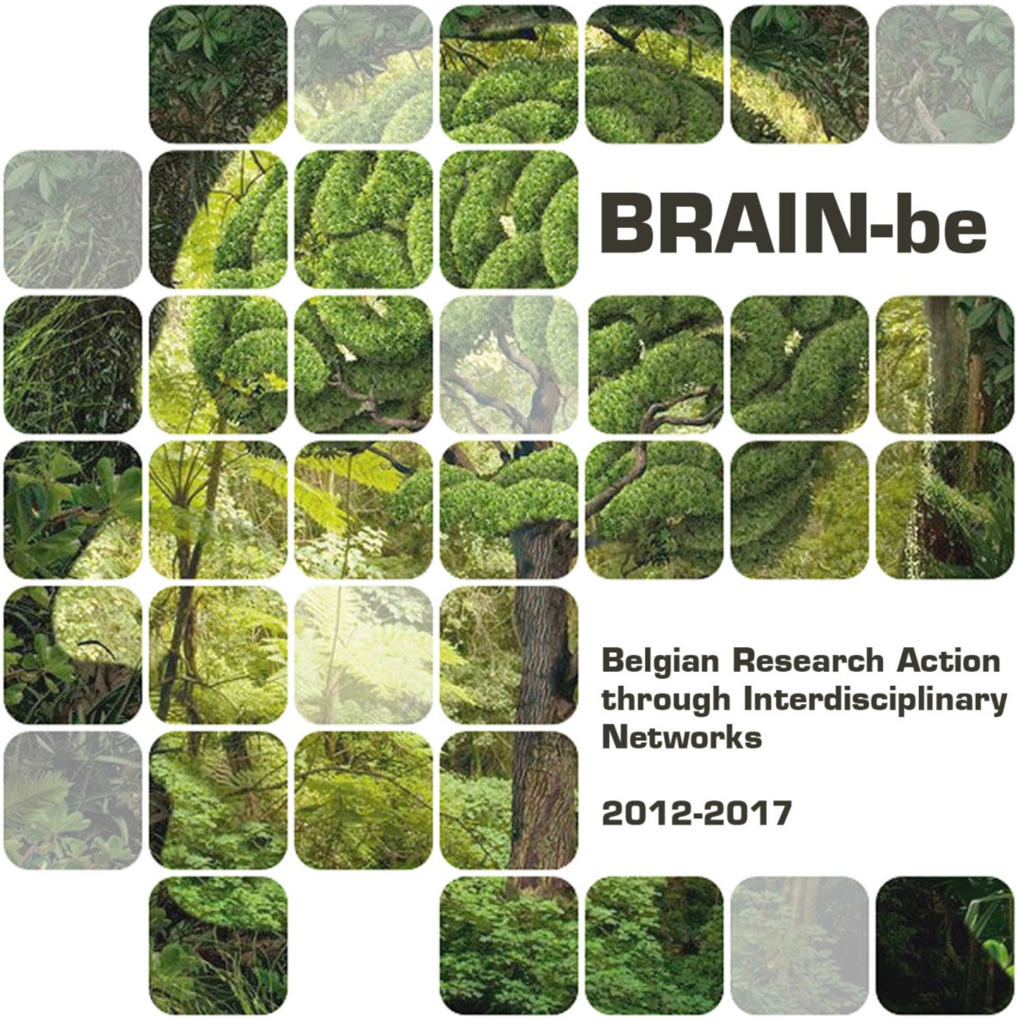

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2012-2017

vERSO

Ecosystem Responses to global change: a multiscale approach in the Southern Ocean

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NETWORK PROJECT

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Ecosystem Responses to global change: a multiscale approach in the Southern Ocean

Contract - BR/132/A1/vERSO

FINAL REPORT

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TABLE OF CONTENTS

ABSTRACT (EN)

Context

Environmental changes are now vastly documented for large areas of the Southern Ocean. The response of marine organisms and ecosystem processes to these changes are still not well understood. In this framework, insights in resilience, thresholds and tipping points for species, communities and ecosystems are of paramount importance. Addressing these endpoints is however highly complex, and requires robust, interdisciplinary and collaborative research networks to progressively reach a holistic understanding.

By design, the vERSO project was intended to forge ahead and identify key areas of research in this respect, and in line with the SCAR priorities. Building on the experience gathered by its long-term partners and taking advantage of the overlap period with another BELSPO-funded project (rECTO), the vERSO developments were intentionally novel and ambitious (in experimental, field and integration facets).

Objectives

The goal of the vERSO project was to assess the impact of the main stressors driven by global change on benthic Antarctic ecosystems using an integrated multiscale approach including different representative size classes of the benthos. Two principal regions with current contrasting responses to global change have been considered, namely the Western Antarctic Peninsula and the East Antarctic. To reach this goal, researches on connectivity and adaptation, trophic ecology and sensitivity and resilience were conducted by all partners and integrated using state of the art modelling techniques.

Results and conclusions

vERSO has globally reached its proposed objectives, paving the way for its sister project, rECTO. vERSO members have participated in 11 expeditions to the Antarctic. Specific efforts were devoted to involving several consortium partners in the fieldwork to optimize the exchange of know-how and crosslinkages using the obtained results. This is reflected in the authorships of the papers and datasets published so far. Most of the experimental work has been carried out successfully, including in logistically-challenging conditions. Some of the explorative, long-term experiments, are still ongoing in the framework of rECTO.

A dedicated Information System was setup and has been merged in various long-term initiatives, dedicated to the discovery and publication of raw data. To date, vERSO has published 52 papers and book chapters and submitted 4 others. Over 50 datasets have been generated and are being documented and published. vERSO was represented 97 times in international conferences.

The unique opportunity offered by the rECTO/vERSO overlap period allowed efficient synergies which have been largely exploited to maximize data and know-how flows. The visibility of the projects peaked in July 2017, during the SCAR Biology Symposium, which will be held in Leuven. This conference gathered 402 people from 32 countries.

Keywords

Southern Ocean; biodiversity; global change; plasticity; connectivity; model coupling

RESUME (FR)

Contexte

Les changements environnementaux affectant l'océan Austral sont maintenant largement documentés. Les réponses des organismes marins, et des processus écosystémiques à ces changements sont encore très mal connus. Dans ce cadre, l'appréciation de la résilience, des seuils et des points de basculement des espèces, communautés et écosystèmes et d'une importance capitale. Tenter de caractériser ces éléments est généralement hautement complexe, et nécessite la mobilisation de réseaux de recherche robustes, collaboratifs, et interdisciplinaires pour atteindre une compréhension complète de ces réponses.

Par nature, le projet vERSO a été conçu pour explorer et identifier une série de priorités de recherche, en ligne avec les priorités de recherche de la communauté du SCAR. Se fondant sur l'expérience accumulée pendant des décennies par ses partenaires, et prenant avantage de la période de recouvrement avec le projet rECTO, également financé par BELSPO, les développements menés par vERSO étaient intentionnellement novateurs et ambitieux (dans ses facettes expérimentales, de terrain et dans leur intégration).

Objectifs

L'objectif général du projet vERSO était de caractériser l'impact des principaux stresseurs environnementaux liés au changement global, sur les écosystèmes benthiques de l'océan Austral, à l'aide d'une approche multi-échelle intégrant différentes classes de taille d'organismes benthiques. Deux régions contrastées du point de vue des changements environnementaux ont été considérées, la Péninsule Antarctique et l'Est Antarctique. Pour atteindre ce but, des recherches sur la connectivité et l'adaptation, l'écologie trophique et la résilience ont été menées par les partenaires et intégrées en utilisant des techniques de modélisation.

Résultats et conclusions

vERSO a globalement atteint ses objectifs, pavant la route pour son projet-sœur, rECTO. Les membres de vERSO ont participé à 11 expéditions en Antarctique et dans le Subantarctique. Des efforts spécifiques ont été alloués pour inclure un maximum de membres du consortium dans le travail de terrain et de laboratoire afin d'optimiser les échanges de savoir-faire, en particulier entre les jeunes chercheurs. Cet effort se matérialise par les combinaisons d'auteurs responsables des publications du consortium. La majeure partie du travail expérimental a pu être menée avec succès, y compris dans des conditions logistiques parfois difficiles. Certaines expériences très exploratoires, de longue durée, sont encore en cours et seront finalisées dans le cadre de rECTO.

Un système d'information dédié a été mis en œuvre et est à présent en cours de fusion avec différentes initiatives soutenues à long terme, et dédiées à la découverte et à la publication de données brutes. A ce jour, le consortium vERSO a publié 52 articles et chapitres de et en a soumis 4 autres. Plus de 50 jeux de données ont été générés et sont en cours de documentation et publication. vERSO a été représenté à 97 reprises dans des conférences internationales.
L'opportunité exceptionnelle représentée par une période de recouvrement entre deux projets-sœurs a permis des synergies efficaces qui ont été mises à profit pour optimiser les

échanges de données et de savoir-faire au sein et entre les équipes. La visibilité des projets a atteint un point d'orgue dans le cadre de la conférence « SCAR Biology Symposium », organisée à Leuven en juillet 2017. Cette conférence a attiré 402 participants de 32 pays.

Mots-clé:

Océan Austral; biodiversité; « global change »; plasticité; connectivité; couplage de modèles

OVERZICHT (NL)

Verband

Niettegenstaande veranderingen in het milieu veelvuldig zijn gedocumenteerd voor grote delen van de Zuidelijke Oceaan, is de respons van mariene organismen en ecosysteemprocessen op deze veranderingen nog steeds niet goed begrepen. In deze context zijn inzichten in veerkracht, drempelwaarden en kantelmomenten voor soorten, gemeenschappen en ecosystemen van het grootste belang. Het begrijpen van deze processen en identificeren van tolerantiegrenzen is echter zeer complex en vereist robuuste, interdisciplinaire en collaboratieve onderzoeksnetwerken om een geïntegreerd en holistisch inzicht te verwerven. Het vERSO-project had als doel belangrijke onderzoeksvragen in deze context te beantwoorden, en dit in lijn met de SCAR-prioriteiten. Voortbouwend op de ervaring van zijn lange-termijnpartners en gebruikmakend van een overlappingsperiode met een ander door BELSPO gefinancierd project (rECTO), waren de doelstellingen binnen het vERSO- nieuw en ambitieus (zowel wat experimentele, veld- en integratie-facetten betreft).

Doelstellingen

Het doel van het vERSO-project was om de impact van de belangrijkste stressoren als gevolg van ‘global change’ op benthische Antarctische ecosystemen te ontrafelen aan de hand van een geïntegreerde benadering over verschillende schalen inclusief de belangrijkste grootteklassen van het benthos. Twee belangrijke regio's met contrasterende reacties op de globale veranderingen zijn bestudeerd in deze context, namelijk het Westelijk Antarctisch Schiereiland en het Oost-Antarctisch Gebied. Om dit doel te bereiken, werd door alle partners onderzoek verricht naar connectiviteit en adaptatie, trofische ecologie, toleranties en veerkracht en de resultaten hiervan werden geïntegreerd met behulp van geavanceerde modelleertechnieken.

Resultaten en conclusies

In het geheel heeft vERSO vooropgestelde doelstellingen bereikt, waardoor het ook relevante informatie aanlevert aan het zusterproject, rECTO. vERSO-leden hebben deelgenomen aan 11 expedities naar Antarctica. Er zijn specifieke inspanningen geleverd om verschillende consortiumpartners bij het veldwerk te betrekken om de uitwisseling van knowhow en samenwerkingen te optimaliseren op basis van de beoogde resultaten. Dit komt tot uiting in de auteurschappen van de tot nu toe gepubliceerde papers en datasets. Het merendeel van het experimentele werk is met succes uitgevoerd, onder meer in logistiek extreme omstandigheden. Sommige van de verkennende, lange-termijnexperimenten zijn nog steeds lopende in het kader van rECTO.

Een speciaal informatiesysteem werd opgezet en samengevoegd in verschillende lange-termijninitiatieven, gericht op het ontdekken en publiceren van onbewerkte gegevens. Tot op heden heeft vERSO 52 wetenschappelijke artikels en boekhoofdstukken gepubliceerd en 4 andere ingediend. Meer dan 50 datasets zijn gegenereerd en worden momenteel verder gedocumenteerd en gepubliceerd. vERSO werd 97 keer vertegenwoordigd in internationale congressen. De unieke kans die de overlappingsperiode rECTO / vERSO bood, maakte efficiënte synergieën mogelijk die grotendeels werden benut om de gegevens- en kennisstromen te maximaliseren. De zichtbaarheid van de projecten piekte in juli 2017, tijdens het SCAR Biology Symposium, dat in Leuven plaatsvond . Deze conferentie bracht 402 mensen samen uit 32 landen.

Sleutelwoorden:

Zuidelijke Oceaan; biodiversiteit; “global change”; plasticiteit; connectiviteit; model koppeling

1. INTRODUCTION

Today it is widely agreed that anthropogenic-driven climate change exists. Although life on Earth has always been evolving as a consequence of natural variations in the climate (Kaiser et al., 2013), many of the environmental changes that are observed since the 20th century are now confirmed to be caused by increasing CO2 in the atmosphere resulting from anthropogenic activities (IPCC, 2013). Therefore, the Paris Conference of the Parties (COP21) of the United Nations Framework Convention on Climate Change (UNFCCC) in November 2015 has finally resulted in the first internationally legally binding agreement to reduce global warming worldwide (Gutt, 2016). The effects of climate change are not the same everywhere, and polar oceans are particularly affected. For instance, while average air temperatures have increased by 0.6°C during the last century, the Antarctic Peninsula and large parts of the Southern Ocean have warmed five times faster. The West Antarctic Peninsula (WAP) is also one of Earth's regions where we observe the most rapid and dramatic environmental changes in marine ecosystems, with appreciable variation in the duration of the sea ice season, extended glacier retreats, ice shelves collapse, warming of the upper water column and changes in local primary production (Ducklow et al., 2013, Stammerjohn et al., 2008, Turner et al., 2013). Furthermore, future global warming related environmental changes are expected for large areas of the Southern Ocean in terms of sea ice cover and glacier melting amongst other parameters (Pasotti et al., 2015). The response of marine organisms and ecosystem processes to such environmental changes are not well known until today. Insights on resilience, thresholds and tipping points for species, communities and ecosystems are therefore of paramount importance to the understanding of the ongoing large-scale changes (Convey et al., 2014, Kennicutt et al., 2014, Oliver et al., 2015).

Addressing responses at the ecosystem level is highly complex, and requires robust, interdisciplinary and collaborative research networks to progressively reach a holistic understanding (Parsons et al. 2011, Ingels et al. 2012, Gutt et al. 2012).

By design, the vERSO project was intended to forge ahead and identify key areas of research for another BRAIN-BE project, RECTO, which started after vERSO, with a 2-year overlap. Hence, some aspects and ideas from vERSO were specifically including novel, high-risks attempts (in experimental, field and integration realms). Funded by the Belgian Science Policy Office, RECTO and vERSO are two BRAIN-be research projects aiming at understanding the potential effects of global change on Southern Ocean ecosystems. Our knowledge about the biodiversity of shallow environments in the Southern Ocean is still very limited, and thus quite different to existing information in other oceans. These habitats are currently exposed to fast-paced changes in key environmental parameters (seawater temperature, salinity, primary production, sea-ice regimes), which will have the potential to induce profound effects on the organisms living there and change the function and structure of these ecosystems. On top of understanding these aspects, the RECTO/vERSO projects have identified diversification, plasticities (trophic, dispersive) and connectivities as key research areas to understand the impact of the environmental changes on Antarctic ecosystems. By focusing on selected key sites, where regional scale studies will help elucidate ecosystem response at different biological scales to the full range of environmental variation, vERSO had the ambition to significantly contribute to this understanding. Seamless integration of vERSO output into the new SCAR Scientific Research Programs (SRPs – AntERA and AntECO) is set as a fundamental priority to meet societal expectations in terms of sustainable management and control strategies, and true cross-disciplinary approaches.

2. STATE OF THE ART AND OBJECTIVES

2.1 State of the Art

The Southern Ocean covers about 34.8 million km2 and the Antarctic contains roughly 11% of the world's continental-shelf area (Zwally et al. 2002), harboring a large share of the planet marine diversity (Barnes and Peck 2008; Brandt et al. 2007; Clarke and Johnston 2003). The region is experiencing environmental changes happening at an unprecedented rate, across broad temporal and spatial scales and it is now critically important to assess the potential responses of the Southern Ocean ecosystems to these changes with no further delay (Turner et al. 2009, Orr et al. 2005, Smith et al. 2006, Barnes & Peck 2008, Montes-Hugo et al. 2009). The threat of global change can fundamentally change the Southern Ocean biology, inducing massive, far-reaching modifications that ecosystems have not experienced in millions of years (Convey et al. 2009). In the marine realm, changes in physico-chemical or biological parameters have the potential to affect many species in different ways and the possible responses of organisms to environmental stressors can widely vary across process scales, from gene to ecosystem, in a complex, intertwined fashion (Ingels et al. 2012). Furthermore, not all Antarctic regions are affected to the same extent: for example, the western Antarctic Peninsula (WAP) is the most rapidly warming region in the Southern hemisphere (King et al. 1994). Concurrent with atmospheric warming there are significant increases in the freshwater input to the ocean from glaciers along the WAP, potentially leading to a shift in phytoplankton assemblages and biomass (Meredith et al. 2013). The WAP area (Bellingshausen/ Amundsen seas), is also the only region of the Antarctic where sea ice extent (SIE) decreased over time, while elsewhere around Antarctica it has increased, possibly in relation to changes in atmospheric circulation (this increase is predicted to slow down and then reverse if the ozone hole closes) (Parkinson and Cavalieri 2012). In contrast to the situation along the WAP, the Ross Sea area has been marked by the largest increase of SIE over the past 30 years and this also holds true for the Western Pacific sector of Antarctica, although to a lesser extent (Parkinson and Cavalieri 2012). Increase in high sea ice algal biomasses release (up to 200 mg Chl-a m-2) due to increase sea-ice melting has important consequences for biogeochemical cycling, bentho-pelagic coupling and the sequestration of organic carbon into sediments (Arrigo and Thomas, 2004; Smith et al. 2006). Recently, the efficiency of this export of organic matter from sea ice has been re-evaluated and shown to be significantly larger than thought previously (Buesseler et al. 2010). For the WAP area, Buesseler et al. (2010) reported that some 10% of the primary production is actually exported to the subsurface layers and the seafloor, highlighting the importance of sea ice and pelagic production for the benthic ecosystem. This condition is thought to be consistent with short food chains and high carbon fluxes associated with blooms of large diatoms, and fecal pellet production by krill (Buesseler et al. 2010). Export production in the seasonally ice-covered areas shows a highly periodic seasonal pattern, with short pulses related to ice retreat (Ducklow et al. 2008) which may have resulted in adaptive feeding strategies for benthic feeders (Arrigo and Thomas 2004 and references therein; Gili et al. 2001; Beaulieu 2002). Continued environmental stress is causing a cascade of effects, yet, comprehensive studies on how these stressors will impact marine ecosystems and their different components are sparse. If major changes in coastal and shelf pelagic systems have already been documented (Dierssen et al. 2002, Ducklow et al. 2007, Montes-Hugo et al. 2009), very little information is available in benthic systems. The response of organisms to a changing environment depends on their capacity to cope with the physiological cost imposed by the new conditions (Peck 2004, 2005, Pörtner 2008) and the outcome of change is determined by the ability of populations to sustain themselves. Individuals may be able to cope physiologically or trophically but reduced genetic connectivity between populations caused by hydrodynamic changes, environmental shifts changing the boundaries of physiological sustenance, and biological alterations may change species distributions and/or affect the survival of populations. In turn, it may stimulate future speciation. At the community level, biological interactions play a crucial role (Ingels et al. 2012). Therefore, addressing potential climate change effects requires robust integration of macro-ecological concepts, experimental evidence and modelling approaches with energy budgets incorporated in life cycle models (Russell et al. 2011). Over the past decade, there has been a significant advance in the knowledge on Antarctic biodiversity through initiatives like the Census of Antarctic Marine Life (CAML). However, for most of the Southern Ocean and its environment the scale at which data is available is far from satisfactory and continues to limit analyses (Schiaparelli et al. 2013; Danis et al. 2013). As a long- term legacy of CAML, information networks such as SCAR-MarBIN (De Broyer et al. 2013), ANTABIF (Danis et al. 2013) or the upcoming biodiversity.aq (Van de Putte et al. 2013) are becoming useful tools in assessing biodiversity and identifying areas that are vulnerable or unique, but also in identifying knowledge gaps (Griffiths et al. 2011). Among these, an important category includes gaps in information available at small and regional scales, which require the refinement and development of dedicated frameworks to categorise and assess ecological processes. Pursuing these efforts collaboratively will contribute significantly to our understanding of the main drivers of Antarctic ecological diversity (Brandt and Ebbe, 2009; Clarke and Johnston, 2003; Griffiths, 2010; Ingels et al. 2012).

2.2 Objectives

The goal of the vERSO project was to assess the impact of the main stressors driven by global change on benthic Antarctic ecosystems using an integrated multiscale approach including different representative size classes of the benthos. Two principal regions with current contrasting responses to global change have been considered, namely the Western Antarctic Peninsula and the East Antarctic. To reach this goal, researches on connectivity and adaptation, trophic ecology and sensitivity and resilience were conducted by all partners and integrated using state of the art modelling techniques. The vERSO research was distributed among four interactive work packages.

In the first work package **(WP1 – Connectivity and Adaptation)** vERSO identified the contemporaneous and past connectivities in a range of widespread and common taxa along the continental shelf of the Antarctic continent. The specific spatio-temporal molecular patterns were used to expand the predictive power and resolution of the models used in WP4.

In the second work package **(WP2 – Trophic Ecology)** vERSO will delineate general trophic web structure and carbon pathways in contrasted coastal habitats and assess trophic variability (i.e. specific plasticity, ontogenic shifts, degree of specific and individual specialization...) in order to estimate the adaptive potential of communities to future trophic changes.

In the third work package **(WP3 – Sensitivity and Resilience)** vERSO will characterize the sensitivity and resilience of key benthic taxa and communities by running integrated experiments to assess the combined effects of temperature, acidification, and food quality and quantity on nutrient fluxes and metabolism of significant components of sediment communities in contrasting regions. The output of these experiments will be used in models of WP4. Resilience analysis will be based on openly available long-term data and on modelling using sensitivity, connectivity and trophic ecology data.

The fourth work package **(WP4 – Integrative modelling)** will run predictive models and will attempt integrating biogeographical, connectivity, trophic, sensitivity and environmental data to assess the severity of potential shifts using innovative approaches. Fine scale data will be used to validate predictive species distribution models. WP4 will play a dual role in vERSO, both as a science driver and as an integrator.

3. METHODOLOGY

Sampling - general

Samples were collected during campaigns to the Southern Ocean, onboard research vessels (e.g. R.V. *Polarstern*) or from research stations in the areas of interest (WAP and Terre Adélie). In the framework of vERSO an integrated, multiscale approach was envisioned to optimize interactions between partners and work packages. The composite vERSO sampling effort included (1) the development of a large-scale sample library, (2) an integrated micro and mesoscale experiment and (3) a fine-scale mapping exercise using ROV-based imaging.

1. Large scale. Many samples had already been collected during previous cruises or land-based samplings (e.g. CEAMARC, REVOLTA, PROTEKER, ANT XXIX-3, Dallman laboratory) and were available and deposited in natural history museums. These samples constituted the initial vERSO library. To complete this library, macro- and mega-benthos samples were collected during future research cruises (ANT 29-9 Filchner Ice Shelf Benthos Sampling 2013-2014, SYSTCO III 2014- 2015) in which vERSO was already involved. Agassiz trawl, bottom trawl, plankton net (ichthyoplankton) were used to collect macrobenthos and their larvae. Samples for meiofauna were collected during the same cruises using a multicorer (MUC) device at scales of cm’s up to 1000 km’s (in different stations). As far as possible, the same samples were used for community and molecular genetics as well as for isotopic analysis. This procedure ensured a truly integrated approach between the different WPs, as well as robust data interoperability.

To optimize niche modelisation potential and multiscaling, various georeferenced environmental parameters were recorded simultaneously in each station, as far as possible. These parameters included bottom temperature, salinity and depth (CTD), current velocity and direction (ADCP), as well as a description of the habitat conditions (substrate characteristics).

2. Regional scale. In two selected sites (land-based laboratories) from contrasted regions (Western Antarctic Peninsula – WAP) and Terre Adélie, we intended to follow primary production over a significant part of the growth season (during a 2-month survey), starting

when the selected sites were still covered by sea ice. Integrated sensitivity experiments were be conducted in the same sites to the best extent feasible.

3. Fine scale benthic mapping. This mapping technique was used both for initial exploration of the sampling regions (selecting optimal location and determining surrounding assemblages) and to carry out a reality-check of the Species Distribution Models (SDMs) outputs. Attempts to carry out this mapping were done using ROV survey and subsequent image analysis (using OFOP software (Ocean Floor Observation Protocol), Huetten and Greinert 2008).

