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Xth SCAR International Biology Symposium on “Antarctic Biology in the 21st Century—Advances in and beyond IPY—”: A brief overview

Mitsuo Fukuchi, Kathleen Elizabeth Conlan

The Xth SCAR International Biology Symposium was held under the theme of “Antarctic Biology in the 21st Century—Advances in and beyond IPY—“ at the Conference Hall, Hokkaido University, between July 26 and 31, 2009. A total of 113 oral presentations and 122 poster presentations were given under six sub-themes. This special issue was edited by six guest editors under the Editor-in-Chief of “Polar Science”, in accordance with the editorial system of “Polar Science” and contains one overview paper and five review papers and 18 research papers.

‘Antarctic biology in the 21st century – Advances in, and beyond the international polar year 2007–2008’

Michael Stoddart

The International Polar Year 2007–2008 (IPY) has provided an opportunity for biology to show itself as an important part of Antarctic science in a manner in which it was not seen during earlier Polar Years. Of the 15 endorsed biological projects in Antarctica, 7 included more than 20 scientists and could be deemed truly international. Four were conducted in the marine environment, and one each in the fields of biological invasions, microbial ecology, and terrestrial ecology, and one was SCAR’s over-arching ‘Evolution and Biodiversity in the Antarctic’. The marine projects have left a robust legacy of data for future research into the consequences of environmental change, and into future decisions about marine protected areas. Studies on introductions of exotic organisms reveal an ever-present threat to the warmer parts of the high-latitude Southern Ocean, or parts which might become warmer with climate change. Studies on microbial ecology reveal great complexity of ecosystems with high numbers of unknown species. Terrestrial research has shown how vulnerable the Antarctic is to accidental introductions, and how productive the soils can be under changed climate conditions. Antarctic biology has come-of-age during IPY 2007–2008 and the campaign has set the scene for future research.

Evidence for widespread endemism among Antarctic micro-organisms

Wim Vyverman, Elie Verleyen, Annick Wilmotte, Dominic A. Hodgson, Anne Willems, Karolien Peeters, Bart Van de Vijver, Aaike De Wever, Frederik Leliaert, Koen Sabbe

Understanding the enormous diversity of microbes, their multiple roles in the functioning of ecosystems, and their response to large-scale environmental and climatic changes, are at the forefront of the international research agenda. In Antarctica, where terrestrial and lacustrine environments are predominantly microbial realms, an active and growing community of microbial ecologists is probing this diversity and its role in ecosystem processes. In a broader context, this work has the potential to make a significant contribution to the long-standing debate as to whether microbes are fundamentally different from macroorganisms in their biogeography. According to the ubiquity hypothesis, microbial community composition is not constrained by dispersal limitation and is solely the result of species sorting along environmental gradients. However, recent work on several groups of microalgae is challenging this view. Global analyses using morphology-based diatom inventories have demonstrated that, in addition to environmental harshness, geographical isolation underlies the strong latitudinal gradients in local and regional diversity in the Southern hemisphere. Increasing evidence points to a strong regionalization of diatom floras in the Antarctic and sub-Antarctic regions, mirroring the biogeographical regions that have been recognized for macroorganisms. Likewise, the application of molecular-phylogenetic techniques to cultured and uncultured diversity revealed a high number of Antarctic endemics among cyanobacteria and green algae. Calibration of these phylogenies suggests that several clades have an ancient evolutionary history within the Antarctic continent, possibly dating back to 330 Ma. These findings are in line with the current view on the origin of Antarctic terrestrial metazoa, including springtails, chironomids and mites, with most evidence suggesting a long history of geographic isolation on a multi-million year, even pre-Gondwana break-up timescale.

