Zooplankton species identified from NOAA Ship Ronald H. Brown RHB0603 in the Sargasso Sea and Southeast North Atlantic Ocean from 2006-2006 (CMarZ_2004-2010 project)

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Project
» Census of Marine Zooplankton-2004-2010 (CMarZ_2004-2010)

Program
» Census of Marine Life (CoML)

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Dataset Description

Species of zooplankton were identified by a number of taxonomic experts from net tows in the Sargasso Sea in April 2006. Samples were collected aboard the Ronald H. Brown cruise 0603 from 5 stations.

Taxonomic Group	Taxonomist	Institution
Copepoda	Leo Blanco **Bercial**	Universidad de Oviedo, Spain
Euphausiacea	Nancy **Copley**	Woods Hole Oceanographic Inst. (WHOI), USA
Copepoda	Astrid **Cornils**	Alfred Wegener Institute for Polar and Marine Research (AWI), Bremerhaven, Germany
fish larvae	Lalithambika **Devi**	National Institute of Oceanography, Kochi, India
Decapoda	Hege Øverbø **Hansen**	Institute of Marine Research, Bergen, Norway
Larvacea	Russ **Hopcroft**	Institute of Marine Science, University of Alaska Fairbanks, USA
Copepoda	Mikiko **Kuriyama** & Hiroyuki **Matsuura**	Plankton Laboratory,Ocean Research Institute, University of Tokyo, Japan
jellies, amphipods, etc.	Dhugal **Lindsay**	Japan Agency for Marine-Earth Science and Technology (JAMSTEC), Yokosuka, JAPAN
Thaliacea	Larry **Madin**	Woods Hole Oceanographic Inst. (WHOI), USA
jellies, amphipods, etc.	Francesc **Pagès**	Institut de Ciències del Mar (CSIC), Spain
Mysidae	Saramma **Panampunnayil**	National Institute of Oceanography, Kochi, India
Foraminifera	Silvia **Watanabe**	Museo Argentino de Ciencias Naturales, Buenos Aires, Argentina

Methods & Sampling

"Zooplankton and micronekton were quantitatively sampled throughout the water column using a 1-m, and a 10-m MOCNESS (Multiple Opening/Closing Net and Environmental Sensing System; Wiebe et al., 1985; The MOCNESS telemetered data continuously to the ship, including depth, temperature, salinity, horizontal speed, and volume filtered. This allowed on-the-fly adjustment of sampling depths or times, and completion of a continuous series of stratified hauls in a relatively short time. All data were recorded electronically for subsequent analysis. MOC-10 tows generally took 10 to 12 hours to complete, MOC-1 tows took about 3.5 hours. In addition, a 2-hour time block was allocated for two blue-water dives. Not shown on this scheme was time for opportunistic sampling with ring nets or water collection with the Niskin bottle. In reality, neither replicate samples with all net systems nor blue-water dives were obtained at all the stations, because of time and weather limitations, and gear malfunctions." (from RV Ronald H. Brown Cruise 06-03 Report)

Data Processing Description

"Samples collected with the MOCNESS's were processed using a standard protocol. On Deck: With completion of the tow, the nets were immediately washed with seawater as they were pulled on deck and the plankton still in the nets carefully moved into the cod-end. The cod-ends were placed in buckets with ice packs to cool the samples and moved expeditiously into the walk-in cold room to await analysis. Specimen removal: One by one the cod-ends were taken into the wet lab for digital photographing, and the picking and removal of large individuals of 1) gelatinous forms, 2) fish, and 3) macrozooplankton/nekton. Pickers described what was being removed and a recorder logged the information. The specimens removed were placed in numbered jars, shell vials, or dishes and the recorder wrote down all specimen information on the data sheets provided, linking the container number to specimen and collection data. This was done so that the actual taxonomic composition and species count for each sample can be reconstructed. The removed specimens were subject to a variety of procedures including further identification, dissection, preservation (in alcohol, frozen nitrogen, or formalin as appropriate), or taken for photographic imaging prior to preservation. Sample splitting and preservation: Within a few minutes of arrival, the stratified samples (with most large gelatinous forms, fish, and macrozooplankton/nekton removed) were passed to the individuals responsible for splitting the samples Generally ½ (split A) was preserved in formalin for future studies, including biomass estimates (e.g., displacement volume), species counts, and other quantitative analyses. The other half was split again with ¼ (split B) for live picking in the main lab and subsequent preservaton in alcohol for later taxonomic analysis. The other ¼ (split C) was immediately preserved in alcohol. After picking, the integrated sample (net 0) was generally split into two halves with one preserved in alcohol and the other in formalin." (from RV Ronald H.