WP 1: Connectivity and Adaptation

Connectivity

Contemporaneous connectivity is shaped by physical forces (characteristics of the continental shelf and regional hydrodynamics) and the life history traits of the organisms. Larval stages with a pelagic phase or highly mobile adults influence the chances to homogenize their populations. The main aim was to identify and understand the dispersal-related processes that explain the distribution patterns and biodiversity of Southern Ocean taxa in a community perspective. We were interested in the relative importance of both environmental and dispersal-related sets of explanatory variables in determining distribution and biodiversity patterns. The hypothesis was that the relative importance of dispersal-related processes increases with geographical scale, and that on smaller scales environmental processes play a larger role. Five taxonomic groups were studied:

Nematoda **-** We assessed the population genetic structure of some dominant nematode species at local to regional spatial scales by applying both morphological and molecular techniques in parallel. The mitochondrial cytochrome oxidase c subunit 1 (COI) gene or the nuclear ribosomal internal transcribed spacer region (ITS) was amplified, sequenced and aligned using several individuals (approx. 20) per population to provide information on genetic diversity within and between populations. Both ITS and COI have been proven especially useful in reconstructing phylogeographic patterns and colonisation history because these genes have sufficient intraspecific variability (Derycke et al. 2008)

Amphipoda **-** Mitochondrial DNA markers and microsatellites were used to investigate the medium- and fine-scale population structuring of selected amphipod groups (Eusiridae and Lysianassoidea) and to test for dispersal. Microsatellites were developed using Next Generation Sequencing (NGS) methods, jointly by RBINS and KU Leuven.

Holothuroidea **-** The obligate symbiont *Echinopsolus acanthocola* of cidaroid echinoids (O' Loughlin et al. 2011) is a brooder that seems unable to move freely in the surroundings. Despite this, it has a circumpolar distribution (Ross Sea, Bransfield Strait, Weddell Sea and Terre Adélie) and a relatively large depth range from *ca.* 200 m to 850 m. Newly developed microsatellites and mitochondrial DNA were used to study genetic relationships between individuals at the local scale (i.e. considering the same infrapopulation, and then different infrapopulations from the same station) and regionally (e.g., Weddell Sea versus Bransfield Strait). Each infrapopulation corresponded to the holothurians occurring on one individual host. Adults-adults and adults-juveniles links were examined in order to assess (1) the mobility of holothurians (parents and offspring on a single host or not) and (2) the weight of brooding in the isolation of infrapopulations. Genotypes of all groups were analyzed through standard methods (genetic diversity and structure, neutral divergence), assignment and by incorporating community and geographical features (GIS and seascape genetics; Manel et al. 2003).

Crinoidea - The COI mitochondrial gene had already been extensively and successfully used to assess population structure, demographic trends and gene fluxes of broadcast spawners over the whole Southern Ocean (Hemery et al. 2012). This approach was extended to species with contrasting life history traits (e.g. brooders such as species of the genera *Isometra* and *Notocrinus*). In addition, microsatellites were developed for the *Promachocrinus kerguelensis* complex and the well-spread brooder *Notocrinus virilis*.

Asteroidea - Based on current knowledge (Mah, pers. com.) and preliminary results of our extensive barcoding effort (Eléaume, unpublished results), we focused on four Antarctic asteroid genera: *Bathybiaster* (one potentially broadcasting species known in the Southern Ocean but with high morphologic and genetic diversity, another deep-sea species in the Atlantic); *Diplasterias* (from the Southern Ocean only, six nominal brooding species with at least one undescribed); *Porania* (bipolar genus with two species, great morphologic and genetic diversity of the Antarctic broadcast species); *Psilaster* (a dozen species known worldwide, only one in Antarctica, broadcaster with high genetic diversity). The mitochondrial (COI) and nuclear (ATP synthase beta subunit intron 6, and Elongation factor-1 alpha subunit intron 4 – see Foltz et al. 2013) genes were sequenced. Microsatellites or SNPs have been developed for two contrasting well-spread species *Bathybiaster loripes* and *Diplasterias brucei*.

Fish - Reduced representation sequencing approaches were developed and optimized to genotype thousands of genetic markers, more specifically single nucleotide polymorphisms (SNPs), in Antarctic notothenioid fishes. The protocols used included a modified version of the double digest restriction-associated DNA (ddRAD) sequencing (Peterson et al. 2012) as described in Palaikostas et al. (2015) and a modified version of the genotyping-by-sequencing (GBS) approach (Elshire et al. 2011) as described e.g. in Raeymaekers et al. (2017). Samples from across the Antarctic (WAP and Terre Adélie) at various geographical scales were genotyped at neutral and adaptive markers in order to differentiate between gene flow (neutral evolution) and adaptation.

Adaptation

Environmental variability induces phenotypes to adapt, especially those linked to life-history traits, trophic ecology and the metabolic-reproductive axis (Araujo et al. 2012, De Santis and Jerry, 2007). Changes in the genome pay testimony to the impact and hence the systematic screening for gene-linked variation is a good indicator of adaptation (Feder and Michell-Olds, 2003). Therefore, outlier behavior of potentially gene-linked SNP markers and candidate genes in reference to historical samples will be used as an indication of adaptation. This was applied to fish. Populations were genotyped with thousands of markers, analyzed through multivariate frequentist and Bayesian approaches, screened for outliers (Shikano et al. 2010) and geographical features (using GIS and seascape genetics; Manel et al. 2003).

Feedback mechanisms with other WPs

The spatial patterns originating from the population genetic analyses were compiled per species to a spatially explicit database and used for habitat modelling through a correlative approach between environmental and ecological factors (Gutt et al. 2012). For dynamic modelling, seascape genetics were used to understand the dynamics of patterns of marine organisms (e.g. Galindo et al. 2010; Selkoe et al. 2010). Details of the modelling methodology is provided under WP 4.

WP 2: Trophic Ecology

Primary production and flux to the seafloor

Samples were treated following a protocol already tested during the SIPEX 2 expedition (Oct.-Dec. 2012). Spikes of ^{13}C-bicarbonate + ^{15}N-nitrate were added to core 1 and ^{13}C-bicarbonate + ^{15}N-NH$_4$ to core 2. A 3rd core was used for Si-uptake after spiking with ^{30}Si (collaboration with F. Fripiat, ULB). Polycarbonate bottles were inserted into Perspex cylinders which are fitted into the drilled holes and left for 24 h. Light levels, temperature, salinity were recorded at beginning of the incubations. Incubations were ended by adding $HgCl_2$ to the samples which were then left to thaw slowly. Thawed samples were filtered on Whatman GF/F; these filters were dried and stored till analysis per IRMS. Ice core parts set aside for initial conditions are also treated with HgCl2, thawed, filtered and dried. In conditions of open waters we sampled the euphotic layer (delimited by the 0.1% PAR level) at 3 to 4 light levels using Niskin bottle samplers. Seawater was transferred to 1 L PC bottles and spiking (^{13}C-HCO$_3$ + ^{15}NO$_3$; ^{13}C-HCO$_3$ + ^{15}NH$_4$) was done following Cavagna et al. (2011). Polycarbonate bottles were incubated in land incubators wrapped with light-filter screens mimicking the in-situ light levels. Incubations were terminated by filtering the samples on GF/F. Filters were handled and stored as above. Isotopic enrichment was measured by IRMS and uptake rates calculated as in Cavagna et al. (2011). We also analysed seawater and brines for natural nitrate isotopic composition. Samples were filtered and stored at -20°C till analysis, applying the bacterial denitrifier method, elaborated by Sigman et al. (2001).

The Carbon export flux to the seafloor was assessed using the ^{234}Th method (Pike et al. 2005; Buesseler et al. 2010; Planchon et al. 2013). The method relies on the particle-reactive and naturally occurring ^{234}Th (1/2 life 24.1 days) produced from its conservative parent ^{238}U (constancy with salinity). Deficits of ^{234}Th activity vs. ^{238}U activities integrated between surface and depth where both isotopes are in secular equilibrium (usually within the upper 200m), reflect export on sinking particles. Several depths (up to 10) were sampled (4L) and total ^{234}Th (dissolved + particulate) activity in the upper water column (till 300m) measured within 48 hours after sampling, using a low-beta RISØ counter. After counting samples were saved for later measurement of background activity and ^{234}Th recovery. Thereafter final ^{234}Th fluxes could be calculated. To translate the ^{234}Th fluxes into POC fluxes large quantities (several 100 L) of seawater were filtered using a stand-alone in-situ pump to collect suspended material (2 size classes: 1-53 µm and > 53 µm) from 150 to 200m depth. These filters were also measured for ^{234}Th activity and for POC, PN content. From the POC/^{234}Th ratio of sinking particles and the ^{234}Th flux, the export of flux of POC, PN to the sediments was calculated.

Benthic food web interactions

The identification of energy pathways through major ecosystem components is a basic element of food web studies. How different consumers process the primary produced material and convert organic matter as it passes through each trophic link has significant consequences for ecosystem properties, such as food web stability, carbon turnover and nutrient regeneration. The specific aim of the field study was the identification of major food web interactions in two contrasting areas of the Antarctic. Here, we used a community approach trying to delineate general food web structure. Based on the principle of 'you are what you eat', a biomarker analysis provided insight into whether the same taxa from both study areas had similar isotopic compositions and/or differences in biomarkers composition or ratios and, in turn, predicting possible correlation between climate change and food webs variation. For this purpose, two types of biomarkers (stable isotopes and fatty acids), which yield complementary information, were used (Nyssen et al. 2005). While analyses are traditionally performed on bulk tissues or even whole organisms, it was recently shown that compound-specific stable isotope ratios of amino acids may be useful to determine both the trophic position of an animal inside a given food web and the contribution of a source to its diet (Chikaraishi et al. 2010). Here, we investigated bulk ratios of stable isotopes of carbon, nitrogen in muscle tissues of consumers, as well carbon and nitrogen ratios of amino acids. Whereas stable isotope analysis allows to identify trophic levels ($\delta^{15}N$) and bulk food sources ($\delta^{13}C$) (Layman et al. 2012), lipid analysis reveals a more specific characterization of the selectivity in food uptake (Pond et al, 2000). For instance, the presence of particular Poly Unsaturated Fatty acids (PUFA's) points to the importance of phytoplankton derived food sources (Suhr et al. 2003), while bacteria also revealed specific fatty acid composition (Nichols and Mc Meekin 2002). To estimate the respective contribution of potential food sources in animal diet, we applied mixing model approach (SIAR modelling) (Parnell et al. 2010).

Tracing experiment

Stable isotope (^{13}C)-labeling experiments were carried out to quantify the importance of different food sources (different bacterial functional groups and diatoms) as a food source for dominant meiofauna and macrofauna taxa. Both primary producers and bacterial functional groups wereisotopically enriched in a microcosm approach with different substrates such as ^{13}C-glucose, ^{13}C - acetate, ^{13}C -bicarbonate, and ^{13}C -amino acids injected into sediments collected. Incorporation of the 13C label into phospholipid-derived fatty acids (PLFAs) of the food sources and different benthic organisms in the sediment can be followed over time (up to 2 weeks). The ^{13}C dynamics of the benthic groups can be fitted with a simple isotope turnover model to derive the importance of the diatoms and different bacterial functional groups as carbon sources for the benthos (Guilini et al. 2010). The results of these experiments helped choosing the food sources used in WP3.

Trophic variability

To assess trophic niche and diet variability, we targeted dominant species with diverse and varying diet types of the following macro or megafaunal groups: echinoids, amphipods, and fish. We determined individual and populational diet metrics describing trophic niches based on gut content analysis (Bolnick et al. 2002) and isotopic approach (Newsome et al. 2007). The SIBER metrics proposed by Jackson et al. (2011) using bulk isotopic analysis of carbon and nitrogen were applied. Comparison of diet metrics (both from gut content and stable isotopes data) allowed to assess the sensitivity of target species to change of their trophic environment. Moreover, for echinoids, a set of representative species were examined that belong to the genus *Sterechinus*, and to the families Cidaridae and Schizasteridae. We assessed the impact of food regime on sea urchin growth (allometry relations between lantern size and test diameter) (see e.g., Ebert et al. 1999), and studied their associated digestive transient microflora (identification of bacteria by pyrosequencing and inference of their enzymatic activities). Bacterial communities and their stable isotope composition were also analyzed for surface sediments in order to determine to what extent they contribute to the digestive microflora of the echinoids.

WP 3: Sensitivity and Resilience

Experiments were conducted in land-based Antarctic laboratories in closed or open circuit aquaria (depending on availability) during two to three weeks. Stressor gradients generated by hydrothermal vents (Deception Island, WAP) were also used as analogs of global change. pH conditions (present, - 0.3, -0.6) were manipulated by adding CO_2 through a computer-assisted system. All experiments were conducted following guidelines provided by Riebesell et al. (2010). Different food concentration and qualities (phytoplanktonic and benthic microalgae, artificial food enriched in proteins) will be provided simultaneously on the surface of the sediment mixed or not with soft sediment added to mimic increased sedimentation rates. These food sources will be enriched in heavy stable isotopes of C and N. Experiments will be carried out at two different scales. A first mesocosm scale experiment will use sediment collected *in situ* by divers in large enough quantities (but therefore in disturbed state) to include all considered benthic size groups and their representative taxa. Diverse smaller microcosm scale experiments will use undisturbed sediment cores of different sizes obtained either by divers or from a small boat to obtain better constrained results on specific responses and interactions of smaller benthic organisms (excluding the megafauna).

In both meso- and microcosm experiment, denitrification and dissimilatory nitrate reduction to ammonium by sediments will be assessed by spiking with $^{15}NO_3$ and measuring the ^{15}N enrichment of N_2, N_2O and NH_4 (Steingruber et al. 2001; Dong et al. 2011). Nutrient profiles (NO_3, NH_4, PO_4) in the sediment was measured using “Rhizomes” or Diffusion Equilibration Thin films (DET; Mortimer et al. 2002).
In both meso- and microcosm experiments for selected species (amphipods, echinoids) and species assemblages (prokaryotes, nematods), the following variables will be monitored :

- Metabolism (all size groups)

o Oxygen consumption (using an optode)
o Food assimilation rates (measuring isotopic enrichment in the consumers)
o Catabolism of proteins and amino acids assessed through ammonium concentration excreted in sea water (the latter samples will be collected in respiration chambers) (amphipods, echinoids, nematodes)
o Potential metabolic activities of bacteria were inferred from community structure (presence/absence of key groups involved in specific activities like nitrification, sulfate reduction, methane oxidation etc.). In addition, community- level physiological profiling will be performed at different time and scale points. In this approach, sediment samples are incubated with different carbon and nitrogen sources in miniaturized systems and respiration is detected by the reduction of a tetrazolium dye (Biolog "Ecoplates" or "Phenotype Microarray Microplates" technology)

In echinoids and starfish, the following variables were monitored:

- Acid-base balance
  Extracellular pH, buffer capacity (alkalinity) and DIC concentration of the coelomic fluid, measured, respectively, with microelectrode, microtitration and isotopic analysis following methods described in Collard *et al* (2016)
- Impact on the skeleton: corrosion (analyzed by SEM analysis) and biomechanics
- Taxonomical and functional structure

By analysis of shifts in functional structure and species composition of the meiofauna and prokaryotes in different treatments of the experiments, community responses can be inferred in terms of altered species interactions and functional complexity; for prokaryotes, community structure will be studied at the level of DNA (total community) and RNA (active community)

The effects of acidification, temperature sedimentation and food quality/quantity on metabolism, acid-base balance, species interactions and functional structure on selected taxa and assemblages were related to changes in biochemical conditions and nutrient fluxes. A tentative energy budget of the community according to conditions will be established.

Resilience is the capacity of an ecosystem to cope with disturbance without shifting to an alternative state and losing function, after passing a tipping point. In the framework of the Census of Antarctic Marine Life, a thorough census of Admiralty Bay benthic biodiversity was completed through the synthesis of data, acquired from more than 30 years of observations (Sicinski et al. 2011). This data collection, published through SCAR-MarBIN (ABBED, the Admiralty Bay Benthos Biodiversity Database) is freely available and includes most of the available records collected from successive Polish and Brazilian expeditions organized since 1977, until the International Polar Year (2007–2009). Data from approximately 1300 species of benthic organisms (excluding bacteria, fungi and parasites) have been recorded from the bay's entire depth range (0–500 m). Admiralty Bay represents a legacy site, and a robust benchmark for a resilience study where continued, systematically integrated data sampling has been carried out. Using available data, the spatial signature of resilience was addressed to evaluate spatio-temporal fluctuations. We used time-series analysis tools to identify variations in assemblages over time and try to identify time lags in responses to environmental change that would form an interesting basis for future monitoring. Parameters such as species richness will also be measured.

WP 4: Integrative modelling

vERSO Information System (VIS)

Large amounts of biodiversity data are available from a range of dedicated data portals, including ANTABIF, OBIS or GBIF. Offering a single access to relevant data, the main source of primary biodiversity data for vERSO will be biodiversity.aq, which includes 2.5M occurrence records on 5000+ taxa in 5000+ datasets. This data is compliant with international standards such as DarwinCore 2.0 (TDWG, Taxonomic Database Working Group) and Open Geospatial Consortium (OGC). After running an initial gap analysis, the vERSO information system was completed with targeted resources mined by exploring the

Antarctic Master Directory (AMD) and through work on fine scale benthic mapping, collections, literature, or networks of collaborators. Environmental parameters have been compiled and published online.

Offline modelling

Using its Information System, vERSO will run predictive distribution models based on selected sets of benchmark data and perform statistical analyses of the environmental variables in order to explain biodiversity patterns and the processes driving them. vERSO will explore modelling runs using an array of Species Distribution Models (SDMs) and taking advantage on the experience acquired in the framework of the Biogeographic Atlas of the Southern Ocean and initial runs carried out by one of vERSO's subcontractant (Biogéosciences, Université de Bourgogne). SDMs will be built using different software packages or custom workflows. Software packages include ArcVIEW (10.1), MaxENT (3.3.3), MGET (0.8a44), GARP (1.1.6). Custom workflows include BRT (Boosted Regression Trees, Irisson et al. 2013), GDM (Generalized Dissimilarity Models, Irisson et al. 2013), GLM (Generalized Linear Model), GAM (Generalized Additive Models) approaches, and will be run for different environmental parameters, scales and species.

Incorporating adaptation and genetic information from WP1 involves exploring spatial patterns originating from the population genetic analyses. Seascape genetics will help understanding the dynamics of patterns of marine organisms and the relative importance of environmental predictors of genetic structure (Selkoe et al. 2010). For this purpose, associations between genetic and environmental factors will be delineated using procedures such as GESTE, BIOENV (in PRIMER v.5) and Mantel tests (as in the "vegan" package in R) (Selkoe et al. 2008, 2010). Some aspect of trophic niche variability and individual specialization in animal populations (WP2) are also related to genetic traits and variability (Araujo et al. 2011, Bolnick et al. 2011) and therefore genetic seascape could also be use to understand capacities of different populations to vary their trophic niche and to adapt to change.

Integration of ecological and physiological sensitivity/resilience from WP3 will be resolved by incorporating an explicit ecophysiological "first principle" component into the model using the latest version of the model developed by Cheung et al. (2011). This model simulates changes in metabolic rates in function of environmental parameters in the ocean, and predicting their effect on growth, reproduction and mortality rates of the studies species.

Finally, a reality-check and further refinement of modelling parameters will be performed by confronting SDM outputs to data obtained by high-resolution benthic mapping carried out by an ROV survey in the two contrasting regions envisioned in the framework of the vERSO proposal (VideoRay PRO3 GTO). ROV imaging will be analyzed using the OFOP software (Ocean Floor Observation Protocol, Huetten & Greinert 2008). DarwinCore archives (DwC v2.0) will be produced for species occurrence records as well as spatially-explicit datasets for habitat.

Online modelling

As part of its Open Source philosophy and taking advantage of ongoing development in the SCAR Antarctic Biodiversity Informatics expert group, as series of developments are envisaged as part of the vERSO modelling workpackage. Based on the GDM and BRT GUI developed under the BASO project (De Broyer et al 2013, Irisson et al. 2013), dedicated SDM modelling webservices can be developed for the biodiversity.aq project. A similar approach has been successfully used for the Atlas of Living Australia (http://www.ala.org.au/spatial-portal-help/gdm/). For this purpose, a dedicated R-server will be setup and maintained by the biodiversity.aq team at RBINS. Other services can be developed such as a set of Taverna (v2.4) workflows which will be published in Lifewatch Biovel e-laboratories. Involvement of important data providers, portals (channels to users) that play key roles in BioVeL workflows. These services and workflows will be specifically documented in the AMD using SERF (Service Entry Resource Format).

4. SCIENTIFIC RESULTS AND RECOMMENDATIONS

In the framework of the vERSO project, the following high-level activities were envisioned by the end of the project, and have all been addressed, as well as additional deliverables. Intermediate results have been detailed in previous reports.

1. Improved knowledge on and understanding of contemporaneous connectivity in a range of widespread and common taxa along the continental shelf of the Antarctic continent
2. Improved knowledge on and understanding of general trophic web structure and carbon pathways in contrasted coastal habitats and trophic variability of main targeted species
3. Improved knowledge on and understanding of the effects of acidification, temperature, food availability on sediment communities, including their resilience
4. Set of predictive models including multiple spatial and temporal scales and scenarios, and whenever feasible, integration of different levels of biological complexity and combination of different taxa.
5. Policy-relevant information and visualization products made available through relevant information systems (i.e. Antarctic Environments Portal)
6. Publications in peer-reviewed (preferably open-access) journals, including reviews and syntheses identifying current state of knowledge and important future research directions
7. Communications in influential Antarctic-specific symposia, especially SCAR OSC and Biology Symposia, and participation in focused workshops, eg related to long-term observation systems (SOOS)
8. Training and graduation of post graduate students (MSc and PhD), mentoring of young scientists beyond the project (through APECS)
9. Relevant media activities

These different topics are developed in detail in the rest of the present report.

The design of the data flows architecture has been developed in the first months of the projects, striving to achieve a perfect match with the SCAR data policy. The vERSO data and metadata records are compatible with broadly-used standards, including DarwinCore (DwC), Data Interchange Format (DIF), ISO19115, and is progressively published in recognized repositories, including the Global Change Master Directory (GCMD), biodiversity.aq, the Ocean Biogeographic Information System (iOBIS), the Global Biodiversity Information Facility (GBIF), the National Center for Biotechnology Information (NCBI), or other relevant depositories, according to the data type.

The vERSO metadata portal is hosted by NASA and forms an IDN (Internal Directory Name) of the GCMD. This ensures a high level of visibility for the vERSO-generated data, and a direct integration in the Antarctic Master Directory (AMD), as requested by SCADM (Standing Committee on Antarctic Data Management) and the SCAR data policy. vERSO partners are now using a vERSO metadata template to document the datasets which will be published along the way. One dataset affiliated with the vERSO project has been described in the portal and over 40 are now being documented with metadata and are in the process of being integrated in the vERSO information system.

Below, we describe the activities pertaining to the project's different workpackages. For each of these items, a short comment is provided.

WP 1: Connectivity and Adaptation

WP *1.1. Documentation of available samples, exchange and new collection of nematodes, amphipods, holothurians, crinoids, starfish and fish. Responsible: RBINS (MNHN), KU Leuven, ULB (UB)*

Amphipods:

New samples were collected during two *Polarstern* cruises (PS 82 (December 2013 – February 2014, RV *Polarstern*, Weddell Sea) and PS89 (December 2014-February 2015, RV *Polarstern*, Lazarev Sea). Samples from the collections of the Royal Belgian institute for Natural sciences (RBINS) were also available. Collaborations with colleagues in the United Kingdom, France, Germany, New Zealand and Australia ensured the addition of additional samples. In April 2017, 17 *Waldeckia obesa* and 21 *Eusirus perdentatus* have been sorted from raw material and collected at the British Antarctic Survey in Cambridge, UK, thanks to a collaboration with Drs Huw Griffiths and Katrin Linse. In October 2016, 20 *Eusirus perdentatus* have been collected from the Alfred Wegener Institute in Bremerhaven, Germany, thanks to a collaboration with Dr Christoph Held. In September 2017, 47 *Eusirus perdentatus* collected in the Ross Sea were sent to RBINS by the National Institute of Water and Atmospheric Research (NIWA), Wellington, New Zealand, by Sadie Mills and Diana Macpherson. In October 2017, 64 *Eusirus perdentatus* specimens from CEAMARC expeditions (Adélie Coast) were sent to RBINS by the Australian Antarctic Division (AAD), thanks to a collaboration with Drs Helena Baird and Glenn Johnstone.

Crinoids:

400 frozen samples from Auburn University have been added to the 1500 already collected and sequenced. These samples are used to develop the RADseq strategy for crinoids population genetics. Ken Halanych (Auburn University) is collaborating with us on various projects, including the sequencing of the *Promachocrinus kerguelensis* transcriptome. New crinoid samples (82) have been collected this year during the REVOLTA 2015-2016 cruise, the *Polarstern* PS96 and the *James Clark Ross* JR15005 cruises. These samples will be used in two ways: 1- complete the heterochronic population sampling of *Promachocrinus kerguelensis* / *Florometra mawsoni* and, 2- transcriptome sequencing for new genetic markers design in order to reorganize crinoid Antarctic species in the crinoid phylogeny.

