

# 18s DNA sequences of planktonic animals that are potential prey of siphonophores in water off California USA from 2016-2020

**Website:** <https://www.bco-dmo.org/dataset/935469>

**Data Type:** Cruise Results, experimental, Other Field Results

**Version:** 1

**Version Date:** 2024-12-05

## Project

» [Collaborative research: The effects of predator traits on the structure of oceanic food webs](#) (SiphWeb)

Contributors	Affiliation	Role
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## Abstract

This dataset contains 18s DNA sequences of planktonic animals that are potential prey of siphonophores. Siphonophores (Cnidaria: Hydrozoa) are abundant and diverse gelatinous predators in open-ocean ecosystems. This dataset expands the ability to study the feeding ecology of siphonophores and the structure of the open-ocean food web by facilitating the molecular identification of siphonophore gut contents. The new data presented here are for species that were underrepresented in existing sequence datasets.

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## Coverage

**Location:** Offshore California Current Ecosystem (OCCE) and off Bermuda in the Sargasso Sea

**Spatial Extent:** N:41.06 E:-64.58 S:19.58 W:-160.37

**Temporal Extent:** 2016-06-11 - 2020-10-04

## Methods & Sampling

The methods below are adapted from Damian-Serrano, Hetherington et al. (2022).

We built an 18S gene barcoding database of potential siphonophore prey items to expand on the available reference sequences in public databases. To do this, we collected 60 specimens of 30 species of zooplankton and micronekton from the California Current using a Tucker trawl. We targeted plausible prey species from motile open-ocean taxa that cohabitate with siphonophores and are underrepresented in SILVA databases (high quality ribosomal RNA databases, [arb-silva.de](#)), including fishes, crustaceans, jellyfishes, urochordates, chaetognaths, polychaetes, and mollusks. Specimens were

photographed alive, then tissue was sampled and frozen, and finally the rest of the animal was fixed in formalin as a voucher to be identified and preserved at the Yale Peabody Museum of Natural History.

DNA extraction, quality control, PCR, and amplicon cleanup was carried out in a similar fashion as the metabarcoding protocol described above (and detailed in Damian Serrano 2022, doi: 10.17504/protocols.io.5qpvo57o7l4o/v2), using the PCR program with an annealing temperature of 54°C, and a single pair of primers (166F and 134R), spanning the full extent of the sequence containing all barcode regions used in the gut content metabarcoding (from V3 to V9). Purified amplicons were sent in plates with the forward and reverse primer separately for Sanger sequencing from both ends at the Yale DNA Analysis Facility. A total of 89 newly-submitted sequences were then assembled and trimmed at a 95% quality cutoff in Geneious and concatenated with the latest SILVA database (SILVA\_138\_SSURef\_NR99 downloaded on February 23, 2021) pruned to remove non-eukaryotic sequences.

Taxonomic identities of the reads in siphonophore gut contents were assigned using the assignment software METAXA2 (Bengtsson-Palme 2015) with a 70% reliability cutoff, comparing the sequences against our custom-built library built using SILVA138 that includes the new prey sequences.

### **Siphonophore collection**

In order to sample a representative set of taxa across the siphonophore phylogeny, we targeted a set of 41 species (aiming for 10 specimens per species) including cystonects, apolemiids, pyrostephids, euphysonects, and calyphorans from shallow and deep waters. Most species were sampled from the Offshore California Current Ecosystem (OCCE) except for the Portuguese man-o-war *Physalia physalis*, which was collected off Bermuda in the Sargasso Sea; *Sulculeolaria chuni* and some *Nanomia* spp. (labeled as “Atlantic”) which were collected off Rhode Island in the Block Island sound; *Forskalia* sp. M123-SS8 and shallow *Nanomia* sp. KiloMoana2018-BW7-4 which were collected off the coast of Hawaii. While all the *Nanomia* populations sampled in this study have been referred to as *Nanomia bijuga*, we suspect that there may be undescribed cryptic *Nanomia* species among the specimens sampled based on the disparate tentillum morphologies we observed. Therefore, we decided to have them labeled at the genus level. One *Nanomia* specimen (KiloMoana2018-BW7-4) was collected off the coast of Kona, Hawaii. The pleustonic (surface floating) *P. physalis* samples were collected manually using a bucket from a small boat. Species found between the 0-20m deep were collected using blue water diving techniques following the guidelines in Haddock & Heine (2005). Species from 200-4000m were collected using ROVs. All animals were collected live and brought back to the ship (or field station in Bermuda for *P. Physalis*) for dissection. Live colonies were photographed (sometimes recorded on video), and zooids of diagnostic value (nectophores, bracts, tentacles) were dissected, when possible, fixed in 4% formalin, and stored as vouchers at the Yale Peabody Museum of Natural History (voucher catalog numbers provided in specimen metadata S15 Table of Damian-Serrano et al., 2022, doi: 10.1371/journal.pone.0267761).

