic resolution, and is becoming an integral tool used to analyze prey items from stomach contents in both terrestrial and aquatic organisms (King et al. 2008; Pampanon et al. 2012). Hargrove et al. (2012) noted the clear advantage of using molecular methods in addition to direct microscopy to decrease the percentage of unidentifiable prey items the stomach contents of French grunt (*Haemulon flavolineatum*). This method is especially important in species whose diets contain mostly soft-bodied prey more susceptible to digestion (Hargrove et al. 2012), cryptic prey species (Deagle et al. 2009) or for organisms that take chunks of prey (Dunn et al. 2010).

Endoparasitism

Parasitism is a common association in aquatic environments, and in big game fishes like wahoo, endoparasitism is quite commonplace (Williams, Jr. and Williams 1996). The digenetic trematode *Hirudinella ventricosa*, is common endoparasite found in wahoo stomachs (Iverson and Yoshida 1957; Manooch et al. 1983; Romeo et al. 2005; Calhoun et al. 2013) as well as the stomachs of tunas (Nakamura and Yuen 1961; Eggleston and Bochenek 1989), blue marlin (Calhoun et al. 2013), and mahimahi (Dyer et al. 1997). Manooch and Hogarth (1983) did not find any biological or environmental covariates in the wahoo samples that were related to parasite occurrence, but did highlight geographic differences in parasite infection.

Objectives

The present synthesis explored the diet composition of wahoo in the Central North Pacific during the summer and fall of 2014. The main objective of this study was to provide detailed diet information of a widely commercial and recreational fish species in an area where information was lacking. The feeding habits of wahoo were examined between individuals collected from the nearshore Hawaiian troll fishery and those collected from the offshore longline fishery. Predators caught in vastly different environments were expected to have differing diets, so the analysis was separated by fishery. To increase the taxonomic resolution of prey identifications, the CO1 region of the mtDNA genome was sequenced for individual prey items that could not be identified to species level visually.

METHODS

Sample Collection and Processing

Stomachs from wahoo caught from the longline fishery were collected by observers from the National Oceanic and Atmospheric Administration (NOAA) Pacific Islands Regional Office Longline Observer Program from June to December 2014. The observer program operates with the Hawaii longline tuna and swordfish vessels and collects stomachs while the catch is being gutted and cleaned at sea. The Hawaii longline fishery operates mainly in the central North Pacific from 4 – 33 °N and 140 – 168 °W (Figure 1). Geographical position and capture date of each individual were recorded on board and stomachs were then immediately frozen. For clarity, the longline fishery will hereafter be referred to as the offshore fishery.

Individuals caught on trolling vessels were collected at the United Fishing Agency fish auction. These fishes were often still intact, and thus entrails were provided by willing seafood wholesalers. Location of capture was not recorded for specimens collected in the nearshore fishery, however the fishers in the troll fishery who sell their catches to the United Fishing Agency usually operate around the island of Oahu, Hawaii. Fork length (FL) of trolled wahoo was recorded to the nearest centimeter at the fish auction and sexed during stomach processing, and weight was recorded to the nearest pound from the identification tag associated with each fish sold at the auction. All stomachs were either processed immediately after retrieval, or kept frozen for future processing. The date when the specimens were tagged at the auction was considered the date that the stomach was collected, but note that the specimens were caught one to three days before they arrived at the auction block. For clarity, the troll fishery will hereafter be referred to as the nearshore fishery.

Hirudinella ventricosa parasites were counted, weighed, and removed from the stomach. Pacific saury, or sanma (*Cololabis saira*) is used as bait in the longline fishery, and these carcasses were also removed from the stomach. It can be assumed for the purposes of this study that artificial lures were used exclusively in the nearshore fishery. A fullness coefficient was then qualitatively assigned to each stomach, as follows: (1) empty, (2) 1 – 50% full, or (3) 51 – 100% full. The fullness coefficient was assigned after the removal of *H. ventricosa* and *C. saira* from the stomach.

Prey Identifications

Prey items were first identified to the lowest taxonomic level visually using available taxonomic keys. Each prey item was given a rank based on digestion state, using the scale system of Choy et al. (2013): (1) intact with some or most skin on, (2) relatively intact with some soft parts digested, (3) soft parts mostly or all digested, but skeletons or remains whole or nearly whole, (4) individuals not identifiable, mostly hard parts remaining (e.g., fish otoliths, cephalopod beaks, loose vertebrae, bones). Depending on the physical quality of the prey items, fork, standard, or mantle lengths of prey items were also recorded.

Pieces of muscle or mantle tissue from prey items of rank 3 or 4 that could not be identified from taxonomic keys were carefully excised and stored in DMSO-salt buffer. Scalpels and forceps used to dissect tissue were thoroughly rinsed with water followed by 70% isopropyl between tissue excisions. DNA was extracted via the Hot Sodium Hydroxide and Tris method (HotSHOT; Meeker et al. 2007). Periodically, tissue samples from prey items of rank 1 that could be identified to species level were collected and sequenced to serve as an internal control.

The CO1 region of the mitochondrial genome was amplified using primers BOL-F1 (5' TCA ACY AAT CAY AAA GAT ATY GGC AC 3') and BOL-R1 (5' ACT TCY GGG TGR

CCR AAR AAT CA 3') for fishes (Ward et al. 2005). Each 20 μ L reaction included: 8.6 μ L nanopure H₂O, 10 μ L MangoMix (2x; Biorline), 0.2 μ L of each primer (10 μ M), and 1 μ L DNA. The thermocycling regime was as follows: 94 °C for 3 min, 30 cycles consisting of 94 °C for 30 s, 55 °C for 45 s, and 72 °C for 45 s, and then a final extension period of 72 °C for 10 min.

Primers mIColintF (5'GGW ACW GGW TGA ACW GTW TAY CCY CC 3') and jgHCO2198 (5' TAI ACY TCI GGR TGI CCR AAR AAY CA 3') as recommended by Leray et al. (2013) were used for cephalopod DNA. Each 20 μ L reaction included: 8.5 μ L nanopure H₂O, 10 μ L MangoMix (2x), 0.2 μ L of each primer (10 μ M), 0.15 μ L bovine serum albumin (10 mg mL⁻¹), and 1 μ L DNA. The thermocycling regime was as follows: 94 °C for 4 min, followed by 300 cycles consisting of 94 °C for 30 s, 50 °C for 30 s, and 72 °C for 45 s, 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 bold band around 600 bp for the Ward et al. (2005) primers or 300 bp for the primer set recommended by Leray et al. (2013). The post-PCR cleanup process consisted of 6 μ L PCR product and 0.9 μ L ExoFap (Affymetrix) subjected to 37 °C for 30 min and then 85 °C for 15 min. Lastly, 1 μ L (10 μ M) of primer was added. Cleaned PCR products were sent to the Advanced Studies in Genomic, Proteomics, and Bioinformatics Genomics Laboratory at the University of Hawaii at Manoa for sequencing. Sequences were compared to the BOLD and GenBank databases using to infer taxonomic identity. A threshold of 97% nucleotide similarity was used to distinguish a species-level identification.

Preliminary Statistical Analyses

For wahoo collected from the nearshore fishery, a two-parameter power function was fitted to the length (L) and weight (W) data. Weights were not provided from the observer program and

thus the L-W analysis was only limited to wahoo collected from the nearshore fishery. The power function with scaling factor a and exponent b was fitted with multiplicative lognormal errors (ϵ) as follows:

$$W = aL^b e^\epsilon$$

Log-transformed, the relationship becomes linear with normal additive errors:

$$\log(W) = \log(a) + b \log(L) + \epsilon$$

Sampling effort was evaluated using a species accumulation curve, produced for the longline-caught and troll-caught wahoo separately. Estimates of asymptotic species richness with percentile confidence intervals were based on methods by Chao (1984; 1987) and conducted using the vegan package in the R statistical software (Oksanen et al. 2014; R Core Team).

Population-Level Diet Analyses

Multiple bulk indices were used to assess prey taxa dominance. Abundance (N) was recorded as count data, weight (W) was recorded as continuous, and frequency (F) was recorded as presence/absence (1 or 0, respectively). Percent weight (%W) and percent abundance (%N) were calculated over j stomachs for the i^{th} prey taxon as follows:

$$\%W_i = 100\% \left(\frac{\sum_j W_{ij}}{\sum_i \sum_j W_{ij}} \right)$$

$$\%N_i = 100\% \left(\frac{\sum_j N_{ij}}{\sum_i \sum_j N_{ij}} \right)$$

Percent Frequency (%F) was calculated as the proportion of stomachs a particular prey taxon was discovered, where n is the total number of predators sampled with prey items in the stomach:

$$\%F_i = 100\% \left(\frac{\sum_j F_{ij}}{n} \right)$$

A percent index of relative importance (%IRI) for the i^{th} prey taxon was then calculated using the equation (Pinkas et al. 1971):

$$IRI_i = (\%N_i + \%W_i)(\%F_i)$$

IRI values were then standardized to equal 100% (%IRI).

Bulk measurements were initially calculated for unidentified fishes and cephalopods to evaluate the proportion of the data that consisted of unidentified prey items. Due to their ability to accumulate in stomachs for long periods of time, cephalopod beaks were not included in this analysis but were quite frequent in wahoo stomachs. %IRI for each prey taxa was then recalculated excluding unidentified fishes and cephalopods.

Individual-Level Diet Analyses

A suite of multivariate analyses was used to describe the variability of the prey composition and its relationship with various biological and environmental covariates. Taxonomic information was condensed to family level to reduce the number of prey taxa for the analysis. Due to low stomach samples in the fall months, wahoo specimens collected in October, November, and December were pooled into a single three-month category (OND).

For the multivariate analyses the diet composition was transformed to a community composition matrix. Let \mathbf{A} be a $p \times n$ matrix containing the abundance data for each of the i^{th} ($i = 1, 2, 3, \dots, n$) prey family in the j^{th} ($j = 1, 2, 3, \dots, p$) predator and \mathbf{B} be a $p \times n$ matrix containing the weight data for each of the i^{th} prey family in the j^{th} predator. For each row (i.e, each of p predators), the total number of prey items a_j and the total weight of prey items b_j in the j^{th} stomach was calculated. The abundance and weight matrices were standardized as \mathbf{A}^* and \mathbf{B}^* , respectively:

$$A^* = \frac{A}{a_i}$$

$$B^* = \frac{B}{b_i}$$

Matrices **A*** and **B*** were averaged to produce a matrix, **%GII**, of percent geometric index of importance (%GII; Assis 1996) and used as the community composition matrix:

$$\%GII = 100\% \left(\frac{A^* + B^*}{2} \right)$$

A Principal Components Analysis (PCA) was separately conducted for both the nearshore- and offshore-caught wahoo to explore inter- and intra-predator variation in diet composition using the vegan package in the R statistical software (Oksanen et al. 2014; R Core Team 2014). A permutation analysis of variance was conducted with a %GII prey matrix as the response variable using sampling month, sex, and predator fork length as explanatory variables for the nearshore fishery (Anderson 2001; McArdle and Anderson 2001). For the offshore fishery, sampling month and a southwest-northeast gradient was used as explanatory variables. The SW-NE gradient was created because most of the sites were aligned on this axis. Briefly, a straight line was drawn through the Hawaiian archipelago by connecting the most extreme southeastern and northwestern islands, Hawaii Island (19.57 N, 155.50 W) and Kure Atoll (28.42 N, 178.33 W), respectively. For each site, the shortest distance to that line (orthogonal distance) was calculated. The SW-NE gradient was calculated as a continuous variable, with positive residuals correspond to sites northeast of the Hawaiian archipelago and negative residuals correspond to sites southwest of the Hawaiian archipelago. A Canonical Correspondence Analysis (CCA; ter Braak et al. 1995) was performed to parse out major axes of variation for statistically significant explanatory variables as suggested by the permutation ANOVA.

Endoparasite Analysis

Parasite-host interactions were explored through a suite of regression models relating predator size from both fisheries to various characteristics of endoparasitism. Mean parasite weight was calculated while also accounting for host or 'subject' effects as random effects, allowing for the calculation of inter-stomach (σ_b^2) and intra-stomach (σ^2) variation in parasite weight using the nlme package in the R statistical software (Pinheiro et al. 2014). This model was compared to one without the subject effect and using both AIC and likelihood ratio test. The intra-stomach correlation (r) was calculated as:

$$r = \frac{\sigma_b^2}{\sigma_b^2 + \sigma^2}$$

To evaluate the relationship between average parasite weight and host weight, a weighted linear regression was fitted using the nlme package in the R statistical software (Pinheiro et al. 2014). Parasites from stomachs collected from the offshore fishery were excluded because predator information was missing. Datum weights were based on within-stomach sample size (i.e., stomachs with more parasites had higher precision of mean parasite weight). Total parasite load, defined as the summed total of parasite weight in a stomach, was also regressed against host weight. Lastly, Parasite abundance was also regressed against host weight using a Poisson linear model.

RESULTS

Stomach Collections

A total of 439 wahoo stomachs were collected from both fisheries, with 206 stomachs from the nearshore fishery and 233 stomachs from the offshore fishery (Table 1). Stomach collection by month was higher during the summer months than in the fall months for both fisheries, reflecting the seasonal availability of wahoo especially in the nearshore fishery. Proportion of empty stomachs was slightly higher for the stomachs collected from the nearshore fishery (36%) than that from the offshore fishery (25%), with most of the full stomachs < 50% full. Within-stomach prey abundance was negatively binomially distributed, with mean 2.49 (SE: 1.07), variance 13.4, and shape parameter (θ) 0.740 (SE: 0.0713; Venables and Ripley 2002) (Figure 2). The maximum number of prey items recorded in an individual stomach was 27 prey items.

Prey Barcodes

Seventy-three fish and cephalopod species in total were identified from 399 prey sequences. Of the 399 prey sequences, 215 sequences matched sequences in the BOLD database with > 99% similarity, and the remaining 184 sequences matched known sequences in the GenBank database with > 97% nucleotide similarity. Matches between species identification between the BOLD and GenBank databases were very close. Of the 184 sequences matched in GenBank, 31 sequences had nucleotide similarities < 97% and were thus classified as unidentified prey items. Fifty-three prey species were identified from wahoo collected from the offshore fishery, of which 40 species were identified exclusively using the molecular approach. Thirty-nine prey species were identified from wahoo collected from the nearshore fishery, of which 26 species were identified exclusively using the molecular approach. Twenty tissue samples from known prey

items set aside for internal validation were all correctly identified with > 97% nucleotide similarity. All barcode identifications, their nucleotide similarities to the BOLD and GenBank databases, GenBank Accession Numbers, and internal validation barcodes are provided in Appendix 3.

Diet Composition of Wahoo Collected from the Nearshore Fishery

Weights and lengths measured from wahoo collected from the nearshore fishery followed an allometric growth pattern (Figure 3), with a scaling factor (a) of $4.15e-06$ [95% CI: $6.74e-06$, $1.24e-05$] scaling and exponent (b) of 3.23 (95% CI: 3.17, 3.30), statistics indicative of its elongated body form. The nearshore-caught specimens used for the diet analysis ranged from 98 – 156 cm FL and 1.36 – 25.4 kg. Fork length was sporadically recorded for wahoo collected from the offshore fishery, however the range of FLs of wahoo collected from the offshore fishery was comparable to the nearshore fishery.