Sea stars:

13,510 occurrence records of Asteroidea (Echinodermata) have been compiled from literature, data papers and global biodiversity information systems sources within the RAMS area of interest and matched against the relevant RAMS species list. The number of Asteroidea species in RAMS has increased by ca. 50%, now reaching 299 accepted species. The biogeographic data will be released (through the biodiversity.aq data portal) in parallel with the publication of the related data paper (Moreau et al. in prep., see section 7.1). In the framework of a Lifewatch grant, the following work has also been achieved for this class of echinoderms: 97 unregistered species were added to the RAMS context together with a general update of the Asteroidea data; 5 legacy volumes were digitized, uploaded into the VLIZ (Flanders Marine Institute) Catalogus (linked to the Biodiversity Heritage Library, now providing open-access links to 40 original descriptions to the RAMS sea star species); new macro pictures of the specimens (oral and aboral surfaces, 42 species) were taken and uploaded on RAMS; a prototype identification key was created for the family Odontasteridae (15 species) from the Southern Ocean and will be presented during a digital taxonomy event from the SCAR Biology Symposium 2017; new links to Barcode of Life for 9 species were added to RAMS, as well as links to the Antarctic field guides (http://afg.biodiversity.aq) (7 species). All COI sequences produced by MNHN, NIWA, MNA and ULB have also been compiled in a working database of available and DNA-Isotopes friendly specimens. A total of more than 4,600 specimens are available for further analysis, to be carried out in parallel by the RECTO project teams.

Fish:

Since the last report only few additions to the already extensive fish collection (now > 3000) have been added. Latest additions were 164 fish (mainly *N. coriiceps*, *N. rossii*, *T. newnesi*, *T. bernacchii* and *H. antarcticus*) from the B121 expedition and 52 fish of various species (including non-notothenioids such as liparids and macrourids) form *Polarstern* expedition PS 118. The total, final fish sample database shall be compiled and published in an online repository in the course of 2019, in conjunction with data activities occurring in the framework of the BRAIN-BE RECTO project.

WP 1.2. *Marker development in nematodes, amphipods, sea urchins and fish. Responsible: RBINS (MNHN), KU Leuven, UGent, ULB (UB)*

Nematodes:

Phylogeographic and population genetic analyses were carried out for several species within the nematode genera *Sabatieria* and *Desmodora*, at locations along the Antarctic Peninsula and eastern Weddell Sea. Samples were collected during expedition PS79/ANT-XXVII/3 of RV Polarstern in February – April 2011, using a multicorer device (MUC, 12 cores, inner diameter 57mm, surface area 25.52 cm^2). Faunal samples were collected in two sediment depth layers (0-3 and 3-5cm) and stored on DESS. In the lab, all meiofauna was extracted and individuals of both targeted genera were handpicked from the DESS samples and individually stored in Worm Lysis Buffer before DNA extraction. Using a combination of existing and newly developed primer sets, we were able to perform PCR reactions using both mitochondrial (cytochrome oxidase I COI) and nuclear (internal transcribed spacer ITS + small subunit ribosomal DNA 18S) markers. Amplified products were sequenced by MACROGEN (Macrogen Inc, Europe). For *Sabatieria*, this resulted in 326 sequences for ITS, 42 for 18S and 16 for COI (after removing bad sequences and those without good match in GenBANK). For *Desmodora*, we were less successful and could only obtain 25 ITS and 37 COI sequences. In both cases, several protocols were tested and refined before obtaining these results. Sequence datasets were then subjected to phylogenetic and population genetic (using ITS for *Sabatieria* and COI for *Desmodora*) analyses to assess species diversity and genetic structure.

Amphipods:

From the existing amphipod collections, comprising samples from various expeditions (ANT XXVII/3, ANT XXVIII/3, ICEAGE II, REVOLTA, Icefish etc.), 162 DNA extractions of several lysianassoid species were carried out (Lysianassoidea: *Pseudorchomene*, *Waldeckia*, *Abyssorchomene*, indet spp.). Due to the departure of the postdoc working on the lysianassoid species, this work has been suspended and reoriented towards the eusiroid group, for which a strong expertise remains in the institute. DNA extractions were obtained for 329 eusiroid specimens belonging to the species complex *Eusirus* cf. *perdentatus*. Standard markers have been sequenced using all these new extractions, along with *Eusirus* spp. extractions from previous studies. For *Eusirus* complex *perdentatus*, 242 COI sequences were obtained, along with about 30 sequences of ITS2 and CytB. Moreover, 56 additional COI and 98 28S sequences of Antarctic *Eusirus* spp. were produced.. Microsatellites were developed for two species of *Eusirus* complex *perdentatus*. In total, 16 loci were successfully amplified and genotyped for 296 specimens of these two species. These data will, amongst others, yield information about species identification and general phylogenetic and phylogeographic analyses.

Crinoids :

Preliminary studies on *Promachocrinus kerguelensis* population structure in the Southern Ocean revealed that this species is a complex of 7 lineages probably not panmictic. Moreover, *Florometra mawsoni* was shown to be closely related to *P. kerguelensis*, and even probably nested within the 7 lineages of *P. kerguelensis*, supporting morphological evidence. A rough estimate of divergence times was done using mutation rates derived from sea urchin sister species separated by the closing of the Isthmus of Panama. Earliest divergence time was estimated to 1 Mya. Among the 1500 COI sequences produced by the MNHN, some are heterochronic, i.e. sampled from populations from the same broad areas at different years. These heterochronic sequences were used to estimate separately effective population size and mutation rate. Earliest divergence time using this method was estimated to 1000 ya. To test these hypotheses, we decided to use fast-evolving markers, SNPs, sampled from the whole genome. RADseq sequencing needs to be tested against the particular species we want to study. DNA was extracted from 40 specimens : 10 *Promachocrinus* clade A from CEAMARC (Terre Adélie), 10 *Promachocrinus* clade A from POKER II (Kerguelen), 10 *Florometra mawsoni* from CEAMARC and 10 *Florometra mawsoni* from POKER II. DNA quality was tested on each sample and only 10 of them proved to contain too small amount of DNA. Double Digest RADseq using EcoR1 and MspI has been essayed on 20 specimens of *Promachocrinus sensu largo* (i.e. including *Florometra mawsoni*) that had already been genotyped for a previous study. Each specimen was tagged separately, and sequencing was done using the MNHN PGM. Sequencing yielded 3 million reads of an average size of 200 bp. All libraries didn’t yield similar number of reads. *Florometra mawsoni* library yielded a reduced number of reads (372) probably because the DNA quality was different with more inhibitors in *Florometra*.

Sea urchins:

Reconstructing the phylogeny of Antarctic schizasterid sea urchins proved extremely challenging, from several points of view. Studies using several independent genetic markers have been carried out for years by a team in Marseille (A. Chenuil & JP Féral – IMBE) but no robust phylogenies were obtained. The main reason is that most species are closely related to each other and few molecular characters provide an interesting phylogenetic signal. In addition, samples are difficult to collect, the accepted taxonomy is based on non-apomorphic morphological characters that are difficult to identify and several samples collected in the field were misidentified, impeding using them in molecular studies. However, taking advantage of the whole transcriptome sequences very recently obtained for three species of Schizasterid echinoids (Romiguier et al. 2014), the team from Marseille (A Chenuil and JP Féral) associated to the partner from UB (T. Saucède & B. David) developed genetic markers from expressed genes based on the divergence among the three schizasterids *Abatus cordatus*, *Abatus agassizii* and *Tripylus abatoides*. They selected exon sequences displaying variability among those species and used online genetic and genomic databases and bioinformatics tools (NCBI, Blasts, ...) to identify the position of introns in transcriptomic sequences, based on the whole genome of the echinoid *Strongylocentrotus purpuratus*. Primer pairs were then identified to amplify dozens of loci within exons. All primer pairs amplified successfully and produced fragments of the expected size, despite the estimated 180 My time of divergence between the reference genome and the schizasterid species under study.

Fish:

DNA of more than 1200 specimens has been extracted. Approximately 400 of these have been used to generate COI sequences, which were used for species verifications/preliminary insights into phylogeographic patterns of fish diversity (bachelor theses; samples from JR150005 off South Orkney Islands). In regard to high-throughput DNA sequencing one double-digest restriction-associated (ddRAD) sequencing library comprising 144 individuals and four genotyping-by-sequencing (GBS) libraries comprising 96 individuals have been sequenced. The ddRAD library yielded 1,500 – 3,000 markers, i.e. single nucleotide polymorphisms (SNPs). As discussed previously attempts with a different protocol (GBS) were made in order to increase the number of markers. GBS data is not fully analysed yet, but appears to yield up to 15,000 good quality SNPs. The protocol changes can therefore be regarded as successful. Finally, 8 libraries were prepared (following the ddRAD protocol mentioned above) and sequenced containing 698 individuals from 9 species of the genus *Trematomus.* These data will be used to assess population structure of this genus around Antarctica as well as to assess the speciation within the genus. Libraries have been demultiplexed and are currently analyzed.

WP 1.3. *Genotyping and genotype analysis of nematodes, amphipods, sea urchins and fish. Responsible: KU Leuven, RBINS (MNHN), UGent, ULB (UB)*

Amphipods:

Given issues with the development of the ddRAD protocol work, on this has been suspended. Cryptic species have shown to be present in the studied lysianassoid and eusiroid amphipods. For this reason, all specimens will be barcoded using COI sequences.

Regarding lysianassoid amphipods, results on *Eurythenes* species were published (Havermans, 2016), and barcoding is ongoing for the *Waldeckia* spp..For eusiroid amphipods, COI and 28S sequences were used to reconstruct Bayesian (BI) and Maximum Likelihood (ML) phylogenetic trees of the genus *Eusirus*, including almost all existing Antarctic species and a few Arctic ones. The trees show that the Antarctic species are monophyletic. A BEAST analysis was also performed on this dataset, using molecular rates from the literature inferred for other amphipods, and provided a rough dating of the initial diversification of the Antarctic clade at 11 [5.1, 18.6] Mya. *Eusirus* amphipods therefore likely colonized the Antarctic shelf after its isolation from other oceans' shelves, about 34-30 Mya. During the Middle Miocene climatic transition 14.2-13.8 Mya, a major cooling of the region and possible increase of the Antarctic Circumpolar Current flow occurred, and this could have participated in the isolation and diversification of an Antarctic *Eusirus* clade. Phylogenetic trees (ML and BI) of the clade formed by *Eusirus* cf. *perdentatus* and *giganteus* specimens was reconstructed using new and existing COI, ITS2 and CytB sequences. Species delimitations methods (ABGD, PTP, bPTP, GMYC, bGMYC) were applied on these trees and revealed putative (pseudo-)cryptic species within both nominal species. The morphology of *Eusirus* cf. *perdentatus* specimens was examined and a new species was described, which presents a distinct coloration pattern than the true *E. perdentatus* ("marbled" versus "spotted"), and also a number of small morphological differences. A population genetics study was performed on these two species, using COI data and 16 microsatellite loci. Populations from the main regions sampled (Peninsula, Eastern Weddell Sea, Adélie Coast, Tressler Bank) were found to be significantly differentiated. Finer-scale genetic structure was found between populations from two Peninsula stations of the "marbled" species, whereas all "spotted" specimens from the Peninsula appeared panmictic, which could indicate behavioral or ecological differences between the two species. Additional population genetics analyses are ongoing.

Crinoids:

82 specimens have been genotyped. Morphological identification has been checked against reference sequences in BOLD and GenBank. Some discrepancies need to be considered into more details. However, we discovered at least one new species of *Pentametrocrinus* and one of Thalassometridae. It is possible that other specimens belong to new species.

Sea stars:

Asteroids from various collections have been barcoded and identified. Two sets of COI sequences from specimens belonging to these collections are now in the public domain: ANDEEP3, ANDEEP-SYSTCO (190 specimens) and Tristan da Cunha - Terra Nova Bay (95 specimens) and openly accessible through BOLD. 700 COI sequences have been collected and the specimens have all been identified by Christopher Mah (Smithsonian Institution). We will use these to compare morphological grouping to molecular clusters. COI sequences have been aligned and a preliminary analysis has been initiated. Species delineation methods ABGD and GMYC have been explored. A total of 1300 sequences are currently available. Targeted species will be studied into more details (morphology and use of nuclear markers) to better understand the presence of several distinct clades within each of them, in the framework of the RECTO project.

Sea urchins:

About a hundred samples representatives of almost all Antarctic and sub-Antarctic schizasterid species could be sequenced (A. Chenuil), specimens being thoroughly identified at species level based on morphological evidences accepted so far in taxonomy (T. Saucède). Most of the studied specimens were collected during cruises PS81 and CEAMARC. Works are in progress and final phylogenetic results are expected by the end of summer 2017. This brand-new phylogeny of schizasterid sea urchins will be of important because it will very likely question the present-day systematics of schizasterids, preliminary results suggesting that most genera are paraphyletic. Such results will have many outcomes regarding macroecology, biogeography and evolutionary scenarios of sea urchin diversification in the Southern Ocean.

Fish:

Genotyping of 528 fish (including some replicates for error estimation) has been concluded (in regard to sequencing) or is in progress (in regard to bioinformatics/biostatistics). Subtle genetic differentiation was observed in species with a mobile and long pelagic larval duration – a pattern not discernible with traditional (low throughput) sequencing methods. These results are soon to be submitted for publication (*Notothenia coriiceps*). Similar analyses are in progress for *Notothenia rossii* and five species of Trematomus. These will also be complemented with individual-based oceanographic dispersal modeling. Raw reads from reduced representation sequencing is or will be available at NCBIs short read archive. DNA barcoding data is available from the Barcode of Life Data Systems (BOLD) repository.

WP 1.4. *Community analysis of patterns. Responsible: RBINS, KU Leuven, UGent, ULB (UB)*

Nematodes:

During the ANT-XXVII/3 cruise, additional samples were collected at the same locations as those for molecular analysis to look at community dynamics of nematodes (both at genus and species level). For this, random subsets of nematodes from each sample were first identified to genus, and later to species level. Again, sampling was hierarchical, to be able to gather information at various spatial scales. Turnover patterns at three different spatial levels (within multicorer cores, between multicorer cores of the same deployment, and between sampling locations) were assessed by beta-diversity partitioning and linked to environmental data collected at the same spatial resolution. We repeated the sampling of soft sediment macrofauna at three investigated sites within Potter Cove (King George Island, WAP) for the understanding of temporal patterns in the community (November 2015 – March 2016). These samples offer a within-year seasonal analysis and comparing them with the samples from 2011, we can observe potential temporal patterns in relation to the ongoing changes. We also carried out a ROV exploration in Potter Cove and Marian Cove during the past sampling campaign in the area. We compared the two adjacent fjords where we find very different environmental processes happening and structuring the communities.

Sea stars:

Using the occurrence database (see above, section 1.1), we analyzed sea stars biogeographical patterns in the Southern Ocean (SO) and tested whether reproductive strategy (brooder *vs.* broadcaster) is a life-history trait that can explain the distribution patterns we observe for the entire class. Patterns were explored and compared to previous results obtained from other marine invertebrates. The analyses were carried out using complementary methods: Bootstrapped Spanning Network (BSN) and multivariate analyses (nMDS and clustering) to analyze the spatial structure of faunal similarities amongst 25 distinct bioregions. The main biogeographical patterns were congruent with results from previous studies based on other taxa and highlight isolation of New Zealand from other regions of the SO, high richness in the Scotia Arc area and particularly of brooding species, East West-Antarctica differentiation and faunal affinities between South America and sub-Antarctic Islands. In contrast, asteroids showed lower endemism level than previously reported, 29% of species occurring only in Antarctica. Asteroids from Tierra Del Fuego turned out to show affinities with those of West-Antarctica at species level suggesting a recent mixing of assemblages. We found that asteroids biogeographic patterns are highly linked to species reproductive strategy. Patterns also differed according to taxonomic level considered, revealing the role of historical factors.

WP 2: Trophic Ecology

WP 2.1. *Measurement of carbon fluxes associated to different primary producers (= in situ experiment)(+ link to WP integrated modelling and interoperability). Responsible: VUB*

The VUB partner investigated the carbon, nitrogen pools uptake rates and isotopic composition of nitrate in sea ice for three land fast ice (i.e., attached to the shore) locations in East Antarctica (Figure 1): Terre Adélie (REVOLTA expedition; Dumont D’Urville), Prydz Bay (Davis station) and Ross Sea (YROSIAE expedition; Scott Base).

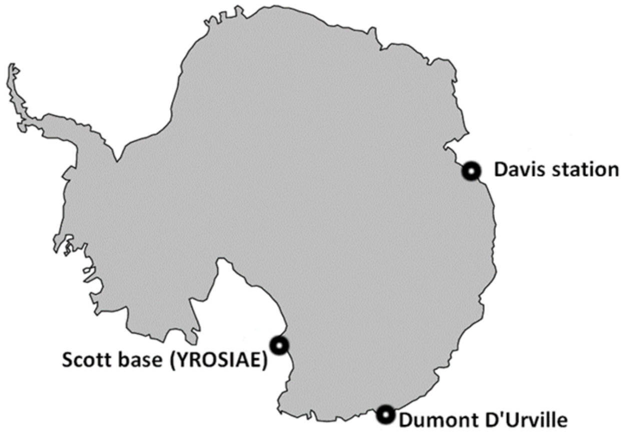


Figure 1: Sampling took place at Davis Station (Prydz Bay) during the austral spring of 2015 (Oct. 27th – Dec. 11th) and at Dumont D’Urville Station (Terre Adélie) on January 4th. The dataset from Davis Station was extended with field measurements from Scott Base (Ross Sea) sampled between Sept. 19 and Nov. 30, 2012 during the YROSIAE campaign. The latter data set spans the full growth season.

Dumont D'Urville Station

An *in-situ* sea-ice uptake experiment was carried out in the framework of the 2014-2015 Terre Adélie expedition (REVOLTA) led by Loïc Michel (ULg) with the help of Philippe Dubois (ULB). Ice cores were taken near the Dumont d'Urville station, to gather data on salinity, temperature, particulate matter content, nutrient content, nitrate isotopic composition, dissolved gases. For C, N uptake experiments, samples of the bottom layer of sea ice and underlying water column (taken by divers) were spiked with 13C and 15N (nitrate, ammonium) substrates and incubated for 6 hours in-situ. Samples have been returned to VUB for analysis. The presence of divers at DDU allowed us to carry out incubation experiments under the ice without disturbing the snow cover, which has a significant impact on the light levels below the ice. At a single occasion (4th Jan 2015) the ice was sampled for background parameters (salinity, temperature, nutrients, particulate matter). Samples of underlying seawater were taken at two depths by divers. The bottom layer of the ice was sampled from above by ice coring (sampling for algae trapped in the ice) and below by divers (sampling of filamentous algae, suspended in water). The collected samples were processed and spiked with stable isotope tracers (^{13}C, ^{15}N) and incubated in-situ for 6h. Primary production was highest in the bottom of the ice (6.7 µmol/L/d) whereas carbon uptake in the water column under the ice was very low. Integrated carbon uptake was 1.9 µmol/m^2/d of which one third was focused in the bottom 10cm of the sea ice (0.67 µmol/m^2/d) making it an ideal feeding ground for higher tropic levels. Nitrogen uptake rates were highest in the bottom of the ice. Ammonium was preferred over nitrate as the main nitrogen source. This could indicate that the sea ice algae bloom was already in an advanced stage with more regenerated primary production and less new production. As observed for carbon uptake of N in the underlying water column was low.

Davis station (Prydz Bay)

During Austral spring of 2015 (Oct. 27th – Dec. 11th) the VUB team contributed to field work on fast ice at the Australian Davis station, Prydz Bay (68°34.0' S, 77°56.4' E). Focus was on the nitrogen and carbon cycle and the pivotal role of sea-ice algae. On 6 occasions during the one-month period at site, sea ice cores were taken for the measurement of inorganic nutrients, particulate matter (POC and PN) and stable isotope compositions. To allow a better interpretation of the results these were combined with those obtained for a longer time series, sampled earlier nearby Scott Base (New Zealand permanent Antarctic research station) during the Year-Round survey of Ocean-Sea Ice-Atmosphere Exchanges (YROSIAE).

Scott Base (Ross Sea, YROSIAE)

This campaign consisted of two legs: the first one from October 10 to December 24, 2011 and the second one during from September 19 to November 30, 2012. Ice cores were collected on 12 occasions about 1 km off Cape Evans (Main site: 77°38' S, 166°23' E). Work was done in collaboration with T. Haskell (Industrial Research Limited), P. Langhorne (University of Otago) and Antarctica New Zealand.

Physical setting at Davis Station

Sea ice thickness was relatively constant during the one-month sampling period at Davis, with an average thickness of 158 cm (S.D. = 5 cm). Temperature profiles (Figure 22) showed low values (-6 to -5 °C) at the surface during the first three sampling stations (DOY 320-326). Starting from DOY 330 there was a gradual increase in sea ice temperature and by day 336 isothermal conditions (> -3 °C) prevailed. Salinity profiles had a typical C-shape with high salinities in the surface and bottom parts of the ice. Surface salinities ranged from 5 to 9, while the internal ice salinity was between 4 and 5. Bottom ice salinities were the highest with values between 8 and 13. Rayleigh numbers indicated a gradual increase in the convection potential at the ice surface. A maximal value of 5 was reached at station 5 (DOY 333), though this remained below the critical threshold value of 10 (Notz and Worster 2009). The observed increase and subsequent decrease in Rayleigh numbers might still indicate that full ice convection took place.

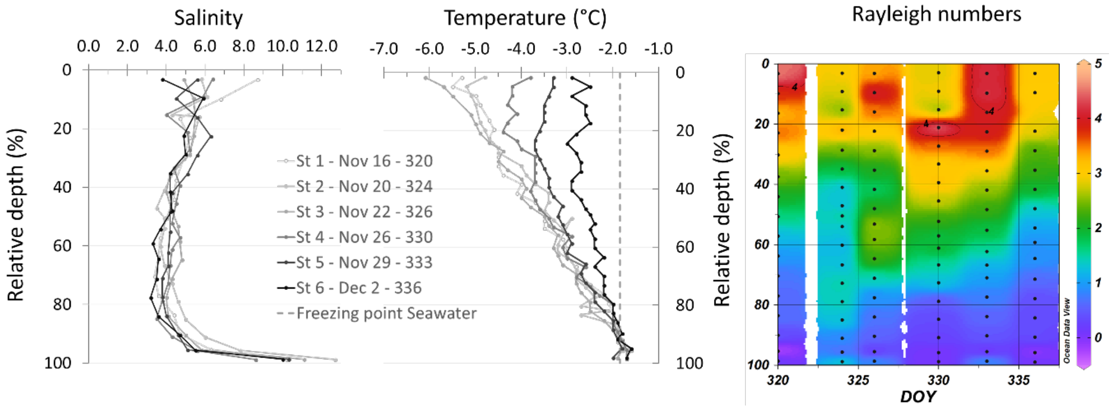


Figure 2: Physical parameters for fast ice at Davis Station. Salinity; temperature (°C); Rayleigh numbers. Salinity remained rather constant during the sampling period. An increase in air temperature resulted in warming of the ice. A maximum in Rayleigh number (4.5) indicates an increase in convection potential toward the end of spring.

Although sampling at Davis station only covered a one-month period, it captured a transition in sea ice temperature that initiated the start of bottom ice melt. By day 336 the bottom ice was clearly melting and the skeletal layer was lost (Figure 3). A drastic change in bottom ice biomass concentration was observed between station 5 (DOY 333) and 6 (DOY 336). Figure 3 reveals that the bottom 3 cm of ice lost a substantial part of biomass while a deeper layer of algae was still fixed in the ice.

Figure 3: Upside down picture of bottom ice at Davis Station. Algal biomass was concentrated in the bottom 4 cm of the ice. Towards the end of the sampling period, algae closer to the ice/water interface where lost due to bottom ice melt, while deeper in the ice algae remained trapped.

Biogeochemical parameters (Davis station & YROSIAE)

Results for different biogeochemical parameters are as expected for fast ice in spring and are shown in combination with the older results from YROSIAE (2012; Scott Base, Ross Sea) which cover a longer time series (Figure 4). At Davis Station, particulate organic carbon (POC) and particulate nitrogen (PN) were high, ranging between 500-1500 µM and 75-200 µM, respectively. Salinity normalised nitrate concentrations were very high, ranging from 50 to 200 µM, thus well above seawater concentrations (30 µM). Also, normalised phosphate concentrations were above the seawater level of 2 µM. Ammonium concentrations ranged between 2 and 8 µM and exceeded those in seawater (< 1µM). Normalised silicic acid concentrations ranged between 10 and 70 µM. Such concentrations, though lower than those in seawater (84 µM), still reflect silicic acid repleteness.