Estimating the biodiversity of the East Antarctic shelf and oceanic zone for ecoregionalisation: Example of the ichthyofauna of the CEAMARC (Collaborative East Antarctic Marine Census) CAML surveys

Philippe Koubbi, Catherine Ozouf-Costaz, Anne Goarant, Masato Moteki, Percy-Alexander Hulley, Romain Causse, Agnès Dettai, Guy Duhamel, Patrice Pruvost, Eric Tavernier, Alexandra L. Post, Robin J. Beaman, Stephen R. Rintoul, Toru Hirawake, Daisuke Hirano, Takashi Ishimaru, Martin Riddle, Graham Hosie

Ecoregions are defined in terms of community structure as a function of abiotic or even anthropogenic forcing. They are meso-scale structures defined as the potential habitat of a species or the predicted communities geographic extent. We assume

that they can be more easily defined for long-lived species, such as benthos or neritic fish, in the marine environment. Uncertainties exist for the pelagic realm because of its higher variability, plus little is known about the meso- and bathypelagic zones. A changing environment and modification of habitats will probably drive new communities from plankton to fish or top predators. We need baseline studies, such as those of the Census of Antarctic Marine Life, and databases like SCAR-MarBIN as tools for integrating all of these observations. Our objective is to understand the biodiversity patterns in the Southern Ocean and how these might change through time.

Terrestrial biodiversity in Antarctica – Recent advances and future challenges

Peter Convey

Although its major components have been known almost since the earliest exploring expeditions, even today the terrestrial biota of Antarctica is surprisingly poorly described in detail. It is clear that most currently ice-free ground in Antarctica would have been covered and scoured by glacial advances at the Last Glacial Maximum or previous maxima. Exceptions to this generalisation include parts of the Victoria Land Dry Valleys and some inland nunataks and mountain ranges at altitude, which host their own largely unique biota. However, as new baseline survey data have become available, in combination with the application of techniques of molecular biological analysis, new evidence has been obtained indicating that long-term persistence and regional isolation is a feature of the Antarctic terrestrial biota whose generality has not previously been appreciated. As well as creating a new paradigm in which to consider the evolution and adaptation of Antarctic terrestrial biota, this opens important new cross-disciplinary linkages in the field of understanding the geological and glaciological history of the continent itself. Superimposed on this emerging historical template of Antarctic biogeography, this biota now faces the twin challenges of responding to the complex processes of climate change facing some parts of the continent, and the direct impacts associated with human occupation and travel to and between the spatially very limited areas of terrestrial habitat.

Antarctic sea ice change and variability – Physical and ecological implications

Robert A. Massom, Sharon E. Stammerjohn

Although Antarctic sea ice is undergoing a slight increase in overall extent, major regional changes are occurring in its spatio-temporal characteristics (most notably in sea ice seasonality). Biologically significant aspects of Antarctic sea ice are evaluated, emphasising the importance of scale and thermodynamics versus dynamics. Changing sea ice coverage is having major direct and indirect though regionally-dependent effects on ecosystem structure and function, with the most

dramatic known effects to date occurring in the West Antarctic Peninsula region. There is mounting evidence that loss of sea ice has affected multiple levels of the marine food web in a complex fashion and has triggered cascading effects. Impacts on primary production, Antarctic krill, fish, marine mammals and birds are assessed, and are both negative and positive. The review includes recent analysis of change/variability in polynyas and fast ice, and also highlights the significance of extreme events (which have paradoxical impacts). Possible future scenarios are investigated in the light of the predicted decline in sea ice by 2100 e.g. increased storminess/waviness, numbers of icebergs and snowfall. Our current lack of knowledge on many aspects of sea ice-related change and biological response is emphasised.

Geochemical features and sources of hydrocarbons and fatty acids in soils from the McMurdo Dry Valleys in the Antarctic

Genki I. Matsumoto, Eisuke Honda, Kazuhiko Sonoda, Shuichi Yamamoto, Tetsuo Takemura

