The J. Frederick Grassle Scientific Symposium on the Census of Marine Life
Poster Session

Lead Author	Poster Title	Co-Authors	Affiliation	Location
Amaral Zettler, Linda	Attaining Operational Marine Biodiversity Observations	Gustav Paulay, J. Emmett Duffy, Reg Beach, Michael Feldman	USNC	**F24**
Appeltans, Ward	Marine Species Information Systems at VLIZ	Decock Wim, De Hauwere Nathalie, Vandepitte Leen, Claus Simon, Deneudt Klaas, Vanhoorne Bart, Hernandez Francisco, Mees Jan	OBIS	**F26**
Appeltans, Ward	The World Register of Marine Species, the first online inventory of all marine species	Decock Wim, Vanhoorne Bart, Hernandez Francisco, Bouchet Philippe, Boxshall Geoff, Fauchald Kristian, Gordon Dennis, Hoeksema Bert, Poore Gary, van Soest Rob, Stöhr Sabine, Walter Chad, Costello Mark J.	WoRMS	**F29**
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Baker, Maria C.	ChEss – Biogeography of Chemosynthetic Ecosystems in the Deep	Eva Z. Ramirez-Llodra, Paul A. Tyler, Christopher R. German, and 22 members of the ChEss SSC	ChEss	**B5**
Baker, Maria C.	ChEss – New Discoveries around the Globe	Eva Z. Ramirez-Llodra, Paul A. Tyler, Christopher R. German, and 22 members of the ChEss SSC	ChEss	**B6**

Baker, Maria C.	ChEss – Education and Outreach (Education Supplement)	Eva Z. Ramirez-Llodra, Paul A. Tyler, Christopher R. German, and 22 members of the ChEss SSC	ChEss	**B7**
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Bergstad, O.A.	North Atlantic Mid-Ocean Biodiversity: what did we learn?	Ó. Ásthórsson, I. Byrkjedal, A.V. Gebruk, J.A. Perez, U. Piatkowski,I.G. Priede, R. S. Santos, M. Vecchione, P. Lorance	MAR-ECO	**C1**
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Brainard, Rusty	Autonomous Reef Monitoring Structures (ARMS): From Science to Outreach—A Universal Method to Collect Knowledge of the Unknown.	Nancy Knowlton, Julian Caley, Megan Moews, Molly Timmers, Laetitia Plaisance, Amanda Toperoff	CReefs	**D2**
Bucklin, Ann	DNA Barcoding of Marine Zooplankton	Blanco-Bercial, L., R. Machida, B.D. Ortman, R.M. Jennings, and L.M. Nigro	CMarZ	**C4**

Carney, R.	Continental Margin Ecosystems on a worldwide scale – II. Large-scale distribution and diversity patterns revisited along continental slopes	Menot L., Billet D.S.M, Galéron J., Ingole B., Kitazato H., Krylova E., Levin L., Poore G., Lavrado, H. P., Rowe G., Sellanes J., Vanreusel A & Sibuet M.	COMARGE	**B8**
CenSeam Science Community	A Global Census of Marine Life on Seamounts (CenSeam)		CenSeam	**B2**
CenSeam Science Community	Fact, fiction, and the future: a synthesis of seamount ecological paradigms		CenSeam	**B3**
CenSeam Science Community	The impacts of human activities on seamounts: low resilience of biota to trawling and mining		CenSeam	**B4**
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Costello, Mark	Global marine biogeographic analysis using data published through the Ocean Biogeographic Information System	Peter Tsai, Pui Shan Wong, Alan Cheung, Mark Gibbons, Annelies Pierrot, Les Watling	Cross-Project Synthesis	**A10**
Ebbe, B.	Abyssal Plains—from quiescent, lifeless deserts to dynamic hotspots of biodiversity and sensors for climate change	S. Keller, P. Martinez Arbizu, and C. Smith	CeDAMar	**A1**
Ebbe, B.	A decade of discovery on abyssal plains of the world's oceans. What we have learned about the largest ecosystem on Earth.	S. Keller, P. Martinez Arbizu, and C. Smith	CeDAMar	**B1**
Ellis, Sara L.	A Comparison of Regional Marine Biodiversity Studies and Their Application to Ecosystem-Based Management	Lewis S. Incze, Peter Lawton, Brian R. MacKenzie, C. Roland Pitcher, Thomas C. Shirley, Henn Ojaveer, John W. Tunnell, and Margit Eero	GoMA	**D6**
Fautin, Daphne	An Overview of Marine Biodiversity in United States Waters	Melissa Brodeur, Michael Feldman, Andy Rosenberg, Wes Tunnell	USNC	**F25**

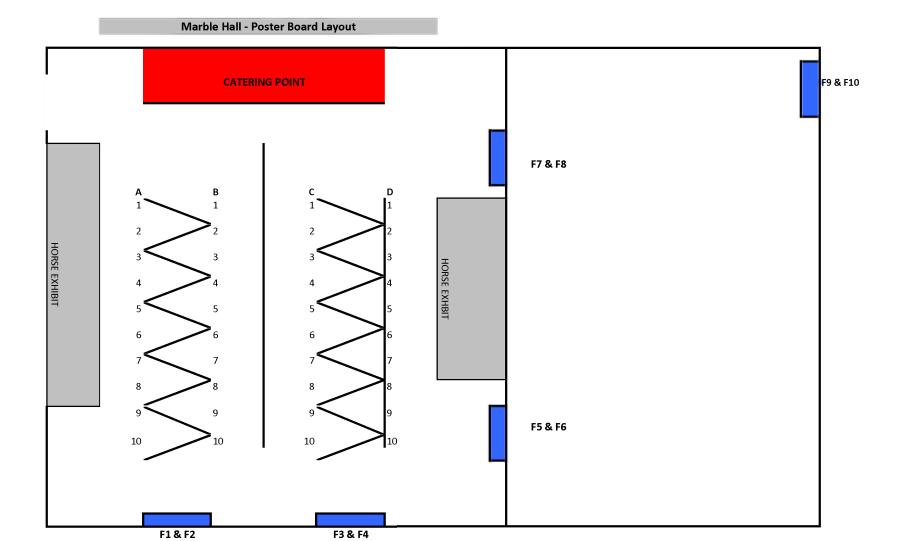| Fernandes, Christabelle E.G.	Benthic bacterial diversity: iron ore dominated mangroves versus ilemenite-rich beach sediment.	Sheryl O. Fernandes, P.A. Loka Bharathi	Indian Ocean	**F18**
Francis, K.X.	Present Status of DNA Barcoding of Marine Species from India	Giridhar, R., Jayachandran, K.V., Vijayalakshmi R Nair, Achuthankutty C.T., Shanta Nair	Indian Ocean	**F19**
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Hopcroft, R.R.	Arctic Ocean Diversity: Exploration in the field	Bluhm BA, Gebruk AV, Gradinger R, Iken K, Kosobokova KN, Weslawski JM, Sirenko BI, and IPY collaborators	ArcOD	**F4**
Hsiang, Stephanie Y.	Synergistic Involvement of High School Students in Graduate Level Research Opportunities: A Foundation for Unprecedented Success in Achieving NaGISA's Goals	Kyle S. Saleeby	Niceville High School	**F28**

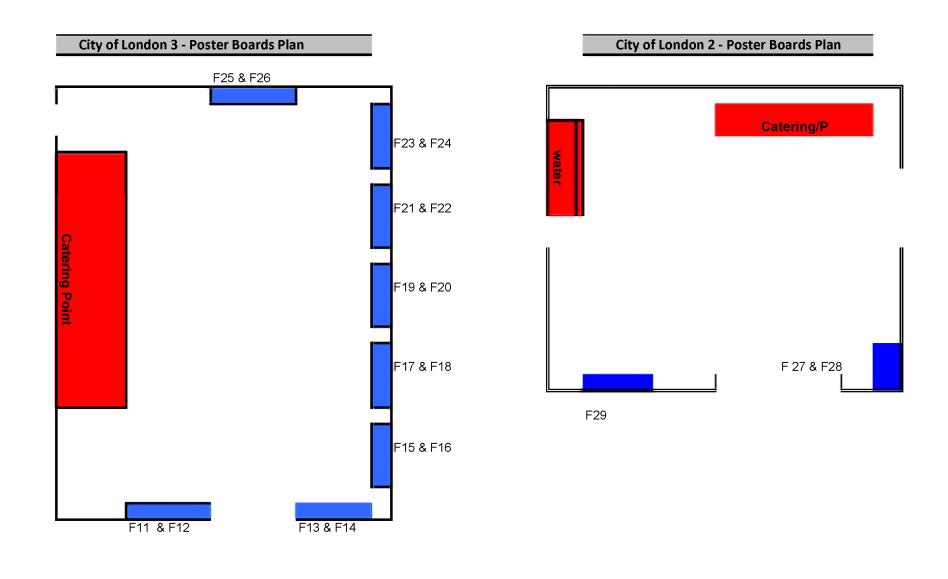| Iken, Katrin	Global-scale biodiversity patterns in nearshore ecosystems	Brenda Konar, Juan Jose Cruz, Lisandro Benedetti-Cecchi, Gerhard Pohle, Patricia Miloslavich, Ann Knowlton, Edward Kimani, Yoshihisa Shirayama	NaGISA	**F5**
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Knowlton, Nancy	Diversity! Census of Coral Reef Ecosystems Scientists Discover New Species and Fascinating Diversity!	Julian Caley, Rusty Brainard, Megan Moews, Laetitia Plaisance, Amanda Toperoff	CReefs	**D4**
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Narayanaswamy, Bhavani E.	Biodiversity of the European Seas	Henn Ojaveer, Marta Coll, Roberto Danovaro	EuroCoML	**F16**
Nishida, S.	Zooplankton species discovery in a biodiversity hotspot: marginal seas of Southeast Asia	S. Ohtsuka, J. Nishikawa, et al.	CMarZ	**C6**

Paulli Pravato, Kira	History of Marine Animal Populations: Stories on Marine Animal Populations and their Exploitation	Anne Husum Marboe, Poul Holm	HMAP	**A8**
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Wei, Chih-Lin	Global Patterns and Predictions of Seafloor Biomass	Gilbert T. Rowe, Elva Escobar-Briones, Antje Boetius, Thomas Soltwedel, Julian Caley, Falk Huettmann, Fangyuan Qu, Zishan Yu, Mary K. Wicksten, Jeffrey G. Baguley, Michael A. Rex, Jyotsna Sharma, Yousria Soliman, Roberto Danovaro, Clifton C. Nunnally, Jody W. Deming, Ian R.MacDonald, Mélanie Lévesque, Jan Marcin Weslawski, Maria Wlodarska-Kowalczuk, Baban S. Ingole, Brian J. Bett, Bodil A. Bluhm, Katrin Iken, Bhavani E Narayanaswamy, Paul Montagna	Cross-Project Synthesis	A3
Welch, David Mark	Measuring Alpha Diversity Across Microbial Ocean Realms	Susan Huse and Linda Amaral-Zettler on behalf of the ICoMM Alpha Diversity Working Group	ICoMM	D10
White, William	New Australian Sharks and Rays		Australia	F10
Wiebe, P. H.	Sampling the deep sea: zooplankton and fish of the North Atlantic	S. Schnack-Schiel, T.T. Sutton, L.P. Madin, M.V. Angel, F. Pagés*, R.R. Hopcroft, D. Lindsay, others	CMarZ	C7
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Williams, Allen	Seamount Ecosystems Conserved in the Huon Commonwealth Marine Reserve, Australia		Australia	**F12**
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Worm, Boris	The Future of Marine Animal Populations Project	Heike K. Lotze, Ian Jonsen, Derek Tittensor, Camilo Mora, Marta Coll, Arliss Winship, Catherine Muir	FMAP	**A7**
Zaiko, Anastasija	Invasive Alien Species in European Marine Ecosystems	Sergej Olenin	EuroCoML	**F15**

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Attaining Operational Marine Biodiversity Observations

Linda Amaral Zettler, Gustav Paulay, J. Emmett Duffy, Reg Beach, Michael Feldman*

*Ocean Leadership, 1201 New York Ave., NW, Fourth Floor, Washington, DC 20005

With the accelerating loss of biodiversity brought on by global climate change, ocean acidification and man's activities, it is increasingly urgent to monitor the status and trends of biodiversity. With guidance from the U.S. National Committee, a federally sponsored workshop will be held 24-27 May 2010 to determine the status of current marine biodiversity observation capabilities and to scope future solutions which may provide for the development of biodiversity proxies, with national and global applications. Utilizing many of the CoML projects** as starting points for operational biodiversity observing, the workshop will provide a set of community based options to the federal agencies necessary for the implementation of a national and global biodiversity monitoring network. These recommendations will also be vetted though and an online public forum prior to being finalized.

** CReefs, ICOMM, TOPP, POST, OBIS

Marine Species Information Systems at VLIZ

Appeltans Ward, Decock Wim, De Hauwere Nathalie, Vandepitte Leen, Claus Simon, Deneudt Klaas, Vanhoorne Bart, Hernandez Francisco, Mees Jan (Flanders Marine Institute)

More and better access to high quality information on species is essential to increase our knowledge on biodiversity and to address the global crisis it faces. Computer technologies now provide a workable platform to properly manage this information and standard data schemes and exchange protocols make online systems interoperable. Consequently, a lot of previously scattered information can now be integrated, analyzed and made publicly available. The Flanders Marine Institute has a professional, government funded data centre which takes a lead in marine biodiversity data management on a local and international level. It is host of over 100 websites of projects and organizations and has developed a full suite of inter-linked data systems to archive, document, integrate and disseminate information over the internet.

Because species are the most practical and widely applicable measure of biodiversity, and species names are at the foundation of quality control in biological studies, VLIZ has developed a taxonomic database that is now the single most complete inventory of all marine life (the World Register of Marine Species, WoRMS). WoRMS is the taxonomic backbone and serves as a standard reference for many institutions and projects. VLIZ also hosts the portal of EU-nomen, which is an initiative towards taxonomic standardization in Europe.

The species composition in a particular habitat or area is the most important aspect of biodiversity as it provides a measure of the stability and environmental health of the ecosystem. To manage species occurrences, VLIZ built the European node of the Ocean Biogeographic Information System (EurOBIS) and coordinates the biological lot of the European Marine Observation and Data Network (EMODNET). This inter-operable network of systems of European marine observations provides the best measure of marine biodiversity in Europe.

Geographic Information Systems (GIS) have become indispensable tools in managing and displaying marine biodiversity data. VLIZ developed a standardized register of place names, the VLIZ Marine Gazetteer (VLIMAR). This gazetteer includes a hierarchical dictionary of place names and areas at sea (e.g. islands, sandbanks, bays, sea-mount chains ...) and provides shape files of these areas. VLIMAR is the first international, internet-accessible gazetteer for the marine environment. In parallel with this geographic system, VLIZ plans to build a glossary and standard marine habitat classification system.

To document and archive all these data and information, VLIZ has built the Integrated Marine Information System (IMIS) and Marine Data Archive (MDA). IMIS is a relational database that integrates information on people, institutions, projects, websites, conferences, datasets, infrastructure, maps and literature.