Brown Cruise 06-03 Report)

Cornils, copepods: A total of 63 species of calanoid copepods, primarily Aetideidae and Heterorhabdidae were identified. Only females and males were identified. Because of the ship movements we were unable to dissect individuals smaller than 2 mm, hence, they are probably under-represented in the species list. A lot of them will only be representatively caught in the 1/4-m MOCNESS. Some individuals of the identified species were taken to be "barcoded".

Bercial, copepods: A total of 15 species of calanoid copepods, belonging to 8 families were identified. These are species that were not included in the Cornils and Matsuura and Kuriyama studies.

Matsuura and Kuriyama, copepods: We aimed to obtain samples of these copepods, especially bathypelagic species, to compare the community structure between the Atlantic and Pacific, to see differences in the genetics of morphologically similar species, and obtain knowledge pertaining to the phylogeny of each family. During this cruise, we sorted out 534 Euaugaptilus and 464 scolecitrichids, and identified 25 and 22 species, respectively (Table 6). Among those, 24 Euaugaptilus and 17 scolecitrichid species were picked out for sequencing. After the cruise, we are going to identify the rest of the individuals, sequence COI and the 12S of these species, and discuss the differences between the Atlantic and Pacific, and the phylogeny of these species.

Hansen, decapods. Decapods collected during RHB0603 in the Sargasso Sea Samples were analyzed from the 10-m and 1-m MOCNESS (MOC-10 and MOC-1). A total of 18 tows were analyzed for the presence of Decapod shrimp: 11 samples from the MOC-1 and 7 samples from the MOC-10 (Table 2). Table 2. Tows with MOC-1 and MOC-10 that sampled Decapod shrimp at the five stations. MOC-1 MOC-10 Tow # Tow # Station 1 1, 2 1 Station 2 3, 4 2 Station 3 5, 7, 8 3 Station 4 9,10 4, 5 Station 5 11, 12 6, 7 A total of 366 individuals were sampled and analyzed from MOC-1 and MOC-10.

Copley, euphausiids: Euphausiids were identified from the live portions of several tows. Thysanopoda obtusifrons, a fairly large species (15-20 mm), was commonly found in the samples. Only about 47 individuals from 13 species were identified due to the small amount of time devoted to this activity. There was a shortage of microscopes and the euphausiids can be examined on land post-cruise whereas the gelatinous zooplankton needed to be identified immediately, while still alive. Nineteen identified specimens from eleven species were submitted for barcoding. For station 4, tow 10, net 3 and station 5, tow 11 nets 3, 4 and 5, and all nets from station 5, tow 13, the euphausiids were identified and measured in the lab from the formalin preserved split in March 2011 for a related project (WHOI-OLI). Some shrinkage may have occurred. Abundances (#/m^3) for these later samples are reported under the 'counts' column for these tows.

Watanabe, foraminifera: Skeletonized microzooplanktonic taxa were isolated and identified to species. Pictures were taken of specimens, and material were preserved for further morphological and genetic analyses. Effort was on the planktonic foraminifera, but significant data was collected on the radiolarians and phytoplanktonic coccolithophores as well.