We studied the geochemical features and compound-specific (CS)- $\delta^{13}\text{C}$ of hydrocarbons and fatty acids in soil samples from the McMurdo Dry Valleys in the Antarctic to elucidate their source organisms and characteristics of their environments. Total organic carbon contents in soil samples were extremely low reflecting extremely harsh environments for organisms. Normal-alkanes ranging in carbon chain length from $n\text{-C}_{14}$ to $n\text{-C}_{38}$ with the predominance of odd-carbon numbers were found, together with n -alkenes ($n\text{-C}_{23:1}$ to $n\text{-C}_{27:1}$). Normal-alkanoic acids ranging in carbon chain length from $n\text{-C}_{10}$ to $n\text{-C}_{30}$ with the predominance of even-carbon numbers were detected in the samples, along with small amounts of branched (*iso* and *anteiso*) and n -alkenoic acids. CS- $\delta^{13}\text{C}$ values of long-chain n -alkanes ($n\text{-C}_{20}$ to $n\text{-C}_{29}$) ranged from -30.4 to -26.6‰ . CS- $\delta^{13}\text{C}$ values of n -alkanoic acids with short-chain carbon numbers ($n\text{-C}_{14}$ to $n\text{-C}_{19}$) ranging from -27.7 to -21.7‰ were much higher than those of long-chain carbon numbers ($n\text{-C}_{20}$ to $n\text{-C}_{30}$, -32.5 to -25.3‰). The geochemical features and CS- $\delta^{13}\text{C}$ values of long-chain n -alkanes and n -alkanoic acids revealed that they are originated from lichen and/or vascular plant debris from the pre- and inter-glacial periods in this region, whereas short-chain n -alkanoic acids are come from microalgae and cyanobacterial debris. CS- $\delta^{13}\text{C}$ values suggest that they are derived from gymnosperms and/or C_4 plants in the cold and dry environments of the pre- and inter-glacial periods of the McMurdo Dry Valleys region.

The limnology and biology of the Dufek Massif, Transantarctic Mountains 82° South

Dominic A. Hodgson, Peter Convey, Elie Verleyen, Wim Vyverman, Sandra J.

McInnes, Chester J. Sands, Rafael Fernández–Carazo, Annick Wilmotte, Aaike De Wever, Karolien Peeters, Ines Tavernier, Anne Willems

Very little is known about the higher latitude inland biology of continental Antarctica. In this paper we describe the limnology and biology of the Dufek Massif, using a range of observational, microscopic and molecular methods. Here two dry valleys are home to some of the southernmost biota on Earth. Cyanobacteria were the dominant life forms, being found in lakes and ponds, in hypersaline brines, summer melt water, relict pond beds and in exposed terrestrial habitats. Their species diversity was the lowest yet observed in Antarctic lakes. Green algae, cercozoa and bacteria were present, but diatoms were absent except for a single valve; likely windblown. Mosses were absent and only one lichen specimen was found. The Metazoa included three microbivorous tardigrades (*Acutuncus antarcticus*, *Diphascon sanae* and *Echiniscus* (cf) *pseudowendti*) and bdelloid rotifer species, but no arthropods or nematodes. These simple faunal and floral communities are missing most of the elements normally present at lower latitudes in the Antarctic which is probably a result of the very harsh environmental conditions in the area.

Bacterial communities in two Antarctic ice cores analyzed by 16S rRNA gene sequencing analysis

Takahiro Segawa, Kazunari Ushida, Hideki Narita, Hiroshi Kanda, Shiro Kohshima

Antarctic ice cores could preserve ancient airborne microorganisms. We examined bacteria in two Antarctic ice core samples, an interglacial age sample from Mizuho Base and a glacial age sample from the Yamato Mountains, by 16S rRNA gene sequencing analysis. Bacterial density, the number of bacterial OTUs and Simpson's diversity index was larger in the Mizuho sample than in the Yamato sample. The 16S rDNA clone library from the Mizuho sample was dominated by the phylum Firmicutes, while the large part of that from the Yamato sample was composed of the Gamma proteobacteria group. Major sources of these identified bacteria estimated from their database records also differed between the samples: in the Mizuho sample bacterial species recorded from animals were higher than that of the Yamato sample, while in the Yamato sample bacteria from aquatic and snow-ice environments were higher than that of the Mizuho sample. The results suggest that these bacteria were past airborne bacteria that would vary in density, diversity and species composition depending on global environmental change. Our results imply that bacteria in Antarctic ice cores could be used as new environmental markers for past environmental studies.

