

On the Abundance and Diversity of Oceanic Life: The 2010 Census of Marine Life

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Prior to the decadal Census of Marine Life (CoML) supported by the Alfred P. Sloan Foundation, studies of oceanic species focused mostly on ocean productivity and the food webs that determine the abundance of commercially valuable species including fish, sharks, marine mammals, squid, as well as species related to human health such as the dinoflagellate species that cause harmful algal blooms. At the starts of the census in 2000, there was a surprising lack of common knowledge about the richness of life in the open ocean and deep-sea sediments. In 1995, I participated in the development of a 1995 U.S. National Research Council Report, *Understanding Marine Biodiversity*¹, which proposed "a fundamental change in the approach by which biodiversity is measured and studied in the ocean by emphasizing and integrated regional scale strategy." Despite the wide circulation of the report, it was unsuccessful in gathering financial support for studies of marine species diversity in the ocean.

About the Census of Marine Life

CoML was conceived following a meeting in 1996 with Jesse Ausubel, a professor at Rockefeller University and a Program Manager for the Alfred P. Sloan Foundation. At the time, the foundation had embarked on a digital survey of the stars and there was a discussion about the parallel possibility of exploring the diversity of living organisms in the ocean for their intrinsic interest. Ausubel conferred with other scientists and assembled experts on fish diversity to plan a census of the fishes. The meetings were successful and the present structure of the census began to take shape. Three main questions were posed: (1) What lives in the ocean?; (2) What did live in the ocean?; (3) What will live in the ocean? CoML officially began in 2000 under the guidance of Ausubel and a steering committee (chaired by this author). To determine what now lives in the ocean, there are twelve regional and national implementation committees and fourteen research projects, each with a separate team of scientists, under the leadership of CoML co-senior scientists, Ron O'Dor and Patricia Miloslavich.

As the culmination of the census approaches in 2010, more than 2,000 scientists from 81 countries throughout the world are focused on the completion of articles, scientific papers, essays, films, lectures, and books that will provide a synoptic view of life in the marine realm—sea to sea, pole to pole, and from the depths of the abyssal plains and seamounts to continental slopes and shelves, canyons, mid-ocean ridges, coral reefs, and also landward into coastal bays and tidal rivers. Accurate measures of patterns of distribution and the abundances of species depend on quantitative sampling techniques and taxonomic authorities to confirm species identifications. One of the obstacles to the completion of the census is the scarcity of taxonomic authorities to identify species accurately. Discovery of relatively simple, inexpensive, and unambiguous molecular techniques for species identification has led to a parallel project supported by the Sloan Foundation called the Barcode of Life. A short sequence of the enzyme cytochrome oxidase 1 gene was shown to provide enough information to be used as a distinct "barcode" capable of separating and identifying most animal species.² The Consortium for the Barcode of Life³ (BCOL) and the Barcode of Life Data Systems⁴ (BOLD) projects have led to widespread use of these new techniques to accurately recognize species. This tool helps overcome what international conversation organizations have called the "taxonomic impediment."

Knowledge of habits and habitats of each species and their genetic, behavioral, and ecological relationships with other species are important for understanding processes that maintain marine ecosystems. New data and tools to visualize data have been developed to illustrate and communicate the patterns of species distribution

that define marine habitats in time and oceanic space⁵ to an unprecedented scale. Field projects and national and regional implementation committees, each with their own teams of scientists, technologies, and sampling programs⁶ are engaged in an intense effort to synthesize and summarize these results by the end of 2010. Publications (including several books synthesizing the results of the census) related before the end of 2010 and the Ocean Biogeographic Information System⁷ (OBIS) will collectively summarize the first global Census of Marine Life.

Open Ocean Life from Top to Bottom – Tagging of Pacific Pelagics (TOPP), Mid-Atlantic Ridge Ecosystem Project (MAR-ECO), and the Census of Marine Zooplankton (CMarZ)

Among the most visible and important inhabitants in the ocean are species of migratory fish, squid, turtles, sharks, birds, and marine mammals. These predatory species play a major role in structuring marine ecosystems. The Tagging of Ocean Pacific Predators (TOPP) projects uses electronic tags and satellite tracing capabilities to follow movements of spectacular animals such as squid, salmon, white sharks, short-fin mako sharks, salmon sharks, leather-back turtles, sooty shearwaters, black-footed albatross, Pacific blue-fin tuna, elephant seals, and whales. The migratory patterns, in a global context, define the habitat of each species in space and time—including breeding grounds and major feeding areas. Individuals range widely in both depth and location, occupying habitats that frequently cross boundaries between water masses and oceans. The attached tags regularly report geographic location, depth, and environmental data via satellites, thus documenting the odysseys of each global traveler.⁸ These peripatetic animal oceanographers reveal the best places to live for each species of marine mammal, turtle, fish, or seabird and relay their environmental data from their travels for use by scientists. The data collected by each animal provides unique perspectives on global ocean biogeography and the connectivity among marine populations. With the exception of seabirds, these species are highly valued as food and must be better protected by laws against overfishing. The TOPP database provides critical insights that guide conservation efforts.