The expertise in biodiversity data management, the networking and communication skills and the long-term support VLIZ can provide, makes their systems authoritative and world-class standard references respected by many national and international organizations. These marine species information systems significantly improve and maximize the use of biodiversity data and information for science, the public at large and for generations to come.

The World Register of Marine Species, the first online inventory of all marine species

Appeltans Ward[1,2], Decock Wim[2], Vanhoorne Bart[2], Hernandez Francisco[2], Bouchet Philippe[1], Boxshall Geoff[1], Fauchald Kristian[1], Gordon Dennis[1], Hoeksema Bert[1], Poore Gary[1], van Soest Rob[1], Stöhr Sabine[1], Walter Chad[1], Costello Mark J. [1]

[1]WoRMS Steering Committee
[2]Flanders Marine Institute (VLIZ), Oostende, Belgium

The World Register of Marine Species (WoRMS) is a collaborative effort by over 200 world-leading taxonomists from 27 countries to create an authoritative, open-access web-resource for all marine species (and where editors wish, their terrestrial and freshwater relatives).

In 2007, this register of marine species grew out of the European Register of Marine Species (ERMS), and its combination with several other species registers maintained at the Flanders Marine Institute (VLIZ) in the framework of the EU Network of Excellence 'Marine Biodiversity and Ecosystem Functioning' (MarBEF). It now integrates and hosts over 20 global (Cetacea, Porifera, Copepoda, Isopoda …), regional (Europe, Antarctica, Canada, Eastern Africa …) and thematic (harmful algae, invasive species …) databases. Rather than building separate registers for all projects, and to make sure the taxonomy used in these different projects is consistent, VLIZ developed a single consolidated database. Editors are provided with privileged online access to the taxa they are responsible for and only need to edit the information once.

WoRMS works with related initiatives to ensure complementarity and makes its content permanently available to readers and to other databases, including the Ocean Biogeographic Information System, Species 2000's Catalogue of Life, SeaLifeBase and the Encyclopedia of Life. Via our website, web services and full download access, many institutions, national and international data centres and research groups are using WoRMS as their standard taxonomic reference and therefore it provides an important quality control mechanism.

WoRMS is one of the very few online resources with a permanent host institution. VLIZ has a government funded professional data centre with a strong focus on biological data management. The intellectual property rights of WoRMS are governed by the scientific Society for the Management of Electronic Biodiversity Data (SMEBD). All editors are life-members of SMEBD and elect a governing council which appoints host institutions for its databases, rather like a society may have a publisher for its journal.

As of 1st May 2010, WoRMS contains 330,000 scientific (Latin) names, of which 176,000 valid species names and 90,000 important synonyms (i.e. incorrect names in use), 18,000 vernacular names, 137,000 key literature references, 42,000 specimen details, 224,000 published distributions, 90,000 web links, 12,000 images and many other species related information (biology, habitat, feeding type …).

WoRMS is recognized as an affiliated project by the Census of Marine Life and we cooperate to achieve our common goal of inventorying all described marine species by the end of 2010.

Towards a pan-Arctic inventory of the species diversity of the macro- and megabenthic fauna of the Arctic shelf seas

Archambault; P., Piepenburg, D., Ambrose, W. G., Blanchard, A., Bluhm, B. A., Carroll, M. L. Conlan, K. E., Cusson, M., Feder, H. M., Grebmeier, J. M., Jewett, S. C., Lévesque, M., Petryashev, V. V., Sejr, M. K., Sirenko, B. I., Włodarska-Kowalczuk, M.

Although the knowledge of Arctic seas increased tremendously in the past decade, benthic diversity was investigated at regional scales only, and no attempt has been made to examine it across the entire Arctic. We present a first pan-Arctic account of the species diversity of the macro- and megabenthic fauna of the Arctic marginal shelf seas. It is based on an analysis of 25 published and unpublished species-level data sets, together encompassing 14 of the 19 marine Arctic shelf ecoregions and comprising a total of 2636 species, including 847 Arthropoda, 668 Annelida, 392 Mollusca, 228 Echinodermata, 205 Bryozoa, and 296 species of other phyla. For the four major phyla, we also analyze the differences in faunal composition and diversity among the ecoregions. Furthermore, we compute gross estimates of the expected species numbers of these phyla on a regional scale. Extrapolated to the entire fauna and study area, we arrive at the conservative estimate that 3900 to 4700 macro- and megabenthic species can be expected to occur on the Arctic shelves. These numbers are smaller than analogous estimates for the Antarctic shelf but the difference is on the order of about two and thus less pronounced than previously assumed. On a global scale, both polar biomes are characterized by intermediate species numbers. Our preliminary pan-Arctic inventory provides an urgently needed assessment of current diversity patterns that can be used by future investigations for evaluating the effects of climate change and anthropogenic activities in the Arctic.

North Atlantic Mid-Ocean Biodiversity: What did we Share?

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Abstract

The story that mid-ocean ridges are the unknown mountain chains of the world, inhabited by weird creatures seldom observed or disturbed by the prying eyes of humans, proved powerful and surprising to wide audiences of all ages. Reporting from the deep ocean as it was being explored, using a multitude of technologies and approaches, resulted in major public impact and enhanced awareness. Critical factors were the good planning from the concept stage and conscious integration of dedicated scientists and students with professional dissemination partners and producers, and supportive sponsors outside the science community. Successes and some shortcomings are presented, and examples of responses from the wider community. Is there a lasting legacy?

ChEss – Biogeography of Chemosynthetic Ecosystems in the Deep Sea (ChEss Times)

Maria C. Baker, Eva Z. Ramirez-Llodra, Paul A. Tyler, Christopher R. German, and 22 members of the ChEss SSC.

Since 2002, the collaborative efforts of ChEss scientists have enhanced our knowledge of the biogeography of deep water chemosynthetically-driven ecosystems around the globe. Collectively, ChEss scientists have discovered many new sites of hot- and cold-water venting including the deepest, hottest, most northerly (Arctic) and most southerly (Antarctic) hydrothermal black smoker vents known to science and the largest known cold seep on the planet. Many of these discoveries were achieved using pioneering robotic techniques that have enhanced our exploration efficiency. ChEss associated taxonomists have so far described over 200 species of mega-, macro- and meiofauna from chemosynthetically-driven environments that are new to science – a discovery rate equivalent to 1 new species every 2 weeks - and there are hundreds more awaiting description. Analysis of faunal distributions, affinities, dispersal pathways and ecological processes for chemosynthetically-driven ecosystems is beginning to shed light on the some of the patterns and processes that shape this astonishing deep-water world. ChEss has increased public awareness of these environments through outreach efforts, often in collaboration with Census groups. ChEss scientists are using their expertise to highlight the vulnerability of these ecosystems to anthropogenic impacts and are working with all stakeholders towards sustainable management regimes.

ChEss – Education and Outreach (Education Supplement)

Maria C. Baker, Eva Z. Ramirez-Llodra, Paul A. Tyler, Christopher R. German, and 22 members of the ChEss SSC.

ChEss has conducted a wealth of educational activities during the course of the programme including the provision of peer-reviewed grants for taxonomists in training (TAWNI), scientist and student exchange visits, student travel bursaries for conferences, taxonomy workshops and cruises and a series of ChEss mini-grants for ChEss synthesis legacy products. ChEss has also increased public awareness of these interesting environments through outreach efforts such as contributions to a number of deep-sea guide books, exhibits and art competitions and have even produced their own educational comic book about the discovery of hydrothermal vents. Many public lectures have been given by ChEss SSC members relating to the work of the Census and the ChEss office have laid on a number of outreach events, including live ship-to-shore broadcasts. The ChEss website is host to well-visited education pages about vents, seeps and whale falls and has maps, visualizations and animations aimed at public education. One of the most important outreach objectives for ChEss has been in providing leadership in highlighting the vulnerability of deep-water chemosynthetic ecosystems to anthropogenic impacts and this activity will undoubtedly continue way beyond the end of the Census.

ChEss – New Discoveries around the Globe (Travel Supplement)

Maria C. Baker, Eva Z. Ramirez-Llodra, Paul A. Tyler, Christopher R. German, and 22 members of the ChEss SSC.

Investigations of chemosynthetic environments in the deep sea span just three decades, owing to their relatively recent discovery. In 2002, ChEss outlined a field programme for the strategic exploration and investigation of chemosynthetic ecosystems in key areas that would provide essential information to close some of the main gaps in our knowledge. This program was motivated by three scientific questions: (1) What are the taxonomic relationships among different chemosynthetic habitats? (2) What are the conduits and barriers to gene flow among those habitats? (3) What are the environmental factors that control diversity and distribution of chemosynthetically driven fauna? To address these questions at the global scale, four key geographic areas were selected for exploration and investigation: the Atlantic Equatorial Belt (AEB), the New Zealand Region (RENEWZ), the Polar Regions (Arctic and Antarctic), and the southeast Pacific off Chile region (INSPIRE). To that end, ChEss scientists have embarked on a large number of research cruises during the past 8 years and, using state of the art technologies and methodologies, and with international coordination of efforts, have made extraordinary advances in our knowledge of chemosynthetic systems.

NaGISA-FMAP Cross-project
Spatial homogenization of species richness in marine ecosystems

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Increasing climatic instabilities and human disturbances are causing rapid shifts in environmental conditions at global and local scales. Despite growing concern about the ecological consequences of compound perturbations, a clear understanding of how natural and anthropogenic environmental variables combine to shape macroecological patterns of biodiversity has remained elusive. We examined how five natural and nine anthropogenic environmental variables influence spatial patterns of species richness across 4324 sites in nine large marine ecosystems. We found that a spatial model that included the interaction between natural and anthropogenic environmental drivers provided a better fit to estimates of species richness than an additive model that ignored synergistic effects among drivers. Residual analysis indicated that anthropogenic environmental variables contributed to maintain significant self-similar (autocorrelated) patterns in species richness over regional spatial scales (100s to 1000s km). These results suggest that anthropogenic perturbations can reduce natural fluctuations in species richness contributing to large-scale spatial homogenization of marine biodiversity.

North Atlantic Mid-Ocean Biodiversity: what did we learn?

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Abstract

Mid-ocean ridges are major features of all oceans. Prior to CoML ridge research was mainly either geological or fisheries-orientated, and the rather limited ecological research targeted oceanic islands, seamounts, and hydrothermal vent systems. MAR-ECO mobilised comprehensive new technologies and a multidisciplinary team to study the photosynthetic communities associated with the mid-ocean ridge. A diverse and abundant fauna of around 1000 macro- and megafaunal species and their major patterns of distribution were documented. Food-web structure was revealed and major processes identified. Challenges in future studies are high-quality sampling of the benthic boundary layer and time-series studies of distribution and abundance dynamics. CoML made a difference, but mid-ocean ecosystems remain remote places where the 'unknown' far exceeds the 'known'.

Tagging of Pacific Predators: Understanding Apex Marine Predator Movements in a Dynamic Ocean

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Marine pelagic predators face unprecedented challenges and for many, uncertain futures. Overexploitation and climate change are impacting the abundance and distribution of top predators in ocean ecosystems. Extinctions, the loss of biodiversity and ecosystem services can only be overcome through an understanding of ecological and evolutionary processes, distribution patterns, and ecosystem function. Our understanding of pelagic ecosystems is complicated by the challenges of synoptically studying multiple species in a biome that covers 70% of the planet. Recent advances in biologging techniques have provided tools for detailing the movements and migrations of animals in relation to ocean processes across a range of ecological scales. The Tagging of Pacific Predators (TOPP), a field program of the Census of Marine Life, deployed 4,300 tags on 23 species in the North Pacific, resulting in a biologging data set of unprecedented scale, covering 268,000 days spanning 2001-2010. TOPP is the first ocean basin scale cross-taxa study of marine predator distribution and movement patterns. Using tracks obtained with electronic tags and filtered using Bayesian state-space models, we describe fidelity to migration pathways and multi-species hot spots, characterize these hot spots oceanographically, and illustrate niche partitioning within and among congener guilds. Our results indicate that the California Current ecosystem and North Pacific Transition Zone are both attractive and retentive to a diverse range of marine vertebrates, and there is seasonal occupation driven by organismal preferences for thermal zones and oceanographic processes that enhance productivity. Knowledge of how pelagic animals exploit the marine environment is critical for establishing effective ocean protection strategies across multi-national boundaries.

Arctic Ocean Diversity (ArcOD): The strategy

Bluhm BA, Clarke C, Gebruk AV, Gradinger R, Hopcroft RR, Huettmann F, Kosobokova KN, Mecklenburg C, Raskoff K, Sirenko BI, Smirnov I

ArcOD's strategy has been directed to three key tasks: compilation of existing data, taxonomic identification of existing samples, and new collections focusing on regional and taxonomic gaps with all efforts conducted in the sea ice, water column and at the sea floor. This was achieved through pan-Arctic involvement with an international 13 member steering group, centers in Fairbanks and Moscow/St. Petersburg and a total of ~100 people from a dozen countries participating in field work, data contributions, mini-grants, species identifications, publications and presentations. ArcOD was also the cluster lead for the Arctic Marine Biodiversity Cluster of the International Polar Year 2007-9 containing 13 projects. ArcOD has created an online open-access database and web portal set up to be harvested by OBIS and GBIF. As of April 2010, 42 data sets comprising close to 200,000 taxonomic records have been contributed by Arctic scientists or compiled from scattered electronic and paper-only sources; ~10,000 of those are records of fish verified through museum visits around the world. ArcOD activities were widely communicated (i) to the science community in several special conference sessions including a 3-day session at the 2010 Arctic Frontiers Conference in Norway and (ii) by the international media in more than 50 countries with continued interest attracted through ArcOD's sought after photography of Arctic fauna and habitat.

AN EXTENSIVE LIPID STRUCTURE AND MASS SPECTROMETRY DATABASE TO RECOGNIZE MARINE MICROORGANISMS

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Background & Aims

To date, most databases for biochemical components of marine microbial origin focus on gene and protein sequences. For lipids, the most extensive library is LIPID MAPS, though it lacks marine microbial data [1]. Therefore, the International Consensus of Marine Microbes (ICoMM) collaborates with LIPID MAPS to generate a universal lipid database that also includes the diverse set of lipid structures unique to marine microorganisms [2]. A search engine will enhance this systematic lipid catalogue and a link a mass spectrometric library and geospatial information will further facilitate the recognition of lipid biomarker data in modern and ancient environments.

Methods & Results

So far we have submitted several types of lipid structures such as ladderane lipids bacteriohopanols, all-*cis* hentriaconta-9,15,22-triene, glycerolethers, derived from bacteria and archaea.

Conclusions

A large collection of marine microbial lipids will be instrumental in the identification of microbial life and concomitantly the inventory of microbial diversity.

References

[1] LIPID MAPS: http://www.lipidmaps.org/
[2] ICoMM: http://icomm.mbl.edu/

Autonomous Reef Monitoring Structures (ARMS):
From Science to Outreach—A Universal Method to Collect Knowledge of the Unknown.