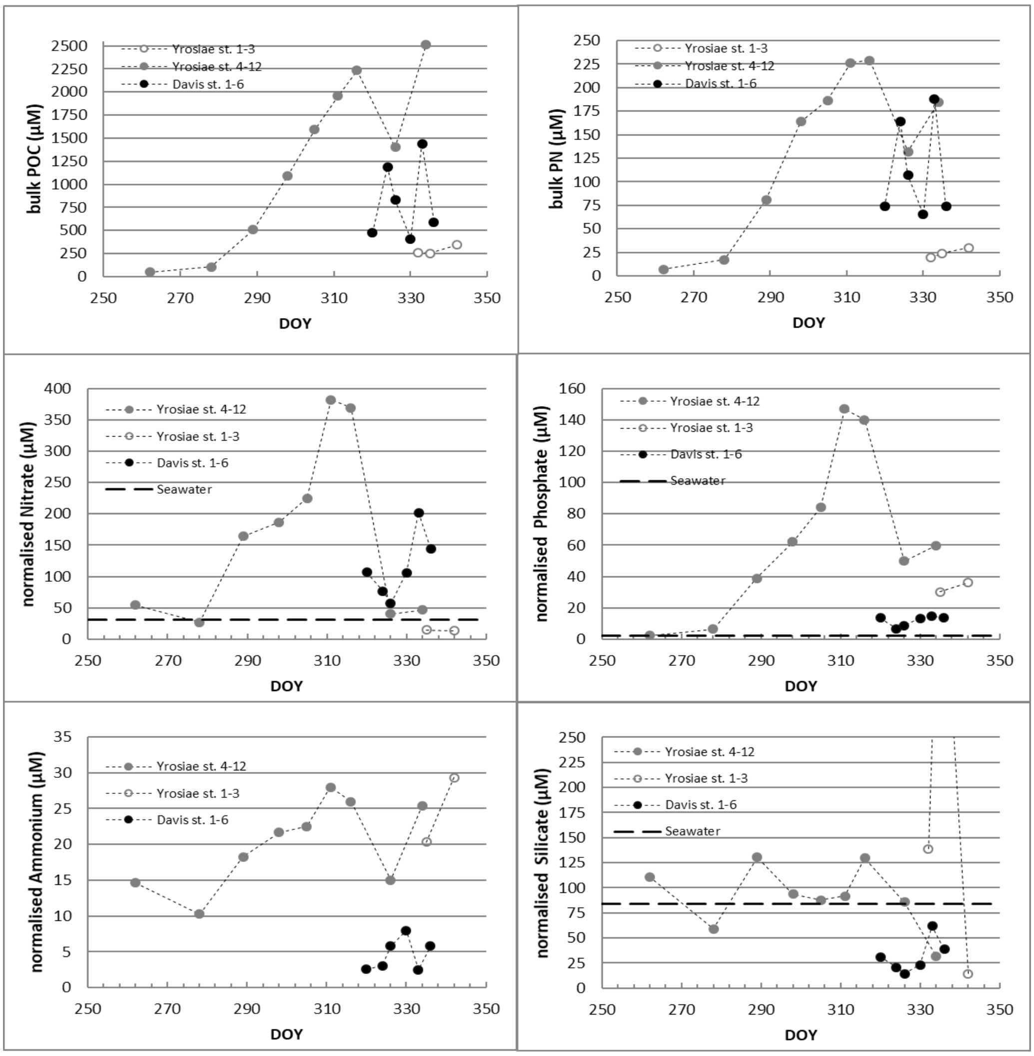


Figure 4: Biogeochemical parameters at Davis Station and Scott Base (YROSIAE). Bulk particulate organic carbon (POC) and particultate nitrogen (PN). Normalised nutrient

concentrations for nitrate, phosphate, ammonium and silicic acid. Dotted lines are the concentrations in the underlying seawater.

Dual N, O isotope signatures for nitrate at Davis and YROSIAE are shown in Figure 5 and 6. Isotope signals for N and O of seawater nitrate were constant at 5.1 - 5.3 ‰ (S.D. = 0.1 ‰) and 2.05 - 2.2 ‰ (S.D. = 0.3 ‰), respectively. This is in the range of published values for the Southern Ocean (DiFiore et al. 2009; Rafter et al. 2013). Results for bottom ice were similar at Davis Station and Scott Base, with $\delta^{15}N$-NO_3 values ranging between 17 and 25 ‰. For $\delta^{18}O$-NO_3 values ranged between 14 and 25 ‰. There was a seasonal evolution with lower values of 10.8 ‰ at DOY 262, but as soon as nitrate started to increase in the ice, $\delta^{15}N$-NO_3^- values increased also to remain around 20 ‰ till DOY 310, and to increase again till 25 ‰ after DOY 330.

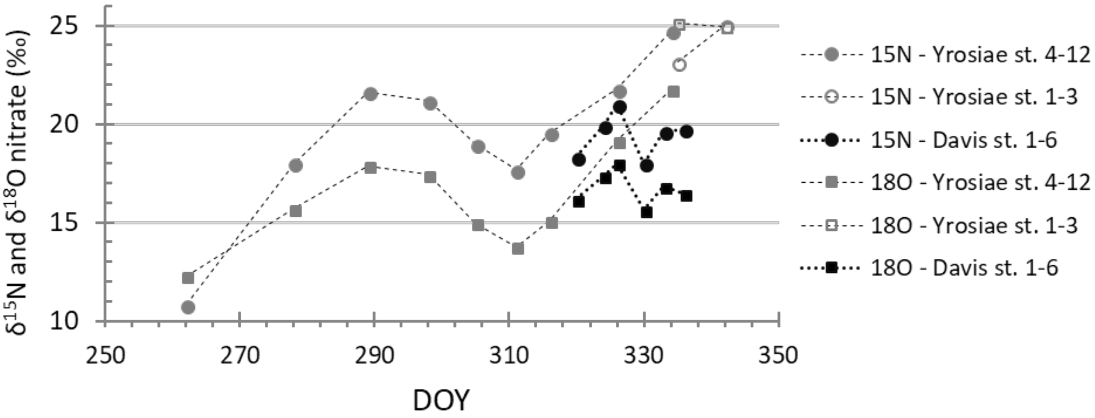


Figure 5: Temporal evolution of nitrate isotopic signatures in bottom ice at Davis Station (black symbols) and Scott Base (YROSIAE; grey and white symbols). Circles = $\delta^{15}N$-NO_3; squares = $\delta^{18}O$-NO_3. For N most values are between 17 and 25 ‰ during the bloom. Values for O isotope signatures are slightly lower and vary between 14 and 22 ‰. O and N follow a similar seasonal trend.

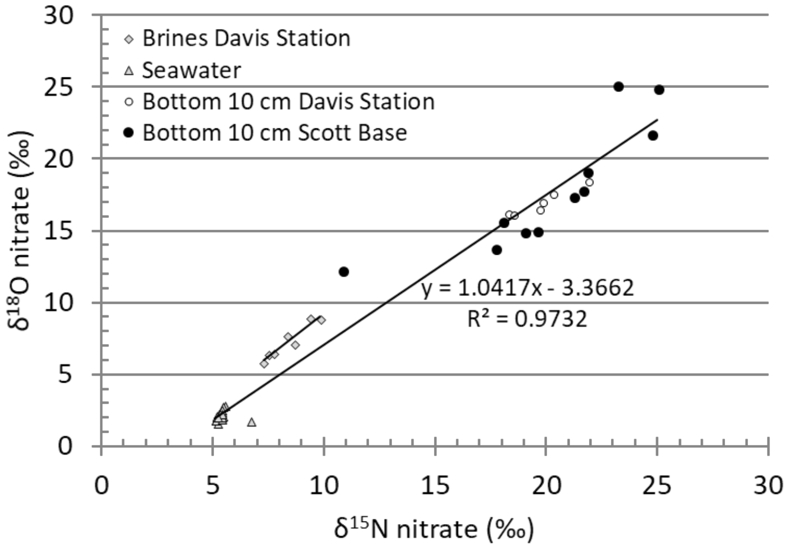


Figure 6: Nitrate isotopic signatures; $\delta^{18}O$-NO_3 (y-axis) vs $\delta^{15}N$-NO_3 (x-axis) for seawater (triangles), brines (diamonds) and bottom sea ice at Scott Base (closed circles) and Davis Station (open circles). The coupling between N and O isotope signatures in nitrate is strong, with samples in bottom sea ice close to a 1:1 slope starting from seawater values. Brine isotope signatures are also coupled but values are slightly higher for oxygen.

In Figure 6, bottom sea ice nitrate $\delta^{18}O$-NO_3 isotope values are plotted vs $\delta^{15}N$-NO_3. Data points fall on a 1:1 slope, reflecting the fact that isotope discriminations (ε) for N and O are similar (i.e., 15ε = 18ε). The graph shows the significant isotope enrichment of the sea ice nitrate relative to seawater nitrate (Figure 6).

Uptake experiments

Primary production (PP) and N- uptake rates were measured by adding stable isotope tracers (^{13}C-bicarbonate; ^{15}N-NO_3, ^{15}N-NH_4) to crushed sea ice samples taken from the internal and the bottom part of the ice cores. These crushed ice samples were inserted in polycarbonate bottles and placed back in situ. Samples were left to incubate for 6h (DDU) or 24h (Davis Station). Stable isotope enrichments and POC concentrations were measured using an elemental analyser isotope ratio mass spectrometer (EA-IRMS) and results used to calculate the rate of carbon incorporation. More details about the method can be found in Roukaerts et al. (2016).

At Davis station carbon uptake rates reached between 0.1 and 4 µmol C L^{-1} d^{-1} (Figure 7). The highest rate (4 µmol C L^{-1} $d^{-1)}$ was reached in the bottom ice layer on November 29th and coincided with the highest POC concentration (1310 µM). C-uptake for internal ice (at about 1 m depth in the ice) never exceeded 0.2 µmol C L^{-1} d^{-1} and POC concentration remained below 100 µM.

At Dumont D'Urville C-uptake rates on January 4th were in the same range as for Davis. reaching 3 µmol C L^{-1} d^{-1} in the bottom ice section at 2 m depth (

Figure 8a). Just below the sea ice, at the top of the underlying water column, carbon uptake was already < 1 µmol C L^{-1} d^{-1} and decreased further with increasing depth in the water column. C-uptake in bottom sea ice was quite variable between the two duplicates (1.2 and 5.1 µmol C L^{-1} d^{-1}). Nitrogen uptake (

Figure 8b) was highest in bottom ice (45 nmol N L^{-1} d^{-1}) and decreased with depth in the underlying water column. In the ice, uptake rates of nitrate and ammonium were similar, while just below the ice ammonium was the main nitrogen source.

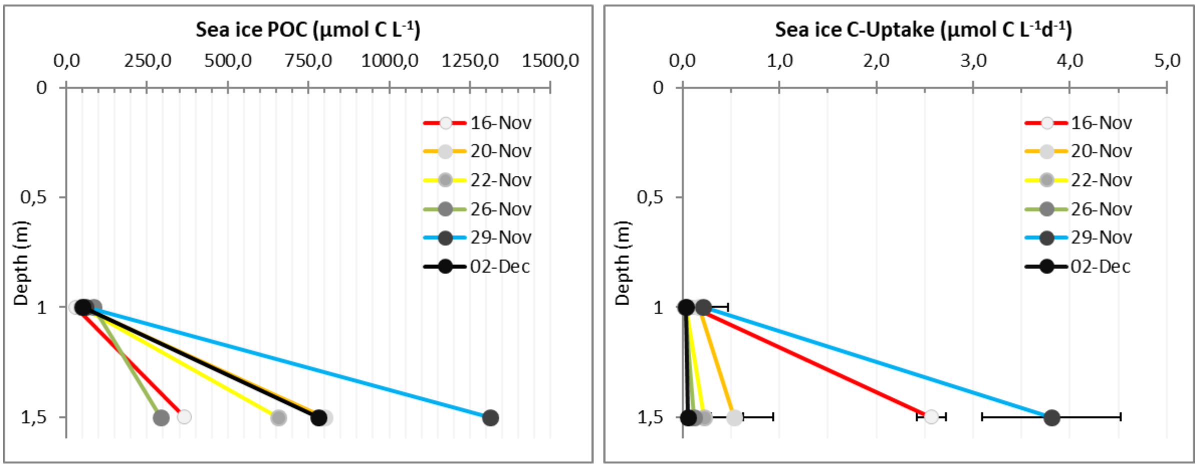


*Figure 7: **a** Particulate organic carbon concentration (µM) at Davis Station for internal ice and bottom ice. **b** Primary production rates (µmol C L^{-1} d^{-1}).*

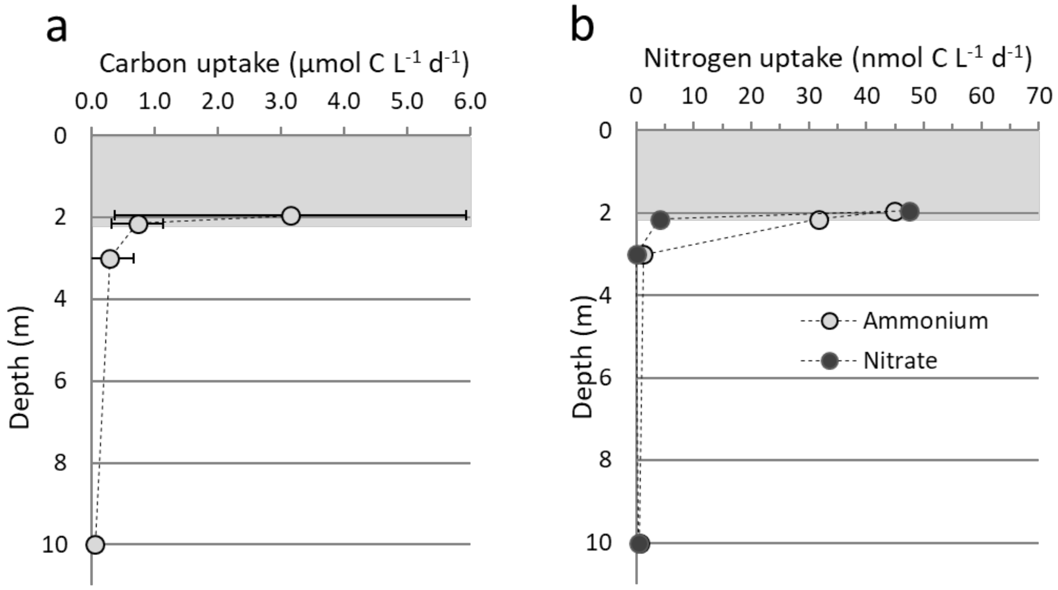


*Figure 8: DDU. Results for incubations in bottom sea ice, in the surface water at the ice/water interface and in the underlying water colmun at 3 and 10m depth. **a:** Primary*

*production rates (µmol C L^{-1} d^{-1}); **b:** Nitrate uptake rates (nmol N L^{-1} d^{-1}) and Ammonium uptake rates (nmol N L^{-1} d^{-1}).*

Discussion

Sea ice nutrient concentrations exceeding those in underlying seawater indicate there was significant remineralisation of organic matter within the sea ice. Although the time series at Davis Station did not cover the start of the bloom, previous results from Scott Base (YROSIAE) do show that the increase of inorganic nutrients in sea ice is synchronous with biomass increase. This observation implies a decoupling in the nitrogen cycle with regenerated nutrients accumulating and not directly accessible for primary producers. A spatial decoupling in the bottom 10 cm of the ice is thus required (**Error! Reference source not found.**).

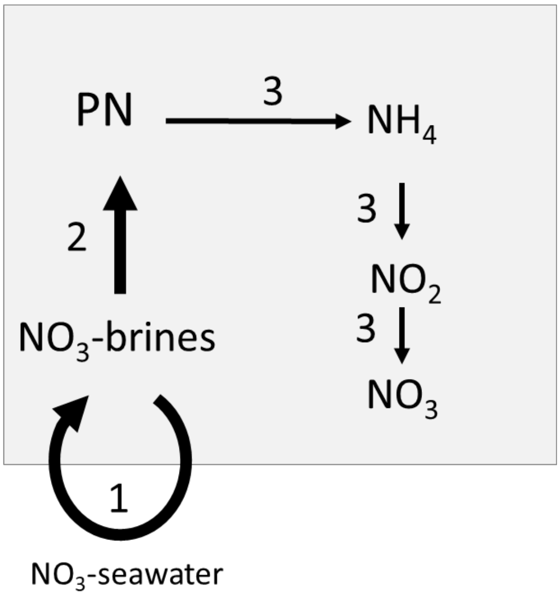


Figure 9: Simplified nitrogen cycle for sea ice with spatial decoupling between the processes of uptake and remineralisation. Arrow 1: exchange between seawater and brines (convection and diffusion). Arrow 2: assimilation of nitrate by photosynthetic algae (PN). Arrow 3: remineralisation of organic matter (PN) and release of nitrate. To reach high biomass concentrations nutrients are brought into the brines and consumed by algae, pumping nitrogen into the ice. Part of this biomass is remineralised, with the resulting nitrate being no longer directly accessible for autotrophic growth. Nitrate concentrations can then increase to exceed those observed in seawater. Remineralisation (arrow 3) needs to be smaller than assimilation (arrow 2) for biomass to increase further.

NPZD-modelling showed that the presence of a biofilm is required to explain the coupled increase of both biomass and nutrients. This biofilm would allow the formation of micro-environments, allowing contrasting processes to take place in close proximity of each other. In case remineralisation of organic matter within the ice is high, the presence of a biofilm could even sustain low oxygen zones. Although the sampling period at Davis Station was too short to verify this, it is likely that the presence of a microbial biofilm might also have affected the biogeochemistry at this location. At first sight the strong coupling of nitrate N and O isotope signatures (Figure 6) suggests a consumption process such as assimilation. However, the very high nitrate concentrations indicate that release of nitrate via nitrification must be significant (Fripiat et al. 2014). Considering fractionation factors reported in literature (Fripiat et al. 2015), a combination of assimilation and nitrification can increase the isotope signature significantly, in agreement with observed $\delta^{15}N\text{-}NO_3^-$ values reaching from 6 to 22.6 ‰. At Scott Base and Davis Station $\delta^{15}N\text{-}NO_3^-$ values mostly fall within this range, with some YROSIAE samples showing even slightly higher $\delta^{15}N\text{-}NO_3^-$ values (25 ‰). However, for $\delta^{18}O\text{-}NO_3^-$ the combined assimilation and nitrification would yield a range of 4 – 11 ‰ which is lower than observed at Scott Base and Davis Station where $\delta^{18}O\text{-}NO_3^-$ values ranged between 15 and 22 ‰. A second process that may play a role is denitrification. As for assimilation, denitrification will also increase the nitrate N, O isotope signatures keeping a 1:1 relation ($15\varepsilon = 18\varepsilon$) but the isotope fractionation of denitrification is significantly larger than for assimilation. It varies between 20 and 30 ‰ (Voss et al. 2001; Naqvi et al. 2006; Wunderlich et al. 2012; Frey et al. 2014) compared to the 5 - 10 ‰ observed for assimilation (Difiore et al. 2010). This means that for a similar loss of nitrate, the isotope signature of the remaining nitrate will increase more in case of denitrification (Dähnke and Thamdrup 2013). A priori denitrification is not a process that is expected in the 'net' oxygenated bottom sea ice since an important condition for denitrification to take place is lack of oxygen. However, such anoxic zones could be present in the ice if we consider the presence of biofilm that hosts micro-environments.

Primary production measurements at Davis Station and Dumont D'Urville ranged between 0.1 and 4 µmol C L^{-1} d^{-1}, equivalent to 1.2 and 4.8 mg C m^{-2} d^{-1}, respectively. Data on sea ice primary production in literature are scarce and show large seasonal and spatial variability. For bottom fast ice at McMurdo Sound in spring, Grossi et al. (1987) reported values between 0.5 and 84 mg C m^{-2} d^{-1} and Archer et al. (1996) measured values up to 140 mg C m^{-2} d^{-1} for Prydz Bay. Both authors used in situ incubations with ^{14}C-tracers. Using oxygen microelectrodes deployed in situ under the ice at McMurdo Sound Trenerry et al. (2002) report an uptake of 7 to 21 mg C m^{-2} d^{-1} for bottom ice. Our results for DDU and Scott Base do fit with literature data, but they are at the lower end of this rather wide range of values.

A large discrepancy exists between the carbon assimilation rates and POC accumulation. Maximal uptake rates for fast ice at Dumont D'Urville and Davis Station never exceed 5 µmol C L^{-1} d^{-1}. This rate can result in a maximal biomass accumulation of 300 µM POC over a 2-month growth period, while the POC accumulation in bottom ice reached as high 1300 µM. Hence the measured uptake rates from tracer experiments are 4 times lower than suggested by the observed increase in biomass concentrations. Below we overview the possible reasons for this low uptake rates from tracer experiments.

The C-assimilation rates as assessed via incubations following spiking with ^{13}C-tracer include the effect of autotrophic respiration. Uptake rates thus represent net primary production (NPP = Gross production - respiration). Any loss of synthesised POC due to grazing or other heterotrophic activity is considered negligible. On the other hand, the increase of POC content in sea ice over the season would represent net community production (NCP). NCP is the difference between net primary production (NPP) and loss in organic carbon due to grazing and other heterotrophic activity. Although NCP underestimates NPP it can be considered as a good minimal estimate of NPP.

Net Primary Production (NPP) = Gross Primary Production (GPP) – Respiration

Net Community Production (NCP) = Net Primary Production (NPP) – Heterotrophic activity – Grazing

Assuming POC content at Davis Station starts increasing in early spring, the observed maximal value of 1300 µM POC had accumulated over a two-month period. Assuming a constant primary production rate during this 2-month period, NCP would need to be at least 21 µmol C L^{-1} d^{-1}. NPP results obtained via incubation experiments are < 4 µmol C L^{-1} d^{-1} , so clearly much lower than NCP. For the tracer addition incubation experiments the aimed at ^{13}C-enrichment of the bicarbonate substrate was 10 %. In case diffusion of the tracer into the brine channels where the algae thrive is slow, the true ^{13}C-DIC enrichment experienced by the algae will be lower than the bulk enrichment value (10 %) used to calculate the C-uptake rate. As a result, the true carbon uptake rate will in fact be higher than the calculated one. For instance, if we consider that the true ^{13}C enrichment was between 5 % and 1.5 % (instead of 10%) the NPP rates would be 20-35 µmol C L^{-1} d^{-1} and thus slightly exceed the NCP value, as expected. This discrepancy could occur when the added tracers are not well dispersed or are diluted by strong respiration (i.e., DIC release), thus resulting in a large underestimation of primary production.

The presence of a biofilm may also affect the outcome of the incubation experiments. The diffusion of the tracer into a biofilm might be slow in comparison with the duration of the incubation experiment (6 to 24 h). If this is the case, a concentration gradient over the biofilm can develop resulting in a non-homogenous tracer distribution, with lower enrichment in the biofilm, where the autotrophic growth takes place (Figure 10). In case a microbial biofilm is present in the ice and affects the diffusion of added tracers, tracer incubations might not be the best approach for quantifying primary production. In this case calculating NCP, based on POC accumulation over time, might be the best approach to obtain a minimal estimate for sea ice primary production. However, this approach requires long periods of observation (full season), which is rarely possible because of logistic constraints.

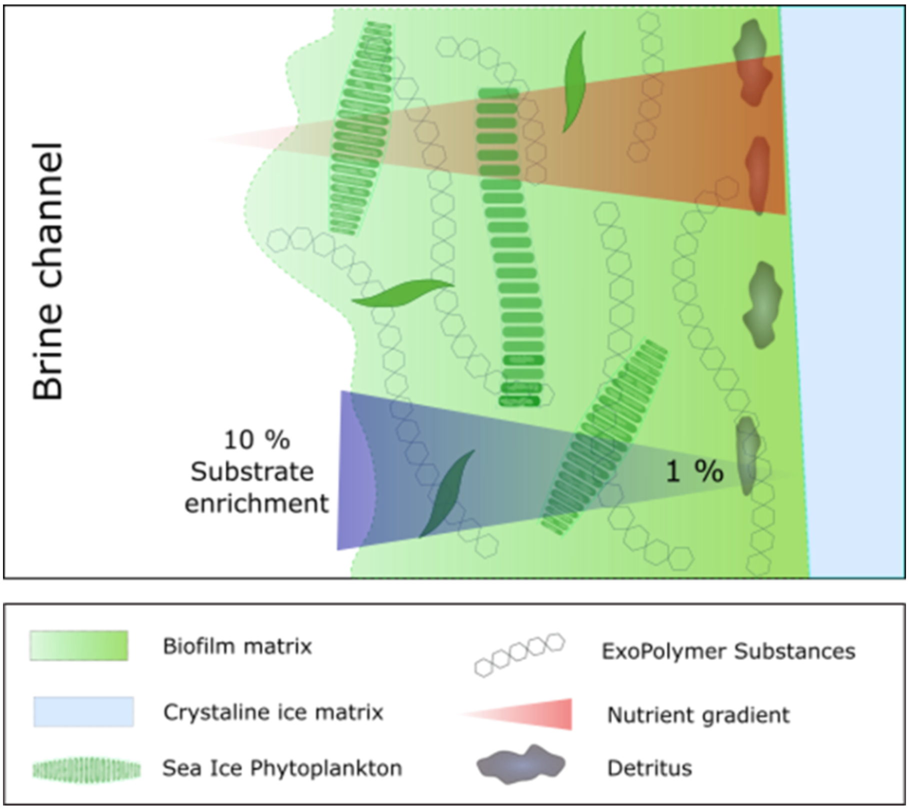


Figure 10: Schematic view of a biofilm in sea ice. A network of exopolymer substances forms a biofilm in which algae grow. Nutrients are supplied from the underlying seawater through the brine channels and are consumed by sea ice algae. Recycling of organic detritus generates inorganic nutrients such as nitrate and phosphate that are trapped in the biofilm as they are produced faster than their diffusion out of the biofilm. A stable isotope spike would easily disperse in the liquid brines but its diffusion into the biofilm could be slow. In this case, the enrichment in the biofilm would not reach the 10 % enrichment within the timeframe of the incubation.