Penguin response to the Eocene climate and ecosystem change in the northern Antarctic Peninsula region

Piotr Jadwiszczak

Eocene Antarctic penguins are known solely from the La Meseta Formation (Seymour Island, James Ross Basin). They are most numerous and taxonomically diverse (at least ten species present) within strata formed at the end of this epoch, which is concomitant with a significant cooling trend and biotic turnover prior to the onset of glaciation. Moreover, all newly appeared taxa were small-bodied, and most probably evolved in situ. Interestingly, some chemical proxies suggest enhanced nutrient upwelling events that coincided with obvious changes in the record of La Meseta penguins.

The water-born protein pheromones of the polar protozoan ciliate, *Euplotes nobilii*: Coding genes and molecular structures

Adriana Vallesi, Claudio Alimenti, Graziano Di Giuseppe, Fernando Dini, Bill Pedrini, Kurt Wüthrich, Pierangelo Luporini

The protozoan ciliate *Euplotes nobilii* found in Antarctic and Arctic coastal waters relies on secretion of water-soluble cell type-specific signal proteins (pheromones) to regulate its vegetative growth and sexual mating. For three of these psychrophilic pheromones we previously determined the three-dimensional structures by nuclear magnetic resonance (NMR) spectroscopy with protein solutions purified from the natural sources, which led to evidence that their adaptation to cold is primarily achieved by increased flexibility through an extension of regions free of regular secondary structures, and by increased exposure of negative charges on the protein surface. Then we cloned the coding genes of these *E. nobilii* pheromones from the transcriptionally active cell somatic nucleus (macronucleus) and characterized the full-length sequences. These sequences all contain an open reading frame of 252–285 nucleotides, which is specific for a cytoplasmic pheromone precursor that requires two proteolytic cleavages to remove a signal peptide and a pro segment before release of the mature protein into the extracellular environment. The 5′ and 3′ non-coding regions are two- to three-fold longer than the coding region and appear to be tightly conserved, probably in relation to the inclusion of intron sequences destined to be alternatively removed to play key regulatory roles in the mechanism of the pheromone gene expression.

Molecular adaptations in Antarctic fish and bacteria

Roberta Russo, Alessia Riccio, Guido di Prisco, Cinzia Verde, Daniela Giordano

Marine organisms, living in the cold waters of the Southern Ocean, are exposed to high oxygen concentrations. Cold-adapted organisms have developed networks of defence mechanisms to protect themselves against oxidative stress. The dominant suborder Notothenioidei of the Southern Ocean is one of the most interesting models, within vertebrates, to study the evolutionary biological responses to extreme environment. Within bacteria, the psychrophilic Antarctic bacterium

Pseudoalteromonas haloplanktis TAC125 gives the opportunity to explore the cellular strategies adopted in vivo by cold-adapted microorganisms to cope with cold and high oxygen concentration. Understanding the molecular mechanisms underlying how a range of Antarctic organisms have responded to climate change in the past will enable predictions as to how they and other species will adapt to global climate change, in terms of physiological function, distribution patterns and ecosystem balance.

Shell structure characteristics of pelagic and benthic molluscs from Antarctic waters

Waka Sato-Okoshi, Kenji Okoshi, Hiroshi Sasaki, Fumihiko Akiha

The surface of the shell of the pelagic Antarctic gastropod, *Limacina helicina antarctica* forma *antarctica*, was smooth, with rib-like structures also observed. The larger specimen, with six to seven whorls, had visible ribs on its most outer whorl. The shell thickness of *L. helicina antarctica* forma *antarctica* was very thin, approximately 5–7 μm , on an individual with a shell diameter of 1.4 mm. Shell microstructure, as examined by SEM, was composed mostly of a crossed-lamellar structure. Shell thickness of the dominant benthic bivalve *Laternula elliptica*, was approximately 99–132 μm on an individual of shell length 19 mm. It was composed of two calcareous layers, including a thick outer homogeneous or granular layer and a thin nacreous inner layer. The characteristics of shell structure are discussed with reference to previous results, and in terms of adaptation to Antarctic waters.

