

## Editorial - Arctic Ocean Diversity: synthesis

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Accepted: 22 December 2010 / Published online: 29 January 2011  
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The most fundamental attributes of marine ecosystems are their Communities associated species composition, along with their specific abundances and biomass. Process-oriented understanding of rates and interactions within ecosystems hinges on this first-order descriptive framework. While we know the major species and understand their roles in many parts of the world ocean, the fragmented nature of discrete studies has not fostered synthetic approaches. The societal need for such basic information has increased in recent decades as major facets of the human footprint are altering marine communities around the globe (i.e. climate change, species invasions, fisheries effects, oil and gas exploration, tourism). To understand such change, biodiversity studies spanning species inventories to functional linkages between diversity and ecosystems are necessary. Within this context, as well as driven by simple human curiosity, the International Census of Marine Life (CoML) was launched in 2000 (Yarincik and O’Dor 2005). CoML grew to a global network of researchers in more than 80 nations engaged in a 10-year scientific initiative to assess and explain the diversity, distribution, and abundance of life in the oceans. CoML addressed the fundamental questions “What lived in the oceans in the past, what lives in the oceans now, and what will live in the oceans in the future” (McIntyre 2010).

The Arctic component of CoML, the Arctic Ocean Diversity project (ArcOD), was launched in 2004 (Gradinger

et al. 2010), with a sister project launched in the Antarctic shortly thereafter (Schiaparelli and Hopcroft 2011). Globally, gaps in biodiversity knowledge are greatest in areas where the logistics limit access. In this regard, the Arctic is understudied due the challenges of sampling in remote ice-covered waters. There is increased urgency to fill these gaps because climate change effects are strongly expressed in the Arctic, as apparent from the rapid loss of its sea ice over the past decades. The ArcOD umbrella sought to inventory biodiversity in the Arctic sea ice, water column and sea floor (Fig. 1)—from the shallow shelves to the deep basins—using a three-level approach: compilation of existing data, taxonomic identification of existing samples, and new collections focusing on taxonomic and regional gaps. While ArcOD was initiated mainly by US-based and Russian scientists, over 100 scientists in a dozen nations have contributed to ArcOD-related efforts, including many conducted during the International Polar Year 2007–9.

In October 2010, the Census reported ‘A decade of discovery’ across regions and realms at the Royal Society in London. This present special issue presents a core contribution of ArcOD’s synthesis and contains pieces originally presented in their preliminary form at the Arctic Frontiers meeting in January 2010 in Tromsø, Norway in the ‘Marine Biodiversity under Change’ session. The articles in this and the subsequent issue (Hop et al. 2011) have a strong focus on biodiversity, on a species, community and/or habitat level. Articles in this issue are pan-Arctic in spatial coverage with international author teams from ten countries and more than 25 institutions contributing the required expertise and majority of the data. The contributions in this issue are arranged in taxonomic order and span from microbes to marine mammals. Most contain new synthetic numerical analyses, as well as reviews of current knowledge, contemporary perspectives, and several presently expected

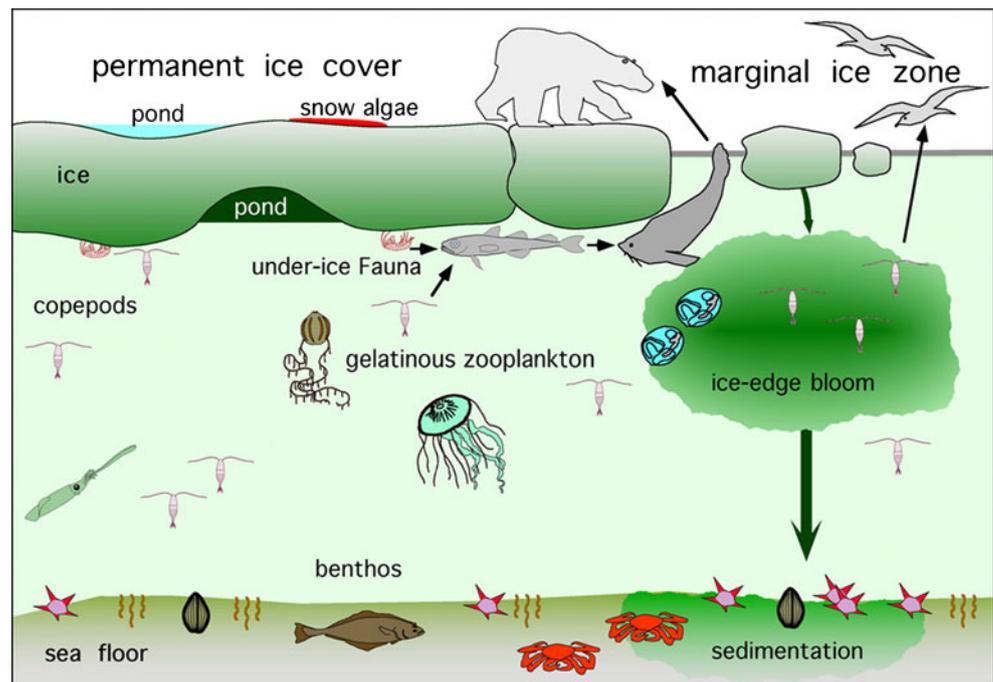
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This article belongs to the special issue “Arctic Ocean Diversity Synthesis”

