B121 Cruise report

23rd February to 24th March 2019

To the crew of R/V *Australis*
To our families and friends

Executive Summary

The Belgica121 expedition (B121) ventured to explore the marine biodiversity of the West Antarctic Peninsula (WAP) to test the concept of using a nimble sampling platform, the R/V *Australis*, a steel hulled, fully rigged motor sailor. Named as a tribute to the first international scientific expedition in Antarctica lead by Adrien de Gerlache in 1897-99 (onboard the *Belgica*), B121 took place between February and March 2019, sampling 15 stations in 22 working days in an area extending from the Berthelot (65°19.751 S, 64°08.263 W) to the Melchior Islands (64°19.246 S, 62°55.375W). Deploying 20 different types of gear (both traditional and modern), the B121 team gathered over 1700 samples that will be brought back to Belgium for further identification (by taxonomic experts) and analyses (isotopes, population genetics or genomics…). The team focused on biodiversity assessments, from the intertidal to subtidal zone (20 m) in coastal areas with contrasting characteristics regarding their exposure to glaciers, oceanographic characteristics and intensity of touristic activities. Other projects included population genetics studies, trophic ecology, environmental DNA, microplastics surveys and more (see full report below for details).

The use of R/V *Australis* for coastal studies deemed to be extremely efficient, in terms of environmental impact (ca. 150x less CO_2 emissions than a Polar class icebreaker) and reactivity, allowing the team to adapt the sampling efforts in function of the weather or anchoring conditions. Fully devoted to the expedition, the ship allowed the B121 team to sample in shallow areas, not accessible to icebreaker and too far away from research stations, and which have been under sampled.

Regarding the biodiversity census, the B121 expedition worked on various realms/taxonomic levels including the intertidal, soft sediments, macro- and megabenthos, fish, birds and marine mammals. Seven stations were investigated for the intertidal (MI, NH, UI, SK, HI, GR and FH) with a total of 121 measurements in quadrats. The average number of species per station was 18. *Kidderia bicolor* (bivalve), *Obrimoposthia wandeli* (flat worm) and *Laevilitorina caliginosa* (gastropod) were the most abundant organisms (up to thousands of individuals per m^2).

Sediment type (9 to 22 meters depth) ranged from complete silt in the anoxic inner basin at the anchorage site of Hovgaard Island or Neko Harbor, to sandier and well oxygenated sediments of Green Reef. At a first glance the macrofauna pre-sieved samples showed very poor communities in the anoxic sediments, with only small gastropods and few motile taxa such as amphipods, which were present in small numbers. A qualitative analysis of macrofauna will be carried out and biomass will be estimated for both soft sediment metazoan size classes and referred either to surface (for the core and Van Veen sampling) or to sediment volume (for the scooping sampling method).

Regarding the mega/macro benthos (9 to 20 meters depth), 53 common species were identified. They were frequently observed directly *in situ* during the 38 dives performed at the nine sites, or after the dives when watching the 12 video transects... In total, 164 fish specimens were collected, most of them belonging to five species, i.e. *Trematomus newnesi*, *Notothenia coriiceps*, *Harpagifer antarcticus*, *Trematomus bernacchii* and *Notothenia rossii*. The spatial distribution of samples is patchy with most specimens collected at Føyn Harbor and Useful Island. Several localities yielded less than a dozen fish preventing spatial comparisons of fish catches. Fish samples collected represent a valuable collection of the Antarctic shallow water fish fauna, which is dominated by notothenioids. Regarding the birds and marine mammals, a total of 46 standard counts were carried out all along the

cruise track (from the Beagle channel to the southernmost visited site of the cruise at Berthelot Islands along the Antarctic Peninsula and the Drake passage. 26 species of birds, 3 species of cetaceans and 4 species of pinnipeds were observed. Finally, several attempts (in 4 different locations) were unsuccessfully ran to sample snow petrel feathers for a project on this species phylogeography and taxonomy.

Other projects were carried out during the expedition, focusing on habitat mapping, population genomics and eDNA sampling to gain further insights into the region's biodiversity levels. Twelve video transects were carried out, one or two at each station, to characterize the shallow habitats. Although Antarctic shallow benthic communities are usually considered depauperated with very low biomass and abundances compared to deeper communities of the Antarctic continental shelf, preliminary results suggest the occurrence of highly diverse shallow communities depending on local conditions. A preliminary correspondence analysis of common taxon distribution suggests marked differences between the considered stations. An in- analysis of the video transects and the relative surface mapped will help further describe biotic interactions and community composition and diversity. The population genomics project was carried out to advance a technological pilot study undergoing in the framework of the RECTO project. A range of organisms were sampled for this purpose, including 83 ostracods, 227 amphipods, 65 bivalves, 16 sea stars and 81 fish.The pilot study focuses on the evaluation and optimization of reduced representation sequencing protocols, more specifically RADseq.. Eventually, RADseq should yield thousands of genotypes per specimen, which will help to identify any potential local adaptation patterns possibly linked to the contrasting environmental and community conditions. For the eDNA project, 8 sampling events were conducted at four major stations that correspond roughly to the widest spatial extent of the expedition. DNA will be extracted from the filters in dedicated eDNA lab spaces at the KU Leuven. Subsequent high-throughput sequencing of the obtained metabarcoding libraries should enable species-level presence-absence detection.
Complimentary projects were ran during the expedition, including a microplastics survey, oceanographic measurements in selected sites, biogeochemistry and trophic ecology as well as macrophotography. For the microplastics survey, a total of 36 samples of sediment and organisms were taken at eight sites between 5m and 20m depth. Sea stars and filter feeding bivalve were sampled for the biotic part of this project. Analyses will be performed in collaboration with Heriot Watt University (Edinburgh, UK) as a part of a PhD thesis ongoing at the ULB Marine Biology Lab. With regards to the oceanographic measurements, 17 CTD casts were carried out in ten sites to characterize water masses parameters. A deep (400m) cast was carried out before Arctowski Peninsula (AP) in conjunction with an eDNA sampling effort. Biogeochemistry analysis will be carried out on soft sediment from the different sampling sites. Sediments will be characterized at the University of Ghent analyses to determine the granulometry (median grain size, size fraction%), total organic matter content (TOM), Total Organic Carbon (TOC%) content, Total nitrogen content (TN%), and pigments content. For trophic ecology, 156 samples counting 24 different species and over 650 specimens were collected at seven sites between 8m and 20m depth. Water and sediment samples were collected at each site. Specimens of seaweeds were sampled as potential food sources while other organisms were collected from different trophic guilds, among primary and secondary consumers, filter feeders, predators/scavengers and terminal consumers. Isotope analysis of $\partial^{13}C$, $\partial^{15}N$, and $\partial^{34}S$ will be carried out at the University of

Liège. Trophic models will be developed to characterize species trophic niches and plasticity, as well as the main structures of trophic networks in shallow coastal habitats of the visited sites. Finally, 143 specimens were macro-photographed during the expedition. The most photographed phyla were Arthropoda (56 specimens) followed by Echinodermata (23), Mollusca (18), Polychaeta (14) and Chordata (10). Both overview and close up pictures of the specimens were captured.

From the initial results, in terms of sampling diversity of projects and fuel efficiency, it appears that the B121 expedition was extremely successful. Further analysis is of course needed to better characterize the biodiversity and run the multiple analysis, but it is recommended that the concept of using a more nimble platform for shallow biodiversity works in the Southern Ocean should be more widely considered, as a complementary approach to traditional approaches which are either based in research station, or along logistics-driven polar icebreaker routes.

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Background

There is a dearth of knowledge about biological and habitat diversity levels found in shallow areas from the Southern Ocean, a situation opposite to that found in other oceans. These ecosystems are exposed to fast-paced changes in key environmental parameters (seawater temperature, salinity, primary production, sea-ice regimes, ice-shelf loss/collapse) and host organisms which have been facing past events shaping the function and structure of ecosystems. The RECTO/vERSO projects funded by the Belgian Science Policy Office (BELSPO) have identified plasticities (trophic, dispersive) and connectivities as key areas of research to understand the response of Antarctic ecosystems to environmental changes.
The Belgica 121 (B121) expedition aims at exploring the surroundings of the Gerlache Strait (Western Antarctic Peninsula) and to carry out a biodiversity census focusing on intertidal and shallow areas using both classic descriptive marine ecology methods as well as state-of-the art techniques (habitat mapping, genetics, trophic ecology). The expedition also bears a strong historic link to the first scientific expedition to overwinter in Antarctica in 1897-99 recording the first intertidal biodiversity data 121 years ago. This historic expedition was led by Adrien de Gerlache onboard the *Belgica*.
The present report gives a detailed account of the preliminary results of the B121 expedition.

Objectives of the expedition

The overarching objective of the expedition was to gather samples and data to help building a benchmark to better understand the response of shallow benthic communities to contrasting glacial regimes in a fast-warming region of the Southern Ocean, the West Antarctic Peninsula (WAP). It is hoped that the collected samples will refine insights gained in the plasticity/resilience of these communities in the framework of the RECTO/vERSO projects.
The objective was tackled by using a multi-faceted approach matched by the complementary competences of the scientific crew and the sampling gear.
The expedition was a unique opportunity to address a series of underlying scientific/logistic questions including:

- to test the concept of using a nimble platform for Antarctic marine biology field work and its potential to fill knowledge gaps with a limited environmental impact
- to map the marine habitats in selected locations of the Gerlache Strait
- to assess the levels of biodiversity in various locations in the West Antarctic Peninsula (WAP), from the supratidal to 20 m depth
- to model trophic networks in fast-changing environmental conditions
- to run a survey of plastic contamination, including adsorbed pollutants (organic and inorganic)

Expedition members

Expedition leader:
Bruno Danis[1]

R/V *Australis* Crew
Skipper: Ben Wallis[7]
First mate: Ryan Houston[7]
Stewardess: Katy Lucas[7]

Scientific team:
Camille Moreau[1, 4]
Charlène Guillaumot[1, 4] (diver)
Francesca Pasotti[2] (diver)
Franz Heindler[3]
Henri Robert[6]
Henrik Christiansen[3]
Quentin Jossart[5]
Thomas Saucède[4] (diver)

Affiliations :

1. Université Libre de Bruxelles
2. Gent Universiteit
3. KU Leuven
4. Université Bourgogne Franche-Comté
5. Vrije Universiteit Brussel
6. EMC[2]
7. Ocean Expeditions

Figure 1: the B121 expedition crew, photo by Henri Robert

The R/V *Australis*

Research vessel AUSTRALIS is a steel hulled, fully rigged motor sailor registered as a commercial – Category 0 (zero – Unrestricted) vessel for cargo and passengers. She carries a comprehensive range of safety, operational and navigational equipment. A 180hp Gardner diesel engine powers the vessel and she is equipped with 2 zodiac tenders. She sails very well and has a powerful engine to push her along at 8+ knots when needed. The general layout of the boat is shown in Figure 2 and Figure 3.

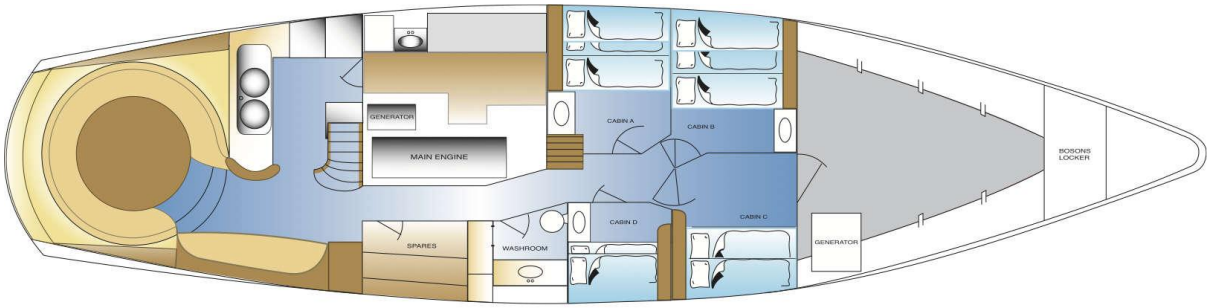

Figure 2: general layout of the cabins of R/V Australis

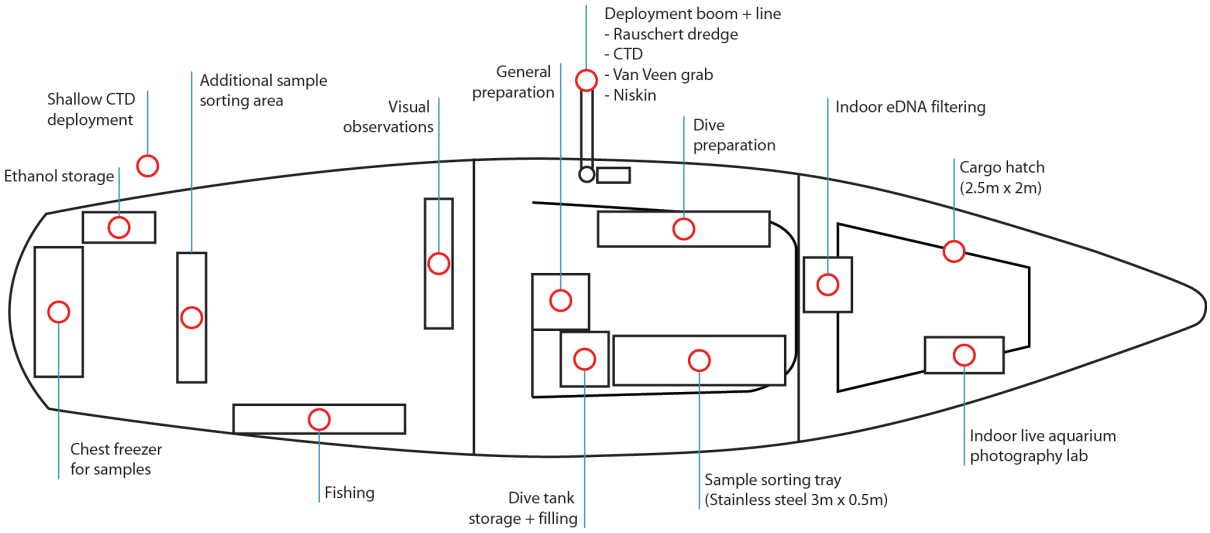

Figure 3: deck layout – deploy and working areas of R/V Australis

Specific equipment was added to the vessel in order to run the scientific mission and deploy the sampling gear in an efficient manner (Figure 3). This gear included a deploy boom and 400 m x 8 mm Dyneema deploy line (SLW 2800kg), a 2 x 0.6 m stainless steel sample sorting tray, a Van Veen benthic grab, and air compressors for diving tanks.

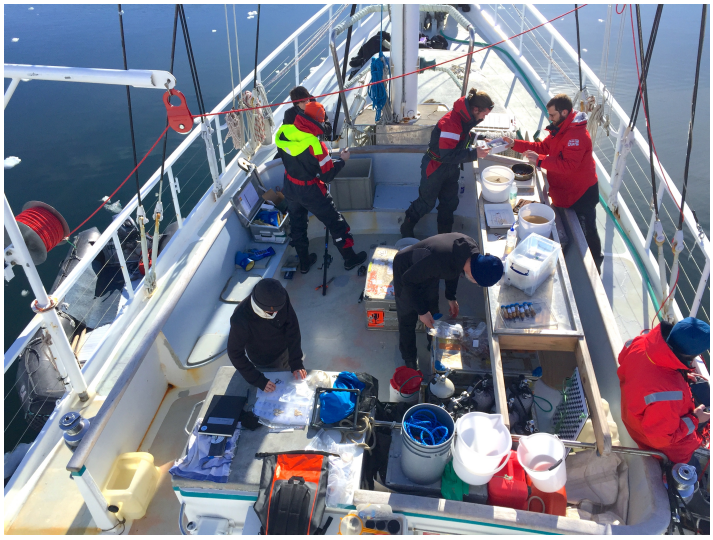

Figure 4: general view of the outdoor working space

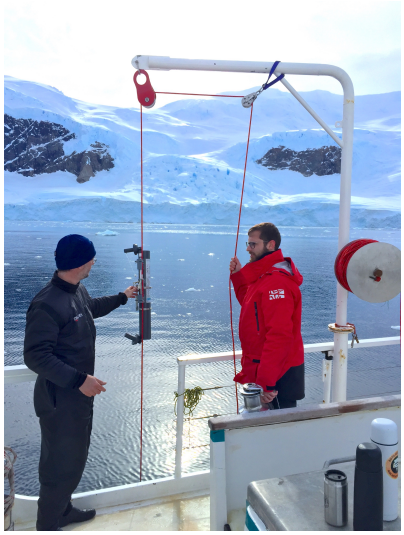

Figure 5: Deploying the Niskin bottle using the deployment boom.

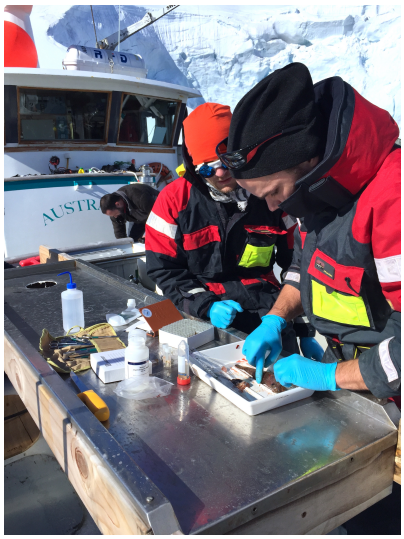

Figure 6: Sorting and processing samples on the tray

Calendar

The expedition took place between Feb 23rd and March 24th, 2019. The *Australis* departed from Ushuaia (Argentina) on Feb 23rd and arrived at the first sampling station (Melchior Islands) on Feb 27th after crossing the Drake passage in strong headwinds. The last station was completed on March 20th and the expedition returned to Ushuaia on March 24th, a total of 22 days was devoted to the sampling effort, including birds and marine mammals observations.

The timing of the main sampling operations conducted during the expedition is detailed in Table 1 and Table 2. A total of 15 stations were visited, amongst which 7 were fully sampled during the 22 operational days.

Table 1: simplified view of the overall calendar of the B121 expedition

	Monday	Tuesday	Wednesday	Thursday	Friday	Saturday	Sunday
February		19	20	21	22	23	24
	25	26	27	28	1	2	3
March	4	5	6	7	8	9	10
	11	12	13	14	15	16	17
	18	19	20	21	22	23	24
	25	26					

Mobilisation/Demobilisation
CapeHorn/Drake transit
Sampling

Table 2: station list including location and sampling dates. Fully sampled stations are in bold.

Stations		*lat (S)*	*long (W)*	*Arrival*	*Departure*
MI	**Melchior Island**	**64°19.246**	**62°55.375**	**27/02/2019**	**03/03/2019**
MP	Metchnikoff Point	64°02.395	62°34.078	03/03/2019	03/03/2019
NH	**Nekko Harbor**	**64°50.565**	**62°32.009**	**03/03/2019**	**06/03/2019**
SM	SeaMount	64°51.283	62°36.136	06/03/2019	06/03/2019
UI	**Useful Island**	**64°43.146**	**62°52.159**	**06/03/2019**	**08/03/2019**
SK	**Skontorp Cove**	**64°54.190**	**62°51.845**	**08/03/2019**	**10/03/2019**
AC	Alvaro Cove	64°52.206	63°00.054	10/03/2019	11/03/2019
HI	**Hovgaard Islands**	**65°06.057**	**64°04.992**	**11/03/2019**	**13/03/2019**
BI	Berthelot Islands	65°19.751	64°08.263	14/03/2019	14/03/2019
VS	Vernadsky Station	65°14.746	64°15.420	14/03/2019	15/03/2019
CT	Cape Tuxen	64°46.765	63°40.381	15/03/2019	15/03/2019
GR	**Green Reef**	**64°43.590**	**63°16.974**	**15/03/2019**	**17/03/2019**

AP	Arctowski Peninsula	64°35.362	62°31.400	18/03/2019	18/03/2019
FH	**Foyn Harbour**	**64°32.798**	**61°59.885**	**18/03/2019**	**20/03/2019**
EI	Enterprise Islands	64°32.420	61°59.899	20/03/2019	20/03/2019

Sampling Area

The sampling area focused on the West Antarctic Peninsula (WAP) and extended from the Berthelot Islands to the SW to Enterprise Islands to the NE and included a total of 15 stations. Certain stations were exhaustively sampled (see Table 1, in bold) while others were partially worked out as timing, priorities, anchoring and weather allowed. Metchnikoff Point (MP) was visited in order to check the status of historic monument #45.

Figure 7: general map of the sampling area. Red rectangles: complete stations; Orange rectangles: partial stations; Green rectangle: historic monument visit. Modified after MAP "Brabant Islands to Argentine Islands", British Antarctic Survey, Edition 1, 2008.

The expedition track reached a total mileage of 1727 nm, and is shown in Figure 8 (full track) and Figure 9 (sampling area).