Authors: Rusty Brainard[1], Nancy Knowlton[2], Julian Caley[3], Megan Moews[1], Molly Timmers[1], Laetitia Plaisance[2], Amanda Toperoff[1]

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The Census of Coral Reef Ecosystems (CReefs) and the National Oceanic and Atmospheric Administration (NOAA) are leading the development of a Census of Marine Life Scientific and Outreach Legacy—the Autonomous Reef Monitoring Structures (ARMS). ARMS roughly mimic the complexity of coral reefs to attract and collect colonizing non-coral invertebrates. They provide a systematic, consistent, and comparable method to assess and monitor cryptic reef diversity globally and over time, while also providing the world with a glimpse into this fascinating realm of understudied species through "Hands-on-ARMS" outreach. This standardized method for taxonomic and molecular analysis is further utilized to enhance ecosystem-based management and increase the ability to monitor/predict ecological impacts of global climate change, particularly ocean warming and acidification.

Over 500 ARMS have been deployed worldwide throughout the Pacific, Indian, and Atlantic Oceans for scientific research, as well as public outreach. They have been deployed in the Line and Phoenix Islands, American Samoa, the Northwestern and Main Hawaiian Islands, Wake Atoll, Guam, the Commonwealth of the Northern Mariana Islands, Lizard and Heron Islands on the Great Barrier Reef and Ningaloo Reef in Australia, Reunion, Europa, and Glorieuses Islands in the Indian Ocean, Moorea in French Polynesia, Florida's northern reef tract, Indian River Lagoon, Kimbe Bay in Papua New Guinea, Indonesia, Panama (as a successional study), and off of Honolulu, Hawaii (for testing and outreach). Further ARMS are planned for deployment in Puerto Rico, throughout the Coral Triangle, U.S. Sanctuaries, and possibly Taiwan, Turks and Caicos, and Belize.

With an increasing scarcity of trained invertebrate taxonomists, ARMS will enable researchers to obtain information more quickly and effectively using molecular techniques, particularly for the small, cryptic organisms that constitute the bulk of reef diversity. Genetic analysis of ARMS samples using 454 environmental sequencing protocols is currently under development through partnerships with the Smithsonian and California State University. At the same time, "Hands-on-ARMS" outreach is attracting new interest in these organisms and their

conservation.   ARMS deployed for outreach purposes have been collected for pilot living reef "Hands-on-ARMS" exhibits/demonstrations, which have already reached over 6,000 people of all ages at schools, science fairs and other public outreach events.

Background:
Coral reefs are among the most diverse ecosystems on earth, and yet they are also among the most threatened ecosystems on the planet due to the effects of climate change (global warming, coral bleaching, ocean acidification, and sea level rise) and other anthropogenic and natural threats. Coral species however, constitute only a small fraction of reef diversity, most of which consists of cryptic and usually poorly-known organisms. Consequently, with current estimates of global reef diversity remaining generally course and understudied, we know almost nothing about the extent to which reef degradation threatens reef diversity. With the exception of corals, concerns about reef loss have focused almost exclusively on ecosystem services and largely ignored biodiversity loss. As a result, the Census of Marine Life, Census of Coral Reef Ecosystems (CReefs) partners globally are focused on the research and understanding of types/distribution of understudied species obligately associated with healthy coral reefs, along with patterns of species diversity in relation to gradients of human disturbance and in lieu of climate change and ocean acidification.

DNA Barcoding of Marine Zooplankton
Authors: A. Bucklin, B.D. Ortman, R.M. Jennings, L.M. Nigro, J. Bradford-Grieve, M. Angel, R. Hopcroft, and N.J. Copley.

The Census of Marine Zooplankton (CMarZ) has a goal to determine DNA barcodes (short DNA sequences for species recognition and discovery) for the ~7,000 described species of holozooplankton (animals that drift with ocean currents throughout their lives). DNA barcodes are useful to ensure accurate species identification, assess species diversity, and reveal taxonomically significant geographic variation and cryptic species. CMarZ barcoding efforts have focused on some of the most common and ecologically important holozooplankton groups (e.g. calanoid copepods and euphausiids). Also, CMarZ has provided DNA barcodes for some of the most taxonomically challenging and least known groups (e.g., bathypelagic ostracods and chaetognaths).

Continental Margin Ecosystems on a worldwide scale – II. Large-scale distribution and diversity patterns revisited along continental slopes

Carney R., Menot L., Billet D.S.M, Galéron J., Ingole B., Kitazato H., Krylova E., Levin L., Poore G., Lavrado, H. P., Rowe G., Sellanes J., Vanreusel A & Sibuet M.

The continental slope lies in between the vast abyssal seafloor and relatively wide continental shelf as a narrow ribbon of ocean bottom characterized by dramatic transitions in pressure, temperature, currents and food influx. Continental margins are thus the widest gradient-dominated ecosystems on Earth, a unique trait that profoundly influences distribution and diversity patterns.

Deep-sea biologists have debated different hypotheses to explain depth-related patterns of the distribution and diversity of benthic and demersal organisms, in particular:
- that the diversity reaches a maximum at mid- to lower-slope depth,
- that the fauna is zoned into bands according to water depth,
- that faunal assemblages are dissimilar between depth zones but have a circum-margin distribution within a depth zone,
- and that the width of the zones increases with depth.

Since these observations were initially made (1880's – 1960's), numerous data have been collected on continental margins but few syntheses have been attempted. The COMARGE project explored several ways to test those old but still unresolved hypotheses. The first approach was to focus on two widespread taxa on continental margins, the squat lobsters and nematodes. The second approach was to undertake meta-analyses across taxa from data either mined from the literature and available in databases (OBIS and COMARGIS) or directly provided by members of the COMARGE network.

Results show that a depth change in species composition is a global pattern but one that is modulated along margins by local oceanographic processes. Similarly a maximum in diversity at mid-slope depth is commonly observed but the shape of the pattern and the depth of the maximum varies across taxa and locations.

This poster intends to illustrate progress made in the documentation and understanding of large-scale distribution and diversity patterns along continental margins. Illustrations will include global maps of available data pointing to graphics showing either the zonation of species or the relationships between diversity indexes and depth, organic carbon fluxes or temperature in different regions of the globe.

A Global Census of Marine Life on Seamounts (CenSeam)
Authors: CenSeam Science Community

Seamounts are widespread features of the world's oceans and can support high levels of biodiversity and endemism, and can play an important role in patterns of marine biogeography. They can be highly productive ecosystems acting as feeding grounds for fishes, marine mammals, and seabirds. Seamounts are targeted for resource extraction such as fisheries and minerals exploration, but are ecologically vulnerable to exploitation. Recognizing a limited sampling effort (both in terms of number sampled and geographic scope) and understanding of seamount ecosystems, the Census of Marine Life field programme CenSeam (a global census of marine life on seamounts) commenced in 2005.

CenSeam has facilitated a variety of seamount research and been instrumental in connecting, focusing, and collating the efforts of many international researchers. The result is a substantial reduction in the unknowns of seamount biodiversity, and many significant advances towards a global understanding of seamount ecosystems.

The programme has successfully addressed the two CenSeam research themes: **Theme 1:** *What factors drive community composition and diversity on seamounts, including any differences between seamounts and other habitat types?* And, recognizing the need to advise seamount managers and policy makers on potential fishing and mining impacts, **Theme 2:** *What are the impacts of human activities on seamount community structure and function?*

CenSeam researchers have critically examined and shaped a new set of seamount paradigms, and gained insight into the threats to seamount ecosystems. The CenSeam database SeamountsOnline has been populated with the latest quality-assured data available, and a large number of new species have been added to the Encyclopedia of Life. Furthermore CenSeam continues to support major voyages to under-sampled oceanic regions e.g. Indian Ocean, South Atlantic.

CenSeam results have had a significant positive influence on marine policy development at both national and international levels, leading to improved management of seamount resources and conservation of seamount habitats. The programme results over the past 5 years have paved the way for the next era of seamount research, and major highlights will be showcased in this poster.

Fact, fiction, and the future: a synthesis of seamount ecological paradigms
Authors: CenSeam Science Community

Despite the relatively short history of seamount ecology a number of ecological paradigms have developed in the scientific literature and in conservation advocacy. Seamounts are frequently referred to as special or unique habitats, and as having faunal communities sufficiently different from those of other deep-sea habitats to warrant particular scientific attention. These concepts, coupled with human threats (such as fishing) to seamount habitat and communities, have provided the motivation for a number of seamount-focused research projects in recent years and the drive for the Census of Marine Life field project CenSeam (a global census of marine life on seamounts).

Drawing on CenSeam activities and products we will evaluate the evolution and robustness of existing paradigms in seamount ecology, as well as identify emerging paradigms - in particular that seamounts are highly variable in their community structure and function; some seamounts can have a rich biodiversity and high levels of endemism, but this cannot be generalised to all seamounts; and that seamount faunal composition is typically derived from a broad regional pool, although relative abundances may differ from adjacent areas of continental slope and other topographic features such as canyons and rises.

Based on the results of efforts over the life of CenSeam, and considering the results of all deep-sea field programmes, we will conclude by suggesting that future seamount research endeavors consider seamounts in the context of the wider deep-sea.

The impacts of human activities on seamounts: Low resilience of biota to trawling and mining
Authors: CenSeam Science Community

One of the central questions of the Census of Marine life project CenSeam (a global census of marine life on seamounts) is *what are the impacts of human activities on seamount community structure and function*? Seamounts are the target of major trawl fisheries and are of increasing interest for mineral resources, and as such seamount conservation has gained momentum.

CenSeam has carried out a number of studies using data from around the world to assess the vulnerability and resilience of seamount communities to the impacts of fishing and mining operations. Here we will review some of the key results.

Since the 1960s, seamounts have been subject to large-scale bottom trawl fisheries. Few fisheries have proven sustainable with most fish stocks showing strong declines. Bottom trawling has been proven to cause severe damage to benthic fauna, physically removing most of the mega benthos, with deep-sea corals and associated invertebrate assemblages being most susceptible. Few taxa are physically resistant to trawling impacts and overall the resilience of seamount ecosystems is very low. We have found no evidence that benthic assemblages recover in the short term (10 years) following spatial fishing closures.

Mining has recently emerged as a potential threat to seamount communities. However, whilst mining could have an equally damaging physical impact as trawling, the long-term effects are hypothesized to be less severe. For example, we have found the benthos of cobalt-rich ferromanganese crusts on seamounts could be similar to the fauna on non cobalt-rich crusts. However, those fauna found in areas of hydrothermal venting (where faunal assemblages can have high levels of endemism), of interest for polymetallic sulphides, have high conservation significance.

We conclude that seamount communities generally have low tolerance to human disturbance. Networks of spatial closures, allocated using systematic conservation planning, could be an effective option allowing exploitation and conservation to coexist.

The results of these studies have been widely disseminated through conference and stakeholder presentations, as well as scientific papers and reports. CenSeam has worked with, and advised, a range of international bodies, including UNEP, IUCN, FAO, COFI, CBD, SBSTTA, ISA, and several RFMOs on seamount issues in a concerted effort to inform resource management and conservation bodies.

Images from the Census of Marine Zooplankton
Authors: N.J. Copley, R.R. Hopcroft, C, Clarke-Hopcroft, L.P. Madin, and K. Joyce.

Zooplankton are highly diverse in form, color, and size. Striking images of living zooplankton species – some newly discovered by CMarZ scientists – are presented in a visually pleasing display. All the images are in natural color and show living zooplankton collected from CMarZ expeditions to the Sargasso Sea, Eastern Atlantic, Northwestern Australia, and elsewhere. The sizes of the images are approximately relative to actual size of the organisms. The posters are available from the WHOI Exhibit Center Shop, http://shop.whoi.edu.

Global marine biogeographic analysis using data published through the Ocean Biogeographic Information System

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We mapped the biogeography of marine species at a global scale, using the over 100,000 species with distribution data published through the Ocean Biogeographic Information System. Data analysis was preceded by cleaning (a) the taxonomy of species names to recognise synonyms, misspellings, and incomplete names, and (b) removal of erroneous and insufficiently geo-referenced data. Analysis used Sorensen's coefficient of similarity, a measure of species turnover and beta-diversity on presence only data, as this avoided bias by species absences due to incomplete sampling. All species were treated equally, so no adjustment (or transformation) was applied for sampling methods or abundance.

Analyses that used actual locations where species were recorded did not show coherent geographic patterns, indicating the affects of sampling bias. Species ranges were thus interpolated from the records to enable re-analysis of a spatially enriched dataset that more accurately reflected a species true distribution than sampled locations. Species were categorised according to whether they were primarily benthic or pelagic, so as to compare whether these life-styles affected species biogeography. A new topographic map of the world's oceans was prepared and enabled matching of species to depth and other topographical features. Both the primary (locations with species records) and secondary (species ranges) databases would be amenable to modelling against environmental data to provide more refined species range maps. When species occurrences were matched to the standard map of seas and oceans of the world as surrogates of species ranges, analyses produced geographically contiguous clusters of sea areas that would be predicted from previous comparisons of marine fauna in the literature.

Maps of species richness adjusted for sampling effort show highest diversity in coastal, tropical and sub-tropical areas. Correlations between sampling effort (number of records) and species richness against seabed and sea-surface area were negative and not statistically significant. This indicated that either the well-established species – area relationship does not apply in the oceans, and/or (most likely) that sampling effort has not been well-distributed across the oceans. The results of these analyses are presented, and show that the oceans are well connected in terms of their species composition, with no indications of sharp biogeographic boundaries. Such connectivity may partly explain why there are less species in the oceans than on land. These findings aid understanding of the evolution of ocean biodiversity, and could be applied in planning a global network of Marine Protected Areas that is representative of the oceans' biodiversity.

Abyssal Plains—from quiescent, lifeless deserts to dynamic hotspots of biodiversity and sensors for climate change

B. Ebbe, S. Keller, P. Martinez Arbizu, and C. Smith

The general perception of the abyssal plains was until very recently one of huge desert-like, quiescent areas of fine mud harboring only very few highly specialized lifeforms – often suspected to be living fossils from a distant time - that barely survived under the harsh conditions of the deep sea. Reproduction as well as evolutionary processes were thought not to take place in the abyss.

This image of the abyssal plains has changed profoundly, particularly during the past decade when data were collected in areas hitherto essentially unknown. In some areas, such as the central Pacific Ocean near the Hawaiian islands, biodiversity was found to be so high as to justify characterization as hotspots of biodiversity. However, as the abyssal ecosystem is devoid of primary production, the only source of nutrients is decaying material from surface waters, the so-called marine snow. Climate change, particularly global warming of the oceans, may change not only the quantity, but also the quality of marine snow. Different algae were shown to aggregate differently, potentially posing a major threat of starvation to abyssal organisms. As the diversity is so high that about every other animal in any sample belongs to a different species, it is likely to be affected as much as abundance. The abyssal seafloor, strange as it may sound, is likely one of the most sensitive indicators of beginning global change.

A decade of discovery on abyssal plains of the world's oceans: What we have learned about the largest ecosystem on Earth?

