

types, different current regimes and different water masses. Our objectives on this expedition were to collect statistically meaningful numbers of selected taxa from as many varying locations as possible across the Filchner area of continental shelf, and by collaboration, work up a detailed picture of the physical environment of each station. The taxa we focused on were crustaceans, glass sponges, gorgonians and ophiuroids. A further objective was to collect samples suitable for stable isotope analysis to strengthen existing models of trophic interactions around the Antarctic.

Work at sea

The specimens for ecological and evolutionary genetic work were collected using Agassiz trawl (AGT), bottom trawl (BT) and Rauschert dredge (RD). The RD was deployed mid-ships. The frame was lowered at 0.4 ms^{-1} until the cable length was 50 m longer than the depth. The trawl began at 0.5 kn for 10 min, after which the trawl was recovered at 0.3 ms^{-1} until the frame was clear of the sea floor, then increased to 0.5 ms^{-1} .

Specimens were sorted, labelled and photographed to obtain information about the colour patterns of the different species while still alive. Ophiuroids and crustaceans were fixed whole in 96 % ethanol. For gorgonians and poriferans, a tissue sample, were fixed in 100 % ethanol, a second gorgonian fragment was fixed in 70 % ethanol for further identification at the stereomicroscope on board. Gorgonian colonies and some poriferan tissue samples were frozen at $-20 \text{ }^{\circ}\text{C}$ for DNA studies. For some gorgonian specimens, tissue was buffered in 50mM Tris-HCl pH 8.0 for DNA storage in FTA cards. Moreover, some tissue of selected gorgonian and crustacean specimens were fixed in RNA lather and stored at $-20 \text{ }^{\circ}\text{C}$ for RNA analysis. Cnidarians (other than gorgonians) were fixed for morphological studies (histology, anatomy, etc.) in buffered 4 - 8 % formaldehyde, fragments of each morphospecies were also fixed in 100 % ethanol for further molecular analysis. Once in the laboratory, all specimens will be preserved in 70 % ethanol.

For stable isotope analysis, invertebrates and fishes were collected from bottom trawls, Agassiz trawls, dredges and baited traps. Small organisms were sampled completely, while from macro- and megafaunal specimens' body wall pieces or muscle tissue samples were taken for analysis. All samples were rinsed with distilled water and frozen at $-20 \text{ }^{\circ}\text{C}$ until further analysis of stable isotope ratios (N, C) at home. For later validation of the taxonomy reference animals were preserved in 70 % ethanol.

Preliminary (expected) results

The RD was deployed at 10 stations. Positions and depth are provided in Table 3.3.3.2.1. Details of the AGT and BT can be found in sections 3.3.3.3 and 3.3.4.1, respectively.

Tab. 3.3.3.2.1: Station details for each RD deployment

Station	Date	Time	Latitude	Longitude	Depth [m]
PS82/127-1	19/01/2014	15:05	75° 28.78 S	27° 21.66 W	275.5
PS82/134-1	20/01/2014	13:28	75° 19.52 S	27° 35.93 W	364.5
PS82/148-1	21/01/2014	20:08	74° 49.58 S	25° 10.51 W	691.7
PS82/169-1	24/01/2014	16:58	74° 52.32 S	26° 35.77 W	319.7

3.3.3 Benthos communities

Station	Date	Time	Latitude	Longitude	Depth [m]
PS82/176-1	25/01/2014	14:05	74° 32.05 S	30° 56.50 W	528.7
PS82/251-1	02/03/2014	19:15	74° 29.58 S	37° 29.96 W	385.5
PS82/283-1	02/07/2014	17:16	74° 58.63 S	29° 23.79 W	408.2
PS82/295-1	02/08/2014	12:17	75° 31.34 S	28° 49.66 W	420.5
PS82/307-1	02/09/2014	14:47	75° 5.38 S	28° 39.95 W	445.5
PS82/351-1	16/02/2014	17:28	70° 56.41 S	10° 32.58 W	314.5

- Crustaceans

The Southern Ocean is considered as a hotspot for biodiversity and endemism for several orders of peracarid crustaceans (e.g. isopods, amphipods) that have undergone spectacular adaptive radiations. Of these, amphipods are the most speciose animal group in Antarctic coastal and shelf regions. Although extensively sampled and studied in several regions of the Southern Ocean (e.g. Antarctic Peninsula and Scotia Sea), recent studies show that most species are inadequately described or composed of several genetically heterogeneous species complexes, with allopatric or sympatric distributions. Hence, the underexplored Filchner area could provide a number of species new to science for several crustacean groups and information regarding the connectivity between these shelf areas, surrounding regions and abyssal basins.

Species numbers and abundances per station are summarized for several crustacean taxa (Amphipoda, Decapoda, Cumacea, Cirripedia, Euphausiacea, Mysidacea, Tanaidacea) in Tab. 3.3.3.2.2 a and b, Tab. 3.3.3.2.3 and Tab. 3.3.3.2.4 for the three different gears used. Finally, sampling by means of amphipod traps attached to the fish trap lander system at station PS82/118 provided thousands of scavenging lysianassoid amphipod species, which can be used for population genetic studies.