The diet composition of wahoo collected from the nearshore fishery consisted of 39 species from 18 fish and cephalopod families. Prey species richness in the nearshore fishery was within the 95% CI of the asymptotic species richness estimate of 44 (95% CI: [40, 62]; Figure 4A). Carangidae (i.e., *Decapterus macarellus*), Scombridae (i.e., *K. pelamis*), and Priacanthidae (i.e., presumably pelagic stages of juvenile *Heteropriacanthus cruentatus*) were the most frequent prey items found in the nearshore-caught wahoo. Juvenile (presumably pelagic-staged) reef fishes from various families (e.g., Chaetodontidae, Monacanthidae, and Dactylopteridae) were also numerically abundant, but less frequent. Two species, *H. cruentatus* and *D. macarellus* dominated the prey composition, accounting for over half the %IRI. Other lesser-observed taxa included: *Auxis rochei*, *Promethichthys prometheus*, and pelagic stages of the reef fish species *Dactyloptena orientalis*, *Chaetodon kleinii*, and *Pervagor spilosoma*. A full list of the observed

prey species and their corresponding bulk measurement indices in the diet of nearshore-caught wahoo is provided in Appendix 1.

Carangidae, Scombridae, and Priacanthidae were dominant prey families shown from the PCA bi-plot (Figure 5). The first two principal components explained 57% of the total variance. The scores of the stomachs on the bi-plot revealed a range of inter-predator foraging habits. For example, stomachs with scores placed near the arrow ends of the three dominant prey families were feeding primarily on that prey family at the time of capture. Stomachs with scores placed near the origin were feeding on rare prey items, or were generalist feeders consuming a mixture of the three dominant prey items.

A permutation ANOVA showed month to be the only predictor that explained a significant ($p < 0.001$) portion of the variability in the prey composition. Month of capture explained 11% of the total variation in the prey composition data. The first two CCA axes explained 72% of the constrained variation. CCA axis one was primarily a temporal gradient, separating the early summer from the autumn months (Figure 7). Carangidae was strongly associated with CCA axis one and was situated near the later summer and fall months. Other numerically abundant reef associated fish families (e.g., Priacanthidae, Monacanthidae, and Chaetodontidae) and Scombridae were associated with the early summer months.

Table 2 shows prey families with the highest %GII from wahoo stomachs collected from the nearshore fishery separated by month. There was a shift in prey dominance from Priacanthidae and Scombridae in the summer to Carangidae (*Decapterus* spp.) in the fall. Certain prey families are considerable portions of the diet only in single months. Of note are Dactylopteridae (*D. orientalis*) and Monacanthidae (*P. spilosoma*) in June, Gempylidae in July,

Ommastrephidae and Alepisauridae in August, Tetraodontidae and Acanthuridae in September, and Balistidae and Molidae in late autumn.

Diet Composition of Wahoo Collected from the Offshore Fishery

Fifty-three prey species from 28 fish and cephalopod families were found in the stomachs of wahoo collected from the offshore fishery. A prey species accumulation curve indicated that species richness was slightly underrepresented, with an estimated prey species richness of 76 (95% CI: [65, 155]; Figure 4B).

From the PCA bi-plots, Gempylidae, Echeneidae, and Molidae were dominant prey items (Figure 6). The first two principal component axes explained 43% of the variance. The scores of the stomachs show a varied array of feeding habits at the time of capture. Snake mackerel (*Gempylus serpens*) dominated the diet of the offshore-caught wahoo in both frequency, abundance, and weight. *Remora brachyptera* (Echeneidae) and *Ranzania laevis* (Molidae) were present in 26 and 21% of the stomachs, respectively, and were also major component of the diet. Bramidae (e.g., *Brama orcini*), Scombridae (e.g., *Thunnus* spp., and *K. pelamis*), and Balistidae (*Melichthys* spp.) were lesser-observed prey families. A full list of the observed prey species and their corresponding bulk measurement indices can be found in the diet of offshore-caught wahoo is provided in Appendix 2.

There were significant temporal and spatial differences in prey composition from the permutation ANOVA tests. Month of capture and position along the SW-NE gradient explained 5% of the total variation in prey composition. The first two CCA axes explained 68% of the constrained variation. The first CCA axis was primarily a spatial axis separating sites northeast and southwest of the Hawaiian archipelago. Molidae was strongly associated with the SW-NE gradient, usually observed in the stomachs of wahoo collected northeast of the Hawaiian

archipelago. In contrast, juvenile pelagic-stage reef-associated balistids were mostly observed in stomachs of wahoo collected southwest of the Hawaiian archipelago. Temporal variation was characterized by inter-monthly differences in the prey composition (Table 3). The three dominant prey families (Gempylidae, Echeneidae, and Molidae) were consistently dominant prey items across the sampling months. Reef-associated balistids were common in July and August and diodontids were common in the fall months.

Endoparasitism

Of the 439 stomachs collected from both fisheries, 96% were parasitized by *H. ventricosa*. Physical condition of the parasite was varied from emaciated to fully turgid. Generally, parasites were positioned towards the posterior end of the stomach if the stomach was full and spread out along the stomach lining if the stomach was empty. Some parasites were still attached upon stomach processing, leaving behind a circular ulcer along a row of ulcers (Figure 10).

Parasite abundance was approximately Poisson distributed with a mode of 2 parasites (mean = 2.17, variance = 1.13) with one stomach having 13 parasites, the maximum number of parasites observed in a stomach (Figure 11). A random effects model was fitted to include both inter- and intra-stomach variability in mean parasite weight. The mean weight of a parasite was 6.01 g and including additional subject effects were statistically significant ($p < 0.001$). The inter-subject standard deviation (1.69) is slightly higher than the within-stomach or residual standard deviation (1.46). There was a considerable correlation in mean parasite weight among stomachs, with an intra-stomach correlation of 0.57.

There was a significant ($p < 0.001$) positive relationship between average parasite weight and host weight. Similarly, total parasite load was positively related ($p < 0.001$) with host

weight. Both models had low explanatory power ($R^2 = 0.2$ Figure 12). There was not a significant linear relationship ($p = 0.44$) between parasite abundance and host weight.

DISCUSSION

General Notes on Foraging Patterns

The PCA bi-plots showed the degree of intra- and inter-specific variability of wahoo collected from both fisheries (Crispen de Billy et al. 2000). Wahoo in the Central North Pacific fed primarily on a few prey items but will also feed on a wide variety of infrequent prey items. Fish prey were mainly consisting smaller juvenile individuals, with the exception of smaller tunas like skipjack and bullet/frigate tunas. Wahoo are highly migratory and thus a nomadic feeding strategy is complementary to the variety of environments this type of predator interacts with. High inter-predator variation was exhibited among predators feeding on primarily dominant prey items or on rare prey items. Since only one or two prey items were usually found in stomachs (Figure 2), feeding on infrequent prey items was probably occurring more than generalist feeding on a mixture of prey items.

The relatively small number of prey items in the stomach may indicate that wahoo seek out individual prey items, using their immense swimming power and teeth to capture prey. Most stomachs with prey only had one prey item (Figure 2), and this pattern was evident for stomachs collected from both fisheries. All of the fully-intact skipjack tuna observed from stomachs of wahoo caught in both fisheries were sectioned into three parts, indicating that individuals were not swallowing the tuna whole, but instead consuming the tuna in sections. A considerable portion of the mackerel scad and *Remora* spp. observed in the diet were found in two or three pieces in the stomach. Snake mackerel were never found in one piece and provided some challenges when enumerating individuals within a stomach. Teeth markings evidenced by punctures in the bodies of other fishes also highlight this type of prey acquisition.

The diet composition of wahoo collected from the Central North Pacific and around the Hawaiian Islands consisted of a diverse prey field spanning reef, neritic, epipelagic, and mesopelagic ecosystems. Wahoo caught in the Gulf of Mexico consumed mainly cephalopods, Exocoetidae, Coryphaenidae, Carangidae, and Scombridae (Frank et al. 2008). In the Indian Ocean, squids were present in nearly half of wahoo stomachs, with Exocoetidae also dominantly present (Malone et al. 2011). *Cyprinus cyanopterus* was a heavily consumed exocoetid consumed by wahoo caught in the equatorial Atlantic Ocean (Vaske et al. 2003). Exocoetids were not commonly found in the stomachs of wahoo collected in this fishery, however wahoo caught in the equatorial Pacific just south of our sampling domain (Iverson and Yoshida 1957) and in the Western Central Pacific (Allain 2003) also were not consuming exocoetids. Wahoo in the North Atlantic Ocean were also not feeding on exocoetids, but selective on scombrids (*Auxis* spp.; Rundershausen et al. 2010). The vast regional differences in the diets of wahoo highlight that foraging habits of wahoo are not generalizable across ocean basins.

The species richness of the diet composition of wahoo collected from the offshore fishery was substantially higher than that of wahoo collected from the nearshore fishery. This observation could be due to the fact that wahoo in the pelagic realm are feeding from vastly different ecosystems than wahoo patrolling the nearshore environment. Whereas wahoo caught nearshore are feeding on juvenile stages of reef fishes, squids, and pelagic scombrids, wahoo caught offshore feed from mesopelagic and bathypelagic fishes that feed higher in the water column at night. The diversity of pelagic fishes that are in the diets of offshore-caught wahoo are also more expansive than the diversity of pelagic fishes that were recorded from the nearshore-caught wahoo. Although the reef environment is more speciose than the pelagic environment, many early life history attributes will influence whether certain reef groups are consumed by

wahoo. Because wahoo were mostly consuming juvenile individuals, reef fish families with extended life history phases in the pelagic realm (e.g., Balistidae, Diodontidae) are more susceptible to predation by wahoo. General size while in the pelagic phase is also important, as most of the juvenile prey items were between 50 and 100 mm.

Diet Composition of Wahoo Collected from the Nearshore Fishery

There was a clear temporal trend in the diet composition for wahoo collected from the nearshore from a mixed diet that consisted of various families of reef fishes and scombrids in the summer to a diet dominated by carangids, specifically *D. macarellus*, in late summer and fall (Figure 7). The presence of reef fishes in the diet in the early summer months coincides with peak recruitment of juvenile reef fishes (Walsh 1987). Wahoo are seasonally available in the nearshore fishery during spring and summer, possibly concurrent with a spawning period of wahoo in the nearshore area (Boggs and Uchiyama). These large schools of juvenile reef fishes returning to the reefs to settle would be an easily acquirable source of food for wahoo and other pelagic predators in the nearshore environment during the summer. *Decapterus macarellus* is also the most common mackerel scad caught in the nearshore hoopnet and handline fisheries in Hawaii (McNaughton 2008). *Decapterus* spp. are a common forage fish predated by many piscivores including seabirds (Brown 1975; Harrison et al. 1983), jacks (Humphreys and Kramer 1984), and various scombrids (Yamaguchi 1953). Iverson and Yoshida (1957) conducted a diet study on wahoo in the equatorial Pacific Ocean and reported *Decapterus* spp., *K. pelamis*, and various squids as major components of the diet with a noticeable dearth of reef-associated fishes. Their study did not sample individuals during the summer period and thus it remains to be seen whether reef fishes were also major prey constituents in the diet. The switch to *Decapterus* spp.

in the later summer to early fall may correspond with a decrease in juvenile reef fishes as they settle into their reef habitats.

The dominance of juvenile reef fishes in the diet of the nearshore-caught wahoo illustrate a clear trophic interaction between reef and pelagic ecosystems. The summer of 2014 was an anomalously successful year for reef fish recruitment from various reef fish families (R. Humphreys, personal communication). Fish recruitment often exhibits high inter-annual variability and thus different reef species could be observed if this study was done in a different sampling year. Many reef fishes observed in the diets of wahoo have reportedly episodic periods of strong recruitment (e.g., *Pervagor spilosoma* and *Priacanthus meeki*; Hobson and Chess 1996; Stimson 2005). Other diet studies on nearshore-caught pelagic fishes have noted the importance of a diverse group of reef fishes (e.g., Tetraodontiformes, Acanthuridae, Priacanthidae, Chaetodontidae) to their diets (e.g., Brock 1984; Buckley and Miller 1994). The juvenile stages of reef fishes thus provide an important link in the marine food web as seasonal sources of easily acquirable prey.

Diet Composition of Wahoo Collected from the Offshore Fishery

There were significant spatiotemporal trends in diet composition of wahoo collected from the offshore fishery. Month of capture was a significant explanatory of diet composition; the change in diet composition was not chronological but inter-monthly, highlighting the variability of juvenile reef fish recruitment patterns with emphasis on families in the Order Tetraodontiformes especially in July and August (Table 3). In the offshore samples, there were clear spatial patterns where different prey families were observed in stomachs. Families in Order Tetraodontiformes are known to have extended juvenile stages in the pelagic zone (Leis 1978; Leis and Moyer 1985). Their presence in stomachs caught west of the archipelago may be

indicative of a westward flow from the Hawaiian archipelago predicated by westward-progressing mesoscale eddies and/or westward transport from the North Equatorial Current. Johnston Atoll and the Hawaiian Archipelago flank these southwestern sites and thus this area may have more of a reef signature than sites northeast of the Hawaiian Archipelago. Juvenile *R. laevis* (Molidae) were generally concentrated at sites northeast of the Hawaiian Archipelago. These organisms could be following the Transition Zone Chlorophyll Front (TZCF) that is positioned just north of the sampling domain (Polovina et al. 2001). The TZCF is a dynamic oceanographic feature where certain marine organisms like tunas and turtles congregate to forage (Polovina et al. 2001). Very little is known of the ecology of *R. laevis* and so it is unknown whether the apparent congregation of *R. laevis* northeast of the Hawaiian archipelago is due to characteristics associated with spawning and/or its juvenile life history.

Echeneids (*R. brachyptera*) were present in 26% of full stomachs of wahoo collected from the Central North Pacific. *Remora brachyptera* was also a major component of the abundance and gravimetric components of the diet (15 and 17%, respectively). Sizes of *R. brachyptera* ranged from 72 – 143 mm (SL). The relative importance of this particular species of *Remora* to the diet of wahoo in the Central Pacific is striking because the conventional notion is that Echeneids are usually not consumed by their hosts, or by other pelagic fishes or mammals. Eldridge and Wares (1974) reported one *R. brachyptera* individual in a blue marlin (*Makaira nigricans*). Echeneids, namely from genera *Echeneis* and *Remora*, usually have close relationships with sharks and billfishes (Cressey and Lachner 1970; Morota and Fujita 1995; O’Toole 2002) that are either commensal (phoresy) or symbiotic (parasite-removing). Wahoo could be consuming freely swimming *Remora* spp. from the water column or could very well be removing attached *Remora* spp. individuals from their hosts. Remoras will detach from their

hosts briefly to catch prey (Strasburg 1962), and thus wahoo could be hunting remoras temporarily detached from their hosts. The removal of attached *Remora* spp. would indicate selectivity in the feeding strategy of wahoo. Empirical evidence of this behavior has yet to be recorded, but is a reasonable explanation for this apparent phenomenon.

Snake mackerel (*G. serpens*) was the most ubiquitous prey item among wahoo collected from the offshore fishery. It is often caught as noncommercial bycatch in the offshore fishery and occupies the same depth range as wahoo (Nakano et al. 1997). Snake mackerel was found in diet of various marine birds, indicating that snake mackerel inhabits the epipelagic zone during the daytime (Harrison et al. 1983). Snake mackerel were usually in an advanced stage of digestion and thus it was difficult to record the prey length, however based on body width, it is plausible that wahoo were consuming smaller juvenile snake mackerel that occupy shallower depths during the daytime (Nakamura and Parin 1993). Catch rates of snake mackerel in the offshore fishery over a 16-year period (1996 – 2011) indicated a fishery-induced change in the composition of fish predators, with increased catch rates of mid-trophic level fishes like snake mackerel, escolar, and lancetfish (Polovina et al. 2009; Polovina and Woodworth-Jefcoats 2013). A decrease in top-level predators and a concurrent increase in mid-trophic bycatch fish species is concurrent with their ubiquity in the diet of wahoo in this study.