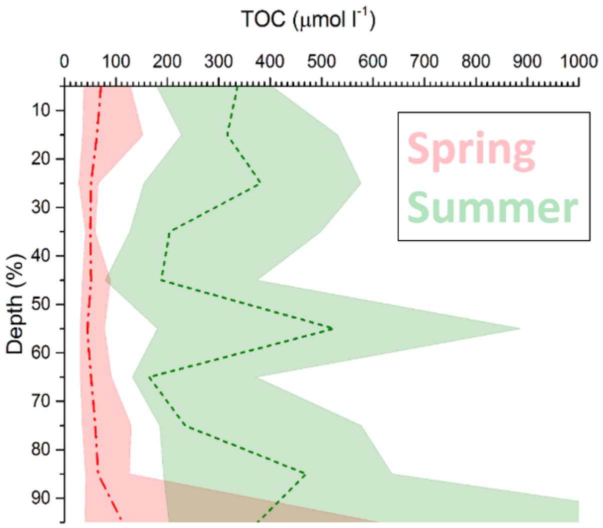
A further possible cause of underestimation primary production using ^{13}C-labelled HCO_3^- might be related with uptake of dissolved organic carbon (DOC) as a source of carbon, either directly or indirectly underestimating primary production. The direct assimilation of DOC (mixothropy) has been reported for flagellates and ciliates (Mitra et al. 2014) but is not assessed when using labelled dissolved inorganic carbon (DIC) tracers in incubation experiments. Also, indirect DOC assimilation might occur, with DOC being remineralised to DIC which dilutes the added $H^{13}CO_3$ isotope tracer. With true enrichment being lower than assumed enrichment used for calculation of uptake rate, the latter will be lower than the true uptake rate (see discussion above). While DOC could also explain the underestimations observed, it requires presence of large amounts of DOC in the ice or a large transport of DOC into the ice from the underlying seawater. To explain the observed discrepancy, at least 1000 µM of the carbon biomass increase at Davis needs to be sustained by DOC assimilation. This DOC needs to be present in the ice before spring (before the bloom) or must be supplied from the underlying seawater. DOC levels up to 1300 µmol C L^{-1} were observed in Antarctic sea ice but these appear to be highly related to particulate biomass and the annual bloom in spring fast ice (Cozzi 2008). A similar observation was done by

Paterson and Laybourn-Parry (2012) reporting DOC concentrations reaching 1050 µmol C L^{-1} by Oct-Nov. No large sea ice DOC pool has been observed during winter, serving as a major carbon source at the onset of the spring bloom. Large DOC concentrations are only observed later in the growth season and are more likely the result of high biomass concentrations, rather than supporting high biomass accumulation. Although DOC trapped in the sea ice can be a carbon source for algal growth, it is unlikely to support a large fraction of the biomass accumulation in spring.

Estimation of ice algae production (NCP) from POC accumulation

As stated above calculating sea ice NCP from organic carbon accumulation over time, may be the best way for estimating primary production and for comparing PP of different sea ice environments. Biomass growth in fast ice is relatively homogeneous and grazing is limited. The down side is that long time series are needed, and heterotrophic activity is not accounted for. Also, this approach is not an option for short term pack ice sampling experiments. However, by mining a large dataset and thereby averaging out spatial variability, a net community production could be calculated for Antarctic pack-ice. In the framework of SCOR working group BEPSII (Biogeochemical Exchange Processes at Sea Ice Interfaces) we compiled historical data for total organic carbon content (TOC) available for some 3000 ice core sections from more than 25 different Antarctic expeditions. The aim is to estimate the primary production for a one-year period (Figure 11) and assess its contribution to primary production of the Seasonal Ice Zone (SIZ) and the whole Southern Ocean. The outcome will be compared with results from sea ice biogeochemical models (i.e., Saenz and Arrigo, 2014). Preliminary results show that NCP of Antarctic sea ice reaches 35.3 Tg C y^{-1} and represents around 20 % of the primary production of the ice-free SIZ (180 Tg C y^{-1}; Saenz and Arrigo, 2014). Such results are in good agreement with previous estimations based on sea ice biogeochemical models (23.7 Tg C y^{-1}; Saenz and Arrigo, 2014) but are lower than a previous estimation by Legendre et al. (1992) which, ranged from 63 to 70 Tg C y^{-1}.

Based on our results for land fast-ice from Davis Station and Scott Base (YROSIAE), integrated POC content amounts of 250 to 300 mmol C m^{-2} in summer. This amount of carbon can potential fuel pelagic and/or benthic communities when released during sea ice melting and can be traced because of its distinct isotopic composition (with δ^{13}C-POC ranging from -19‰ to -12‰ in bottom of fast ice, Davis Station)



	Spring	**Summer**	
[TOC] *(µmol L^{-1})*	*63*	*320*	*Our preliminary study*
Ice thickness *(m)*	*0.81*	*1.17*	*(Saenz and Arrigo 2014)*
Ice extent Impacted *(x10^6 km^2)*	*10*	*6.5*	*(Worby et al. 2008)*
Net community production *(Tg C y^{-1})*	*6.12*	*29.20*	***Sum: 35.32***

PP in the SIZ (Tg C y^{-1}) (Saenz and Arrigo 2014)	***180***	***(19.6 %)***
PP in whole Southern Ocean (Tg C y^{-1}) (Saenz and Arrigo 2014)	***1949***	***(1.8 %)***

Figure 11: Preliminary results of NCP based on the accumulation of TOC in sea ice over the growth season. Top figure: median relative profiles returned from the historical data compilation, with the lines representing the median values and the shaded areas defining the 25-75% intervals. Table: first calculations of NCP based on the TOC accumulation, the ice thickness and the ice extent. Estimates of primary production for the SIZ and Southern Ocean are indicated, with values in brackets representing the relative contributions (%) of sea ice NCP.

Potter Cove (King George Island):

To investigate the effects of glacier retreat on biogeochemical cycling at the sediment-water interface of three shallow sites within Potter Cove (WAP) with similar granulometric characteristics, but different time since glacier retreat (10-25-50 years). We performed three deployments during summer (February 2015), two during winter (September 2015) and again three in spring (December 2015), in order to cover all seasons in one year. At these three sites, we deployed by scuba diving a total of 6 benthic chambers and took water samples to measure the fluxes of oxygen, inorganic carbon, nutrients, sulfide and sulfate and manganese and iron at the sediment-water interface. Three dark chambers allowed only respiration, three transparent chambers included both respiration and benthic primary production. Afterwards, the sediment was characterized in terms of granulometry, organic carbon and nitrogen content, pigment concentration and microphytobenthic, microbial, meiofauna (by means of sediment cores) and macrofaunal abundance (sampling by Van Veen grabs) and community structure. Light and temperature were logged continuously during these 20h incubations. We repeated the last deployment this past spring December 2015. During the summer 2015 (February) an automated profiler was deployed at the sea floor and high-resolution profiles of oxygen, pH and H_2S were measured in the upper sediment layers to calculate diffusive oxygen uptake and sulfide fluxes. We also initiated the processing of the samples gathered from the previous campaign laboratory experiment on ^{13}C pre-labelled macroalgae degradation by meio- and macrofauna.

In November 2016, we deployed benthic chambers and an automated profiler with the aim to estimate soft sediment benthic assemblages energy fluxes and contribution to the overall food web. The samples from the *in situ* Benthic Chambers Deployment (Feb 15, Sep 15 and Dec 15) at the three contrasting sites (9 m depth) within Potter Cove have been processed during the past year for soft benthic organisms (prokaryotes, meiofauna, macrofauna) standing stocks (Fig. 1), sediment characteristics (sediment granulometry and pigments) and energy fluxes (total oxygen uptake, diffusive oxygen uptake, nutrient cycling). Preliminary results showed that the soft sediment communities do display a remineralisation potential comparable to that of temperate regions with fauna mediated uptake being high and mostly driven by the larger macrofauna.

During the past year we also processed the samples from the macroalgae degradation experiment during which we gave pre-labelled (^{13}C) macroalgae detritus (two differently palatable species, *Palmaria* and *Desmarestia*) to soft sediment assemblages in a microcosm setup (enclosed Plexiglas cores). We followed the path of carbon through the food web from sediment prokaryotes to meiofauna and finally macrofauna. From preliminary results we can state that macroalgae do enter the food web via prokaryotic reworking, although it seems that after 20 days only a limited amount of the initially given carbon is taken up as bacterial biomass (about 8%). Fauna samples are yet to be analyzed but they are being processed.

Finally, during the last Antarctic campaign at Potter Cove (November 2016), an experiment on microphytobenhtos has been carried out where benthic microalgae primary production (Oxygen production) were measured exposing in situ sampled sediment to different light regimes and oxygen production was measured. Samples and data are still being processed.

WP 2.2. *Delineation of general food web interactions in the benthic compartment (meiofauna, echinoderms, amphipods, fish) (in situ sampling – experiment). Responsible: UGent, ULg, VUB, ULB*

Terre Adélie:

During reporting year 2014-2015, ULiège carried out joint fieldwork with ULB at the Dumont-d'Urville research station (French Polar Institute - IPEV), in the framework of our collaboration with the French National Museum of Natural History (MNHN - REVOLTA research program). This campaign gave us an unique opportunity to understand ecological implications of sea ice cover increase. Indeed, we studied benthic food web structure on the coasts of Adélie Land during an event of unusually high sea ice cover (i.e. two successive austral summers without seasonal breakup). Over 20 dives and several bait trapping operations were performed, allowing collection of >700 samples, including 28 consumer taxa as well as most potential food items for benthic consumers. All samples have been analyzed for elemental content and stable isotope ratios of C, N and S. This data was used to build two ecological models: a mixing model aiming to identify which food items supported populations of consumers (horizontal structure of the food web) and a trophic position model (vertical structure of the food web). The mixing model clearly indicated that many taxa relied predominantly on sea ice algae, a finding that markedly differs from literature data about those invertebrates. The other model suggested that trophic position of several consumers was lower than expected, and notably that many omnivores relied directly on primary producers and/or organic matter pools for their nutrition. Moreover, comparison of our results with a smaller sample set collected in the year before makes us confident in the fact that the observed trends are linked with actual changes in invertebrate diets during this peculiar year without seasonal breakup. Overall, our results provide insights about how Antarctic benthic consumers might adapt their feeding habits in response to sudden changes in environmental conditions and trophic resource availability. They also show that local and/or global trends of sea ice increase in Antarctica have the potential to cause drastic changes in food web structure, and therefore to impact benthic communities. Those results have been presented in 6 conferences (cf. list below) and are the object of an article that is currently submitted.

Kerguelen Islands:

In the framework of vERSO and PROTEKER programs (French Polar Institute - IPEV), ULg, ULB and UB are currently taking part in a collaborative effort to delineate food web structure in coastal habitats of Sub Antarctic Kerguelen Islands. These islands harbor complex coastal ecosystems featuring multiple primary producers and contrasted habitats. The aim of the research depicted in this section are 1) to highlight major trophic interactions among macrozoobenthos; 2) to identify primary producers and/or organic matter sources that act as main food items for dominant benthic invertebrates; and 3) to identify which components of the food web might be the most vulnerable to environmental modifications linked with climate change. These objectives will be met by combining gut content examination and use of integrative trophic markers (stable isotope ratios of C, N and S). During the reporting year 2015-2016, a joint field campaign was undertaken by ULB and UB. During this campaign, specimens of sea urchins, ascidians, sea cucumbers, molluscs and macroalgae as well as samples of sediment and suspended particulate organic matter were collected. Samples could be analyzed between February and April 2017 (morphological, isotopic and gut content analyses). Results show contrasting trophic niches and plasticity levels between the species analyzed, highlighting larger isotopic niches and potentially less vulnerable species within omnivorous consumers compared to carnivorous and detrivorous species. In November and December 2016, a joint field campaign was undertaken by UB, ULiège and ULB. ULièges main focus in this campaign was to collect material of dominant benthic consumers and their potential food items to achieve as complete as possible reconstruction of processes ruling food webs in Giant kelp (*Macrocystis pyrifera*) beds of Kerguelen Islands. In total, 10 dives were performed and complemented by direct hand collection operations in the intertidal zone. Over 600 samples were collected, representing around 25 consumer taxa (sponges, gastropods, bivalves, polychaetes, amphipods, isopods, decapods, brittle stars, sea urchins, sea cucumbers and sea stars) and 8 potential food items (6 species of macroalgae, suspended particulate organic matter, and sediment-associated particulate organic matter). Most of them have been analysed for elemental content and stable isotope ratios of C, N and S. Results show that complex trophic interactions take place in Kerguelen Islands' kelp beds, as multiple production pathways support invertebrate consumers. *Macrocystis pyrifera* itself does not seem to be a major contributor to benthic organisms' diet. Conversely, *Ulva* sp., suspended organic matter, and possibly epilithic biofilms seem to be preferentially consumed by both taxa.

Prydz Bay:

Isotope ratios for particulate matter (δ^{15}N-PN, δ^{13}C-POC) were measured in fast ice and the underlying seawater at Davis station. δ^{15}N-PN results for internal ice are between 5 and 15‰, decreasing in bottom ice to values between 0 and 5‰. Concentrations in the underlying seawater were too low to obtain values for δ^{15}N-PN signatures. The δ^{13}C-POC values are close to -27‰ in internal sea ice, increasing progressively in the bottom 30 cm reaching values up to -15‰ in the last 4cm layer. POC in the underlying seawater has a δ^{13}C-value of -24‰ ± 1.9‰. Carbon budget calculations (both mass and isotope signature) are in progress to estimate the export flux of POC from sea ice to underlying seawater.

The isotope signatures for POC and PN depend on the substrate used and the isotope fractionation. Signatures in bottom fast ice are clearly distinct from those observed in the underlying seawater though the substrates are the same (DIC and nitrate). In an open system such as the underlying seawater there is an isotope fractionation for the light isotope during assimilation. As a result, particulate matter (PM) will be lighter than the initial substrate. In a closed system no new substrate is supplied and the isotope signature of the cumulative product will depend of the fraction of substrate remaining. The higher values for δ^{13}C-POC in the bottom ice suggest that this is a semi-closed system with the supply of substrate being limited by diffusion and/or convection. This difference in isotope signature of particulate organic matter between seawater and sea ice can help differentiate the carbon sources that benthic organisms use.

WP 2.3. *Assessment of trophic variability (in situ sampling) and plasticity (lab experiment) of targeted species. Responsible: ULg, ULB (UB), UGent*

Nematodes:

Shallow soft-sediment communities (meiofauna and in benthic macrofauna) of Potter Cove (King George Island) have been investigated in terms of their stable isotopic signature and their food web characteristics in a qualitative (bi-plot δ13C, δ15N values) and quantitative fashion (by means of community metrics and the application of Bayesian based approaches to the Standard Ellipse Distribution).

Amphipods:

Through collaboration with RBINS (Marie Verheye and Cédric d'Udekem d'Acoz), ULg gained access to 248 Antarctic amphipods specimens. These samples originate from RBINS and MNHN collections. Available specimens cover a wide geographic area that encompasses both the Western Antarctic Peninsula area (Drake Passage, Bransfield Strait, and multiple zones of Weddell Sea) and East Antarctica (Adélie Land and Dumont-d'Urville Sea). All specimens belong to the Iphimediidae family. They include 19 species spanning 7 genera, ensuring a broad taxonomical coverage of this family. In order to limit damage caused to specimens, only pleopods are used for C and N stable isotope analysis. . This procedure ensures that analyzed specimens can still be used for morphological studies. Results were explored through isotopic niche modelling. The isotopic niche of the whole amphipod assemblage was wider in WAP than in AL. This was true for both total (proxy of the whole range of resources exploited by animals) and the core (proxy of the most commonly used resources) isotopic niches. The ratio between total and core isotopic niches was smaller in WAP than in AL (4.13 vs. 5.74), suggesting that in WAP, animals commonly use a greater relative percentage of the resources to which they have access. Niche modelling at the specific level revealed that this trend was not found in all taxa. For example, niches of *Gnathiphimedia sexdentata* and *Iphimediella microdentata* were bigger in WAP than in AL, following the general pattern. On the other hand, niches of *Echiniphimedia echinata* and *E. hodgsoni* had the same width in both areas. Moreover, relative niche overlap between these two species was much higher in WAP than in AL. Our results indicate that the widely different environmental conditions encountered by the animals in these two zones clearly influence their ecology. Overall, Iphimediidae amphipods tend to exploit more resources in WAP, i.e. in the zone where impacts of global change (temperature increase, sea ice cover decrease) are the strongest. Niche overlap between some closely related (i.e. congeneric) species was also more important in WAP. Ultimately, environmental changes in this region might reinforce these trends, which might lead to competition and perturb amphipod community structure. Those results were presented at two conferences (see list below).

Sea urchins:

During the Austral summer of 2013-2014 (RV *Polarstern* PS81 - ANTXXIX/3 cruise), sea urchins were sampled by the ULB team in three neighboring areas (Drake Passage, Bransfield Strait and Weddell Sea) featuring several depth-related habitats offering different trophic environments to benthic consumers. Three families with contrasting feeding modes were studied: Cidaridae (epifaunal browsers with preferences towards animal food items), Echinidae (generalist consumers) and Schizasteridae (sediment feeders). The objectives of this study were to (1) To characterize the range of food sources used by the target species in referential stations in order to document trophic networks within communities, (2) to compare (intraspecific comparisons) the trophic behaviors of echinoids across contrasted environments in order to visualize feeding flexibility and further document potential vulnerability in front of environmental changes (cf. changes in food availability). Results suggested that each family has specific adaptations to variation in trophic environment (i.e. food availability and/or composition). These results were presented in 2 conferences and published in *Polar Biology* (Michel et al. 2016). During the last reporting year, efforts were made to generalize these findings to other regions, including and Kerguelen Islands (Sub Antarctic). During the 2015 Kerguelen campaign, the three echinoid families were accessible between 0 and 20m depth at three reference stations of Gulf of Morbihan (Kerguelen Islands). Specimens (20 – 30 individuals / species / station) were collected (SCUBA diving) and dissected in PAF laboratory (BIOMAR). Subsamples were prepared for further analyses to be done in ULiège, ULB or UBFC) that encompass (1°) inventory of gut contents (microscopy), (2°) stable isotopes analyses ($\delta^{15}N$, $\delta^{13}C$); (3°) characterization of the gut bacteria (genetic analyses - DNA and RNA), (4°) morphology and size of the Aristotle's lanterns, (5°) calculation of the gonadic index (gonads weight/ teguments weight) and identification of the gonad stages (histology). Some of these analyses were incorporated in a paper that is currently submitted to *CCAMLR Science* (cf. list below). Moreover, during the 2017 Kerguelen campaign, we performed a spike experiment (injecting labeled ^{13}Carbon in the sediment and overlying waters) where we investigate the role of bacterial (BAC) and microphytobenthos (MPB) in meiofauna (and when possible macrofauna organisms) diet at one station in Potter Cove. We tackled the contribution of BAC and MPB to the Carbon fluxes within the sediment. We targeted MPB by adding ^{13}C bicarbonate ($Na^{13}CO_3^-$) in the overlying water column (5 cm water column) and exposed the cores to in situ photoperiod (15:9 light:dark, light intensity of ~20 µmoles). To investigate the BAC contribution and to label this benthic biota we used 2 treatments: sodium acetate-2-^{13}C ($^{13}CH_3CO_2Na$) to label Sulfate reducing bacteria, ^{13}C glucose ($^{13}C_6H_{12}O_6$) to label Heterotrophic bacteria and again ^{13}C bicarbonate ($Na^{13}CO_3^-$) to label chemoautotrophic bacteria. Preliminary results show little or no uptake of carbon by nematodes in those treatments with as food pathway target the microphytobenthos. The processing of the rest of the material is ongoing.

Sea stars:

In the framework of B. Le Bourg's PhD thesis, and through collaboration with the ULB team, the National Museum of Natural History (MNHN, Paris, France), the Institute of Oceanology of the Polish Academy of Sciences (IOPAN, Sopot, Poland the British Antarctic Survey (BAS, Cambridge, United Kingdom), ULiège gained access to over 1000 specimens of sea stars belonging to over 100 species spread over 44 genera. Those sea stars come from multiple and contrasted habitats across Subantarctic (South Georgia, South Sandwich Islands, Falkland Islands, Kerguelen Islands, Kerguelen Plateau) and Antarctic (South Shetland Islands, South Orkney Islands, Western Antarctic Peninsula, Weddell Sea, Adélie Land, d'Urville Sea, Georges V Land, Princess Elizabeth Land) locations. Temporal coverage is wide, ranging from 1985 to 2017. For each specimen, tegument and/or podial vesicles samples are analysed for stable isotope composition of C, N and S, and data are explored through isotopic niche modelling. Analysis is still ongoing, and preliminary results indicate a high trophic plasticity of many taxa of Southern Ocean sea stars. Moreover, regional variations in environmental conditions, including sea ice coverage and dynamics, seem to influence resource partitioning and niche overlap among co-occurring taxa. These results have been presented in 5 conferences (see list below). Parallel to data acquisition, the ULiège team set up a long-term experiment aiming at understanding how different preservation modes (freezing, ethanol and formalin) influence isotopic composition of sea star tissues. This experiment started in April 2016 and lasted for 2 years. Results suggest that effects of preservation methods on some of the metrics used for isotopic niche modelling are limited. This opened up new opportunities to use samples obtained through inter-institution exchanges (cf. above). A publication about those results, which also have been presented in 4 conferences, is currently in preparation.

Fish:

Through collaboration with KUL and exploitation of old samples collected during the BIANZO project, ULg gathered over 400 samples from 41 taxa of Notothenioid fishes sampled between 2002 and 2015 in the Scotia Sea and Weddell Sea. These samples were analysed for stable isotope ratios of carbon and nitrogen, and data were explored trough niche modelling. Moreover, the cephalic morphology of selected taxa has also been studied in order to shed lights on links between feeding habits and head shape and size. Overall, results revealed a great variation in isotopic compositions of Notothenioid fishes, suggesting that they exploit a wide array of resources. Temporal evolution of niches suggested that taxon-specific ecological plasticity in response to variation in environmental parameters and/or in prey availability exists. In old samples (2002/2004), isotopic niches of the dominant *Trematomus* and *Lepidonotothen* genera were overlapping, highlighting a possible past competition for resources. This overlap was not observed anymore in more recent samples, suggesting that resource partitioning between the two genera increased over the studied period. Those results were presented in 3 conferences, and plans are currently made to combine them with existing literature data to achieve a characterization of icefish trophic ecology at the scale of the whole Antarctic continent.

WP 3: Sensitivity and Resilience

WP 3.1. *Integrated mesocosm scale experiment at WAP site for metabolic responses of selected taxa and benthic groups. Responsibles: UGent, ULB, VUB, ULg*

Due to logistics constraints, this experiment could not be carried out (see also WP3.3).

WP 3.2. *Integrated mesocosm scale experiment at Terre Adélie for metabolic responses of selected taxa and benthic groups. Responsibles: ULB, RBINS (MNHN), UGent, VUB, ULg*

A first experiment was ran at DDU, aiming at determining the capacity *Sterechinus neumayeri* (Echinodermata: Echinoidea), one of the Southern Ocean's keystone species, to regulate the pH of its extracellular fluids, an important feature to cope with Ocean Acidification. Sea urchins *Sterechinus neumayeri* responded to OA forecasted to occur in 2100 ($pH_{T\text{-}SW}$ = 7.7, corresponding to -0.3 pH units in comparison with present values) similarly to temperate and tropical sea urchins of the same taxon (regular euechinoids). They increased the alkalinity of their extracellular fluid, which resulted in no difference in their extracellular fluid pH as compared to control sea urchins, after 5 days at target pH_{SW}. This indicates that *S. neumayeri* from Adélie Land have an adequate acid-base machinery to compensate OA as expected in 2100.

The experiment performed at DDU was replicated during the campaign 2015/2016 at Potter Cove (WAP) a site with contrasted environmental conditions and subject to fast warming. An extra treatment of pH_T was added (pH_T=7.4). Same response in acid/base regulation was observed in the experiments at Potter Cove where animals were subject to a considerably larger range of temperature.

Sterechinus neumayeri and *Odontaster validus* were also sampled, in 2018, in Port Foster, the immerged caldera of Deception Island (Antarctic Peninsula), along temperature and pH gradients generated by several well characterized hydrothermal vents. These samples allowed to assess the long-term impact of global change stressors on these two species. *S. neumayeri* proved to be able to maintain its acid-base homeostasy thanks to an accumulation of bicarbonate as in short-term experiments, demonstrating that this capacity is sustainable during the whole life of the sea urchin. On the contrary, *O.validus* did not compensate its extracellular pH, similarly to temperate species. Analysis of the effects of temperature and pH on the skeleton functional aspects is in progress.

WP 3.3. *Microcosm scale experiments at WAP for the identification of changes in interactions between microbiota, meiofauna and macrofauna respectively in different crossed pH, temperature, sedimentation and food treatments. Responsibles: UGent, ULB, VUB, ULg*

During this Antarctic campaign 2015/2016 in Potter Cove (WAP) we tried to carry out a microcosm acidification experiment. Unfortunately, after one week in the experiment, it failed due to facilities-related issues. We replicated the acidification experiment previously carried out in Terre Adélie on the sea urchin *Sterechinus neumayeri*. We also performed an acidification experiment on *Ophionotus victoriae* to assess the effect of an acidified environment on the biomechanics of its heavily calcified body. We undertook other experiment to assess the temperature stress response of two brooding sea stars, *Granaster nutrix* and *Neosmilaster georgianus,* this was done in temperature ramping experiments where temperature was increased slowly (mean of 0.25C /day) and metabolic rate (measured as oxygen consumption) was measured every time tempeature was increased by 2 – 3 degrees (every 4 – 8 days). The condition of the Potter Cove population of *Odontaster validus* was also recorded by sampling specimens and recording parameters such as length-weight distributions and organ indices.

WP 3.4. *Microcosm scale experiments in Terre Adelie for the identification of changes in interactions between microbiota, meiofauna and macrofauna respectively in different crossed pH, temperature, sedimentation and food treatments. Responsibles: UGent, RBINS (MNHN), ULB, VUB, ULg*

Due to logistics constraints, this experiment could not be carried out (see also WP3.3).