The Mid-Atlantic Ridge Ecosystem Project (MAR-ECO) and its international team of scientists survey ocean life from surface waters to the deep sea along a major section of the underwater mountain chain that forms the Mid-Atlantic Ridge from Iceland to the Azores. The MAR-ECO ship, *RV G.O. Sars*, was built specially to survey mid-ocean ridges using many channels of underway acoustic imaging to survey bottom topography as well as concentrations of organisms at any depth simultaneously. Trawls and plankton nets are deployed to capture phytoplankton, zooplankton, fish, squid, and marine mammals. Remotely operated vehicles are also used to supplement water column sampling and complete high-resolution visual surveys in the water column and on the bottom. Before MAR-ECO, the interior of the ocean, in and around the topographically complex mid-ocean ridges, had not been adequately explored and still much remains to be done. Plans are well underway for the study of the Mid-Atlantic Ridge in the South Atlantic, a bottom feature that has previously been largely unexplored.

The Census of Marine Zooplankton (CMarZ) samples the open ocean from surface to near bottom in many parts of the world with a series of opening and closing nets that drift with ocean currents and water masses. With the aid of barcoding technologies and taxonomic experts, CMarZ expects to have documented about 7,000 species, thus providing a new understanding of the world of oceanic zooplankton.

Census of Marine Life of the Deep-Sea Abyssal Plains, Continental Margins, Mid-Ocean Ridges, Seamounts, Vents and Seeps, and Antarctic and Arctic Oceans

Despite ample evidence to the contrary, deep-sea environmentalists were generally thought to be a veritable desert occupied by a few strange-looking predatory fish and large invertebrates. Animals on the deep-sea floor are smaller than in shallow water and earlier deep-sea samples were processed using nets or screens too coarse to retain the diversity of animals. Use of fine screens (0.3 mm mesh) reveals a diversity of deep-sea animals as great as that found in the most diverse tropical, shallow-water environments. In 2010, the Census of Marine Life will provide a classification of many different deep-sea marine habitats, each with its own diverse assemblage of unfamiliar animals and microorganisms. Deep-sea animals were thought to feed mostly on the remains of organisms settling to the bottom from surface layers of the ocean. Now, due to intensive sampling of deep-sea sediments and the discovery of many animals with chemosynthetic symbionts (bacteria associated with different types of animals that use chemical energy rather than photosynthesis

to grow and reproduce at hydrothermal vents, this is only the beginning of an era of discover of the diversity of deep-sea life. Typically, less than half of the species in each sediments sample from a previously unsampled area of the deep sea have been described. A small fraction of species in most animals groups are well-sampled and the full magnitude of the task is only beginning to be appreciated using barcoding to distinguish species. More complete data on abundance and distribution of fish are revealing the full dangers of overfishing in most regions of the world. Many ocean habitats are being seen by scientists for the first time and exploration of life in the ocean will continue to be a major research frontier for the foreseeable future. Sponges were among the first multicellular animals to evolve in the ocean. The Census of Diversity of Abyssal marine Life (CeDARar) found seventy-six species of small carnivorous sponges of the coast of Antarctica and the Census of marine Life on Seamounts (CenSeam) found another seventeen species. These small sponges are remnants of a time when Foraminifera and other organisms began to evolve shells for protection about half a billion years ago. The Census of Antarctic Marine Life (CAML) was noted among *Time's* Top Ten Scientific Discoveries of 2007, and on May 17, 2007, one little deep-sea carnivorous sponge made the cover of the scientific journal *Nature*. That same year *Discover* cited the Census of Marine Life as "one of the most important experiments in the world."

Since their initial discovery in 1977, hydrothermal vents and seeps have been found at all oceans depths and in many localities throughout the world. These isolated ecosystems are fueled by hot and cold flows of hydrothermal fluid replete with reduced compounds such as hydrogen sulfide and methane. It is now thirty years since the discovery of microorganisms and animals at the Galapagos hydrothermal vents that depend on chemical energy from within the Earth. These oases occur in areas of lava flows and vent that release hydrothermal fluid at temperatures up to 350° C. Fluids at these temperatures support Archaea, microorganisms adapted to high temperatures and now accepted as one of three separate domains of life distinct from bacteria and the Eukaryota, the third major division of life that includes most familiar groups of one-celled organisms as well as plants and animals. The most distinctive vent animals are large, brilliant, red-plumed worms up to three centimeters in width and meters in length, which secrete thick white tubes that provide both support and protection from predators. Vent microorganisms and their enzymes are being used in commercially-valuable chemical processes. Flows from cold and hot seeps and vents of varying chemical compositions, and unusual features such as mud volcanoes are among the habitats for hydrothermal vent animals such as "Pompeii" worms that live at very high temperatures, corals, several kinds of abundant chemosynthetic mussels and clams, and tubeworm thickets. Chemosynthetic symbionts are now recognized in animals from hydrothermal environments at all ocean depths.⁹ The list of animals with chemosynthetic bacteria include species of sponges, clams, mussels, snails, shrimp, and almost all the major groups of worms. A recent addition, the Yeti crab,¹⁰ is covered in long, hairy-looking setae that host microbial mat microorganisms, thought to serve as a nutritional supplement.