Metagenomic analyses of the dominant bacterial community in the Fildes Peninsula, King George Island (South Shetland Islands)

Choon Pin Foong, Clemente Michael Wong Vui Ling, Marcelo González

There is little information on the bacterial diversity of the Fildes Peninsula, King George Island. Hence, this study was conducted to determine the bacterial population of sediments and soils from the lakes, river, glacier and an abandoned oil tank area in the Fildes Peninsula, using a metagenomic approach. DNA was extracted from the sediment and soil samples, and analyzed using the 16S rDNA polymerase chain reaction-denaturing gradient gel electrophoresis (PCR-DGGE). A total of 299 DNA fragments resolved using the DGGE were sequenced. The results of the analysis provided an overview of the predominant groups of bacteria and the diversity of the bacterial communities. The most abundant phyla of bacteria in Fildes Peninsula were Bacteroidetes, Proteobacteria, Acidobacteria, Gemmatimonadetes, Nitrospira, Firmicutes, Actinobacteria, Chloroflexi, Cyanobacteria, Spirochaetes, *Deinococcus-Thermus*, WS3 and BRC1. All of the sediment samples from the lakes had different representatives of dominant bacterial species. Interestingly, 15% of the operational taxonomic units (OTUs) did not group into any of the existing phyla in

the Ribosomal Database Project (RDP). One of the OTUs had a similarity of <0.90 when compared to the GenBank sequences and probably was a novel bacterium specific to that location. The majority of the bacterial 16S rDNA sequences were found to be closely related to those found elsewhere.

Monitoring and identification of airborne fungi at historic locations on Ross Island, Antarctica

Shona M. Duncan, Roberta L. Farrell, Neville Jordan, Joel A. Jurgens, Robert A. Blanchette

Air sampling in the 'Heroic Era' historic huts on Ross Island, Antarctica confirmed fungal presence, viability and winter survival. Cultivation and consensus sequence-based identification of *Cladosporium cladosporioides*, *Pseudeurotium desertorum*, *Geomyces* sp. and *Antarctomyces psychrotrophicus* demonstrated that they dominated the air environment within the huts. *Cadophora* sp. and *Thebolus* sp. were also isolated from the air and identified by morphological characteristics. Viable fungal colony forming units generally dropped in winter 2007 samplings from levels recorded in summer 2006 but were still substantial and greater than observed in summer 2008 and summer 2009 sampling at some locations. Comparing interior to exterior sampling, at the Hut Point and Cape Evans sites, there were more fungi recovered from the air in the interiors but at Cape Royds location, more fungi were recovered from the outside environment, possibly due to the impact of large amounts of organic material from the nearby Adélie penguin rookery. This research reveals airborne fungal biodiversity in summer and winter and demonstrates spores are widespread particularly in the interiors of the huts. Completed conservation efforts appear to have reduced fungal blooms and spores, which should reduce future adverse impacts to wood, textiles, paper and other artefacts so that this important polar heritage can be preserved.

PhAP protease from *Pseudoalteromonas haloplanktis* TAC125: Gene cloning, recombinant production in *E. coli* and enzyme characterization

D. de Pascale, M. Giuliani, C. De Santi, N. Bergamasco, A. Amoresano, A. Carpentieri, E. Parrilli, M.L. Tutino

Cold-adapted proteases have been found to be the dominant activity throughout the cold marine environment, indicating their importance in bacterial acquisition of nitrogen-rich complex organic compounds. However, few extracellular proteases from marine organisms have been characterized so far, and the mechanisms that enable their activity in situ are still largely unknown. Aside from their ecological importance and use as model enzyme for structure/function investigations, cold-active proteolytic enzymes offer great potential for biotechnological applications. Our studies on cold adapted proteases were performed on exo-enzyme produced by

the Antarctic marine bacterium *Pseudoalteromonas haloplanktis* TAC125. By applying a proteomic approach, we identified several proteolytic activities from its culture supernatant. PhAP protease was selected for further investigations. The encoding gene was cloned and the protein was recombinantly produced in *E. coli* cells. The homogeneous product was biochemically characterised and it turned out that the enzyme is a Zn-dependent aminopeptidase, with an activity dependence from assay temperature typical of psychrophilic enzymes.