- Decapoda

Only three species of decapods were recovered. The two species *Notocrangon antarcticus* and *Chorismus antarcticus* were found together in all shelf depth trawls except for the shelf station at Austasen. In the AGT station at the eastern shelf break/slope around 1,750 m depth and the northern bottom trawl stations PS82/331 (760 m) and PS82/341 (740 m), these species were replaced by *Nematocarcinus longirostris*, present in high numbers (300, 205 and 45 specimens respectively).

- Amphipoda

The AGT recovered the highest abundance (> 1,100 specimens) and species richness (80 different species) at the easternmost station on the southern shelf (PS82/91; 290 m). Most species belonged to the family Iphimediidae, as associated fauna to the large quantities of bryozoans that characterized this catch. The stations at the Filchner Trench (i.e. PS82/67, PS82/111, PS82/115) were characterized by a low abundance and species richness of amphipods, and crustaceans in general. BT catches were characterized by a high diversity and abundance of epimeriid and iphimediid species. The station with the highest species richness and abundance was situated at the NE shelf (PS82/11; 300 m). The two northernmost stations sampled using the RD were characterized by the highest abundance and species richness (+/- 50 species) of amphipods.

Tab. 3.3.3.2.2.a: see electronic supplement

Tab. 3.3.3.2.2.b: Species numbers and abundances for crustacean taxa

Taxa	Stations		296-1		306-1		316-1		331-1		341-1		357-1	
	Sp	N	Sp	N	Sp	N	Sp	N	Sp	N	Sp	N	Sp	N
Amphipoda														
Ampeliscidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Epimeriidae	1	1	0	0	2	4	3	4	1	2	1	1	1	1
Eusiroidea	2	3	1	1	0	0	0	0	0	0	0	0	0	0
Iphimediidae	3	4	1	1	1	1	1	1	0	0	0	0	0	0
Leucothoidea	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lysianassoidea	0	0	0	0	0	0	1	1	0	0	0	0	0	0
Melitidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Oedicerotidae	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Stenothoidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Stilipedidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Indet	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Decapoda														
<i>Notocrangon antarcticus</i>	1	18	1	14	0	0	0	0	0	0	0	0	0	0
<i>Nematocarcinus longirostris</i>	0	0	0	0	1	2	1	205	1	45	0	0	0	0
<i>Chorismus antarcticus</i>	0	0	1	1	0	0	0	0	0	0	0	0	1	4
Euphausiacea	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Isopoda														
Flabellifera - Serolidae	1	1	1	1	0	0	0	0	0	0	0	0	0	0
Flabellifera - Gnathiidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Flabellifera - <i>Natanolana</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Valvifera - Arcturidae	0	0	1	1	0	0	0	0	0	0	0	0	0	0
Valvifera - <i>Glyptonotus</i>	1	1	0	0	0	0	0	0	0	0	0	0	0	0
Indet	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Mysidacea	1	18	1	1	1	2	1	2	1	3	0	0	0	0
Tanaidacea	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Total species number	10		7		5		7		3		3			
Total abundance	46		20		9		213		50		6			

Tab. 3.3.3.2.3: see electronic supplement

3.3.3 Benthos communities

Tab. 3.3.3.2.4: Species numbers and abundances per station are summarized for several crustacean taxa