Figure 8: Belgica121 expedition track. The red rectangle corresponds to the closeup displayed in Figure 9

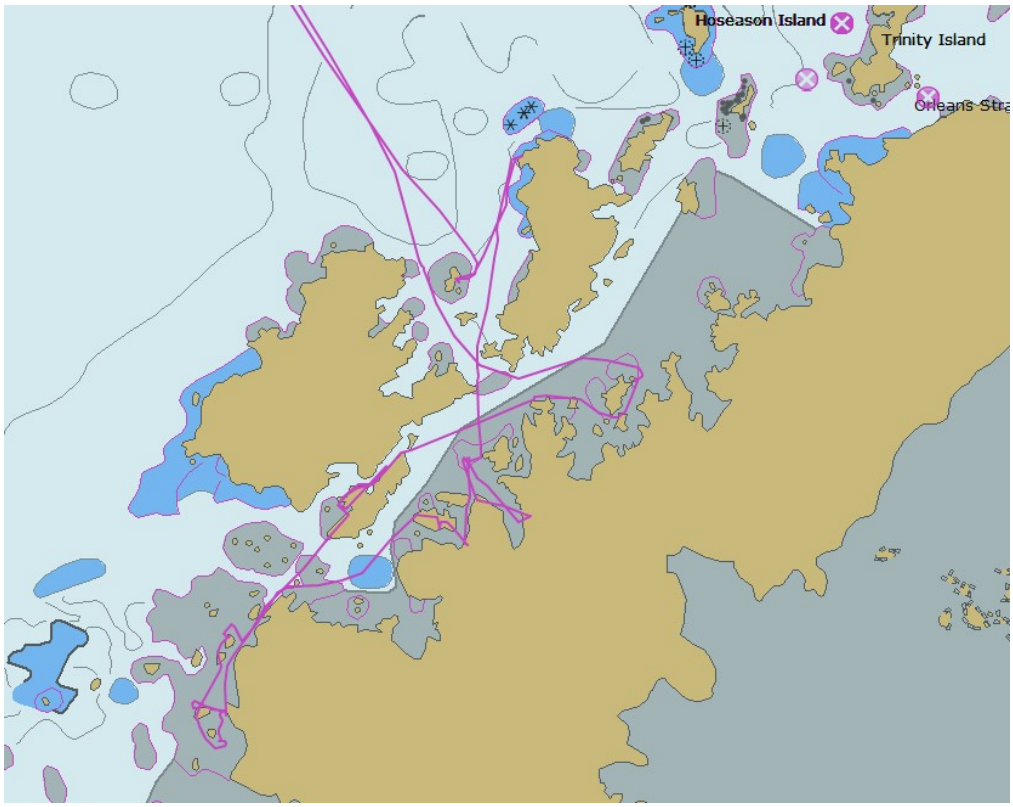

Figure 9: Closeup on the Belgica121 track in the sampling area

The different stations were selected in shallow areas that differ in their geographic location inside and outside Gerlache Strait and their environmental settings: from open sea conditions to protected areas, with contrasting glacier influence and conditions of ice disturbance the proximity of penguin colonies and number of tourists visiting and type of related toruism-activities (landing, zodiac/kayak tours, boat anchorage).

A series of bathymetric maps have been generated using the *Australis* sonar system and are displayed below, for each visited station. All maps use the following codes to describe the sampling effort carried out: intertidal (smiley and figure), dives (red dots and figures), video transects (red rectangles and numbers), Rauschert dredge (yellow lines and figures), Van Veen grabs (yellow triangles and figures), amphipod trap (yellow circle), fish trap (green circle) and gill nets (green arrows and figures).

Melchior Islands (MI)

Figure 10: general view of the anchorage in Melchior Island. Picture: Francesca Pasotti

Location: Palmer Archipelago. North of Gerlache Strait. Open to Drake Passage
Settings:

- protected inner bay. muddy bottom with gravels and dropstones
- low glacier activity and ice disturbance
- no penguin colony
- regularly visited by tourists: usual boat anchorage. kayak and zodiac tours. no landing

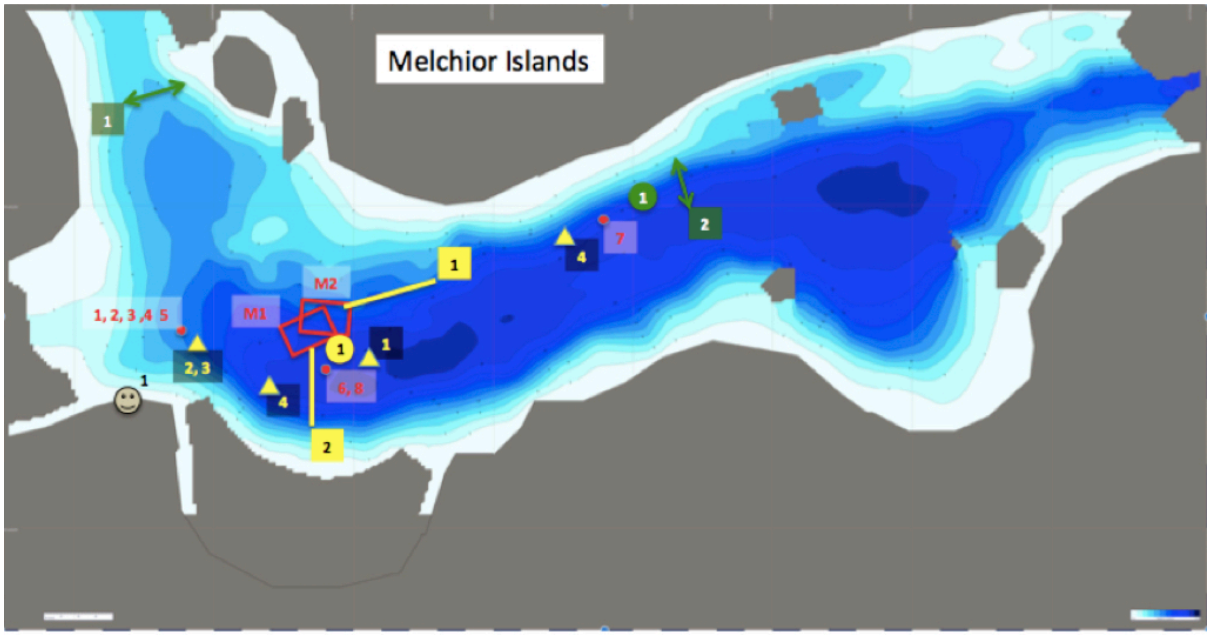

Figure 11: Melchior Islands inner bay. Bathymetric chart showing location of all sampling events. Bathymetric chart is courtesy of Ben Wallis (Ocean Expeditions).

Metchnikoff Point (MP)

Location: western extremity of Pasteur Peninsula in northern Brabant Island.
This station was only visited to inspect historic monument #45 (see section "ASPA Plaque Visit – Metchnikoff Point (MP)").

Neko Harbor (NH)

Figure 12: general view of the anchorage in Neko Harbour. Picture: Francesca Pasotti

Location: Andvord Bay. South East Gerlache Strait
Settings:

- open continental fjord. rocky and gravely bottom with fine sand patches
- High glacier activity and ice disturbance (intense glacier calving and iceberg scouring)
- Gentoo penguin colony
- highly visited by tourists: 20-30.000 landings a year

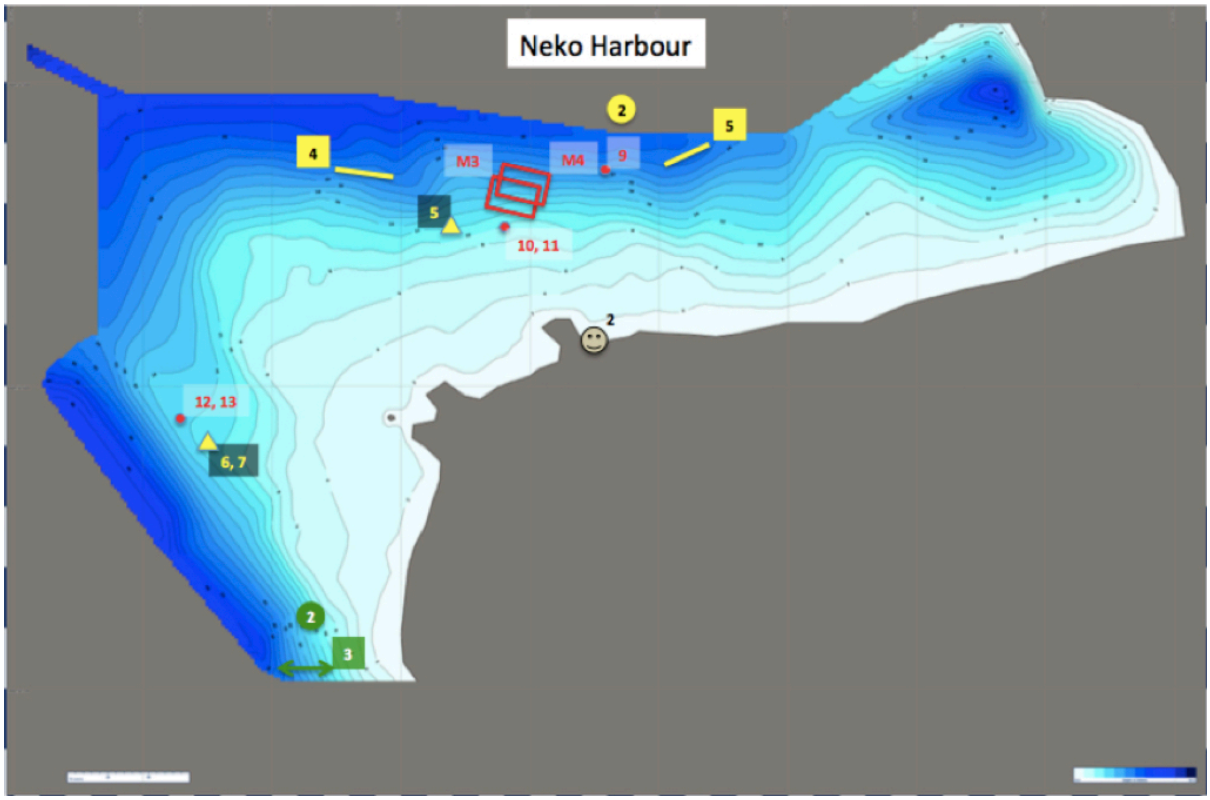

Figure 13: Neko Harbour. Bathymetric chart showing location of all sampling events. Bathymetric chart is courtesy of Ben Wallis (Ocean Expeditions).

Seamount (SM)

Location: Andvord Bay. South East Gerlache Strait

Settings:

- Open continental fjord
- Isolated shallow sea mount
- Many cruise ships passing by

Remark: the seamount was only sampled using a Rauschert Dredge and an ROV dive.

Useful Island (UI)

Figure 14: general view of the anchorage in Useful Island. Picture: Francesca Pasotti

Location: Central South Gerlache Strait
Settings:

- open sea conditions. rocky shallows to muddy substrate with gravels at depth
- no glacier activity. regular but shallow iceberg disturbance
- Gentoo penguin colony
- low tourist activity: zodiac tours mostly

Figure 15: Useful Island. Bathymetric chart showing location of all sampling events. Bathymetric chart is courtesy of Ben Wallis (Ocean Expeditions).

Skontorp Cove (SC)

Figure 16: general view of the anchorage in Skontorp Cove. Picture: Francesca Pasotti

Location: Paradise Harbour. South Gerlache Strait

Settings:

- highly protected inner cove with muddy bottoms
- High glacier activity and ice disturbance (regular glacier calving and iceberg scouring)
- no penguin colony
- highly visited by tourists: landings in nearby Brown base. kayak and zodiac tours, boat anchorage

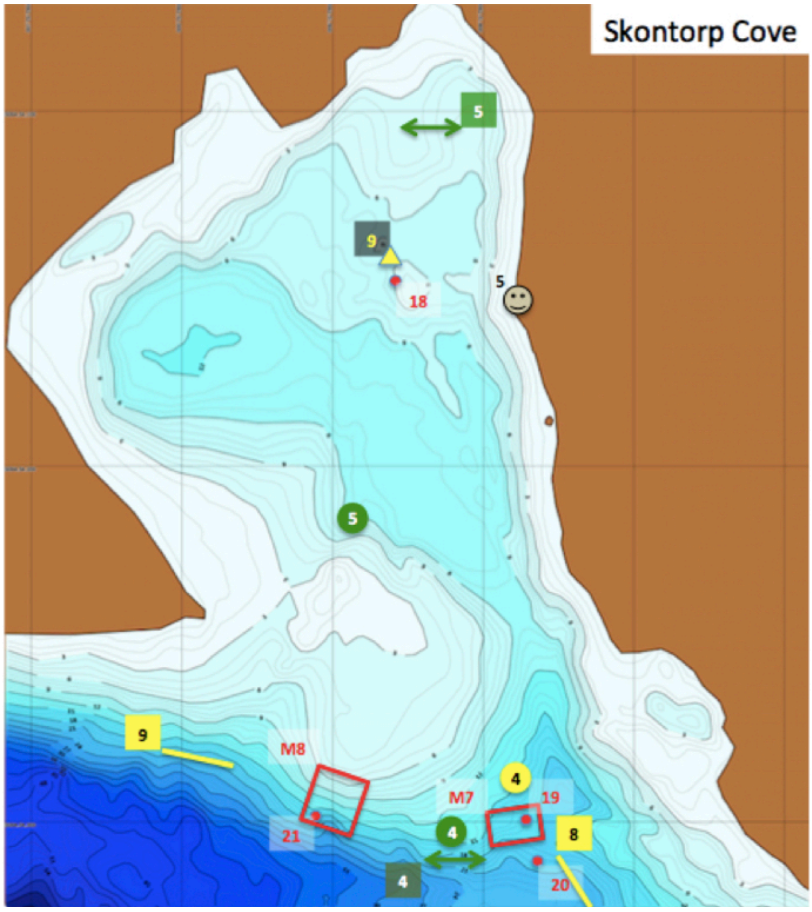

Figure 17: Skontorp Cove. Bathymetric chart showing location of all sampling events. Bathymetric chart is courtesy of Ben Wallis (Ocean Expeditions).

Alvaro Cove (AC)

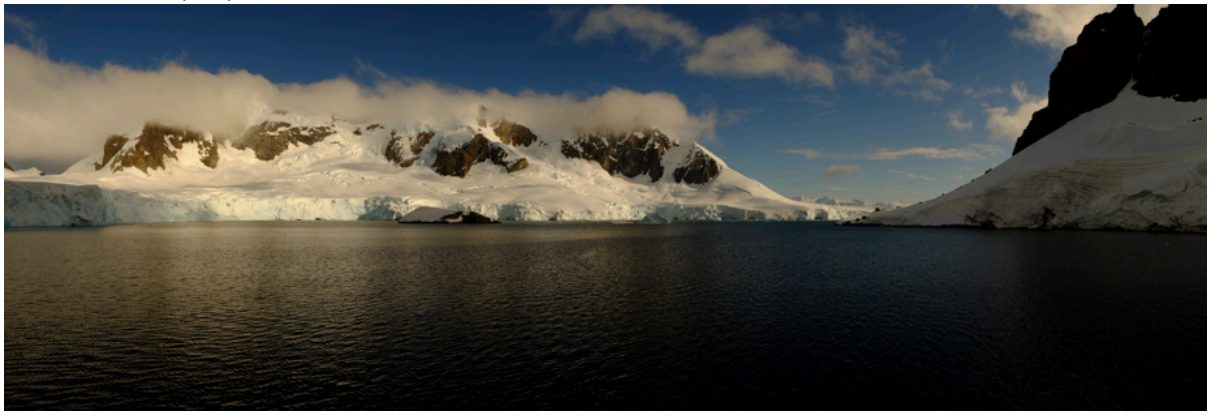

Figure 18: general view of the anchorage in Alvaro Cove. Picture: Francesca Pasotti

Location: north side of Bryde Island, Danco Coast

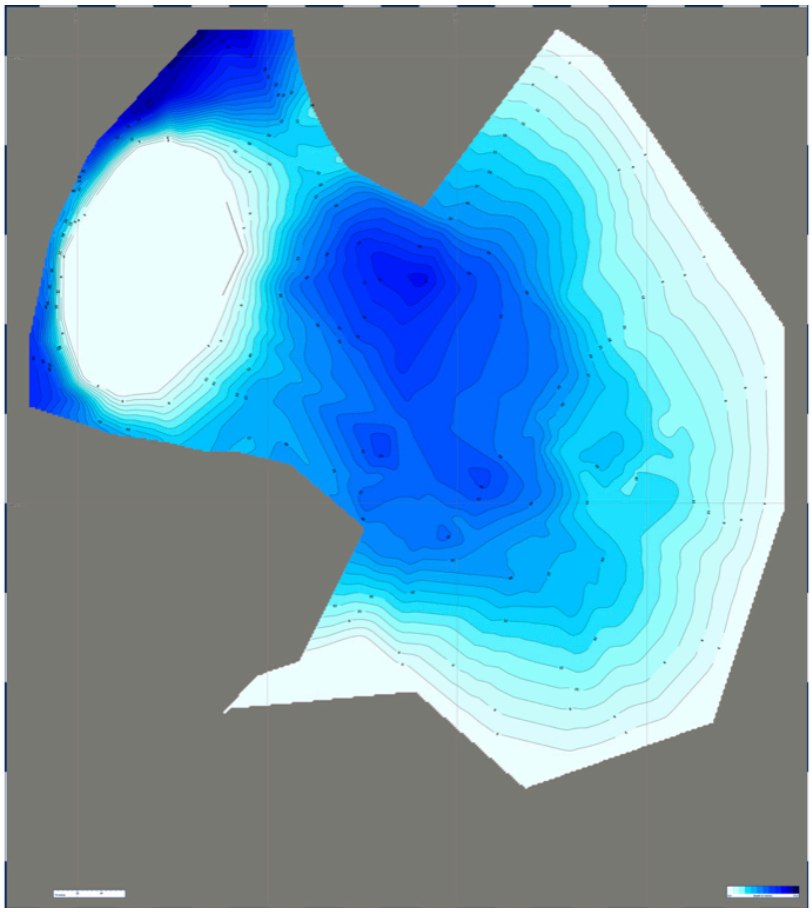

Figure 19: Alvaro Cove. Bathymetric charts are courtesy of Ben Wallis (Ocean Expeditions).

Hovgaard Islands (HI)

Figure 20: general view of the anchorage in Hovgaard Islands. Picture: Francesca Pasotti

Location: Wilhelm Archipelago. South of Gerlache Strait. open to Drake Passage and Antarctic Coastal Current influence
Settings:

- highly protected and almost enclosed inner bay
- no glacier activity nor direct ice influence
- no penguin colony
- low visit level but reknown anchorage site: 30 boats a year

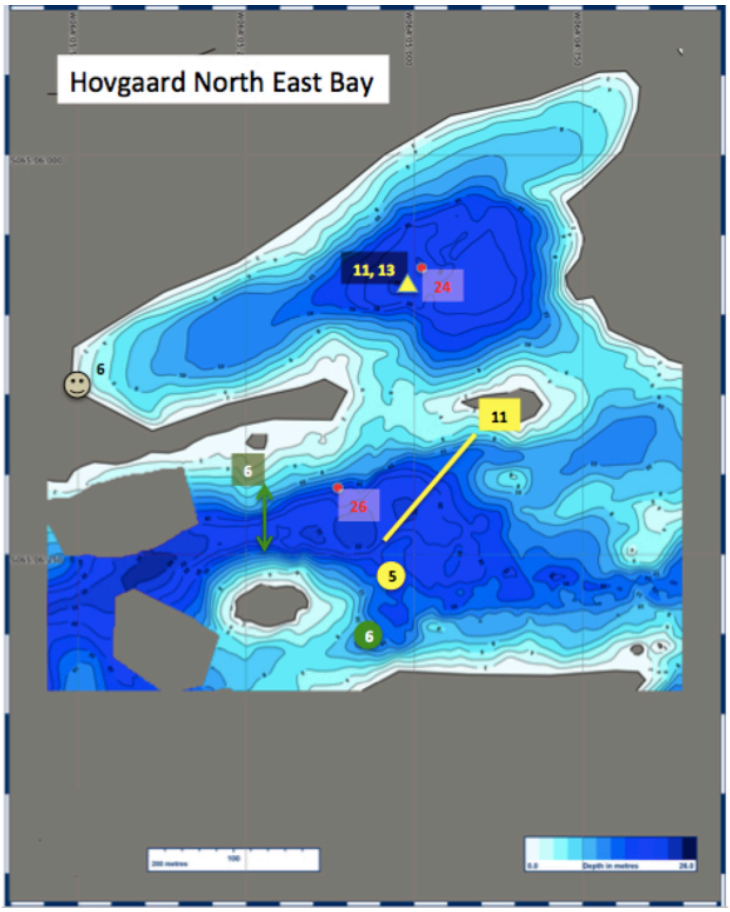

Figure 21: Hovgaard Islands, North East Bay. Bathymetric charts are courtesy of Ben Wallis (Ocean Expeditions).

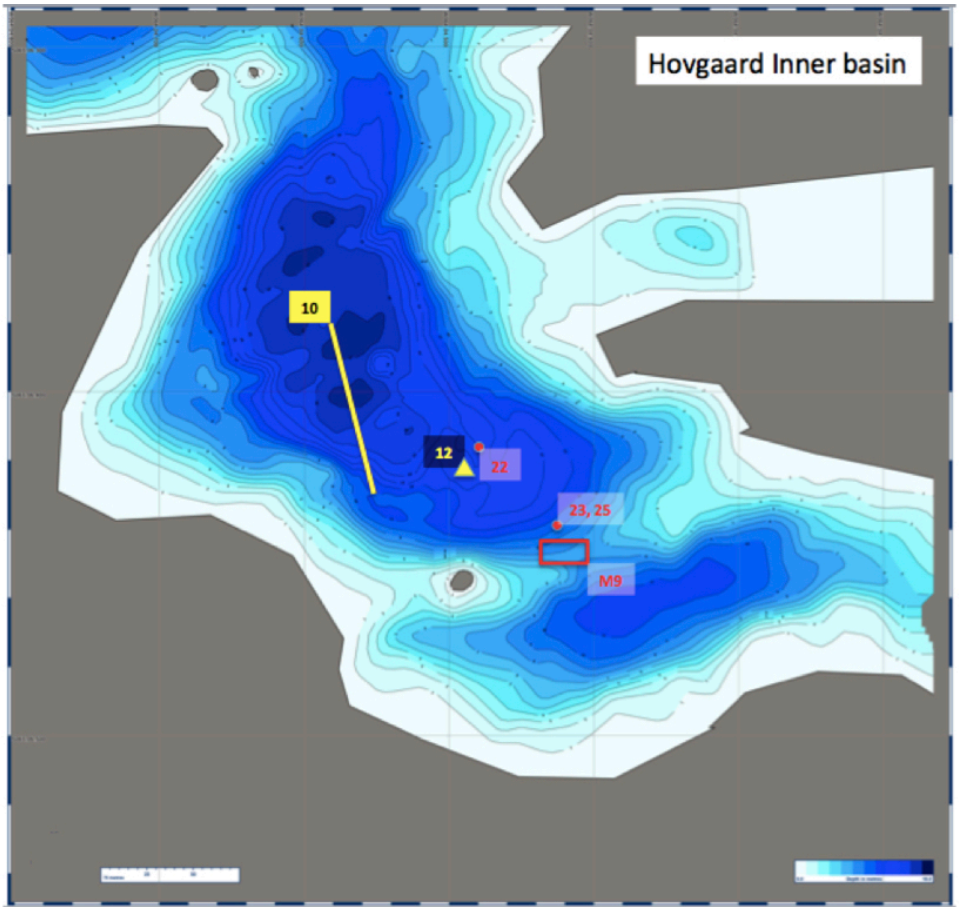

Figure 22: Hovgaard Islands, inner basin. Bathymetric charts are courtesy of Ben Wallis (Ocean Expeditions).