B. Ebbe, S. Keller, P. Martinez Arbizu, and C. Smith

The known, unknown and unknowable within the three main themes of the Census, abundance, diversity and distribution, is shown with regard to the abyssal plains. The general layout of the poster will reflect a matrix of known/unknown/unknowable and abundance/diversity/distribution, but hopefully text and images can be arranged in a way that represents the KUU and ADD grid without having to actually mention these categories. The astounding diversity of life that was discovered, possible dramatic changes in abundance that were once thought impossible, and new insights regarding cosmopolitism in an environment that to human eyes is much more homogeneous than it obviously is to its inhabitants will be presented along with an outlook on the many things we still do not know and possibly never will, converting the very general experience of generating a plethora of new questions along with each answer one finds.

A Comparison of Regional Marine Biodiversity Studies and Their Application to Ecosystem-Based Management

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Every study of an ecosystem is a compromise based on resources, time, interests of investigators and funding agencies, and social, legal and economic drivers. Each study therefore has unique approaches, opportunities, findings, and recommendations. We compare the motivations, objectives, approaches, and achievements of four ecosystem-level studies of marine biodiversity that have contributed to the first Census of Marne Life: the Gulf of Maine Area Census Program, Baltic History of Marine Animal Populations, Great Barrier Reef Seabed Biodiversity Project, and Gulf of Mexico Biodiversity Project. The purpose of this comparison is to identify how information and results from biodiversity studies can be used to improve decision-making on marine and coastal issues.

Each program was designed to improve understanding at the ecosystem level, but they were created independently and proceeded in different ways. All four programs were designed for durations of 8-10 years, and each required considerable time—up to several years—to develop networks among scientists, managers, social scientists and historians, and to create consensus on how to move ahead, and to assemble funding. All four resulted in improved baseline data and in new, or substantially revised, data systems. Each contributed to the evolution of new interdisciplinary teams and science-management linkages and networking.

The programs focused on different aspects of biodiversity. Although biodiversity is now widely considered an essential consideration in ecosystem-based management (EBM), this single descriptor does not capture the complexity of diversity within an ecosystem. One approach is to split biodiversity organization into three principal elements—composition, structure and function (CSF) —each of which can be further represented through a hierarchy of spatial scales ranging from ecoregions to genes. We term this hierarchical view of biodiversity a "CSF template." We use this template to examine the relative focus of the four research programs and to analyze existing ecosystem-wide biodiversity knowledge. This approach helps assess what is known and where gaps may lie and thus may be useful in planning future studies and prioritizing needs. The CSF template may be a useful vehicle for communicating between scientists, managers, and stakeholders. Building a general approach that captures how various studies have focused on biodiversity organizational elements will contribute to ongoing meta-analyses of worldwide experience in EBM-related research.

An Overview of Marine Biodiversity in United States Waters

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Marine biodiversity of the United States is extensively documented, but data assembled by the United States National Committee (USNC) for the Census of Marine Life (Census) demonstrate that even the most complete taxonomic inventories are based on records scattered in space and time. The USNC has summarized the knowledge—and some of the major gaps in knowledge—of marine biodiversity of the United States and to our knowledge, this is the first time such an exercise has been attempted. It is clear from the biotic diversity inventories compiled in our six geographically based sections, four of which are more or less coincident with large marine ecosystems (LMEs), knowledge of U.S. marine biodiversity is fragmentary. Lists, such as these six regions, and the composite one for the country as a whole, are essential as baselines for making management decisions and for assessing biotic changes.

Benthic bacterial diversity: iron ore dominated mangroves versus ilemenite-rich beach sediment.

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Massively parallel tag sequencing of the V6 region of 16S rRNA genes was used to examine the diversity of benthic bacterial community in two iron dominated ecosystems- Divar mangrove swamp and the Kalbadevi berm sediment, west coast of India. The Fe in mangroves is mainly from Fe-Mn mining activities while in the berm sediments, it is mainly from ilemenite-rich placer deposits. The poster discusses the implication of the ready availability of iron to these microbes. Some of the major bacterial groups encountered from these sediments were affiliated to the phyla Proteobacteria, Acidobacteria, Actinobacteria and an unknown phylum. The phylum Proteobacteria was the most dominant in the mangrove sediment comprising ~46% of the total tag sequences. Within the phylum Proteobacteria, the Gammaproteobacteria accounted for nearly 36% of the tags.

Gammaproteobacteria are generally found in organic C–rich systems and are known to be potentially pathogenic in nature. In the berm sediment, Firmicutes dominated at 40% and Bacilli accounted for ~70% of the tag sequences.

Firmicutes are known to occur in pristine soils generally dominated by terrestrial vegetation like *Casuarina* and this presentation highlights their role as degraders of polymers in these systems. The additional role of iron as a co-factor for the expression of many enzymes involved in degradation of complex polymers is stressed. Though both the ecosystems are Fe-rich, and could promote iron respiration and improve bio-availability of this element to the systems, the bacterial community in these habitats are influenced by the prevailing environmental conditions. Each represented an unique population structure with very little overlap between OTU clusters at 3% dissimilarity. The bacterial community of the mangrove swamps was mostly dominated by enteric forms whereas in the berm sediments, it is more comprised of those involved in sediment degradative processes.

PRESENT STATUS OF DNA BARCODING OF MARINE SPECIES FROM INDIA

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India has a vast diversity of marine species (of the order 13,000 and higher) which is acquired from its exclusive economic zone (EEZ) of about 2.172-million km^2 in the sea all along the 7500 km long coastline around her. Species identification of certain groups of marine organisms has been challenging as there is lack of expert taxonomists. Hence in our present study, we have conducted intense sampling along the Indian coast targeting species which are taxonomically difficult to identify. Seven genera of shrimps (Genus *Caridina*, *Enwpalaemon*, *Nematocarcinus*, *Parapenaeopsis*, *Penaeus*, *Solenocera* and *Trachypenaeus*) and 10 genera of zooplankton (Genus *Acartia*, *Canthocalanus*, *Eucalanus*, *Euphausia*, *Euterpina*, *Labidocera*, *Rhopalopthalmus*, *Sagitta*, *Stylocheiron* and *Thysanopoda*) were identified using their phenotypic characters. DNA Barcodes viz., cytochrome oxidase I (COI) gene, 16S and 18S gene were sequenced and their grouping effectiveness in interpreting the phylogenetic information and evolutionary relationship were observed. The clusters formed with these sequence information were in good agreement with the traditional classification of species. This study proves the effectiveness of multiple DNA barcodes in resolving the phylogenetic tree of the taxa under study.

Global Patterns of Marine Microbial Communities

Jed A. Fuhrman (University of Southern California), for the ICoMM Beta Diversity Working Group

Microorganisms are astronomically abundant in marine habitats and are crucial to all major biological and biogeochemical cycles, yet are the least understood organisms anywhere. The International Census of Marine Microbes (ICoMM) used high throughput molecular genetic analysis to characterize the identities and relative abundances of bacteria, archaea, and protists, with the ability to portray even extremely rare organisms. Several hundred samples from around the world were investigated, including plankton, sediments, hydrothermal vents, corals, sponges, mats, and marshes. The Beta Diversity Working Group was organized to define and address overarching questions that could be answered using this global dataset. Among the questions addressed by the group are: What factors create microbial community assembly patterns: to what extent are communities defined environmentally (i.e. influenced by habitat or geography), historically (i.e. influenced by time and by processes such as mixing and dispersal), or biologically (i.e. influenced through relationships among the organisms in the community)? Can microbial community similarity be predicted from environmental similarity? Are there biomes for microbes, and can we predict the habitat based on finding specific microbes (or vice versa)? How do microbes follow classical ecological patterns such as the relationships between distance and diversity, or time and diversity, and are these patterns robust at different taxonomic levels and at local, regional and global scales? What does it mean to be a rare microbe, and what are the contributions of rare microbes to ecological function and to processes that lead to the overall distribution of organisms? At this time we have some interesting preliminary results. Mapping the distribution of microbes globally, we can begin to delineate biomes or habitat zones for microbial species. Bacterial diversity patterns on a global scale appear largely related to latitude in upper water column samples, whereas water depth is the main spatial factor explaining beta-diversity in coastal sediments. Latitude and water depth are most likely proxies for changes in temperature, nutrient supply, and possibly productivity, of these two broadly defined environments. The slope of the distance-decay relationship is significantly higher in sediments, suggesting higher community turnover, probably reflecting the fragmentation and reduced dispersal in these habitats. Correlation networks of individual taxa over different environments, suggest ecological succession within the microbial communities, allowing for hypotheses on ecological and biogeochemical roles for known and unknown microbes, and allow for the comparison of microbial community structures with implications about the fragility or robustness of specific ecosystems. These results show above all that microbial communities are far from randomly distributed at the global scale, and they reveal patterns with ecological and broader biological relevance. We believe these observations will inform the future of microbial ecology, oceanography, and ecological theory, and will assist our quest to understand universal "laws" in biology that apply to animals, plants, fungi, and microbes alike.

Japan: a marine biodiversity hotspot!

Katsunori Fujikura, Dhugal John Lindsay, Hiroshi Kitazato, Shuhei Nishida and Yoshihisa Shirayama

To ascertain the level of marine biodiversity in Japanese waters, we have compiled information on the marine biota, including the number of described species (species richness), the number of identified but undescribed species, and our current state of knowledge about each taxon. This is the first attempt to estimate species richness for all marine species in Japanese waters.

A total of 33,629 species have been reported to occur in Japanese waters. The total number of identified but undescribed species was at least 121,913. The total number of described species combined with the number of identified but undescribed species reached 155,542. This is the best estimate of the total number of species in Japanese waters and indicates that more than 70% of Japan's marine biodiversity remains un-described.

Japan's Exclusive Economic Zone (EEZ) extends from approximately 17° N to 48° N, and from 122° E to 158° E. The land area of Japan is small at 3.78×10^5 km², but the EEZ ranks sixth largest in the world, or approximately 12 times the area of the land. The total area of Japan's EEZ is only 1.2% of the area of the global ocean. According to OBIS, the total number of marine species described from the global ocean is estimated at about 230,000. A total of 33,629 species approaches 14.6% of all marine species. Thus, Japan's marine species richness is high considering the small area and volume of Japanese waters.

The state of knowledge was extremely variable, with taxa containing many inconspicuous, smaller species tending to be less well known. Although Japan's marine biota can be considered relatively well known, at least within the Asian-Pacific region, considering the vast number of different marine environments such as coral reefs, ocean trenches, ice-bound waters, methane seeps, and hydrothermal vents, much work remains to be done. The number of invasive species reported as recently introduced into Japanese waters was 39.

We assume global climate change to have a tremendous impact on marine biodiversity and ecosystems. The present result will be the good baseline to monitor (detect) the impact of environmental change on marine biodiversity.

Arctic Ocean Diversity (ArcOD) Synthesis: How many species are there?

Gradinger R, Bluhm BA, Gebruk AV, Hopcroft RR, Huettmann F, Kosobokova KN, Kovacs K, Lovejoy C, Mecklenburg K, Mincks Hardy SL, Piepenburg D, Poulin M, Sirenko BI, Weslawski JM

ArcOD's mission was the first complete inventory of biodiversity in the three major Arctic realms: sea ice, water column and seafloor – from the shallow shelves to the deep basins. The current inventory demonstrates highest diversity in the smallest size classes with: 4500 OTUs (operational taxonomic units) of archaea (estimate), 45,000 OTUs of bacteria (estimate), close to 2000 single-celled eukaryote phytoplankton species, >1000 single-celled eukaryote ice-associated species, ~60 ice-associated metazoans, ~300 zooplankton species with more than half of those occurring in deep water, close to 3000 benthic shelf macro- and megafaunal species, >1000 benthic deep-sea species (incl. meiofauna), >200 fish species and 16 marine mammal species. More than 60 undescribed species were discovered during field expeditions. Species inventories are rather complete for zooplankton, but not for benthos. Within the metazoan fauna, crustaceans dominate species richness in all three realms while diatoms dominate ice algal and phytoplankton richness. There appears to be no zoogeographical barrier between the Eurasian and Amerasian basins in all three realms. A mid-depth (500-2000 m) peak in species richness was found for zooplankton but not for benthic taxa. Distinct zooplankton communities exist for different depth zones with high within-depth similarity. For benthic communities, regional differences appear to be larger on the shelves than in the deep sea. Recent changes in diversity include range extensions, changed ratios of warm water to cold water species and changes in densities and are probably related to climate change.

Marine biodiversity in South Africa: evaluation of current states of knowledge

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Continental South Africa has a coastline of 3 650 km and an EEZ of over 1 million km^2. This extends to a depth of 5 700 m, with over 65% deeper than 2000 m. The currently described marine biota comprises 12 760 species, of which 4233 (33%) are endemic. In terms of regional and depth coverage the coastal zone is relatively well sampled, while some 2 522 grab, dredge or trawl samples of benthic invertebrate communities having been taken offshore. Few of these, however, were collected after 1980 and over 99% are from depths shallower than 1 000 m – indeed 83% are from less than 100 m!

In this poster we map the depth distribution of the regional seas and overlay the distribution of samples taken; tabulate the numbers of described and endemic species in each major taxonomic group; estimate how well each group is known and plot patterns of endemicity of major groups around the coast.

In evaluating the current state of knowledge we conclude that, given its status as a developing nation, South Africa has a relatively strong history of marine taxonomic research, good regional guidebooks and comprehensive and well-curated museum collections. However, many taxa, particularly those of small body size, remain poorly documented and the abyssal zone is almost completely unexplored. On the plus side the region offers rich potential for scientific discovery. A photographic montage of some exciting new species recently discovered in the region is used to illustrate this potential.

CoML and the Encyclopedia of Life: Integrating marine biodiversity information online

Hammock, J., Schultz, K., Parr, C. Encyclopedia of Life, National Museum of Natural History, Washington, DC, USA. E-mail: hammockj@si.edu

Most of the ~200 000 known species of marine plants, animals, and microorganisms are poorly understood, and what little information we have is usually scattered across libraries, museums, databases, and other storehouses of expert knowledge. The Encyclopedia of Life (http://eol.org) is an unprecedented partnership between the scientific community and the general public with the goal to describe and illustrate all species known to science. In order to build a comprehensive, freely accessible online system of biodiversity information, we aggregate materials from a variety of expert and amateur data partners and we digitize the biological literature of the past. Text, data, photographs, video, maps, etc. from multiple sources are integrated, and specialist curators ensure quality of the collection by monitoring materials within their area of expertise.

The Census of Marine Life has been a key partner in the organization of marine biodiversity data online. The work of CoML researchers has greatly increased our knowledge of marine biodiversity, and that information is already making its way online and into the public eye. Their participation in classification revision via the World Register of Marine Species , Assembling the Tree of Life, and the European Distributed Institute of Taxonomy, is providing an up-to-date classification of marine biodiversity. EOL's compatibility with all of these systems provides a common venue for comparing, discussing and reconciling these classification projects.

CoML projects have also produced high-quality images and other data on thousands of species, and this is currently linked to EOL from a variety of sources, including directly from CoML websites which showcase species from their project habitat. In addition, species lists produced by CoML projects for their habitats support filters which allow EOL to present comprehensive Encyclopedias of particular habitats, eg.: the Encyclopedia of Seamount Life. We anticipate these will engage both the interested public, by providing focused subject matter, and the research community, by providing a common forum for community ecologists and other specialists to disseminate new information and share ideas targeted to their particular research community.