Taxa	Stations 127-1		134-1		148-1		169-1		176-1		251-1		283-1		295-1		307-1		351-1		
	Sp	N	Sp	N	Sp	N	Sp	N	Sp	N	Sp	N	Sp	N	Sp	N	Sp	N	Sp	N	
Amphipoda																					
Amathillopsidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ampeliscidae	1	2	1	1	0	0	1	1	35	1	6	2	8	1	2	2	1	3	2	2	2
Calliopidae	0	0	0	0	0	0	0	0	0	0	0	1	111	0	0	0	1	2	1	3	3
Caprellidea	0	0	0	0	0	0	0	0	5	5	0	0	0	0	3	8	0	0	0	0	0
Corophioidea	0	0	0	0	0	0	1	2	3	6	5	7	7	3	0	0	0	0	0	0	0
Epimeriidae	1	3	2	2	0	0	4	5	3	3	3	10	1	1	1	1	0	0	0	0	0
Eusiroidea	2	5	2	6	0	0	3	11	3	35	6	31	3	6	1	2	0	0	2	2	2
Iphimediidae	4	5	6	7	0	0	4	5	2	6	0	0	0	0	0	1	3	0	0	0	0
Isaeidae	1	2	1	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0
Ischyroceridae	0	0	0	0	0	0	0	0	2	4	1	5	0	0	0	0	0	0	0	0	0
Lepechinellidae	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0
Leucothoidea	0	0	1	1	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0
Liljeborgiidae	1	3	1	1	0	0	0	0	0	0	3	4	1	1	1	1	0	0	0	0	0
Lysianassoidea	2	6	1	1	0	0	1	1	7	10	8	166	6	9	3	3	2	3	3	3	3
Melphippidae	0	0	1	1	0	0	0	0	2	44	1	7	2	7	1	4	0	0	1	1	1
Oedicerotidae	0	0	0	0	0	0	2	12	3	51	1	1	1	1	1	2	1	1	0	0	0
Phoxocephalidae	0	0	0	0	0	0	0	0	0	0	1	1	0	0	2	2	1	1	0	0	0
Podoceridae	1	1	0	0	0	0	0	0	2	22	1	2	0	0	1	3	1	1	0	0	0
Stegocephalidae	0	0	0	0	0	0	0	0	2	10	2	9	0	0	2	3	1	1	0	0	0
Stenothoidea	0	0	0	0	0	0	0	0	0	0	1	27	0	0	0	0	1	1	0	0	0
Stilipedidae	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0
Synopiidae	0	0	0	0	0	0	1	6	0	0	1	8	1	6	1	7	0	0	0	0	0
Indet	10	>50	11	46	3	4	11	71	10	129	10	112	10	15	13	31	7	8	1	1	1
Cumacea	5	>50	2	16	2	8	8	44	7	67	3	3	7	91	12	85	8	13	4	5	5

Stations		127-1	134-1	148-1	169-1	176-1	251-1	283-1	295-1	307-1	351-1												
Taxa	Sp	N	Sp	N																			
Decapoda																							
<i>Notocrangon antarcticus</i>	0	0	1	2	0	0	1	4	0	0	1	5	1	1	1	1	0	0	0	0	0		
indet	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	
Euphausiacea	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Isopoda																							
Asellota	0	0	0	0	1	1	3	4	4	17	5	13	1	1	2	2	1	1	1	1	2	2	
Flabellifera – Serolidae	0	0	0	0	0	0	0	2	7	1	1	1	0	0	0	0	0	0	0	0	0	0	0
Flabellifera – Gnathiidae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
Flabellifera – Natatolana	0	0	0	0	0	0	0	1	1	1	1	124	0	0	1	1	1	1	1	0	0	0	0
Valvifera – Arcturidae	1	1	0	0	0	0	1	6	4	15	1	6	2	4	1	4	2	4	2	2	2	1	1
Valvifera – Glyptonotus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Indet	1	1	1	1	0	0	0	1	5	0	0	0	1	1	0	0	0	0	0	0	0	1	2
Mysidacea	1	2	1	2	3	7	4	22	4	55	5	31	1	1	3	12	4	4	4	4	3	3	3
Tanaidacea	0	0	0	0	0	0	0	0	1	1	0	0	1	1	0	0	0	0	0	0	0	0	0
Total species number	32	31	9	31	44	75	66	43	54	32	21	66	43	54	32	21	66	43	54	32	21	66	43
Total abundance	> 134	88	20	239	520	697	151	202	44	25	134	88	20	239	520	697	151	202	44	25	134	88	20

3.3.3 Benthos communities

In the amphipod traps, a total of 8 amphipod species and 1 isopod species (*Natatolana* sp.) were found. The lysianassoid species *Orchomenella* (*O.*) *pinguides*, *Uristes* sp. and *Waldeckia* spp. were the most abundant. Other amphipod species included the lysianassoid species of the genera *Hirondellea* and *Pseudorchomene*, an unidentified lysianassoid species and *Eusirus* sp.

- Isopoda

Serolid species were most abundant at the AGT stations PS82/43 and PS82/73 on the outer shelf at +/- 470 m and the southern shelf at +/- 570 m depth, respectively, as well as at the bottom trawl stations PS82/11 (300 m) and PS/249 (370 m). Other most abundant species recovered in BT and AGT were *Natatolana* spp. and *Glyptonotus antarcticus*.

- Cumacea

Cumaceans were more dominant than amphipods in the RD samples characterised by gravel and fine sediment, in contrast to dredge samples dominated by sponge spicules or bryozoans. The most diverse catch was that at station PS82/295 (420 m), with 12 different species and a number of 85 specimens. Station PS82/283 (408 m) was characterized by the highest abundance (91 specimens, belonging to 7 different species). The AGT deployed at station PS82/151 (1,750 m) contained the highest number of specimens (33) for all trawls, indicating that the relative abundance of cumaceans increases with depth.