Berthelot Islands (BI)

Figure 23: general view of the anchorage in Berthelot Islands. Picture: Francesca Pasotti

Location: Grandidier Channel, South of Gerlache Strait
Settings:

- protected bay facing continent. but open sea conditions. rocky and gravely bottom
- High glacier activity and ice disturbance (proximity of very active Trooz glacier front)
- no penguin colony
- almost no visitors except for few tourist zodiac tours and scientific landings (from Vernadsky station)

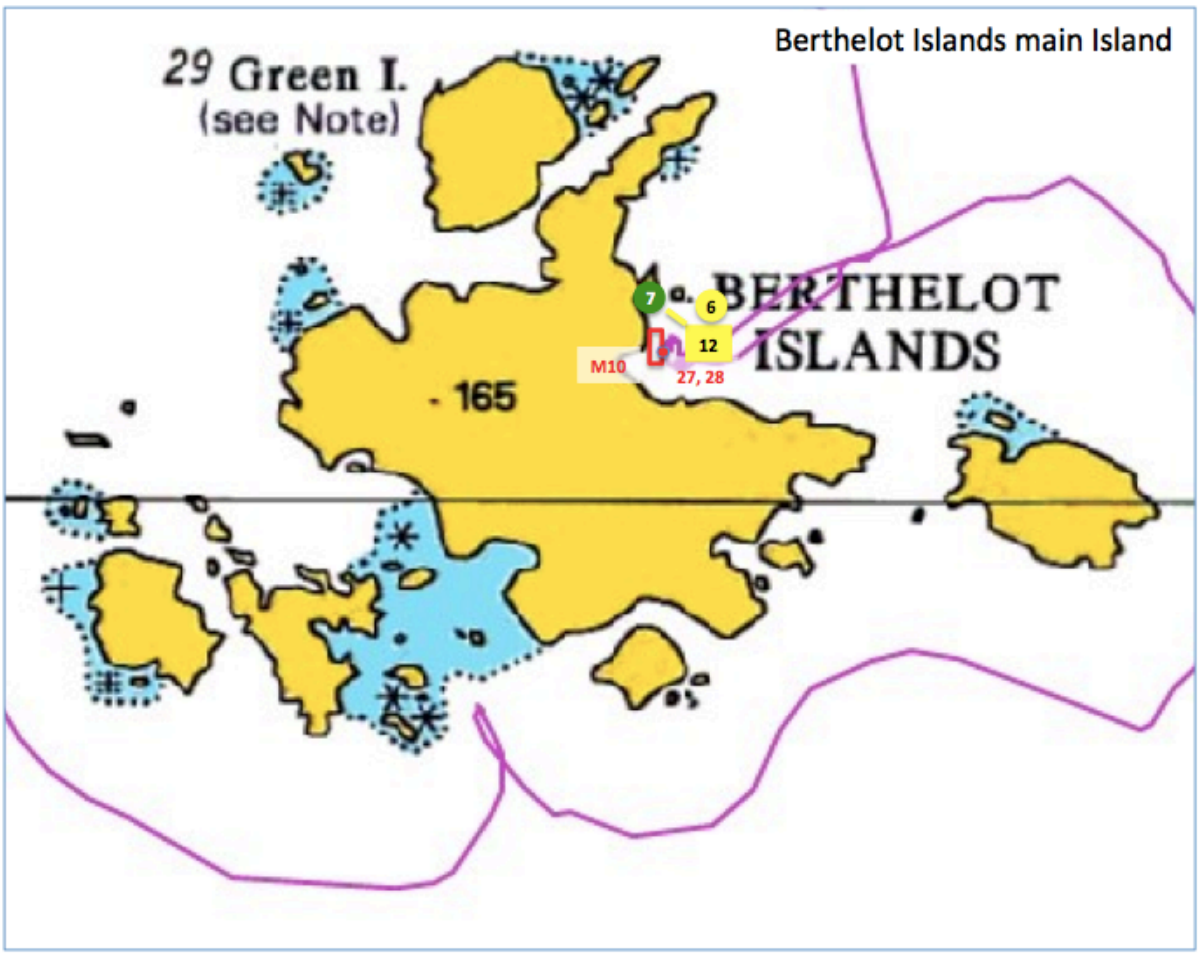

Figure 24: Berthelot Islands. Map showing location of all sampling events.

Vernadsky Station (VS)

Location: Galindez Island, Grandidier Channel
Remark: only fishing gear was deployed at this station

Cape Tuxen (CT)

Location: Waddington Bay, Grandidier Channel
Remark: a landing was carried out to seek for snow Petrel samples

Green Reef (GR)

Figure 25: general view of the anchorage in Green Reef. Picture: Francesca Pasotti

Location: Neumayer Channel. North West Gerlache Strait
Settings:

- open to Neumayer Channel. muddy bottom with gravels
- High glacier activity and ice disturbance
- no penguin colony
- no visitors but proximity of highly steamed Neumayer Channel

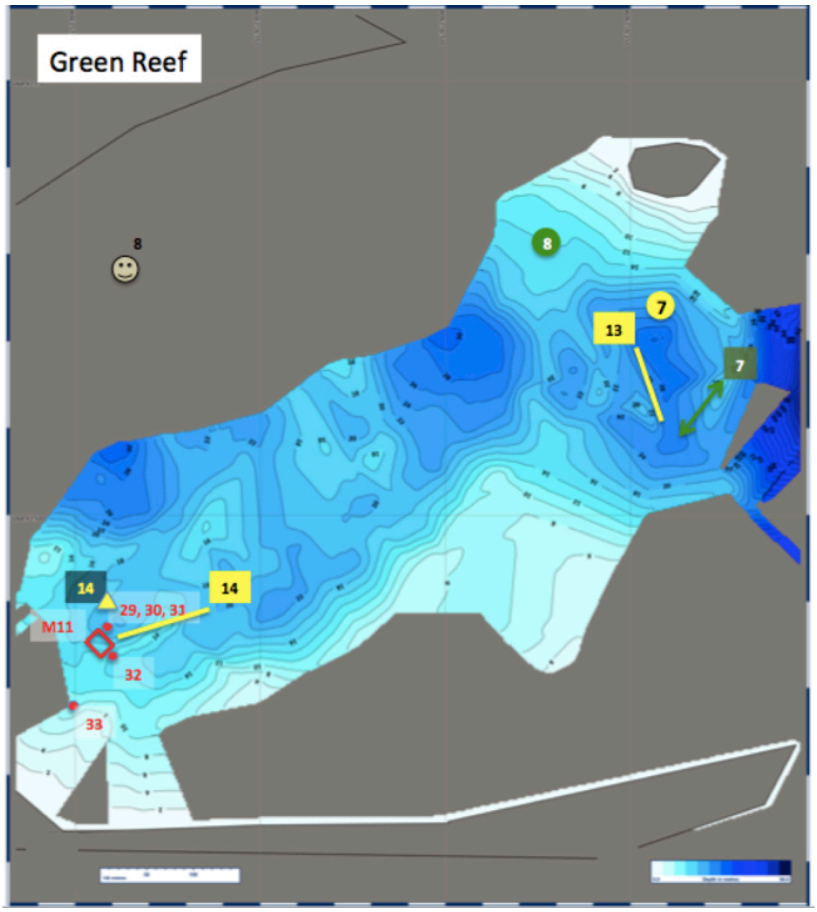

Figure 26: Green Reef. Bathymetric chart showing location of all sampling events. Bathymetric chart is courtesy of Ben Wallis (Ocean Expeditions).

Arktowski Peninsula (AP)

Location: Gerlache Strait, off Cape Anna
Remark: only used to sample eDNA, in deeper areas.

Føyn Harbor (FH)

Location: between Nansen Island and Enterprise Island NE Gerlache Strait, off Bancroft Bay
Settings:

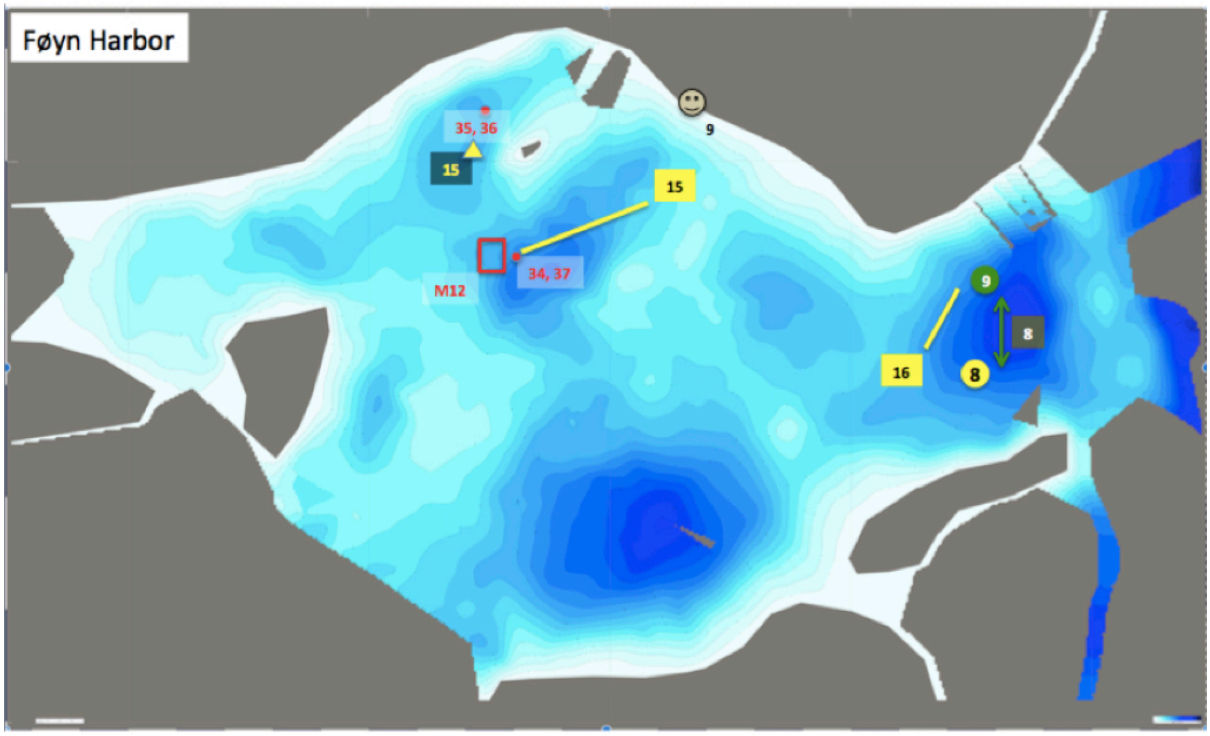

Figure 27: Føyn Harbor. Bathymetric chart showing location of all sampling events. Bathymetric chart is courtesy of Ben Wallis (Ocean Expeditions).

Enterprise Islands (EI)

Location: NE Gerlache Strait, off Bancroft Bay
Remark: very close to Føyn Harbour, only sampled for a video transect by divers over the wreck of a whaling factory ship (Guvernøren).

Data management

In the framework of the B121 expedition, data was aggregated and organized to ensure optimal use in the future for data publication in authoritative repositories and sample management. A series of data types were collected pertaining to navigation, weather conditions and sampling efforts (both biological and oceanographic).

General procedures

- Logbooks: hard copies of logbooks were completed on a daily basis by the B121 team. Data was organized in 4 different logbooks: sample, events, photo, diving. Logbooks were digitized and backed up on a daily basis.
- Spreadsheets: data from the logbooks was entered in dedicated spreadsheet on a daily basis by two members of the B121 team: Charlène Guillaumot and Bruno Danis. A quality control (QC) was performed on the fly and feedback was given to the researchers on an adhoc basis.
- Backup procedures: digital data and samples were backed up on a daily basis on 2 computers and 2 external hard drives.

Sample (biodiversity) data

Sample data was gathered in MS Excel spreadsheets, specially prepared for the expedition. The structure of the spreadsheet is based upon the Darwin Core (DwC) standard, expanded for specific data and sample management needs.
A template of the spreadsheet is provided in annex for future use by other users.

Media data

Large amounts of video data were gathered in the framework of the expedition, both for outreach and research purposes.
Underwater footage was taken by Bruno Danis and Henri Robert using a Remotely Operated Vehicle (ROV: OpenROV Trident). The footage was used essentially for exploration and dive site confirmation purposes.
Aerial footage was shot by Franz Heindler, Camille Moreau and Bruno Danis using two DJI Mavic Pro drones, for documentation purposes.
Documentary footage was mostly shot by Franz Heindler and other members of the team. For more details, see the dedicated section below.

Data publication

In the spirit of the Antarctic Treaty, Art. 3.1.c, the data emerging from the Belgica 121 sampling efforts will be made openly and freely available, in the best possible time limits and will follow the standards, policies and norms of behavior as established by the Scientific Committee on Antarctic Research (SCAR). In particular, raw biodiversity data will be shared using dedicated, community-driven platforms such as the biodiversity.aq initiative.
Processed data will be made available through scientific publications and through the Belgica 121 website (www.belgica121.be).

Work at sea and preliminary results

1. Sampling efficiency

Bruno Danis & Ben Wallis

Context

One of the objectives of the Belgica121 expedition was to test the use of a nimble platform (a 75' steel-hulled motor sailor) for marine biodiversity works in the Southern Ocean. Recent efforts in documenting the Southern Ocean biodiversity has shown that the sampling intensity varies considerably with the considered geographic location (Griffiths & Danis 2011, De Broyer et al. 2014). Key elements in the distribution of sampling intensity are the locations of the various national bases and the routes of major research icebreakers. In fact, much of the sampling, tagging, and observing of animals has been done in the nearby coastal areas around the research bases. Further, much of the open water sampling efforts have been carried out along the transit routes of the vessels that regularly visit these bases mostly for logistic reasons (Griffiths 2010).

Hence, benthic ecosystems remain poorly studied in the subpolar Antarctic, including those in extensive fjords along the West Antarctic Peninsula (WAP). Recent studies have shown that WAP fjord basins exhibited 3 to 38-fold greater benthic megafaunal abundance than the open shelf, and local species diversity and trophic complexity remained high from outer to inner fjord basins (Grange & Smith 2013). Furthermore, WAP fjords contained distinct species composition, substantially contributing to beta and gamma diversity at 400–700 m depths along the WAP. Rapid warming along the WAP will increase meltwater and sediment inputs, deleteriously impacting these biodiversity hotspots. Because WAP fjords also provide important habitat and foraging areas for Antarctic krill and baleen whales, there is an urgent need to develop better understanding of the structure, dynamics and climate-sensitivity of WAP subpolar fjord ecosystems (Grange & Smith 2013).

The B121 expedition strived at filling knowledge gaps in this potential biodiversity hotspot and remain consistent by limiting its environmental footprint, by making use of a light sampling platform.

Methods

By design, the expedition was aimed to focus on carrying out a detailed biodiversity census, from the intertidal to the subtidal zones (up to 20m) in stations along the Gerlache Strait. The stations were chosen for their contrasting conditions in terms of exposure to glaciers influence, to different water masses (Drake, Gerlache Strait, etc…), and geomorphology. Multiple gears were deployed (see Table 3), combining traditional instruments and modern techniques, and the team mostly included young scientists who were acquainted to using several techniques. Each team had a specific project (see specific section, "Work at sea and preliminary results") and was able to help others during sample processing stages.

The initial stages of the expedition were exploratory (one full station would need up to 4 days to be completed) and were followed with more efficient sampling (1.5 – 2 days per station). Opportunistically, certain stations were partially sampled in function of the priorities and weather/anchoring conditions.

Results

Even if preliminary a series of key figures are presented in this section, mostly to demonstrate the potential of the approach chosen for the B121 expedition. 17 types of gear were deployed during the expedition (see Table 3). The SCUBA divers ("DIV" in Table 3) were tasked with carrying out video transects, sampling sediments, macrofaunal organisms or bottom water for the various projects.

Table 3: types of gear deployed during the B121 expedition

Code	*Full Name*
AT	Amphipod Trap
BN	Bongo net
CTD	CTD
DIV	Scuba divers
DR	Drone
GN	Gillnet
ITD	Intertidal sampling
KELP	Kelp Survey
LF	Line Fishing
LL	Long Line fishing
NIS	Niskin Bottle
RD	Rauschert Dredge
ROV	Remotely Operated Vehicle
SP	Snow Petrel
TER	Terrestrial Survey
TOP	Top Predator Survey
VV	Van Veen Grab

15 stations were visited in total, amongst which 7 were extensively sampled. The number of samples taken in the different stations was variable as well as the number of gear deployments by the B121 team (see Table 4). An average of 10 deployments per day were successfully carried out. A total of 1739 samples were collected during the expedition (76 samples.day^{-1}).

Table 4: number of samples and gear deployments gathered at each station (additional samples were taken outside the stations and are not accounted for).

Station	*Samples*	*Deployments*
MI	310	36
MP	2	2
NH	168	29
SM	17	2
UI	278	18
SK	201	24
AC	8	4

HI	212	25
BI	54	9
VS	14	2
CT	2	2
GR	142	22
AP	9	1
FH	201	24
EI	1	1

In terms of CO_2 emissions, the total fuel consumption of the expedition (from Ushuaia to Ushuaia) was 4280 l, including the usage by the vessel, generators, tenders, electricity, heating, fresh water production. This fuel consumption can be compared to an average 40 $T.d^{-1}$ for a Polar class ice-breaker sailing in open waters (12 $T.d^{-1}$ when stationary). The fuel efficiency was therefore around 140 times better (21d at anchor, 9 d steaming) in the case of the B121 expedition.

Perspectives

The concept of using a nimble research vessel for Antarctic marine biodiversity studies in shallow waters has proven its efficiency and is probably worth expanding in a region that combines a very high biodiversity, important knowledge gaps and exposure to rapid shifts in environmental conditions. Details on the B121 expedition will soon be published in a concept paper which will also bring perspective on its efficiency in filling knowledge gaps as identified during the Census of Antarctic Marine Life (Schiaparelli et al. 2013).
Another important aspect is the dependency on fuel costs and how it affects Antarctic research: during the International Polar Year, which ran from March 2007 to March 2009, many research projects were under threat because of the steep rise in marine-fuel costs. Icebreakers are fueled by marine diesel oil (MDO), which average price had increased fivefold between 2003 and 2007 (Schiermeier, 2008).
Unless absolutely necessary, quite a few biodiversity-oriented expeditions could avoid unnecessary costs and environmental footprint by choosing a similar setup as that used for the B121 expedition.

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2. Intertidal diversity

Quentin Jossart & Camille Moreau

Context

The Antarctic intertidal environment is considerably less sampled than the surrounding deeper waters, the opposite situation of almost anywhere else in the world (Brandt 2005). The Antarctic intertidal environment is characterized by intense seasonal ice-scouring, winter ice encasement, freshwater input in summer, high UV radiation and important variation in temperature (Peck et al 2006). However, despite the general view that the Antarctic intertidal conditions are too extreme to allow macrofaunal life, little known historic and recent studies have shown that intertidal communities can establish (and persist) in these extreme conditions as illustrated by a wide diversity of taxa and functional groups (Waller 2013, Aghmich et al 2016, Griffiths & Waller 2016).

Methods

Explorations with inflatable boat were conducted to find suitable areas (allowing landing and sampling). General description and overview pictures were taken for each site to characterize the environmental settings (topography, shore length, nature of the substrate, occurrence of intertidal pools…). Two sampling procedures were used to characterize the biodiversity and abundance on each site: (1) 10 quadrats (25cm X 25cm) were randomly disposed at the low tide level (Figure 28). Presence and abundance of each species (morphotypes) were recorded within each quadrat and specimens were preserved in 96% ethanol for further identification and analyses; (2) to obtain a better overview of the total biodiversity, an exploration (1 hour) in the vicinity of quadrats was also done to look for any species not found inside the quadrats. When needed, a sieving step was done before the counting (using 5mm and 1 mm meshes).

Figure 28: Quadrat randomly disposed in the intertidal zone

Results

Seven stations were investigated for the intertidal (MI, NH, UI, SK, HI, GR and FH) with a total of 121 measurements in quadrats. For each station, the quadrats were done at low tide (from 0.55m to 0.75m). In some stations, we also complemented with higher heights (MI, SK) or intertidal pools (MI, NH, UI). The average number of species per station was 18 with a maximum in FH (24) and a minimum in NH (8) (Table 5).

Table 5: Number of species per intertidal station

Station	***N of species***
MI	20
NH	8
UI	21
SK	20
HI	13
GR	21
FH	24

Kidderia bicolor, *Obrimoposthia wandeli and Laevilitorina caliginosa* (Figure 29) were the most abundant organisms (up to thousands of individuals per m²) at all stations but NH. The most represented phyla were Arthropoda (12 species) followed by Mollusca (10), Polychaeta (5) and Echinodermata (5).

Figure 29: Most abundant taxa found in the intertidal (Kidderia bicolor: left, Obrimoposthia wandeli: center, Laevilitorina caliginosa: right). Scale bar: 0.3cm

Perspectives

Further analyses will be carried on all samples at their return to Belgium to morphologically identify them. Specialists of each concerned taxa will be contacted to achieve that goal. In the meantime, all morphotypes will be barcoded (COI mitochondrial region) to create a first comprehensive baseline of intertidal genetic diversity. Diversity indexes and a quantitative approach will also allow a comparison among the sampling locations with regards to their environmental characteristics.

