



Editorial

The Census of Antarctic Marine Life: Diversity and change in Southern Ocean Ecosystems

1. Introduction

The Census of Antarctic Marine Life (CAML) represented the largest survey undertaken of Antarctic marine life, and contributed one of the larger programmatic efforts to the International Polar Year (IPY) 2007/2008. It coordinated 19 research voyages distributed broadly throughout the Southern Ocean and Antarctic shelves, and supported by a network of over 300 biologists from 30 countries.

CAML tackled the multiple tasks of contributing to the Census of Marine Life (CoML) in Antarctica, by assessing the *Known*, the *Unknown* and the *Unknowable* in this vast region; and, fulfilling the IPY themes, of providing a robust baseline against which to assess any changes in diversity and/or community structure at these high latitudes under the increasing pressure of dramatic climate-associated changes. Given that Polar Regions experience the greatest rates of climate change on the Planet, their detailed assessment should be regarded by the scientific community and decision makers as an urgent priority.

To accomplish its multiple missions, CAML has continuously engaged Antarctic researchers – from students to veterans – involved in various national and international programs, creating a single international collaborative network, where new partnerships among scientists, and the exchange of human resources and materials, have become commonplace. Through leveraging of core funding provided by the Census of Marine Life, a variety of national funds and workshop opportunities have been harnessed, allowing the completion of synthetic studies, which would have been impossible without such a coordinated effort.

During CAML's 5-year life span, two seminal meetings of its international Scientific Steering Committee and invited participants developed the program features and operative framework. In Brussels during May 2005, the draft CAML Science Plan was produced and reasonably achievable targets for research projects were proposed. In Białowieża (Poland) during May 2007, coordination details and standardized sampling protocols were refined prior to the launch of most IPY cruises. These efforts laid the essential foundation for future integration.

The major achievements of this unprecedented assessment were presented at the CAML Final Symposium, entitled “*Diversity and Change in Southern Ocean Ecosystems*”, hosted and organized by the Italian National Antarctic Museum in Genoa during May 2009. From the 42 different contributions presented at this symposium, 25 have been assembled for this Special Issue dedicated to CAML. We offer this product to the scientific community, hoping that it will stimulate new, or better defined, questions and hypotheses about the evolution, dynamics and history of Antarctic ecosystems.

This issue begins with two synthetic efforts summarizing our knowledge of the Antarctic's biodiversity. De Broyer and Danis (2011), together with 64 taxonomic editors, assessed the “*Known, Unknown and Unknowable*” of Antarctic marine biodiversity using the Register of Antarctic Marine Species (RAMS). Their estimate of the *Known* is amazingly more than 8,019 valid species, and about 15,500 taxon names, overturning the long-standing paradigm of decreasing diversity with increasing latitude in the southern hemisphere. Undoubtedly, the Southern Ocean is an area of high speciation and endemism, at levels which could not be imagined just a few years ago. Secondly, Griffiths et al. (2011) illustrate the importance of SCAR-MarBIN in the compilation and management of information on Antarctic marine biodiversity, with its more than 140 different datasets containing over one million distribution records. Hot spots, as well as under-sampled regions or taxa, can now be visualized. These monumental consolidations of information represent key enduring legacies of CAML, enabling future studies to fill gaps in knowledge and compare new observations with these biodiversity baselines.

The next section of the issue is devoted to studies looking at more regionally or taxonomically focused topics, often working to improve our basic inventory of Antarctic marine species. Siciński et al. (2011) present a comprehensive census of the Admiralty Bay area benthos, with approximately 1300 metazoan species identified during more than 30 years of observations. Admiralty Bay is now one of the best studied Antarctic areas, recently designated a legacy site, where continued, systematically integrated sampling could measure effects of climate change on marine life. The exploration of the Antarctic deep sea and adjoining basins has been one of the major themes within the CAML community, showing the unexpectedly high diversity in the Antarctic abyss (e.g. Brandt et al., 2007) and deep-water dispersal pathways through the thermohaline circulation (Strugnell et al., 2008). In this issue, Schrödl et al. (2011) focuses on gastropod molluscs along a deep-sea transect in the South Atlantic, from the equator to Antarctica, finding that only 5 out of the 27 species collected are currently described. Diversity increased moving southward, again in clear contrast to the paradigm of a decreasing marine diversity from lower to higher latitudes, but observations also challenge earlier suggestions of a hyper-diverse global abyssal gastropod macrofauna. Further south, Rapp et al. (2011) describe three new species of *Calcarea* sponges from Antarctic abyssal depths that, despite their rarity, seem to constitute a consistent component of the fauna and suggest many more new species will likely be discovered in future. In the following contribution, Mühlenhardt-Siegel. (2011) considers the high degree of endemism of Antarctic

deep-sea Cumaceans, where up to 75% of the morphospecies collected in the past 15 years are represented by new species.