### **Gut content metabarcoding**

Shortly after collection of the live specimens, we dissected and pooled several gastrozooids from each colony, making sure that those with visible gut contents are included in addition to several other without conspicuous prey, and also including visible egested food pellets at the bottom of the sampling container.

To extract DNA, we digested the samples with proteinase K at 56°C for 1-2h, and used the DNeasy Blood & Tissue kit (Qiagen, Hilden, Germany) eluting twice at 56°C for 10min into a final volume of 100µl. For barcode amplification, we used a set of six primer pairs that amplify six barcode regions within the 18S gene ('V3', 'V5-V7S', 'V5-V7L', 'V7', 'V7p+V8', and 'V9'). The primers were designed using Geneious 11.1.5 (Kearse 2012), constraining the search to short (>300 bp) amplicon products with a high chance of remaining uncleaved after digestion in the gastrozooid, flanked by priming sites conserved (to a maximum mismatch of 3bp) across metazoans. The search for conserved priming sites was conducted on an alignment of 18S genes from 975 species across all metazoan phyla downloaded from GenBank (available in [github.com/dunnlab/siphweb\\_metabarcoding/Primer\\_design](https://github.com/dunnlab/siphweb_metabarcoding/Primer_design)). The primer search was optimized to only retrieve non-degenerate primer pairs with compatible annealing temperatures and without problematic dimerization and hairpin temperatures. Primer sequences are shown in Table 1 (Damian Serrano 2022, doi: 10.1371/journal.pone.0267761), and their properties can be found in Table T1 in the protocol (Damian Serrano 2022).

## Prey reference database

In order to enhance the accuracy of the taxonomic assignments of reads, we also built an 18S gene barcoding database of potential prey items to expand on the available reference sequences in public databases. To do this, we collected 60 specimens of 30 species of zooplankton and micronekton from the OCCE using a Tucker trawl. We targeted plausible prey species from motile open-ocean taxa that cohabitate with siphonophores and are underrepresented in SILVA databases, including fishes, crustaceans, jellyfishes, urochordates, chaetognaths, polychaetes, and mollusks. Specimens were photographed alive, then tissue was sampled and frozen, and finally the rest of the animal was fixed in formalin as a voucher to be identified and preserved at the Yale Peabody Museum of Natural History. DNA extraction, quality control, PCR, and amplicon cleanup was carried out in a similar fashion as the metabarcoding protocol described above (and detailed in Damian Serrano 2022, doi: 10.17504/protocols.io.5qpvo57o7l4o/v2), using the PCR program with an annealing temperature of 54°C, and a single pair of primers (166F and 134R), spanning the full extent of the sequence containing all barcode regions used in the gut content metabarcoding (from V3 to V9). Purified amplicons were sent in plates with the forward and reverse primer separately for Sanger sequencing from both ends at the Yale DNA Analysis Facility. A total of 89 newly-submitted sequences were then assembled and trimmed at a 95% quality cutoff in Geneious and concatenated with the latest SILVA database (SILVA\_138\_SSURef\_NR99 downloaded on February 23, 2021) pruned to remove non-eukaryotic sequences.