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3. Soft sediments biodiversity

Francesca Pasotti

Context

Soft sediments represent the majority of the World's Oceans, and the Southern Ocean shelf constitutes 11 % of the planet's bottoms. Despite the importance of such ecosystems, the sediment benthos is even less well studied than hard rock substrate communities. The role of meiofauna and macrofauna is crucial in the marine systems, for they are tightly linked to the sediment organic matter pool and hence they are directly involved in the benthic-pelagic coupling and the energetics of shallow and shelf/deep waters (Giere 2009). Organisms such as meiobenthic nematodes which are the most abundant taxon among the size class, are able to directly feed on the microbial biota while they are eaten directly or indirectly by other larger higher trophic levels organisms (Woodward 2010). Macrobenthic polychaetes or some bivalves are able to oxygenate the deeper layers of the sediment by burrowing activities (Queiros et al. 2013). The diversity and functional diversity of the meio- and macrobenthos are crucial for a complete understanding of the resilience of Antarctic ecosystems and their contribution to the Ocean's carbon cycle (Cook et al. 2009, Stammerjohn et al. 2008, Clarke et al. 2007, Ducklow et al. 2013). Climate change and glacier retreat are among the main threats to the shallow water coastal areas of the Antarctic. Scouring has been observed to have rather long-term effects on the soft sediment communities (Lee et al. 2001), with meiofauna often being a better competitor in the recolonisation of scoured sediment compare to the larger macrofauna, which is more affected by mechanical disturbance (Pasotti et al., 2014, Giere 2009).

Methods

As for the biogeochemistry sampling, samples for meiofauna assemblage structure (taxa diversity, nematodes diversity, biomass), have been sampled at each location by divers either by means of perspex push cores (3.6 cm diameter, quantitative) or by surface sediment scooping (qualitative).Where the sediment characteristics allowed core sampling, the sediment was sliced in different layers profiles (0-1 cm, 1-2 cm, 2-5 cm 5-10 cm) for the whole core depth. At least 3R were always taken for the meiofauna characterisation at each location dive event. Nevertheless in light of the different nature of the sediments in the various stations, the sediment depth layers may vary in resolution. Macrobenthos on the other hand was sampled either by means of Vanveen grab (and sediment volume noted) or where the Vanveen would not work in light of the dense presence of rocks or large bodied

organisms, surface sediment scooping was performed by means of large 1L vials. Not at every location macrofauna samples were taken. Once retrieved, the sediment was sieved on a 1 mm mesh size sieve and the sample stored in ziplock bags and stored in the freezer (-20°C) for further analysis. When individuals belonging to desired bivalve species (*Aequiyoldia eightsi*, *Laternula elliptica*) for genomic studies of connectivity, these were either stored separately as to be dedicated to genetic analysis, or kept for biomass estimation of the soft sediment macrofauna.

Table 6: Meiofauna and biogeochemistry sampling list

Analysis	*DATE*	*LOCATION*	*DEPTH (m)*	*LAT*	*LON*	*SAMPLING GEAR*
Meiofauna and biogeochemistry	01/03/2019	Melchior Island	17	S064.19.257	W062.55.467	3.6 cm perspex push cores
Meiofauna and biogeochemistry	02/03/2019	Melchior Island	18	S064.19.195	W062.55.157	3.6 cm perspex push cores
Meiofauna and biogeochemistry	05/03/2019	Neko Harbour	15	S064.50.636	W062.32.036	Scooping by means of 2 x 500ml pot, 2 x 200 ml pot
Meiofauna and biogeochemistry	05/03/2019	Neko Harbour	9	S064.50.642	W062.31.991	Scooping by means of 1 x 500ml pot, 2 x 200 ml pot
Meiofauna and biogeochemistry	08/03/2019	Useful Island	22	S064.43.141	W062.52.150	Scooping by means of 2 x 200 ml
Meiofauna and biogeochemistry	08/03/2019	Useful Island	22	S064.43.141	W062.52.150	3.6 cm perspex push cores
Meiofauna and biogeochemistry	09/03/2019	Skontorp Cove	10	S064.54.1791	W062.51.8324	3.6 cm perspex push cores
Meiofauna and biogeochemistry	10/03/2019	Skontorp Cove	17	S064.54.3072	W062.51.8128	Scooping by means of 1x 200ml scooped /1 x 3.6 cm core / 4 x 3.6 cm core/ Scooping by means of 2 x 200ml scooped sediment
Meiofauna and biogeochemistry	12/03/2019	Hovgaard Island	14,7	65°06.057'S	64°04.992'W	3.6 cm perspex push cores
Meiofauna and biogeochemistry	13/03/2019	Hovgaard Island	20	65°06.398'S	64°04.532'W	Subcoring of Vanveens

Meiofauna and biogeochemistry	14/03/2019	Berthelot Island	15,5	65°19.713'S	64°08.310'W	Surface sediment scooping with 200ml pots
Meiofauna and biogeochemistry	16/03/2019	Green Reef	17,9	64°43.550'S	63°16.959'W	3.6 cm perspex push cores
Meiofauna and biogeochemistry	17/03/2019	Green Reef	9	64°43.395'S	63°16.961'W	Scooping by means 200 ml pots surface sediment scooping
Meiofauna and biogeochemistry	19/03/2019	Foyn Harbour	17	64°32.762'S	61°59.914'W	3.6 cm perspex push cores
Meiofauna and biogeochemistry	20/03/2019	Foyn Harbour	12	64°32.762'S	61°59.914'W	3.6 cm perspex push cores

Table 7: Macrofauna sampling list

Analysis	***DATE***	***LOCATION***	***DEPTH (m)***	***LAT***	***LON***	***GEAR***
Macrofauna - qualitative	02/03/2019	Melchior Island	18	S064.19.257	W062.55.467	Van Veen grab
Macrofauna - qualitative	02/03/2019	Melchior Island	18	S064.19.195	W062.55.157	Van Veen grab
Macrofauna - qualitative	02/03/2019	Melchior Island	18	S064.19.195	W062.55.157	Van Veen grab
Macrofauna qualitative	05/03/2019	Neko Harbour	15	S064.50.636	W062.32.036	Scooping by means of 1L pots
Macrofauna qualitative	05/03/2019	Neko Harbour	9	S064.50.642	W062.31.991	Scooping by means of 1L pots

Macrofauna qualitative	07/03/2019	Useful Island	20	S064.43.141	W062.52.150	Scooping by means of 1.1L
Macrofauna qualitative	07/03/2019	Useful Island	15	S064.43.141	W062.52.150	Scooping by means of 1L pots
Macrofauna quantitative	10/03/2019	Skontorp Cove	10	S064.54.1791	W062.51.8324	Van Veen grab
Macrofauna quantitative	13/03/2019	Hovgaard Island	14,7	65°06.057'S	64°04.992'W	Van Veen grab
Macrofauna quantitiative	13/03/2019	Hovgaard Island	20	65°06.398'S	64°04.532'W	Van Veen grab
Meiofauna quantitiative bulk + biogeochemistry	13/03/2019	Hovgaard Island	20	65°06.398'S	64°04.532'W	Subcores of Van Veen grab
Macrofauna quantitative	17/03/2019	Green Reef	18	64°43.550'S	63°16.959'W	Van Veen grab
Macrofauna quantitative	19/03/2019	Foyn Harbour	15	64°32.762'S	61°59.914'W	Van Veen grab

Results

Soft sediments were scarce in locations with steep slope or very open waters-exposed topography. The locations where mostly characterized by rocky shores and depending on the slope, drop stones and pebbles would be interspersed in between softer sediment patches. On locations where slope was rather homogeneous or not too prominent and the tidal influence would not be too intense, sediment could accumulate and form deep layers of silt which could be mixed with fine sand. In this case we could sample by means of cores or Van Veen grab and the sediment layer seemed to be at least 5-10 cm deep before encountering bedrock and higher density of pebbles that hindered the use of these sampling gears. The very surface layer would always be composed by glacial silt, which would create a resuspension cloud once touched. Often microphytobenthos or algal associations that formed a brown mat on top of the sediment would be present. Sediment type ranged from complete silt in the anoxic inner basin at the anchorage site of Hovgaard Island or Neko Harbor, to sandier and well oxygenated sediments of Green Reef. At a first glance (hence not by means of a microscope) the macrofauna pre-sieved samples showed very poor communities in the anoxic sediments, with only small gastropods and few motile taxa such as amphipods, which were present in small numbers. The highest overall diversity appeared to be found from the pre-sieving of the 18m samples in Green Reef, where *Aequiyoldia eightsi* and likely *Thracia sp.* bivalves were present together with tube worms and amphipods. These taxa are known to be active burrowers and to keep the sediment oxygenated well below 10 cm depth facilitating organic matter degradation and remineralisation. In general, the quantitative analysis of soft sediment macrobenthos has been made difficult by the nature of the chosen sites within the locations: not always the sediment was of the type that can be properly sampled by means of Van Veen grab. Hence in many sites a qualitative analysis of macrofauna will be carried out and abundances/biomasses will be referred to volume of sediment sieved more than to the surface sampled by the Van Veen grab.

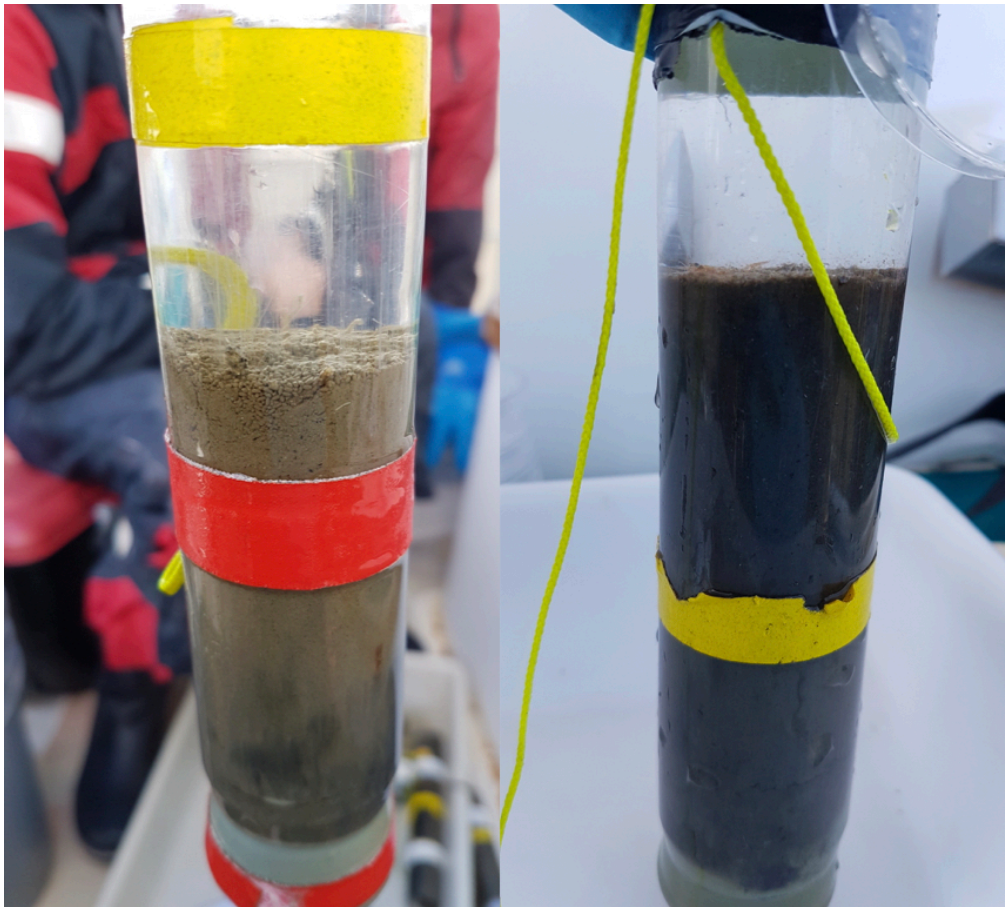

Figure 30: cores sampling, displaying different levels of oxygenation in sediments. Photo: Francesca Pasotti

Perspectives

Meiofauna will be analyzed for higher taxon composition and also for Nematode genus diversity and trophic guild ecology. Macrofauna will be identified at species level where possible. Biomass will be estimated for both soft sediment metazoan size classes and referred either to surface (for the core and Van Veen sampling) or to sediment volume (for the scooping sampling method).

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4. Macro- and megabenthos diversity

Thomas Saucède, Charlène Guillaumot, Henri Robert

Context

On the background of biodiversity erosion and environmental changes, species inventories have become essential to implementation of conservation policies in order to mitigate biodiversity loss and maintain ecosystem services (Balmford and Gaston 1999, Gaston 2005, May 2011). Considering the rapid climate and oceanographic changes already affecting (Turner et al. 2013) or expected (Gutt et al. 2015) to affect Southern Ocean organisms, identifying taxa and areas the most at risk has become a priority (Griffiths 2010). It is also of importance to studying the multiple effects of direct and indirect abiotic and biotic stressors on species and ecosystems (Smith 2002, Pendlebury & Barnes-Keoghan 2007, Molinos et al. 2015) and study species and community responses to environmental changes, a key question of the 'Antarctic life on the precipice' topic of the Science Horizon Scan (Kennicutt et al 2014). Finally, naming species and using taxonomic and biodiversity information is importance to all scientists in life sciences as it is a prerequisite to any biodiversity study (Chapman 2005) in various fields such as phylogenetics, biogeography, conservation, natural resource management, bio-prospecting, and education (Chapman 2005, Costello et al 2015). During the B121 cruise, inventory of macro- and megabenthos diversity was conducted using various sampling gears and investigation means as a necessary preliminary step to further ecological analyses, from individual species systematics to trophic and community analyses.

Methods

Most common and key species (engineers or top predators) of the surveyed shallow water habitats (between 5 and 20 m depth) could be observed and identified during the dives, some of them sampled by hand picking, or identified on video transects. This first inventory was widely complemented by samples collected with a Rauschert dredge, Van Veen grab and amphipod trap.

Diving results

A preliminary list of 53 common species (Table 8) could be identified during the 38 dives performed during this mission. They were frequently observed directly *in situ* at the nine visited sites, or after the dives when watching the 12 video transects. Some specimens of most species were sampled for further taxonomic investigations and for isotopic and molecular analyses (the quantity of sampled specimens strictly followed the pre-established protocols and was maintained at a minimum number required for analyses). All specimens were either photographed after sampling and/or shot on video transects during the dives.

Table 8: List of most common species identified and observed during the dives

Higher taxonomic ranks	*Identified species*	*Images*
Ochrophyta	*Adenocystis utricularis*	video M06
	Himantothallus grandifolius	video M03
	Cystosphaera jacquinotii	
	Desmarestia anceps	video M03
	Desmarestia antarctica	video M11
Rhodophyta	*Iridae cordata*	video M01
	Trematocarpus antarcticus	video M01
	Plocamium hookeri	video M11
	Gigartina skottsbergii	video M03
Chlorophyta	*Monostroma hariotii*	video M03
Demospongiae	*Dendrilla antarctica*	video M01
	Homaxinella balfourensis	photo
	Mycale acerata	video M05
	Cinachyra barbata	video M05
Anthozoa	*Glyphoperidium bursa*	photo
Nemertea	*Parborlasia corrugatus*	photo
Gastropoda	*Nacella concinna*	photo
	Margarella antarctica	photo
	Austrodoris kerguelenensis	photo
Bivalvia	*Laternula elliptica*	photo
	Aequiyoldia eightsii	photo
	Limatula hodgsoni	video M01
Polychaeta	*Flabelligeridae* sp	video M10
	Sabellidae sp	video M09
	Terrebellidae sp	video M09
Pycnogonida	*Pycnogonida* sp	photo
Amphipoda	*Paraceradocus miersi*	photo
	Abyssorchomene sp	video M03
Isopoda	*Glyptonotus antarcticus*	photo
Asteroidea	*Odontaster validus*	photo
	Odontaster meridionalis	photo
	Odontaster pearsei	photo
	Psilaster charcoti	photo
	Diplasterias brucei	photo
	Lysasterias sp	photo
	Granaster nutrix	photo
	Cuenotaster involutus	photo
	Acondontaster hodgsoni	photo
	Labidiaster annulatus	photo
	Perknaster sp	photo
	Neosmilaster georgianus	photo
	Henricia sp	photo

Ophiuroidea	*Ophionotus victoriae*	photo
Echinoidea	*Sterechinus neumayeri*	photo
Holothuroidea	*Heterocucumis steineni*	photo
Brachiopoda	*Liothyrella uva*	video DIV38
Tunicata	*Aplidium* sp	
	Molgula pedunculata	video M12
	Pyura sp	video M09
	Cnemidocarpa verrucosa	video M10
Actinopterygii	*Parachaenichthys charcoti*	video DIV03
	Trematomus newnesi	video DIV03
	Notothenia coriiceps	video M08

Amphipod sampling results

With over 850 named species, amphipods are the most speciose animal group in the Southern Ocean, where it is present at all depths, in all environments and where it occupies a vast array of trophic niches. The high species richness of amphipods and the dominant role they play in the Antarctic ecosystems justifies in depth taxonomical, ecological and biogeographical studies on these crustaceans. Such studies and sampling campaign should be carried out on a regular basis, as the biota of the Antarctic Peninsula in particular is already experiencing major climatic and anthropogenic alterations. Repeated and standardized sampling effort will allow to detect how different taxa will react to these alterations.

Amphipods were collected at all stations during the cruise using a Rauschert dredge (deployed at a depth ranging from 18 to 22 meters for approximatively 40 meter on the sea floor) and a pair of baited amphipod trap (40x25x20cm with a 2cm and a 4cm entry hole deployed at each station for 24 hours at 20 meter depth).

Table 9: Rauschert dredge sampling preliminary data

Area	*Deployment #*	*Sorted taxa*	*Total individuals*
MI	1	7	*243*
MI	2	11	*347*
MI	3	17	*187*
NH	4	20	*660*
NH	5	17	*1074*
SM	6	14	*292*
UI	7	20	*131*
UI	8	9	*175*
SK	9	17	*474*
SK	10	10	*344*
HI	11	15	*339*
HI	12	31	*782*
BI	13	23	*996*
GR	14	11	*285*
GR	15	9	*463*
FH	16	19	*859*
FH	17	8	*362*

Table 10: Amphipod trap sampling preliminary data

Area	Deployment #	Sorted taxa	Total number of individuals
MI	1	5	563
NH	2	6	1403
UI	3	11	12144 (18000 released)
SK	4	3	5100 (12000 released)
HI	5	2	12001 (21600 released)
BI	6	2	101
GR	7	4	531
FH	8	3	1207 (20600 released)

Perspectives

A large number of samples was gathered (both physical and virtual, as video/pictures). This specific part of the results will need to be addressed by dedicated efforts, which will materialize as identification workshops, barcoding efforts, etc…
A special effort will also be devoted to the publication of the data pertaining to collections, and the possibility to publish an "Illustrated Field guide" is also envisioned at this point

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5. Fish diversity

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Context

The Antarctic fish fauna is largely dominated by endemic, specially adapted notothenioids (Eastman, 1993, 2005). This clade of perciform fishes is a rare example of a marine adaptive radiation (Matschiner et al., 2015) and widely used to investigate ecological and evolutionary questions (e.g. Rutschmann et al., 2011; Volckaert et al., Carlig et al., 2018). Despite large efforts for biodiversity research in the Southern Ocean, obtaining samples of shallow water fish fauna can still be difficult and spatially restricted. Many samples may be caught from Antarctic research bases possibly causing bias in the obtained data toward "sample-hotspots", while the areas between bases may be under-represented. Shallow water fish species can exhibit small scale differences in ecological traits and site fidelity (Casaux & Barrera-Oro, 1996). Recognizing such local variability is important to make sure biologically relevant variation is not neglected in current management and protection plans. In addition, multidisciplinary approaches are needed to understand the interplay between ecology and evolution that shapes the morphometry and life style of Antarctic fishes. Consequently, during the B121 expedition extensive fish sampling across many localities in a confined region of the Antarctic Peninsula took place. A multilayer approach comprising sampling for prey item and microbiome composition, stable isotope analyses (see 9.), population genomics (see section on Population genomics) and associated parasite fauna, ecological and morphometric data was used.

Methods

Three methods to collect fish were used: (1) angling with hooks, line and sinker, (2) gill nets, and (3) a cylindrical fish trap or fyke. Angling took place with standard commercial fishing rods, braided fishing line, and rigs (Sabikis) equipped with multiple hooks of varying sizes, and small, colorful lures, luminescent plastic beads, and weights at the end in depth of 5 – 50 m. Hooks were sometimes baited with fish, mollusk or shrimp and used actively (jigging during daytime from the ship or zodiacs) or passively (fixed to the ship overnight). Two types of gill nets were used, measuring approximately 18 m in width and 1.5 m in height and with 4 cm and 8 cm mesh size (stretched), respectively. The smaller mesh size was only used in FH after the other net had been ripped. Nets were set in depths of 10 – 30 m and usually perpendicular to observed currents (see station maps for approximate positions). The fish trap was deployed for at least 8 h in depths of 10 – 30 m, baited with fish, mollusks, or shrimp. All three methods were employed at all major stations (MI, NH, UI, SK, HI, GR, FH) and additional, opportunistic fishing was conducted at minor stations (AC, VS, CT, BI, EI). A few fish were taken incidentally from sampling devices not designed to catch fish. After landing, fish were kept alive in ambient water for maximum 12 hours before processing. Total and standard length were noted, specimens dissected and sex and maturity stage recorded. A liver biopsy was collected in RNAlater and a muscle biopsy directly frozen. Subsequently, further samples were taken and preserved in absolute, pre-chilled ethanol: two fin clips, another muscle biopsy, a hindgut sample, stomach content, a gonad sample, and, if present, a sample of endoparasites from the body cavity. In few cases external parasites were found and collected in ethanol as well. The heads of most smaller specimens were preserved in ethanol. If the head was discarded, otoliths and gill rakers were collected

instead whenever possible. Detailed pictures were taken of selected specimens. Finally, in all *T. newnesi* three previously recognized morphs, namely “typical”, “intermediate” and “large mouth” (Eastman & DeVries, 1997; Piacentino & Barrera-Oro, 2009; Barrera-Oro et al., 2012), were determined and recorded alongside with measurements of the head length, upper jaw length, gape width, and orbit diameter, all taken to the nearest half millimeter. For these fish and some *N. coriiceps*, notes were also taken on the coloration pattern of live specimens.