Some of the CAML-IPY cruises were totally or partially dedicated to the exploration of unstudied Antarctic areas or to the short and long-term consequences of changing ice cover to Antarctic communities. We begin with the Gutt et al. (2011) survey of the Larsen A and B areas along the Antarctic Peninsula 5 and 12 years after the shelves' collapse, discovering an impoverished benthic fauna with the deep-sea species encountered presumed to be survivors from previous ice-covered conditions. New colonizers were slowly changing the formerly oligotrophic sub-ice-shelf ecosystem to a newly productive one. Hardy et al. (2011) also examined recolonization processes in areas freed of ice, showing that epibionts associated with cidaroid echinoids could contribute to benthic colonization of the seafloor. Thinking on longer time-frames, Kaiser et al. (2011) studied benthic Antarctic assemblages from several cruises to the Weddell and Scotia Seas, with emphasis on cheilostome bryozoans, isopods, ostracods and echinoids. They demonstrated that there is no longer strong support to the hypothesis of a homogenous and unique Antarctic slope fauna, and that the slope was probably not a universal refuge for Antarctic shelf fauna during glacial expansions. With similar goals, Post et al. (2011) studied the physical and biological characteristics of benthic communities across the George V Shelf, suggesting that seafloor communities are the result of asynchronous recruitments from deep water propagules sources, or from neighboring shelf refugia, following the last retreat of the icesheet and glaciers. Finally, Bowden et al. (2011) discovered striking assemblages dominated by stalked crinoids and brachiopods on isolated knolls of the Admiralty Seamount. Sediments mainly formed by crinoid ossicles indicate that these assemblages had persisted there for considerable time, suggesting that during glaciation these seamount systems acted as refugia allowing the survival of assemblages that have no extant relatives in the modern Antarctic biota.

In the CAML assessment of Antarctic marine life, all sizes of life, from bacteria to whales have been considered, often asking broader questions beyond simply diversity. At the smallest end of the spectrum, Nakayama et al. (2011) focused on Antarctic archaeal communities and their role in controlling the dynamics of biogenic methanogenesis in Admiralty Bay. Differences in archaeal densities occurred with depth and granulometry, while 16S clone libraries revealed archaeal groups not previously described in Antarctic samples. Moving to eucaryotes, Olgúin and Alder (2011) examined the 167 diatom species from the subantarctic Argentinian shelf to Antarctic waters to understand biogeographic linkages, and the barrier effect of the Polar Front. Within the Subantarctic region, diatom density and biomass values were low and uncorrelated to chlorophyll, while in Antarctic waters, diatom biomass was directly related with chlorophyll, confirming their important contribution to the Antarctic phytoplankton stock.

Within the invertebrates, Würzberg et al. (2011) employed 18 Southern Ocean polychaete families, from the shelf to the deep sea, to identify trophic biomarkers and successfully elucidated feeding preferences using fatty acid (FA) composition. Fatty acids suggested consistent feeding patterns within families in the deep sea, while the FA composition differed between the deep and the shelf stations, even within the same family. In the following paper, Eléaume et al. (2011) used the feeding behavior of comatulid crinoids – as recorded in still images and video transects – to infer the directions of near bottom currents, supporting the existence of a counter-clockwise gyre in the deep George V Basin, and delineating its boundaries. This novel method integrated biological and physical data, and allows characterization of water movements over large bottom areas where instrumentation is operationally limited.

For fishes, Koubbi et al. (2011) demonstrated the spatial distribution of myctophids is highly influenced by meso- or sub-mesoscale oceanographic features using historical surveys and recent CAML cruise data to model species assemblages in the Indian sector of the Southern Ocean by using Generalized Dissimilarity Modeling. These novel models represent powerful tools to move from bioregionalization based on abiotic factors only, to the ecoregionalization, which takes into account species assemblages. Next, O'Driscoll et al. (2011) studied the Antarctic silverfish *Pleuragramma antarcticum*, using a combined approach of mid-water-demersal trawls and multifrequency acoustic surveys, showing that silverfish marks could be discriminated from those of krill and other associated species.

Close to one-third of the contributions to this issue have embraced molecular techniques as a means to resolve diversity and phylogeny. These papers reflect not only a new phase of research in Antarctica, but also CAML's specific affiliation to the Barcode of Life project (Grant and Linse, 2009). Through agreement with the Canadian Center for DNA Barcoding in Guelph, more than 15,000 sequences representing more than 1,500 species have been produced from the Antarctic region that are now publicly available. Molecular tools are providing information about taxonomic boundaries, the extent of cryptic speciation, and the phylogeography of Antarctic species. It is remarkable that the first major steps in the marine molecular field undertaken in Antarctica are little less than a decade old, with important early efforts showing that the rate of molecular evolution is not slowed at low temperatures (e.g. Held, 2001), and that cryptic speciation occurs in Antarctic waters (e.g. isopods—Held, 2003).