Arctic Ocean Diversity: Exploration in the field

Hopcroft RR, Bluhm BA, Gebruk AV, Gradinger R, Iken K, Kosobokova KN, Weslawski JM, Sirenko BI, and IPY collaborators

Over its 6 years, ArcOD conducted a total of ~30 field activities scattered across the majority of the recognized Arctic habitats, many under the Marine Biodiversity Cluster of the International Polar Year 2007-9. Regional focus areas included the Chukchi Sea as the gateway of the Pacific to the Arctic; the Canada Basin as the most poorly explored, deep-sea area; and Svalbard Fjords for which complete inventories and long-term time series are well underway. The tools for discovery comprised a combination of the traditional collection gear (ice corers, plankton nets, benthic grabs, seafloor corers and trawls) as well as modern technology such as remotely operated vehicles, camera platforms, and under-ice diver-operated *in situ* devices. Sampling included several unstudied unique habitats includingd sea ice pressure ridges, deep-water pockmarks, and encompassed the ice-covered Arctic Seas from nearshore to ocean ridges and from surface waters to the abyss. Shipboard collections provided a solid base for barcoding of ~400 Arctic multicelluar species of fish and invertebrates.

Synergistic Involvement of High School Students in Graduate Level Research Opportunities: A Foundation for Unprecedented Success in Achieving NaGISA's Goals

Stephanie Y. Hsiang (Student Author, Head of Analyses), and Kyle S. Saleeby (Student Author, Dive Team Leader), Niceville High School, Niceville, FL, USA

In 2003, Niceville High School teacher, Mr. Richard Hernandez, was invited by NaGISA Principal Investigator, Dr. Yoshihisa Shirayama to participate in the Census of Marine Life's NaGISA program. Upon Mr. Hernandez's acceptance, Niceville High School became a test case to see whether high schools globally would be able to provide representative samples of marine life from shores in their areas as part of the NaGISA's fifty-year biodiversity study. The student-run NaGISA program at Niceville High School stands where it is today because the test proved to be an overwhelming success.

Currently in its seventh year of involvement, the Northwest Florida NaGISA Team at Niceville High School has assisted in expanding the NaGISA program to three high schools in the United States, as well as three more high schools throughout the world. Niceville High School has established or assisted with the establishment of NaGISA High School Initiative collection sites at Kizimkazi, Tanzania; Crete, Greece; and, most recently, Sharm el-Sheikh, Egypt. These sites represent collection sites on the Indian Ocean, Mediterranean Sea, and Red Sea, respectively.

Incidentally, the NaGISA program in Northwest Florida has become even more significant in view of BP's Transocean Deepwater Horizon oil rig spill in the Gulf of Mexico in April 2010. Because Niceville High School's periodic collection occurred only days prior to the oil spill, their NaGISA data collection is particularly significant as providing evidence of the effects of the oil spill on the Gulf of Mexico's marine life in the Northwest Florida region.

Overall, the inclusion of high schools into the NaGISA program is significant holistically in that it not only provides opportunities for students to get involved in vastly different cultures and real world science, but also it advances the educational community as well. Students involved develop interpersonal and leadership skills, as a successful NaGISA collection demands the effective organization of students and the High School Initiative emphasizes their interaction with other high schools and their university mentors. Involvement in this project offers the benefits of performing university graduate level research while still involved at a high school level.

Global-scale biodiversity patterns in nearshore ecosystems

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Global NaGISA biodiversity data for rocky shore communities and for individual taxa such as macroalgae, polychaetes, echinoderms, gastropods and decapods show that nearshore marine systems do not display universal spatial patterns. Diversity of taxa is highest in either high or low latitudes or peaks in regional hotspots rather than following clear latitudinal gradients as suggested in the literature. Multiple natural and human-influenced environmental drivers influence nearshore assemblages mostly at large spatial scales (within and across continents) but less defined at small, regional scales. NaGISA results suggest that nearshore rocky shore assemblages may respond differently to environmental drivers than terrestrial assemblages, where biodiversity patterns typically tend to be more unified. This opens new and exciting questions about the complexities and interdependencies in marine nearshore environments that will be important for future understanding, planning and conservation of the nearshore.

Size-Scale Strategies for Understanding Biodiversity in the Gulf of Maine Area

Lewis S. Incze[1], Peter Lawton[2,3], Sara L. Ellis[1], Peter J. Auster[4], Anna Metaxas[5], Ellen Kenchington[6], Paul V.R. Snelgrove[7], Nicholas H. Wolff[1], Stephen J. Smith[6], Michelle E. Greenlaw[2]

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The Gulf of Maine Area (GoMA) covers 228,000 km^2 and extends from the intertidal to ~3,000 m depth, and from approximately 40° to 44.5° N along the North American Atlantic coast and to 45.8° N in the Bay of Fundy. The region is one of the most studied marine environments in the world, yet in 2000 there existed no systematic assessment of the known biodiversity and no coordinated, system-level framework for identifying gaps in biodiversity knowledge, promoting research, and using the results to help understand and sustain ecological functioning at the regional scale. This poster looks at three examples of work on biodiversity patterns and processes at different levels of detail and spatial scale within this system, and how they can be used. Comparisons include a national marine sanctuary (2,181 km^2, the smallest scale and greatest over-all detail presented here); a wide "corridor" containing numerous "representative" benthic and pelagic habitats extending from the coast to the continental slope; and a gulf-wide analysis of multiple benthic (infaunal and epifaunal) and demersal fish databases collected over many years.

The smallest scale allows, as much as possible, for an analysis of benthic and pelagic processes and their interactions, including the effects of advection, migrations, natural events, climate change and direct anthropogenic impacts. Additional information is needed for the context of full biodiversity, but the sanctuary presents a good focal point in a heterogeneous section of coastal shelf with considerable historical data and public use and interest. The corridor (named "The Discovery Corridor") promotes the concept of sampling all depth, hydrologic and substrate environments as a requirement for understanding the entire ecosystem. The size of the corridor dictates a nested strategy of selected sites within a geophysically varied but conceptually coherent environmental context. It is not scientifically necessary to confine sampling to sites within the corridor, but this approach affords ample habitats for comparison within and

outside the corridor, and has the advantage of providing a readily visualized mission that the public and managers can support as well as a context for communicating results to them. The gulf-wide analysis enables comparison of broad-scale patterns and environmental influences on a taxonomic subset of the other two scales. The three scales and data sets do not intermesh perfectly, yet they represent a wealth of information that contributes to a regionally integrated approach to biodiversity.

Benthic Biodiversity of the Indian Ocean

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Abstract

The International Indian Ocean Expedition (IIOE) carried out in the 1960's provided a certain level of understanding of the marine biodiversity of the Indian Ocean. Over the last four decades, large volume of biological data collected by numerous Indian expeditions as evident from various scientific reports demonstrates that bulks of the earlier studies are devoted to the zooplankton communities and very few reported the benthic diversity from the continental margin and the deep-sea regions of the Indian Ocean. Indian Ocean is a home to diverse array of ancient and unique faunal assemblages due to the habitat heterogeneity. However, knowledge of the benthic biodiversity of the Indian Ocean is limited, in comparison with Atlantic and Pacific Oceans.

In this poster we summarize the data on the nearshore, continental margin and the deep-sea benthos collected since 2000. Although, majority of the data is on the macrofauna, some information is also given on meio- and megafauna. Polychaetes were the dominant group among all the macrobenthic communities and comprised of ~150 genera from 60 families. About 75% of the polychaete species were restricted to the shallower depths (10 – 200 m) and only 25% were from the deeper regions including oxygen minimum zone (OMZ), canyons, ridges, seamounts and basins. Crustaceans were represented by many species of amphipods, isopods, tanaids, cumaceans. However due to the non-availability of taxanomic expertise their identification is limited to the group level. Nearly 400 species of soft and hard corals and 15 species of hexactinellid sponges are reported from the region. Interestingly, the study resulted in describing few new species (harapacticoid 1; halacarid 1; sponge 1) and is suggestive of tremendous scope for exploration of various records of deep-sea sponges, crustaceans and echinoderms perhaps remarkable to science. Echinoderms, bryozoans, mollusks and minor phyla of the deeper regions are poorly explored. The recent addition of the macrofaunal communities in the western Indian continental margin showed different community patterns, compared to other regions in the world oceans. Among the metazoan meiofauna, Nematoda is the dominant groups with ~ 90 species.

This poster also demonstrates the influence of habitat heterogeneity on the benthic biodiversity along and across the Indian coast. Biodiversity is presented in the graphic and tabular forms and will illustrate the relationship between the biotic and abiotic factors. It also includes some images of newly discovered and potential new species of the region.

The Diversity of Coral Reefs:
Molecular Tools Help Us Understand What Exists and What We Could be Losing

Authors: Nancy Knowlton[1], Julian Caley[2], Rusty Brainard[3], Laetitia Plaisance[1], Ryuji Machida[1], Megan Moews[3]

Smithsonian Institution[1], Australian Institute of Marine Science[2], NOAA Pacific Islands Fisheries Science Center, Coral Reef Ecosystem Division[3]

Traditionally, large and well-studied reef-associated macrofauna, such as corals and fishes, have been used as surrogates to achieve rapid strategic biodiversity assessments and relative measures of reef health. This is in part, because identifying the multitude of cryptic species is either impossible or extremely labor intensive. Diversity data on the numerous reef-associated cryptofauna remains scarce and scattered and it is questionable whether the use of surrogate groups for biodiversity assessment on coral reefs adequately reflects general patterns of diversity among all organisms.

To help answer this question, in the first global study of its kind, CReefs scientists, partnering with the Smithsonian and California State University, are providing new biodiversity estimates of reef-associated cryptofauna using molecular techniques based on DNA barcodes and environmental genomics. In this study, barcodes were extracted from standardized samples found in natural reef environments and artificial settlement structures (ARMS) throughout the tropics (Pacific Ocean - The Line Islands, French Polynesia, Northwestern Hawaiian Islands, the Great Barrier Reef's Lizard and Heron Islands; Indian Ocean - Western Australia: Atlantic Ocean – Panama) and across gradients of human impacts. Specific datasets were then assayed using 454 sequencing, a method that is increasingly applied to microbes but has never been used for complex multi-cellular communities.

This study provides total biodiversity estimates using statistical diversity estimators, allowing for the estimate of total numbers of species as a function of location and reef condition. Results have revealed the high prevalence of low-abundance species and high species turnover between localities and across reef habitats. These numbers, combined with results from past studies, yield the most comprehensive understanding of reef diversity to date, including estimates of the numbers of species yet to be described or at risk of extinction.

Background:

Coral reefs are among the most diverse ecosystems on earth, and yet they are also among the most threatened ecosystems on the planet due to the effects of climate change (global warming, coral bleaching, ocean acidification, and sea level rise) and other anthropogenic and natural threats. Coral species however, constitute only a small fraction of reef diversity, most of which consists of cryptic and usually poorly-known organisms. Consequently, with current estimates of global reef diversity remaining generally course and understudied, we know almost nothing about the extent to which reef degradation threatens reef diversity. With the exception of corals, concerns about reef loss have focused almost exclusively on ecosystem services and largely ignored biodiversity loss. As a result, the Census of Marine Life, Census of Coral Reef Ecosystems (CReefs) partners globally are focused on the research and understanding of types/distribution of understudied species obligately associated with healthy coral reefs, along with patterns of species diversity in relation to gradients of human disturbance and in lieu of climate change and ocean acidification.

Diversity!
Census of Coral Reef Ecosystems Scientists Discover New Species and Fascinating Diversity!

Authors: Nancy Knowlton[1], Julian Caley[2], Rusty Brainard[3], Megan Moews[3], Laetitia Plaisance[1], Amanda Toperoff[3]

Smithsonian Institution[1], Australian Institute of Marine Science[2], NOAA Pacific Islands Fisheries Science Center, Coral Reef Ecosystem Division[3]

In an unprecedented global census of coral reef ecosystems, CReefs scientists and collaborators have developed and utilized an array of new sampling methodologies (eg Autonomous Reef Monitoring Structures (ARMS) and DNA-based technologies) to conduct comprehensive and taxonomically diversified research of lesser known species. In the effort to learn more about the abundance, diversity and distribution of these understudied organisms, teams of scientists globally have collected thousands of new and fascinating species throughout the world's oceans. This visually stimulating poster will give viewers a glimpse into the amazing intricacy of the under-celebrated life that makes up the most diverse and biologically complex marine ecosystems in the world's oceans. From orange crabs with yellow pompoms and clear shrimp covered in striking red mazes to spaghetti worms with their colorful gills, nudibranches or "sea slugs" with vibrant variation and even new species of tiny octopi, these specimens will catch the eye and draw in scientists and the public alike. *We will also provide a smaller version of the poster as a handout.*

Background:
Coral reefs are among the most diverse ecosystems on earth, and yet they are also among the most threatened ecosystems on the planet due to the effects of climate change (global warming, coral bleaching, ocean acidification, and sea level rise) and other anthropogenic and natural threats. Coral species however, constitute only a small fraction of reef diversity, most of which consists of cryptic and usually poorly-known organisms. Consequently, with current estimates of global reef diversity remaining generally course and understudied, we know almost nothing about the extent to which reef degradation threatens reef diversity. With the exception of corals, concerns about reef loss have focused almost exclusively on ecosystem services and largely ignored biodiversity loss. As a result, the Census of Marine Life, Census of Coral Reef Ecosystems (CReefs) partners globally are focused on the research and understanding of types/distribution of understudied species obligately associated with healthy coral reefs, along with patterns of species diversity in relation to gradients of human disturbance and in lieu of climate change and ocean acidification.

Exploring the Nearshore: Educating the Next Generation

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Education and training of the next generation of scientists and of stakeholders was a core objective of the NaGISA project and one of its legacies. Taxonomic training and sampling workshops prepared university students and coastal researchers from over 25 countries to engage in NaGISA sampling, monitoring and conservation of the nearshore environment. The growing network of the NaGISA High School Initiative has not only introduced standardized scientific methodology into the classroom, but also provided common ground for global interactions between young scientists. Incorporation of the NaGISA protocols into educational programs such as university and high school courses is an invaluable asset for educating stakeholders and training students.

A hierarchical framework for classifying seabed biodiversity with application to planning and managing Australia's marine biological resources

Authors: Peter R. Last, Vincent D. Lyne, Alan Williams, Campbell R. Davies, Alan J. Butler, Gordon K. Yearsley, Daniel C. Gledhill

Abstract:
- Biodiversity can be interpreted in many ways. Classifications can include biotic and/or abiotic components, depend on scale and context, and often reflect the disciplinary bias of the authors.

- Marine biodiversity has almost exclusively been examined at the scale of local or modern processes, which are often less informative than biogeographic or ancient processes for understanding species richness patterns. However, modern and ancient processes are the endpoints of a natural hierarchy where different processes influence distribution at each level. Patterns and processes of biodiversity are scale dependent, with lower levels fully or partially nested in those above. Comparisons that omit this scale dependency will be compromised.