The hemoglobins of sub-Antarctic fishes of the suborder Notothenioidei

Daniela Coppola, Daniela Giordano, Alessandro Vergara, Lelio Mazzarella, Guido di Prisco, Cinzia Verde, Roberta Russo

Fishes of the perciform suborder Notothenioidei provide an excellent opportunity for studying the evolution and functional importance of evolutionary adaptations to temperature. To understand the unique biochemical features of high-Antarctic notothenioids, it is important to improve our knowledge of these highly cold-adapted stenotherms with new information on their sub-Antarctic relatives. This paper focuses on the oxygen-transport system of two non-Antarctic species, *Eleginops maclovinus* and *Bovichtus diacanthus*. Unlike most Antarctic notothenioids, the blood of *E. maclovinus* and *B. diacanthus* displays high hemoglobin (Hb) multiplicity. *E. maclovinus*, the sister group of Antarctic notothenioids, has one cathodal (Hb C) and two anodal components (Hb 1, Hb 2). *B. diacanthus*, one of the most northern notothenioids, has three major Hbs. The multiple Hbs may have been maintained as a response to temperature differences and fluctuations of temperate waters, much larger than in the Antarctic. Although non-Antarctic notothenioids have never developed cold adaptation, the amino-acid sequence reveals high identity with the globins of Antarctic notothenioids. Hbs of sub-Antarctic notothenioids are characterised by high oxygen affinity and Root effect. Phylogenetic analyses are consistent with the hypothesis that Bovichtidae and Eleginopidae diverged after they became established in more temperate waters north of the Antarctic Polar Front.

Fine-scale feeding behavior of Weddell seals revealed by a mandible accelerometer

Yasuhiko Naito, Horst Bornemann, Akinori Takahashi, Trevor McIntyre, Joachim Plötz

We used a mandible accelerometer to document feeding events in two free-ranging adult female Weddell seals in Atka Bay, Antarctica. Using spectral analysis, we isolated several patterns in the mandible acceleration data. The shorter, un-attenuated signals are thought to represent feeding. The longer, attenuating signals are thought to represent vocalizing activities. The depth data suggest that one seal dived under the base of the iceberg. During these dives we detected a unique type of feeding signal. These signals were characterized by patterns of low amplitude and

irregular peaks. A second signal type, characterized by a larger amplitude, was observed 75 times at depths shallower than 60 m. The number of feeding signals per dive was higher for iceberg associated dives (>60 m, 11.3 signals/dive) than for dives to midwater depths (<60 m, 0.5 signals/dive). Our results support the hypothesis that underwater surface of icebergs serves as a habitat for marine fauna. We recorded the first vocalization related signals in seals using a mandible accelerometer. One seal spent significantly more time in shallow water and foraged less than the second seal. This seal also vocalized more often (135 events) than the second individual (29 events), possibly due to an emphasis on mating behavior.

Comparison of zooplankton distribution patterns between four seasons in the Indian Ocean sector of the Southern Ocean

Kunio T. Takahashi, Graham W. Hosie, John A. Kitchener, David J. McLeod, Tsuneo Odate, Mitsuo Fukuchi

We investigated the composition, distribution and abundance of zooplankton in the Indian Ocean sector of the Southern Ocean during the austral summer (December/January) of 2004/05, 2005/06, 2007/08 and 2008/09 using a Continuous Plankton Recorder (CPR). CPR tows were conducted along two transects during voyages south of Cape Town to north of Syowa station and from north of the Mawson station area to south of Fremantle. High zooplankton abundance was recorded on each transect in the Polar Frontal Zone (PFZ) and the northern area of the Antarctic Zone (AZ). Community structure in these zones was dominated by common taxa including the ubiquitous *Oithona similis* and calanoid copepodites, accounting for >50% of total abundance, and *Calanus simillimus*, *Ctenocalanus citer*, *Clausocalanus laticeps* and *Metridia lucens* also occurred in high densities. Appendicularians of the genus *Fritillaria* were the most important component in the Cape Town to Syowa station area in 2008, with 36.9% of total abundance. The average chlorophyll a level at this time of year was the lowest (0.32 mg m⁻³) among all transects. Appendicularians are suited to oceanic oligotrophic waters; therefore, they are suited to low phytoplankton density. Foraminiferans were numerically dominant throughout the Mawson station area to Fremantle transect in 2005. Unlike *Fritillaria* spp., foraminiferans prefer high phytoplankton density. The elevated average chlorophyll a biomass in 2005 (0.64 mg m⁻³) provided favorable conditions for Foraminifera, which were dominant and widespread. CPR surveys provide information on the fine scale structure of the inter-annual distribution changes in micro- and meso- zooplankton assemblages, and the CPR is one of ideal method to monitor organisms that are indicators of environmental change.