Hopcroft, larvacea: Two principle purposes were addressed during the cruise: general photography of zooplankton, and identification of larvacean species for the barcoding (sequencing) effort. Approximately 1500 useful images have been taken of ~100 different living species of zooplankton at 4 MPix resolution. Depending on the species, from one to 20 pictures have been taken per specimen. In regard to the larvaceans, progress during the cruise was disappointing. Only 12 or 13 of the ~70 species described in this group were encountered during this cruise. With the possible exception of the smallest MOCNESS, these collecting systems extruded most of the larvaceans, and rendered those remaining unidentifiable in the collections. The Reeve net was generally successful, but densities of animals were unusually low. Even for the Reeve net, there appeared to be a relatively limited time-window over which material in the collection remained in a useful condition, and this may have contributed to an underestimation of species present. Only the most common tropical species were encountered, with the notable exception of the giant "mesopelagic" species, Bathochordaeus stygius. There appear to have been several distinct faunal shifts between stations. In the future, some method of slowing the degradation rate of the samples must be found for this specific group; perhaps partial "preservation" with ethanol while sorting the samples will work better.

Devi, larval fish: The fish larvae were picked live from the whole sample and were kept in the cold room for further analysis. The subsampled zooplankton preserved in ethanol and formaldehyde were also examined and the larvae picked out. The fish larvae were identified into different taxa. ! 43 species belonging to 18 families were present in the live samples analyzed. ! The rest of the samples were preserved in formaldehyde for further studies after the cruise. ! Maximum abundance and diversity(4 families and 7 species) were observed at lat 29o 57'N and lon 71o 01'W (MOC1 Tow 3 Net 5). ! Abundance and diversity decreased from there. Only 2 families with 7 species were found at 25o 00'N and 59o 56'W (taken from 0-1000m). ! At lat 33o 38'N and lon

69o 47'W, 5 species were encountered in 4 families (MOC10 Tow 1 Net 4). ! In all the three locations, the mesopelagic groups Myctophidae and Gonostomatidae were dominant. ! Two of the Cyclothone species (C. braueri and C. pallida) contributed the most to the numerical abundance. ! Maximum species diversity was observed in the family Myctophidae (15 species). ! Notoscopelus resplendens and Benthosema glaciale were the dominant species found in the area. ! Thunnus sp. was found only in one sample (MOC10 Tow5 Net 4) at 19o 49'N and 54o 44'W. ! The members of the Percoids were rare. ! 15 species were given for barcoding.

Panampunnayil, mysids: Five stations were sampled between 33 and 14 degrees N and 70 and 54 degrees W. At each station samples were collected using 1/4-m MOCNESS (upper 500m), 1-m MOCNESS (9 nets, upper 1000m) and 10-m MOCNESS (5 nets, down to 5000m), both day and night. Each sample was split. 50% was preserved in 5% formalin for silhouette analysis and later taxonomic analysis; 50% was preserved in alcohol for taxonomic analysis on board and removal of identified species for barcoding. Mysids were picked out of the samples preserved in alcohol and identified.

Madin, thaliacea: Thaliacea collected during RHB0603 in the Sargasso Sea Collections of Thaliacea (salps, doliolids, pyrosomes) were rather sparse on this track, although 17 species were obtained either in the net tows, or more often, from the dives. Net collected samples included: 1. Cyclosalpa polae (aggregate) 2. Thalia democratica (solo & aggregate) 3. Salpa cylindrica (solo) 4. Iasis zonaria (solo & aggregate) 5. Salpa aspera (aggregate) 6. Salpa fusiformis (solo & aggregate) 7. Helicosalpa virgula (solo) 8. Dolioletta gegenbauri 9. Doliopsis sp. 10. Doliolina sp. 11. Doliolum denticulatum 12. Pyrosoma atlanticum 13. Pyrosomella sp. Most of these were in the shallower nets, and were only found in small numbers (1 to 4 of each). Species collected during dives included: Brooksia rostrata (aggregate) Iasis zonaria (aggregate) Salpa aspera (solo & aggregate) Salpa fusiformis (solo & aggregate) Salpa maxima (solo & aggregate) Salpa cylindrical (solo) Pegea bicaudata (aggregate) Pegea confoederata (aggregate) Dolioletta gegenbauri Doliolina sp. Pyrosoma atlanticum All salps were identified and measured, and good specimens (mainly from dives) examined and photographed for anatomical details. These descriptions will become part of the detailed morphological information which will accompany the genetic data. A parallel project to develop a morphological and molecular phylogeny of the Thaliacea will be carried out by Madin and Bucklin over the next two years.

