

# Ostracod species from the Sargasso Sea collected on NOAA Ship Ronald H. Brown (RHB0603) in April 2006 (CMarZ\_2004-2010 project)

**Website:** <https://www.bco-dmo.org/dataset/2998>

**Data Type:** Cruise Results

**Version:** 3

**Version Date:** 2016-05-06

## Project

» [Census of Marine Zooplankton-2004-2010](#) (CMarZ\_2004-2010)

## Program

» [Census of Marine Life](#) (CoML)

Contributors	Affiliation	Role
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## Coverage

**Spatial Extent:** N:33.6425 E:33.6425 S:14.0417 W:-75.0334

**Temporal Extent:** 2006-04-11 - 2006-04-26

## Dataset Description

Counts of ostracods from the Sargasso Sea collected on the NOAA Ship Ronald H. Brown, April 10-30, 2006. NCBI GenBank accession numbers included were possible.

Note, these are counts, not abundance. The volume filtered by the net and the fraction of the sample examined are not factored into the values.

### Related Reference:

Nigro LM, Angel MV, Blachowiak-Samolyk K, Hopcroft RR, Bucklin A (2016) Identification, Discrimination, and Discovery of Species of Marine Planktonic Ostracods Using DNA Barcodes. PLoS ONE 11(1): e0146327. doi:10.1371/journal.pone.0146327

## Methods & Sampling

Ostracods were identified by microscopic examination of specimens for previously-documented diagnostic morphological characters. Identification was done of living specimens prior to preservation in 95% ethanol. For DNA extraction and processing details, see Nigro et al (2016).

### **P.I. Notes:**

The total number of species sorted from the samples and identified during the cruise was 80. There will have been several which could not be identified onboard ship so the final number will probably approach 90. This includes 6-8 species that are either certainly or probably novel, which all came from the deep tows. These new species increase the number of species currently known to inhabit the Atlantic (140) by nearly 6%. For example three individuals of the seven specimens belonging to the deep-living genus *Bathypochoecia* are each representatives of previously undescribed species; two of the others are strikingly sculptured specimens of a species that has previously been collected at depths of 4000m off NW Africa, but still remains undescribed. The same is true for the 20 or so specimens of a *Fellia* species taken in the deep nets at stations 4 and 5.

A number of other notable species, which are rare in oceanographic collections, were taken in the deep tows, including:

1. *Gigantocypris dracontovalis*, which is smaller than its better known and more abundant congener *G. muelleri* (of which only a single specimen was recorded) and has golden reflectors in its large naupliar eyes;
2. *Mollicia tyloda* that has only been recorded a couple of times since it was first described by G.W. Muller in 1906, and
3. *Macrochoecia macroreticulata* and *M. spinireticulata* only recently described from deep water in the NE Atlantic, which were both abundant in the deeper MOC-10 samples.

Seventeen of the species were collected at all five stations, but a further four that were not recorded at station 4 are likely to be in those samples, increasing the number of ubiquitous species to 21. Eleven species were collected for the first time at station 5, including the largest of the halocyprids, *Alacia valdiviae*, which is over 6 mm long and bright red in color, and so unlikely to have been overlooked previously.

There were considerable changes in the species dominance. *Orthochoecia secernenda* that had been the commonest large ostracod was replaced by *O. atlantica*, *Halocypris globosa* by *Halocypris inflata*, and *Orthochoecia secernenda* by *O. atlantica*.

Before the cruise began, I set a target of 50 species to be sequenced. Thanks to the large number of species that made their first appearance at station 5, the target was exceeded. In all, 58 species were picked out for sequencing and these are the first halocyprids ever to be sequenced. They represent 39% of the species known to occur in the whole of the Atlantic (now 148, which includes the new species collected on the cruise) and 25% of the global inventory of planktonic ostracods (230). Hence we have already achieved substantial progress towards providing a powerful identification tool for planktonologists studying this abundant group that has largely been overlooked because of the problems associated with their identification.

\*\* For station 3 cast 5, changed instrument from MOC-10 to MOC-1 because the station number and cast number don't match. Net could have spent most of its time at 200 m. None of nets worked right.