## Data Processing Description

### Bioinformatic pipeline

Amplicon libraries were demultiplexed by primer sequence using custom bash code. Primer sequences were removed using *cutadapt* (Martin 2011). The forward and reverse reads were matched and repaired using *bbtools* (Bushnell 2017), then denoised and de-replicated using the DADA2 (Callahan 2016) plugin in QIIME2 (Bolyen 2019) with a truncation quality threshold of 28. We *de novo* clustered the unique features into operational taxonomic units (OTUs) using the VSEARCH (Rognes 2016) plugin in QIIME2 with a similarity threshold of 95%. To reduce computational load, only the top 100 most abundant features among the clustered OTUs were selected for taxonomic assignment. Taxonomic identities were assigned using the assignment software METAXA2 (Bengtsson-Palme 2015) with a 70% reliability cutoff, comparing the sequences against the SILVA123.1 reference library (Quast 2012), and against our custom-built library built using SILVA138 as a foundation. The SILVA123.1 database contains 61383 eukaryotic reference sequences, while our custom database (built off SILVA138.1) contains 79044. Animals in the SILVA123.1 taxonomy are annotated to the ranks of superphylum, phylum, subphylum, class, subclass, order, family, genus, and species. However, the SILVA138.1 animal taxonomy was annotated at the levels of clade (e.g. Bilateria, Protostomia, Deuterostomia, Ecdysozoa, Lophotrochozoa), phylum, class, subclass, order, suborder, and species. All bioinformatics analyses were carried out in the Yale High Performance Computing Cluster. The taxonomic assignments and read count data were merged, then parsed to match the sample of origin and the DNA sequence they derived from. Sequence post-processing scripts can be found in the GitHub repository [https://github.com/dunnlab/siphweb\\_metabarcoding/Scripts](https://github.com/dunnlab/siphweb_metabarcoding/Scripts) (Damian-Serrano, 2024).

## BCO-DMO Processing Description

Processed submitted files using the BCO-DMO tool named Laminar to create the primary data file named 935469\_v1\_gut\_dna\_seq\_potential\_preym\_of\_siphonophores.csv and the supplemental data file named 935469\_supl\_rrna\_partial\_seq\_potential\_preym\_of\_siphonophores.

- Created a SRA Run Info table which was downloaded from NCBI on page listing experiments <https://www.ncbi.nlm.nih.gov/sra/?term=SRP321688>

Added to this table to include information about Spots.

Additional metadata: spots bases spots\_with\_mates avgLength size\_MB TaxID

The SRA Run Info table was named SraRunInfo.csv.

- Imported the submitted file named Example\_Dunn\_NCBI\_SRA\_RunTable.xlsx and the SRA Run Info file SraRunInfo.csv into Laminar.

- Renamed parameters in the file Example\_Dunn\_NCBI\_SRA\_RunTable.xlsx to follow BCO-DMO naming convention by replacing spaces with underscores.

- Removed two fields, `geo_loc_name_country` and `geo_loc_name_country_continent`, which contained the value of 'uncalculated' as it doesn't add any information to the dataset. The values for these two parameters was not entered in the NCBI submission, and that's why the value is 'uncalculated'. The location information of 'Water off California' is included on the dataset page.

- Joined the two submitted files into one table by joining on the parameter `Run`.

- Removed the parameter `Bytes` since the parameter `size_MB` is the same information with the size in MB which is easier to read.

- Converted the `Collection_Date` parameter format from `%m-%d-%y` to `%Y-%m-%d` to be in the ISO 8601 format.

- Renamed any parameters in the joined table that have spaces in their names with an underscore to follow BCO-DMO naming conventions.

- Split the column `lat_lon` which contained both latitude and longitude values into separate latitude and longitude columns. Then converted latitude values to positive or negative values following the convention of South is negative. And converted longitude values to positive or negative values following the convention of West is negative. Finally, deleted the `lat_lon` column since the information is now in separate columns.

- Renamed this table to `935469_supl_rrna_partial_seq_potential_preய_of_siphonophores`.

- Imported the submitted file named `Dunn_NCBI_MZ_data.xlsx` into Laminar to process it. These are the steps performed for this file.

- Removed parameters with no values except for the `Cruise_ID` parameter which is filled in with information from the submitter.

- Removed the column `Date` because the submitter requested it in an email dated 10/15/2024. This is the comment from that email "Sorry about the double date columns. That is the result of a table join I did to integrate two different tables. Please disregard the `Date` column."

- Renamed parameters by replacing spaces with underscores according to BCO-DMO naming convention.

- Added a prefix of `NCBI_` to the `Accession` parameter to make it clear where the Accession number comes from.

- Replaced Clade value for prey organism *Calanus pacificus* from Ctenophora to Copepoda. This change was performed from referencing the NCBI accession value and the taxonomy listed for the organism: Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Crustacea; Multicrustacea; Hexanauplia; Copepoda; Calanoida; Calanidae; Calanus.