Results

In total, 164 fish specimens were collected (Table 11). Most of these belonged to five species, i.e. *Trematomus newnesi* (N = 60), *Notothenia coriiceps* (N = 33), *Harpagifer antarcticus* (N = 27), *Trematomus bernacchii* (N = 21), and *Notothenia rossii* (N = 12), and were collected by either line fishing (N = 83) or gill net fishing (N = 49). The littoral fish *H. antarcticus* was frequently collected by hand in the intertidal (N = 23), as well as one *N. coriiceps*. One *H. antarcticus* was also taken incidentally with a Van Veen grab and three further individuals by gill net. The fish trap performed rather poorly as only three fish (two *N. coriiceps*, one *T. bernacchii*) were caught in nine deployments. Three fish, one *N. coriiceps* and two small bathydraconids were collected opportunistically by divers and one *T. bernacchii* was caught in the amphipod trap. Line and gill net fishing also yielded three *Lepidonotothen nudifrons*, three *Gobionotothen gibberifrons* and two *Chaenocephalus aceratus.* The spatial distribution of samples is patchy with most specimens collected at Føyn Harbor (N = 57) and Useful Island (N = 42). Several localities yielded less than a dozen fish preventing spatial comparisons of fish catches. This comparatively small total amount of fishes enabled us to sample the specimens in great detail, exercising the entire sampling protocol on 142 fish. Nineteen fish were frozen whole and three individuals were released after taking fin clips. Entire heads were preserved in 116 cases and head measurements of all *T. newnesi* (N = 60) were recorded. Sixteen specimens (at least one per species) were photographed.

Table 11: Fish specimens collected during the B121 expedition by species and station

Station	*T. bernacchii*	*T. newnesi*	*N. coriiceps*	*N. rossii*	*G. gibberifrons*	*C. aceratus*	*L. nudifrons*	*R. glacialis*	*H. antarcticus*	*undet.*	*total*
MI	14		5	2	1	1					23
NH			1				1	2			4
UI		37	4				1				42
SK			3								3
AC	1										1
HI			10								10
VS		11	2			1	1				15
GR		4	2						2		8
CT	1										1
FH	5	8	6	10	2				25	1	57
total	21	60	33	12	3	2	3	2	27	1	164

Perspectives

The fish samples collected here represent a valuable collection of the Antarctic shallow water fish fauna, which is dominated by notothenioids. However, much of the diversity of the Notothenioidei is primarily found in deeper waters (Eastman 2017), likely linked to the glacial submergence of the Antarctic shelves (Eastman 1993). Consequently, Artedidraconidae are for example completely absent in the samples collected here. Instead, especially *Trematomus newnesi* and *Notothenia coriiceps* appear as dominant species of the shallow waters around the Gerlache Strait. The diversity data should not be regarded as representative though, as it was collected with selective gear and variable catch efforts. The comprehensive sample of *T. newnesi* will enable detailed morphometric, genetic, and trophic ecology analyses on this example of phenotypic plasticity in Antarctic fishes. Despite previous diet and buoyancy analyses (Eastman & DeVries, 1997, Eastman & Barrera-Oro, 2010), a causal explanation for this morphism is still lacking. The combination of the aforementioned techniques may be powerful to resolve at least whether the head shape morphology of *T. newnesi* is genetically pre-determined or entirely plastic. The bullhead notothen *N. coriiceps* is one of the most abundant shallow water notothenioids and is a common study species for ecology, cold adaptation, genomics, and development (Shin et al., 2014, Postlethwait et al., 2016, Amores et al., 2017, Cali et al., 2017). Yet, spatio-temporal genetic diversity patterns are still largely unknown. The samples taken during this expedition can be used together with samples from other campaigns to conduct detailed population genomic and connectivity analyses. It is important to establish a clear understanding of the spatial distribution of possibly locally adapted populations to facilitate appropriate management of this key component of the coastal Antarctic ecosystem. Similar analyses can be conducted with complementary samples of *T. bernacchii* (see also Table 11), a species for which genetic differentiation between East and West Antarctica is documented (Van de Putte et al., 2012), but processes that shape this divergence remain unclear. Lastly, *Harpagifer antarcticus* is the only known harpagiferid occurring at the Antarctic Peninsula. The species diverged from its South American congener *H. bispinis* probably 1.7 Ma ago (Hüne et al., 2015). As a littoral species it is a key link between highly abundant shallow water amphipods and higher trophic levels. Several potential prey organisms were also collected (see 2.) and may serve as an important reference database. Samples collected here can therefore potentially be used for molecular analyses of intraspecific levels of diversity in the species' genome, its diet, and gastrointestinal microbiome community.

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6. Birds and marine mammals' diversity

Henri Robert

Context

The Biology Conservation Unit (RBINS – OD Nature) has collected presence and abundance data on seabirds and marine mammals in the Southern Ocean for more than 11 years. The aim of this long-term program is to monitor marine top predators during transect onboard research vessels (e.g. RV Polarstern, RV Sonne, RV Belgica) or ice breaker container carrier (Ivan Papanin) in order to detect possible shifts in wildlife population presence and/or densities. On the medium to long term these data allow us to assess the effects of anthropogenic pressure and climate change on the species and can serve as a lever for conservation measures. Field data are collected following a standardized protocol described hereunder to allow comparison both geographically and along a time spectrum.

This cruise was also the opportunity to provide support and samples to the whaleswim project, led by Jen Jackson (BAS, find details here: https://best-whaleswim.eu/help-us/) by taking pictures of whales encountered.

Method

Continuous monitoring of birds and marine mammals (species identification and headcount) is performed from the bridge or a spot offering the best visibility on deck. Bird/mammal standard counts are 30 min non-stop observation with binoculars for identification (if required) and age/sex determination when possible. A 300 mm tele objective camera is used for documentation and identification of species that pose identification issues in the field (e.g. *Catharacta* spp., *Pachyptila* spp.). GPS ship position and climatic conditions are recorded at each start and end position of counts. Counts are performed during daylight (from dawn to dusk), while visibility permitting (counts must be stopped when visibility is poor due to heavy fog or precipitation) to avoid bias in animal detection and subsequent false population estimates.

Equipment used for the survey:

- Binoculars Leica Ultravid 10*40
- Camera+long lense (Nikon D300+Nikkor 70-300mm)
- Garmin Oregon 600 GPS
- Drone Mavic Pro DJI

Work at sea and results

During the Belgica121 mission over 30 standard counts were performed (from the Beagle channel to the southernmost visited site of the cruise at Bethelot Island along the Antarctic Peninsula and the Drake passage. 28 species of birds, 3 species of cetaceans and 4 species of pinnipeds were observed between the 23rd of February and March 23rd, 2019.

Species encountered in the Drake Passage and at the Antarctic Peninsula with preliminary considerations:

1- BIRDS

Diomedidae

- Wandering Albatross (*Diomedea exulans exulans*): common in the open waters of Drake passage
- Black-browed Albatross (*Thalassarche melanophrys*): very common in the open waters of the Southern Ocean (particularily from the channels of the Magellanic area to the Drake passage)
- Grey-headed Albatross (*Thalassarche chrysostoma*): few specimens sighted south of Cape Horn and in the Drake passage
- Light-mantled Sooty Albatross (*Phoebetria palpebrata*): few specimens sighted in the Drake passage in the vicinity of the Antarctic Peninsula

Procellaridae

- Southern Giant petrel (*Macronectes giganteus*): circum Antarctic species. Common in the Gerlache strait and the Drake passage
- Southern Fulmar (*Fulmarus glacialoides*): Few specimens sighted in the Gerlache strait, more common in the Drake passage
- Antarctic Petrel (*Thalassoica antarctica*): few specimen observed in the southern part of the Drake passage
- Cape Petrel (*Daption capense capense*): few specimen observed near Cape Horn and during the crossing of the Drake passage
- Snow Petrel (*Pagodroma nivea*): 4 individuals sighted in the Gerlache strait (1 near Cape Tuxen, 2 at Skontorp Cove and 1 near Metchnikoff Point)
- White-headed Petrel (*Pterodroma Lessonii*): few specimens observed during the crossing of the Drake passage
- Soft-plumaged Petrel (*Pterodroma mollis mollis*): few specimens observed the crossing of the Drake passage
- White-chinned Petrel (*Procellaria aequinoctialis*): common species in the Magellanic area and the northern part of the Drake passage
- Kerguelen Petrel (*Lugensa brevirostris*): one specimen observed in the Drake passage
- Sooty Shearwater (*Puffinus griseus*): common near Cape Horn and in the Beagle channel
- Antarctic/Slender-billed Prion (*Pachyptila sp. cf. desolata/belcheri*): very common around the continental slope of the Magellanic area. Few other individuals observed in the northern part of the Drake passage.

Hydrobatidae
- Wilson's Storm Petrel (*Oceanites oceanicus)*: common in the Drake passage and the Gerlache strait (circum Antarctic).
- Black bellied Storm Petrel (*Fregetta tropica*): few specimens observed in the northern part of the Drake passage.

Pelecanoididae
- Common Diving Petrel (*Pelecanoides urinatrix*): few specimens observed in the northern half of the drake passage.

Phalacrocoracidae
- Antarctic Shag (*Phalacrocorax brandsfieldensis*): common all along the Gerlache strait.

Chionidae
- Pale-faced Sheathbill (*Chionix alba*): few specimen observed on Gentoo and Chinstrap penguin colonies all along the Gerlache Strait.

Stercorariidae
- Brown Skua (*Catharacta lonnbergi*): commonly observed in the Gerlache Strait, north of Lemaire Channel (confusion with South Polar Skua likely in the Gerlache strait).
- South Polar Skua (*Catharacta maccormicki*): few specimens observed south of the Lemaire Channel.

Laridae

- Kelp Gull (*Larus dominicanensis*): few specimens observed near Gentoo Penguin colonies along the Gerlache Strait

Sternidae
- Antarctic Tern (*Sterna vittata*): commonly encountered all along the Gerlache Strait and Lemaire Channel

Sphenicidae
- Gentoo Penguine (*Pygoscelis papua*): dominant and common species breeding on many locations along the Gerlache Strait.
- Magellanic Penguin (*Spheniscus magellanicus*): few specimen observed near Cape Horn , common in the Beagle Channel.
- Chinstrap Penguin (*Pygoscelis antarctica*): one colony of several thousand individuals at Metchnikoff Island
- Adelie Penguin (*Pygoscelis adeliae*): two individuals observed at Berthelot Islands.

2- MARINE MAMMALS

Otariidae
- Antarctic Fur Seal (*Arctocephalus gazelle*): common in the Gerlache strait.

Phocidae
- Leopard Seal (*Hydrurga leptonyx*): several specimens observed at the vicinity of most Gentoo Penguin colonies.
- Weddell Seal (*Leptonychotes weddellii*): one observed at Mechior islands
- Crabeater Seal (*Lobodon carcinophaga*): common along the Gerlache strait and very common in the Lemaire Channel and Penola Strait.

Delphinidae
- Hourglass Dolphin (*Lagenorhynchus australis*): two pods of few specimens observed in the southern part of the Drake passage
- Dusky Dolphin (*Lagenorhynchus obscurus*): common in the Beagle Channel

Balaenopteridae
- Antarctic Minke Whale (*Balaenoptera bonaerensis*): common in the Gerlache strait, Lemaire and Penola Channel. Few individuals observed in the Beagle Channel.
- Humpback Whale (*Megaptera novaeangliae*): common and dominant cetacean observed in the Gerlache Strait, particularly abundant at the southern opening of the Lemaire Channel

The following table present the species list of birds and marine mammals observed during B121. For each species and every area prospected, an abundance index is given (I= one observation or rare species; II= fairly abundant species; III= dominant species).

Table 12: Checklist of birds and marine mammals observed during the expedition. LC = Lemaire Channel; DP= Drake Passage

Vernacular name	Latin name	MI	NH	UI	SK	HI	BI	LC	FH	DP
Black-browed Albatross	*Thalassarche melanophrys*									III
Wandering Albatross	*Diomedea exulans*									II
Grey-headed Albatross	*Thalassarche chrysostoma*									II
Light-manteled Albatross	*Phoebetria palpebrata*									II
Soft-plumage Petrel	*Pterodroma mollis*									I
Cape Petrel	*Daption capense*						I			II
Snow Petrel	*Pagodroma nivea*									
Antarctic Petrel	*Pterodroma incerta*									I
Kerguelen Petrel	*Lugensa brevirostris*									I
Southern Fulmar	*Fulmarus glacialoides*	I								II
Southern Giant Petrel	*Macronectes giganteus*			II			I	II		II
Sooty Shearwater	*Puffinus griseus*									II
White-shinned Petrel	*Procellaria aequinoctialis*									II
Grey Petrel	*Procellaria cinerea*									I
Blue Petrel	*Halobaena caerulea*									III
Antarctic Prion	*Pachyptila desolata*									III
Slender-billed Prion	*Pachyptila belcheri*									III
Common Diving Petrel	*Pelecanoides urinatrix*									II
Wilson's Storm Petrel	*Oceanites oceanicus*	I	II	II	I		II	I	I	II
Black-bellied Storm Petrel	*Fregetta tropica*									II
Kelp Gull	*Larus dominicanus*	II	II	II	II	II		II	III	
Antarctic Tern	*Sterna vittata*	III		II	III	II	II	III	II	
Skua sp. (cf. brown)	*Catharacta cf. lonnbergi*	II	II	II	II			I	I	I
South Polar Skua	*Catharacta maccormicki*					II	II			
Gentoo Penguin	*Pygoscelis papua*		III	III	II	III	I	III		
Adelie Penguin	*Pygoscelis adeliae*						II			
Antarctic Shag	*Phalacrocorax brandsfieldensis*	II	II	II	II	II	I	II	III	
Snowy Sheathbill	*Chionis albus*			II					II	
Humpback Whale	*Megaptera novaeangliae*		II	II				II	II	I
Minke Whale	*Balaenoptera bonaerensis*		II		II	I		II		I
Hourglass Dolphins	*Lagenorhynchus cruciger*									II
Crabeater Seal	*Lobodon carcinophaga*	II	II		I	II	III	III		
Weddell Seal	*Leptonychotes weddellii*	I								
Leopard Seal	*Hydrurga leptonyx*		II							
Ant. Fur Seal	*Arctocephalus gazella*	II		II					II	

7. Habitat mapping

Bruno Danis, Charlène Guillaumot, Thomas Saucède

Context

Habitat mapping is a powerful tool that interpolates seafloor landscapes according to patchy observations by studying the inferences between environment and biotic diversity. We will follow the directions provided by similar works in other Antarctic regions (Jerosch et al. 2016. Post et al. 2011. 2017).

Gutt (2007) and Gutt et al (2013) proposed a classification of Antarctic macrobenthic communities; they mainly distinguished between "Sessile suspension feeders and associated fauna" dominated by sponges and associated fauna of predators (gastropods and asteroids) or other organisms (holothuroids, ophiuroids) and "mobile deposit feeders, infauna and grazers" dominated by asteroids, sea urchins, or infaunal bivalves, among others. They also proposed a "mixed" community category but no devoted category to shallow water nor kelp-dominated habitats. Seabed images have proved to be relevant tools to characterize Antarctic benthic communities (Gutt et al. 2013) using either Ocean Floor Observation System (Segelken-Voigt et al. 2016), ROV (Watson et al. 2018) or optics attached to sampling gears (Pineda-Metz and Gerdes 2018). Photographic transects of the seafloor constitute a non-invasive, efficient technique for benthic studies, providing data on the abundance and distribution patterns at small spatial scale (Segelken-Voigt et al. 2016). Objectives of this project were to characterize the main traits of shallow habitat communities composition using the non-invasive seabed images technique and compare shallow habitats of the studied site with Gutt's categories and former shallow community studies. Results are also expected to contribute to the inventory of the macro- and megabenthic diversity (see section on Macro- and megabenthos diversity) and prove useful to help precise trophic relationships between target species (see section on Trophic ecology).

Methods

A set-up composed of two GoPro (PeauPro87 3.37mm GoPro H4 Black), and two video torches (BigBlue VL 6500Tri) was used by a diver to obtain videos of the seafloor. For each video transect, an average surface of 100m^2 was covered in approximately 15 minutes, in order to have video footages slow enough to enable clear identification of organisms based on screenshot images. The orientation and profile of each transect was defined by a buddy

diver, following a depth ascending profile along a slope (generally 20 to 15 meters) and the orientation given by a compass.

Figure 31: the "mobylette", used for habitat mapping during the B121 expedition

The GoPros were positioned according to a stereo-video system (Hammar et al. 2012, Harvey et al. 2004, 2008) (Figure 31) that was calibrated using a chess-board of black and white squares of known length before diving (Figure 32). The videos obtained by the front

and rear cameras will be analysed using the VideoSync software and will enable measuring the different objects.

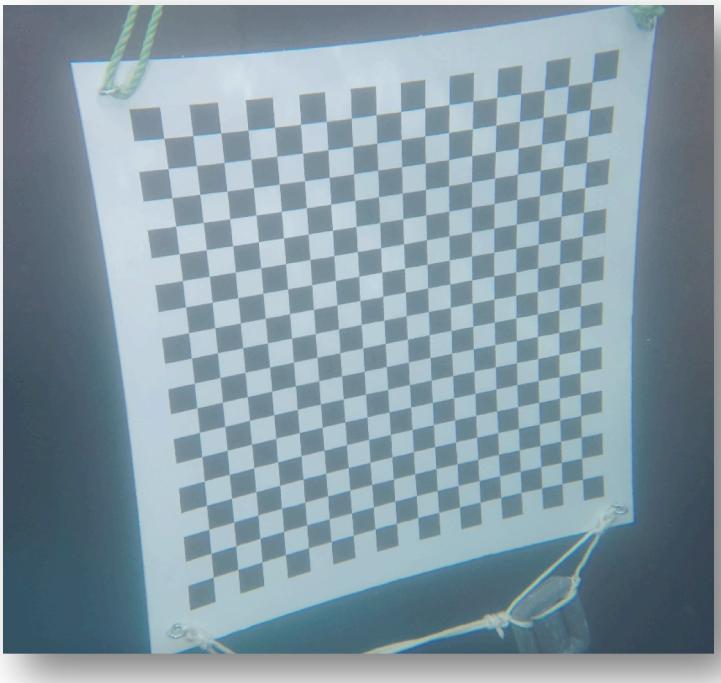

Figure 32: Chess mat used to calibrate the GoPro at the start of each dive

Results

Twelve video transects were carried out, one or two at each station, to characterize the shallow habitats where samples were taken for the trophic study. Transects were usually performed along a gentle slope in between 20m and 15m depth, along a depth gradient (from deeper towards shallower areas), except in HI where it was performed at 8m depth. Shallow kelp habitats with high diversity were preferred. Two transects were realized in most stations to document habitat heterogeneity due to the diversity of substrates (from muddy to rocky in UI), depth (MI, NH) or topography (channel and slope in SC).
Although Antarctic shallow benthic communities are usually considered depauperated with very low biomass and abundances compared to deeper communities of the Antarctic continental shelf, due to the impact of ice scouring and/or anchor ice and to prevailing oligotrophic situations under or close to the ice-shelves (Gutt 2001, Gutt et al 2013), preliminary results suggest the occurrence of various shallow communities depending on local conditions (Table 13, Figure 33), mainly driven by ice disturbance in NH, SC, BI and GR, whereas sponge-related communities dominate in more stable environmental conditions.