Upon return in the home laboratory, DNA extractions will be carried out on several taxa of interest for molecular studies. For amphipods, these taxa include the families Lysianassoidea, Epimeriidae and Iphimediidae, for which an extensive DNA barcode (COI) library has been established so far. Lysianassoid samples will be used to complement on-going phylogenetic and phylogeographic studies (see Havermans et al. 2010, 2011; Havermans *in press*) by means of sequencing of mitochondrial (COI, 16S rDNA) and nuclear (28S rDNA, 18S rDNA) gene fragments. Population genetic studies will be initiated using abundant amphipod taxa such as *Orchomenella* (*O.*) *pinguides*, *Waldeckia obesa*, *Eusirus* spp. and iphimediid species by developing microsatellite or SNP markers based on Next-Generation Sequencing data. Ongoing or past population genetic studies on decapods (*N. antarcticus*, *C. antarcticus*) and isopods (serolids, *Glyptonotus antarcticus*) can be complemented by the numerous samples obtained during this expedition.

- Ophiuroids

There are 219 species of ophiuroids to be found in Antarctic waters of which 126 are endemic (Marin-Ledo & López-González 2013). The majority of species are small and morphologically cryptic. However, the more common, large ophiuroids are possible for a non-expert taxonomist to identify. Ophiuroids were collected from all stations and tentative identifications are given in Tab. 3.3.3.2.5. The most common species was *Ophiacantha antarctica*, present at most stations. Other common species include *Ophionotus victoriae*, *Ophioplinthus gelida*, *Ophiocten dubium*, *Ophioceres incipiens* and *Ophioperla koehleri*. *Ophioperla koehleri* was only found in shallower regions, (max depth found 570 m).

Based on non-expert morphotype sorting some biogeographical patterns were apparent suggesting distinct assemblages for the eastern shelf region, the trough

and western shelf region, the shelf break, and the Filchner Trench in the south. The Filchner Trench itself was impoverished with only *O. victoriae* collected from the two southernmost stations. This contrasts with the eastern shelf fauna (i.e., shallower regions close to the continent) that even at the southernmost shelf station was considerably more diverse. This may be related to depth, substrate and current regimes. There was no obvious difference between the ophiuroid assemblages from the north or south of the eastern shelf. Typical species that defined this inner shelf assemblage include *Astrotoma agassizi*, *Ophiosteira* sp. and, at shallower stations, *Ophiura caranifera*. The shelf break was another clearly definable assemblage. *Ophiacantha pentactis* was collected exclusively and in large numbers from these stations (PS82/233, western shelf break at 830 m; PS82/266, mid trough shelf break at 720 m; PS82/314 eastern shelf break at 710 m), but not from deeper slope station (e.g. PS82/151 eastern slope 1,750 m) nor from stations of similar depth but clearly on the shelf itself (e.g. PS82/264 mid trough close to shelf break at 650 m). *Astrochlamys sol* was also collected only from shelf break stations. The stations south of the shelf break, both in the trough itself and to the shallower regions to the west of the trough, had similar assemblages consisting mostly of the common species *Ophiacantha antarctica*, *Ophioplithus gelida* and *Ophionotus victoriae*.

On return samples will be identified by a taxonomist specializing in Antarctic ophiuroids, DNA will be extracted from all individuals and the Cytochrome c Oxidase subunit one gene amplified for molecular identification and initial phylogenetic analyses. Specific hypotheses will be tested using double digested restriction associated DNA sequencing (ddRAD). Species presence data will be submitted to the SCAR MarBIN database. DNA sequences will be submitted to GENBANK.

- Poriferans

Poriferans are a regionally important element in some Antarctic benthic communities. They can be considered as ecosystem engineers as they provide structure to the sea-floor positively influencing the diversity and composition of Antarctic benthic communities, facilitating recruitment of other sessile organisms, and serve as refuge various species including juvenile stages of fish (Kaiser et al. 2013). *Rossella racovitzae* and *Anoxycalyx joubini* are two dominant species that form these extensive assemblages, and are suspected to reproduce actively by asexual reproduction (Teixidó et al. 2006). However the extent of asexual reproduction and the balance sexual/asexual reproduction that contributes to the assemblage structure is unknown. The major aim of this study was to investigate the population structure of both species at a microscale (within sampling sites) and regional scale (between sampling sites) using population genetic techniques to better understand species dispersal capacities and genetic variability within and among the different localities.

Ten to 30 samples of *R. racovitzae* and 7 to 27 samples of *A. joubini* were collected using AGT and BT from 5 stations (Tab. 3.3.3.2.6).