## **Data Processing Description**

### **BCO-DMO Processing:**

- added conventional header with dataset name, PI name, version date, reference information
- renamed parameters to BCO-DMO standard
- manually found and added the accession numbers. Only a handful (23) of the records have accessions. Some records in this dataset have 2 to 4 accessions associated with it because each accession is for a single individual and the dataset may have multiple specimens of a single species from a single sample (net).
- revised species names as per M. Angel's instructions

v.2016-04-06 replaced v.2013-05-15. Accession numbers were added as per PLOS ONE paper, and species names were updated by Martin Angel.

v2016-05-04 replaced v. 2016-04-06. Added live links to GenBank, shortened 1 very long comment that

wouldn't serve.

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## Data Files

File
<b>sargasso_ostrcods_2016.csv</b> (Comma Separated Values (.csv), 94.46 KB) MD5:aa7ef5a5e023c83d7655e1cfc263bed8
Primary data file for dataset ID 2998

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## Parameters

Parameter	Description	Units
station	station name	
instrument	instrument used to sample	
cast	tow identification number	
lat	latitude of the station. North is positive, South is negative.	decimal degrees
lon	longitude of the station. East is positive, West is negative	decimal degrees
date_local	month, day and year of start of station	
net	net number/identification	
depth_min	minimum depth: where the net was closed for MOC nets	meters
depth_max	maximum depth: where the net was opened	meters
depth_mid	depth in meters at the midpoint of the opened net, used with MOCNESS tows	meters
species	animal identification: genus and species name	
species_comment	comments related to identification	
sex_stage	gender or life stage of identified animal(s)	
length_mm	length of each identified animal	millimeters
sequenced	were specimens given for DNA sequencing	
comments	comments related to sampling and/or sorting	
count	number of individuals identified in the sample	

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## Instruments

<b>Dataset-specific Instrument Name</b>	
<b>Generic Instrument Name</b>	Automated DNA Sequencer
<b>Dataset-specific Description</b>	Applied Biosystems 3130 capillary DNA Sequencer
<b>Generic Instrument Description</b>	General term for a laboratory instrument used for deciphering the order of bases in a strand of DNA. Sanger sequencers detect fluorescence from different dyes that are used to identify the A, C, G, and T extension reactions. Contemporary or Pyrosequencer methods are based on detecting the activity of DNA polymerase (a DNA synthesizing enzyme) with another chemoluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step.

<b>Dataset-specific Instrument Name</b>	MOCNESS10
<b>Generic Instrument Name</b>	MOCNESS10
<b>Dataset-specific Description</b>	This MOCNESS-10 was equipped with 333 micron mesh.
<b>Generic Instrument Description</b>	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 <sup>2</sup> 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).

<b>Dataset-specific Instrument Name</b>	
<b>Generic Instrument Name</b>	Thermal Cycler
<b>Dataset-specific Description</b>	Applied Biosystems 9600 Thermal cycler or in a Perkin Elmer 480 thermal cycler using the GoTaq Flexi DNA polymerase (Promega)
<b>Generic Instrument Description</b>	A thermal cycler or "thermocycler" is a general term for a type of laboratory apparatus, commonly used for performing polymerase chain reaction (PCR), that is capable of repeatedly altering and maintaining specific temperatures for defined periods of time. The device has a thermal block with holes where tubes with the PCR reaction mixtures can be inserted. The cycler then raises and lowers the temperature of the block in discrete, pre-programmed steps. They can also be used to facilitate other temperature-sensitive reactions, including restriction enzyme digestion or rapid diagnostics. (adapted from <a href="http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html">http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html</a> )

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## Deployments

### RHB0603

<b>Website</b>	<a href="https://www.bco-dmo.org/deployment/57686">https://www.bco-dmo.org/deployment/57686</a>
<b>Platform</b>	NOAA Ship Ronald H. Brown
<b>Report</b>	<a href="http://www.cmarz.org/CMarZ_RHBrown_April06/Cruise_Report/working.htm">http://www.cmarz.org/CMarZ_RHBrown_April06/Cruise_Report/working.htm</a>
<b>Start Date</b>	2006-04-10
<b>End Date</b>	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](http://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
NOAA Ocean Exploration	<a href="#">unknown CMarZ_2004-2010 NOAA OEP</a>

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