Molecular Barcoding in Diet Studies

Molecular barcoding is becoming a viable way to assess the diets of many fishes of diverse foraging ecologies from zooplanktivores (Leray et al. 2013) to apex top predators (Dunn et al. 2010; Cote et al. 2013). Wahoo are an ideal predator for prey barcoding, because large prey items are usually consumed, and although the prey items are in an advanced state of digestion, enough tissue can still be excised for DNA extraction. This is a clear advantage to the visual method, in

which enumerable body parts are often required (e.g., vertebrae, fin rays) or identification, parts that are easily amenable to digestion or partial digestion. The utility of the barcoding approach is evidenced by the low proportions of unidentified fishes and squids in the prey tables. Without the use of genetic techniques, unidentified fishes and squids would have been majority of the bulk indices (i.e., %N, %F, and %W). Detailing the specific identities of prey items allowed for a closer analysis of the prey field reported in this study. Because unidentified prey items are usually not integrated into the diet analysis, the low contribution of unknown prey items increases confidence that the sample of the diet reported is representative of what the predator was consuming in the area and during the period of sample collection.

Unidentified prey items, in considerable proportions, have the potential to mask the interpretation of this diet analysis. Barcoding individual prey items allowed for more infrequently observed species to be discovered and thus increased the species richness of the diet composition. Species accumulation curves can be affected by the identification of more prey taxa by delaying the asymptote of species richness. Because unidentified prey were excluded from the multivariate analyses, the detection of opportunistic feeding on infrequent prey items would not have been concluded had those prey items not been identified.

The level of taxonomic aggregation will also affect the interpretation of a diet analysis. At coarser taxonomic levels, prey taxa can accumulate and asymptote with fewer stomach observed than at finer taxonomic levels. This can lead to the possibly erroneous conclusion that enough stomach were collected to represent the diversity of the diet. For the offshore-caught wahoo, when prey groups were grouped at family levels, the prey accumulation curve reached asymptote while when grouped at the species level, the asymptote was not yet reached. However, because most of the prey families observed consisted of one species, aggregations on either the species

level or the family level would have led to similar results with respect to the multivariate analyses. This was especially true for the species and families that occurred most frequently in the diets.

Methodological Considerations

Sample size was important to assess how well the diet composition observed was representative of the diet of the predator during the time and where it was collected. The sampling effort for the nearshore fishery was adequate as the prey accumulation curve for stomachs collected was reaching the asymptotic species richness. Species richness for the offshore fishery was slightly underrepresented for the offshore fishery. Regardless, the samples collected in this project provided an adequate representation of the prey composition of wahoo during the time period and across the spatial range of the sampling domain.

Among the three individual bulk indices of abundance (%F, %N, and %W), %F can provide an adequate representation of important prey taxa. All three bulk indices were all highly positively correlated with %IRI as expected because these three indices in tandem characterize the calculating of the IRI. However, %F and %N were more strongly correlated ($r = 0.97$ and 0.95 , respectively) with %IRI than %W ($r = 0.87$), indicating %F or %N to be just as robust as compound indices (i.e., %IRI). %F and %N also had higher R^2 values ($R^2 = 0.94$ and 0.90 , respectively) than %W ($R^2 = 0.75$) when used as a single variable in a log-linear model with %IRI as the response variable. Gravimetric measurements are the most variable of the bulk indices because of differential digestion of prey items. In this case, %F and %N were both similarly as robust as %IRI, a finding concurrent with a review by Baker et al. (2014). With an adequate sample size, %F can solely provide an easily measurable metric to evaluate relatively

important prey items in the diet if information on abundance and/or weight of prey items cannot be collected or are unreliable.

Endoparasitism

The high association of wahoo with the parasite *H. ventricosa* was not surprising, with 96% of the stomachs having at least one parasite (Williams, Jr. and Williams 1996). There was considerable variability in the average weight of a parasite observed in wahoo stomachs (Figure 12). A considerable portion of the variability can be explained by predator weight, however variability in weight among stomachs can also be due to the general condition the stomachs at the time of processing and whether the parasites were feeding and thus turgid at the time of processing.

The weight of the host is an important factor when considering its relationship with the parasites that inhabit its stomach. Positive relationships between average parasite weight and predator weight suggested that parasites inhabit their host for most of their host's life and are growing in tandem with their host. The digenetic characteristic of the parasite indicates that wahoo become parasitized by consuming a secondary or tertiary host. The pairing of parasites observed in 78% of parasitized stomachs could be due to density dependence with relation to the space provided by the stomach. The parasite also creates ulcers to form on the stomach lining, and so there may be an unknown regulation between the host and parasite to control parasite capacity. The parasite may enter the wahoo stomach through an intermediate host consumed in its juvenile or larval stages, information that is lacking in our analysis. Wahoo could also be readily consuming intermediary hosts and density-dependent factors brought on by the wahoo host or the parasites may limit the number of parasites in a particular stomach. Our data does not

present any empirical insight into the parasitic pathway of *H. ventricosa* and further work should investigate the parasitic ecology and genetic structure of this extremely common endoparasite.

CONCLUSIONS

Diet studies not only allow for exploration of the foraging ecology of the predator under study, but they also provide pertinent ecological information of the environment it occupies. This study has contributed to the understanding of not only this pelagic predator, but the diverse prey field it relies on for sustenance. For instance, the period of time reef fishes spend in early life stages in the pelagic realm is an enigma and diet studies allow for a narrowed perspective of the pelagic juvenile stages of reef fishes. The summer of 2014 was considered a boom recruitment year for many families of fishes in Hawaii and was definitely manifested in the diet of the nearshore-caught ono. The presence of reef-associated tetraodontids in wahoo caught west of the Hawaiian Archipelago in the summer also highlights a unique characteristic of early life history strategy for some reef fishes.

Wahoo feed on fishes and squids from nearshore reef to epipelagic to mesopelagic environments and are thus an important trophic linkage among these radically different ecosystems. Wahoo were somewhat opportunistic in terms of their fish prey, however there is some evidence of feeding selectivity towards a few dominant groups in the water column. Size was also an important characteristic, as most fish prey items were juveniles with the exception of tunas. Schooling juvenile reef fishes provide an ephemeral source of abundant food during summer and may be a reason along with spawning that epipelagic predators like wahoo have seasonal peaks in the nearshore troll fishery during summer.

It should be noted that due to the fisheries-dependent nature of the sample collections, the size range of the wahoo represents the size range of the wahoo caught in the fishery. The lower bound of the size range corresponds to approximately a year old, with most of the wahoo surveyed in this project between 0.5 – 3 years old (Zischke et al. 2013b). Smaller juvenile

specimens were not collected in this study and thus require further study due to the fact that the highest growth rates occur during the first year of life.

Molecular barcoding played an important role elucidating the fine details of the wahoo and had mixed effects in terms of its influence of the interpretation of the diet analysis. Barcoding decreased the percentage frequency, weight, and abundance of unidentified fishes and squids to below 15%, statistics that are generally low for diet studies. Combined with the analysis of sample size, we are confident that the analysis conducted here provided an adequate representation of the diet of wahoo in the context of where and when they were caught. With respect to the multivariate analyses, the level of opportunism shown by the increased diversity of the prey field in wahoo caught in both fisheries could not have been explored without species-specific identifications from the barcoding. However, the additional layer of taxonomic detail did not influence the interpretation of the major axes of variation in the prey composition when comparing aggregation at the family and species level because many of the families were represented by just one species, especially the dominant prey families.

In the context of ecosystem-based management of fisheries, diet studies allow for the integration of interactions among predators and their prey fields. Current data-poor assessments of fish population are not capable of integrating diet. The next advances of methods in the direction of ecosystem-level assessments may utilize diet information to quantify the interactions in multiple-species fisheries like the Hawaii longline fishery. Diet studies may be transformed from important ecological studies to important data requirements in the assessment of ecosystem health.

FIGURES

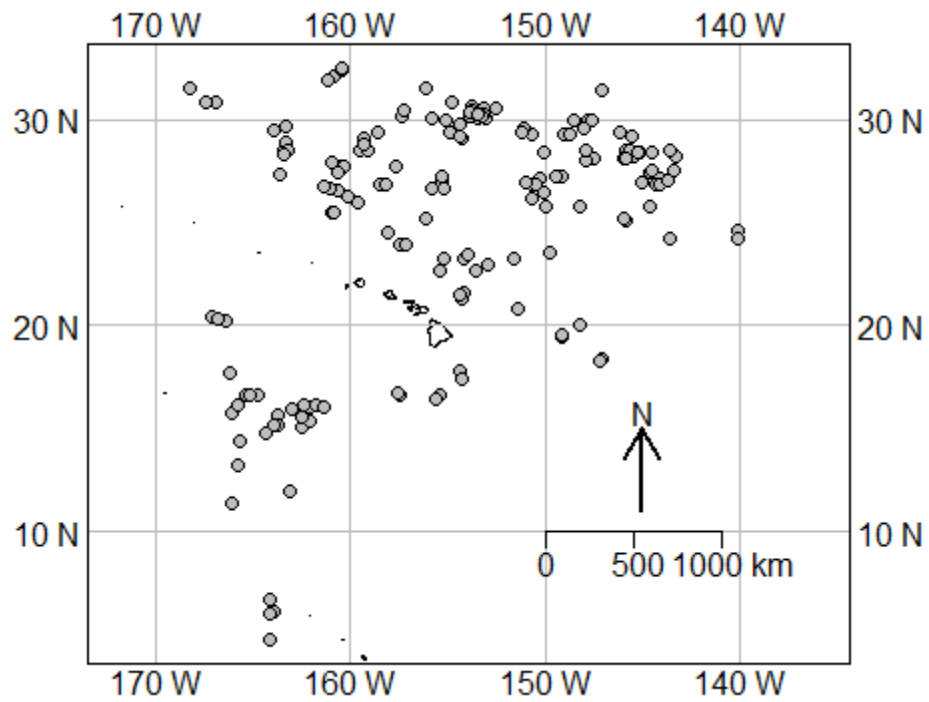


Figure 1: Sites (gray dots) where stomachs were collected from wahoo collected from the Hawaii longline fishery from June to December 2014. The black square around the island of Oahu approximates the domain of the stomach collections from the nearshore troll fishery.

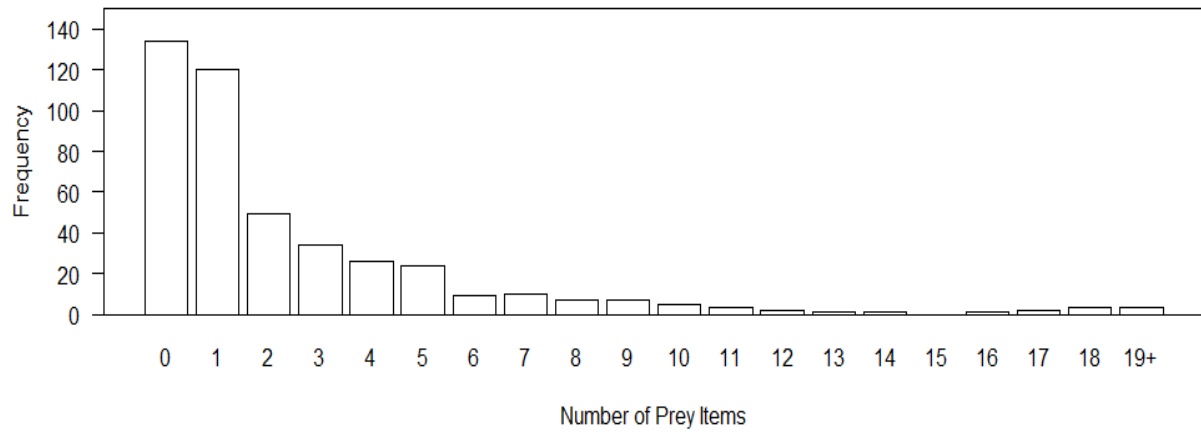


Figure 2: Number of prey items observed in wahoo stomachs from both offshore and nearshore fisheries. 19+ refers to stomachs with 19 or more prey items. The tail of the distribution extends to 27 prey items.

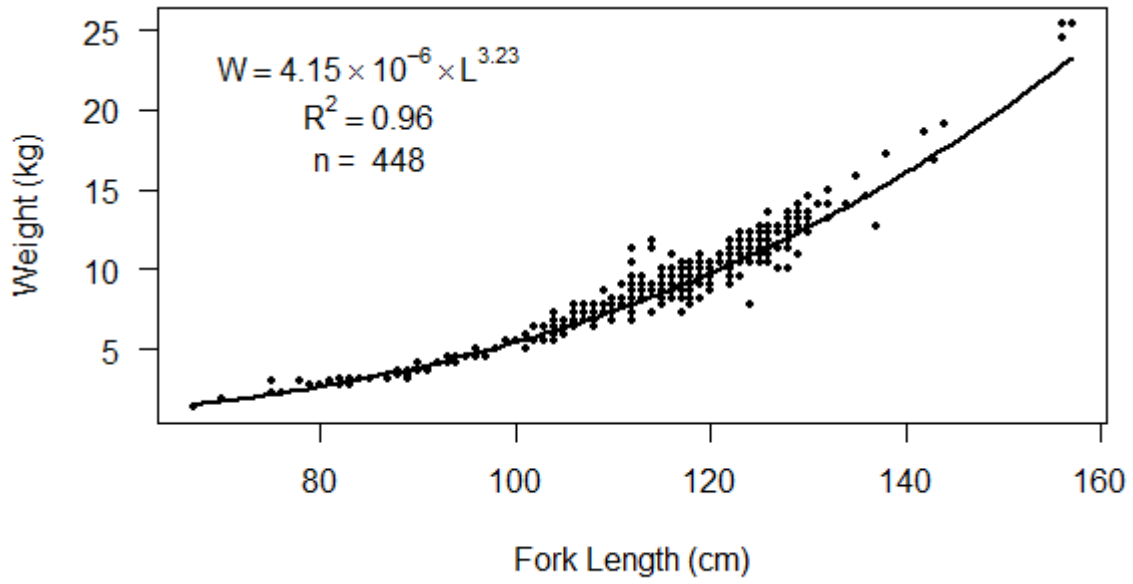


Figure 3: Weight-length plot of wahoo collected from the nearshore fishery. These samples include individuals that were not used in the diet analysis. The curve is the fitted weight-length power function as described in the plot. Weights were not available for the offshore-caught wahoo samples.