- We present a hierarchical framework for describing the structure of marine demersal biodiversity across all spatial scales. This system explicitly recognizes the overarching influence of large-scale biodiversity patterns at realm (ocean basin and tectonic), provincial (palaeohistorical) and bathomic (depth-related) levels. The functional roles and spatial scales are captured within ten nested levels within realms, where the first seven are primarily spatially nested and ecosystem based, and the lowest levels represent units of taxonomic inheritance. The framework is conceptual and each level needs to be validated for its general applicability.

- Our hierarchical framework was developed to guide marine resource planning and management in Australia. The system has been used successfully for continental-scale bioregionalisation, including identification of Australia's National Representative Systems of Marine Protected Areas, and has wider application at a global scale.

Biodiversity Knowledge and its Application in the Gulf of Maine Area, Northwest Atlantic Shelf

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Primary objectives of the Gulf of Maine Area Program of the Census of Marine Life (GoMA) were to summarize knowledge of regional biodiversity, support development of information systems, and integrate biodiversity knowledge for use in decision making. We have found a hierarchical view, organized around compositional, structural, and functional diversity elements, to be useful in deriving and communicating overviews of biodiversity knowledge. Here we profile conclusions from regional expert groups convened to summarize knowledge on compositional, structural, and functional aspects of biodiversity within six major "ecosystem compartments": Coastal Margins, Benthic and Demersal Habitats, Slope and Seamounts, Microbial Communities, Zooplankton and Pelagic Nekton, and Upper Trophic Level Predators. We also summarize findings from GoMA-sponsored research that has consolidated information on compositional aspects of biodiversity at the regional ecosystem level.

Compositional elements represent the identity and variety of biodiversity at different levels from ecoregions to genes. We focused much of our work at the species level, assembling a Gulf of Maine Register of Marine Species (GoMRMS) based on species either known to exist here (using a variety of sources) or expected in the region based on a larger Northwest Atlantic register. The total number of species within GoMRMS is now just over 3,100. More than 1,400 additional species reported in the area are under review for inclusion in GoMRMS, bringing the provisional total to over 4,500 (excluding viruses, bacteria, and archaea). To convey how much is known and unknown about

diversity at the regional scale, we developed a length-based representation of compositional diversity for all adult stages of biota from viruses to the largest whales.

Structural diversity elements are concerned with the physical organization or pattern within the system from ecoregion- to habitat-scales, including both biotic and abiotic variables that modulate patterns. In biodiversity monitoring frameworks, *functional* diversity elements are those abiotic and biotic factors (or processes) that are influential in either maintaining characteristic biodiversity features within the system, or which contribute to changes. These range from genetic processes to regional natural and anthropogenic forcing variables that operate at various spatial, ecological and evolutionary scales. To accommodate the complexity and spatial extent of different structural features in the system and to help clarify the connections and transfer of knowledge between research and management applications, we considered the system as a nested set of spatial domains that range from fine-scale micro-habitat features influencing occupancy, through seascapes, to the broad scale of the ecoregion itself.

Oceanographically modulated processes, such as bentho-pelagic coupling, transport, and mixing, promote connectivity across these spatial domains and represent an important considerations for spatial management under Ecosystem-Based Management. Temporal variability, including year-to-year variations (natural and human) and secular change (climate and community trajectories), is layered on top of this spatial matrix of habitats, organisms, and linkages. Conceptually, it can be argued that while discovery-based research is interested in investigation across the full range of these spatial domains, monitoring and spatial planning largely remain focused on periodic assessments and decision-making above a certain minimum domain size and at lower levels of complexity.

Marine Biodiversity of Korea

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Korea is a peninsular surrounded by marginal seas in the west Pacific. It is rich in marine fauna and flora due to diverse habitats and occurrence of both warm and cold currents. The East Sea is deep down to 4,000m in depth and provides rocky or sandy shores. The south sea has thousands of islands and well-developed wetlands on the shores. The west sea is featured by a few kilometer-wide tidal flats. The warm and cold current systems bring subarctic, temperate, and subtropical marine organisms to the Korean waters. In these waters, approximately 9,700 marine species are reported to date. Diatoms (1,835 species), dinoflagellates (328), and silicoflagellates (6) comprise the main groups of phytoplankton. Marine algae include Rhodophyta (566), Phaeophyta (176), and Chlorophyta (128). Marine invertebrates are represented by 5,443 species of which the main groups are mollusks (1,882), Crustacea (1,387), annelids (513), Cnidarian (324), Poriferan (267), and Echinoderms (186). Fish species reaches up to 1,121 in number consisting of 219 families and 613 genera with high diversities in Perciformes (46.5% of Actinopterygii), Scorpaeniformes (13.7%), Tetraodontiformes (6.5%), and Pleuronectiformes (6.3%). It is expected that twenty thousands more species would be found in Korean waters. In relation to cataloguing the marine organisms, a general survey on Korea marine ecosystem and a marine biodiversity conservation program are being carried out. The information on Korea marine organisms is stored in both KOMBIS (Korea marine biodiversity information system) and KOBIS (Korea ocean biogeographic information system), and serviced to the public.

Continental Margin Ecosystems on a worldwide scale – III. Influence of the newly perceived habitat heterogeneity on biodiversity

Levin L., Menot L., Billet D.S.M, Carney, R., Galéron J., Ingole B., Kitazato H., Krylova E., Poore G., Lavrado, H. P., Rowe G., Sellanes J., Vanreusel A. & Sibuet M.

During the past few decades, our understanding of deep continental-margin habitats (from the shelf break to the abyssal rise, 200 - 4000m water depth) has changed more than for any other large area of Earth. While it has been long known that the ocean margins are a mixture of rugged mountainous scenery and sediment covered slopes, it is only recently, with higher resolution bathymetry and increased bottom sampling, the tremendous complexity and diversity of margin settings has been uncovered. Continental margins are active regions ecologically, geologically, chemically, and hydrodynamically. Collectively, these processes create unique ecosystems characterized by distinctly high biomass, high productivity, unique physiological adaptations and apparent high species endemicity. Such hotspots are associated with very large-scale oceanographic features such as the boundaries of oxygen minimum zones, reef-like coral mounds, canyons, and cold seeps. Within each of these settings, a heterogeneous mix of soft and hard, sometimes biotic substrates creates a mosaic of settings that enhances regional diversity.

Margin heterogeneity thus exists in many forms and on multiple space and time scales; it is also perceived differently depending on the size, mobility and lifestyles of the species considered. The COMARGE focus on how different sources and scales of heterogeneity influence margin biodiversity has spanned a wide range of taxa, from protozoa to megabenthos, in diverse settings across the globe. Perhaps the most universal finding is that heterogeneity acts in a hierarchical, scale-dependent manner to influence margin diversity: (i) at the largest scale with strong effect is hydrography associated with water masses and overlying productivity; (ii) at meso scales (10s km) there is topographic control in the form of canyons, banks, ridges, pinnacles, and sediment fans; (iii) at small scales there are earth and tectonic processes that control fluid seepage and sediment disturbance and (iv) at the smallest scales there are habitats formed by ecosystem engineers that influence diversity through provision of substrate, food, refuge and various biotic interactions.

This poster illustrates continental margin habitat heterogeneity at meso to small spatial scales and demonstrates its influence on biodiversity. Images will reveal the mosaic of habitats found on continental margins, graphics will demonstrate the influence of habitat heterogeneity on diversity and a 3D-diagram will summarize the interplay between large-scale environmental gradients and fragmented habitats in shaping margin biodiversity. We will highlight some of the truly unique animals and communities discovered in recent explorations of margin heterogeneity.

Migratory behavior and habitat use of North American green sturgeon

Authors: Steve Lindley(1), Dan Erickson(2), and Mary Moser(3)

Abstract: The green sturgeon (*Acipenser medirostris*) is a rare and elusive anadromous fish, and a decade ago, little was known about its basic life history, including its migratory behavior and use of different habitats. It was generally appreciated that green sturgeon spend much of their lives in the coastal ocean, and that they could be found aggregating in certain estuaries along the Pacific coast in summer months. That green sturgeon were thought to spawn in just three rivers in northern California and southern Oregon, and had been encountered in coastal waters as far south as Baja California, Mexico and as far north as the Bering Sea, implies that at least some green sturgeon undertake extensive migrations among diverse habitats. Extensive migrations could subject green sturgeon to many threats, including several fisheries and kinds of habitat degradation. Understanding the interactions of highly migratory animals with potential threats is critical to their conservation.

The development of electronic tags offered a way to build such understanding. We used acoustic and pop-off satellite archival tags to track the movements of green sturgeon among spawning rivers, non-natal estuaries and the coastal ocean between central California and southeast Alaska. Acoustic tags and the Pacific Ocean Shelf Tracking hydrophone system revealed that green sturgeon have a distinctive seasonal migration pattern, rapidly moving long distances from natal rivers and non-natal estuaries in the summer to overwintering grounds near to or north of northern Vancouver Island, with a return south the following spring. Spawning adults did not subsequently return to their natal rivers for at least two years, usually spending summers in non-natal estuaries in non-spawning years. Movements among estuaries were common within summers. Within this generalized migration pattern, distinctive variation in the use of particular habitats was apparent within and among populations, suggesting that green sturgeon form migratory contingents like some other anadromous fish such as striped bass and freshwater eels. PAT tags revealed that green sturgeon remain within a narrow range of temperatures and depths while in the ocean. The results of our tagging studies have been used to designate critical habitat and design regulations to conserve green sturgeon.

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Marine biodiversity in the Caribbean: increasing awareness through the Census of Marine Life program

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The Census program began in the Caribbean in 2004 with the goal of reviewing the state of knowledge of marine biodiversity, establishing links with research and conservation regional programs, and implementing Census projects in the region.

The Caribbean engaged in the historical project of the CoML as well as in the exploration projects studying biodiversity in the nearshore, the continental margins, the chemosynthetic ecosystems, and establishing a network of marine microbial research. Caribbean-CoML has contributed with 60,368 records to the Ocean Biogeographic Information System (OBIS) database, representing 5,601 species. The tropical ecosystems that characterize the Caribbean incorporate a high diversity of associated flora and fauna, encompassing a major global marine biodiversity hot spot. A total of 12,046 marine species have been reported for this region. Sampling effort has been greatest in shallow, nearshore waters; offshore and deep environments have been less studied. The currently accepted classification of marine ecoregions of the Caribbean did not apply for the benthic distributions of five relatively well known taxonomic groups. Coastal species richness tends to concentrate along the Antillean arc (Cuba to the southernmost Antilles) and the northern coast of South America (Venezuela – Colombia), while no pattern can be observed in the deep sea with the available data. Several

factors make it impossible to determine the extent to which these distribution patterns accurately reflect the true situation for marine biodiversity in general: (1) highly localized concentrations of collecting effort and a lack of collecting in many areas and ecosystems, (2) high variability among collecting methods, (3) limited taxonomic expertise for many groups, and (4) differing levels of activity in the study of different taxa.

Biodiversity of the European Seas

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The European Regional Seas cover a vast area; with the boundaries ranging from the mid-Atlantic ridge in the west through to Vladivostock in the east, and from the warm waters of the Mediterranean in the south to the cold waters of the Arctic in the north.

The European Seas are some of the most well studied waters in the world with species data having been collected for many centuries; at present there are more than 10,000 species which are known to inhabit the Western European Margin (Arctic, North Sea and NE Atlantic), more than 17,000 species in the Mediterranean and greater than 5,600 species in the Baltic Sea. Even so, we are still finding and describing many new species in these regions. It is only with the support of the Census of Marine Life that many of the datasets have been made accessible and centralised in one location; for Europe it is EurOBIS.

Results from the recent synthesis of European marine waters has found that the ecosystems in the European Seas are some of the most well known globally. However, the synthesis work undertaken has higlighted where there are major gaps in our knowledge and how these ecosystems are facing increasing threats from a range of human induced impacts. The threats that the marine species face range from habitat loss and degradation, fishing and its associated impacts on the fauna, exploration for oil/gas and minerals, eutrophication, invasion of alien species and climate change. Changes in the climate are having huge impacts on the biodiversity of the European Seas; for example by increasing the water temperature there is a move northwards by warm water species as well as increasing the threat of alien species invasions to high latitudes. It is important that future research focuses on what is still to be discovered e.g. the diversity if the microbial world is not that well known as well as the consequences of the growing threats and incorporation of biodiversity aspects into marine management advice.

Zooplankton species discovery in a biodiversity hotspot in Southeast Asia

Authors: S. Nishida, S. Ohtsuka, J. Nishikawa, et al.

Comprehensive CMarZ research has been conducted in the embayed waters, coastal areas, and marginal seas of Southeast Asia. This is a major biodiversity hotspot in the world and has a very complicated geography and geological history. New species discoveries here have been dominated by copepods and mysids collected using sledge nets from coastal near-bottom habitats and by night-time or SCUBA sampling in coral reefs, indicating that the high diversity of these habitats has been overlooked by conventional daytime net sampling. The Sulu Sea, a semi-enclosed marginal sea in the tropical Western Pacific Ocean, has been a particular focus for CMarZ studies and has yielded a number of discoveries of new species and genera, including copepods. Species discoveries by CMarZ within the Copepoda have added another 8% to the total number of copepod species in Southeast Asia (another 2% to the global total), and new species discoveries of Mysidacea in Southeast Asia have added 15% to the global total for that group.

Surveying the patterns of life in the understudied depths of the South Atlantic: continuing the legacy of the MAR-ECO project (CoML) into the southern mid-Atlantic ridge.

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Abstract

The South Atlantic is the newest of all major oceans and the only one to be directly connected to all of them. It is also economically important as it sustains a large portion of the Atlantic pelagic and demersal fisheries. Yet our knowledge on its patterns of deep-water diversity and distribution is scarce and concentrated on the slope areas of the African and South American margins. Besides these major gaps of knowledge on diversity, important questions remain concerning the role of mid-oceanic ridge, and its adjacent seamounts, in deep-water fauna dispersal processes between the coasts of Africa and South America and among the north Atlantic, Pacific, Indian and Antarctic oceans.

These questions motivated an international initiative conceived to extend the CoML's MAR-ECO project and scientific approach to the southern mid-Atlantic ridge and adjacent seamount chains (St. Peter's & St. Paul's Rocks, Rio Grande Rise and Walvis Ridge). During three years, a team of scientists leaded by South America and Africa, have collaborated on developing a strategy to sample ridge-associated biota, from bacteria to whales, capable of (a) increasing data on South Atlantic deep pelagic and benthic diversity and distribution, and (b) integrating South American and African communities in the challenge of exploring the deep waters between them, identifying fishing opportunities and needs for conservation.

In 2009, a consortium established between the A.P. Sloan Foundation, the International Centre for Genetic Engineering and Biotechnology (ICGEB), MAR-ECO and the Shirshov

Institute of Oceanology (Russia) provided the first opportunity for field activity as part of the annual South Atlantic voyage of the R/V Akademik Ioffe. During a 34-day trip that started in Gran Canaria (Spain) and ended in Cape Town (South Africa), scientists from Brazil, Russia, Uruguay and New Zealand conducted a total of 63 sampling events down to 4700 m depths on the southern mid-Atlantic ridge and Walvis Ridge. A total of 976 animals (mostly fish and cephalopods) were preliminary identified during the trip. Many samples, however, particularly from plankton and benthos stations, were stored and sent for identification by taxonomists in Brazil, South Africa and Russia. Over 175 species of fish, 44 cephalopods and around 200 species of benthic invertebrates have been currently identified. These figures will certainly increase, as the majority of specimens remains to be examined. Nearly 300 bacteria were isolated from deep sediment and water samples, 50 of them showing potential for biotechnological uses. Continuous records of whales, birds and the distribution of the Deep Sound Scattering Layer (DSSL) were systematically obtained along the ship´s track and will provide information on the influence of the ridge system on the overlaying epipelagic habitats.