Molecular taxonomy and identification within the Antarctic genus *Trematomus* (Notothenioidei, Teleostei): How valuable is barcoding with COI?

A.-C. Lautredou, C. Bonillo, G. Denys, C. Cruaud, C. Ozouf-Costaz, G. Lecointre, A. Dettai

The Trematominae are a particularly interesting subfamily within the antarctic suborder Notothenioidei (Teleostei). The 14 closely related species occupy a large range of ecological niches, extremely useful for evolutionary and biogeography studies in the Antarctic Ocean. But some Trematomus species can be difficult to identify by using morphological criteria, specially young stages and damaged specimens. Molecular identification would therefore be highly useful, however the suitability of the cytochrome oxidase I gene in a barcoding approach needs to be assessed. We evaluated species delineation within the genus Trematomus comparing morphological identification, nuclear markers (the rhodopsin retrogene and a new nuclear marker *pkd1*: polycystic kidney disease 1) and COI. We show that Trematomus vicarius is not distinguishable from Trematomus bernacchii with the molecular markers used, and neither is Trematomus loennbergii from Trematomus lepidorhinus. We suggest that until this is investigated further, studies including these species list them as T. loennbergii/T. lepidorhinus group, and keep voucher samples and specimens. Generally, COI gives a congruent result with the rhodopsin retrogene, and except for the previously cited species pairs, COI barcoding is efficient for identification in this group. Moreover *pkd1* might not be suitable for a phylogenetic study at this scale for this group.

Zooplankton Atlas of the Southern Ocean: The SCAR SO-CPR Survey (1991–2008)
David J. McLeod, Graham W. Hosie, John A. Kitchener, Kunio T. Takahashi, Brian P.V. Hunt

The SCAR Southern Ocean Continuous Plankton Recorder (SO-CPR) Survey produces one of the largest and most accessed zooplankton data sets in the world. These data serve as a reference for other Southern Ocean monitoring programmes such as those run by the Commission for the Conservation of Antarctic Marine Living Resources (CCAMLR) and the developing Southern Ocean Observing System (SOOS). It has been instrumental in providing baseline data on zooplankton composition, communities, and distribution patterns on the ocean basin scale. The SO-CPR Survey is publishing the first detailed geographical atlas of the near-surface Southern Ocean zooplankton. This atlas is based on 22,553 CPR samples collected from 1991 to 2008 from voyages operated by Australia, Japan, Germany, New Zealand, USA and Russia. The Atlas documents the distribution and abundance of the 50 most abundant zooplankton taxa amongst the 200+ taxa sampled. The maps are printed in alphabetical order of the genera within each taxon and nomenclature is based on the Register of Antarctic Marine Species (RAMS) developed by the SCAR Marine Biodiversity Information Network (SCAR-MarBIN). The SO-CPR Atlas will operate as a ready reference to researchers interested in the distribution of zooplankton in the Southern Ocean, for example knowing the

distribution of grazers in relation to phytoplankton production or the availability of prey for higher predators.