Table 13: Semi-quantitative distribution of 22 main components (genus) of the investigated macrobenthic communities in the different stations based on video surveys. White (0): absent, yellow (+): present; orange (++): frequent; red (+++): abundant to dominant

	Seaweeds					µalgae	Porifera				Actinaria	Nemertea
sites	***Himanthothallus***	***Iridea***	***Desmarestia***	***Plocamium***	***Trematocarpus***	***Filamentous***	***Cinachyra***	***Mycale***	***Dendrilla***	***Homaxinella***	***Glyphoperidium***	***Parborlasia***
MI	+	+++	0	+	+	0	0	0	++	0	+	++
NH	+++	+++	++	0	+	0	0	0	0	0	0	+
UI	++	++	+	0	+	++	++	+	0	0	+	++
SC	+	+	+	0	+	+++	0	+	0	0	+	+
HI	0	0	0	0	++	+	0	0	+	++	+++	+
BI	0	+	0	0	++	++	0	+	+	0	++	++
GR	+	+	++	++	+	+	0	+	+	0	+	++
FH	+	++	0	0	+++	0	0	0	++	0	+	+

	Annelida	Bivalvia	Gastropoda	Isopoda	Chelicerata	Asteroidea		Ophiuroidea	Echinoidea	Holothuroidea
sites	***Terebellidae***	***Laternula***	***Austrodoris***	***Glyptonotus***	***Pycnogonida***	***Odontaster***	***Labidiaster***	***Ophionotus***	***Sterechinus***	***Heterocucumis***
MI	+	++	++	0	0	0	0	0	+++	0
NH	0	++	0	0	0	+++	++	0	0	0
UI	++	+	0	0	+	+++	0	+	+	++
SC	+++	+	0	+	0	+++	+	++	0	+
HI	+	+++	0	+++	0	0	0	0	+++	+++
BI	++	+++	+	0	++	+++	0	+	+	+
GR	+	+++	+	+++	0	++	0	0	+	0
FH	+	++	+++	+	0	+	0	0	+++	0

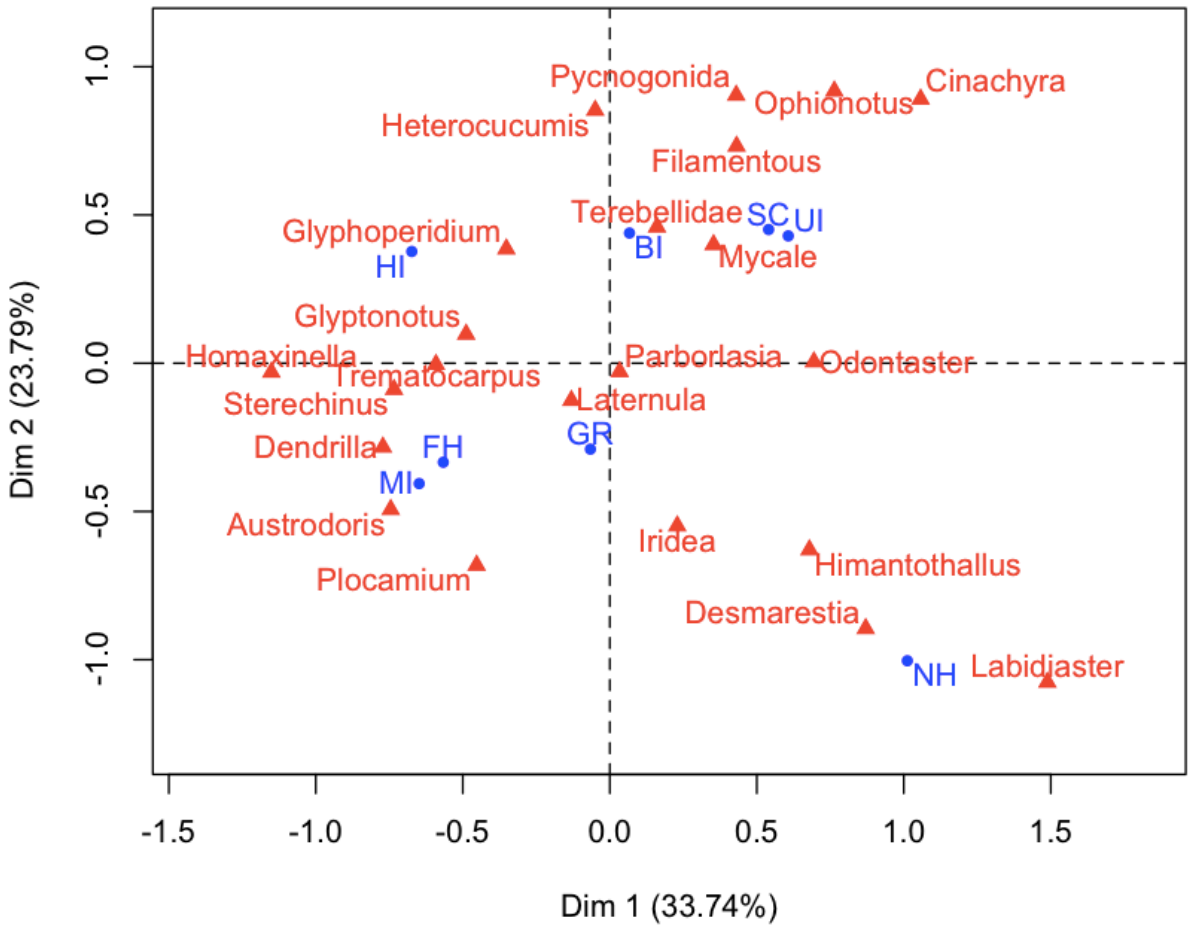

Figure 33: Plot of the first two components of a correspondence analysis based on the contingency Table 13. Genus names are in red, station codes in blue.

A preliminary correspondence analysis of common taxon distribution (Figure 33, Table 13) suggest the occurrence of contrasting shallow habitats and the importance of some biotic interactions such as: between the mollusk *Austrodoris* and the sponge *Dendrilla* upon which it has been observed feeding; the association between filamentous microalgae and terebellids, pycnogonids and the holothuroid *Heterocucumis*, the exclusion between the sea urchin *Sterechinus neumayeri* and the starfish *Odontaster validus*. Certain taxa were systematically present (*Laternula elliptica, Parborlasia corrugatus*).

Perspectives

A more quantitative and fine-tuned analysis using the video transects and the relative surface mapped will help further describe biotic interactions and community composition and diversity. Images will be extracted from video transects using Agisoft PhotoScan software and pictures analyses will be performed using PhotoQuad software to characterize habitat main features. Quantified species richness and abundance (cover) will be linked to abiotic and other biotic environmental settings investigated at the studied stations (oceanography, meiofauna, seabed properties characterised by the VanVeen samples) and to stations properties (visitors frequency, glacier influence) following the methods adopted for similar works in other Antarctic regions (Jerosch et al. 2016. Post et al. 2011, 2017).

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8. Trophic ecology

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Context

Over the last decades, stable isotopes proved to be one of the most reliable integrative trophic markers and have become a near-universal tool in ecology (Boecklen *et al.*, 2011). The concept underlying this technique can be summarized by the idiom "you are what you eat". whereby the isotopic composition of a consumer is a proportional mixture of the isotopic compositions of its food sources, with a slight enrichment towards the heaviest isotope (Boecklen et al.. 2011; Layman et al.. 2012). Moreover, stable isotope ratios of each element have specific properties. making the different tracers complementary. Carbon stable isotope ratios ($\delta^{13}C$) are mostly influenced by processes occurring at the base of food webs, and $\delta^{13}C$ variations throughout the subsequent trophic steps are typically low. This makes $\delta^{13}C$ a useful tracer of the food items directly, or indirectly supporting a consumer population (DeNiro and Epstein. 1978; Layman et al.. 2012). Conversely, nitrogen stable isotope ratios ($\delta^{15}N$) exhibit a marked stepwise increase with increasing trophic levels making $\delta^{15}N$ a useful indicator of both the food sources and the trophic position of consumers (DeNiro and Epstein. 1981;

Layman et al.. 2012). The ratio of sulphur isotopes ($\partial^{34}S$) varies substantially among primary producers, but changes relatively little with progression through a food web, and also can be used to identify important resource pools (Layman et al.. 2012). Recently, it has been proposed that stable isotope ratios of consumers can be used to build an isotopic niche, which can be considered as a proxy of the realized ecological niche (Newsome et al.. 2007; Jackson et al.. 2011). This isotopic niche is influenced by both habitat and trophic sources used (Newsome et al.. 2007; Flaherty and Ben-David. 2010). Therefore it can be used as a descriptor of consumer trophic ecology but also of the main food web structures (Layman and Allgeier. 2012. Layman et al.. 2012). The aim of this trophic workpackage was to assess trophic web structures and the trophic niche of target species in kelp habitats not covered with sea ice using the stable isotopes approach and to compare them to former data collected at Dumont d'Urville (Adelie Land, East Antarctica).

Methods

To characterize the trophic ecology (ecological niche and plasticity) of target species of starfish (*Odontaster validus* and *Psilaster charcoti*), sea urchin (*Sterechinus neumayeri*) and dominant fish species (*Trematomus newnesi*, *Trematomus bernacchii* and *Notothenia coriiceps*; see section “Fish diversity”) as well as the main structures of trophic networks at the investigated sites, potential resource pools of the sea water (plankton and suspended particular organic matter near the surface and above the bottom) at the bottom (sediment organic matter and primary producers) and representatives of main consumers of benthic communities encompassing dominant taxa and dominant trophic guilds were sampled for further isotope analyses. For analysis of the sea water Suspended Particular Organic Matter (SPOM), water samples were collected near the surface and at the sea bottom using a 3 litre Niskin bottle operated either from the vessel *Australis* or one of its tenders. Two samples (replicates) were taken at 2.5m depth and two samples at 1m above the bottom at each site whenever possible. Each water sample was filtered using a 47mm diameter 0.7 µm size Whatman GF/F glass microfiber filters (No. 1825-047) mounted on a Nalgene 500ml receiver, filtration being performed using a man-powered foot pump. Filters were then frozen at -20°C and stored in ziplock plastic bags separately. For analysis of the sediment organic matter, six sediment samples were taken by scuba diving at each site by scooping the first 2 cm of soft bottoms within 200ml vials. Excessive water was removed from vials after the dives and each sample was frozen at -20°C. Sampling of the representatives of most common and key organisms of each site community was done by hand picking during the dives. Whenever possible, 10 specimens of the most abundant and common species of seaweeds and benthic invertebrates were collected at seven sites. Specimens were sorted after each dive, species identified at best and entire specimens stored in ziplock plastic bags at -20°C. Only pieces of seaweed leaves were preserved.

Results

156 samples counting 24 different species and over 650 specimens were collected at seven sites between 8m and 20m depth (Table 14), plus 161 samples/specimens for fish (see section “Fish diversity”). Water and sediment samples were collected at each site. Specimens of seaweeds were sampled as potential food sources among the species *Himanthothallus grandifolius, Desmarestia antarctica, Iridea cordata*, *Plocamium hookeri*, or *Trematocarpus antarcticus*. Other organisms were collected in different guilds, among primary (gastropods *Margarella refulgens* and *Nacella concinna*) and secondary consumers

(gastropod *Austrodoris kerguelensis*), filter feeders (sponges *Dendrilla antarctica*, *Mycale acerata* or *Homaxinella balfourensis*, bivalves *Aequiyoldia eightsii* and *Laternula elliptica*, holothuroid *Heterocucumis steineni*), omnivorous/grazers (sea urchin *Sterechinus neumayeri*, ophiuroid *Ophionotus victoriae*), predators/scavengers (*Glyptonotus antarcticus*. *Parborlasia corrugatus*) and terminal consumers / predators (sea anemone *Glyphoperidium bursa*, starfishes *Odontaster validus*, *Psilaster charcoti* and *Labidiaster annulatus*).

Table 14: Samples collected by scuba diving at each site for trophic analyses, excluding fish samples which are listed in Table 11. Specimens marked with GN or FT were collected by gill net or fish trap, respectively.

Site	*latitude*	*longitude*	*depth*	*species*	*sample #*	*Nb*
MI	-64.3208167	-62.922983	20	*Sterechinus neumayeri*	128_2	1
MI	-64.3208167	-62.922983	20	*Sterechinus neumayeri*	129_2	1
MI	-64.3208167	-62.922983	20	*Sterechinus neumayeri*	130_2	1
MI	-64.3208167	-62.922983	20	*Sterechinus neumayeri*	131_2	1
MI	-64.3208167	-62.922983	20	*Sterechinus neumayeri*	132_2	1
MI	-64.3208167	-62.922983	20	*Sterechinus neumayeri*	133_2	1
MI	-64.3208167	-62.922983	20	*Sterechinus neumayeri*	134_2	1
MI	-64.3208167	-62.922983	20	*Sterechinus neumayeri*	135_2	1
MI	-64.3208167	-62.922983	20	*Sterechinus neumayeri*	136_2	1
MI	-64.3208167	-62.922983	20	*Sterechinus neumayeri*	137_2	1
MI	-64.3208167	-62.922983	20	*Iridea cordata*	122	10
MI	-64.3208167	-62.922983	20	*Psilaster charcoti*	123	4
MI	-64.3208167	-62.922983	20	*Psilaster charcoti*	123	4
MI	-64.3208167	-62.922983	20	*Parborlasia corrugatus*	124	5
MI	-64.3208167	-62.922983	20	*Dendrilla antarctica*	125	2
MI	-64.3208167	-62.922983	20	*Austrodoris kerguelensis*	126	7
MI	-64.3208167	-62.922983	20	*Margarella refulgens*	127	14
MI	-64.3208167	-62.922983	20	*Dendrilla antarctica*	196	7
MI	-64.3208167	-62.922983	20	*Psilaster charcoti*	198	1
MI	-64.3208167	-62.922983	20	*Psilaster charcoti*	199	1
MI	-64.3208167	-62.922983	17	SPOM	245	3L
MI	-64.3208167	-62.922983	2.5	SPOM	246	3L
MI	-64.3208167	-62.922983	20	*Aequiyoldia eightsii*	254	10
MI	-64.3208167	-62.922983	20	*Laternula elliptica*	256	6
MI	-64.3208167	-62.922983	20	*Nacella concinna*	281	12
MI	-64.3208167	-62.922983	20	sediment	195	3
MI	-64.3208167	-62.922983	20	sediment	210	3
NH	-64.842767	-62.533967	20	sediment	382	6
NH	-64.842767	-62.533967	20	*Nacella concinna*	383	9
NH	-64.842767	-62.533967	20	*Himanthothallus grandifolius*	384	2
NH	-64.842767	-62.533967	20	*Himanthothallus grandifolius*	443	7
NH	-64.842767	-62.533967	20	*Iridea cordata*	445	9
NH	-64.842767	-62.533967	20	*Odontaster validus*	446	1
NH	-64.842767	-62.533967	20	*Odontaster validus*	448	10
NH	-64.842767	-62.533967	20	*Labidiaster validus*	448	3
NH	-64.842767	-62.533967	20	*Parborlasia corrugatus*	449	2
NH	-64.8439	-62.53365	2.5	SPOM	478	3L
NH	-64.8439	-62.53365	2.5	SPOM	479	3L
NH	-64.8439	-62.53365	20	SPOM	502	3L
NH	-64.8439	-62.53365	20	SPOM	503	3L
UI	-64.7189	-62.86967	20	*Himanthothallus grandifolius*	623	10
UI	-64.7189	-62.86967	20	*Iridea cordata*	624	10
UI	-64.7189	-62.86967	20	*Odontaster validus*	625	10

UI	-64.7189	-62.86967	20	*Margarella refulgens*	627	20
UI	-64.7189	-62.86967	20	*Parborlasia corrugatus*	628	6
UI	-64.7189	-62.86967	20	*Mycale cf acerata*	629	1
UI	-64.7189	-62.86967	20	*Nacella concinna*	631	10
UI	-64.7189	-62.86967	20	*Mycale cf acerata*	671	9
UI	-64.7189	-62.86967	20	sediment	670	6
UI	-64.7189	-62.86967	20	SPOM	692	3L
UI	-64.7189	-62.86967	20	SPOM	693	3L
UI	-64.7189	-62.86967	20	SPOM	698	3L
UI	-64.7189	-62.86967	20	SPOM	699	3L
UI	-64.7189	-62.86967	20	*Sterechinus neumayeri*	793	1
UI	-64.7189	-62.86967	20	*Sterechinus neumayeri*	794	1
UI	-64.7189	-62.86967	20	*Sterechinus neumayeri*	795	1
UI	-64.7189	-62.86967	20	*Sterechinus neumayeri*	796	1
SC	-64.903267	-62.8569	20	*Himanthothallus grandifolius*	852	10
SC	-64.903267	-62.8569	20	*Odontaster validus*	846	10
SC	-64.903267	-62.8569	20	*Ophionotus victoriae*	855	1
SC	-64.903267	-62.8569	20	*Parborlasia corrugatus*	856	1
SC	-64.903267	-62.8569	20	*Nacella concinna*	857	3
SC	-64.903267	-62.8569	20	sediment	882	6
SC	-64.903267	-62.8569	2.5	SPOM	920	3L
SC	-64.903267	-62.8569	2.5	SPOM	921	3L
SC	-64.903267	-62.8569	20	SPOM	922	3L
SC	-64.903267	-62.8569	20	SPOM	923	3L
SC	-64.904983	-62.864967	20	*Iridea cordata*	927	10
SC	-64.904983	-62.864967	20	*Labidiaster annulatus*	929	1
SC	-64.904983	-62.864967	20	*Parborlasia corrugatus*	930	1
SC	-64.904983	-62.864967	20	*Ophionotus victoriae*	932	6
SC	-64.904983	-62.864967	20	*Nacella concinna*	933	19
SC	-64.904983	-62.864967	20	*Parborlasia corrugatus*	934	2
HI	-65.10664	-64.07552	15	sediment	986	6
HI	-65.10664	-64.07552	8	*Nacella concinna*	1014	1
HI	-65.10664	-64.07552	8	*Homaxinella balfourensis ?*	1015	1
HI	-65.10664	-64.07552	8	*Sterechinus neumayeri*	1016	10
HI	-65.10664	-64.07552	8	*Glyphoperidium bursa*	1017	1
HI	-65.10664	-64.07552	8	*Glyphoperidium bursa*	1018	3
HI	-65.10664	-64.07552	8	*Homaxinella balfourensis ?*	1019	10
HI	-65.10664	-64.07552	8	*Nacella concinna*	1020	10
HI	-65.10664	-64.07552	8	*Glyptonotus antarcticus*	1057	1
HI	-65.10664	-64.07552	8	*Glyptonotus antarcticus*	1058	4
HI	-65.10664	-64.07552	8	*Glyphoperidium bursa*	1064	9
HI	-65.10664	-64.07552	8	*Trematocarpus antarcticus*	1061	10
HI	-65.10664	-64.07552	8	*Heterocucumis steineni*	1062	1
HI	-65.10664	-64.07552	8	*Heterocucumis steineni*	1065	1
HI	-65.10664	-64.07552	8	*Parborlasia corrugatus*	1059	6
HI	-65.10664	-64.07552	8	sediment	1056	3
HI	-65.10664	-64.07552	8	SPOM	1095	3L
HI	-65.10664	-64.07552	8	SPOM	1096	3L
HI	-65.10664	-64.07552	8	SPOM	1097	3L
GR	-64.7257167	-63.282683	18	*Parborlasia corrugatus*	1213	9
GR	-64.7257167	-63.282683	18	*Glyptonotus antarcticus*	1214	4
GR	-64.7257167	-63.282683	18	*Nacella concinna*	1215	3
GR	-64.7257167	-63.282683	18	*Iridea cordata*	1216	10
GR	-64.7257167	-63.282683	18	*Odontaster validus*	1217	9
GR	-64.7257167	-63.282683	18	*Laternula elliptica*	1225	6
GR	-64.7257167	-63.282683	18	sediment	1239	6
GR	-64.7257167	-63.282683	18	*Laternula elliptica*	1240	1

GR	-64.7257167	-63.282683	18	*Laternula elliptica*	1241	6
GR	-64.7257167	-63.282683	18	*Nacella concinna*	1242	7
GR	-64.7257167	-63.282683	18	*Glyptonotus antarcticus*	1243	7
GR	-64.7257167	-63.282683	18	*Mycale cf acerata*	1244	3
GR	-64.7257167	-63.282683	18	*Aequiyoldia eightsii*	1246	2
GR	-64.7265	-63.283033	15	*Himanthothallus grandifolius*	1284	10
GR	-64.7265	-63.283033	15	*Plocamium hookeri*	1285	10
GR	-64.7265	-63.283033	15	*Sterechinus neumayeri*	1286	5
GR	-64.7265	-63.283033	15	*Desmarestia antarctica*	1288	10
GR	-64.7265	-63.283033	15	*Margarella refulgens*	1289	11
GR	-64.7257167	-63.282683	2.5	SPOM	1293	3L
GR	-64.7257167	-63.282683	2.5	SPOM	1294	3L
GR	-64.7257167	-63.282683	18	SPOM	1295	3L
GR	-64.7257167	-63.282683	18	SPOM	1296	3L
FH	-64,5465833	-61,9979833	18	*Iridea cordata*	1331	10
FH	-64,5465833	-61,9979833	18	*Sterechinus neumayeri*	1332	10
FH	-64,5465833	-61,9979833	18	*Nacella concinna*	1333	15
FH	-64,5465833	-61,9979833	18	*Trematocarpus antarcticus*	1334	10
FH	-64,5465833	-61,9979833	18	*Margarella refulgens*	1335	5
FH	-64,5465833	-61,9979833	2,5	SPOM	1369	3L
FH	-64,5465833	-61,9979833	2,5	SPOM	1370	3L
FH	-64,5465833	-61,9979833	15	SPOM	1371	3L
FH	-64,5465833	-61,9979833	15	SPOM	1372	3L
FH	-64,5465833	-61,9979833	20	*Aequiyoldia eightsii*	1465	2
FH	-64,5465833	-61,9979833	20	*Laternula elliptica*	1466	11
FH	-64,5465833	-61,9979833	20	*Odontaster validus*	1467	10
FH	-64,5465833	-61,9979833	20	*Dendrilla antarctica*	1468	10
FH	-64,5465833	-61,9979833	20	sediment	1469	6
FH	-64,5465833	-61,9979833	20	*Odontaster validus*	1471	1
FH	-64,5465833	-61,9979833	20	*Parborlasia corrugatus*	1472	9
FH	-64,5465833	-61,9979833	20	*Austrodoris* sp	1473	13
FH	-64,5465833	-61,9979833	20	*Margarella refulgens*	1474	15
FH	-64,5465833	-61,9979833	20	*Glyptonotus antarcticus*	1475	5
FH	-64,5465833	-61,9979833	20	Ascidian (type *Pyura* ?)	1476	8
FH	-64,5465833	-61,9979833	20	*Glyphoperidium bursa*	1477	4

Perspectives

Isotope analysis of $\delta^{13}C$, $\delta^{15}N$, and $\delta^{34}S$ will be performed in ULG by G. Lepoint and L. Michel. Trophic models will be developed to characterize species trophic niches and plasticity, as well as the main structures of trophic networks in shallow coastal habitats of the visited sites.

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9. Population genomics

Henrik Christiansen, Bruno Danis, Franz Heindler, Quentin Jossart, Camille Moreau, Francesca Pasotti, Henri Robert

Context

Understanding the spatial distribution of genomic diversity of Antarctic organisms is crucial in times of rapid environmental change, because standing genetic variation is the dominant prerequisite for adaptation responses (e.g. Bernatchez 2016). Genetic variability can make species more resilient and eventually enable them to adapt to changing conditions (e.g. Peck 2018). In addition, inter-population connectivity patterns and drivers of population structure in the Southern Ocean remain partially elusive, particularly across taxa with contrasting biological properties (Halanych & Mahon, 2018; Moon et al., 2017; Young et al., 2015). Massive reductions in cost render high-throughput sequencing now amenable to many non-model species (Andrews et al., 2016), such as most Antarctic taxa. In the framework of the RECTO-vERSO projects, several ecologically important species have been selected as target organisms for detailed spatial population genomic analyses. These taxa include species of ostracods (genus *Macroscapha*), amphipods (*Charcotia* and *Eusirus*), bivalves (*Aequiyoldia* and *Laternula*), sea stars (*Bathybiaster* and *Psilaster*), fish (*Trematomus*), and birds (*Pagodroma*). Specific efforts have been devoted during this expedition to collect samples of these target groups for population genomics. Ultimately, parallel, multispecies analyses of genetic population structure and connectivity may help unravel the importance of biological traits such as mobility, fertility and dispersal characteristics in defining genetic differentiation across (parts of) the Southern Ocean.