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**Fig. 1** The Arctic's three realms: sea ice, water column, and benthos, with examples of their biodiversity. Modified from Gradinger et al. (2010)



future scenarios. Many include pan-Arctic species inventories by realm and regions, for invertebrates building on the unprecedented list by Sirenko (2001), and provide 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. The Arctic Register of Marine Species containing these inventories is now available at [www.marinespecies.org/arms/](http://www.marinespecies.org/arms/) and the majority of taxon distribution records underlying the register—and the papers in this issue—are available through the Ocean Biogeographic Information System (OBIS: [www.iobis.org](http://www.iobis.org)) and ArcOD's webportal ([www.arcodiv.org](http://www.arcodiv.org)) with microbial data within MICROBIS (<http://icomm.mbl.edu/microbis/>). The following paragraphs highlight some of the core findings from each article.

Most marine microbe groups are present in Arctic marine waters (Lovejoy et al. 2010). Estimates of operational taxonomic units for picoplankton, based on the small subunit rRNA gene (SS rRNA) are: ~500 pico-Eucarya and Archaea each per water mass (of which 300 are unique to that water mass) for a total of 4,500 for each group (assuming 15 water masses). The number of bacterial OTUs is estimated to be an order of magnitude higher: 45,000. Similar to other taxa, these microbes are a combination of Arctic and more cosmopolitan forms. Bacterial and archaeal communities differ somewhat from their temperate counterparts, although Proteobacteria among the Bacteria dominate in surface and deep waters as in other oceans.

A total of 2,106 marine single-celled protists have been described from the Alaskan, Canadian, Scandinavian,

Greenlandic, and Russian Arctic based on morphological studies, consisting of 1,874 phytoplankton and 1,027 sympagic (ice-associated) taxa (Poulin et al. 2010). For comparison, ~5,000 phytoplankton species are recognized in the world's oceans. The Arctic taxa represent four of the six super-groups of the now widely accepted eukaryote classification, and the Chromalveolata contain most of the taxa. The new list is primarily comprised of cells >20  $\mu\text{m}$ , with large knowledge gaps in the pico- and nano-biota size classes.

In the sea ice itself, dozens of metazoans live within the sea ice brine channels or at the ice–water interface. For sea ice meiofauna, these includes, for example, at least 8 species of Rotifera, 3 Nematoda, and 11 Arthropoda, while a more species-rich community occurs at the ice–water interface (e.g., 11 species of Amphipoda) due to exchange with the plankton. Sea ice endemic species have been described for Cnidaria, Nematoda and Amphipoda (Gradinger et al. 2010) and the inventory is not yet complete. Our GIS modeling efforts (Gradinger, Bluhm, Iken, Huettmann, Hop, and Werner, unpublished) revealed pan-Arctic distribution patterns for the pack-ice biota with distinctly different patterns for the fast ice.

ArcOD's current register of metazoan holozooplankton is close to 350 species (Sirenko et al. 2010). On Arctic shelves, zooplankton communities range from those consisting largely of Arctic endemics to those dominated seasonally by sub-arctic expatriates in large portions of the Barents and Chukchi Seas. While nearly 200 species appear largely restricted to the shelves, there is overlap with the basin species approaching the shelf break. While efforts

remain underway to characterize the complexity of shelf habitats (Hopcroft et al., unpublished), exploring the patterns of the deep basins represented a more manageable task. A total of 174 multi-cellular zooplankton species from eight phyla were registered from the central Arctic basins, dominated by crustaceans, and primarily copepods (Kosobokova et al. 2010). New taxon records including new species were generally from bathypelagic layers. No zoogeographical barrier was apparent between the Eurasian and Canadian basins, although Pacific and Atlantic expatriates accounted for basin-scale differences in the upper layer. Communities were distinctly different between depth layers. Diversity indices increased with depth to a maximum within the Atlantic layer, followed by a decrease in the deepest strata.