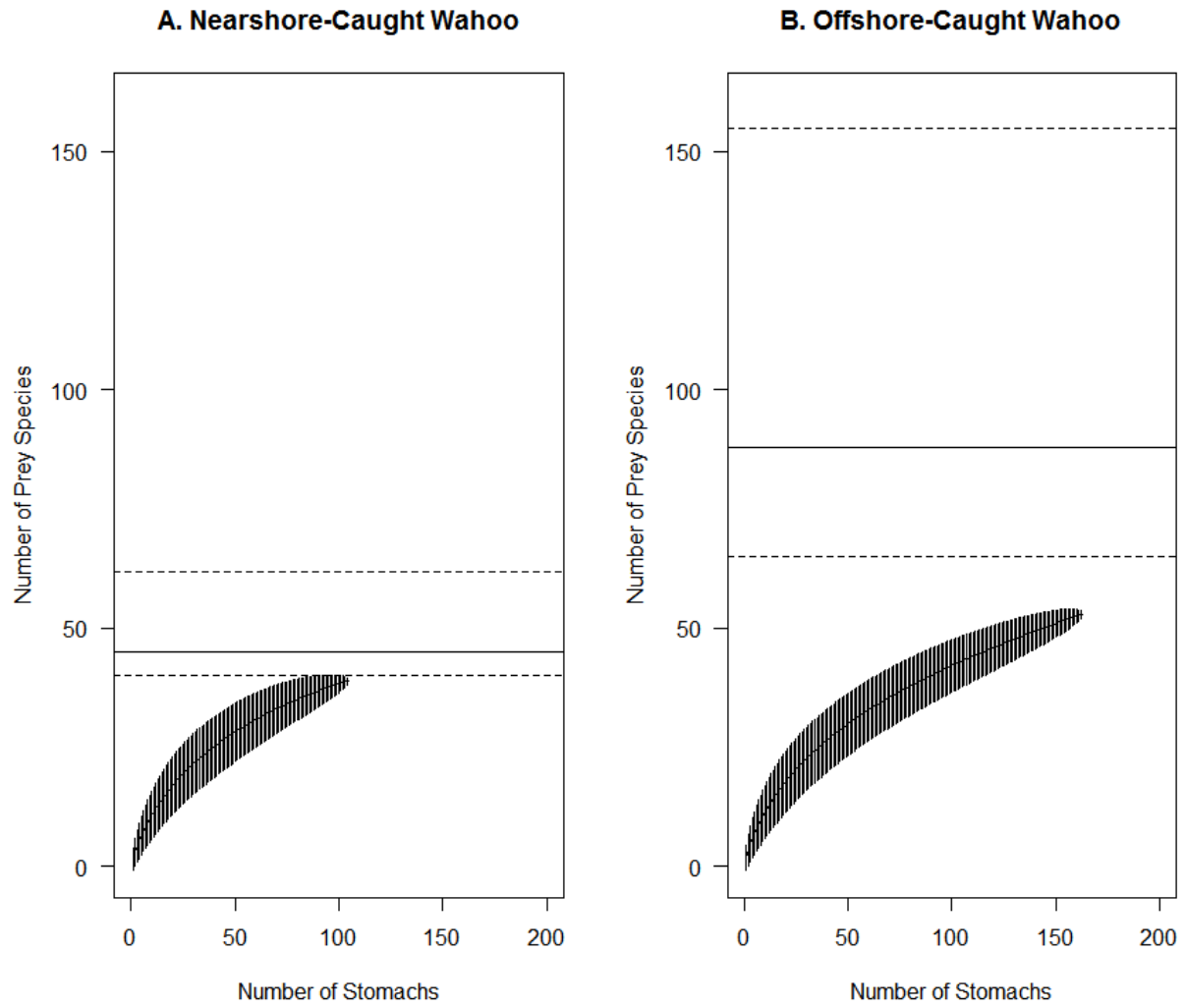


Figure 4: Prey accumulation curves (with 95% CIs) using species as the taxonomic unit for wahoo collected from the (A) nearshore and (B) offshore fisheries. The solid horizontal lines are the estimated species richness asymptote with 95% CIs (dotted horizontal lines).

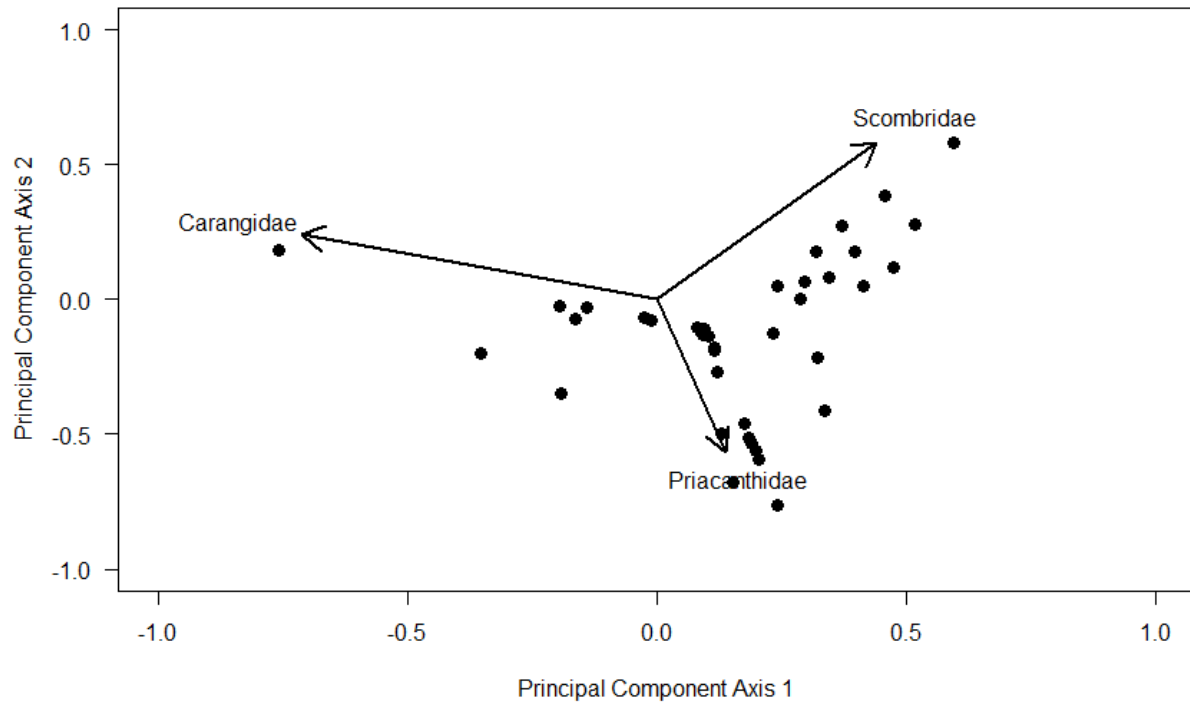


Figure 5: PCA bi-plot of the prey composition for wahoo collected from the nearshore fishery along the first two axes. Black dots are scores for individual predators. For clarity, only the loadings for the three most dominant prey families—Carangidae, Priacanthidae, and Scombridae—are shown.

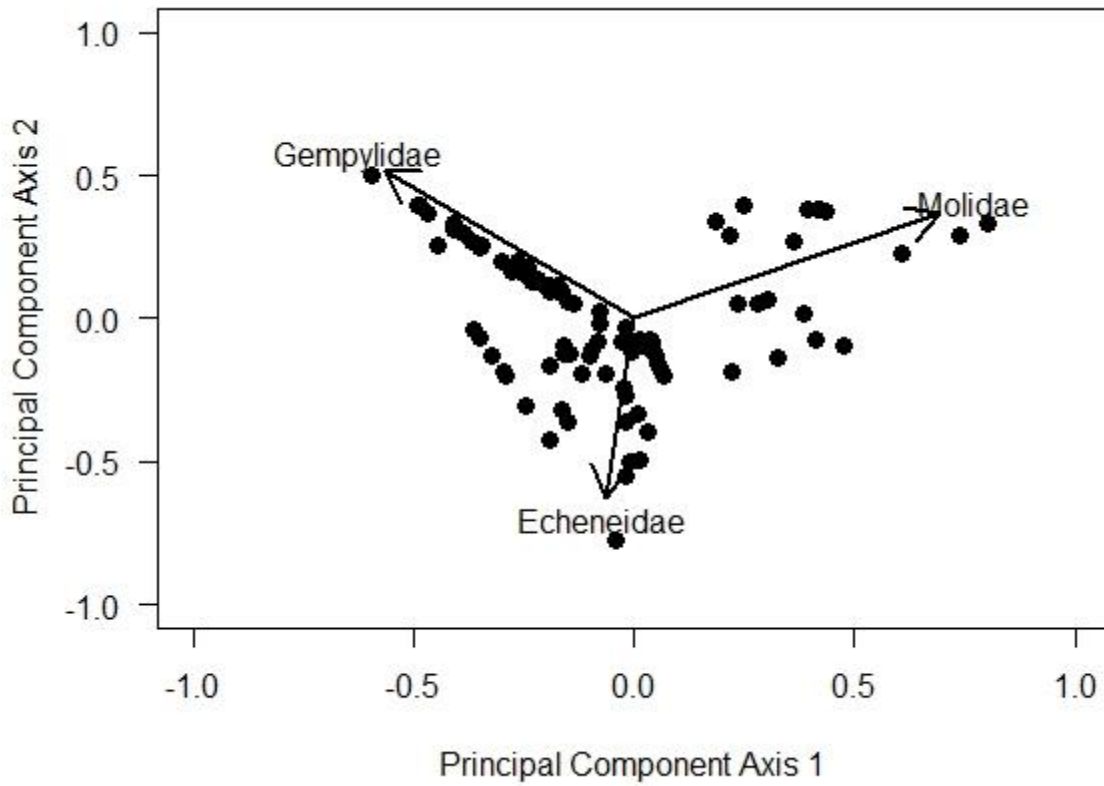


Figure 6: PCA bi-plot of the prey composition for wahoo collected from the offshore fishery. Open circles are scores of samples collected NE of the Hawaiian archipelago and open triangles are scores of samples collected southwest of the islands. For clarity, only the loadings for the three most dominant prey families—Gempylidae, Echeneidae, and Molidae—are shown.

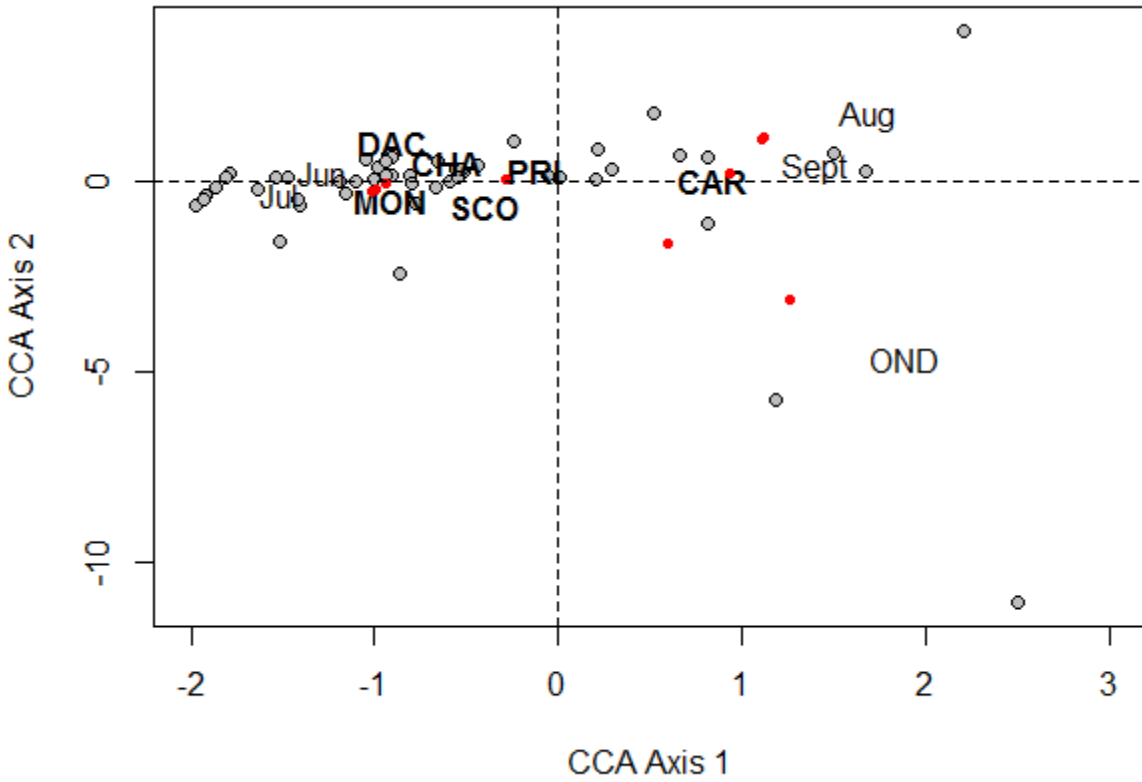


Figure 7: CCA bi-plots of the prey composition of wahoo collected from the offshore (left) and nearshore (right) fisheries. Grey open dots represent individual predator stomachs, and red solid dots are less frequent prey taxa. Centroid codes are formatted by month (regular text) and species (bold capital letters). DAC: Dactylopteridae; CHA: Chaetodontidae; MON: Monacanthidae; SCO: Scombridae; PRI: Priacanthidae; CAR: Carangidae; OND: Pooled samples from October, November, and December.

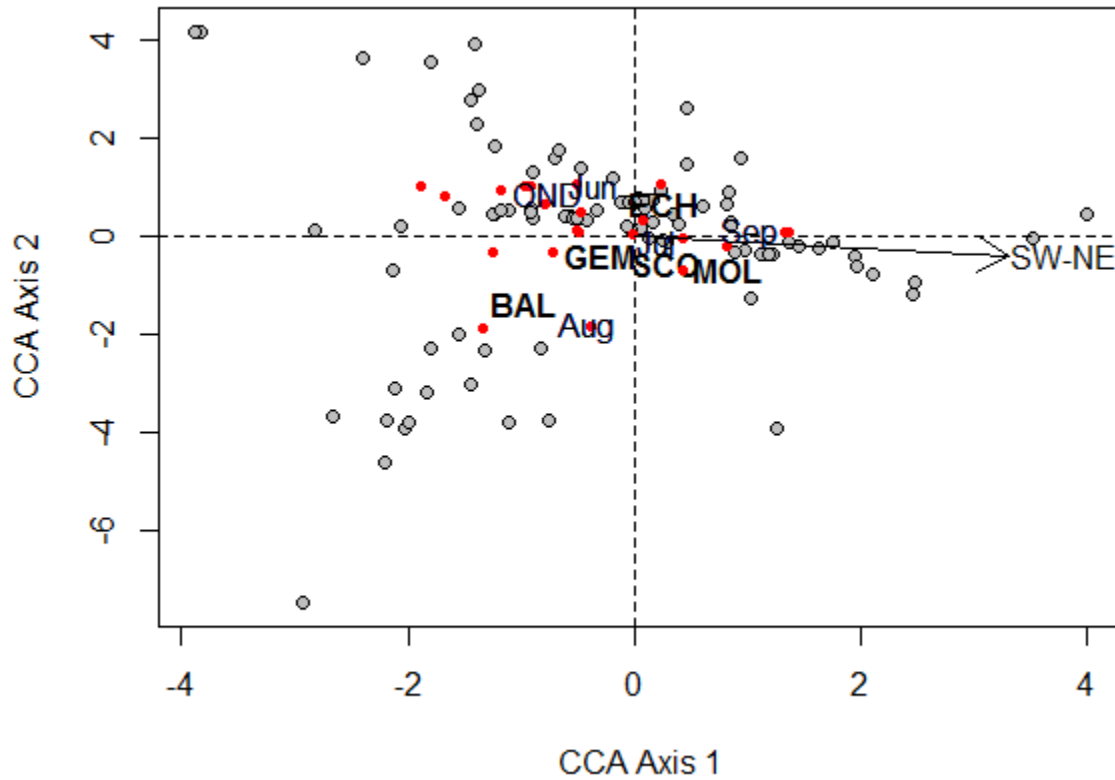


Figure 8: CCA bi-plots of the prey composition of wahoo collected from the offshore (left) and nearshore (right) fisheries. Grey open dots represent individual predator stomachs, and red solid dots are lesser observed prey taxa. Centroid codes are formatted by month (regular text) and species (bold capital letters). BAL: Balistidae; GEM: Gempylidae; SCO: Scombridae; ECH: Echeneidae; MOL: Molidae; OND: Pooled samples from October, November, and December.