Seamounts are underwater mountains that constitute a plethora of unique, globally distributed habitats where, despite many highly successful CoML expeditions, the diversity of living creatures is only beginning to be described. Large seamounts fed by hot spots in the Earth's mantle may become island chains, such as the Azores, Galapagos, Hawaiian, and Malay archipelagos. The year 2099 is the 200th anniversary of Charles Darwin's birthday thus the importance of island archipelagoes in the development of the theory of evolution is being recognized. Darwin was highly influenced by his discoveries in the Galapagos Islands and Alfred Russell Wallace was similarly impressed by the evidence for evolutionary processes he observed in the Malay Archipelago. New Zealand plans to protect seamounts in ten percent of its 1.7 million-hectare exclusive economic zone by 2010. The United States established the Papahānaumokuākea National Marine Monument in 2006 to protect 360,000 KM² of ocean waters and ten islands and atolls in the Northwestern Hawaiian Islands, an area that also includes numerous seamounts. Before leaving office, President George W. Bush proposed protection of the Lind Islands and another area in a large section of the Northern Mariana Islands. A more complete sampling of these areas will have an enormous influence on our future understanding of the origins and maintenance of biodiversity in tropical marine environments.

International Census of Marine Microbes (ICOMM)

The ICOMM team (led by Mitchell Sogin and Linda Amaral Zettler of the Marine Biological Laboratory in Woods Hole and Jan de Leeuw of the Royal Netherlands Institute for Marine Research) is using modern gene-sequencing equipment to obtain "sequence tags" that define microbial "operational taxonomic units" as proxies for species. These techniques are revealing an unexplored universe of microorganisms at all depths in the ocean in a variety of deep-sea habitats.¹¹ Modern molecular methods using high-speed computers to analyze gene sequence data enable definition of thousands of distinct low-abundance populations of marine

“species,” which appear to represent a massive number of species and many higher-level taxa. Thousands of new species of marine microbes appear to be present in water samples from the deep North Atlantic and two deep-sea hydrothermal vents in the vicinity of Axial Seamount on the Juan de Fuca Ridge. Most previous estimates of the species richness of microbial life in the ocean are much lower. These new findings will change the way we think about microbial activities in the deep sea, which we know will change the way we think about microbial activities in the deep sea, which we know play an important role in maintaining the ocean’s chemical composition. But a clear understanding will be difficult, given that most “species” are represented by single individuals in either samples or clusters of samples from the same site; a far greater sampling effort will be required to represent the diversity of oceanic microbial life.

Archaea thrive at temperatures up to 400°C mostly in hot springs on land and hydrothermal vents and seeps throughout the mid-ocean ridge system. Oceanic microbes, such as those that thrive on free mercury at high concentrations (up to 11 nmol/litre) in acid waters (pH 3.3-3.8) and temperatures in excess of 300°C, are likely to be relatives of early life on the planet.¹² An understanding of the distribution of microorganisms, including rare species, requires a massive effort using molecular approaches to measure species diversity and a variety of quantitative sampling methods to identify microhabitats at all depths.

The discovery of abundant microorganisms dependent on methane at all depths in the ocean and thousands of meters below the sea floor¹³ increases the likelihood of finding life elsewhere in the universe. Methane and water have been found on Mars suggesting that, in a later decade, a census of Martian life may be a real possibility.

Exploration Beyond 2010

CoML is beginning to delineate the broad ranges of marine habitats and their species richness and abundance, but full exploration of the vast sediment-covered ocean floor; continental, island and seamount margins; the mid-ocean ridges; and the approximately 1.3 billion KM³ volume of the ocean will require a continuing commitment. The rate of CoML’s discovery of new species has accelerated rapidly. The greatest numbers of marine species have been found in tropical coral reefs (CReefs); the vast areas of the deep-sea abyssal plains (CeDAMar); continental margins (COMARGE); polar areas (CAML) and Arctic Ocean Diversity (ArcOD); and seamounts (CenSeam). About half of all species from each newly explored areas of deep-sea floor have never been seen before. Present estimates of the number of deep-sea animal species range from 500,000 to 10 million—the uncertainty of these estimates is a true reflection of how relatively unexplored the deep sea truly is. Our grasp of known and unknown species diversity is generally greater in shallow water environments, which are often better sampled, but coral reefs represent another habitat where the correct order of magnitude of species diversity is still unknown. Much has been accomplished in the first Census of Marine Life—but there is clearly much more work to do. As the gargantuan effort to describe life in the ocean in 2010 comes to completion, a new generation of young scientists is planning the next census of ocean life to be completed in 2020.