Long distances, deep and rough topography, time and technology constraints were some of the shortcomings that limited sampling on the Southern mid-Atlantic ridge. But scientific results emerging from this first experience are already substantial and expected to reveal "unknowns" on deep water diversity of such poorly studied area. More than that, they have increased the general motivations to continue the MAR-ECO project legacy beyond CoML and sample more and better the overlooked depths of the South Atlantic Ocean.

Great Barrier Reef Seabed Biodiversity
(A CoML Affiliated Project)

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The shelf seabed habitats and associated biodiversity of the GBR Marine Park were mapped by deploying towed video, epibenthic sled and trawl at almost 1,400 sites throughout the 210,000 km² shelf area, from 2003 to 2006, to provide information for conservation planning and to assess sustainability of the region's prawn trawl fishery. Initially, analyses of pre-existing data assessed the potential for using bio-physical relationships between seabed species and the physical environment for statistical prediction mapping of assemblages, 'communities' and species biomass. These analyses also identified and ranked the importance of physical variables (eg. bathymetry, sediments, currents, water chemistry, ocean colour) that appeared to structure patterns in seabed biodiversity, and hence for stratification in a sampling design that aimed to representatively sample the 'environment space' of the region. The sampling yielded an inventory of >5,300 species of benthos, bycatch and fishes. Two-stage GLM bio-physical models were developed to predict maps of the distribution and abundance throughout the GBR shelf region of ~850 seabed species that were present at >25 sites. The predictive performance of the bio-physical models was typically better for the presence/absence stage (ROC AUC>0.75 for ~83% of species) than for the biomass stage (deviance ratio >0.3 for ~52% of species). The most frequently selected variables were sediment size fractions and carbonate, depth, benthic irradiance, current stress, then bottom water chemistry, seasonality, turbidity, and other temporal effects. The inventories & maps were used to estimate indicators of exposure to trawling and sustainability risk for ~850 bycatch species, seabed assemblages and habitats, and also assess the comprehensiveness of protected areas.

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Exploring the role of environmental variables in shaping patterns of biodiversity composition in seabed assemblages

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Biodiversity pattern distribution information is fundamental for planning and management in the marine environment yet is severely lacking for most marine regions — partly due to the great expense and time required for biodiversity surveys. To serve the immediate need, more readily available physical data coverages are often used as surrogates for biodiversity patterns. However, physical variables are measured on arbitrary scales unlikely to be directly relevant to biology — to make the connection, knowledge of the relationships between biological patterns and physical variables is essential. As a contribution to the synthesis phase of the International Census of Marine Life (CoML), we explored these relationships by applying a novel analysis approach, based on modification of the statistical method randomForest (a bootstrapped randomized partitioning tree method). This approach elucidates the shapes and magnitude of multiple species responses to as many as 30 physical gradients, including thresholds, quantifies the extent to which physical surrogates explain biological patterns, and identifies the importance of each physical variable. These responses were compared for meso-scale biological and physical datasets from contrasting shelf biogeographic regions in tropical Australia, deep Gulf of Mexico and temperate Gulf of Maine. The biological survey datasets comprised site-by-species abundance data from trawls, benthic sleds, and grabs/cores. The modified randomForest analysis collates split points and Δdeviance information for each physical variable from 100s of regression trees for each species. These results are expressed as cumulative distributions of splits deviance, weighted by variance explained. When summed over multiple species, these distributions represent patterns of biological compositional change response along gradients for each physical variable. We believe this approach has significant potential as a robust method of quantitatively integrating information from across multiple disparate surveys that used different sampling devices. The results show that biological compositional change is non-linear along gradients, that some variables are more important than others (though variable importance differs for different survey types and regions) and that overall the physical surrogates may explain 10-30% of biological abundance patterns (range 0-80%). Such information contributes to understanding the role of physical gradients in determining species distributions at mesoscales, provides information to facilitate design of future biodiversity sampling programs, and can be applied, through "biologically-informed" transformations of the more readily available physical data, to provide predictive maps of expected seabed beta diversity patterns. Further, we hope this information will focus more routine production of biologically relevant variables from the marine geological and oceanographic community.

History of Marine Animal Populations:
Stories on marine animal populations and their exploitation.

Kira Paulli Pravato, Anne Husum Marboe, Poul Holm

HMAP is a global research initiative to study past ocean life and human interaction with the sea. Since 2000 about 100 researchers have undertaken an interdisciplinary research program using historical and environmental archives. We have analyzed marine population data before and after human impacts on the ocean became significant. The principal goal of the program has been to enhance knowledge and understanding of how and why the diversity, distribution and abundance of marine life in the worlds oceans changes over the long term. The poster reflects on the project's major achievements.

Sampling the deep tropical/subtropical Eastern Atlantic on the RV Polarstern

Authors: S. Schnack-Schiel, P.H. Wiebe, A. Pierrot-Bults, A. Cornils, L. Blanco-Bercial

Abstract: In November 2007, an international CMarZ team of taxonomic experts and molecular specialists joined a Polarstern cruise from Bremerhaven/Germany to Cape Town/South Africa. The zooplankton research concentrated on the hitherto understudies tropical/subtropical waters of the eastern Atlantic Ocean in order to collect and identify the zooplankton distributed throughout the entire water column, with a focus on the under-sampled meso- and bathypelagic zones. The overriding project goal was to produce accurate and complete information on zooplankton species diversity, biomass, biogeographic distribution, genetic diversity, and community structure.

Continental Margin Ecosystems on a worldwide scale (COMARGE) – I. Species rich, complex and fragile deep-sea landscapes within human reach.

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The field project "Continental Margin Ecosystems on a world-wide scale", COMARGE was launched in 2005 to address key issues on the ecology of continental slopes. Along a depth gradient that begins at the shelf break (~200m) and ends at abyssal plains (~4000m), continental margin experiences sharp variations in temperature, pressure, food influx or currents. Along this depth gradient, distribution patterns, the zonation of species in depth bands, and a maximum in diversity at mid-slope depth, were known locally but still needed to be confirmed globally and explained. Over the last 10 years, new technological means of exploring the deep-sea floor, in-situ or remotely, have revealed that continental margins are not monotonous muddy slopes but instead have a high degree of complexity formed of biologically rich, unique habitats including oxygen minimum zones, canyons, cold seeps and reef like coral mounds. We have also discovered that these settings are subject to degradation through exploitation of living or mineral resources and from ocean warming, acidification, and deoxygenation associated with climate change.

In an attempt to merge known but unexplained ecological patterns with new habitat discoveries, to highlight the societal value of continental margins and to assess potential anthropogenic threats, COMARGE focused on three main questions:

- Are large-scale biodiversity patterns such as zonation or diversity-depth trends ubiquitous and what are their drivers?

- What are the margin habitats and what is the relationship between diversity and habitat heterogeneity?

- How continental margin biota, communities and ecosystems respond to anthropogenic disturbances?

A network of over 100 scientists held discussions and generated syntheses through four thematic workshops. Data integration was achieved either through the Ocean Biogeographic Information System (OBIS, www.iobis.org) or via the COMARGE Information System (COMARGIS), ecologically orientated.

The aim of this poster is to (1) introduce COMARGE, its realm of concern, its scientific questions and its major achievements in terms of international networking and (2) illustrate the human footprint on continental margins and the imperative for continued, integrated researches in an international context. Illustrations will include a map of COMARGE-associated cruises and habitats sampled as well as a map of human footprints from various activities (Fishing, oil&gas, cables…) in the Northeast Atlantic, and a map of margins environments most threatened by different facets of climate change.

Measuring the Regional Effect of 19th C American Offshore Whaling Voyages

Tim D. Smith, Randall Reeves

American whaling was by far the most spatially extensive fishery the world had seen by the mid-1800s. The spatial distribution of American whaling over the 19th century is shown using data from daily logbooks from a sample of roughly 10% of the voyages made (Frame A). Quantitative knowledge of this distribution has formed a basis for determining the impact of American whalers on the regional populations of whales in all parts of the world's oceans. American whaling began in the Atlantic (Frame B), and expanded out of the Atlantic in the early 19th century, with vessels routinely traveling around Africa and South America by 1820 (Frame C). Around the Cape of Good Hope the fishery extended into the Indian Ocean and then across to Australia and into the Pacific, focusing on right whales and sperm whales. Around Cape Horn the fishery extended to the northwest in the Pacific Ocean, focusing initially on sperm whales and subsequently on right whales, bowhead whales, gray whales and humpback whales. Later in the 19th century the fishery collapsed back into the Atlantic (Frame D), focusing again primarily on sperm whales, as it began its slow decline into the early 20th century. Quantitative knowledge of these spatial patterns has formed a basis for determining the temporal patters of the regional impacts of the fishery on the whales.

Mobilizing Marine Biodiversity Research: The Canadian Healthy Oceans Network

Snelgrove, P. V. R., Archambault, P., Juniper, S. K., Lawton, P., Metaxas, A., McKindsey, C., Pepin, P., and Tunnicliffe, V.

The Census of Marine Life has provided a framework for collaborative research in marine biodiversity. Here we present a model for academic and government partnership that has created the Canadian Healthy Oceans Network (CHONe), a national research program that is uniting researchers to provide new insights into marine biodiversity and provide scientific guidelines for policy in conservation and sustainable use of marine biodiversity resources in Canada's three oceans. This initiative is structured around three interlinking themes. Theme Marine Biodiversity addresses the relationships between biodiversity and habitat diversity by testing hypotheses that link functional and species biodiversity to habitat complexity. Theme Ecosystem Function addresses how ecosystem function and health are linked to biodiversity and natural and anthropogenic disturbances. Theme Population Connectivity addresses how dispersal of marine organisms, typically by early life stages, influences patterns of diversity, resilience, and source/sink dynamics of species and biological communities using source-sink studies of existing management areas as model systems, and comparative studies of different dispersal metrics to estimate metapopulation connectivity. We will synthesize the outcomes of these themes across the Network to identify approaches to bridge science and policy, and communicate these results to the complex networks of user groups who ultimately influence policy application.

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The International Census of Marine Microbes (ICoMM)

Mitchell L. Sogin[1], Jan W. de Leeuw[2], and Linda A. Amaral-Zettler[1] on behalf of the ICoMM Scientific Organizing Committee and Scientific Advisory Council

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The International Census of Marine Microbes (ICoMM) seeks to determine the range of genetic diversity and relative numbers of different microbial organisms at sampling sites throughout the world's oceans. Rather than focusing on individual taxa, ICoMM explores how entire complex microbial population structures vary as a function of geographical location, depth, and an array of contextual parameters. ICoMM explores those issues over different spatial and temporal time scales. Important questions include 1) How many different kinds of microorganisms inhabit all ocean realms combined? 2) Do microbial populations exhibit geographical and temporal distribution patterns? 3) How is the microbial world connected by circulation patterns? 4) Are there co-occurrence patterns of specific microbial taxa? 5) Are there specific correlations in community composition with contextual parameters such as depth, pH, salinity, latitude, longitude, seasonality etc.? 6) How do microbial populations shift and evolve in response to changes in marine environments? 7) What is the extent of the "rare biosphere" and what is its spatial and temporal distribution? ICoMM employs "next generation" sequencing to address these questions over different spatial (millimeter to kilometer) and temporal (monthly to annual) scales at globally distributed sampling sites.

Laboratories from 25 countries have participated in ICoMM which represents the largest global survey to date of marine microbial populations. Early in this survey, ICoMM investigators produced compelling evidence documenting the existence of the Rare Biosphere which includes many thousands of low abundance microbial populations of yet to be determined genomic diversity. More recently ICoMM has made the surprising observation that microbial community compositions in the deep ocean display biogeographical distributions in which land masses and currents separate distinct microbial communities. Characteristics of the sediments likely play a role in structuring these communities and may contribute to the biogeographical distribution patterns. This contrasts with the idea that all organisms are everywhere and that the environment selects for specific communities. A similar analysis of microbial communities at the hydrothermal environment "Lost City" discovered that rare microbial populations in young chimneys are often more abundant in older chimneys, indicating that these species can remain very rare in a chimney for 1000 years before 'blooming' and suddenly becoming dominant when the environmental conditions allow. A long history of selection over many cycles of chimney growth and death selected for numerous closely related species at Lost City. Finally, a rare biosphere of diverse microbial eukaryotes has also been revealed in the low oxygen reaches of the ocean in the Framvaren Fjord, Norway and the Cariaco deep-sea basin, Venezuela. Here taxa with less than ten sequence tags represented more than 90% of the diversity present including a substantial number of taxonomic groups undetected by previous methods from surveys of both sampling sites.

ICoMM investigators have also explored the relationship between community composition and different water chemistry. Distinct salinity, temperature and nutrient characteristics define several water masses making them distinguishable over thousands of kilometers in thermohaline ocean circulation. The existence of biogeochemical provinces in the sea as defined by water masses appears to define unique clusters of bacterial and archaeal diversity. The group III Euryarchaeota dominated the deep Atlantic water masses from the central Arctic and represented the second most abundant group in two other deep-water samples. Group III Euryarchaeota in the deep Arctic water may serve a key role in the nitrogen cycle at high latitudes. In the North Atlantic, our census has shown that distinct deep-water masses exhibit specific bacterial communities. The composition of both abundant and rare phylotypes grouped according to water masses. Bacterial communities from the same water mass but separated by thousands of kilometers were more related to each other than communities only separated by a few 100 meters at individual sites but originating from different water masses. Finally, a study of porifera microbiomes identified approximately 3,000 bacterial Operational Taxonomic Units spanning 27 bacterial phyla within the microbial communities of 3 different Australian sponges. Separate specimens for the same sponge species were remarkably similar at all phylogenetic levels, but different sponge species from the same environment possess distinct microbial population structures.

"Acoustic tracking of marine animals in the Northeast Pacific"

Jonathan Thar

The Pacific Ocean Shelf Tracking (POST) Project was conceived in 2001 to determine the scientific value and feasibility of building a permanent, large-scale acoustic telemetry network for studying the movement and behavior of marine animals. From 2001-2005, the concept of deploying highly efficient lines, or "curtains", of acoustic receivers on the ocean bottom was tested mainly in the inland waters of Vancouver Island, British Columbia. Concurrently, trials of the utility of those curtains for experimental science were completed mostly by tracking the out-migrations of various salmonid stocks from regional river systems, taking advantage of the acoustic technology that works seamlessly between fresh- and saltwater. After a successful proof of concept phase, the initial permanent POST array was deployed in 2006, using lines of receivers running from shore to 200m depth, that can detect nearly 100% of all acoustically tagged animals passing through them. Today, this array has grown to stretch along 3,000km of the Northeast Pacific coast, from Prince William Sound, Alaska to Point Reyes, California. Over 45 independent researchers contribute to and receive data from POST's freely accessible database, having tagged more than 13,000 individuals of 18 different species. The platform serves as an accessible research tool available to academe, resource agencies and the public, contributing to the advancement of scientific knowledge and the conservation and stewardship of marine resources.