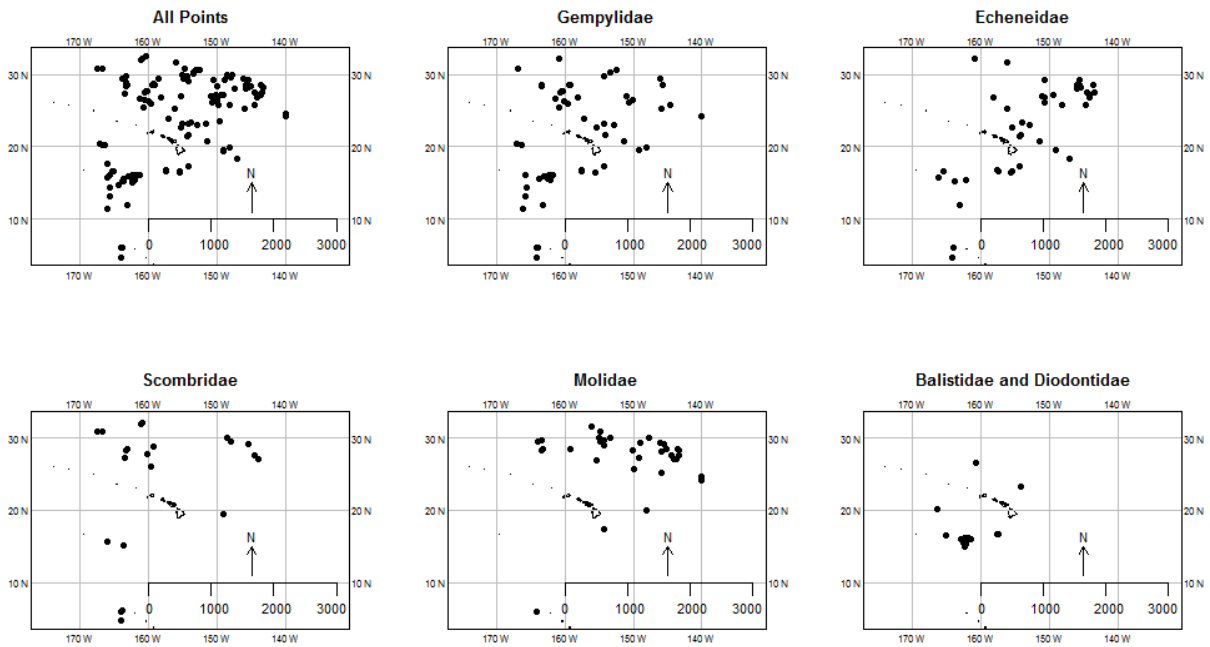


Figure 9: Locations (black dots) of dominant prey families observed in wahoo collected from the offshore fishery.



Figure 10: Stomach lining of a wahoo stomach with rows of circular ulcers created by *H. ventricosa*. Scale bars not given, but the diameter of the ulcer was usually approximately 5 mm.

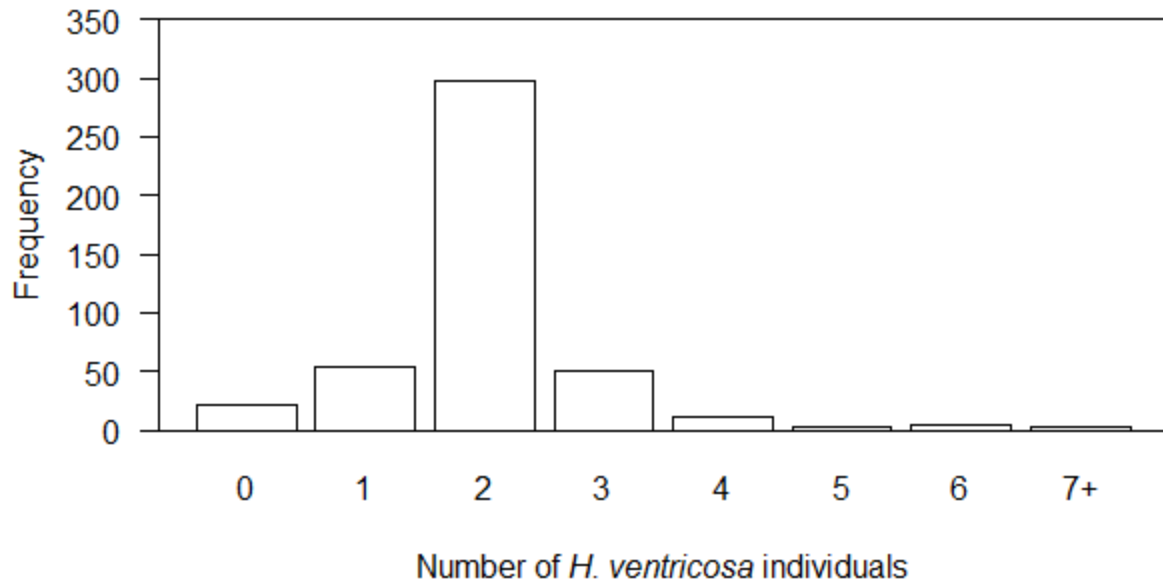


Figure 11: Frequency of *H. ventricosa* parasites in wahoo stomachs collected from the nearshore fishery. The tail of the distribution extends to 13 parasites.

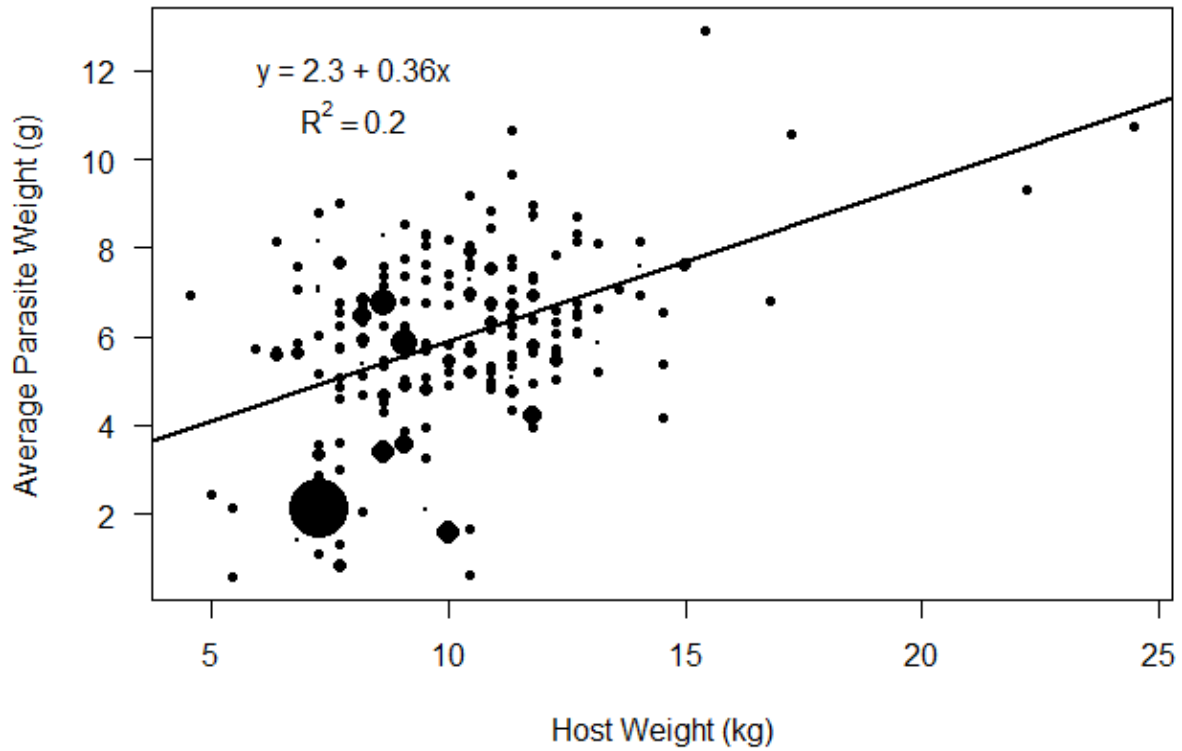


Figure 12: Average parasite weight plotted over host weight. The solid line is the estimated linear function as stated in the plot. The relative size of the dot denotes the sample size that was used to calculate a particular average value.

TABLES

Table 1: Total wahoo stomachs collected, number of stomachs with prey, and proportions of stomach fullness separated by fishery.

	Nearshore Fishery	Offshore Fishery
Total Stomachs	206	233
Stomachs with Prey	133	175
% Empty Stomachs	36%	25%
% Stomachs 0-50% Full	37%	52%
% Stomachs 50-100% Full	26%	23%

Table 2: Prey families with the five highest %GII values across sampling month for wahoo collected from the nearshore fishery.

June n = 39		July n = 35		August n = 24		September n = 27		OND n = 10	
	%GII		%GII		%GII		%GII		%GII
Priacanthidae	35.8	Scombridae	33.2	Carangidae	39.4	Carangidae	51.3	Carangidae	68.6
Scombridae	21.3	Gempylidae	16.6	Priacanthidae	29.5	Priacanthidae	13.7	Scombridae	13.9
Dactylopteridae	13.1	Chaetodontidae	14.7	Ommastrephidae	14.4	Acanthuridae	8.2	Moridae	12.6
Monacanthidae	12.0	Priacanthidae	12.3	Scombridae	13.1	Tetraodontidae	7.4	Balistidae	4.9
Carangidae	9.2	Carangidae	6.7	Alepisauridae	2.4	Scombridae	6.0		

Table 3: Prey families with the five highest %GII values across sampling month for wahoo collected from the offshore fishery.

June n = 40	%GII	July n = 41	%GII	August n = 32	%GII	September n = 38	%GII	OND n = 24	%GII
Gempylidae	20.08	Molidae	25.13	Molidae	19.42	Echeneidae	35.59	Gempylidae	31.33
Echeneidae	18.92	Gempylidae	21.06	Balistidae	18.82	Molidae	28.36	Scombridae	15.31
Scombridae	17.6	Scombridae	13.76	Gempylidae	18.64	Gempylidae	12.58	Diodontidae	13.76
Tetraodontidae	11.17	Echeneidae	10.98	Echeneidae	10.69	Bramidae	6.3	Echeneidae	13.09
Molidae	9.42	Balistidae	9.57	Scombridae	9.53	Argonautidae	3.36	Molidae	10.93

APPENDICES

Appendix 1: Prey table at species resolution for wahoo collected from the nearshore fishery. Bulk indices for unidentified fishes and squids are shown but were excluded from the bulk and compound indices calculations. A “+” in the last two columns indicate whether a prey taxon was identified visually (VIS) or using the molecular barcoding approach (MOL).

Taxon	%N	%W	%F	%IRI	VIS	MOL
<u>FISH</u>						
Aulopiformes						
Alepisauridae						
<i>Alepisaurus ferox</i>	0.24	0.43	0.85	< 0.1%		+
Perciformes						
Acanthuridae						
<i>Acanthurus nigrofuscus</i>	0.72	0.05	1.71	< 0.1%		+
<i>Acanthurus olivaceus</i>	0.24	0.11	0.85	< 0.1%		+
<i>Naso lituratus</i>	0.48	0.09	0.85	< 0.1%		+
<i>Naso unicornis</i>	2.63	0.46	2.56	0.31		+
Bramidae						
<i>Brama orcini</i>	1.2	0.72	3.42	0.26		+
<i>Brama</i> sp.	0.24	0.28	0.85	< 0.1%		+
Unidentified Bramidae	0.24	0.17	0.85	< 0.1%	+	
Carangidae						
<i>Caranx melampygus</i>	1.44	0.63	1.71	0.14		+
<i>Decapterus macarellus</i>	7.42	29.66	19.66	28.88	+	+
<i>Decapterus macrosoma</i>	1.44	2.46	5.13	0.79		+
<i>Decapterus maruadsi</i>	0.48	0.72	1.71	< 0.1%		+
<i>Decapterus</i> sp.	1.44	6.65	5.13	1.64	+	
<i>Selar crumenophthalmus</i>	0.48	0.48	1.71	< 0.1%		+
Chaetodontidae						
<i>Chaetodon kleinii</i>	8.61	0.55	6.84	2.48		+
<i>Chaetodon unimaculatus</i>	1.2	0.18	0.85	< 0.1%		+
<i>Forcipiger flavissimus</i>	0.48	0.09	1.71	< 0.1%	+	+
<i>Hemitaurichthys polylepis</i>	0.24	0.07	0.85	< 0.1%		+
<i>Heniochus acuminatus</i>	0.48	0.02	1.71	< 0.1%		+
Unidentified Chaetodontidae	2.15	0.28	2.56	0.25	+	
Gempylidae						
<i>Gempylus serpens</i>	0.72	0.72	1.71	< 0.1%		+
<i>Promethichthys prometheus</i>	5.5	3.49	5.13	1.83	+	+
Istiophoridae						
<i>Makaira nigricans</i>	0.24	0.22	0.85	< 0.1%		+
Lutjanidae						
<i>Lutjanus kasmira</i>	0.24	0.03	0.85	< 0.1%		+
Mullidae						

<i>Mulloidichthys vanicolensis</i>	0.48	0.16	0.85	< 0.1%		+
Priacanthidae						
<i>Heteropriacanthus cruentatus</i>	23.68	16.86	28.21	45.31	+	+
Unidentified Priacanthidae	0.24	0.06	0.85	< 0.1%	+	
Scombridae						
<i>Acanthocybium solandri</i>	4.07	2.26	6.84	1.72		+
<i>Auxis rochei</i>	1.67	11.83	5.13	2.74	+	+
<i>Auxis thazard</i>	0.24	0.24	0.85	< 0.1%	+	+
<i>Katsuwonus pelamis</i>	4.55	7.66	12.82	6.20	+	+
<i>Thunnus obesus</i>	0.48	1.01	1.71	0.10		+
Unidentified Scombridae	0.72	2.27	2.56	0.30	+	
Siganidae						
<i>Siganus spinus</i>	0.72	0.06	1.71	< 0.1%	+	
Scorpaeniformes						
Dactylopteridae						
<i>Dactyloptena orientalis</i>	8.85	1.15	7.69	3.05	+	+
Tetraodontiformes						
Balistidae						
<i>Melichthys vidua</i>	0.24	0.21	0.85	< 0.1%	+	+
<i>Sufflamen bursa</i>	0.48	0.03	1.71	< 0.1%		+
<i>Sufflamen fraenatum</i>	1.67	0.26	2.56	0.20		+
Molidae						
<i>Ranzania laevis</i>	0.48	1.19	1.71	0.11	+	+
Monacanthidae						
<i>Cantherhines pardalis</i>	1.2	0.17	0.85	< 0.1%		+
<i>Pervagor spilosoma</i>	5.5	0.87	5.13	1.29	+	+
Unidentified Monacanthidae	3.83	0.65	5.98	1.06	+	
Tetraodontidae						
<i>Lagocephalus lagocephalus</i>	0.24	0.28	0.85	< 0.1%	+	+
Unidentified Tetraodontidae	0.24	2.4	0.85	< 0.1%	+	
Unidentified Fish	10.69	4.14	15.07			
<u>CEPHALOPODS</u>						
Teuthida						
Ommastrephidae						
<i>Notodarus hawaiiensis</i>	1.67	1.77	3.42	0.47		+
<i>Sthenoteuthis oualaniensis</i>	0.24	0.1	0.85	< 0.1%		+
Unidentified Cephalopods	5.04	2.59	9.52			

Appendix 2: Prey table at species resolution for wahoo collected from the offshore fishery. Bulk indices for unidentified fishes and squids are shown but were excluded from the bulk and compound indices calculations. A “+” in the last two columns indicate whether a prey taxon was identified visually (VIS) or using the molecular barcoding approach (MOL).