Pagès and Lindsay, other zooplankton: Copepods, Ctenophores, Amphipods and Cephalopods collected during RHB0603 in Sargasso Sea. Ctenophore forms that were identified from net samples included several cydippids belonging to the Haeckeliidae (Aulacoctena acuminata), the Bathyctenidae (Bathyctena chuni), the Pleurobrachiidae (Hormiphora palmata, Pleurobrachia sp.1), the Mertensiidae (Charistephane fugiens), and others. Lobates such as Kiyohimea usagi and Ocyropsis maculata maculata, the Cestoid Cestum veneris, and several Beroe species were also caught in net tows. Blue water diving allowed the collection of several individuals of the lobate Eurhamphaena vexilligera and the Thalassocalycid Thalassocalyce inconstans, in addition to some of the forms listed above. Twelve species of amphipods were sorted from the live samples, most of them large Physocephalata that were easy to spot. Many more species will undoubtedly be found upon examination of the formalin and ethanol-preserved samples. More than half of the gelatinous organisms captured during the blue-water SCUBA dives were host to hyperiid amphipods at varying stages of development. In many cases it was impossible to identify the hyperiid embryos to species or indeed genus level due to their early developmental stages. Individuals were extracted from the canals or gelatinous matrix of their hosts and placed in ethanol for sequencing. This should allow determination of any species specificity in host/parasite relationships as a factor contributing to species diversity maintenance mechanisms in the pelagic zone. The paucity of species belonging to the Physosomata at meso- and bathypelagic depths may have been a consequence of the dominance of these ecosystems by small siphonophores rather than the larger cnidarians that usually host these animals. Submersible dives should be conducted in this area to directly assess the types and numbers of large ctenophore and cnidarian forms to compare with the data gained on amphipods by net systems such as the MOCNESS. Thirteen species of cephalopods were identified in the MOCNESS samples. Of these, three were octopods (Cirrothauma murrayi, Bolitaena pygmaea, Tremoctopus violaceus), one was a vampyromorph (Vampyroteuthis infernalis), and the remaining nine were various squids belonging to at least five major groups (Bathyteuthids, Chiroteuthids, Cranchids, Histioteuthids, and Enoploteuthids). Many larval individuals were also sampled and these were recorded photographically, dissected to obtain tissue for DNA analysis, and preserved in formalin for subsequent taxonomic analysis. Sampling with larger trawls will be necessary to assess the true diversity of the cephalopod fauna at these sites, but the 335 micron mesh yielded specimens in immaculate condition, greatly simplifying taxonomic analyses.

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Data Files

File
zoop_RHB0603.csv (Comma Separated Values (.csv), 125.59 KB) MD5:1b505c0cb6a3e1fbecb29c5a9c1464f1 Primary data file for dataset ID 3295

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Parameters

Parameter	Description	Units
instrument	The instrument used to catch the animals.	
station	station number	
tow	tow number	
date_local	mm/dd/yy	
time_local	hhmm. 24 hour clock	
yrday_local	Decimal days since Jan. 1. Jan 1 at noon is 001.5.	decimal days
lat	North is positive and south is negative.	decimal degrees
lon	West is negative longitude and east is positive.	decimal degrees
net	Which net in a multiple net system.	
depth_range	The min and max depths over which the net was open.	meters
depth_mid	One depth to represent the sample collection depth if one depth is necessary. The middle of the depth range over which the net was sampled.	meters
taxon	The taxonomic group to which the species belongs. May be order, class, family, etc.	
count	How many animals were picked from the tow. Sometimes this was a subsample of the total found in the net, sometime it was the total found in a particular net.	
size	The size or length of the animal in mm.	mm

comments	In this dataset, the comments column is used to denote which subsample the animals came from.	
species	the species name	
depth_max	maximum depth of sample	meters
depth_min	minimum depth of sample	mg/m^3
identified_by	taxonomist's name	

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Instruments

Dataset-specific Instrument Name	MOCNESS.25
Generic Instrument Name	MOCNESS.25
Dataset-specific Description	64 micron mesh, fished to 500 meters depth, for collection of microzooplankton.
Generic Instrument Description	The Multiple Opening/Closing Net and Environmental Sensing System or MOCNESS is a family of net systems based on the Tucker Trawl principle. The MOCNESS-1/4 carries nine 1/4-m2 nets usually of 64 micrometer mesh and is used to sample the larger micro-zooplankton.