Footnotes

Ocean Studies Board and National Research Council, *Oceanography in the Next Decade: Building New Partnerships* (Washington, D.C.: National Academy Press, 1992). Ocean Yearbook 24: 1-8.

P.D.N. Hebert, A. Cywinska, S.L. Ball and J.R. deWaard, “Biological Identifications through DNA Barcodes,” *Proceedings of the Royal Society of London B* (2003) 270:313-321

Available online: www.barcodinglife.org/views/login.php.

Available online: www.barcoding.si.edu.

Available online: www.comlmaps.org.

Available online: www.coml.org/projects/projects.

Available online: www.iobis.marine.rutgers.edu.

Available online: www.topp.org.

N. Dubilier, C. Bergin and C. Lorr, “Symbiotic Diversity in Marine Animals: The Art of Harnessing Chemosynthesis,” *Nature Reviews Microbiology* 6 (2009): 725-740.

E. MacPherson, W. Jones and M. Segonzac, “A New Squat Lobster Family of Galatheaidea (Crustacea, Decapoda, Anomura) from the Hydrothermal Vents of the Pacific-Antarctic Ridge,” *Zoostema* 27, no. 4 (2005): 709-723.

M.L. Sagin, H.G. Morrison, J.A. Huber, D.M. Welch, S.M. Huse, P.R. Neal, J.M. Arrieta and G.J. Herndl, “Microbial Diversity in the Deep Sea and the Underexplored ‘Rare Biosphere,’” *Proc. Natl. Acad. Sci.* 103, no. 32 (2006): 12115-12120.

M. Crespo-Medina, A. Chatziefthimiou, N. Bloom, G. Luther, D. Wright, J. Reinfelder, C. Vetriani and T. Barkay, “Adaptation of Chemosynthetic Microorganisms in Elevated Mercury Concentrations in Deep-Sea Hydrothermal Vents,” *Limnology and Oceanography* 54, no. 1 (2009): 41-49.

S. D’Hondt, B.B. Jorgensen, D.J. Miller, A. Batzke, R. Blake, B.A. Cragg, H. Cyplonka, G.R. Dickens, T. Ferdman, K.U. Hinrichs, N.G. Holm, R. Mitterer, A. Spivack, G. Wang, B. Bekins, B. Engelman, K. Ford, G. Gettemy, S.D. Rutherford, H. Sass, C.G. Skillbeck, I.W. Aiello, G. Guerin, C.H. House, F. Inagaki, P. Meister, T. Naehr, S. Nitsuma, R.J. Parkes, A. Schippers, D.C. Smith, A. Teske, J. Wiegand, C.N. Padilla and J.L.S. Acosta, “Distributions of Microbial Activities in Deep Seafloor Sediments,” *Science* 306 (2004): 2216-2219.

The Census of Marine Life was 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" was released in 2010 in London.^[1] Contents. 1 Census program.Â Census researchers undertook the task of constructing the history of marine animal populations since human predation became important, roughly the last 500 years. This program component is the History of Marine Animal Populations (HMAP). The largest component of the Census involved investigating what now lives in the world's oceans through 14 field projects. Life in the World's Oceans: Diversity, Abundance and Distribution is a true landmark publication. Comprising the synthesis and analysis of the results of the Census of Marine Life this most important book brings together the work of around 2000 scientists from 80 nations around the globe.Â Comprising the synthesis and analysis of the results of the Census of Marine Life this most important book brings together the work of around 2000 scientists from 80 nations around the globe. The book is broadly divided into four sections, covering oceans past, oceans present, oceans future and a final section covering the utilisation of the data which has been gathered, and the coordination and communication of the results. -- Forms a baseline of marine life's diversity, distribution, and abundance against which future change can be measured. OBIS Network. Stakeholders.Â In Nagoya October 2010, the 10th Conference of the Parties to the Convention on Biological Diversity (Decision COP10/29 para 10 and 35;) requested Member States to further enhance globally networked scientific efforts, such as the Ocean Biogeographic Information System (OBIS), to continue to update a comprehensive and accessible global database of all forms of life in the sea, and further assess and map the distribution and abundance of species in the sea. Ecologically or Biologically Significant Areas (EBSAs): Criteria.