Taxon	%N	%W	%F	%IRI	VIS	MOL
<u>FISH</u>						
Aulopiformes						
Alepisauridae						
<i>Alepisaurus ferox</i>	0.58	0.24	1.8	< 0.1%		+
Beloniformes						
Exocoetidae						
<i>Exocoetus monocirrhus</i>	1.16	0.78	2.4	0.14	+	
<i>Unidentified Exocoetidae</i>	0.19	0.2	0.6	< 0.1%	+	
Hemiramphidae						
<i>Oxyporhamphus micropterus</i>	1.16	0.77	1.8	< 0.1%		+
Berciformes						
Anoplogastridae						
<i>Anoplogaster cornuta</i>	0.39	0.09	1.2	< 0.1%		+
Berycidae						
<i>Beryx splendens</i>	0.19	0.14	0.6	< 0.1%		+
Lampriformes						
Lophotidae						
<i>Lophotus lacepede</i>	0.19	0.86	0.6	< 0.1%		+
Perciformes						
Bramidae						
<i>Brama dussumieri</i>	0.77	0.16	1.8	< 0.1%		+
<i>Brama orcini</i>	4.82	1.76	10.78	2.11		+
<i>Brama</i> sp.	0.19	0.07	0.6	< 0.1%		+
<i>Pteraclis aesticola</i>	0.58	0.23	1.8	< 0.1%		+
<i>Taractichthys steindachneri</i>	1.35	1.63	4.19	0.37		+
Carangidae						
<i>Decapterus macarellus</i>	0.39	0.16	1.2	< 0.1%		+
<i>Decapterus macrosoma</i>	0.19	0.2	0.6	< 0.1%		+
<i>Naucrates ductor</i>	0.19	0.01	0.6	< 0.1%		+
Chaetodontidae						
<i>Forcipiger flavissimus</i>	0.39	0.08	0.6	< 0.1%	+	
<i>Forcipiger longirostris</i>	0.39	0.08	0.6	< 0.1%	+	
<i>Hemitaurichthys thompsoni</i>	0.19	0.21	0.6	< 0.1%		+
<i>Heniochus acuminatus</i>	0.19	0	0.6	< 0.1%		+
Chiasmodontidae						
<i>Dysalotus alcocki</i>	2.12	0.35	6.59	0.48	+	+
Echeneidae						
<i>Remora brachyptera</i>	14.84	16.89	26.35	24.90	+	+

<i>Remora</i> sp.	1.73	1.52	2.99	0.29	+	
Gempylidae						
<i>Gempylus serpens</i>	19.27	12.45	41.92	39.60	+	+
<i>Lepidocybium flavobrunneum</i>	3.08	0.6	2.99	0.33	+	+
<i>Nealotus tripes</i>	2.12	0.89	4.79	0.43	+	+
<i>Ruvettus pretiosus</i>	0.58	0.1	0.6	< 0.1%		+
Nomeidae						
<i>Cubiceps baxteri</i>	0.39	0.08	1.2	< 0.1%		+
<i>Cubiceps paradoxus</i>	0.19	0.03	0.6	< 0.1%		+
<i>Cubiceps pauciradiatus</i>	0.19	0.06	0.6	< 0.1%		+
<i>Psenes cyanophrys</i>	1.35	0.49	2.4	0.13		+
<i>Psenes maculatus</i>	0.39	0.67	1.2	< 0.1%		+
Scombridae						
<i>Acanthocybium solandri</i>	2.5	1.03	4.79	0.50		+
<i>Auxis rochei</i>	0.19	2.09	0.6	< 0.1%	+	+
<i>Katsuwonus pelamis</i>	2.31	10.39	5.99	2.27	+	+
<i>Thunnus alalunga</i>	0.19	0.32	0.6	< 0.1%		+
<i>Thunnus obesus</i>	0.58	4.78	1.8	0.29		+
Scombrolabrachidae						
<i>Scombrolabrax heterolepis</i>	0.19	0.01	0.6	< 0.1%		+
Zanclidae						
<i>Zanclus cornutus</i>	0.19	0.01	0.6	< 0.1%		+
Scorpaeniformes						
Dactylopteridae						
<i>Dactyloptena orientalis</i>	0.19	0.03	0.6	< 0.1%	+	
Syngnathiformes						
Fistulariidae						
<i>Fistularia petimba</i>	0.19	0.03	0.6	< 0.1%		+
Tetraodontiformes						
Balistidae						
<i>Melichthys niger</i>	6.94	4.59	7.19	2.47	+	+
<i>Melichthys vidua</i>	0.39	0.38	1.2	< 0.1%		+
<i>Sufflamen fraenatum</i>	0.19	0.03	0.6	< 0.1%		+
Unidentified Balistidae	0.19	0.24	0.6	< 0.1%	+	
Diodontidae						
<i>Chilomycterus reticulatus</i>	0.19	0.1	0.6	< 0.1%		+
<i>Diodon</i> sp.	0.19	0.21	0.6	< 0.1%	+	
<i>Diodon hystrix</i>	0.19	0.1	0.6	< 0.1%		+
Unidentified Diodontidae	1.73	3.94	4.19	0.71	+	
Molidae						
<i>Masturus lanceolatus</i>	0.58	0.18	1.2	< 0.1%		+
<i>Ranzania laevis</i>	13.68	23.72	20.96	23.34	+	+
Tetraodontidae						
<i>Lagocephalus lagocephalus</i>	1.35	1.25	2.99	0.23		+

<i>Sphoeroides pachygaster</i>	0.19	0.47	0.6	< 0.1%		+
Unidentified Tetraodontidae	3.85	2.19	1.2	0.22		+
Unidentified Fish	6.81	1.84	12.2			
<u>CEPHALOPODS</u>						
Octopoda						
Argonautidae						
<i>Argonauta nodosa</i>	1.54	0.74	3.59	0.24		+
Unidentified Octopoda	0.19	0.26	0.6	< 0.1%		+
Oegopsida						
Ommastrephidae						
<i>Hyaloteuthis pelagica</i>	0.19	0.02	0.6	< 0.1%		+
Teuthida						
Enoploteuthidae						
<i>Enoploteuthis reticulata</i>	0.19	0.01	0.6	< 0.1%		+
Ommastrephidae						
<i>Sthenoteuthis oualaniensis</i>	1.54	0.81	4.79	0.34		+
Onychoteuthidae						
<i>Onykia sp.</i>	0.19	0.24	0.6	< 0.1%		+
Unidentified Cephalopods	2.96	1.53	9.88			

Appendix 3: Sequences identifications and percent similarities from the BOLD and GenBank databases. Sequence length and accession numbers from the GenBank output are also included. Records in bold were sequences used as internal validation.

	Species (BOLD)	% similarity (BOLD)	Species (GenBank)	ACCN (Genbank)	% similarity (GenBank)	Sequence Length
1	No Match		<i>Siganus spinus</i>	JQ432158.1	83	626
2	No Match		<i>Taractichthys steindachneri</i>	EF609477.1	87	213
3	No Match		<i>Acanthocybium solandri</i>	KC970444.1	89	301
4	No Match		<i>Acanthocybium solandri</i>	KC970444.1	90	266
5	No Match		<i>Brama orcini</i>	KF489508.1	90	619
6	No Match		<i>Katsuwonus pelamis</i>	KM605252.1	90	275
7	No Match		<i>Brama orcini</i>	KF489508.1	91	588
8	No Match		<i>Brama orcini</i>	KF489508.1	91	636
9	No Match		<i>Brama orcini</i>	KF489508.1	91	635
10	No Match		<i>Brama orcini</i>	KF489508.1	91	622
11	No Match		<i>Brama orcini</i>	KF489508.1	91	629
12	No Match		<i>Brama orcini</i>	KF489508.1	91	632
13	No Match		<i>Brama orcini</i>	KF489508.1	91	630
14	No Match		<i>Brama orcini</i>	KF489508.1	91	631
15	No Match		<i>Brama orcini</i>	KF489508.1	91	598
16	<i>Decapterus tabl</i>	100	<i>Decapterus maruadsi</i>	KJ004518.1	91	626
17	<i>Decapterus tabl</i>	100	<i>Decapterus maruadsi</i>	KM006769.1	91	634
18	No Match		<i>Brama orcini</i>	KF489508.1	92	268
19	No Match		<i>Brama orcini</i>	KF489508.1	92	344
20	No Match		<i>Brama sp.</i>	KM366110.1	92	436
21	<i>Decapterus tabl</i>	100	<i>Decapterus maruadsi</i>	JX261400.1	92	407
22	No Match		<i>Exocoetus monocirrhus</i>	JF493488.1	92	289
23	No Match		<i>Exocoetus monocirrhus</i>	JF493488.1	93	306

24	No Match		<i>Exocoetus monocirrhus</i>	JF493488.1	93	301
25	No Match		<i>Exocoetus monocirrhus</i>	JF493488.1	94	620
26	No Match		<i>Katsuwonus pelamis</i>	KM605252.1	94	273
27	No Match		<i>Acanthocybium solandri</i>	DQ107694.1	95	604
28	No Match		<i>Brama orcini</i>	KF489508.1	95	233
29	No Match		<i>Cubiceps paradoxus</i>	AB205442.1	95	632
30	No Match		<i>Dysalotus alcocki</i>	AP006814.1	95	233
31	No Match		<i>Fistularia petimba</i>	JQ365355.1	95	223
32	<i>Promethichthys prometheus</i>	99	<i>Promethichthys prometheus</i>	EU263807.1	95	581
33	<i>Acanthocybium solandri</i>	99	<i>Acanthocybium solandri</i>	KF009559.1	96	664
34	No Match		<i>Chaetodon kleinii</i>	JQ349876.1	96	194
35	No Match		<i>Heteropriacanthus cruentatus</i>	JQ431859.1	96	649
36	<i>Hyaloteuthis pelagica</i>	100	<i>Hyaloteuthis pelagica</i>	AB270947.1	96	286
37	No Match		<i>Oxyporhamphus micropterus</i>	JF494032.1	96	297
38	<i>Sthenoteuthis oualaniensis</i>	98	<i>Sthenoteuthis oualaniensis</i>	AB270943.1	96	273
39	<i>Acanthocybium solandri</i>	99	<i>Acanthocybium solandri</i>	JQ840407.1	97	414
40	<i>Acanthocybium solandri</i>	99	<i>Acanthocybium solandri</i>	GU225520.1	97	435
41	No Match		<i>Acanthocybium solandri</i>	GU225519.1	97	549
42	<i>Acanthocybium solandri</i>	100	<i>Acanthocybium solandri</i>	DQ835834.1	97	282

43	No Match		<i>Decapterus macarellus</i>	KM986880.1	97	258
44	No Match		<i>Enoploteuthis reticulata</i>	AF000039.1	97	304
45	No Match		<i>Gempylus serpens</i>	AP012502.1	97	632
46	No Match		<i>Katsuwonus pelamis</i>	KM605252.1	97	320
47	No Match		<i>Lagocephalus lagocephalus</i>	JQ681798.1	97	257
48	<i>Naso unicornis</i>	99	<i>Naso unicornis</i>	KF714984.1	97	189
49	<i>Nealotus tripes</i>	99	<i>Nealotus tripes</i>	AP012521.1	97	358
50	<i>Nealotus tripes</i>	99	<i>Nealotus tripes</i>	AP012521.1	97	212
51	No Match		<i>Nealotus tripes</i>	AP012521.1	97	301
52	<i>Notodarus hawaiiensis</i>	97	<i>Notodarus hawaiiensis</i>	AB270937.1	97	300
53	<i>Notodarus hawaiiensis</i>	98	<i>Notodarus hawaiiensis</i>	AB270937.1	97	299
54	<i>Notodarus hawaiiensis</i>	98	<i>Notodarus hawaiiensis</i>	AB270937.1	97	317
55	<i>Notodarus hawaiiensis</i>	98	<i>Notodarus hawaiiensis</i>	AB270937.1	97	309
56	<i>Onykia sp.</i>	98	<i>Onykia sp.</i>	AB264122.1	97	300
57	<i>Oxyporhamphus micropterus</i>	97	<i>Oxyporhamphus micropterus</i>	JF494032.1	97	278
58	<i>Oxyporhamphus micropterus</i>	97	<i>Oxyporhamphus micropterus</i>	JF494032.1	97	310
59	<i>Pervagor spilosoma</i>	98	<i>Pervagor spilosoma</i>	DQ521020.1	97	514
60	<i>Remora brachyptera</i>	100	<i>Remora brachyptera</i>	GU440496.1	97	276
61	No Match		<i>Remora brachyptera</i>	GU440496.1	97	469
62	No Match		<i>Remora brachyptera</i>	GU440496.1	97	176

63	<i>Thunnus obesus</i>	100	<i>Thunnus obesus</i>	KP975909.1	97	143
64	<i>Acanthocybium solandri</i>	100	<i>Acanthocybium solandri</i>	KF009559.1	98	592
65	<i>Acanthocybium solandri</i>	99	<i>Acanthocybium solandri</i>	GU225519.1	98	609
66	No Match		<i>Acanthocybium solandri</i>	GU225520.1	98	461
67	No Match		<i>Acanthocybium solandri</i>	GU225508.1	98	634
68	No Match		<i>Acanthurus nigrofuscus</i>	KC187743.1	98	276
69	<i>Anoplogaster cornuta</i>	99	<i>Anoplogaster cornuta</i>	JQ353973.1	98	586
70	<i>Argonauta nodosa</i>	99	<i>Argonauta nodosa</i>	AY557517.1	98	252
71	<i>Argonauta nodosa</i>	98	<i>Argonauta nodosa</i>	AY557517.1	98	302
72	No Match		<i>Brama orcini</i>	KF489508.1	98	639
73	<i>Chaetodon kleinii</i>	99	<i>Chaetodon kleinii</i>	HQ561505.1	98	565
74	<i>Chaetodon unimaculatus</i>	100	<i>Chaetodon unimaculatus</i>	JQ431594.1	98	327
75	<i>Cubiceps baxteri</i>	98	<i>Cubiceps baxteri</i>	DQ107605.1	98	443
76	<i>Cubiceps baxteri</i>	98	<i>Cubiceps baxteri</i>	DQ107605.1	98	456
77	No Match		<i>Dactyloptena orientalis</i>	KJ968015.1	98	377
78	<i>Decapterus sp.</i>	100	<i>Decapterus macarellus</i>	KM986880.1	98	616
79	<i>Decapterus macarellus</i>	100	<i>Decapterus macarellus</i>	KM986880.1	98	287
80	No Match		<i>Decapterus macarellus</i>	KM986880.1	98	639
81	No Match		<i>Dysalotus alcocki</i>	AP006814.1	98	277
82	No Match		<i>Dysalotus alcocki</i>	AP006814.1	98	272

83	No Match		<i>Forcipiger flavissimus</i>	KF929889.1	98	245
84	No Match		<i>Gempylus serpens</i>	AP012502.1	98	480
85	<i>Gempylus serpens</i>	100	<i>Gempylus serpens</i>	AP012502.1	98	638
86	<i>Gempylus serpens</i>	99	<i>Gempylus serpens</i>	AP012502.1	98	566
87	No Match		<i>Gempylus serpens</i>	AP012502.1	98	465
88	No Match		<i>Gempylus serpens</i>	AP012502.1	98	275
89	No Match		<i>Gempylus serpens</i>	AP012502.1	98	286
90	No Match		<i>Gempylus serpens</i>	AP012502.1	98	587
91	No Match		<i>Katsuwonus pelamis</i>	KM605252.1	98	608
92	<i>Lagocephalus lagocephalus</i>	100	<i>Lagocephalus lagocephalus</i>	AP011933.1	98	637
93	No Match		<i>Melichthys niger</i>	JQ431903.1	98	313
94	<i>Melichthys niger</i>	100	<i>Melichthys niger</i>	JQ841279.1	98	392
95	No Match		<i>Mulloidichthys vanicolensis</i>	KF489653.1	98	518
96	No Match		<i>Mulloidichthys vanicolensis</i>	KF489653.1	98	294
97	<i>Naso lituratus</i>	100	<i>Naso lituratus</i>	KF714982.1	98	153
98	<i>Nealotus tripes</i>	100	<i>Nealotus tripes</i>	AP012521.1	98	628
99	<i>Nealotus tripes</i>	100	<i>Nealotus tripes</i>	AP012521.1	98	644
100	<i>Nealotus tripes</i>	100	<i>Nealotus tripes</i>	AP012521.1	98	628
101	No Match		<i>Nealotus tripes</i>	AP012521.1	98	625
102	<i>Nealotus tripes</i>	99	<i>Nealotus tripes</i>	AP012521.1	98	512