Dataset-specific Instrument Name	MOCNESS1
Generic Instrument Name	MOCNESS1
Dataset-specific Description	335 micron mesh, fished to 1000 meters depth.
Generic Instrument Description	The Multiple Opening/Closing Net and Environmental Sensing System or MOCNESS is a family of net systems based on the Tucker Trawl principle. The MOCNESS-1 carries nine 1-m2 nets usually of 335 micrometer mesh and is intended for use with the macrozooplankton. All nets are black to reduce contrast with the background. A motor/toggle release assembly is mounted on the top portion of the frame and stainless steel cables with swaged fittings are used to attach the net bar to the toggle release. A stepping motor in a pressure compensated case filled with oil turns the escapement crankshaft of the toggle release which sequentially releases the nets to an open then closed position on command from the surface. -- from the MOCNESS Operations Manual (1999 + 2003).

Dataset-specific Instrument Name	MOCNESS10
Generic Instrument Name	MOCNESS10
Dataset-specific Description	Special fine mesh (335 micron) nets were used for collecting zooplankton from large volumes of water in the deep sea, to 5000m. The down-haul used a 3 mm mesh net.
Generic Instrument Description	The Multiple Opening/Closing Net and Environmental Sensing System (MOCNESS) is based on the Tucker Trawl principle (Tucker, 1951). The MOCNESS-10 (with 10 m^2 nets) carries 6 nets of 3.0-mm circular mesh which are opened and closed sequentially by commands through conducting cable from the surface (Wiebe et al., 1976). In this system, "the underwater unit sends a data frame, comprising temperature, depth, conductivity, net-frame angle, flow count, time, number of open net, and net opening/closing, to the deck unit in a compressed hexadecimal format every 2 seconds and from the deck unit to a microcomputer every 4 seconds" (Wiebe et al., 1985).

Dataset-specific Instrument Name	RingNet
Generic Instrument Name	Ring Net
Dataset-specific Description	3.4 meter diameter
Generic Instrument Description	A Ring Net is a generic plankton net, made by attaching a net of any mesh size to a metal ring of any diameter. There are 1 meter, .75 meter, .25 meter and .5 meter nets that are used regularly. The most common zooplankton ring net is 1 meter in diameter and of mesh size .333mm, also known as a 'meter net' (see Meter Net).

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Deployments

RHB0603

Website	https://www.bco-dmo.org/deployment/57686
Platform	NOAA Ship Ronald H. Brown
Report	http://www.cmarz.org/CMarZ_RHBrown_April06/Cruise_Report/working.htm
Start Date	2006-04-10
End Date	2006-04-30

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Project Information

Census of Marine Zooplankton-2004-2010 (CMarZ_2004-2010)

Website: http://www.cmarz.org/

Coverage: Global ocean

The Census of Marine Zooplankton (CMarZ) is a field project of the Census of Marine Life (see www.CoML.org). CMarZ is working toward a taxonomically comprehensive assessment of biodiversity of animal plankton throughout the world ocean. The project goal is to produce accurate and complete information on zooplankton species diversity, biomass, biogeographical distribution, genetic diversity, and community structure by 2010. Our taxonomic focus is the animals that drift with ocean currents throughout their lives (i.e., the holozooplankton, Fig. 1). This assemblage currently includes ~6,800 described species in fifteen phyla; our expectation is that at least that many new species will be discovered as a result of our efforts. The census encompasses unique marine environments and those likely to be inhabited by endemic and undescribed zooplankton species.