- Replaced Clade value for prey organism *Parasagitta elegans* from Ctenophora to Chaetognatha. This change was performed from referencing the NCBI accession value and the taxonomy listed for the organism: Eukaryota; Metazoa; Spiralia; Gnathifera; Chaetognatha; Sagittoidea; Apheroglossa; Ctenodonta; Sagittidae; Parasagitta.

- Replaced Clade value for prey organism *Pleurobrachia bachei* from Ostracoda to Ctenophora. This change was performed from referencing the NCBI accession value and the taxonomy listed for the organism: Eukaryota; Metazoa; Ctenophora; Tentaculata; Cydippida; Pleurobrachiidae; Pleurobrachia.

- Renamed this processed file to `935469_supl_rrna_partial_seq_potential_preய_of_siphonophores`.

Created a taxonomy file named `species_taxonomy_of_hosts_found_in_primary_file.csv` that contains taxonomy information from the World Register of Marine Species (WoRMS) at <https://www.marinespecies.org/index.php> for the hosts listed in the primary dataset file `935469_v1_gut_dna_seq_potential_preய_of_siphonophores.csv`.

Created a taxonomy file named `species_taxonomy_of_preய_found_in_supplemental_file.csv` that contains taxonomy information from the World Register of Marine Species (WoRMS) at <https://www.marinespecies.org/index.php> for the prey listed in the supplemental dataset file `935469_supl_rrna_partial_seq_potential_preய_of_siphonophores.csv`.

## Related Publications

Alejandro Damian-Serrano, & Casey Dunn. (2024). dunnlab/siphweb\_metabarcoding: Published analyses (1.0). Zenodo. <https://doi.org/10.5281/zenodo.13936376>  
*Software*

Bengtsson-Palme, J., Hartmann, M., Eriksson, K. M., Pal, C., Thorell, K., Larsson, D. G. J., & Nilsson, R. H. (2015). metaxa2: improved identification and taxonomic classification of small and large subunit rRNA in metagenomic data. *Molecular Ecology Resources*, 15(6), 1403–1414. Portico. <https://doi.org/10.1111/1755-0998.12399>  
*Software*

*Software*

Bolyen, E., Rideout, J. R., Dillon, M. R., Bokulich, N. A., Abnet, C. C., Al-Ghalith, G. A., ... Asnicar, F. (2019). Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology*, 37(8), 852–857. doi:[10.1038/s41587-019-0209-9](https://doi.org/10.1038/s41587-019-0209-9)  
*Software*

Bushnell, B., Rood, J., & Singer, E. (2017). BBMerge – Accurate paired shotgun read merging via overlap. *PLOS ONE*, 12(10), e0185056. <https://doi.org/10.1371/journal.pone.0185056>  
*Software*

Callahan, B. J., McMurdie, P. J., Rosen, M. J., Han, A. W., Johnson, A. J. A., & Holmes, S. P. (2016). DADA2: High-resolution sample inference from Illumina amplicon data. *Nature Methods*, 13(7), 581–583. doi:[10.1038/nmeth.3869](https://doi.org/10.1038/nmeth.3869)  
*Software*

Damian Serrano, A. (2022). DNA metabarcoding protocol for siphonophore gut contents v2. <https://doi.org/10.17504/protocols.io.5qpvo57o7l4o/v2>  
*Methods*

Damian-Serrano, A., Hetherington, E. D., Choy, C. A., Haddock, S. H. D., Lapidés, A., & Dunn, C. W. (2022). Characterizing the secret diets of siphonophores (Cnidaria: Hydrozoa) using DNA metabarcoding. *PLOS ONE*, 17(5), e0267761. <https://doi.org/10.1371/journal.pone.0267761>  
*Results*

Haddock, S. H. D., Heine, J. N., United States National Oceanic and Atmospheric Administration, California Sea Grant College Program, & National Sea Grant College Program (U.S.). (2005). *Scientific blue-water diving*. California Sea Grant College Program. <https://isbsearch.org/isbn/9781888691139>  
*Methods*

Kearse, M., Moir, R., Wilson, A., Stones-Havas, S., Cheung, M., Sturrock, S., ... Drummond, A. (2012). Geneious Basic: An integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics*, 28(12), 1647–1649. doi:[10.1093/bioinformatics/bts199](https://doi.org/10.1093/bioinformatics/bts199)  
*Software*

Martin, M. (2011). Cutadapt removes adapter sequences from high-throughput sequencing reads. *EMBnet journal*, 17(1), 10. doi:[10.14806/ej.17.1.200](https://doi.org/10.14806/ej.17.1.200)  
*Software*