3.3.3 Benthos communities

Tab. 3.3.3.2.5: Identified ophiuroids collected at stations using AGT and BT

	<i>Amphipura</i> sp	<i>Astrochilomya bruneus</i>	<i>Astrochilomya sol</i>	<i>Astrotoma egrassizi</i>	<i>Ophiacantha antarctica</i>	<i>Ophiacantha pentactis</i>	<i>Ophiacantha</i> sp	<i>Ophiolima antarctica</i>	<i>Ophioparta gigas</i>	<i>Ophiocten dubium</i>	<i>Ophiocten</i> sp	<i>Ophioleuce regulare</i>	<i>Ophioceres incipiens</i>	<i>Ophiosteira</i> sp	<i>Ophioperla koehleri</i>	<i>Ophioplinius gelida</i>	<i>Ophioplinius</i> sp	<i>Ophipura caranifera</i>	<i>Ophipura</i> sp	<i>Ophiomastus</i> sp	<i>Ophiomusium</i> sp	<i>Ophiionotus victoriae</i>	UNKNOWN	ASSORTED SMALL UNKNOWN
AGT																								
PSR7/43	X			X	X		X			X	X			X	X	X						X	X	
PSR7/50																X	X	X					X	X
PSR7/67									X	X													X	
PSR7/73				X	X					X				X	X		X					X	X	
PSR7/91				X												X		X				X		X
PSR7/97				X											X		X	X				X		
PSR7/117																						X		
PSR7/115																						X		
PSR7/151					X																	X	X	
PSR7/233					X	X		X				X					X						X	
PSR7/264	X									X			X				X							
PSR7/266			X		X	X											X							
PSR7/284	X				X					X					X	X								
PSR7/293	X				X			X		X						X				X		X	X	
PSR7/308	X				X					X					X							X	X	
PSR7/314			X		X	X							X											
PSR7/349													X	X		X	X	X						
BT					X			X	X	X				X	X	X				X	X			
PSR7/11					X			X	X	X				X	X	X				X	X			
PSR7/18	X				X			X	X			X		X	X	X					X			X
PSR7/39					X			X	X					X										
PSR7/53	X		X					X	X				X		X		X				X	X	X	
PSR7/78				X		X				X			X									X	X	
PSR7/84	X		X	X			X	X	X					X	X	X					X			
PSR7/88	X		X	X				X	X				X		X	X						X	X	
PSR7/126					X																X		X	
PSR7/129																								
PSR7/166	X				X				X					X	X	X					X		X	
PSR7/175					X									X		X					X			
PSR7/201					X																			
PSR7/244															X	X	X							
PSR7/248	X				X										X		X						X	
PSR7/249					X								X										X	X
PSR7/287	X	X			X				X					X								X		
PSR7/296	X			X	X				X														X	X
PSR7/306				X	X				X					X								X	X	
PSR7/316					X	X			X	X														
PSR7/331					X	X		X				X	X	X				X		X			X	
PSR7/341				X	X	X			X				X			X								
PSR7/357				X	X		X					X		X	X	X						X		

Tab. 3.3.3.2.6: Sampling sites and number of individuals per sponge species collected at each station

Station	Gear	Depth [m]	<i>Rosella racovitzae</i>	<i>Anoxycalys joubini</i>
PS82/011	BT	406	10	9
PS82/053	BT	261	18	10
PS82/088	BT	265	28	27
PS82/166	BT	306	10	7
PS82/349	AGT	225	30	14

Four stations were located in the Filchner area and one was in Austasen. Samples from both areas were collected on a depth range 220-410 m. Presence of propagules was recorded and, where present, these were sampled and preserved for further analysis. Two different preservation treatments were used, -20 °C storage temperature and 100 % ethanol and storage in cool chambers, in order to ensure a suitable preservation for further DNA isolation. The genetic analyses will be done at the home laboratory. For the molecular genetics analysis, RAD-Seq (restriction site associated DNA sequencing) will be used. This genetic approach is exceedingly sensitive and is able to provide information on the maintenance and/or extinction of local populations, the recovery after disturbance, and the colonization of new areas.

Gorgonians

The cnidarian material collected during PS82 was obtained from 21 Bottom Trawls, 14 Agassiz Trawls, 2 Multicorers, 2 Multigrabs and one Rauschert Dredge. More than 1,200 individuals/colonies have been preliminarily identified on board, although most are awaiting further morphological studies in the laboratory (e.g. histology, SEM). The specimens belong to 95 morphospecies, of which 14 belong to Hydrozoans, 5 to jellyfishes and 76 to Anthozoans. This last group includes 44 species belonging to Octocorallia and 32 to the Hexacorallia. The hexacoral species consisted of 22 actinarians, 7 scleractinians and 3 zoanthideans. While the octocoral material collected consisted of 3 species of pennatulaceans, 3 bamboo corals, 4 soft corals and 34 primnoid species.

Preliminary results on the primnoids composition showed that shallow stations from the east flank of the Filchner Trough are more diverse than deeper ones (>1,000m), and than stations from the west flank. Data from the shelf break stations suggests they are less diverse than the eastern shelf. In the northern stations (up 76°) gorgonian communities are dominated by *Dasystenella acanthina*, while in the southern stations *Thouarella* species seem to be the dominant (Fig. 3.3.3.2.1).

For the present study on the gorgonian population structure and connectivity genomic DNA will be extracted from seven primnoid species. For each species we collected a minimum of 5 specimens at each station, but not all species have been found in the same stations (Tab. 3.3.3.2.7).