Methods

The full array of sampling techniques employed during the Belgica 121 expedition was used to collect samples for population genomics. Target taxa were identified to the highest taxonomic rank possible and subsequently the entire specimen or a suitable biopsy was stored in absolute ethanol at -20° C. Ostracods were specifically searched for and isolated from the Rauschert dredge trawls. Amphipods were isolated from Rauschert dredge and amphipod trap collections and hand-picked by divers. Bivalves were collected mainly with the Van Veen grab and hand-picked by divers. Sea stars were collected by divers and incidentally through line fishing. Fish were collected as described in 6. Attempts to collect feathers of snow petrels were made as described in 7.

Results

Approximately 83 ostracods were collected at six localities (MI, UI, SK, HI, BI, FH). Taxonomic identification will take place after the expedition. More than 200 *Charcotia* sp. from MI, NH, SM, BI, and FG and at least 27 *Eusirus* sp. from UI, SK and GR were preserved. For bivalves a total of 44 individuals of *Aequiyoldia eightsi* from MI, NH, UI, AC, HI and 21 *Laternula elliptica* from MI, AC, GI were collected. A total of 16 sea stars of the species *Psilaster charcoti* (14 in MI and 2 in HI) was collected by divers and line fishing. Twenty-one *Trematomus bernacchii* and 60 *Trematomus newnesi* were collected at four localities (see 6.). Potential nesting sites of the snow petrel *Pagodroma nivea* as indicated in Croxall et al. (1995) were visited, but only one potential snow petrel feather could be collected.

Perspectives

A comprehensive technological pilot experiment is currently underway to evaluate and optimize reduced representation sequencing protocols, more specifically RADseq (Baird et al., 2008) or ddRADseq (Peterson et al., 2012), for application to the target taxa mentioned here (Christiansen et al., in prep). First results indicate that RADseq is likely a good option for population genomics of all of our targets, except for amphipods. The latter commonly have very large genomes. As the genome size of our specific amphipod target species (*Charcotia* spp., *Eusirus* spp.) is unknown it is difficult to choose appropriate restriction enzymes for genome reduction. An alternative option may be whole mitogenome sequencing. The large amounts of amphipod samples collected here will provide ample opportunity to further test and fine-tune different genetic approaches. For ostracods whole genome amplification is needed after DNA extraction to attain sufficient quantity and quality for RADseq, but this additional procedure provides useful results (de Medeiros & Farrell, 2018). Given the relative scarcity of ostracods in our previous collection attempts, the individuals found here are very important for future ostracod population genomic studies. Many bivalves with good spatial coverage were sampled that can complement existing sample collections to provide an extensive picture of the spatio-temporal genomic diversity of these species. Compared to existing collections, only relatively little additional sea star and fish samples were collected here. Many fish and sea star samples were already available and partly sequenced prior to the expedition. The individuals from this expedition may complement these ongoing efforts. Snow petrels remain elusive, so samples from other campaigns will be used for bird population genomics. Eventually, RADseq should yield thousands of genotypes per specimen, which will help to identify any potential local adaptation patterns possibly linked to the contrasting environmental and community conditions (see 8. & 11.) at the sites visited during the B121 expedition. Across taxa comparisons are additionally expected to help disentangle driving factors of spatial genetic divergence. However, there is sometimes little spatial overlap between target species, which will complicate such analyses.

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10. Microplastics survey

Bruno Danis & Thomas Saucède

Context

Recently a lot of attention has been directed towards the occurrence of plastics in the marine environment. These contaminants occur in many forms. including some of minute size (microplastics) and are generally thought to represent an important threat to marine ecosystems. Microplastics have been found to act as “magnets” to a broad range of marine contaminants. including Persistent Organic Pollutants (POPs). which become adsorbed to their surface due to their physico-chemical properties. In turn. these contaminated plastics. have the capacity to enter food network through different pathways. potentially playing an aggravating role in the bioaccumulation and/or biomagnification of the contaminants load. It was recently shown that the Southern Ocean is far from being an untouched area of the world with respect to plastic contamination (Waller et al. 2017). For example. microplastics have been reported from surface waters to deep-sea sediments.

Methods

Samples for Microplastic analysis were taken in “abiotic” (sediments). and biotic (Bivalvia: *Aequiyoldia eightsii* and Asteroidea: either *Odontaster validus*, *Psilaster charcoti, or Lysasterias perrieri*) compartments by scuba diving. Five specimens were sampled at about 20m depth at each site by hand picking. Sediment samples were collected by scooping the first 2 cm of the sea bottom with 200ml vials. Nine samples were collected at different depths at each site whenever possible: three replicates at 20m. three at 10m and three at 5m. Specimens were sorted after the dives and frozen in Ziplock plastic bags at -20°C. Sediment vials were kept closed after the dives to avoid potential contamination by various plastic sources present on board and directly stored in Ziplock plastic bags at -20°C. This

general protocol (depths and number of samples) was modified at some sites depending on local topograghic and environmental conditions (*e.g.* absence of sediment in the shallows...) (Table 15).

Results

A total of 36 samples of sediment and organisms were taken at eight sites between 5m and 20m depth (Table 15). The starfish *O. validus* was sampled when present, starfish *P. charcoti* or *L. perrieri* in other cases. Specimens of the filter feeding bivalve *A. eightsii* could be sampled at MI only.

Table 15: Check-list of samples collected for microplastics analysis

Site	*latitude*	*longitude*	*depth*	*sample ID*	*sample #*	*Nb*
Melchior Island	-64.3208167	-62.922983	5	sediment	185	3
Melchior Island	-64.3208167	-62.922983	5	sediment	186	3
Melchior Island	-64.3208167	-62.922983	5	sediment	187	3
Melchior Island	-64.3208167	-62.922983	10	sediment	188	3
Melchior Island	-64.3208167	-62.922983	10	sediment	189	3
Melchior Island	-64.3208167	-62.922983	10	sediment	190	3
Melchior Island	-64.3208167	-62.922983	20	sediment	191	3
Melchior Island	-64.3208167	-62.922983	20	sediment	192	3
Melchior Island	-64.3208167	-62.922983	20	sediment	193	3
Melchior Island	-64.3208167	-62.922983	20	*Psilaster charcoti*	194	4
Melchior Island	-64.3208167	-62.922983	20	*Aequiyoldia eightsii*	255	14
Neko Harbour	-64.842767	-62.533967	20	sediment	381	3
Neko Harbour	-64.842767	-62.533967	10	sediment	401	3
Neko Harbour	-64.842767	-62.533967	7	sediment	402	3
Neko Harbour	-64.842767	-62.533967	20	*Odontaster validus*	444	5
Neko Harbour	-64.843583	-62.533367	15	sediment	506	3
Neko Harbour	-64.843583	-62.533367	10	sediment	507	3
Useful Island	-64.7189	-62.86967	10	sediment	668	3
Useful Island	-64.7189	-62.86967	20	sediment	669	3
Useful Island	-64.7189	-62.86967	20	*Odontaster validus*	626	6
Skontorp Cove	-64.90305	-62.86377	10	sediment	835	3
Skontorp Cove	-64.903267	-62.8569	20	*Odontaster validus*	847	5
Skontorp Cove	-64.903267	-62.8569	20	sediment	881	3
Hovgaard Island	-65.10664	-64.07552	15	sediment	987	3
Hovgaard Island	-65.103267	-64.0845	10	sediment	1106	3
Hovgaard Island	-65.103267	-64.0845	20	sediment	1107	3
Berthelot Island	-65.32855	-64.1385	20	sediment	1119	3
Berthelot Island	-65.32855	-64.1385	20	*Odontaster validus*	1120	5
Green Reef	-64.7257167	-63.282683	18	*Odontaster validus*	1218	5
Green Reef	-64.7257167	-63.282683	18	sediment	1238	3
Green Reef	-64.7265	-63.283033	12	sediment	1287	3
Føyn Harbour	-64.54603	-61.998567	18	*Lysasterias perrieri*	1391	4
Føyn Harbour	-64.54603	-61.998567	10	sediment	1392	3
Føyn Harbour	-64.54603	-61.998567	18	sediment	1393	3
Føyn Harbour	-64.54603	-61.998567	18	*Lysasterias perrieri*	1394	1
Føyn Harbour	-64.54603	-61.998567	18	*Perknaster fuscus*	1395	1

Perspectives

Microplastics analyses will be performed in collaboration with Dr Ana Catarino, Institute of Life and Earth Sciences, School of Energy, Geoscience, Infrastructure and Society, Heriot Watt University (Edinburgh, UK). These analyses will be part of the PhD thesis of Ms Marine Pyl (Marine Biology Lab, ULB), under the supervision of Bruno Danis and Marc Metian (REL, International Atomic Energy Agency, Monaco). Plastics will be extracted and analysed using protocols in line with those developed by Catarino et al. (2017).

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11. Oceanography

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Context

Environmental properties play a key role in species distribution, richness and the structure of biotic interactions within communities (Jerosch et al. 2016, Post et al. 2011, 2017). Among these properties, water temperature and salinity are important drivers.

In the context of a collaboration with an ongoing program in the area (FjordPhyto program, Allison Lee and Maria Vernet), we also realised analyses to characterise water turbidity and plankton community structure. The FjordPhyto program aims at looking at the impacts of glacier meltwater on phytoplankton ecology. Until now, the project gathers time series of samples collected at 16 different coastal fjords, among which stations visited during the B121 cruise.

Methods

Oceanographic data were collected using casts of a Starr-Oddi DST compact microprocessor-controlled CTD (conductivity, temperature, depth) recorder conducted at ten different stations (Table 17). The CTD recorder was set up for one measurement per second. Due to recorder sensitivity and response time, deployments were performed at the rate of 10m/min., with 30 sec. stops done every 5 meters. For calibration of conductivity values and correction of potential offset, sea surface conductivity was also measured using a WFW muti 340i portable probe at the start and end of each recorder deployment. CTD data were retrieved from recorder using the SeaStar Application Software (©2010 Star-Oddi).

Vertical sea water turbidity of the water column was characterised using a Secchi disk. The Secchi disk was deployed overboard using a graduated tape reel and Secchi depth was noted when the disk was not visible anymore. During sunny days, the Secchi disk was deployed in the boat shadow. Date and time of each deployment were recorded.

In order to characterise plankton communities at the surface, sea water was collected either by hand or using a bongo net towed behind the zodiac during approximately 10 minutes (mesh size: 20µm, to have a concentrated sample). In each case, the sample was preserved in a brown 120mL Nalgene bottle and fixed with 3mL of Lugol. The remaining water contained in the bongo net cod-end was filtered on 47mm sterile filters provided by the FjordPhyto program and using a man-powered foot pump, mounted on a Nalgene 500mL unit. The filter was afterwards preserved in separate cryotube containing RNAlater and kept frozen until genetic analyses will be carried out by Allison Lee. Water samples from a 3L Niskin bottle were collected at three different depths (2m, 10m, > 30m) whenever possible at the different station (Table 16). Water was filtered using the same material as previously described. Filters were fold following to FjordPhyto protocol and kept frozen in cryotubes until chlorophyll-a content analyses are performed by Allison Lee.

Results

Seventeen CTD recorder casts were performed at ten sites (Table 17, Figure 34) to characterize water masses at each study station. Supplementary deployments were performed at depth in Neko Harbor and Petermann Island to complement former data obtained by Allison Lee in the context of the FjordPhyto Program. A deep (400m) cast was performed before Arctowski Peninsula (AP) to document salinity and temperature data associated to a Niskin deployment for eDNA sampling. Depth values were not treated due to the recorder depth limitation (150 m), acknowledged after the CTD deployment.

Plankton-related samples will be further analysed by Allison Lee. Samples are stored accordingly to the FjordPhyto protocol either frozen or in lugol and kept at CADIC until sent back to San Diego.

Table 16: List of the analyses related to plankton sampling performed for the FjordPhyto project at the corresponding stations

Station	*Position*	*Event; sample number*	*Sample type*	*Date; Time (at station)*	*Remarks*
Melchior Islands	64°19,248S 62°55,378W	PHY_01; #224	Surface sample + lugol	02/03/2019; 10:00am	
			Secchi disk	02/03/2019; 10:00am	
		BN_01; #253	Bongo net surface sample + lugol	02/03/2019; 12:30am	
			Bongo net filtered water for genetics		Not done, no pump available at this moment
			Niskin water samples		Not done, no pump available at this moment
Neko Harbour	64°50,584S 62°32,034W	PHY_02; #442	Surface sample + lugol	05/03/2019; 01:00pm	
		BN_02; #429	Bongo net surface sample + lugol	05/03/2019; 10:30am	
		BN_02; #430	Bongo net filtered water for genetics	05/03/2019; 10:30am	
		NIS_06; #498	Water filtered 3L, 2m depth	05/03/2019; 09:00am	
		NIS_06; #499	Water filtered 3L, 2m depth	05/03/2019; 09:00am	
		NIS_06; #500	Water filtered 3L, 10m depth	05/03/2019; 09:00am	
		NIS_06; #501	Water filtered 3L, 10m depth	05/03/2019; 09:00am	
	64°50,753S 62°32,740W	NIS_07; #521	Water filtered 3L, 35m depth	06/03/2019; 11:30am	
		NIS_07; #521	Water filtered 3L, 35m depth	06/03/2019; 11:30am	
			Secchi disk	06/03/2019; 11:30am	
Useful Island	64°43,129S		Secchi disk	07/03/2019; 08:45am	

	62°52,174W	BN_03; #674	Bongo net surface sample + lugol	07/03/2019; 12:15am	
		BN_03; #675	Bongo net filtered water for genetics	07/03/2019; 12:15am	Half of the cold-end processed (foot pump broken due to over-use and too concentrated samples)
		PHY_03; #797	Surface sample + lugol	07/03/2019; 03:00pm	
		NIS_08; #694	Water filtered 3L, 2.5m depth	08/03/2019; 09:30am	
		NIS_08; #695	Water filtered 3L, 2.5m depth	08/03/2019; 09:30am	
		NIS_08; #696	Water filtered 3L, 10m depth	08/03/2019; 09:30am	
		NIS_08; #697	Water filtered 3L, 10m depth	08/03/2019; 09:30am	
			Niskin > 30m		Not possible for this station due to organisation, anchoring, time…
Brown Cove	64°54.66'S 62°51.94'W	PHY_04; #827	Surface sample + lugol	09/03/2019; 09:15am	
			Secchi disk	10/03/2019; 09:00am	
		BN_04; #924	Bongo net surface sample + lugol	10/03/2019; 12:00am	
		BN_04; #925	Bongo net filtered water for genetics	10/03/2019; 12:00am	
		NIS_09; #916	Water filtered 3L, 2.5m depth	10/03/2019; 12:00am	
		NIS_09; #917	Water filtered 3L, 2.5m depth	10/03/2019; 12:00am	
		NIS_09; #918	Water filtered 3L, 10m depth	10/03/2019; 12:00am	
		NIS_09; #919	Water filtered 3L, 10m depth	10/03/2019; 12:00am	

64°54'221" 62°52'021"	NIS_11; #875	Water filtered 3L, 35m depth	10/03/2019; 06:00pm	
	NIS_11; #938	Water filtered 3L, 35m depth	10/03/2019; 06:00pm	
65°11,079S 64°08,336W		Secchi disk		Aborted, too much boat movment and current
	BN_05; #1125	Bongo net surface sample + lugol	13/03/2019; 06:30pm	
	BN_05; #1126	Bongo net filtered water for genetics	13/03/2019; 06:30pm	
	NIS_15; #1127	Water filtered 3L, 2.5m depth	13/03/2019; 06:30pm	
	NIS_15; #1128	Water filtered 3L, 2.5m depth	13/03/2019; 06:30pm	
	NIS_15; #1129	Water filtered 3L, 10m depth	13/03/2019; 06:30pm	
	NIS_15; #1130	Water filtered 3L, 10m depth	13/03/2019; 06:30pm	
	NIS_15; #1131	Water filtered 3L, 35m depth	13/03/2019; 06:30pm	
	NIS_15; #1132	Water filtered 3L, 35m depth	13/03/2019; 06:30pm	

Table 17: Temperature, salinity and Secchi depth data for the different stations. Uncorrected salinity values. Stations with subzero temperature values are highlighted in yellow

Station	event ID	latitude	longitude	max depth (m)	date (dd/mm/yy)	local time start-end	T (°C) min<mean<max	salinity (psu) min<mean<max	Secchi depth (m)
MI	CTD_01	64°19.249'	62°55.378'	22	27/02/19	11:25-11:34	1.75<2.1<3.24	31.4<32.66<33.4	
MI	CTD_02	64°19.249'	62°55.378'	22	27/02/19	22:00-22:16	0.24<1.5<1.78	32.7<33.28<33.8	
MI	CTD_03	64°19.249'	62°55.378'	15	02/03/19	06:08-06:16	1.43<1.70<2.4	32.5<32.95<33.4	3.3
NH	CTD_04	64°50.576'	62°32.035'	8	04/03/19	14:11-14:17	0.48<1.07<1.82	31.6<32.39<32.7	
NH	CTD_05	64°50.576'	62°32.035'	48	04/03/19	17:35-17:57	0.28<0.39<0.64	31.8<32.54<32.8	8.6
UI	CTD_06	64°43.146'	62°52.160'	19	06/03/19	18:23-18:31	0.76<0.87<0.99	31.7<32.54<33.1	9.7
UI	CTD_07	64°43.146'	62°52.160'	16	08/03/19	17:31-17:40	0.76<0.78<0.84	32.4<32.69<33.1	
SK	CTD_08	64°54.185'	62°51.825'	9	10/03/19	17:26-17:32	0.68<1.01<1.78	31.1<32.48<32.7	7.6
SK	CTD_09	64°54.368'	62°52.035'	47	10/03/19	18:58-19:21	0.48<0.58<1.08	32<32.85<33.1	
HI	CTD_10	65°06.055'	64°04.951'	19	11/03/19	19:28-19:37	-0.13<0.09<0.52	30.5<32.12<33	2
HI	CTD_11	65°06.398'	64°04.532'	15	13/03/19	14:25-14:30	-0.46<-0.03<0.28	30.8<32.29<33	
PI	CTD_12	65°11.079'	64°08.336'	32	13/03/19	18:33-18:52	-0.75<-0.25<-0.05	30.9<32.69<33.3	
BI	CTD_13	65°19.709'	64°08.284'	20	14/03/19	14:41-14-51	-1.16<-1.04<-0.7	31.2<31.82<32.5	4
GR	CTD_14	64°43.548'	63°16.935'	16	16/03/19	08:41-08:50	0.52<0.73<1,51	33<33.3<33.5	6.4
AI	CTD_15	64°35.371'	62°31.168'	400	18/03/19	13:39-14:06	-0.33<-0.14<0.56	30.4<34.07<34.6	
FH	CTD_16	64°32.795'	61°59.879'	15	19/03/19	12:03-12:10	0.7<0.75<1	33.6<33.88<34	7.3
FH	CTD_17	64°32.795'	61°59.879'	15	20/03/19	12:45-12:52	0.2<0.52<0.6	33.2<33.55<33.8	

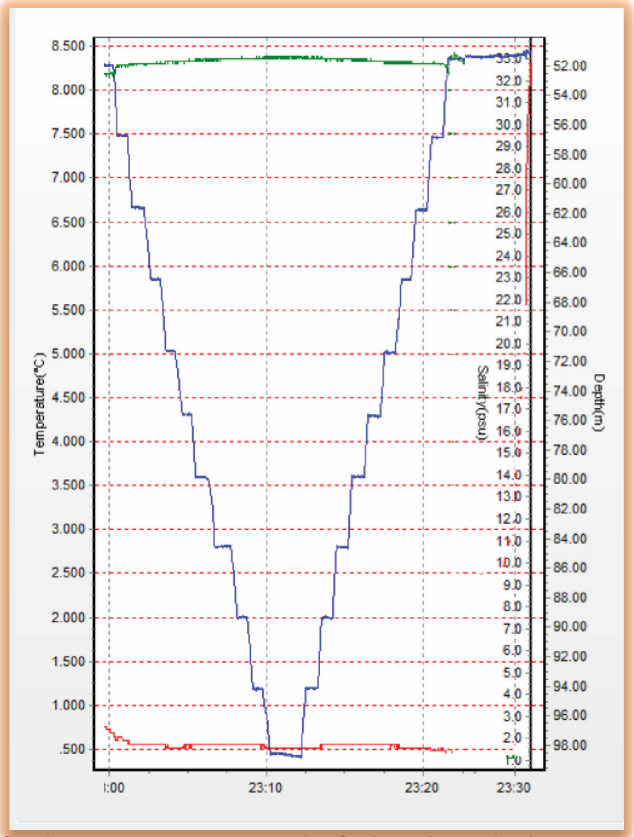

Figure 34: CTD cast #09 data for Skontorp Cove as an example of salinity (green line), temperature (red line), and depth (blue line) profiles (depth values not to scale)

Perspectives

Salinity values will be corrected in lab when back university. Plankton samples will be processed by Allison Lee and will be part of the time series follow up begun by the FjordPhyto project at the sampled station (among several).