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Program Information

Census of Marine Life (CoML)

Website: http://www.coml.org/

Coverage: global

The Census of Marine Life is a global network of researchers in more than 80 nations engaged in a 10-year scientific initiative to assess and explain the diversity, distribution, and abundance of life in the oceans. The world's first comprehensive Census of Marine Life - past, present, and future - will be released in 2010.

The stated purpose of the Census of Marine Life is to assess and explain the diversity, distribution, and abundance of marine life. Each plays an important role in what is known, unknown, and may never be known about what lives in the global ocean.

First, diversity. The Census aims to make for the first time a comprehensive global list of all forms of life in the sea. No such unified list yet exists. Census scientists estimate that about 230,000 species of marine animals have been described and reside in jars in collections in museums of natural history and other repositories. Since the Census began in 2000, researchers have added more than 5600 species to the lists. They aim to add many thousands more by 2010. The database of the Census already includes records for more than 16 million records, old and new. By 2010, the goal is to have all the old and the new species in an on-line encyclopedia with a webpage for every species. In addition, we will estimate how many species remain unknown, that is, remain to be discovered. The number could be astonishingly large, perhaps a million or more, if all small animals and protists are included. For comparison, biologists have described about 1.5 million terrestrial plants and animals.

Second, distribution. The Census aims to produce maps where the animals have been observed or where they could live, that is, the territory or range of the species. Knowing the range matters a lot for people concerned about, for example, possible consequences of global climate change.

Third, abundance. No Census is complete without measures of abundance. We want to know not only that there is such a thing as a Madagascar crab but how many there are. For marine life, populations are being estimated either in numbers or in total kilos, called biomass.

To complete the context, it is important to understand the top motivations for the Census of Marine Life. Most importantly, much of the ocean is unexplored. Most of the records in its database are for observations near the surface, and down to 1000 meters. No observations have been made in most of the deep ocean, while most of the ocean is deep.

Another important issue is that diversity varies in space. Marine hot spots, like the rain forests of the land, exist off for large fish off the coasts of Brazil and Australia. The goal is to know much more about marine hot

spots, to help conserve these large fish. Their abundance and thus their diversity is changing, especially for commercially important species. Between 1952 and 1976, for example, fishermen and their customers emptied many areas of the ocean of tuna.

The Census has evolved a strategy of 14 field projects to touch the major habitats and groups of species in the global ocean. Eleven field projects address habitats, such as seamounts or the Arctic Ocean. Three field projects look globally at animals that either traverse the seas or appear globally distributed: the top predators such as tuna and the plankton and the microbes. The projects employ a mix of technologies. These include acoustics or sound, optics or cameras, tags placed on individual animals that store or report data, and genetics, as well as some actual capture of animals. The technologies complement one another. Sound can survey large areas in the ocean, while light cannot. Light can capture detail and characters that sound cannot. And genetics can make identifications from fragments of specimens or larvae where pictures tell little.

This mix of curiosity, need to know, technology, and scientists willing to investigate the unexplored and undiscovered will result in a Census of Marine Life in 2010 that provides a much clearer picture of what lives below the surface around the globe. Several reasons make such a report timely, indeed urgent. Crises in the sea are reported regularly. One recent study predicted the end of commercial fishery globally by 2050, if current trends persist. Better information is needed to fashion the management that will sustain fisheries, conserve diversity, reverse losses of habitat, reduce impacts of pollution, and respond to global climate change. Hence, there are biological, economic, philosophical and political reasons to push for greater exploration and understanding of the ocean and its inhabitants. Indeed, the United Nations Convention on Biological Diversity requires signatories to collect information on living resources, but, as yet, no nation has a complete baseline of such information. The Census of Marine Life's global network of researchers will help to fill this knowledge gap, providing critical information to help guide decisions on how to manage global marine resources for the future.

[Text copied from the CoML web site, November 5, 2008]

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Funding

Funding Source	Award
Alfred P. Sloan Foundation (Sloan)	unknown CMarZ_2004-2010 Sloan
NOAA Ocean Exploration	unknown CMarZ_2004-2010 NOAA OEP

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