WP 3.5. *Time series analysis of Admiralty Bay data. Responsibles: ULB, RBINS*

Admiralty Bay data was compiled as a followup of the SCAR-MarBIN initiative (De Broyer et al. 2019). The ULB team is in contact with main actors (University of Lodz, Poland and Universidade Federal de Rio de Janeiro) to complete the dataset that was compiled in the framework of the Census of Marine Life (ABBED, Sicinski et al. 2010). This analysis could not be completed to the inadequate quality of the final dataset.

WP 4: Integrative modelling

WP4.1. *Construction of vERSO Information System. Responsibles: RBINS, ULB*

The vERSO information system (vERSO-IS) is operational and accommodated the newly generated data as well as existing data used in the framework of the modelling runs. vERSO-IS is a composite system which uses existing e-infrastructure (GBIF, iOBIS, Lifewatch, biodiversity.aq, GCMD) to allow users to discover and download raw data as it is published by the network. Metadata records are discoverable using the vERSO metadata portal, which points to raw data, as soon as it is published. Metadata records are exposed to search engines to ensure a maximal visibility through the Internet.

For the long-term, the vERSO information system is included in the Global Change Maste Directory (GCMD, metadata and discovery tool) and the biodiversity.aq initiative is harboring raw biodiversity data.

WP4.2. Running of Offline Models. Responsibles: ULB (UB), RBINS, KULeuven

Sea stars:

Offline modelling has started for a variety of model organisms. An augmented database on Southern Ocean asteroids has been assembled and is now used for Species Distribution Models (SDMs). SDMs models for several asteroids has been developed using MaxEnt and GLM approaches, other approaches and stability of those models are currently under investigation. A Dynamic Energy Budget (DEB) model has been developed for *Odontaster validus* Koehler 1906, and is currently being optimized by validation against field collected data and experiments. DEB models are currently under development for other asteroids from the Southern Ocean (*Neosmilaster georgianus* & *Granaster nutrix*). Adult-life-stage-only DEB models are being explored as an alternative simplified model for species for which larval development information is scarce and difficult to obtain. Potential application of coupling both approaches (SDM and DEB) is being explored. Trait based models (TDMs) are being developed using combinations of DEB model output and Southern Ocean productivity models.

Sea urchins:

Offline modelling has started for echinoids, at two spatial scales: the Kerguelen Plateau, and the whole Southern Ocean (south of 45°S). In addition, an augmented database on Southern Ocean echinoids has been assembled and is now used for Species Distribution Models (SDMs). We tested the influence of different temporal and spatial biases in widely used modelling procedures (MaxEnt and BRT), using a dataset from the Kerguelen Plateau, for four echinoid species that display contrasted ecological niches and distribution areas. Presence-only data were compiled from different oceanographic campaigns (led over a long time period: 1872-2015) and show significant sampling heterogeneities. The influence of data quantity and distribution in space and time on model performances was analyzed and compared with the influence of present and future environmental changes. BRT and MaxEnt abilities to project the models over different time periods was also tested, by comparing models based on contemporaneous data with models extrapolated from the past. Results were used to model species potential shifts predicted from IPCC A1B scenarii proposed for 2100 and 2200 AD; they were compared with the magnitude of changes recorded in the past (1955-2012). Models were also produced for six biogeographically and ecologically different species of echinoids at the scale of the SO based on the Random Forest procedure. Robust models were obtained showing both the relevance of the data now available at the scale of the ocean for such models and the importance of cruises recently led in the SO under the umbrella of the CAML for improving the completeness of datasets. A DEB model is currently under development for *Sterechinus neumayeri* (another key Antarctic species).

Fish:

Collaboration with ULB (/MNHN) is planned for species distribution models (SDM) for *Notothenia rossii* and possibly *N. coriiceps*. The same was planned for dynamic energy budget (DEB) modeling. Oceanographic, individual-based modeling (IBM) was planned in collaboration with RBINS and RECTO partners. In general, most of these synergies were identified and planned in conjunction with several RECTO partners and activities (cf. annual RECTO report). Due to time constraints, this aspect could only be explored.

WP 4.3. Deployment of Online Modelling tools. Responsibles: RBINS, ULB (UBFC), KU Leuven

Initial efforts were attempted to develop these tools. Given the dynamic nature of these efforts, they are now maintained under the umbrella of the SCAR Expert Group on Antarctic Biodiversity Informatics and biodiversity.aq initiative, using different development frameworks than anticipated.

WP 4.4. Creation of visualization products. Responsibles: ULB, RBINS, KU Leuven

Visualization products were mostly developed for scientific communication purposes. Please refer to the conference communication and publication lists below for a full account.

Scientific training activities

Bachelor and Master theses (16)

1. Blanchard, A. (2016): Variations géographiques du régime alimentaire des étoiles de mer en Océan Austral. Master's in biology of Organisms and Ecology thesis, successfully defended on 07/09/2016. Supervisor: Loïc Michel.
2. Borghs, J. (2018). Metabarcoding of the stomach and gut content of Antarctic fish. Master thesis Biology, successfully defended on 12/06/2018. Supervisor: Franz M. Heindler & Filip Volckaert.
3. Charpentier, A. (2018). Étude du Réseau trophique benthique de la baie de Port-aux-Français aux îles Kerguelen. Master in Oceanography thesis (Aix-Marseille University), successfully defended in June 2018. Supervisors: Gilles Lepoint & Baptiste Le Bourg. ULiège.
4. Crockaert, G. (2017). Biogéographie des astéries (Echinodermata : Asteroidea) de la région Magellanique. Master Thesis defended on 09/07/2017. Supervisor: Bruno Danis & Camille Moreau, ULB.
5. Demoustier, L. (2018). Cartographie des habitats des astéries (Echinodermata : Asteroidea) du plateau est-Antarctique, Master Thesis, successfully defended on 05/09/2018. Supervisors : Bruno Danis & Charlène Guillaumot, ULB
6. Duysens, J. (2017). Mesure des concentrations en mercure total et des compositions isotopiques d'invertébrés antarctiques (Terre-Adélie). Bachelor's in medical sciences thesis (HELMO Sainte-Julienne), successfully defended in June 2017. Supervisors: Loïc Michel & Gilles Lepoint. ULiège.
7. Goossens, S. (2017). Identification of Antarctic fish through DNA Barcoding. Bachelor thesis Biology successfully defended on 28/04/2017. Supervisor: Henrik Christiansen & Filip Volckaert, KU Leuven.
8. LeFaible, N. (2016). Spatial and temporal dynamics of benthic assemblages in a shallow fjord environment affected by recent glacier retreat. Master thesis, defended on 06/07/2017. Supervisors: Vanreusel Ann, Pasotti Francesca, Ulrike Braeckman, UGent
9. Léger-Bascou, L.(2016). Variations géographiques du régime alimentaire des amphipodes en Océan Austral. Master in Oceanology thesis successfully defended on 06/09/2016. Supervisor: Loïc Michel.
10. Léger-Bascou, L.(2016). Variations géographiques du régime alimentaire des amphipodes en Océan Austral. Master in Oceanology thesis successfully defended on 06/09/2016. Supervisor: Loïc Michel.
11. Maes, S. (2017). Polar cod population structure: connectivity in a changing ecosystem. Master thesis Biology successfully defended on 03/07/2017. Supervisor: Henrik Christiansen & Filip Volckaert, KU Leuven.
12. Marien, V. (2018). Phylogeny of fish from the Southern Ocean (Sub-Antarctic Islands). Bachelor thesis Biochemistry and Biotechnology successfully defended on 24/05/2018. Supervisor: Henrik Christiansen & Filip Volckaert, KU Leuven.
13. Moya, A. (2016) DNA Barcoding van Antarctische Vissen. Bachelor thesis Biology successfully defended on 22/04/2016. Supervisor: Henrik Christiansen & Filip Volckaert, KU Leuven.
14. Peignot, Q. (2017). Etude des variations trophiques chez les poissons des glaces (Notothenioidei, Perciformes) en océan Austral dans un contexte de changement climatique. Master's in environmental sciences thesis (University of Reims Champagne-Ardenne), successfully defended in June 2017. Supervisors: Loïc Michel & Bruno Frédérich. ULiège.
15. Shaw, P. (2018). Interspecific phylogeny of the genus *Lepidonotothen*. Bachelor thesis Biology successfully defended on 24/05/2018. Supervisor: Franz M. Heindler & Filip Volckaert.

16. Smit, T. (2016) Genetic population structure of a Southern Ocean fish, *Notothenia coriiceps*. Master thesis Biology successfully defended on 27/06/2016. Supervisor: Henrik Christiansen & Filip Volckaert, KU Leuven.

PhD theses (7)

1. Cristiansen, H. 2019. Supervisor: Filip Volckaert, KU Leuven
2. Di Giglio, S. 2020. Supervisor: Philippe Dubois, ULB
3. Fabri-Ruiz, S. 2018. Supervisors: Thomas Saucède & Bruno Danis, UBFC & ULB
4. Guillaumot, C. 2021. Supervisors : Bruno Danis & Thomas Saucède, ULB & UBFC
5. Heindler, F.M., 2019. Supervisor: Filip Volckaert, KU Leuven
6. LeBourg, B. 2019. Supervisor: Gilles Lepoint, U Liège
7. Moreau, C. 2019. Supervisors: Bruno Danis & Thomas Saucède, ULB & UBFC

5. DISSEMINATION AND VALORISATION

Working through SCAR and international organizations, vERSO scientists contributed to the development of policy at national and international levels (e.g. strategic and ecosystem-based management of Antarctic marine resources). The development materialized as contributions to various conservation-oriented committees such as the ATCM – CEP or CCAMLR. vERSO partners have experience with both committees through direct input in submission of e.g. Working Papers in ATCM, or in terms of scientific expertise in CCAMLR bioregionalization workshops.

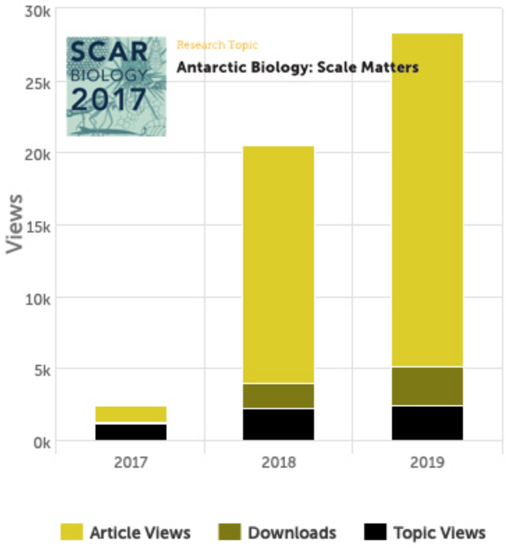
5.1 Organisation of an International Conference

The XIIth SCAR (Scientific Committee on Antarctic Research) biology symposium and affiliated side meetings were held in Leuven, Belgium, between the 8th and 15th of July, and largely organized by the vERSO consortium.

The main theme for the XIIth SCAR (Scientific Committee on Antarctic Research) biology symposium was "Scale matters". From the small molecular scale, through population and large ecosystem scale, biological processes and diversity span all these levels. Understanding these processes as well past and present patterns of biodiversity are essential for understanding possible threats to Antarctic biology and their impact. With this Symposium we wanted to focus on understanding biological distribution and trends as well as adaptation and processes both in the marine and terrestrial realm including the human biology. Special attention was be paid to multidisciplinary research and how combining insight from different fields can help our understanding of biology in this unique region.

Total attendance was 402 people from 32 countries. Attendees were primarily from Europe and equally distributed between genders. 260 people payed the regular fee, 130 an early career fee and there were 12 1-day registrations.

A selection of research presented at the symposium were published in a Frontiers Research Topic. A total of 118 authors contributed to this issue, with a total of 18 articles.



5.2 Organisation of Workshops (6)

1. Christiansen, H., et al. 2017. APECS Science Communication Workshop. Leuven, Belgium, during SCAR Biology Symposium.
2. Danis, B., Ropert-Coudert, Y., Convey, P., Vandeputte, A., 2016. EG/ABi Development of the register of Antarctic Species workshop. Brussels, Belgium
3. Danis, B., Ropert-Coudert, Y., Hindel, M., Vandeputte, A., 2015. EG-BAMM/ABi Retrospective Analysis of Tracking Data (RAATD) workshop. Brussels, Belgium
4. Eléaume, M., Galut, C., 2016. Antarctic Identification workshops. Concarneau, France
5. Volckaert, F., 2017. A molecular tools workshop for vERSO and RECTO partners and external participants. Leuven, Belgium.
6. Volckaert, F., 2017. vERSO-RECTO bioinformatics workshop. Leuven, Belgium.

5.3 Participation in Conferences and Workshops (97)

1. Agüera, A., Danis, B., Guillaumot, C. (2017). Trait distributions of key marine species from the Western Antarctic Peninsula. DEB Symposium, Tromso, Norway. 31 May -2 June 2017. Poster.
2. Christiansen, H. (2017) Polar research across borders – getting involved as Early Career Scientist. NWO and APECS-NL National Polar Symposium, The Hague, Netherlands, 8 December 2017. Oral (Invited speaker).
3. Christiansen, H., Danis, B., Heindler, F.M., Hellemans, B., Jossart, Q., Kochzius, M., Leliaert, F., Moreau, C., Pasotti, F., Patel, T., Robert, H., Van de Putte, A.P., Vanreusel, A., Verheye, M., Volckaert, F.A.M. & Schön, I.M. (2018) Facilitating Southern Ocean population genomics – a RADseq pilot experiment. POLAR 18: SCAR/IASC Open Science Conference, Davos, Switzerland, 15-26 June 2018. Poster.
4. Christiansen, H., Heindler, F. M., Griffiths, H.J., Van de Putte, A.P., Volckaert, F.A.M. (2017) DNA Barcoding of fishes collected off the South Orkney Islands. SCAR Biology Symposium 2017, Leuven, Belgium, 10-14 July, 2017. Poster.
5. Christiansen, H., Heindler, F.M, Dettai, A., Van de Putte, A.P. Barcoding Southern Ocean lanternfish, Myctophidae, and other mesopelagic fish. 2016 Open Science

Conference of the Scientific Committee on Antarctic Research, Kuala Lumpur, Malaysia, 20-30 August 2016. Poster.

6. Christiansen, H., Van de Putte, A.P., Hellemans, B., Heindler, F. M., Barrera-Oro, E., Volckaert, F.A.M. (2017) Population genomics of the marbled rockcod, Notothenia rossii, in the Scotia Sea and Kerguelen plateau. SCAR Biology Symposium 2017, Leuven, Belgium, 10-14 July 2017. Oral.
7. Christiansen, H., Van de Putte, A.P., Volckaert, F.A.M. (2015) Monitoring the genetic status of marine populations - AGenDex. Genotyping by Sequencing Course, Norwich, UK, 8-12 June 2015 (Runner-up Award). Poster.
8. Christiansen, H., Van de Putte, A.P., Volckaert, F.A.M. (2016) Application of ddRAD sequencing for population genomics of Antarctic fish. 15Th Assembly of the Linnaeus Centre for Marine Evolutionary Biology, Tjärnö, Sweden, 26-28 April 2016. Oral.
9. Christiansen, H., Van de Putte, A.P., Volckaert, F.A.M. (2016) Connectivity in the Southern Ocean: population genomics of icefish. Joint Symposium on Eco-Evolutionary Dynamics and Flanders Annual Meeting of Ecology, Ghent, Belgium, 19-21 December 2016. Oral.
10. Christiansen, H., Van de Putte, A.P., Volckaert, F.A.M. (2017) Connectivity in the Southern Ocean: population genomics of icefish. VLIZ Marine Science Day, Brugge, Belgium, 3 March 2017. Poster.
11. Christiansen, H., Van de Putte, A.P., Volckaert, F.A.M. (2018) Large and fine scale population genomics of an Antarctic fish. Marine Evolution, Strömstad, Sweden, 15-17 May 2018. Poster.
12. Christiansen, H., Van de Putte, A.P., Volckaert, F.A.M. Genetic diversity of two notothenioid fish species elucidated by RAD sequencing. 2016 Open Science Conference of the Scientific Committee on Antarctic Research, Kuala Lumpur, Malaysia, 20-30 August 2016. Oral
13. Christiansen, H., Van de Putte, A.P., Volckaert, F.A.M. Riding the current - population genomics of demersal Antarctic fish. 2016 Annual Symposium of the Fisheries Society of the British Isles, Bangor, UK, 18-22 July 2016. Oral.
14. Christiansen, H., Van de Putte, A.P., Volckaert, F.A.M., 2015. Monitoring the genetic status of marine populations - AGenDex. Youmares 6, Bremen, Germany, 14-16 September 2015. Poster.
15. Christiansen, H., Van de Putte, A.P., Volckaert, F.A.M., 2015. Monitoring the genetic status of marine populations - AGenDex. Genotyping by Sequencing Course, Norwich, UK, 8-12 June 2015 (Runner-up Award). Poster.
16. Christiansen, H., Van de Putte, A.P., Volckaert, F.A.M., 2016. Application of ddRAD sequencing for population genomics of Antarctic fish. 15Th Assembly of the Linnaeus Centre for Marine Evolutionary Biology, Tjärnö, Sweden, 26-28 April 2016. Oral.
17. Dehnhard N., Achurch H., Clarke J., Michel L. N., Walters A., Southwell C., Eens M. & Emmerson L (2017). Foraging distribution, habitat preferences and diet of breeding Antarctic fulmarine petrels in East Antarctica. Oral communication accepted for presentation at the "12th SCAR (Scientific Committee on Antarctic Research) Biology Symposium", 10-14/07/2017, Leuven, Belgium.
18. Dehnhard N., Achurch H., Judy C., So K., Michel L., Southwell C., Walters A. & Eens M (2018). Foraging distribution, habitat preferences and diet of Antarctic petrels, cape petrels and southern fulmars – inter-specific overlap as a consequence of high environmental variability? VLIZ Marine Science Day 2018, Bredene, Belgium, 21/03/2018. Oral.
19. Deman, F., Fripiat, F., Roukaerts, A., Meiners, K., Lannuzel, D., Vancoppenolle, M., ... Dehairs, F. (2017). POC, PON, DOC, DON: Antarctic pack ice data compilation. In BEPSII / ECVice meeting, 2017. BEPS II meeting, March 2017, Scripps Institute of Oceanography, California, USA.
20. Deman, F., Roukaerts, A., Delille, B., Fripiat, F., Lannuzel, D., Tison, J. L., & Dehairs, F. (2016). A time series study during spring transition in the fast ice at Davis station,

Antarctica: preliminary results. In International Symposium on Polar Environmental Change and Public Governance: Collection of Abstracts. CHINARE meeting, Oct. 2016 Wuhan, China.

21. Deman, F., Roukaerts, A., Fripiat, F., Lannuzel, D., & Dehairs, F. (2017). Nitrate isotopic composition in landfast sea ice: a time series study. In Gordon Research Conference: Polar Marine Science: Understanding Polar Ecosystem Change Through Time Series Observations, Technological Advances, and Biophysical Coupled Modelling. Gordon Research Conference on Polar Marine Science, March 2017, Ventura, USA.
22. Dery A, Collard M, Dubois Ph. Soft echinoderms to be expected in the future? Impact of ocean acidification on the mechanical properties of the skeleton and underlying mechanisms. 4th International Symposium on the Ocean in a High-CO$_2$ World, Hobart (Tasmania, Australia) 3-6 May 2016. Oral communication.
23. Dettai A., Fournier J., Ameziane N., Amice E., Chauvaud L., da Forno E., Domenjoz O., Dubois P., Freschet E., Jane P., Krygelmans A., Michel L. N., Schaad A., Thébault J., Schiaparelli S., Eléaume M. & Gallut C (2017). Récifs artificiels dans l'Océan Austral, un nouvel outil pour l'étude de la faune fixée de petite taille. 13èmes Journées Scientifiques du Comité National Français de Recherches Arctiques et Antarctiques (CNFRA), Paris, France, 11-12/05/2017. Oral.
24. Dettai, A., Auvinet, J., Frederich, B., Christiansen, H., Aboubakari, N., Bonillo, C., Higuet, D. (2017) Trematominae and Artedidraconinae: contrasted mitogenome evolution for two Antarctic radiations. SCAR Biology Symposium 2017, Leuven, Belgium, 10-14 July 2017. Oral.
25. Di Giglio S., Agüera A., Danis B., Eléaume M., Fournier J., Gallut C., Jane P., Michel L., Pasotti F., Sahade R., Vanreusel A. & Dubois P (2017). Acid-base physiology of the Antarctic sea urchin Sterechinus neumayeri: differences according to environmental conditions? 12th SCAR (Scientific Committee on Antarctic Research) Biology Symposium, Leuven, Belgium, 10-14/07/2017. Poster.
26. Dubois P., Agüera A., Améziane N., Collard M., Danis B., David B., Dehairs F., De Ridder C., Di Giglio S., Eléaume M., Féral J.-P., Fournier J., Gallut C., Gonthier-Maurin M., Jane, P., Marschal C., Michel L., Motreuil S., Pasotti F., Sahade R., Saucède T. & Vanreusel A. (2017). IPEV REVOLTA and PROTEKER programs: Monitoring benthic marine biodiversity in antarctic and subantarctic coastal areas and their responses to environmental changes. International Long-Term Ecological Research Network and Zones Ateliers & Critical Zone Observatory Networks Joint Conference, Nantes, France, 02/10/2017. Oral.
27. Dubois P., Gonthier-Maurin M., Ameziane N., Di Giglio S., Féral J.-P., Marschal C., Michel L., Motreuil S. & Saucède T (2017). Is the Sub-antarctic sea urchin Abatus cordatus threatened by ocean acidification? 12th SCAR (Scientific Committee on Antarctic Research) Biology Symposium, Leuven, Belgium, 10-14/07/2017. Poster.
28. Dubois Ph, et al (21 authors). Acid-base physiology of Antarctic and Sub-antarctic sea urchins and their resilience to ocean acidification. XXIIth SCAR Biology Symposium (Leuven, Belgium) 10-14 July 2017. Oral communication.
29. Dubois Ph, et al (21 authors). Acid-base physiology of Antarctic and Sub-antarctic sea urchins and their resilience to ocean acidification. 16th International Echinoderm Conference (Nagoya, Japan) 27 May – 1st June 2018. Oral communication.
30. Dubois Ph, et al (21 authors). IPEV REVOLTA and PROTEKER programs: Monitoring benthic marine biodiversity in antarctic and subantarctic coastal areas and their responses to environmental changes. International Long-Term Ecological Research Network, Zones Ateliers & Critical Zone Observatory Networks (LTER-France) Joint Conference (Nantes, France). 2-4 October 2017
31. Eleaume M., Améziane N., Dettaï A., Dubois P. Michel L. & Gallut C. (2018). REVOLTA legacy: outcomes of an eight-year Antarctic program. Marine Ecosystem Assessment for the Southern Ocean (MEASO18), Hobart, Australia, 09-13/04/2018. Poster.