For macro- and megabenthic shelf fauna, a first pan-Arctic inventory based on ~68,000 distribution records from 14 of the 19 marine Arctic shelf ecoregions totaled 2,636 species, with a predicted value of 3,900–4,700 species (Piepenburg et al. 2010). Species numbers were highest in the NE Barents Sea, while taxonomic distinctness was highest in the Eastern Bering Sea. As for zooplankton, crustaceans (especially amphipods) dominated species numbers (847 taxa), closely followed by annelids (668 taxa). On a global scale, the Arctic shelves are characterized by intermediate macro- and megabenthic species numbers that are not as low compared to Antarctica as previously believed.

An updated inventory of deep-sea benthos (>500 m) yielded 1,125 taxa (Bluhm et al. 2010), over 400 more than the previous inventory (Sirenko's 2001). The register based on ~6,000 records was again dominated by arthropods (366 taxa), followed by foraminiferans, annelids, and nematodes. About 60% of the taxa overlapped with shelf taxa and half of them were extremely rare. Community abundance, community biomass and polychaete diversity indices decreased with water depth and most decreased marginally with latitude, while evenness increased in both cases. In contrast to other deep-sea regions and the zooplankton, no mid-depth peak in species richness was found. Atlantic influence dominates the register, with modern Pacific fauna virtually absent, and minor regional differences. Again, no barrier effect was suggested for the mid-Arctic ridges.

Faunistic changes—observed and predicted—were explored for the nearshore and fjordic regions with a focus on Svalbard (Weslawski et al. 2010). Increased water temperatures in Pacific and Atlantic inflow areas were reflected in the occurrence of more boreal–subarctic species, while local cold-water species may be suppressed. In coastal areas much less influenced by these advected waters, local benthos is expected to change primarily due to decreasing salinity, reduced ice cover and increased siltation/sedimentation. Together, these factors may lead to habitat homogenization and a subsequent decrease in biodiversity. In

contrast, the innermost basins of Arctic fjords maintain pockets of very cold, dense, saline water and thus may act as refugia for cold-water species.

Increasing availability of genetic data in public databases now facilitates exploration of large-scale patterns in Arctic marine populations (Mincks Hardy et al. 2010). New case studies in meta-population analysis of COI sequence “barcode” data from polychaetes and echinoderms demonstrate phylogeographic applications of these data. Emerging patterns include influences of the Arctic's complex climatic and glacial history on genetic diversity and evolution, along with contrasting patterns of both high gene flow and persistent biogeographic boundaries in contemporary populations. The rapidly expanding genetic libraries are anticipated to provide great insight into the evolutionary history of Arctic communities.

An updated fish inventory yielded 242 species distributed among 45 families, with Cottoidei (71 species) and Zoarcoidei (55) accounting for more than half of all species (Mecklenburg et al. 2010). COI “barcodes” of 106 of these species supported separation of some species and synonymy of others, and sometimes revealed presence of cryptic species. For 34 species, their biogeographic patterns were revised relative to earlier descriptions. Forty-one percent of all species had (predominantly) arctic or arctic–boreal distributions, while the remaining 59% had (predominantly) boreal and wide distributions.

For 27 Arctic sea bird species, predictive models were constructed based on public open-access data archives using Random Forest machine learning algorithms and 26 environmental GIS layers (Huettmann et al. 2010). A compatible taxonomic species cross-walk was also constructed from various sources. Model-prediction scenarios, based on pseudo-absence and expert-derived absence, were run for best accuracy and performance assessments. They showed that the derived models performed poorly for only a few coastal species, but well to very well for most pelagic species. The authors caution that the conservation status for most seabirds is still widely underestimated.

As a consequence of Arctic sea ice decline, some ice-associated marine mammals have shifted distributions, show compromised body conditions, and have experienced declines in production or abundance (Kovacs et al. 2010). Temperate marine mammal species, in contrast, are expanding their ranges northward, likely causing competitive pressure on some endemic species through increased predation, disease and parasite infections. The currently observed negative impacts are expected to continue, and perhaps escalate, in the near future with continued declines in ice cover, thus presenting a serious risk to marine biodiversity among endemic Arctic marine mammal species.

As with many large programs, much work still remains ahead. The scientific network developed through ArcOD

will continue its activities thereby building the foundations for future assessments of Arctic marine biodiversity, and establishing ongoing trends over time. The articles contained here make important first steps in that direction.

**Acknowledgments** We gratefully acknowledge funding for the original field research that was the basis for this synthesis. We thank everyone who contributed to this effort through field work, species identifications, providing data or logistics support. The synthesis effort itself that resulted in this special issue was supported by the Alfred P. Sloan Foundation, with special thanks to its visionary vice director, J. Ausubel. This issue is part of the Census of Marine Life's Arctic Ocean Diversity project synthesis and all papers were originally presented at the Arctic Frontiers Conference in Tromsø, January 2010. The support and initiative of ARCTOS and Arctic Frontiers are gratefully acknowledged, with special thanks to Dr. P. Wassmann for making the connection between ArcOD, ARCTOS and Arctic Frontiers.

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