103	<i>Notodarus hawaiiensis</i>	98	<i>Notodarus hawaiiensis</i>	AB270937.1	98	283
104	No Match		<i>Notodarus hawaiiensis</i>	AB270937.1	98	294
105	<i>Notodarus hawaiiensis</i>	98	<i>Notodarus hawaiiensis</i>	AB270937.1	98	281
106	No Match		<i>Pervagor spilosoma</i>	DQ521020.1	98	642
107	No Match		<i>Promethichthys prometheus</i>	EU263807.1	98	432
108	No Match		<i>Promethichthys prometheus</i>	EU263807.1	98	297
109	No Match		<i>Psenes maculatus</i>	AB205444.1	98	647
110	No Match		<i>Pteraclis aesticola</i>	AP012499.1	98	500
111	No Match		<i>Ranzania laevis</i>	KJ768291.1	98	290
112	<i>Ranzania laevis</i>	100	<i>Ranzania laevis</i>	KF025666.1	98	401
113	No Match		<i>Ranzania laevis</i>	KJ768291.1	98	424
114	No Match		<i>Ranzania laevis</i>	KJ768291.1	98	309
115	<i>Remora brachyptera</i>	100	<i>Remora brachyptera</i>	GU440496.1	98	595
116	No Match		<i>Remora brachyptera</i>	GU440496.1	98	292
117	No Match		<i>Remora brachyptera</i>	GU440496.1	98	571
118	No Match		<i>Remora brachyptera</i>	GU440496.1	98	552
119	No Match		<i>Remora brachyptera</i>	GU440496.1	98	555
120	<i>Remora brachyptera</i>	99	<i>Remora brachyptera</i>	GU440496.1	98	601
121	No Match		<i>Remora brachyptera</i>	GU440496.1	98	289
122	No Match		<i>Remora brachyptera</i>	GU440496.1	98	631
123	No Match		<i>Remora brachyptera</i>	GU440496.1	98	481

124	<i>Sthenoteuthis oualaniensis</i>	99	<i>Sthenoteuthis oualaniensis</i>	DQ885828.1	98	262
125	<i>Sthenoteuthis oualaniensis</i>	99	<i>Sthenoteuthis oualaniensis</i>	EU660576.1	98	303
126	<i>Sthenoteuthis oualaniensis</i>	99	<i>Sthenoteuthis oualaniensis</i>	AB270943.1	98	303
127	<i>Sthenoteuthis oualaniensis</i>	100	<i>Sthenoteuthis oualaniensis</i>	DQ885828.1	98	300
128	<i>Sthenoteuthis oualaniensis</i>	99	<i>Sthenoteuthis oualaniensis</i>	AB270943.1	98	257
129	No Match		<i>Sufflamen fraenatum</i>	AP004456.1	98	628
130	<i>Sufflamen fraenatum</i>	100	<i>Sufflamen fraenatum</i>	AP004456.1	98	331
131	No Match		<i>Sufflamen fraenatum</i>	AP004456.1	98	645
132	No Match		<i>Taractichthys steindachneri</i>	EF609477.1	98	573
133	<i>Zanclus cornutus</i>	99	<i>Zanclus cornutus</i>	KC623652.1	98	599
134	<i>Acanthocybium solandri</i>	100	<i>Acanthocybium solandri</i>	JQ840407.1	99	622
135	<i>Acanthocybium solandri</i>	100	<i>Acanthocybium solandri</i>	GU225520.1	99	468
136	No Match		<i>Acanthocybium solandri</i>	GU225508.1	99	484
137	<i>Acanthocybium solandri</i>	100	<i>Acanthocybium solandri</i>	DQ107694.1	99	597
138	<i>Acanthocybium solandri</i>	100	<i>Acanthocybium solandri</i>	GU440206.1	99	483
139	<i>Acanthocybium solandri</i>	100	<i>Acanthocybium solandri</i>	KF009559.1	99	280
140	No Match		<i>Acanthocybium solandri</i>	GU225520.1	99	446

141	<i>Acanthocybium solandri</i>	100	<i>Acanthocybium solandri</i>	KF009559.1	99	636
142	<i>Acanthocybium solandri</i>	100	<i>Acanthocybium solandri</i>	GU225519.1	99	597
143	<i>Acanthocybium solandri</i>	100	<i>Acanthocybium solandri</i>	GU225508.1	99	602
144	No Match		<i>Acanthocybium solandri</i>	JQ840406.1	99	568
145	<i>Acanthocybium solandri</i>	100	<i>Acanthocybium solandri</i>	JQ840407.1	99	574
146	<i>Acanthurus nigrofuscus</i>	100	<i>Acanthurus nigrofuscus</i>	KC187767.1	99	627
147	<i>Acanthurus olivaceus</i>	100	<i>Acanthurus olivaceus</i>	KJ967832.1	99	580
148	No Match		<i>Alepisaurus ferox</i>	KF929581.1	99	361
149	<i>Alepisaurus ferox</i>	100	<i>Alepisaurus ferox</i>	JQ353961.1	99	632
150	<i>Alepisaurus ferox</i>	100	<i>Alepisaurus ferox</i>	AP004211.1	99	312
151	No Match		<i>Alepisaurus ferox</i>	AP004211.1	99	435
152	No Match		<i>Anoplogaster cornuta</i>	JQ353973.1	99	517
153	No Match		<i>Anoplogaster cornuta</i>	JF965514.1	99	374
154	<i>Argonauta nodosa</i>	100	<i>Argonauta nodosa</i>	AY557517.1	99	289
155	<i>Argonauta nodosa</i>	99	<i>Argonauta nodosa</i>	AY557517.1	99	303
156	<i>Argonauta nodosa</i>	100	<i>Argonauta nodosa</i>	AY557517.1	99	298
157	<i>Argonauta nodosa</i>	99	<i>Argonauta nodosa</i>	AY557517.1	99	299
158	<i>Auxis rochei</i>	100	<i>Auxis rochei</i>	KM651784.1	99	618
159	No Match		<i>Auxis rochei</i>	KM651784.1	99	617
160	<i>Auxis rochei</i>	100	<i>Auxis rochei</i>	AB103468.1	99	643
161	No Match		<i>Auxis rochei</i>	FJ226517.1	99	344
162	<i>Auxis rochei</i>	100	<i>Auxis rochei</i>	KM651784.1	99	372
163	No Match		<i>Auxis rochei</i>	KM651784.1	99	647

164	No Match		<i>Auxis thazard</i>	AB105447.1	99	617
165	No Match		<i>Beryx splendens</i>	AP002939.1	99	631
166	<i>Brama dussumieri</i>		<i>Brama dussumieri</i>	KF461140.1	99	580
167	<i>Brama dussumieri</i>		<i>Brama dussumieri</i>	KJ020208.1	99	484
168	No Match		<i>Brama dussumieri</i>	KJ020208.1	99	546
169	<i>Brama orcini</i>	100	<i>Brama orcini</i>	KF489508.1	99	641
170	<i>Brama orcini</i>	100	<i>Brama orcini</i>	KF489508.1	99	634
171	No Match		<i>Brama orcini</i>	KF489508.1	99	626
172	<i>Brama orcini</i>	100	<i>Brama orcini</i>	KF489508.1	99	583
173	<i>Brama orcini</i>	100	<i>Brama orcini</i>	KF489508.1	99	633
174	No Match		<i>Brama orcini</i>	KF489508.1	99	624
175	No Match		<i>Brama orcini</i>	KF489508.1	99	635
176	No Match		<i>Brama orcini</i>	KF489508.1	99	633
177	No Match		<i>Brama orcini</i>	KF489508.1	99	627
178	No Match		<i>Brama orcini</i>	KF489508.1	99	580
179	<i>Cantherhines pardalis</i>	100	<i>Cantherhines pardalis</i>	KF027512.1	99	623
180	No Match		<i>Caranx melampygus</i>	KC970375.1	99	376
181	No Match		<i>Caranx melampygus</i>	KF649843.1	99	632
182	No Match		<i>Caranx melampygus</i>	KF649843.1	99	640
183	No Match		<i>Caranx melampygus</i>	KC970375.1	99	541
184	<i>Caranx melampygus</i>	100	<i>Caranx melampygus</i>	KF649843.1	99	647
185	No Match		<i>Chaetodon kleinii</i>	HQ561505.1	99	633
186	<i>Chaetodon kleinii</i>	100	<i>Chaetodon kleinii</i>	HQ561505.1	99	588
187	No Match		<i>Chaetodon kleinii</i>	JQ349876.1	99	399

188	No Match		<i>Chaetodon kleinii</i>	JQ349876.1	99	435
189	<i>Chaetodon kleinii</i>	100	<i>Chaetodon kleinii</i>	HQ561505.1	99	404
190	<i>Chaetodon kleinii</i>	100	<i>Chaetodon kleinii</i>	HQ561505.1	99	587
191	<i>Chilomycterus reticulatus</i>	100	<i>Chilomycterus reticulatus</i>	HQ010089.1	99	495
192	<i>Cubiceps pauciradiatus</i>	100	<i>Cubiceps pauciradiatus</i>	KJ968014.1	99	176
193	No Match		<i>Dactyloptena orientalis</i>	KJ968015.1	99	315
194	<i>Dactyloptena orientalis</i>	100	<i>Dactyloptena orientalis</i>	KJ968015.1	99	598
195	<i>Dactyloptena orientalis</i>	100	<i>Dactyloptena orientalis</i>	KJ968015.1	99	601
196	<i>Dactyloptena orientalis</i>	100	<i>Dactyloptena orientalis</i>	KJ968015.1	99	624
197	<i>Decapterus macarellus</i>	100	<i>Decapterus macarellus</i>	KM986880.1	99	612
198	No Match		<i>Decapterus macarellus</i>	KM986880.1	99	355
199	<i>Decapterus sp.</i>	100	<i>Decapterus macarellus</i>	KM986880.1	99	641
200	<i>Decapterus macarellus</i>	100	<i>Decapterus macarellus</i>	KM986880.1	99	265
201	No Match		<i>Decapterus macarellus</i>	KM986880.1	99	634
202	<i>Decapterus macarellus</i>	100	<i>Decapterus macarellus</i>	KM986880.1	99	529
203	<i>Decapterus macarellus</i>	100	<i>Decapterus macarellus</i>	KM986880.1	99	580
204	<i>Decapterus macarellus</i>	100	<i>Decapterus macarellus</i>	KM986880.1	99	221
205	<i>Decapterus macarellus</i>	99	<i>Decapterus macarellus</i>	KM986880.1	99	536
206	<i>Decapterus macarellus</i>	100	<i>Decapterus macarellus</i>	KM986880.1	99	581

207	<i>Decapterus macarellus</i>	99	<i>Decapterus macarellus</i>	KF009585.1	99	462
208	No Match		<i>Decapterus macarellus</i>	KM986880.1	99	592
209	No Match		<i>Decapterus macarellus</i>	KM986880.1	99	636
210	<i>Decapterus sp.</i>	100	<i>Decapterus macarellus</i>	KM986880.1	99	635
211	No Match		<i>Decapterus macarellus</i>	KM986880.1	99	622
212	No Match		<i>Decapterus macarellus</i>	KM986880.1	99	590
213	No Match		<i>Decapterus macarellus</i>	KM986880.1	99	472
214	<i>Decapterus macarellus</i>	100	<i>Decapterus macarellus</i>	KM986880.1	99	612
215	<i>Decapterus macarellus</i>	100	<i>Decapterus macarellus</i>	KM986880.1	99	553
216	No Match		<i>Decapterus macarellus</i>	KM986880.1	99	615
217	No Match		<i>Decapterus macarellus</i>	KM986880.1	99	440
218	No Match		<i>Decapterus macarellus</i>	KM986880.1	99	507
219	No Match		<i>Decapterus macarellus</i>	KM986880.1	99	417
220	No Match		<i>Decapterus macrosoma</i>	KC970467.1	99	437
221	No Match		<i>Decapterus macrosoma</i>	KC970467.1	99	639
222	<i>Decapterus macrosoma</i>	100	<i>Decapterus macrosoma</i>	KF841444.1	99	648
223	<i>Decapterus macrosoma</i>	100	<i>Decapterus macrosoma</i>	KC970467.1	99	644
224	<i>Decapterus macrosoma</i>	100	<i>Decapterus macrosoma</i>	KF841444.1	99	644
225	<i>Decapterus macrosoma</i>	100	<i>Decapterus macrosoma</i>	KF841444.1	99	652
226	<i>Diodon hystrix</i>	100	<i>Diodon hystrix</i>	JQ842830.1	99	592

227	<i>Diodon hystrix</i>	100	<i>Diodon hystrix</i>	JQ842830.1	99	629
228	<i>Diodon hystrix</i>	99	<i>Diodon hystrix</i>	KF025664.1	99	282
229	<i>Diodon hystrix</i>	100	<i>Diodon hystrix</i>	JQ842830.1	99	588
230	No Match		<i>Dysalotus alcocki</i>	AP006814.1	99	639
231	No Match		<i>Dysalotus alcocki</i>	AP006814.1	99	637
232	No Match		<i>Dysalotus alcocki</i>	AP006814.1	99	553
233	No Match		<i>Dysalotus alcocki</i>	AP006814.1	99	342
234	No Match		<i>Forcipiger flavissimus</i>	JQ431744.1	99	633
235	<i>Forcipiger longirostris</i>	100	<i>Forcipiger longirostris</i>	JQ431745.1	99	632
236	No Match		<i>Forcipiger longirostris</i>	JQ431745.1	99	232
237	<i>Gempylus serpens</i>	100	<i>Gempylus serpens</i>	AP012502.1	99	643
238	<i>Gempylus serpens</i>	100	<i>Gempylus serpens</i>	AP012502.1	99	637
239	<i>Gempylus serpens</i>	100	<i>Gempylus serpens</i>	AP012502.1	99	337
240	<i>Gempylus serpens</i>	100	<i>Gempylus serpens</i>	AP012502.1	99	581
241	<i>Gempylus serpens</i>	100	<i>Gempylus serpens</i>	AP012502.1	99	634
242	No Match		<i>Gempylus serpens</i>	AP012502.1	99	625
243	No Match		<i>Gempylus serpens</i>	AP012502.1	99	500
244	No Match		<i>Gempylus serpens</i>	AP012502.1	99	351
245	No Match		<i>Gempylus serpens</i>	AP012502.1	99	584
246	No Match		<i>Gempylus serpens</i>	AP012502.1	99	377