32. Frédérich, B., Heindler, F.M., Christiansen, H., Dettaï, A. & Lepoint, G. (2017). Morphological diversification in the icefishes Trematominae (Notothenioidei, Teleostei). Zoology Symposium, Wageningen, Netherlands, 23-24 November 2017. Poster.
33. Frédérich, B., Heindler, F.M., Christiansen, H., Dettaï, A. & Lepoint, G. (2018) Morphological diversification of the endemic Antarctic fishes Trematominae (Notothenioidei, Teleostei). POLAR 18: SCAR/IASC Open Science Conference, Davos, Switzerland, 15-26 June 2018. Poster.
34. Frédérich, B., Heindler, F.M., Dettaï, A., Christiansen, H., Van de Putte, A.P., Lepoint, G. (2016) Head shape disparity of the cod icefishes Trematominae (Notothenioidei, Teleostei). 23rd Congress of Zoology, Antwerp, Belgium, 15-17 December 2016. Poster.
35. Fripiat F. et al., 2016. Annual meeting of the SCOR working group "Biogeochemical exchange process at the sea ice interface", Paris VI, (UPMC).
36. Fripiat F., 2016. Saroma Lagoon sea ice field trip (Hokkaido, Japan; collaboration with Prof. D. Nomura). Intercalibration experiment for carbonate parameters, algal biomass.
37. Gallut C., Fournier J., Ameziane N., Amice E., Chauvaud L., da Forno E., Domenjoz O., Dubois P., Freschet E., Jane P., Krygelmans A., Michel L. N., Schaad A., Thébault J., Schiaparelli S., Eléaume M. & Dettai A (2017). Autonomous Reef Monitoring Structures in the Southern Ocean, a tool for the study of the understudied small fauna. 12th SCAR (Scientific Committee on Antarctic Research) Biology Symposium, Leuven, Belgium, 10-14/07/2017. Poster.
38. Guillaumot C, Agüera A, Danis B, Deregibus D, Quartino ML, Saravia LA. (2018). Dynamic growth model of Antarctic macroalgae in a fast-changing environment.
39. Guillaumot C, Agüera A, Eléaume M, Danis B. (2018). Physiological modelling in Antarctica: dynamic inferences in a changing environment. 12 minutes talk (English), SCAR Davos, 06/2018
40. Guillaumot C, Artois J, Saucède T, Demoustier L, Moreau C, Eléaume M, Agüera A, Danis B. (2018). Modelled distributions of benthic species of the Southern Ocean in a fast-changing environment. MEASO, Hobart, 04/2018. Poster.
41. Guillaumot C, Martin A, Eléaume M (presenter), Saucède T. (2017). Modelling species distribution: influences of temporal, spatial, and sampling heterogeneities in data-poor areas. An example from the Kerguelen Plateau. Kerguelen Symposium, 11/2017. Poster
42. Guillaumot C, Martin A, Eléaume M, Danis B, Saucède T. (2018). An example from the Kerguelen Plateau. 12 minutes talk (English), MEASO, Hobart, 9-13/04/2018
43. Guillaumot C, Saucède T, Danis B. (2018). Inferring the responses of Southern Ocean benthic species to environmental changes using Dynamic Energy Budget models. ZOOLOGY congress, Anvers, 15/12/2018. 12 minutes talk (English).
44. Guillaumot C, Saucède T, Danis B. (2018). Poster. Strict extrapolation in modelling Southern Ocean species distribution. Zoology congress, Anvers, 15/12/2018.
45. Guillaumot, C., Agüera, A., Danis, B. (2017). Physiological performances of Southern Ocean key species. DEB Symposium, Tromso, Norway. 31 May -2 June 2017. Oral.
46. Guillaumot, C., Agüera, A., Danis, B. (2017). Projecting species energetic performance in a spatially-explicit context: Trait Distribution Modelling of a key antarctic species.. CNFRA, Paris, France. 11-12 May. Oral.
47. Guillaumot, C., Agüera, A., Danis, B. (2017). Projecting species energetic performance in a spatially-explicit context: Trait Distribution Modelling of antarctic benthic species. SOOS Workshop (Southern Ocean Observing System network), British Antarctic Survey, Cambridge, UK. 15-16 May 2017. Poster.
48. Heindler, F. M., Hellemans, B., Christiansen, H., Van de Putte, A.P., Maes, G.E., Volckaert, F.A.M. (2017) Historical DNA Barcoding of trematomid fishes using

museum samples. SCAR Biology Symposium 2017, Leuven, Belgium, 10-14 July, 2017. Poster

49. Heindler, F.M, Christiansen, H., Dettaï, A., Collins, M.A., Steinke, D., Couloux, A., Volckaert, F.A.M., Van de Putte, A.P. (2016) DNA Barcoding of small mesopelagic fish from the Southern Ocean. 23rd Congress of Zoology, Antwerp, Belgium, 15-17 December 2016. Poster.
50. Heindler, F.M., Christiansen, H., Dettaï, A., Collins, M.A., Coloux, A., Volckaert, F.A.M., Van de Putte, A. (2017) DNA barcoding of small mesopelagic fish from the Southern Ocean. VLIZ Marine Science Day, Brugge, Belgium, 3 March 2017. Poster.
51. Heindler, F.M., Hellemans, B., Christiansen, H., Dettaï, A., Van de Putte, A.P., Maes, G.E. & Volckaert, F.A.M. (2017) Ancient marine metabarcoding: A new approach to stomach and microbiome analysis for historical fish. VLIZ Marine Science Day, Bredene, Belgium, 21 March 2018. Oral.
52. Heindler, F.M., Hellemans, B., Christiansen, H., Dettaï, A., Van de Putte, A.P., Maes, G.E. & Volckaert, F.A.M. (2018) Historical DNA Metabarcoding of trematomid fishes using museum samples. POLAR 18: SCAR/IASC Open Science Conference, Davos, Switzerland, 15-26 June 2018. Oral.
53. Lara Y., Lepoint G., Pessi I., Wilmotte A. & Michel L. N (2017). In Search of Marine Antarctic Cyanobacteria. 12th SCAR (Scientific Committee on Antarctic Research) Biology Symposium, Leuven, Belgium, 10-14/07/2017. Poster.
54. Le Bourg B., Blanchard A., Danis B., Jossart Q., Lepoint G., Moreau C. & Michel L. N (2016). Feeding ecology of Southern Ocean sea stars inferred from stable isotope ratios of C, N and S. Zoology 2016, Antwerp, Belgium, 17/12/2016. Oral.
55. Le Bourg B., Blanchard A., Danis B., Jossart Q., Lepoint G., Moreau C. & Michel L. N (2017). Influence of environmental conditions on trophic niche partitioning among sea stars assemblages. 12th SCAR (Scientific Committee on Antarctic Research) Biology Symposium, Leuven, Belgium, 10-14/07/2017. Oral.
56. Le Bourg B., Blanchard A., Danis B., Jossart Q., Lepoint G., Moreau C. & Michel L. N (2018). Feeding ecology of sea stars of the Southern Ocean: potential influence of sea ice on trophic niche partitioning. 16th International Echinoderm Conference, Nagoya, Japan, 31/05/2018. Oral.
57. Le Bourg B., Blanchard A., Danis, B., Lepoint G., Moreau C., Jossart Q. & Michel L. N (2016). Feeding ecology of Southern Ocean sea stars inferred from stable isotopes ratios. Joint European Stable Isotopes User Group Meeting (JESIUM) 2016, Ghent, Belgium, 05/09/2016. Poster.
58. Le Bourg B., Lepoint G. & Michel L. N., 2016. Feeding of Antarctic asteroids: trophic resources, plasticity, and diversity. VLIZ Marine Scientists Day 2016, Bruges, Belgium, 12/02/2016. Poster
59. Le Bourg B., Lepoint G., Balthasart P. & Michel L (2018). Effects of fluid preservation on sea star stable isotope composition: How useful can museum collections be for trophic ecology studies? VLIZ Marine Science Day 2018, Bredene, Belgium, 21/03/2018. Poster.
60. Le Bourg B., Lepoint G., Balthasart P. & Michel L. N (2017). Effects of fluid preservation on sea star stable isotope composition: How useful can be museum collections for trophic ecology studies? Zoology 2017, Wageningen, The Netherlands, 23/11/2017. Poster.
61. Le Bourg B., Lepoint G., Balthasart P. & Michel L. N (2018). Preservation methodology and stable isotope composition in sea stars: Can museum collections be useful for trophic ecology studies? 11th International Conference on the Applications of Stable Isotope Techniques to Ecological Studies (IsoEcol 2018), Viña del Mar, Chile, 30/07-03/08/2018. Oral.
62. Le Bourg B., Lepoint G., Balthasart P. & Michel L. N. (2018). Effects of fluid preservation on sea star stable isotope composition: do they prevent the use of

museum collections for trophic ecology studies? Benelux Association of Stable Isotope Scientists (BASIS) Annual Meeting 2018, Liège, Belgium, 19-20/04/2018. Poster.

63. Maes, S., Christiansen, H., Mark, F.C., Lucassen, M., Van de Putte, A.P., Volckaert, F.A.M. & Flores, H. (2018) Polar cod population structure: connectivity in a changing ecosystem. POLAR 18: SCAR/IASC Open Science Conference, Davos, Switzerland, 15-26 June 2018. Poster.
64. Maes, S., Christiansen, H., Mark, F.M., Lucassen, M., Van de Putte, A.P., Volckaert, F.A.M., Flores, H. (2017) Comparison of spatial genetic structure and its drivers in Arctic and Antarctic fishes. SCAR Biology Symposium 2017, Leuven, Belgium, 10-14 July, 2017. Poster.
65. Michel L. N., d'Udekem d'Acoz C., Frédérich B., Léger-Bascou L., Schön I., Verheye M. & Lepoint G (2017). Effects of environmental changes on ecological niches of Iphimediidae amphipods: a stable isotope comparison of West Antarctic Peninsula and East Antarctica. Developing the West Antarctic Peninsula International Network within the Southern Ocean Observing System workshop, Cambridge, United Kingdom, 15-16/05/2017. Poster.
66. Michel L. N., d'Udekem d'Acoz C., Frédérich B., Léger-Bascou L., Schön I., Verheye M. & Lepoint G (2017). Stable isotopes reveal effects of environmental changes on ecological niches of Iphimediidae amphipods. Poster accepted for presentation at the "12th SCAR (Scientific Committee on Antarctic Research) Biology Symposium", 10-14/07/2017, Leuven, Belgium.
67. Michel L. N., Danis B., Dubois P., Eleaume M., Fournier J., Gallut C., Jane P. & Lepoint G (2017). Increased sea ice cover disrupts food web structure in Antarctic coastal benthic ecosystem. 12th SCAR (Scientific Committee on Antarctic Research) Biology Symposium, Leuven, Belgium, 10-14/07/2017. Oral.
68. Michel L. N., David B., Dubois P., Lepoint G., De Ridder, C., 2016. Trophic plasticity of Antarctic echinoids under contrasted environmental conditions. VLIZ Marine Scientists Day 2016, Bruges, Belgium, 12/02/2016. Poster
69. Michel L. N., Dubois P., Eleaume M., Fournier J., Gallut C., Jane P., Lepoint, G., 2016. Impacts of unusually high sea ice cover on Antarctic coastal benthic food web structure. 10th International Conference on the Applications of Stable Isotope Techniques to Ecological Studies (IsoEcol 2016), Tokyo, Japan, 08/04/2016. Oral
70. Michel L. N., Dubois P., Eleaume M., Fournier J., Gallut C., Jane P., Lepoint, G., 2016. Use of stable isotope ratios to delineate coastal benthic food web structure in Adélie Land (East Antarctica). Belgium National Committee on Antarctic Research (BNCAR) symposium 2016, Brussels, Belgium, 28/04/2016. Poster.
71. Michel L. N., Dubois P., Eleaume M., Fournier J., Gallut C., Jane P. & Lepoint G (2016). Unusually high sea ice cover influences resource use by benthic invertebrates in coastal Antarctica. Joint European Stable Isotopes User group Meeting (JESIUM) 2016, Ghent, Belgium, 05/09/2016. Poster.
72. Michel L. N., Dubois P., Eleaume M., Fournier J., Gallut C., Jane P. & Lepoint G (2017). Increased sea ice cover disrupts food web structure in coastal Antarctica. Oral communication presented on 03/03/2017 at the VLIZ Marine Science Day 2017, Bruges, Belgium, 03/03/2017. Oral.
73. Michel L. N., Dubois P., Eleaume M., Fournier J., Gallut C., Jane P. & Lepoint G (2017). Unusually high sea ice cover influences resource use by benthic invertebrates in coastal Antarctica. Benelux Association of Stable Isotope Scientists (BASIS) Annual Meeting 2017, Utrecht, The Netherlands, 04/05/2017. Oral.
74. Michel L. N., Dubois P., Eleaume M., Fournier J., Gallut C., Jane P. & Lepoint G (2016). Unusually high sea ice cover influences resource use by benthic invertebrates in coastal Antarctica. Poster presented on 05/09/2016 at the "Joint European Stable Isotopes User Group Meeting (JESIUM) 2016", Ghent, Belgium.
75. Moreau, C. Danis, B., 2016. Reproductive strategy as a piece of the biogeographic

puzzle: a case study using Antarctic sea stars (Echinodermata, Asteroidea). Centre Interuniversitaire de Biologie Marine (CIBIM), Mons, Belgium.

76. Moreau, C., Danis, B., 2015. Use of open source data to describe Southern Ocean Asteroidea biogeography. Empowering Biodiversity Research conference, Brussels, Belgium
77. Peignot Q., Frédérich B., Lepoint G. & Michel L (2018). δ13C and δ15N measurements in Antarctic Notothenioid fishes: variation of their trophic ecology. VLIZ Marine Science Day 2018, Bredene, Belgium, 21/03/2018. Poster.
78. Peignot Q., Frédérich B., Lepoint G. & Michel L. N (2017). Trophic ecology of icefishes (Notothenioidei, Perciformes) in a context of climate change. Zoology 2017, Wageningen, The Netherlands, 23/11/2017. Poster.
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80. Roukaerts A., Zhou J., Fripiat F., Tison F.L., Dehairs F., 2015. Missing carbon source or methodological bias? Goldschmidt Conference, Prague.
81. Roukaerts, A., Deman, F., Fripiat, F., & Dehairs, F. (2017). New insights in Antarctic fast ice biogeochemistry, the role of biofilm. In XIITH SCAR biology symposium, Leuven, Belgium.
82. Saucède T., Améziane N., Feral J.-P., Bazin A., Chenuil A., David B., De Ridder C., Gonzalez-Wevar C., Levêque J., Marschal C., Mathieu O., Michel L., Motreuil S. & Poulin E (2015). PROTEKER : Mise en place d’un observatoire sous-marin côtier aux Îles Kerguelen. 3ème colloque biennal des Zones Ateliers du CNRS, Paris, France, 15/10/2015. Poster.
83. Saucède T., Cabessut M., De Ridder C., Dubois P., Fabri-Ruiz S., Fournier J., Gonthier-Maurin M., Marschal C., Marty G., Mateos A., Mathieu O., Michel L., Motreuil S. & Féral J.-P (2017). Plasticité trophique et résilience chez les oursins des Iles Kerguelen. 13èmes Journées Scientifiques du Comité National Français de Recherches Arctiques et Antarctiques (CNFRA), Paris, France, 11-12/05/2017. Oral.
84. Saucède T., De Ridder C., Dubois P., Marschal C., Marty G., Motreuil S., Michel L., Pascal P.-Y., Poulin E. & Féral J.-P (2018). Ecological monitoring of sub-Antarctic coastal marine biodiversity: implementation of a submarine observatory in the Kerguelen Islands (French Southern Territories). Marine Ecosystem Assessment for the Southern Ocean (MEASO18), Hobart, Australia, 09-13/04/2018. Poster.
85. Saucède T., De Ridder C., Michel L., Pascal P.-Y., Cabessut M., Marty G., Mateos A., Mathieu O., Motreuil S. & Féral J.-P (2018). Ecologie trophique des oursins côtiers des Kerguelen. 14èmes Journées Scientifiques du Comité National Français de Recherches Arctiques et Antarctiques (CNFRA), Strasbourg, France, 25/04/2018. Oral.
86. Saucède, T., Bazin, A., Lévêque, J., Milloux, M.-J., Fabri-Ruiz, S., Michel, L., De Ridder C., Féral, J.P., 2016. Etude des réseaux trophiques dans les environnements côtiers des Iles Kerguelen : analyse des régimes alimentaires d’espèces d’oursins et de leur plasticité à l’aide de traceurs isotopiques (δ^{13}C et δ^{15}N). 5ème journée de l’OSU THETA *(Observatoire des Sciences de l’Univers "Terre Homme Environnement Temps Astronomie")*; Geneuille (Franche-Comté-Bourgogne)
87. Saucède, T., Marty, G., Fabri-Ruiz, S., Fournier J., De Ridder, C., 2015. Proteker – Mise en place d’un observatoire sous-marin côtier aux Îles Kerguelen - Etablissement d’une ligne de base pour les suivis écologique et génétique, la protection et la conservation. *Conference on board Marion Dufresne*
88. Saucède, T., Marty, G., Fabri-Ruiz, S., Fournier, De Ridder, C., 2015. Proteker – Bilan de la mission et premiers résultats. *Conference on board Marion Dufresne* SCAR, Davos 06/2018. Poster.
89. Van de Putte, A.P. (2016). A Southern Ocean trophic database, SCAR OSC 2016.

Oral.

90. Van de Putte, A.P. (2016). Biodiversity informatics for Polar Regions - how to transform data into knowledge EncontroCiëncia 2016, Lisbon Portugal. Oral
91. Van de Putte, A.P. (2016). Biodiversity.aq. SCAR OSC 2016. Oral.
92. Van de Putte, A.P. (2016). Register of Antarctic Species workshop. Leuven, Belgium 20-23 September 2016. Organiser
93. Van de Putte, A.P. (2016). SCADM, the Antarctic data management system, making scientific research in Antarctica discoverable. SCAR OSC 2016. Oral.
94. Van de Putte, A.P. (2016). SCAR Biology Symposium. SCAR OSC 2016. Oral.
95. Van de Putte, A.P. (2016). SCAR Open Science Conference and delegates meeting. Kuala Lumpur, Malaysia, 22-30 August 2016. Participation
96. Van de Putte, A.P. (2016). The Relationship between Ecological Specialization and Response to Pleistocene Climate Change. SCAR OSC 2016. Oral.
97. Van de Putte, A.P. (2016). Thirty-fifth Meeting of the Commission for the Conservation of Antarctic Marine Living Resources, Participation to the commission and Scientific Committee meetings. Hobart Tasmania, 17-28 October 2016. Belgian head of delegation

5.4 Outreach and communication activities (4)

1. "Briser la glace", article published in "Le 15ème jour du mois" issue nr. 243 (April 2015), available at http://le15ejour.ulg.ac.be/jcms/c_48540/fr/briser-la-glace
2. Video Faculté des Sciences, available at https://www.youtube.com/watch?list=PLtWiu4yEvwjaRsuQlKtWJZa4gzBIBZZkr&v=xP_2-8KPRF0
3. Outreach covering the work on fast ice at Davis station during our recent fieldwork, November 2015. http://www.wtnschp.be/geowetenschappen/op-zoek-naar-algen-zee-ijs-antarctica/
4. Presentation to “Pool tot Pool” club of “Vissen van de Zuidelijke Oceaan” by Filip Volckaert, Leiden (NL), 12.03.2016

6. PUBLICATIONS

The vERSO consortium, in the course of its 4 years efforts, have published a total of 50 articles in peer-reviewed international journals. The details of the publications are provided below.

6.1 Published or in press (50)

1. Agüera, A., Ahn, I.-Y., Guillaumot, C., & Danis, B. (2017). A Dynamic Energy Budget (DEB) model to describe Laternula elliptica (King, 1832) seasonal feeding and metabolism. *PLoS ONE*, 1–20. http://doi.org/10.1371/journal.pone.0183848

2. Agüera, A., Collard, M., Jossart, Q., Moreau, C., Danis, B., 2015. Parameter Estimations of Dynamic Energy Budget (DEB) Model over the Life History of a Key Antarctic Species: The Antarctic Sea Star Odontaster validus Koehler, 1906. *Plos One*, *10*(10), e0140078.

3. Braeckman U., Pasotti F., et al. “Degradation of macroalgal detritus in shallow coastal Antarctic sediments”, *Limnology & Oceanography* 2018 https://doi.org/10.1002/lno.11125

4. Brasier, M. J., Grant, S. M., Trathan, P. N., Allcock, L., Ashford, O., Blagbrough, H., … Griffiths, H. J. G. (2018). Benthic biodiversity in the South Orkney Islands Southern Shelf Marine Protected Area. *Biodiversity*, *00*(00), 1–15. http://doi.org/10.1080/14888386.2018.1468821

5. Byrne, M., Gall, M., Wolfe, K., Agüera, A., 2016. From pole to pole: the potential for the Arctic seastar *Asterias amurensis* to invade a warming Southern Ocean. *Global Change Biology*.
6. Christiansen, H., Dettai, A., Heindler, F. M., Collins, M. A., Duhamel, G., Hautecoeur, M., … Van de Putte, A. P. (2018). Diversity of Mesopelagic Fishes in the Southern Ocean - A Phylogeographic Perspective Using DNA Barcoding. *Frontiers in Ecology and Evolution*, *6*(September). http://doi.org/10.3389/fevo.2018.00120
7. Collard, M., De Ridder, C., David, B., Dehairs, F., Dubois, P., 2014. Could the acid-base status of Antarctic sea urchins indicate a better-than-expected resilience to near-future ocean acidification? *Global Change Biology*, 21(2): 605–617.
8. Constable, A. J., Costa, D. P., Schofield, O., Newman, L., Urban, E. R., Fulton, E. A., … Willis, Z. (2016). Developing priority variables (“ecosystem Essential Ocean Variables” — eEOVs) for observing dynamics and change in Southern Ocean ecosystems. *Journal of Marine Systems*. http://doi.org/10.1016/j.jmarsys.2016.05.003
9. d’Udekem d’Acoz, C., Havermans, C., 2015. Contribution to the systematics of the genus *Eurythenes* I. Smith in Scudder, 1882 (Crustacea: Amphipoda: Lysianassoidea: Eurytheneidae). *Zootaxa* 3971(1): 001-080.
10. David, B., Saucède, T., Chenuil, A., Steimetz,E., De Ridder, C. 2016. The taxonomic challenge posed by the Antarctic echinoids *Abatus bidens* and *Abatus cavernosus* (Schizasteridae, Echinoidea). *Polar Biology* 39 : 897-912.
11. De Pooter, D., Appeltans, W., Bailly, N., Bristol, S., Deneudt, K., Eliezer, M., … Hernandez, F. (2017). Toward a new data standard for combined marine biological and environmental datasets - expanding OBIS beyond species occurrences. *Biodiversity Data Journal*, *5*, e10989. http://doi.org/10.3897/BDJ.5.e10989
12. Delille, B., Van der Linden, F., Carnat, G., Sapart, C., De Jong, J., Kotovitch, M., Deman, F., Deharis, F., Descy, J-P., Nomura, D., Stammerjohn, S., Ackley, S., Tison, J-L. (2018) Biogeochemistry at the early stages of ice formation; Insights from PIPERS. *Polar 2018: Abstract Proceedings* (pp. 977)
13. Deman, F., Fripiat, F., Roukaerts, A., Meiners, K., Lannuzel, D., Vancoppenolle, M., ... Dehairs, F. (2017). POC, PON, DOC, DON: Antarctic pack ice data compilation. *BEPSII / ECVice meeting* (pp. 3)
14. Deman, F., Roukaerts, A., Delille, B., Fripiat, F., Lannuzel, D., Tison, J. L., & Dehairs, F. (2016). A time series study during spring transition in the fast ice at Davis station, Antarctica: preliminary results. *International Symposium on Polar Environmental Change and Public Governance: Collection of Abstracts* (pp. 19-20)
15. Deman, F., Roukaerts, A., Fripiat, F., Delille, B., Tison, J. L., & Dehairs, F. (2018). Biogeochemistry of Antarctic landfast sea ice and the potential role of biofilm. *Polar 2018: Abstract Proceedings* (pp.975)
16. Deman, F., Roukaerts, A., Fripiat, F., Lannuzel, D., & Dehairs, F. (2017). Nitrate isotopic composition in landfast sea ice: a time series study. *Gordon Research Conference: Polar Marine Science: Understanding Polar Ecosystem Change Through Time Series Observations, Technological Advances, and Biophysical Coupled Modeling*
17. Fabri-Ruiz, S., Danis, B., David, B., & Saucède, T. (2018). Can we generate robust species distribution models at the scale of the Southern Ocean? *Diversity and Distributions*, (July), 1–17. http://doi.org/10.1111/ddi.12835
18. Fripiat F., M. Declercq, C.J. Sapart, L.G. Anderson, V. Bruechert, F. Deman, D. Fonseca-Batista, C. Humborg, A. Roukaerts, I.P. Semiletov, and F. Dehairs, 2018. Influence of the bordering shelves on nutrient distribution in the Arctic halocline

inferred from water column nitrate isotopes, *Limnology and Oceanography*, 63, 2154-2170, https://doi.org/10.1002/lno.10930, https://doi.org/10.1002/lno.10930.