Quast, C., Pruesse, E., Yilmaz, P., Gerken, J., Schweer, T., Yarza, P., Peplies, J., Glöckner, F. O. (2012). The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. *Nucleic Acids Research*, 41(D1), D590–D596. doi:[10.1093/nar/gks1219](https://doi.org/10.1093/nar/gks1219)  
*Methods*

Rognes, T., Flouri, T., Nichols, B., Quince, C., & Mahé, F. (2016). VSEARCH: a versatile open source tool for metagenomics. *PeerJ*, 4, e2584. Portico. <https://doi.org/10.7717/peerj.2584>  
*Software*

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## Parameters

Parameter	Description	Units

BioProject	The NCBI identifier for the BioProject associated with the data	unitless
SRA Study	The NCBI identifier for the SRA study associated with the data	unitless
Experiment	The NCBI identifier for the sequencing experiment	unitless
Run	The unique NCBI identifier for each sequencing run	unitless
BioSample	The NCBI identifier for the BioSample associated with the data	unitless
geo_loc_name	The specific geographical location where the sample was collected	unitless
lat	latitude, South is negative	decimal degrees
lon	longitude, West is negative	decimal degrees
Collection_Date	The date when the sample was collected	unitless
BioSampleModel	The model describing the BioSample (e.g., human, environmental)	unitless
Organism	The scientific name of the organism from which the sample was taken	unitless
TaxID	NCBI taxon identifier	unitless
isolation_source	The source from which the sample was isolated (e.g., soil, blood)	unitless
Host	The host organism from which the sample was obtained	unitless
Sample Name	The name of the sample	unitless
source_material_id	The NCBI identifier for the source material	unitless
spots	The spot model is Illumina GA centric. The flowcells have the locations where the adapters have stuck them to the glass of the lane. There are X and Y coordinates that identify these 'spots'. As the camera reads the fluorescent flashes during sequencing, the coordinates indicate which spot the new base is added to. All of the bases for a single location constitute the spot.	unitless
Bases	The total number of bases sequenced	unitless

spots_with_mates	spots with mates	unitless
AvgSpotLen	The average length of the spots (reads) in the run	Base pairs
size_MB	The total size of the sequencing data files	MB
Extraction	The identifier for the extracted DNA	unitless
Index	Index sequence used in the library preparation	unitless
samp_collect_device	The device used to collect the sample	unitless
Platform	The sequencing platform used (e.g., Illumina, PacBio)	unitless
Instrument	The sequencing instrument used (e.g., Illumina MiSeq)	unitless
Assay_Type	The type of sequencing assay performed (e.g., RNA-Seq, WGS)	unitless
Library_Name	The name of the sequencing library	unitless
LibrarySource	The source material for the library (e.g., genomic, transcriptomic)	unitless
LibraryLayout	The layout of the sequencing library (e.g., paired-end, single-end)	unitless
LibrarySelection	The method used to select the nucleic acid library (e.g., PCR, random)	unitless
Consent	Information on the consent for data usage	unitless
create_date	The date when the submission was created	unitless
ReleaseDate	The date when the data was released to the public	unitless
version	The version of the NCBI submission	unitless
Center_Name	The name of the sequencing center	unitless
DATASTORE_filetype	The file type stored in the NCBI DataStore (e.g., FASTQ, BAM)	unitless

DATASTORE_region	The geographical region of the DataStore	unitless
DATASTORE_provider	The provider of the DataStore where files are kept	unitless

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## Instruments

<b>Dataset-specific Instrument Name</b>	Applied Biosystems SimpliAmp thermal cycler	
<b>Generic Instrument Name</b>	qPCR Thermal Cycler	
<b>Generic Instrument Description</b>	An instrument for quantitative polymerase chain reaction (qPCR), also known as real-time polymerase chain reaction (Real-Time PCR).	

<b>Dataset-specific Instrument Name</b>	Qubit 2.0 fluorometer	
<b>Generic Instrument Name</b>	Qubit fluorometer	
<b>Generic Instrument Description</b>	Benchtop fluorometer. The Invitrogen Qubit Fluorometer accurately and quickly measures the concentration of DNA, RNA, or protein in a single sample. It can also be used to assess RNA integrity and quality. Manufactured by Invitrogen, Carlsbad, CA, USA (Invitrogen is one of several brands under the Thermo Fisher Scientific corporation.)	