Global marine species diversity[a] and richness[b]: patterns and predictors

[a] Derek P. Tittensor, Camilo Mora, Walter Jetz, Heike K. Lotze, Daniel Ricard, Edward Vanden Berghe & Boris Worm

[b] Philippe Bouchet, Derek P. Tittensor, Geoff Boxshall, Terry Erwin, Benoit Fontaine, Camilo Mora & Edward Vanden Berghe

The decade-long Census of Marine Life has dramatically increased our knowledge of marine species and where they live. This process has come about from the numerous research expeditions of individual field projects discovering new species, the compilation of enormous amounts of data by OBIS, and the modeling and synthetic efforts of FMAP and HMAP. Yet if we put all of this data together, and add it to all of the data that pre-dated the Census or was collected alongside it, how much do we *really* know about patterns of marine diversity and distribution? We set up a synthesis group to answer these questions at the broadest possible scales. The first sub-group set out to compile distribution data from zooplankton to whales, from invertebrates to sharks, from corals to fishes, to ask whether there were fundamental similarities in the factors shaping their distributions, where the cross-taxon diversity hotspots were, and what we could learn about the evolutionary or ecological mechanisms that shape the global patterns of marine diversity that we observe today. The second sub-group focused on the purely numerical aspect of whether we could robustly refine estimates of global marine species richness, given the data that we have today. We investigated statistical, macroecological, and taxonomic approaches to answer this intriguing and challenging question. Here we present the results of these studies, and explore the knowns, unknowns, and unknowables of the marine world.

COMPREHENSIVE REGIONAL ASSESSMENT OF KNOWN BIODIVERSITY IN A LARGE MARINE ECOSYSTEM: THE GULF OF MEXICO EFFORT

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An attempt to compile a comprehensive biotic inventory of the Gulf of Mexico (GoMx) has recently been completed. The boundaries of the GoMx were defined geographically and ecologically. A team of 140 experts/taxonomists from 15 countries, representing 80 institutions, worked for four years (2004–2007) to update the knowledge of the fauna and flora. The effort, which covered 40 phyla, listed 15,419 species inhabiting the 1.5 million km² GoMx, and it consists of the most comprehensive account to date for a large marine ecosystem. Among the species, some 1,253 species are listed as endemic to the GoMx, and 552 are listed as nonindigenous. Coverage of the better-known macrobiota, such as birds or marine mammals, is nearly complete, but many of the taxonomic groups with small, rare, soft-bodied or deepwater species are still poorly known. Molecular studies reveal undescribed taxa among even common forms, some long overlooked. Taxonomic revisions and descriptions lag far behind recent molecularly based efforts for most groups.

The GoMx biota checklist, dubbed Phase I of the Biodiversity of the Gulf of Mexico Project (BioGoMx), was published as a book in 2009 (Felder and Camp. *Gulf of Mexico– Origins, Waters, and Biota. Vol. 1. Biodiversity*. Texas A&M Press). Phase II was the conversion of the checklist into a database, currently available through OBIS and NASA. A

more detailed database, with information about habitat, biology, depth and references, will soon be available through GulfBase, a GoMx portal. Phase III, the analysis of the dataset, is currently underway, to identify patterns of biodiversity and gaps in geography and taxonomy.

CENSUS OF ANTARCTIC MARINE LIFE (CAML)

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The Census of Antarctic Marine Life (CAML www.caml.aq) is a project of the Scientific Committee on Antarctic Research, selected as a highlight of the International Polar Year (IPY). CAML has coordinated 18 major voyages in the largest-ever survey of the Southern Ocean. While cataloguing 16,000 species of biota from the Southern Ocean, researchers have discovered new processes of dispersal, colonization and evolution. This broad scope required collaboration among biologists, geoscientists and oceanographers. The CAML network has 350 participants from 33 countries, including a consortium of seven countries with Antarctic programs in South America. Inspired by the IPY, a comparison of species in Antarctic and Arctic waters was possible for the first time. Legacies of CAML are the discovery of hundreds of new species, DNA barcodes for 2,500 species; taxonomic monographs, Antarctic Field Guides, pages for the Encyclopaedia of Life; over 1,000 publications; benthic and pelagic bioregionalisations; contributions to the Southern Ocean Observing System and providing evidence for the declaration of two Vulnerable Marine Ecosystems by the Commission for the Conservation of Antarctic Marine Living Resources. CAML has provided access to a robust baseline of information on the variety of life in the Southern Ocean ecosystem. Future climate change will be measured against this benchmark.

Global Patterns and Predictions of Seafloor Biomass

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Abstract:

A comprehensive global seafloor biomass database has been constructed from Census of Marine Life field projects. Patterns of seafloor biomass are shown to be positive functions of surface primary production and delivery of the particulate organic carbon flux to the sea floor. At a regional scale, seafloor biomass varies on different margins, depending on the width of the continental shelf, seafloor topography, temperature, and terrestrial runoff. Predictive models utilized global primary production, export POC flux, and seafloor relief models. Machine learning algorithms (Random Forest, Multivariate Adaptive Regression Splines, and TreeNet) were employed to optimize biomass prediction precision. For the first time, individual and composite maps of predicted global seafloor biomass were generated for bacteria, meiofauna, macrofauna, and megafauna (invertebrates and fishes). The ensemble of models explains 70% to 80% of observed biomass variance. The predictive maps are important for ocean and fisheries management and are vital components in the development of mechanistic deep-sea food web models.

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Measuring Alpha Diversity Across Microbial Ocean Realms

David Mark Welch, Susan Huse and Linda Amaral-Zettler on behalf of the ICoMM Alpha Diversity Working Group

There are more microbes on Earth than stars in the universe. Nucleic-acid staining technology shows the number of bacteria in the open ocean exceeds 10^{29} cells, with average cell concentrations of 10^6 per milliliter of seawater. In marine surface sediments, cell abundances are 10^8–10^9 per gram, and even in the greatest depths of the subsurface seabed, microbial density exceeds 10^5 cells/gram. The International Census of Marine Microbes is measuring microbial diversity in a broad range of marine ecosystems to facilitate quantification of the magnitude and dynamics of the microbial world and its stability through space and time. Examining the relationships between microbial populations and whole communities within their dynamic environment will allow us to better formulate the definition of what constitutes an ecologically relevant species in the microbial world.

Molecular methods of identifying the largely uncultivable microbial biosphere rely upon sequencing regions of conserved genes such as the 16S ribosomal RNA and using measures of genetic similarity to describe Operational Taxonomic Units (OTUs) or microbial species equivalents. Clustering methods based on either phylogenetic inferences or sequence similarities can define membership in an OTU. For Bacteria and Archaea, cluster sizes are typically set at the 3% difference level to measure richness (alpha diversity). Using extensive quality control measures and conservative methods to assign sequences to OTUs, we clustered more than 10 million bacterial sequence tags from 569 surveys of diverse marine ecosystems and identified 128,000 bacterial OTUs. Using a smaller set of 1.3 million sequence tags from 77 surveys we identified 3,200 archaeal OTUs. This census has significantly increased the estimated number of marine bacterial and archaeal OTUs; however, nearly every survey undersampled every major taxon. We estimate that complete sampling of the ICoMM surveys would yield 440,000 – 460,000 bacterial OTUs and 13,000 – 23,000 archaeal OTUs, and that the ICoMM surveys themselves represent only a fraction of the microbial richness in the world's oceans.

Samples for which we had both water column and sediments represented for a given locale showed that in general the benthos was richer in bacterial diversity than the water column. Preliminary results indicate that sediments in the temperate zone on the continental shelf of New Zealand are among the samples that hosted the greatest bacterial richness observed and estimated in ICoMM samples thus far. It is possible that this area represents an undiscovered hotspot of diversity unexplored until now. Waters of the shallow Azorean Vents were among the samples that showed the greatest bacterial diversity in the water column while Antarctic coastal waters were among those that showed the lowest. We examined many fewer samples for archaeal diversity, but among those examined, temperate waters and sediments appeared to host a higher archaeal richness than tropical waters and sediments overall. Among the least diverse archaeal samples included hydrothermal vent microbial mats from the Lost City

Hydrothermal vent and waters of the Arctic Ocean. In general, observed bacterial diversity was nearly 40 times greater than archaeal diversity in the ICoMM samples examined overall while diversity estimates yielded estimates that were 25 times higher in bacteria than archaea. Observed eukaryotic richness was at least 1 order of magnitude higher than archaeal richness overall but estimates of eukaryotic richness are ideally limited to replicated samples and incidence-based methods which were lacking in most ICoMM samples.

New Australian Sharks and Rays

Author: William White

Abstract:
Since 2007, the CSIRO's Biogeography and Taxonomy team has described 80 new species of sharks, rays and chimaeras from Australian waters, in collaboration with numerous international experts. This represents more than a quarter of Australia's, and about 7% of the world's, shark and ray fauna. Full species accounts are available in the recently published Sharks and Rays of Australia, Second Edition by Peter Last and John Stevens. The collage of the 80 new species featured highlights the very high diversity of sharks, rays and chimaeras found within the Australian region. The Biogeography and Taxonomy team at CSIRO Marine & Atmospheric Research in Hobart consists of: Peter Last, Daniel Gledhill, William White, John Pogonoski, Alastair Graham and Louise Conboy.

Biodiversity in Western Australia's Deep Sea

Author: Alan Williams

Abstract:

- This first large systematic collection of large seabed invertebrates from Australia's deep western continental margin (~100 to 1,100 m depth between North West Cape and Albany), revealed an undiscovered high species richness and novelty in several taxa.

- Within the total collection, 1,979 species make up the major taxa that have comprehensive and consistent species-level discrimination across all samples: Demospongiae, corals (Octocorallia and Antipatharia), Mollusca, Echinodermata, Decapoda, Pycnogonida and Acscidiacea. Richness of other taxa has not yet been determined.

- 59% of the major taxa were estimated to be new or un-named species. Even amongst the decapods, which are relatively well known, 33% of the 524 species collected are believed to be new to science.

- http://www.coml.org.au/photogallerycenseam.html

Seamount ecosystems conserved in the Huon Commonwealth Marine Reserve, Australia

Author: Alan Williams

Abstract:

- The Huon Commonwealth Marine Reserve (CMR) off southern Tasmania covers 12,780 km2 of outer continental shelf, continental slope and deeper seabed. It contains the smaller Tasmanian Seamounts Marine Reserve that was declared in 1999 when the conservation significance of Australia's seamounts and the impact of commercial bottom trawl fishing was first recognized.

- The Huon CMR encloses almost all of Australia's largest known seamount cluster. In April 2007, we mapped about 2200 sq km of the Huon CMR and identified 123 seamounts in 1,000-2,000 m depths – most of which were previously unknown (Figure 1). The seamounts are the cone-shaped remnants of extinct volcanoes, up to 25 km across at the base, and rising 200-500 m from the seabed.

- This seamount area differs from all others identified in the Australian marine jurisdiction and the adjacent Tasman and Coral Seas2, in the large number of seamounts, their relatively shallow depth range, and the preponderance of cone-shape forms.

Statistical methods for synthesizing the world's largest tracking dataset

Arliss J. Winship, Ian D. Jonsen, Salvador Jorgensen, Greg A. Breed, Autumn-Lynn Harrison, James E. Ganong, Scott A. Shaffer, Dan P. Costa, Barbara A. Block

Using state-of-the-art electronic tracking technologies, TOPP has amassed the world's largest single dataset on the movement and distribution of 21 marine predator species in the North Pacific Ocean. The diverse range of species studied and tagging technologies used by TOPP presents a challenge for synthetic efforts to infer relationships between the movements and distributions of marine predators and their environment. Our project draws on FMAP's animal movement modelling efforts to facilitate the synthesis of the TOPP dataset. We used a Bayesian state-space method to derive regular, consistent and comparable estimates of animal locations across species and technologies along with appropriate estimates of the uncertainty in these location estimates. Our method explicitly accounted for data precision allowing us to integrate relatively precise satellite-based data with relatively imprecise light- and sea surface temperature-based geolocation data. We estimated the precision of the geolocation data using data from captive animals at known locations and data from experiments where free-ranging animals were simultaneously 'double-tagged' with satellite and geolocation tags. The estimated locations were combined across individuals and species to examine where total predator density was highest in the eastern North Pacific Ocean. A time weighting scheme was applied to species whose distribution of data records was heavily influenced by tag failure and animal harvest in order to reduce the influence of tagging location on the estimated geographic distribution of these species. Densities were also normalized across species to reduce the effect of differences in sample size when inferring multi-species patterns. Only by applying sophisticated statistical methods, like the state-space approach that we used, can one make proper inferences about stochastic ecological processes such as animal movement while accounting for imperfect observations in large, diverse datasets like that of TOPP.

The Future of Marine Animal Populations Project

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What will live in the oceans? This is the question that has ultimately driven the Future of Marine Animal Populations (FMAP) Project over the past decade. Yet without a solid understanding of past and present trends, it is impossible to make sound future projections. Thus, FMAP's mission has been to describe and synthesize globally changing patterns of species abundance, distribution, and diversity, and to model the effects of fishing, climate change and other key variables on those patterns. This work has been carried out across ocean realms and with an emphasis on understanding past changes and predicting future scenarios. Here, we highlight the main advances that have been made across three major research streams: (1) Marine biodiversity patterns and their drivers, (2) Long-term trends in animal abundance and diversity, and (3) Distribution and movements of individual animals. In the concluding section we provide some insight into what is unknown, and what is currently unknowable, particularly with respect to predicting the future of marine biodiversity.

Invasive Alien Species in European Marine Ecosystems

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Abstract:

Biological invasions by alien species are recognised as an important component of global environmental change, often resulting in a significant loss in the economic value, biological diversity and function of invaded ecosystems. More than 1000 multi-cellular alien species have been recorded from European seas. Approximately 600 taxa have become established with self-sustaining populations; the great majority of them found in the Mediterranean Sea. Zoobenthic organisms are the most dominant group of exotic species across all European Seas. As a result, studying the impact of invasive alien species on native fauna has been an area of research that the European Census of Marine Life has fully supported.

The most important pathway of alien species introductions are: canals (Mediterranean Sea), shipping, aquaculture or stocking activities (Baltic Sea and Atlantic coast). Recently a proposed standardised method, the Bio-Pollution Level (BPL) index, allows us to measure the magnitude of bio-invasive impacts. The estimated BPL is a net result of a combination of abundance and distribution range (ADR), class and impact of alien species on communities (C), invaded habitat (H) and ecosystem functioning (E). For example, the slipper limpet *Crepidula fornicata* in the North Sea and Atlantic coast occurs at densities $>1700/m^2$, resulting in trophic competition, causing reduced growth of commercial bivalves; changes to sediment mud deposits, thus reducing the diversity and abundance of living plants. Therefore the assigned bio-pollution level for the species is strong (BPL=3). Following this approach the bioinvasion impacts of the target alien species can be quantified.