3.3.3 Benthos communities

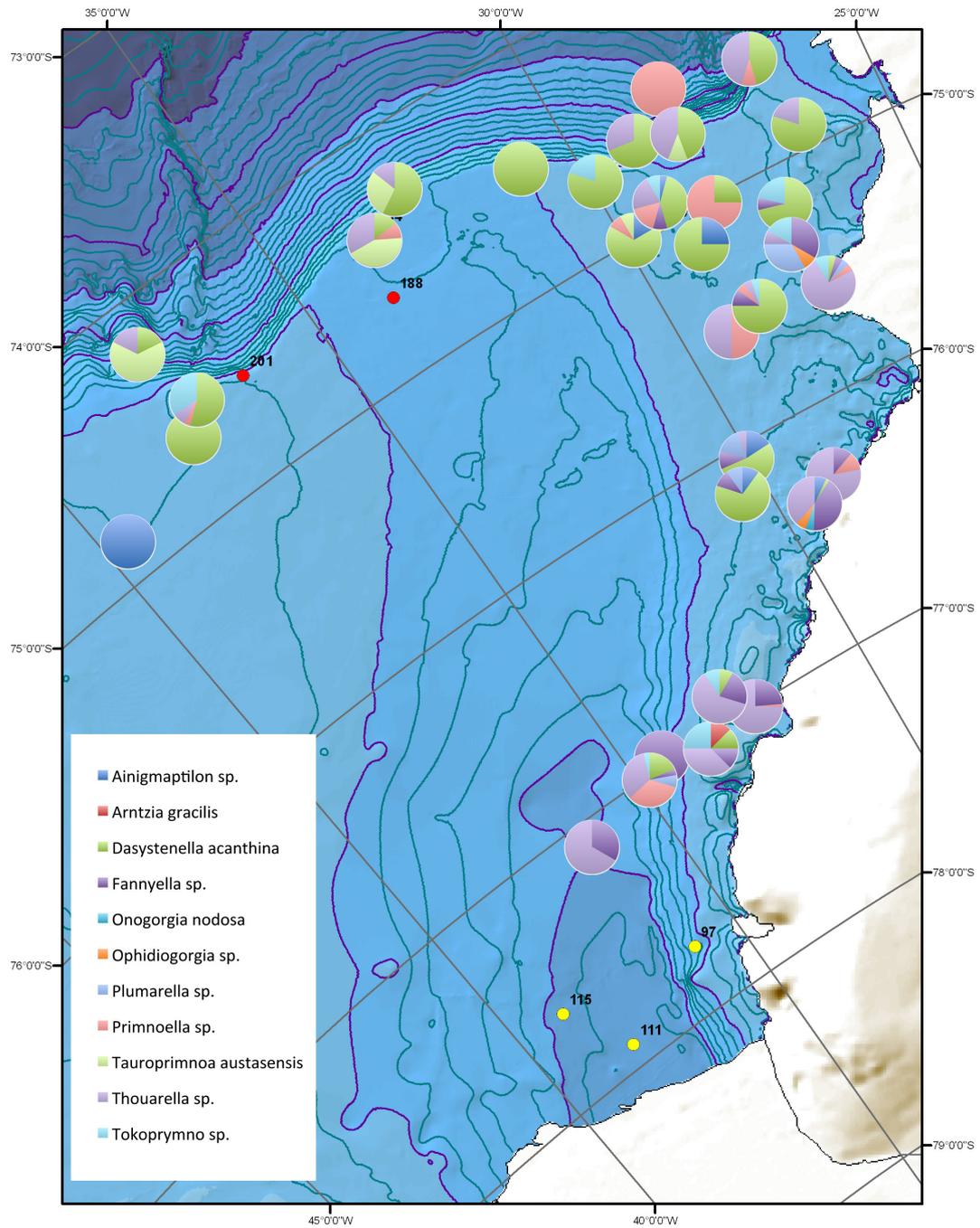


Fig. 3.3.3.2.1: Composition of Antarctic primnoids in the Filchner Outflow System

Tab. 3.3.3.2.7: Number of primnoid specimens collected for population genetic analyses

Taxa	PS82																						
	11	18	39	43	50	53	73	88	91	126	166	175	249	264	282	284	296	314	316	331	341	349	
<i>Ainigmaptilon</i> sp.					7																		18
<i>Dasystenella acanthina</i>	68	10	7	10		5	6			8	9	14			8	10	15	11	19	5		11	
<i>Fannyella rossii</i>					42		16	15															
<i>Thouarella</i> sp1					16		22	21															
<i>Thouarella</i> sp2					5	9		13															
<i>Thouarella</i> sp4					7		17	10	11														
<i>Tokoprymno</i> sp.	17						7					9											

3.3.3 Benthos communities

Populations from the seven Antarctic gorgonians will be compared; five of them found at shallow depths (~250 m) will be compared in a latitudinal gradient. One species has been found at 77° transect at two different depths allowing the comparison in depth of two populations. Moreover, two species have been found at both sides of the Filchner Trench at depths around 400 m, and the primnoid *Dasystenella acanthina*, which seems to have a wider distribution in this area, will be used for detailed studies of the connectivity among the different populations in the Filchner area (Fig. 3.3.3.2.2).