19. Fripiat, F., Sigman, D.M., Fawcett, S.E. , Rafter, P.A. , Weigand, M.A. , Tison, J.L., 2014. New insights into sea ice nitrogen biogeochemical dynamics from nitrogen isotopes. *Global Biogeochemical Cycles* 28(2): 115-130
20. González-Wevar, C.A., Chown, S.L., Morley, S., Coria, N., Saucède, T., Poulin, E. 2016. Out of Antarctica: quaternary colonization of sub-Antarctic Marion Island by the limpet *Nacella* (Patellogastropoda: Nacellidae). *Polar Biology*, 39(1): 77-89,
21. González-Wevar, C.A., Hüne, M., Rosenfeld, S., Saucède, T., Féral, J.P., Mansilla, A., Poulin E., 2016. Patterns of genetic diversity and structure in Antarctic and sub-Antarctic Nacella (Patellogastropoda: Nacellidae) species. *Biodiversity*, http://dx.doi.org/10.1080/14888386.2016.1181573
22. Guillaumot C, Artois J, Saucède T, Demoustier L, Moreau C, Eléaume M, Agüera A, Danis B. accepted. Species distribution models in a data-poor and broad scale context. *Progress in Oceanography*.
23. Guillaumot C, Saucède T, Danis B. accepted. Influence of environmental descriptor choice in modelling Southern Ocean benthic species distributions. *Diversity and Distribution*.
24. Guillaumot, C., Alexis, S. F., Marc, M., Danis, B., & Thomas, J. F. (2018). Benthic species of the Kerguelen Plateau show contrasting distribution shifts in response to environmental changes, (September 2017), 1–16. http://doi.org/10.1002/ece3.4091
25. Gutt, J., Alvaro, M.C., Barco, A., Böhmer, A., Bracher, A., David, B., De Ridder, C., Dorschel, B., Eléaume, M., Janussen, D., Kersken, D., Lopez-González, P.J., Martınez-Baraldés, I., Schröder, M., Segelken-Voigt, A., Teixido, N., 2016. Macroepibenthic communities at the tip of the Antarctic Peninsula, an ecological survey at different spatial scales. *Polar Biology* 39:829–849
26. Hauquier, F., Ballesteros-Redondo, L., Gutt, J., Vanreusel, A., 2016. Community dynamics of nematodes after Larsen ice-shelf collapse in the Eastern Antarctic Peninsula. *Ecology and Evolution*, 6(1): 305–317
27. Hauquier, F., Durán Suja, L., Gutt, J., Veit-Köhler, G., Vanreusel, A., 2015. Different oceanographic regimes in the vicinity of the Antarctic Peninsula reflected in benthic nematode communities. *PLOS ONE,* 10(9)
28. Hauquier, F., Leliaert, F., Rigaux, A., Derycke, S., & Vanreusel, A. (2017). Distinct genetic differentiation and species diversification within two marine nematodes with different habitat preference in Antarctic sediments. *BMC Evolutionary Biology*, *17*(1), 120. http://doi.org/10.1186/s12862-017-0968-1
29. Havermans, C., & Smetacek, V. (2018). Bottom-up and top-down triggers of diversification: A new look at the evolutionary ecology of scavenging amphipods in the deep sea. *Progress in Oceanography*, *164*(July 2017), 37–51. http://doi.org/10.1016/j.pocean.2018.04.008
30. Havermans, C., 2016: Have we so far only seen the tip of the iceberg? Exploring species diversity and distribution of the giant amphipod Eurythenes, Biodiversity, DOI: 10.1080/14888386.2016.1172257
31. Havermans, C., Seefeldt, M. A., & Held, C. (2018). A biodiversity survey of scavenging amphipods in a proposed marine protected area: the Filchner area in the Weddell Sea, Antarctica. *Polar Biology*. http://doi.org/10.1007/s00300-018-2292-7
32. Heindler, F.M., Christiansen, H., Frederich, B., Dettai, A., Lepoint, G., Maes, G.E., Van de Putte, A. P., & Volckaert, F.A.M. (2018). Historicla DNA metabarcoding of the

prey and microbiome of trematomid fishes using museum samples. *Frontiers in Ecology and Evolution*, https://doi.org/10.3389/fevo.2018.00151

33. Hoffmann R., Pasotti F., Vázquez S., Torstensson A., MacCormack W., Wenzhöfer F., Braeckman U. "Spatial variability of biogeochemistry in shallow coastal benthic communities of Potter Cove (Antarctica) and the impact of a melting glacier", *PLoS One,* 2018 doi: 10.1371/journal.pone.0207917
34. Kašparová, E., Van de Putte, A. P., Marshall, C., Janko, K. (2015). Lifestyle and Ice: The Relationship between Ecological Specialization and Response to Pleistocene Climate Change. *Plos One*, *10*(11), e0138766
35. Kocot, K.M, Christiansen, H., Zapata Guardiola, R., Sands, C., Held, C. (2016) 3.2.1 Phylogeny, phylogeography and population genetics of High Antarctic biota. In: Schröder, M. (2016) The Expedition PS96 of the Research Vessel POLARSTERN to the southern Weddell Sea in 2015/2016. Berichte zur Polar- und Meeresforschung.
36. Kotovitch, M., Fripiat, F., Moreau, S., Deman, F., Vanderlinden, F., Tison, J. L., & Delille, B. (2016). Sea Ice - Source or sink for nitrous oxide. *International Symposium on Polar Environmental Change and Public Governance: Collection of Abstracts* (pp. 25-26)
37. Kotovitch, M., Tison, J. L., Fripiat, F., Deman, F., Sapart, C., Carnat, G., ... Delille, B. (2017). N2O production and cycling within Antarctic sea ice. In *Book of abstracts: XIIth SCAR Biology Symposium* (pp. 382)
38. Lannuzel, D., Chever, F., van der Merwe, P., Janssens, J., Roukaerts, A., Cavagna, A. J., Meiners, K. (2016). Iron biogeochemistry in Antarctic pack ice during SIPEX-2. Deep-Sea Research Part II. Topical Studies in Oceanography, 131, 111-122. DOI: 10.1016/j.dsr2.2014.12.003
39. Michel L. N., Danis B., Dubois P., Eleaume M., Fournier J., Gallut C., Jane P. & Lepoint G. (2019). Staying cool has also consequences: Increased sea ice cover disrupts food web structure in East Antarctica. *Scientific Reports* (in press)
40. Michel, L.N., David, B., Dubois, Ph., Lepoint, G., De Ridder, C., 2016. Trophic plasticity of Antarctic echinoids under contrasted environmental conditions. *Polar Biology* 39:913–923
41. Moreau, C., Saucède, T., Jossart, Q., Agüera, A., Brayard, A., & Danis, B. (2017). Reproductive strategy as a piece of the biogeographic puzzle: a case study using Antarctic sea stars (Echinodermata, Asteroidea). *Journal of Biogeography*, doi: 10.1111/jbi.12965
42. Pasotti, F., Manini, E., Giovannelli, D., Wölfl, A.-C., Monien, D., Verleyen, E., Braeckman, U., Abele, D., Vanreusel, A., 2015. Antarctic shallow water benthos in an area of recent rapid glacier retreat, Mar. Ecol. 36(3): 716–733,
43. Pasotti, F., Saravia, L.A., De Troch, M., Tarantelli, M.S., Sahade, R., Vanreusel A., 2015. Benthic trophic interactions in an Antarctic shallow water ecosystem affected by recent glacier retreat. *Plos One,* 10(11): e0141742
44. Roukaerts A, Cavagna A-J, Fripiat F, et al. (2016) Sea-ice algal primary production and nitrogen uptake rates off East Antarctica. *Deep-Sea Research,* Part II, 131:1–10. doi: 10.1016/j.dsr2.2015.08.007.
45. Roukaerts A., Cavagna, A.-J., Fripiat, F., Lannuzel, D., Meiners, K.M., Dehairs, F., 2015. Sea-ice algal primary production and nitrogen uptake rates off East Antarctica, *Deep-Sea Research II*
46. Roukaerts A., D. Nomura, F. Deman, H. Hattori, F. Dehairs, F. Fripiat, 2018. The effect of melting treatments on the assessment of biomass and nutrients in sea ice

(Saroma-ko lagoon, Hokkaido, Japan), *Polar Biology*, (https://doi.org/10.1007/s00300-018-2426-y).

47. Roukaerts, A., Deman, F., Fripiat, F., & Dehairs, F. (2017). New insights in Antarctic fast ice biogeochemistry, the role of biofilm. *Book of abstracts: XIIth SCAR Biology Symposium* (pp. 384)
48. Saucède, T. 2016. Martin Rauschert and Wolf E. Arntz: Antarctic macrobenthos: a field guide of the invertebrates living at the Antarctic seafloor. *Polar Biology*, 39(4): 759-760
49. Saucède, T., Díaz, A., Pierrat, B., Sellanes, J., David, B., Féral, J.-P., Poulin, E. , 2015. The phylogenetic position and taxonomic status of Sterechinus bernasconiae Larrain, 1975 (Echinodermata, Echinoidea), an enigmatic Chilean sea urchin. *Polar Biology* 38:1223–1237
50. Van der Linden, F., Moreau, S., Champenois, W., Heinesch, B., Carnat, G., Kotovitch, M., Fripiat, F., Deman, F., Deharis, F., Haskell, T., Tison, J-L., Delille, B. (2018) Antarctic landfast sea ice: Autotrophy vs. Heterotrophy, Sink vs. Source of CO_2. *Polar 2018: Abstract Proceedings* (pp. 757)

6.2 Submitted (4)

1. Saucède T, Guillaumot C, Michel L, Fabri-Ruiz S, Bazin A, Cabessut M, García-Berro A, Mateos A, Mathieu O, De Ridder C, Dubois P, Danis B, David B, Díaz A, Lepoint G, Motreuil S, Poulin E & Féral JP. *submitted*. Modeling species response to climate change. Case study of echinoids on the Kerguelen Plateau. *CCAMLR Science*.

2. Dehnhard N., Achurch H., Clarke J., , Michel L. N., Southwell C., Sumner M., Eens M. & Emmerson L. High inter- and intra-specific niche overlap among three sympatrically breeding, closely-related seabird species. Generalist foraging as an adaptation to a highly variable environment. Under consideration for possible publication in *Journal of Animal Ecology.*
3. Michel L. N., Danis B., Dubois P., Eleaume M., Fournier J., Gallut C., Jane P. & Lepoint G. Staying cool also has consequences: increased sea ice cover disrupts food web structure in East Antarctica. Under consideration for possible publication in *Scientific Reports*.
4. Saucède T., Guillaumot C., Michel L. N., Fabri-Ruiz S., Bazin A., Cabessut M., García-Berro A., Mateos A., Mathieu O., De Ridder C., Dubois P., Danis B., David B., Díaz A., Lepoint G., Motreuil S., Poulin E. & Féral J.-P. Modeling species response to climate change in Sub-Antarctic islands: Echinoids as a case study for the Kerguelen Plateau. Under consideration for possible publication in *CCAMLR Science*.

6.3 In preparation (12)

1. Christiansen, H., Heindler, F.M., Dettai, A., Collins, M.A., Couloux, A., Duhamel, G., Hautecoeur, M., Steinke, D., Volckaert, F.A.M., Van de Putte, A.P. Diversity of mesopelagic fishes in the Southern Ocean - a phylogeographic perspective.
2. Christiansen, H., Heindler, F.M., Hellemans, B., Jossart, Q., Pasotti, F., Robert, H., Verheye, M., Danis, B., Kochzius, M., Leliaert, F., Moreau, C., Patel, T., Van de Putte, A.P., Vanreusel, A., Volckaert, F.A.M., & Schön, I.. Facilitating Southern Ocean population genomics of non-model species: optimized experimental design for reduced representation sequencing.

3. Christiansen, H., Heindler, F.M., Van de Putte, A.P., Volckaert, F.A.M. Large and fine scale population genomics of the Antarctic fish *Notothenia coriiceps* reveal spatial genetic structure and genotype-environment associations.
4. Di Giglio, S., Angulo-Preckler, C., Pernet, Ph., Avila, C., Dubois, Ph. The future of polar echinoderms assessed in the light of Antarctic hydrothermal vents. to be submitted to *Global Change Biology.*
5. Fripiat F., M. Declercq, C. Sapart, L.G. Anderson, V. Bruechert, F. Deman, D. Fonseca-Batista, C. Humborg, A. Roukaerts, and F. Dehairs, Benthic pelagic coupling in the East Siberian Sea inferred from nitrate isotopes, to be submitted to *Limnology and Oceanography.*
6. Hauquier F., Leliaert F., Derycke S., Rigaux A., Vanreusel., A. Habitat-linked population genetic differentiation and species diversification in two Antarctic nematodes.
7. Hauquier, F., Verleyen, E, Tytgat, B, Vanreusel, A. Different dispersal and drivers for distribution in surface and subsurface benthic nematodes of the Southern Ocean continental shelf zone.
8. Heindler, F.M., Christiansen, H., Maes, S.M.T., Frederich, B., Michel, L.N., Dettai, A., Desvignes, T., Maes, G.E., Van de Putte, A.P., & Volckaert, F.A.M. Combined microbiome and stomach content DNA metabarcoding demonstrate novel food web links and microbiome-host interactions along an evolutionary bentho-pelagic gradient in fishes of the Southern Ocean.
9. Le Bourg B., Lepoint G., Balthasart P. & Michel L. N. Assessment of the influence of preservation methodology on stable isotope compositions in sea stars
10. Michel L. N., Nyssen F., Dauby P. & Verheye M. Mandible morphology does not necessarily reflect feeding habits in Antarctic amphipods.
11. Pasotti, F., Braeckman, U., Lefaible, N., Hoffmann, R. & Vanreusel, A. “Antarctic fjord soft sediment benthos: a snapshot at different scales.”
12. Roukaerts A., D. Nomura, F. Fripiat, H.Hattori, F. Deman, F. Dehairs, The effect of melting protocol on biogeochemical parameters measured in sea ice samples from the Saroma Lagoon (Hokkaido, Japan), to be submitted to *Polar Biology*.

6.4 Data papers (6)

1. Fabri-Ruiz, S., Saucède, T., Danis, B., & David, B. (2017). Southern Ocean Echinoids database – An updated version of Antarctic, Sub-Antarctic and cold temperate echinoid database. *ZooKeys*, *697*, 1–20. http://doi.org/10.3897/zookeys.697.14746
2. Guillaumot, C., Martin, A., Fabri-Ruiz, S., Eleaume, M., & Saucède, T. 2016. Echinoids of the Kerguelen Plateau - occurrence data and environmental setting for past, present, and future species distribution modelling. Zookeys 630: 1-17, doi: 10.3897/zookeys.630.9856
3. Jossart, Q., Moreau, C., Aguera, A., Broyer, C. De, Danis, B., 2015. The Register of Antarctic Marine Species (RAMS): a ten-year appraisal. *ZooKeys*, 524: 137-145
4. Moreau, C., Aguera, A., Jossart, Q., Danis, B., 2015. Southern Ocean Asteroidea: a proposed update for the Register of Antarctic Marine Species. *Biodiversity Data Journal*, 25(3):e7062

5. Moreau, C., Mah, C., Agüera, A., Améziane, N., Barnes, D., Crokaert, G., … Danis, B. (2018). Antarctic and Sub-Antarctic Asteroidea database. *ZooKeys*, *747*, 141–156. http://doi.org/10.3897/zookeys.747.22751
6. Saucède, T., Griffiths, H.J, Moreau, C., Jackson, J., Sands, C., Downey, R., Reed, A. , Mackenzie, M., Geissler, P., Linse, K., 2014. East Weddell Sea echinoids from the JR275 expedition. *ZooKeys 504: 1-10*

6.5 Datasets (51)

The vERSO datasets are progressively documented in the vERSO Information System.

1. Acid-base physiology in echinoderms. *In situ* parameters (temperature, salinity and oxygen saturation) obtained from a CTD. Parameters from seawater samples (pH, alkalinity and DIC). pHT, AT-CF measured in the coelomic fluid of 12 species of echinoderms (Asteroidea, Echinoidea, Holothuroidea)
2. Antarctic Shelf (200-500 m) gene sequence *Desmodora* 18SCOI
3. Antarctic Shelf (200-500 m) gene sequence *Sabatieria* 18S18S
4. Antarctic Shelf (200-500 m) gene sequence *Sabatieria* 18SITS
5. Antarctic Shelf (200-500 m) gene sequence *Sabatieria* COI
6. Antarctic Shelf (200-500 m) gene sequence *Sabatieria* ITS
7. Biogeochemical (Oxygen fluxes, nutrient fluxes, metals, sulfides, TOM, CN, grain size, Chl-a) and biological (meiofauna and macrofauna densities) data from the benthic chambers in situ deployment 2015 (three sites within Potter Cove)
8. Biogeochemical (Oxygen fluxes, nutrient fluxes, TOM, CN, grain size, Chl-a) and biological (meiofauna and macrofauna densities) data from the degradation experiment at Potter Cove
9. Biogeochemical fluxes benthic chambers Potter Cove (King George Island, West Antarctic Peninsula) Benthic chambers biogeochemical fluxes, Pangaea series, Potter Cove, King George Island,West Antarctic Peninsula Processing
10. Biogeochemistry (pigments, sediment grain size, TOM, CN, bacterial abundance and biomass) data of three sites within Potter Cove
11. Biogeochemistry of sediments benthic chambers Potter Cove (King George Island, West Antarctic Peninsula) Benthic chambers biogeochemical fluxes
12. Biological data (densities and biomasses of meiofauna and macrofauna)
13. Carbon, nitrogen and sufur elemental (%C, %N, %S) and stable isotope ($\delta^{13}C$, $\delta^{15}N$, $\delta^{34}S$) compositions of organisms collected during the Proteker 3 campaign (Subantarctic sea urchins, sponges and macro-algae).
14. CO1 sequence data for >1300 asteroids including sample-related metadata (identification, depth, date etc…)
15. Dataset of oceanographic/environmental maps (0.1° resolution) covering the Kerguelen Plateau area for past decades (1955-2012) as well as predictions for 2100 and 2200 (based on IPCC scenario A1B).
16. DNA barcoding data (COI) of 96 putative *T. eulepidotus*, 53 putative *N. coriiceps*, and 29 *Trematomus* spp. (sequenced in the framework of a Bachelor thesis), not published yet, but will be added to BOLD.
17. ROV work at Potter Cove. Benthic diversity mapping data and video transects.
18. Phylogeographic genetic data set with > 1000 COI and few Rho (< 100) sequences of various Antarctic myctophids (lanternfish)
19. Macrofauna biomass Potter Cove 2011 Shallow water meiofauna biomass from three stations at Potter Cove, King George Island, West Antarctic
20. Meiofauna abundance Potter Cove 2010 Shallow water meiofauna abundance from three stations at Potter Cove, King George Island, West Antarctic
21. Meiofauna biomass Potter Cove 2010 Shallow water meiofauna biomass from three stations at Potter Cove, King George Island, West Antarctic

22. Meiofauna biomass Potter Cove 2010 Shallow water meiofauna biomass from three stations at Potter Cove, King George Island, West Antarctic
23. Nematodes DNA sequence data for two genera: *Sabatieria* spp. 18S, ITS and COI ; *Desmodora* spp ITS and COI. All sequences in GENBANK
24. Occurrence data for asteroids from biodiversity information systems (biodiversity.aq; OBIS; GBIF data portal), cleaned, checked and completed with additional data from published literature, including original manuscripts and data papers and cruise reports. 14,000 georeferenced records for latitudes below 45°
25. Physiological measurements in nematodes: extracellular carbon system data, oxygen consumption
26. Potter Cove (King George Island Antarctic Peninsula), West Macrofauna densities Macrofauna densities benthic chambers Pangaea series, Potter Cove, King George Island,West Antarctic
27. Potter Cove (King George Island Antarctic Peninsula), West Macrofauna biomass Macrofauna biomass benthic chambers Pangaea series, Potter Cove, King George Island,West Antarctic
28. Potter Cove (King George Island Antarctic Peninsula), West Macrofauna densities Macrofauna densities spatial/temporal analysis Pangaea series, Potter Cove, King George Island,West Antarctic
29. Potter Cove (King George Island Antarctic Peninsula), West Macrofauna biomass Macrofauna biomass spatial/temporal analysis Pangaea series, Potter Cove, King George Island,West Antarctic
30. Potter Cove (King George Island Antarctic Peninsula), West Macrofauna biomass Macrofauna biomass Macroalgae detritus remineralisation, Pangaea series, Potter Cove, King George Island,West Antarctic
31. Potter Cove (King George Island Antarctic Peninsula), West Meiofauna densities Meiofauna densities benthic chambers Pangaea series, Potter Cove, King George Island,West Antarctic
32. Potter Cove (King George Island Antarctic Peninsula), West Meiofauna biomass Meiofauna biomass benthic chambers Pangaea series, Potter Cove, King George Island,West Antarctic
33. Potter Cove (King George Island Antarctic Peninsula), West Meiofauna densities Meiofauna densities temporal analysis Pangaea series, Potter Cove, King George Island,West Antarctic
34. Potter Cove (King George Island Antarctic Peninsula), West Meiofauna biomass Meiofauna biomass temporal analysis Pangaea series, Potter Cove, King George Island,West Antarctic
35. Potter Cove (King George Island Antarctic Peninsula), West Meiofauna biomass Meiofauna biomass Macroalgae detritus remineralisation, Pangaea series, Potter Cove, King George Island,West Antarctic
36. Stable isotope data of Potter Cove benthos in 2010-2012
37. Stable Isotope data Potter Cove (King George Island, West Antarctic Peninsula) Potter Cove, King George Island, West Antarctic
38. The checklist of Southern Ocean asteroids in the RAMS (Register of Antarctic Marine Species) has been published. 295 accepted species.
39. Two ddRAD data sets with genotypes for 1500 - 3000 SNPs combined, using the same bioinformatics pipeline, with *de novo* assembly and one time aligning to the reference genome of *N. coriiceps*
40. GBS data of *Notothenia ros*sii with ~10000 SNPs genotyped in 354 individuals from the Scotia Arc region and Kerguelen Islands. ddRAD data from 5 Trematomus species.
41. Updated biogeographic dataset of sea urchin occurrence data of the Kerguelen Plateau including a sampling effort time series
42. Two reduced representation sequencing (one ddRAD with *N. coriiceps*, one GBS with *N. rossii*) are available, as well as accompanying COI data for some samples

included in these. Additionally, COI data for 75 fishes from an expedition off the South Orkney Islands is completed. Further COI data of *Trematomus* spp., *Dissostichus mawsoni* and *Aethotaxis mitopteryx* exists. Biological data such as life history parameters for *Notothenia* spp. is being collected at the time of writing. Finally, a large phylogeographic data set of mesopelagic fish of the Southern Ocean is available, consisting of newly created and database harvested COI and Rhodopsin gene sequences.

43. One dataset (120 samples, 11 species) about carbon and nitrogen elemental (%C, %N) and stable isotope (δ^{13}C, δ^{15}N) composition of sea urchins collected during the PS81 (ANTXXIX/3) campaign.
44. One dataset (769 samples) about carbon, nitrogen and sulfur elemental (%C, %N, %S) and stable isotope (δ^{13}C, δ^{15}N, δ^{34}S) composition of benthic invertebrates (28 taxa including sponges, sea anemones, nemerteans, nematods, polychaetes, sipunculians, molluscs, arthropods and echinoderms) and 10 of their potential food items (including benthic macroalgae, benthic biofilm, suspended particulate organic matter, sympagic algae and Pygoscelis adeliae guano) collected during the austral summers 2013-2014 and 2014-2015 on shallow bottoms (0-20 m) around Dumont-d'Urville station (Adélie Land, East Antarctica).
45. One dataset (248 samples, 19 species) about carbon and nitrogen elemental (%C, %N) and stable isotope (δ^{13}C, δ^{15}N) composition of Iphimediidae amphipods collected along the Western Antarctic Peninsula and in Adélie Land between 2006 and 2013.
46. One dataset (419 samples, 41 species) about carbon and nitrogen elemental (%C, %N) and stable isotope (δ^{13}C, δ^{15}N) composition of Notothenioidea fishes collected in the Scotia Sea and Weddell Sea between 2002 and 2015.
47. Carbon and nitrogen elemental (%C, %N) and stable isotope (δ^{13}C, δ^{15}N) composition of sea urchins (120 samples, 11 species) collected during the PS81 (ANTXXIX/3) campaign
48. Carbon and nitrogen elemental (%C, %N) and stable isotope (δ^{13}C, δ^{15}N) composition of Iphimediidae amphipods (248 samples, 19 species) collected along the Western Antarctic Peninsula and in Adélie Land between 2006 and 2013.
49. Carbon and nitrogen elemental (%C, %N) and stable isotope composition (δ^{13}C, δ^{15}N) of Notothenioidea fishes (411 samples, 41 species) collected in the Scotia Sea and Weddell Sea between 2002 and 2015.
50. Carbon, nitrogen and sulfur elemental (%C, %N, %S) and stable isotope (δ^{13}C, δ^{15}N, δ^{34}S) composition of sea stars (currently 1035 samples of 104 taxa, not final) collected in multiple Antarctic and Subantarctic locations from 1985 to 2017.
51. Carbon, nitrogen and sulfur elemental (%C, %N, %S) and stable isotope (δ^{13}C, δ^{15}N, δ^{34}S) composition of benthic invertebrates and their potential food items collected in Kerguelen Islands kelp beds during the Proteker 2016 campaign (currently 342 samples, not final).

6.6 Books (2)

1. David, B., Saucède, T., 2015. Biodiversity of the Southern Ocean. ISTE Press & Elsevier, London, 130 pp.
2. David, B. , Saucède, T., 2015. Biodiversité de l'océan Austral, laboratoire naturel pour l'évolution. ISTE Editions, London, 157 pp.

6.7 Campaign reports (7)

1. Fournier, J., Michel, L., Dubois, P., Gallut, C., Eléaume, M. 2015. REVOLTA - Ressources Ecologiques et Valorisation par un Observatoire à Long terme en Terre Adélie. Programme IPEV n°1124. Année 2. Rapport de campagne d'été 2014-2015, 28 pp.

2. Griffiths, H.J. et al., 2016. SO-AntEco South Orkneys - State of the Antarctic Ecosystem. *RRS James Clark Ross* JR15005 Cruise Report. 149 pp.
3. Kocot, K.M, Christiansen, H., Zapata Guardiola, R., Sands, C., Held, C., 2016. 3.2.1 Phylogeny, phylogeography and population genetics of High Antarctic biota. In: Schröder, M. (2016) The Expedition PS96 of the Research Vessel POLARSTERN to the southern Weddell Sea in 2015/2016. *Berichte zur Polar- und Meeresforschung*.
4. Mark, F.C., Koschnick, N., Scheuffele, H., Papetti, C., Lucassen, M., Strobel, A., Burkhardt-Holm, P., Segner, H., Riginella, E., Mazzoldi, C., La Mesa, M., Christiansen, H., 2016. 3.2.2 Cold adaptation vs. sensitivity to climate change and pollution in Antarctic Notothenioids: Physiological plasticity, genetic regulation, immunology and reproductive traits. In: Schröder, M. (2016) The Expedition PS96 of the Research Vessel POLARSTERN to the southern Weddell Sea in 2015/2016. *Berichte zur Polar- und Meeresforschung.*
5. Saucède, T., Dubois P., Michel L., Motreuil S., 2017. PROTEKER – Impact du changement global sur le benthos et les habitats marins côtiers des Iles Kerguelen. Programme IPEV n°1044 Phase 2, Année 2. Rapport de campagne d’été 3 novembre – 31 décembre 2016, 29 pp.
6. Saucède, T., Dubois P., Motreuil S., 2019. PROTEKER – Impact du changement global sur le benthos et les habitats marins côtiers des Iles Kerguelen. Programme IPEV n°1044 Phase 2, Année 4. Rapport de campagne d’été 3 novembre – 29 décembre 2018, 61 pp.
7. Saucède, T., Marty, G., Fabri-Ruiz, S., Fournier, J., De Ridder, C., 2015. PROTEKER - Impact du changement global sur le benthos et les habitats marins côtiers des Iles Kerguelen. Programme IPEV n°1044 Année 1. Rapport de campagne d’été 18 novembre – 23 décembre 2015, 33 pp.

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