247	<i>Gempylus serpens</i>	100	<i>Gempylus serpens</i>	AP012502.1	99	634
248	<i>Gempylus serpens</i>	100	<i>Gempylus serpens</i>	AP012502.1	99	632
249	No Match		<i>Gempylus serpens</i>	AP012502.1	99	630
250	<i>Gempylus serpens</i>	100	<i>Gempylus serpens</i>	AP012502.1	99	505
251	No Match		<i>Gempylus serpens</i>	AP012502.1	99	203
252	<i>Gempylus serpens</i>	100	<i>Gempylus serpens</i>	AP012502.1	99	278
253	<i>Gempylus serpens</i>	100	<i>Gempylus serpens</i>	AP012502.1	99	539
254	<i>Gempylus serpens</i>	100	<i>Gempylus serpens</i>	AP012502.1	99	571
255	<i>Gempylus serpens</i>	100	<i>Gempylus serpens</i>	AP012502.1	99	498
256	<i>Gempylus serpens</i>	100	<i>Gempylus serpens</i>	AP012502.1	99	629
257	<i>Gempylus serpens</i>	100	<i>Gempylus serpens</i>	AP012502.1	99	307
258	No Match		<i>Gempylus serpens</i>	AP012502.1	99	629
259	<i>Gempylus serpens</i>	100	<i>Gempylus serpens</i>	AP012502.1	99	658
260	No Match		<i>Gempylus serpens</i>	AP012502.1	99	447
261	<i>Gempylus serpens</i>	100	<i>Gempylus serpens</i>	AP012502.1	99	414
262	No Match		<i>Gempylus serpens</i>	AP012502.1	99	289
263	No Match		<i>Hemitaurichthys polylepis</i>	JF435019.1	99	608
264	No Match		<i>Heniochus acuminatus</i>	JQ431852.1	99	526
265	No Match		<i>Heniochus acuminatus</i>	AP006005.1	99	650

266	<i>Heteropriacanthus cruentatus</i>	99	<i>Heteropriacanthus cruentatus</i>	JQ431859.1	99	239
267	<i>Hyaloteuthis pelagica</i>	100	<i>Hyaloteuthis pelagica</i>	AB270947.1	99	293
268	<i>Katsuwonus pelamis</i>	100	<i>Katsuwonus pelamis</i>	DQ107683.1	99	610
269	<i>Katsuwonus pelamis</i>	100	<i>Katsuwonus pelamis</i>	DQ107683.1	99	567
270	<i>Katsuwonus pelamis</i>	100	<i>Katsuwonus pelamis</i>	KF597042.1	99	556
271	<i>Katsuwonus pelamis</i>	100	<i>Katsuwonus pelamis</i>	KF597042.1	99	599
272	<i>Katsuwonus pelamis</i>	100	<i>Katsuwonus pelamis</i>	KM605252.1	99	640
273	<i>Katsuwonus pelamis</i>	100	<i>Katsuwonus pelamis</i>	KJ134898.1	99	627
274	<i>Katsuwonus pelamis</i>	100	<i>Katsuwonus pelamis</i>	KF597042.1	99	628
275	<i>Katsuwonus pelamis</i>	100	<i>Katsuwonus pelamis</i>	KF597042.1	99	621
276	No Match		<i>Katsuwonus pelamis</i>	KM605252.1	99	240
277	No Match		<i>Katsuwonus pelamis</i>	KF528381.1	99	613
278	No Match		<i>Katsuwonus pelamis</i>	KM605252.1	99	627
279	No Match		<i>Katsuwonus pelamis</i>	KM605252.1	99	287
280	No Match		<i>Katsuwonus pelamis</i>	KM605252.1	99	275
281	No Match		<i>Katsuwonus pelamis</i>	KM605252.1	99	640
282	<i>Katsuwonus pelamis</i>	100	<i>Katsuwonus pelamis</i>	KJ134897.1	99	547
283	<i>Katsuwonus pelamis</i>	100	<i>Katsuwonus pelamis</i>	KJ134897.1	99	553
284	<i>Katsuwonus pelamis</i>	100	<i>Katsuwonus pelamis</i>	JN644292.1	99	447

285	<i>Katsuwonus pelamis</i>	100	<i>Katsuwonus pelamis</i>	KM605252.1	99	577
286	<i>Katsuwonus pelamis</i>	100	<i>Katsuwonus pelamis</i>	KM055418.1	99	322
287	No Match		<i>Katsuwonus pelamis</i>	EU014260.1	99	596
288	No Match		<i>Katsuwonus pelamis</i>	EU014260.1	99	283
289	No Match		<i>Katsuwonus pelamis</i>	KM605252.1	99	280
290	<i>Lagocephalus lagocephalus</i>	100	<i>Lagocephalus lagocephalus</i>	JF730881.1	99	393
291	No Match		<i>Lagocephalus lagocephalus</i>	JQ681798.1	99	605
292	<i>Lepidocybium flavobrunneum</i>	100	<i>Lepidocybium flavobrunneum</i>	HM007724.1	99	633
293	<i>Lepidocybium flavobrunneum</i>	100	<i>Lepidocybium flavobrunneum</i>	HM007724.1	99	643
294	<i>Lepidocybium flavobrunneum</i>	100	<i>Lepidocybium flavobrunneum</i>	HM007724.1	99	639
295	<i>Lepidocybium flavobrunneum</i>	100	<i>Lepidocybium flavobrunneum</i>	HM007724.1	99	586
296	<i>Lepidocybium flavobrunneum</i>	100	<i>Lepidocybium flavobrunneum</i>	HM007724.1	99	646
297	<i>Lepidocybium flavobrunneum</i>	100	<i>Lepidocybium flavobrunneum</i>	HM007724.1	99	472

298	<i>Lepidocybium flavobrunneum</i>	100	<i>Lepidocybium flavobrunneum</i>	AP012519.1	99	607
299	No Match		<i>Lophotus lacepede</i>	KF930060.1	99	377
300	<i>Lutjanus kasmira</i>	99	<i>Lutjanus kasmira</i>	KC187825.1	99	563
301	<i>Makaira nigricans</i>	99	<i>Makaira nigricans</i>	KJ968143.1	99	538
302	No Match		<i>Masturus lanceolatus</i>	AP006239.1	99	624
303	<i>Masturus lanceolatus</i>	100	<i>Masturus lanceolatus</i>	AP006239.1	99	603
304	<i>Melichthys niger</i>	100	<i>Melichthys niger</i>	JQ841279.1	99	599
305	No Match		<i>Melichthys niger</i>	JQ841719.1	99	624
306	<i>Melichthys niger</i>	100	<i>Melichthys niger</i>	JQ841719.1	99	627
307	<i>Melichthys niger</i>	100	<i>Melichthys niger</i>	JQ841279.1	99	445
308	<i>Melichthys niger</i>	100	<i>Melichthys niger</i>	JQ841279.1	99	597
309	<i>Melichthys niger</i>	100	<i>Melichthys niger</i>	JQ841279.1	99	588
310	<i>Melichthys niger</i>	100	<i>Melichthys niger</i>	JQ841719.1	99	647
311	<i>Melichthys niger</i>	100	<i>Melichthys niger</i>	JQ841719.1	99	656
312	<i>Melichthys niger</i>	100	<i>Melichthys niger</i>	JQ841719.1	99	639
313	<i>Melichthys niger</i>	100	<i>Melichthys niger</i>	JQ841719.1	99	656
314	No Match		<i>Melichthys vidua</i>	AP009207.1	99	645
315	<i>Naso lituratus</i>	100	<i>Naso lituratus</i>	KF714982.1	99	625
316	No Match		<i>Naucrates ductor</i>	JF493967.1	99	636
317	<i>Pervagor spilosoma</i>	99	<i>Pervagor spilosoma</i>	DQ521020.1	99	589

318	<i>Pervagor spilosoma</i>	100	<i>Pervagor spilosoma</i>	DQ521020.1	99	624
319	No Match		<i>Promethichthys prometheus</i>	EU263807.1	99	477
320	<i>Promethichthys prometheus</i>	100	<i>Promethichthys prometheus</i>	EU263807.1	99	459
321	No Match		<i>Promethichthys prometheus</i>	EU263807.1	99	224
322	<i>Promethichthys prometheus</i>	99	<i>Promethichthys prometheus</i>	EU263807.1	99	652
323	<i>Promethichthys prometheus</i>	100	<i>Promethichthys promethus</i>	EU263807.1	99	648
324	No Match		<i>Promethichthys promethus</i>	EU263807.1	99	70
325	<i>Psenes cyanophrys</i>	100	<i>Psenes cyanophrys</i>	AP011067.1	99	635
326	<i>Psenes cyanophrys</i>	100	<i>Psenes cyanophrys</i>	KJ020210.1	99	615
327	No Match		<i>Psenes maculatus</i>	AB205444.1	99	636
328	No Match		<i>Psenes cyanophrys</i>	AP011067.1	99	634
329	<i>Pteraclis aesticola</i>	98	<i>Pteraclis aesticola</i>	AP012499.1	99	588
330	<i>Pteraclis aesticola</i>	98	<i>Pteraclis aesticola</i>	AP012499.1	99	630
331	<i>Ranzania laevis</i>	100	<i>Ranzania laevis</i>	KF027509.1	99	631
332	No Match		<i>Ranzania laevis</i>	KF025666.1	99	433
333	No Match		<i>Ranzania laevis</i>	AP006047.1	99	647
334	<i>Ranzania laevis</i>	100	<i>Ranzania laevis</i>	KF027509.1	99	652
335	<i>Ranzania laevis</i>	100	<i>Ranzania laevis</i>	KF025666.1	99	519
336	No Match		<i>Ranzania laevis</i>	KJ768291.1	99	246
337	No Match		<i>Ranzania laevis</i>	KF025666.1	99	517

338	<i>Ranzania laevis</i>	100	<i>Ranzania laevis</i>	KF025666.1	99	572
339	No Match		<i>Ranzania laevis</i>	KF025666.1	99	317
340	No Match		<i>Ranzania laevis</i>	KF027509.1	99	637
341	<i>Remora brachyptera</i>	100	<i>Remora brachyptera</i>	GU440496.1	99	467
342	<i>Remora brachyptera</i>	100	<i>Remora brachyptera</i>	GU440496.1	99	627
343	<i>Remora brachyptera</i>	100	<i>Remora brachyptera</i>	GU440496.1	99	533
344	<i>Remora brachyptera</i>	100	<i>Remora brachyptera</i>	GU440496.1	99	634
345	<i>Remora brachyptera</i>	100	<i>Remora brachyptera</i>	GU440496.1	99	631
346	<i>Remora brachyptera</i>	100	<i>Remora brachyptera</i>	GU440496.1	99	572
347	No Match		<i>Remora brachyptera</i>	GU440496.1	99	645
348	No Match		<i>Remora brachyptera</i>	GU440496.1	99	552
349	No Match		<i>Remora brachyptera</i>	GU440496.1	99	366
350	<i>Remora brachyptera</i>	100	<i>Remora brachyptera</i>	GU440496.1	99	630
351	No Match		<i>Remora brachyptera</i>	GU440496.1	99	633
352	No Match		<i>Remora brachyptera</i>	GU440496.1	99	607
353	<i>Remora brachyptera</i>	100	<i>Remora brachyptera</i>	GU440496.1	99	612
354	No Match		<i>Remora brachyptera</i>	U440496.1	99	290
355	No Match		<i>Remora brachyptera</i>	GU440496.1	99	369
356	<i>Remora brachyptera</i>	100	<i>Remora brachyptera</i>	GU440496.1	99	627
357	<i>Ruvettus pretiosus</i>	100	<i>Ruvettus pretiosus</i>	AP012506.1	99	644

358	No Match		<i>Selar crumenophthalmus</i>	KC970506.1	99	280
359	<i>Selar crumenophthalmus</i>	100	<i>Selar crumenophthalmus</i>	KJ148633.1	99	650
360	<i>Spherooides pachygaster</i>	99	<i>Spherooides pachygaster</i>	KJ709636.1	99	303
361	<i>Sthenoteuthis oualaniensis</i>	99	<i>Sthenoteuthis oualaniensis</i>	AB270943.1	99	314
362	<i>Sthenoteuthis oualaniensis</i>	99	<i>Sthenoteuthis oualaniensis</i>	EU660576.1	99	288
363	<i>Sthenoteuthis oualaniensis</i>	100	<i>Sthenoteuthis oualaniensis</i>	DQ885839.1	99	287
364	<i>Sthenoteuthis oualaniensis</i>	100	<i>Sthenoteuthis oualaniensis</i>	AB270943.1	99	305
365	<i>Sthenoteuthis oualaniensis</i>	100	<i>Sthenoteuthis oualaniensis</i>	KF009670.1	99	261
366	No Match		<i>Sufflamen bursa</i>	JQ350376.1	99	627
367	No Match		<i>Sufflamen bursa</i>	JQ350376.1	99	642
368	No Match		<i>Sufflamen fraenatum</i>	JQ432176.1	99	529
369	No Match		<i>Sufflamen fraenatum</i>	AP004456.1	99	650
370	<i>Taractichthys steindachneri</i>	100	<i>Taractichthys steindachneri</i>	EF609477.1	99	520
371	<i>Taractichthys steindachneri</i>	100	<i>Taractichthys steindachneri</i>	EF609477.1	99	557
372	No Match		<i>Taractichthys steindachneri</i>	EF609477.1	99	338

373	<i>Taractichthys steindachneri</i>	100	<i>Taractichthys steindachneri</i>	KC970511.1	99	405
374	<i>Taractichthys steindachneri</i>	100	<i>Taractichthys steindachneri</i>	KC970511.1	99	590
375	No Match		<i>Taractichthys steindachneri</i>	EF609477.1	99	587
376	<i>Thunnus alalunga</i>	100	<i>Thunnus alalunga</i>	KP975847.1	99	472
377	No Match		<i>Thunnus alalunga</i>	KC015953.1	99	440
378	<i>Thunnus albacares</i>	100	<i>Thunnus albacares</i>	KP975904.1	99	591
379	<i>Acanthocybium solandri</i>	100	<i>Acanthocybium solandri</i>	GU225519.1	100	587
380	<i>Acanthocybium solandri</i>	100	<i>Acanthocybium solandri</i>	DQ107694.1	100	627
381	<i>Acanthocybium solandri</i>	100	<i>Acanthocybium solandri</i>	GU225508.1	100	628
382	<i>Auxis rochei</i>	100	<i>Auxis rochei</i>	JF492935.1	100	589
383	<i>Caranx melampygus</i>	100	<i>Caranx melampygus</i>	JQ431544.1	100	634
384	<i>Decapterus macarellus</i>	100	<i>Decapterus macarellus</i>	KM986880.1	100	630
385	No Match		<i>Decapterus macrosoma</i>	KF841444.1	100	617
386	<i>Gempylus serpens</i>	100	<i>Gempylus serpens</i>	AP012502.1	100	588
387	<i>Gempylus serpens</i>	100	<i>Gempylus serpens</i>	AP012502.1	100	641
388	<i>Gempylus serpens</i>	100	<i>Gempylus serpens</i>	AP012502.1	100	589
389	<i>Heteropriacanthus cruentatus</i>	100	<i>Heteropriacanthus cruentatus</i>	KF929967.1	100	588
390	No Match		<i>Katsuwonus pelamis</i>	KF528381.1	100	283

391	No Match		<i>Katsuwonus pelamis</i>	JN653477.1	100	534
392	<i>Katsuwonus pelamis</i>	100	<i>Katsuwonus pelamis</i>	EU014260.1	100	604
393	No Match		<i>Makaira nigricans</i>	HQ945883.1	100	610
394	<i>Melichthys vidua</i>	100	<i>Melichthys vidua</i>	JQ431905.1	100	599
395	<i>Naso unicornis</i>	100	<i>Naso unicornis</i>	KJ658938.1	100	325
396	<i>Promethichthys prometheus</i>	100	<i>Promethichthys prometheus</i>	EU263807.1	100	590
397	No Match		<i>Psenes maculatus</i>	AB205444.1	100	434
398	<i>Remora brachyptera</i>	100	<i>Remora brachyptera</i>	GU440496.1	100	621
399	No Match		<i>Thunnus obesus</i>	KP975848.1	100	285

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