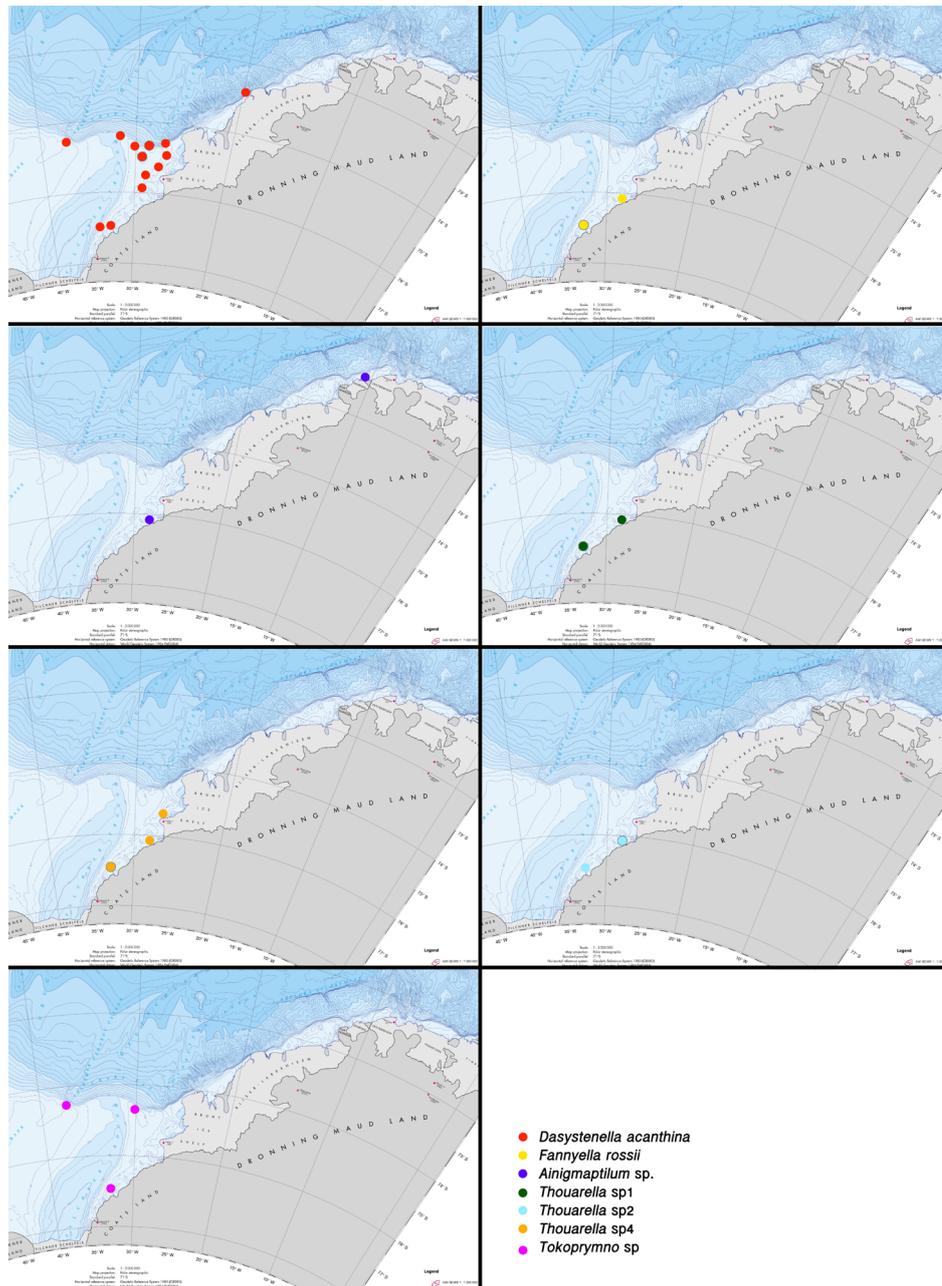


Fig. 3.3.3.2.2: Localities of primnoid species for population comparisons

Stable isotopes

The stable isotopes $\delta^{15}\text{N}$ and $\delta^{13}\text{C}$ are proxies of trophic relationships, with $\delta^{15}\text{N}$ reflecting the trophic position of a consumer and $\delta^{13}\text{C}$ reflecting the basic food sources of the whole community. These isotope signatures are used to identify the trophic position of major components of the Filchner Outflow System. Regarding the high-Antarctic Weddell Sea, previous stable isotope ratio studies on the trophic position of pelagic organisms, benthic invertebrates and vertebrate top predators identified trophic relations within limited sub- systems of the whole network.