Structure of the pelagic cnidarian community in Lützow–Holm Bay in the Indian sector of the Southern Ocean

R. Toda, M. Moteki, A. Ono, N. Horimoto, Y. Tanaka, T. Ishimaru

The structure of the pelagic cnidarian community in Lützow–Holm Bay in the Indian sector of East Antarctica was investigated in January 2005 and 2006. Zooplankton samples from six discrete depths (surface to 2000 m) obtained using an RMT–8 yielded 4666 individuals of 31 species of cnidarian. Cnidarian abundance and carbon biomass were far greater in 2005 than in 2006. The biomass of macrozooplankton was large in the upper 200 m in 2005, but concentrated at 200–500 m in 2006, except for Euphausiacea. The most dominant species was *Diphyes antarctica*, followed by *Dimophyes arctica* and *Muggiaea bargmannae*. Four species had never been collected from East Antarctica; of these, *Solmissus incisa* was a first record in the Southern Ocean. Cluster analysis revealed the following three major communities: the epipelagic (0–200 m), in summer surface, winter, and upper modified circumpolar deep waters (MCDW); the upper mesopelagic (200–500 m), in upper MCDW; and the lower meso– and bathypelagic (500–2000 m), in lower MCDW. The epipelagic and lower meso– and bathypelagic communities are likely reduced in abundance/biomass when primary production is low, due to bottom–up control, while the upper mesopelagic community remains stable.

What shapes edaphic communities in mineral and ornithogenic soils of Cierva Point, Antarctic Peninsula?

G. Mataloni, G. González Garraza, M. Bölter, P. Convey, P. Fermani

Three mineral soil and four ornithogenic soil sites were sampled during summer 2006 at Cierva Point (Antarctic Peninsula) to study their bacterial, microalgal and faunal communities in relation to abiotic and biotic features. Soil moisture, pH, conductivity, organic matter and nutrient contents were consistently lower and more homogeneous in mineral soils. Ornithogenic soils supported larger and more variable bacterial abundances than mineral ones. Algal communities from mineral soils were more diverse than those from ornithogenic soils, although chlorophyll–a concentrations were significantly higher in the latter. This parameter and bacterial abundance were correlated with nutrient and organic matter contents. The meiofauna obtained from mineral soils was homogeneous, with one nematode species dominating all samples. The fauna of ornithogenic soils varied widely in composition and abundance. Tardigrades and rotifers dominated the meiofauna at eutrophic O2, where they supported a large population of the predatory nematode *Coomansus gerlachei*. At site O3, high bacterial abundance was consistent with high densities of

the bacterivorous nematodes *Plectus* spp. This study provides evidence that Antarctic soils are complex and diverse systems, and suggests that biotic interactions (e.g. competition and predation) may have a stronger and more direct influence on community variability in space and time than previously thought.

Archaeal and bacterial community structures in the anoxic sediment of Antarctic meromictic lake Nurume-Ike

Norio Kurosawa, Shota Sato, Yutaka Kawarabayasi, Satoshi Imura, Takeshi Naganuma

Prokaryotic community structures in the anoxic sediment of the Antarctic meromictic Lake Nurume-Ike were revealed by sequence analysis of 16S rRNA gene clones. The archaeal clones obtained (205 total) consisted of only three phylotypes, and were dominantly affiliated with uncultured euryarchaeotes. Specifically, 93% of the clones were identified as marine benthic group-D archaeal phylotype. In contrast to the limited archaeal diversity, 53 phylotypes were detected within 312 bacterial clones. Major bacterial phylotypes were affiliated with α -Proteobacteria (20% of clones), δ -Proteobacteria (9%), Planctmycetales (7%), and Cyanobacteria (7%). A small numbers of clones belonging to γ -Proteobacteria, Actinobacteria, Spirochaetes, Flavobacteria, and Verrucomicrobia were also found. A total of 53% of the bacterial clones, consisting of 13 phylotypes, could not be classified into any known group. These results indicated that the bacterial community of Lake Nurume-Ike sediment consisted of numerous phylogenetic groups and had a diversity comparable to the diversity of other Antarctic lakes communities previously reported. Interestingly, however, there were very few phylotypes shared between the communities of lakes Nurume-Ike and five other lakes located in the Vestfold Hills area. This is the first comprehensive study to analyze more than 500 16S rDNA clones for microbial community analysis of an Antarctic lake sediment sample, and the results significantly expand current views of bacterial diversity in Antarctic lakes.