<b>Dataset-specific Instrument Name</b>	ROV Doc Ricketts	
<b>Generic Instrument Name</b>	ROV Doc Ricketts	
<b>Generic Instrument Description</b>	The remotely operated vehicle (ROV) Doc Ricketts is operated by the Monterey Bay Aquarium Research Institute (MBARI). ROV Doc Ricketts is capable of diving to 4000 meters (about 2.5 miles). The R/V Western Flyer is the support vessel for Doc Ricketts and was designed with a center well whose floor can be opened to allow Doc Ricketts to be launched from within the ship into the water below. For a complete description, see: <a href="https://www.mbari.org/at-sea/vehicles/remotely-operated-vehicles/rov-doc...">https://www.mbari.org/at-sea/vehicles/remotely-operated-vehicles/rov-doc...</a>	

<b>Dataset-specific Instrument Name</b>	NanoDrop 3300	
<b>Generic Instrument Name</b>	Thermo Scientific NanoDrop spectrophotometer	
<b>Generic Instrument Description</b>	Thermo Scientific NanoDrop spectrophotometers provide microvolume quantification and purity assessments of DNA, RNA, and protein samples. NanoDrop spectrophotometers work on the principle of ultraviolet-visible spectrum (UV-Vis) absorbance. The range consists of the NanoDrop One/OneC UV-Vis Spectrophotometers, NanoDrop Eight UV-Vis Spectrophotometer and NanoDrop Lite Plus UV Spectrophotometer.	



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## Project Information

### **Collaborative research: The effects of predator traits on the structure of oceanic food webs (SiphWeb)**

**Coverage:** North Pacific

Food webs describe who eats whom, tracing the flow of energy from plants up to large animals. While many connections in food webs on land are quite familiar (lions eat antelope and antelope eat grass, for example), there are large gaps in our understanding of ocean food webs. Closing these gaps is critical to understanding how nutrients and energy move through ocean ecosystems, how organisms interact in the ocean, and how best to manage ocean resources. This project will study ocean food web structure with a focus on siphonophores, an abundant group of predators in the open ocean that range in length from less than an inch to more than one hundred feet. Siphonophores are closely related to corals and many jellyfish. They are known to be important predators within ocean food webs, but they are difficult to study because they live across great ocean depths and are gelatinous and fragile. The details of what they eat, as well as many other features of their biology, remain poorly known. This project will combine direct observations of feeding, genetic analysis of siphonophore gut contents, and stable isotope analyses to identify what different species of siphonophores eat. The team will also examine why they eat what they do. This will provide a new understanding of how the structure of food webs arise, aiding in our ability to predict future changes to food webs as the global climate shifts. Siphonophores feed in a very unique manner--they have highly specialized tentacles that are used solely for capturing prey--thus, the prey captured is determined largely by the anatomy and function of these tentacles. The project will describe these tentacles, reconstruct their evolutionary history, and investigate how evolutionary shifts in tentacle structure have led to changes in diet. This project will train one PhD student, one Master's student, a postdoc, and undergraduate students, including individuals of underrepresented groups. This project will support the production of scientifically rigorous yet engaging videos, foster the expansion of a citizen-science program, and create K-12 teaching modules.

This project will advance three scientific aims: First, it will identify the diet of a diverse range of siphonophores using DNA metabarcoding of gut contents and prey field, remotely operated vehicle (ROV) video of prey encounters, and stable isotope analysis. These approaches are highly complementary and allow for extensive cross validation. Second, the project will characterize the selectivity of siphonophore diets by comparing them to the relative prey abundances in the habitats of each of these species. Third, the project will characterize the structure of the siphonophore prey capture apparatus across species through detailed morphological analysis of their tentacles and nematocysts. These data will be integrated in an ecological and evolutionary framework to identify predator features associated with prey specialization. In a larger context, addressing these questions will advance our understanding of oceanic predation by revealing how evolutionary changes in predator selectivity correspond to evolutionary changes in habitat and feeding apparatus and how these changes shape current food web structure in the open ocean. We will test and refine an integrated approach to describing the structure and origin of food web topology, and evaluate the potential for phylogenetic relationships to explain prey selectivity.

This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

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## Funding

<b>Funding Source</b>	<b>Award</b>
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1829835</a>

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