In total we collected 620 stable isotope samples from invertebrate organisms belonging to 13 Taxa groups and 199 samples from fishes referring to 20 species (Tab. 3.3.3.2.8).

Tab. 3.3.3.2.8: Major taxa sampled for stable isotope analysis

Major Taxon	[n]	Major Taxon	[n]
Foraminifera	3	Annelida	66
Porifera	31	Chelicerata	16
Cnidaria	34	Crustacea	72
Bryozoa	8	Hemichordata	23
Nemertini	4	Echinodermata	221
Mollusca	90	Tunicata	45
Sipunculida	7	Pisces	199

Data management

Once specimens are identified either by morphotaxonomy or by molecular DNA “Barcoding”, occurrence data for species at each station will be submitted to SCAR MarBIN. DNA sequence data and population genetic matrices will be submitted to NCBI GENBANK.

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3.3.3 Benthos communities

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3.3.3.3 Biomass estimations from AGT and bottom trawls

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Objectives

It has long been recognised that there is spatial heterogeneity among the distribution of Antarctic benthic communities, with assemblages affected by depth, food availability (primary production), currents regimes, sediment type, ice scour and annual ice cover duration (Hedgepeth 1969). Here we use subsamples from Agassiz and bottom trawls to assess abundance and biomass at stations across the Filchner shelf region in an attempt to generalise patterns of diversity and abundance on the scale of 10s to 100s of kilometres.

Work at sea

The AGT was deployed from the stern A-frame gantry. The trawl was lowered at 1 ms⁻¹ with the ship running at 2.3 kn. The position and depth was logged as the trawl frame hit the seafloor, which could be determined by the sudden decrease in wire tension. The cable was further released until there was twice the depth worth of cable length. At this time the ship speed was reduced to 1 kn for trawling with a trawl time of 10 min. Once trawl time elapsed the ship was stopped and hauling began at 0.5 ms⁻¹ until the frame was free of the bottom, then hauling speed was increased to 0.7 ms⁻¹.

Bottom trawls were deployed as detailed in section 3.3.4.1.

Specimens were collected by hand from the trawl material, washed free of sediment, and sorted to phylum or lower taxonomic level where possible. A subsample of material was collected from the AGT and BT for abundance and biomass estimation. The subsample (one 20 L bucket as a proportion of N buckets estimated from the catch) was reserved and sorted separately into phylum and morphotype. Individual morphotypes were photographed and weighed. s species identifications were generally not possible, abundance and wet weights were pooled for lowest confident clade identification.

Preliminary (expected) results

Over the duration of the expedition we conducted 16 AGTs in the Filchner region and one at Austasen outside of the BENDEX area. The locations and depth of each station is given in Tab. 3.3.3.3.1.

Tab. 3.3.3.3.1: Station details for each AGT deployment

Station	Date	Time	Latitude	Longitude	Depth [m]
PS82/043-1	01/07/2014	18:15	76° 4.22 S	30° 8.700 W	473
PS82/050-1	01/08/2014	07:09	76° 19.32 S	29° 0.170 W	228.5
PS82/067-1	01/10/2014	14:46	77° 6.08 S	36° 32.76 W	1101
PS82/073-1	01/11/2014	09:13	77° 0.28 S	34° 9.34 0 W	570
PS82/091-1	14/01/2014	14:52	76° 58.07 S	32° 51.48 W	293.7
PS82/097-1	15/01/2014	13:59	77° 43.45 S	35° 58.84 W	572.5
PS82/111-1	16/01/2014	15:50	77° 54.31 S	38° 12.45 W	1209
PS82/115-1	17/01/2014	06:56	77° 36.68 S	38° 56.33 W	1058.2
PS82/151-1	22/01/2014	10:25	74 ° 32.26 S	28° 31.50 W	1749.5
PS82/233-1	02/01/2014	07:21	74° 14.65 S	37° 42.35 W	833.5
PS82/264-1	02/05/2014	12:32	74° 22.41 S	33° 23.03 W	649
PS82/266-1	02/05/2014	20:37	74° 18.39 S	32° 50.05 W	718.2
PS82/283-2	02/07/2014	18:19	74° 59.87 S	29° 22.90 W	409.2
PS82/293-1	02/08/2014	09:34	75° 31.50 S	28° 59.08 W	462.2
PS82/308-1	02/09/2014	15:39	75° 5.32 S	28° 38.92 W	452.7
PS82/314-1	02/10/2014	08:27	74° 39.93 S	28° 41.89 W	712.2
PS82/349-1	16/02/2014	12:38	70° 55.57 S	10° 28.22 W	213.5

Estimates of Abundance and Biomass

From the sub sample we estimated relative abundance and biomass of the clades collected from counts and wet weights of individuals given in Table 3.3.3.3.2. The results can be visualized in Fig. 3.3.3.3.1, where we plotted the location of each sample, specifically marking the four BTs, and scaled the pie chart to indicate total wet biomass per m² taken from each location, and the individual abundance of