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12. Biogeochemistry

Francesca Pasotti

Context

Soft sediments represent the majority of the Southern Ocean sea floor, and their potential in terms of carbon sequestration and/or organic matter remineralization is highly understudied. Prokaryotes and the small sized metazoans known as meiofauna are a crucial component of the micro-food-web of soft sediments (Giere 2009). In the deep, food banks have been documented as one of the main factors for the sustained high biomasses of Antarctic benthos during winter times (Smiths et al., 2003). The strong benthic-pelagic coupling of the deep with the surface high summer productivity leads to a storage of organic matter into the sediments which can be consumed either directly or indirectly via the microbial loop. Similar processes happen as well in the shallower areas of the Antarctic marine ecosystems. Sea ice algae, phytoplankton, microphytobenthos and large seaweeds all play an important role during the summer months in providing a large input of food for the higher consumer, and part of this primary production will be stored in the sediments where it can be remineralized (Braeckman et al., 2018). The granulometry of the sediments represents a very important parameter that influences organic matter reworking and the overall organic matter load. Besides this, different grain sizes of sediment can host different meiobenthic or macrobenthic assemblages, in light of specific adaptations to organic load and oxic/hypoxic/anoxic conditions, and the need for specific sediment size fraction for their motility or burrowing activities (for instance in the case of tube worms). Hence sediment characteristics can be a very good proxy for the energetic status of different study locations and their biogeochemical composition can help us better understand the structure of the local benthic assemblages and the potential effects that glacier retreat and increasing sea water temperatures may have in the alteration of the local dynamics.

Methods

Sediment has been sampled at each location by divers either by means of perspex push cores (3.6 cm diameter) or by surface sediment scooping. This sampling has been done in parallel to the meiofauna sampling (See section 3 for more details). Where the sediment composition allowed core sampling, the sediment was sliced in different layers profiles (0-1 cm, 1-2 cm, 2-5 cm 5-10 cm) for the whole core depth. At least 3R were always taken for biogeochemistry, only in a couple of occasions samples where lost during transport. Moreover, not in every location the same depth layer were possible to be achieved and this will be considered during processing of the data.

For Meiofauna and biogeochemistry sample list see section on Soft sediments biodiversity.

Results

Soft sediment composition among the different locations and between the different sampling sites within locations differed in terms of granulometry and oxic/anoxic conditions. Overall the sites that we explored ranged from very anoxic-silt dominated sites to more oxic-fine-sand sediment sites, with pebbles being a large component of the latter. Historical and ongoing glacial ablation and bottom topography and slope play a major role in the soft sediment grain size and oxygenation status. In general enclosed basins like the anchor site in Hovgaard Island or Skontorp Island which were characterised by a rather gentle sloped

shallow inner basin and a shallow saddle at their entrance were characterised by highly silty sediments with anoxic deeper (below the surface 0-1 cm) layers.Sites more exposed to open water dynamics like Dive_22 at Hovgaard Island and Dive_12 of Neko Harbour were sandier and more oxygenated in the depth. Microphytobenthic mats and algal associations were to be found on the surface of the sediment and will likely be represented by different organic matter content, carbon to nitrogen ratios and Chl-a and other pigments profiles.

Perspectives

In Ghent analyses will be carried out on sediment to study the granulometry (median grain size, size fraction%), total organic matter content (TOM), Total Organic Carbon (TOC%) content, Total nitrogen content (TN%), and pigments analysis (by means of HPLC analysis to have the complete spectrum and proxies of potential direct primary producers) of the sediment samples

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13. Environmental DNA

Henrik Christiansen, Franz Heindler, Quentin Jossart, Camille Moreau

Context

Organisms leave traces in the habitat they use, in form of shed skin, hair, scales, cells, and more. Such remnants are present in both aquatic and terrestrial systems. Recent technological advances make it now feasible to sequence environmental sample concentrates (e.g. from water or soil) from a specific habitat in order to survey and potentially even quantify the species occurring therein in a non-invasive manner (Creer & Seymour 2017). Samples are taken with special attention to anti-contamination measures and stored in sterile containers. Back in the laboratory PCR of specific target fragments (depending on the target taxa, e.g. COI, 12S, D-Loop, mutS, or shotgun sequencing) and subsequent high-throughput sequencing is conducted (Creer et al., 2016). Data from this environmental DNA (eDNA) can thus assist in biodiversity assessment and monitoring and holds great potential to eventually enable large scale, standardized sampling for conservation purposes (Thomsen & Willerslev, 2015; Bohmann et al., 2014). First, however, ground-truthing experiments with solid technical development, careful standardization and

replication are needed. Water samples for eDNA analyses were collected during the B121 expedition to further advance this rapidly developing research field.

Methods

Seawater was collected from zodiacs at two depths using a 3 L, hand-held Niskin bottle, which was sterilized with bleach and rinsed thoroughly in seawater on site between each deployment. Three replicates were taken per depth and stored in individual 1 L plastic containers, which were previously bleached and rinsed, and rinsed again on site with the sampled water, just before collection. Megafauna presence in direct vicinity of eDNA sampling events was noted. Samples were then kept sealed at ambient temperature until filtration. All water samples were filtered by the same person within 24 h using sterile, single-use 50 mL Soft-Ject syringes (VWR, accession code HSWA8300005157) onto Sterivex-GP 0.22 polyethersulfone filters (Merck, accession code SVGPL10RC). The use of these enclosed filters and sterile, single-use equipment should decrease the chances for contamination (Sigsgaard et al., 2016). The entire volume (1 L) was filtered, except when the filter clogged before (but always minimum 800 mL filtered). Filters were immediately closed, put back into their original bag, wrapped with parafilm and stored at -20° C. Working surfaces and non-single-use equipment (markers, scissors) were sterilized with minimum 50 % bleach solution between samples (Goldberg et al., 2016; Wilcox et al., 2016). As a control, 1 L of demineralized water was filtered in the same way after processing all six samples per locality.

Results

Eight sampling events were conducted at four major stations, that correspond roughly to the widest spatial extent of the expedition (i.e. MI, NH, HI, FH; see Fig. 1). At each station, one sampling was carried out in the vicinity of the anchored ship (but with at least a few hundred meters distance) and one sampling further away (few miles). Each sampling event comprises six water samples, three replicates from surface waters (2.5 m depth) and three replicates from near the seafloor (approximately 20 m depth at MI, NH, HI). The last deep sample was taken on the way to Foyn Harbour in the middle of the Gerlache Strait at approximately 400 m depth. Including controls this sampling effort yielded 56 filters containing environmental DNA.

Perspectives

After transport to the home institute, DNA will be extracted from the filters in dedicated eDNA laboratories. Suitable extraction protocols will be tested in advance. Primer sets for metabarcoding will be determined in order to survey diversity of fishes, and possibly also crustaceans, and cetaceans and pinnipeds. If resources allow, marker sets that record intraspecific variation (Sigsgaard et al., 2016) may also be explored. Subsequent high-throughput sequencing of these metabarcoding libraries should enable species-level presence-absence detection. Sequences can also be assessed quantitatively, but the correlation to true abundance is not obvious. Eventually, eDNA results should be compared to census data from traditional methods employed during this expedition as well as published occurrence records. Cowart et al. (2017) have used metagenomic sequencing of eDNA at localities in the same region as studied here. Their results provide another good

opportunity for comparative analyses at a fine spatial scale, paving the way for more systematic use of eDNA for Antarctic biodiversity monitoring.

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14. Macrophotography

Quentin Jossart & Camille Moreau

Context

In parallel to the samplings, a specific timeframe was dedicated to macro-photography. Indeed, the interest of having high quality pictures is twofold. First, pictures of living organisms help in the identification process onboard or after the expedition. Secondly, it is a precious material for future scientific (e.g. papers, conferences…) and outreach activities.

Methods

Species illustrating the biodiversity of the samplings were photographed using an Olympus camera (OMD-EM1), a 60mm macro lens, two flashes and few accessories to diffuse or reflect the light. Photographed specimens were isolated from the others before preservation and were identified at the lowest taxonomic level possible (using the field guides available onboard).

Results

In total, 143 specimens were photographed during the expedition. The most photographed phyla were Arthropoda (56 specimens) followed by Echinodermata (23), Mollusca (18), Polychaeta (14) and Chordata (10). Overview pictures of the specimens were captured (Figure 35) as well as some close-ups to most informative structures (Figure 36). Finally, an Excel sheet containing information on the specimens was compiled (*i.e*. sample and event numbers, size of the individual, taxonomic identification, name of the picture files).

Figure 35: Example of an overview picture (Serolidae; Crustacea – Isopoda). Scale bar = 0,5cm

Figure 36: Example of a close-up picture (spinelets of the sea star Odontaster validus)

Perspectives

Some pictures will be sent to taxonomists to obtain further identifications while others will be used by B121 scientists in their future scientific contributions. Moreover, the pictures and Excel file associated will be uploaded online to improve their accessibility. Other ideas are under consideration and will be evaluated in the upcoming months (*e.g.* upload in the WoRMS taxonomic database, combination with other cruise pictures to produce a field guide…).

15. Phylogeography and taxonomy of the Snow Petrel (*Pagodroma nivea* s.l.)

Henri Robert

Context

The Snow Petrel (*Pagodroma nivea s.l.*) is a common circumpolar Antarctic and Subantarctic seabird that has undergone historic climatic changes. It is therefore a well-suited model organism to predict future scenarios resulting from future global changes. Nowadays, the

taxonomic status of the Snow Petrel remains the subject of considerable controversy (Shirihai. 2007; del Hoyo & Collar. 2014), the current consensus treating it as two distinct subspecies (del Hoyo & Collar. 2014): the Lesser and the Greater Snow Petrel (respectively *P. nivea nivea* and *P. n. major*). Few "pure" parapatric populations of both "subspecies" are known whereas most colonies consist of hybrid morphotypes. The evolutionary history of the species is still uncertain and the existence of the two "subspecies" could be the result of different glacial refugia with the establishment of post glacial hybridization zones (Fraser et al. 2012).

Method

Genetic data will be used to reconstruct the snow Petrel's evolutionary history, detect past refugia and its current phylogeography in order to link histories and refugia to past climate changes.

Biometrical measurements will allow assessment of morphological variance among populations and individuals for birds from various locations of the Antarctic, South Georgia and the Scotia Arc obtained during field campaigns and from other institutions and museums.

Two sampling mission have been organized in the framework of the RECTO project in order to collect DNA samples and morphometric data from distinct, distant populations. The first mission took place in the Sor Rondane Mountains (Queen Maud Land) in the vicinity of Princess Elisabeth Station during the BELARE 2017-2018 austral summer. The second mission being the Belgica 121 expedition to the Gerlache Strait, see the -Calendar and Sampling Area- chapters on page 7 and 8 of the present cruise report.

Work at sea and results

A total four locations known to host Snow Petrel colonies were visited between March 9th and the 15th of March 2019. Target colonies were selected out of the sites recorded and georeferenced by Coxall et al. 1995.

	Localisation	**Coordinates**	**Date of visit**
-	Almirante Brown station	(64°53'S 62°51'W)	09/03/2019
-	Skontorp Cove	(64°54'S 62°51'W)	09/03/2019
-	Alvaro Cove	(64°52.206S 63°00.054W)	11/03/2019
-	Cape Tuxen	(64°46.765S 63°40.3814W)	15/03/2019

Each site was carefully observed from the distance to detect potential breeding sites and then thoroughly surveyed by foot (equipped with crampons and ice axe when necessary) by two to four people in the search for nesting cavities, carcasses or feathers. Despite our efforts to visit known reproduction sites and collect Snow Petrel samples, very few feathers were collected, and no certainty of the species can be assured so far as Antarctic Shag (*Phalacrocorax brandsfieldensis*) were also present in the areas making the identification of the white feathers found uncertain. The relative fail of sample collection can be attributed to two main factors: the breeding season of the Snow Petrel being over by the time of our visit (the fledging time of the chicks occurring usually around the end of the months of February) made the detection of the nesting cavities difficult. Secondly, conversation with colleagues overwintering at the Vernadski station revealed that the Snow Petrel frequentation at the breeding site and therefore the rate of reproduction of the species present in the vicinity of the station has been extremely low this year.

Perspectives

The ultimate goal of this topic is to predict future distributions of the Snow Petrel and its prey under different scenarios by integrating distribution models with models on ocean dynamics, sea ice extent and Lagrangian particles.
Future distributions of the Snow Petrel and its prey will be predicted under different scenarios by integrating spatial and trait distribution models based on physiological limits and ecological niches with state-of-the art models for ocean dynamics (Luyten, 2011), sea ice (Vancoppenolle et al., 2009) and Lagrangian particle models (Dulière et al., 2013).

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16. ASPA Plaque Visit – Metchnikoff Point (MP)

Bruno Danis

Context

The Belgica 121 expedition was tasked by the Belgian Environment Public Service (SPF Environmnet) to visit Metchnikoff Point on Brabant island, in order to check the general status of historic monument N°45 dedicated to the Belgica expedition lead by Adrien de Gerlache in 1897-99. This historic monument is under the responsibility of the Belgian State in application of specific Antarctic dispositions. The monument has not been visited since 1999. The team was also asked to proceed to the reparation of the monument, in case of mild damage.

Methods

After spotting the monument, the *Australis* anchored in a Bay located South of Metchnikoff point (lat: 64°02.395 N, 62°34.078 W). A first team (Bruno Danis, Henri Robert, Franz Heindler) was deployed using a tender on the South side of the Point. A drone was sent to identify an appropriate site to land the rest of the team. The B121 team was deployed using the two tenders on the North coast, more accessible, and at a fair distance of a fur seal

colony. Videos and photos of the monument were taken to document the status of the commemorative plaque.
The B121 team also documented the remaining detritus of an undetermined research camp, which were left downhill of the plaque. The team cleaned part of the camp, gathering 4 full bags of garbage, which were brought back for further documentation.

Results

A large number of pictures and videos were taken at the site as required by the Belgian SPF Environment, as well as additional documentation about the garbage patch. A few pictures are shown below (Figure 37, Figure 38, Figure 39). The plaque itself was in good state, and no particular maintenance was required. A bronze-imitation (plastic) statue of Adrien de Gerlache was found behind the plaque, unattached. It was also documented and put back in place. All documentation pertaining to the historic monument and nearby garbage will be shared by the SPF Environment, which will decide if any further action is required.

Figure 37: general view of the bay below the commemorative plaque. A colony of fur seals can be seen on the beach. Picture by Charlène Guillaumot

Figure 38: general picture of the historic monument. Picture by Charlène Guillaumot.


Figure 39: general view of the garbage patch left from a research camp, before cleaning by the B121 team. Picture by Charlène Guillaumot.

Perspectives

The B121 team delivered the inspection of historic monument n°45 as required by the Belgian SPF Environment. Relevant photos and videos will be shared with the SPF. The

management of the garbage patch remains problematic, as the team was not equipped to properly clean the site, which is under the responsibility of the Belgian State. The relevant authorities will be consulted, and it is hoped that appropriate action shall be taken, in coordination with the Antarctic Treaty's Committee on Environmental Protection.

Diving activities

The B121 diving team was composed of Francesca Pasotti (dive leader), Charlène Guillaumot and Thomas Saucède. Dives were planned and carried our following the rules outlined in the Operational Risk Management which was compiled and signed by the dive leader Francesca Pasotti, signed by the skipper of Australis Ben Wallis, the scientific leader Bruno Danis, the diver and the insurance department of the diver's employer. Daily briefings were carried out to plan the dives following the ROV exploration of each new location's sea bottom and hence deciding the exact points where video transects, hand picking of specimens, and/or sediment sampling for various analyses were supposed to happen. Dives were done within the depth limitations (30 m) outlined by the ORM, with no more than 2 repetitive dives happening during one day for each diver. Ascent to the surface was controlled with a speed of 10 m per minute, and a safety stop of 3 min at 5 meters was done at the end of each dive. Divers dove in a buddy system (or alone depending on task) and a safety on the zodiac, with one diver always tethered to the surface, and the buddy joined to him by a buddy line. Divers dove both directly from the *Australis* and from the zodiacs. Ice conditions (presence of large icebergs or ice growlers, presence of dense pack ice) were monitored and the dives were postponed when necessary. A leopard seal watch was active from aboard the Australis and from the zodiacs during the duration of each dive: dives always happened in vicinity of the Australis to always allow monitoring of the activity by means of a binocular. The refilling of the tanks was carried out by the first mate of the Australis, Ryan Houston who himself is a Diving Instructor with years of experience and he had been trained to take care of the compressor onboard of the Australis. Tanks were filled only when the air was dry, hence not during rainy days or snow to avoid presence of moist in the tanks and prevent freezing at depth. A total of 38 dives were carried out during a total of 19 working days and 3 days off with the collection of up to 333 samples (Table 18).
A full report of the diving activities has been provided to the Belgian Science Policy Office.

Number of operations per diver:
Charlène Guillaumot : 27
Francesca Pasotti : 19
Thomas Saucède : 26

Table 18: Dive Log. Divers: FP = Francesca Pasotti, CG = Charlène Guillaumot, TS = Thomas Saucède

Date	*Dive n°*	*Divers*	*Event_ID*	*Latitude*	*Longitude*	*Total dive time*	*Max Depth*
27/02/2019	1	TS, CG	MI_Dive1	62°19.246	62°55.375	27	20
27/02/2019	2	FP	MI_Dive2	62°19.246	62°55.375	14	16,7
28/02/2019	3	TS, CG	MI_Dive3	62°19.246	62°55.375	36	19,6
01/03/2019	4	FP	MI_Dive4	62°19.246	62°55.375	37	17,8
01/03/2019	5	TS, CG	MI_Dive5	62°19.246	62°55.375	39	20
01/03/2019	6	TS, CG	MI_Dive6	62°19.246	62°55.375	41	22
02/03/2019	7	FP+CG	MI_Dive7	62°19.246	62°55.375	28	18
02/03/2019	8	TS, CG	MI_Dive8	62°19.246	62°55.375	36	19,8
04/03/2019	9	FP, TS	NH_Dive_9	62°50.565	62°32.009	27	23,6
04/03/2019	10	TS, CG	NH_Dive_10	62°50.565	62°32.009	38	16
05/03/2019	11	TS, CG	NH_Dive_11	62°50.565	62°32.009	35	18,6
05/03/2019	12	FP, CG	NH_Dive_12	62°50.565	62°32.009	28	16,4
06/03/2019	13	FP, TS	NH_Dive_13	62°50.565	62°32.009	26	17,9
07/03/2019	14	TS, CG	UI_Dive_14	64° 43.136’	62° 52.173	39	20
07/03/2019	15	FP, TS	UI_Dive_15	64° 43.136’	62° 52.173	35	20
08/03/2019	16	FP, CG	UI_Dive_16	64° 43.136’	62° 52.173	35	22
08/03/2019	17	TS, CG	UI_Dive_17	64° 43.136’	62° 52.173	35	21
09/03/2019	18	FP, CG	SK_Dive_18	64°54,183’	62°51.826’	35	10
09/03/2019	19	TS, CG	SK_Dive_19	64°54.248’	62°51.777’	35	21
10/03/2019	20	FP, TS	SK_Dive_20	64°54.196	62°51.41.4’	35	17,1
10/03/2019	21	TS, CG	SK_Dive_21	64°54.299’	62°51.898’	32	21
12/03/2019	22	FP, CG	HI_Dive_22	65°06.057’	64°04.992’	34	14,7
12/03/2019	23	TS, CG	HI_Dive_23	65°06.057’	64°04.992’	34	11,6
13/03/2019	24	FP	HI_Dive_24	65°06.049’	64°04.920’	9	20

13/03/2019	25	TS, CG	HI_Dive_25	65°06.057’	64°04.992’	24	10
13/03/2019	26	FP, TS	HI_Dive_26	65°06.196’	64°04.042	24	20
14/03/2019	27	TS, CG	BI_Dive_27	65°19.713’	64°08.310’	31	20
14/03/2019	28	FP, CG	BI_Dive_28	65°19.713’	64°08.310’	21	15,5
16/03/2019	29	TS, CG	GR_Dive_29	64° 43.550’	63°16.959’	37	19
16/03/2019	30	FP	GR_Dive_30	64° 43.550’	63°16.959’	26	17,9
16/03/2019	31	TS, CG	GR_Dive_31	64° 43.550’	63°16.959’	29	19
17/03/2019	32	TS, CG	GR_Dive_32	64° 43.550’	63°16.959’	39	19
17/03/2019	33	FP, CG	GR_Dive_33	64° 43.550’	63°16.959’	17	11,8
19/03/2019	34	TS, CG	FH_Dive_34	64°32.801’	61°59.880’	39	21
19/03/2019	35	FP, TS	FH_Dive_35	64°32.762’	61°59.914’	28	18
20/03/2019	36	FP	FH_Dive_36	64°32.762’	61°59.914’	38	18
20/03/2019	37	TS, CG	FH_Dive_37	64°32.801’	61°59.880’	31	24
20/03/2019	38	TS, CG, FP	EI_Dive_38	64°32.420	61°59.899	36	18

Documentary

A documentary about the expedition directed by Lilian Hess will be released in December 2019.It will topic both the original Belgica expedition (1897-1899) as well as the B121 (2019). Financed through a crowdfunding campaign (9.10.2019 – 9.11.2019) and private sponsors (mentioned in the acknowledgments section) it is produced by Lilian Hess, Franz M. Heindler and Bruno Danis. Footage was shot by the crew members during the expedition, and by Lilian Hess for all other occasions.
The synopsis will be an intimate account of a small group of ambitious individuals, who are passionate about introducing a more sustainable way of conducting Polar research to the science community. The harsh beauty of the Antarctic landscape is reflected in the rawness of the footage, which will be captured by the scientists themselves - above and below water. Some of the most deeply poetic and profoundly personal texts have been produced by the original explorers during what we today refer to as the “Heroic Age of Antarctic Exploration”. While the old diaries speak of the struggle for survival, this documentary rather resembles a first-hand video journal about the fervour that comes with realising ones aspirations, the hope for making a change, the strains of the sea, and the intensifying pressure of no escape.

More information about the documentary can be found on the Belgica121 website (www.belgica121.be) as well as on the expedition’s kickstarter page.

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Acknowledgements

The B121 expedition was funded through various channels, for the expedition itself and for the realization of a dedicated documentary. The B121 team has also benefited from a lot of support, time and expertise from the international networks it has been collaborating with since a long time.

Funding of expedition:

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Funding of documentary:

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