Strugnell et al. (2011) begin this molecular section by addressing the evolutionary history of the cosmopolitan, and often deep-water octopus genus *Benthoctopus* using five mitochondrial and one nuclear gene. They suggest that the *Benthoctopus* clade originated in relatively shallow Northern Hemisphere waters and later colonized the Southern Ocean, where the group is now represented by three independent clades, and occurs at shallower depths than non-polar *Benthoctopus* species. Díaz et al. (2011) used the regular sea urchin genus *Sterechinus* and COI to explore the evolutionary relationships between shelf and deep water species, using five nominal species with Antarctic and Subantarctic distributions and different bathymetric ranges. They found two genetically distinct main groups, one formed by the shallow-water Antarctic species *S. neumayeri* and the second included all the other nominal species, regardless their depth habitat or region of origin. Neither the submergence nor emergence hypotheses currently explain the observed relationships between these two clades.

A set of contributions tackled the issue of circumpolarity. Arango et al. (2011) targeted the highly abundant and morphologically variable Antarctic sea spider, *Nymphon australe*, using both COI and 16S. They found a single species with circum-Antarctic and eurybathic distribution, despite the existence of a strong phylogeographic structure and the presence of effectively isolated populations. Similarly, González-Wevar et al. (2011) investigated phylogeographic patterns of the endemic shallow-water Antarctic limpet *Nacella (Patinigera) concinna* along the western Antarctic Peninsula, both morphologically and using COI. They failed to detect any genetic structure, supporting a single genetic unit, and further suggested negative selection for genetic diversity occurs during glacial periods in species which live at shallow depths. Likewise, Havermans et al. (2011) used a barcoding approach to test for circumpolarity in lysianassoid amphipods, finding that the majority of the species studied were characterized by genetic homogeneity, thereby confirming both a circum-Antarctic and a eurybathic distribution. However, four species had genetically divergent lineages and possible cryptic taxa, suggesting that the paradigm of circumpolarity for Antarctic species cannot be generalized, and

needs to be tested species by species. Lastly, Allcock et al. (2011) focused on the genetic structure of the endemic Southern Ocean octopus genus *Pareledone* using COI sequences from 350 specimens obtained from different localities that corresponded to at least 11 different species. They found evidences of cryptic speciation in some taxa and, in one case, a true circumpolar distribution.

Several papers simply sought to determine the usefulness of molecular techniques at resolving species boundaries. Thus, Dettai et al. (2011) explored the effectiveness of the COI gene in discriminating Antarctic teleosts using 538 specimens, collected off Terre Adélie, finding general congruence among molecular and morphological data. Nonetheless, in several cases neither COI, the other molecular markers investigated, nor morphology, unambiguously recovered the currently accepted species. Their work pinpointed the specimens that needed to be re-identified morphologically, and highlighted the teleost groups in which barcoding can be routinely used for specimen identification. Along similar lines, O'Loughlin et al. (2011) studied 187 species of Antarctic holothuroids (including 51 undescribed species) both from a molecular and morphological perspective. Both inter- and intra-regional genetic divergences were revealed in COI sequence data, despite morphological classification suggesting only species with circumpolar distributions. They concluded that morphological data may be misleading, failing to reflect the real level of differentiation in holothuroids.

The 25 papers presented here from the CAML Final Symposium are less than half of those currently published by CAML contributors in peer-reviewed articles. They represent the leading edge of many others expected to be published as the incredible quantity of material collected under the CAML umbrella is processed. The diversity of species from the IPY-CAML surveys has exceeded expectations, and it will take years to inventory all of the species and formally describe the new ones.

The legacies of CAML will continue well beyond the project's official completion in 2010, with all of the CAML data publicly available in permanent repositories for researchers, governments and other national and international organizations concerned with Antarctic Ocean's management. The georeferenced species records, will remain available through CAML's sister project, SCAR-MarBIN (the Scientific Committee on Antarctic Research's Marine Biodiversity Information Network). SCAR-MarBIN is already evolving into ANTABIF (Antarctic Biodiversity Information Facility), which will become the primary Antarctic biodiversity data portal. ANTABIF will coordinate and provide access to a distributed network of contributing databases, including both marine and terrestrial datasets related to the SCAR EBA (Evolution and Biodiversity in Antarctica) program. Analogously, all barcode sequences are permanently available through BOLD (Barcode of Life Database), together with links to the voucher material. Together, these will facilitate future comparisons between new material and that produced under the CAML umbrella, thereby making taxonomic delimitation more straightforward in the future.

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Stefano Schiaparelli*

*Dipartimento per lo studio del Territorio e delle sue Risorse
(Dip. Te. Ris.), Università di Genova, Corso Europa No. 26,
I-16132 Genova, Italy*

*Museo Nazionale dell'Antartide (Sede di Genova),
Viale Benedetto XV, No. 5, I-16132 Genova, Italy
E-mail address: stefano.schiaparelli@unige.it*

Russell R. Hopcroft

*Institute of Marine Science, University of Alaska, Fairbanks,
AK 99775-7220, United States*

* Corresponding author at: Dipartimento per lo studio del Territorio e delle sue Risorse (Dip. Te. Ris.), Università di Genova, Corso Europa 26, I-16132 Genova, Italy. Tel.: +39 010 3538329; fax: +39 010 3538102.