ANT-XXVII/3		PS77/235-3	PS77/239-3	PS77/248-2	PS77/248-3	PS77/250-6	PS77/252-3	PS77/252-7	PS77/257-2	PS77/260-6	PS77/265-2	PS77/275-3
Gear		AGT11	AGT12	AGT13	AGT14	AGT15	AGT16	AGT17	AGT18	AGT19	AGT20	AGT 21
Average depth (m)		295	361	205	429	573	313	333	172	255	ca.500	225
Porifera		0	-	-	-	-	0	0	++	+	++	++
Cnidaria												
	Hydroidea	0	0	+	-		0	0	-	+	-	-
	Actiniaria	0	-	-	0		0	0	-	-	-	-
	Gorgonaria	0	-	-	-	Net torn,	0	0	+	+	++	-
	Pennatularia	0	0	0	-		0	0	0	0	-	0
	Scleractinia	0	0	-	0	almost	0	0	-	-	-	0
Nemertini		0	-	-	0	no catch	0	-	-	0	0	-
Mollusca												
	Bivalvia	0	-	0	0		0	+	-	-	-	-
	Aplacophora	0	0	0	0		0	0	0	0	0	0
	Gastropoda											
	Prosobranchia	0	-	-	0		0	0	-	-	-	-
	Opisthobranchia	0	0	0	0		0	0	0	0	0	0
	Polyplacophora	0	0	0	0		0	0	0	-	0	-
	Cephalopoda / Octopoda	0	-	0	0		0	0	0	-	-	-
	Scaphopoda	0	0	0	+		0	-	0	0	0	0
Polychaeta												
	Sedentaria	-	-	-	0		0	-	-	-	-	-
	Errantia	0	-	-	0	-	-	-	-	-	-	-
Priapulida		-	0	0	0		0	0	0	0	0	0
Sipunculida		-	0	0	0		0	0	-	-	0	0
Echiurida		0	-	0	0	-	-	+	-	0	-	0
Crustacea												
	Cirripedia	0	0	0	0		0	0	0	0	-	0
	Amphipoda	0	-	-	-		0	0	-	-	-	-
	Isopoda	0	-	-	-		0	0	-	-	-	-
	Cumacea	0	0	0	0		0	0	0	0	-	-
	Mysidacea	0	0	0	-		0	0	0	0	0	0
	Stomatopoda	0	0	0	0		0	0	0	0	0	0
	Decapoda											
	Natantia	0	-	0	+	-	0	-	0	-	0	0
	Reptantia	0	0	0	0		0	0	0	0	0	0
Pantopoda		0	-	-	-		0	0	-	+	-	-
Bryozoa		0	0	-	0	-	-	0	-	-	+	-
Brachiopoda		0	0	-	-	-	0	0	-	-	-	-
Pterobranchia		0	0	0	0		0	0	0	0	+	-
Echinodermata												
	Ophiuroidea	-	+	+	-	-	-	-	+	-	+	-
	Asteroidea	0	-	-	-	-	0	0	-	-	-	-
	Echinoidea	0	0	0	0	-	-	0	‡	-	-	-
	Crinoidea	0	-	-	-		0	0	-	-	‡	-
	Holothuroidea	0	+	-	-	-	-	-	-	+	-	-
Ascidiacea		0	0	0	0		-	-	+	-	-	+
Pisces		0	-	-	-	-	0	-	‡	-	-	-

3.1.2 Relative importance of environmental and dispersal-related processes in structuring meiofauna communities in the Southern Ocean

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Objectives

It is believed that both local environmental factors and dispersion ability play key roles in structuring communities and defining geographic/spatial ranges of organisms (referred to as the 'metacommunity concept', Wilson 1992; Leibold

et al. 2004). The main aim of this research is to identify and understand the factors (environmental or dispersal-related) that explain the distribution patterns and biodiversity of Southern Ocean meiofauna. Furthermore, we are interested in the relative importance of both sets of explanatory variables in determining community structure. The prevailing hypotheses are that for large distances the legacy of historical separation may transcend any effect of environmental factors on community structure and biodiversity, whereas at intermediate spatial scales the effect of both historical contingencies and contemporary ecological factors probably shape biodiversity and distribution patterns. At small scales, distance effects would be negligible on community variations. In short, the relative importance of dispersal-related processes becomes more prevalent at larger geographical scales. The validity and generality of these hypotheses for marine benthic organisms remains largely unknown and will be investigated here on free-living marine nematodes and Harpacticoid copepods from the Southern Ocean.

Work at sea

During the ANT-XXVII/3 expedition, samples had been collected with the multicorer (MUC6) at different spatial scales (cm – 1,000 km) in the Southern Ocean for community analysis, including meiofauna (nematodes/copepods) species distribution and biodiversity patterns. Additionally, samples were collected to quantify relevant habitat characteristics (environmental factors) that play a role in either local or regional control of community dynamics. Finally, a number of samples were collected for population genetic analysis on some dominant nematode species present at different spatial scales to identify the distribution and connectivity between populations. Next to the MUC samples, a colonisation experiment was set up during the expedition to test selectivity of meiofauna/ nematodes for certain habitats when settling down from the water column, thereby characterising habitat preference.

In total, 12 hauls of the MUC6 were used for this project at 8 different locations (see Table 3.1.4). Each time the same depth range (between 240 and 450 m) was sampled to rule out depth as a factor. From each haul, two or three cores were used (at the first Larsen A South station we could only recover one core) and samples were collected at scales of cm (subsamples within a core), m (cores from the same MUC deployment), 10 to 100 m (samples from different MUC deployments at the same station) and between 10 to 1,000 km (different stations), because spatial scale has been proven to be an important determinant in structuring meiofauna communities. For every core we divided the upper 5 cm of sediment in two slices (0 - 3 and 3 - 5 cm) and each slice was subsequently divided into 6 parts with a pie-shaped metal piece for the smallest scale sampling. Of these 6 pieces, three were stored in 4 - 7 % formalin for community analysis (meiofauna identification and abundance), one was kept in ethanol for population genetics and two were kept frozen (-20 °C) for abiotic factors, such as grain size, pigment concentration (as a measure of primary production input) and organic C/N content. At each station, bottom temperatures (CTD), geographic position (to calculate distances between habitats) and depth were recorded as well.

All organisms sampled quantitatively with the MUC6 will be sorted and counted on major taxa level at the lab of the Marine Biology Section of Ghent University. Nematodes will be identified down to genus level at the Marine Biology Section of

Ghent University and Harpacticoid copepods will be identified to species level at DZMB.

Preliminary results

Since extraction of animals and the analysis of environmental parameter have to be done in a standardised way in the lab, no preliminary results are available for the meiobenthos.

Tab. 3.1.4: MUC6 stations worked up during ANT-XXVII/3 for small-scale analysis of meiofauna communities. SG NE=South Georgia North-East, SO=South Orkneys, KG MB=King George Maxwell Bay

Station No.	Position Lat	Position Long	Date	Cores	Depth (m)	Area
214-3	54°25,61'S	35°41,79'W	16.02.2011	4,9,12	264,5	SG NE
214-4	54°25,62'S	35°41,86'W	16.02.2011	4,9,12	265,2	SG NE
217-3	61°8,66'S	43°58,00'W	19.02.2011	4,9,12	401,7	SO
222-3	62°13,28'S	58°50,95'W	23.02.2011	4,9,12	244,2	KG MB
226-10	64°56,01'S	60°38,61'W	26.02.2011	4,9,12	242,0	Larsen A_South
231-5	64°56,16'S	60°38,66'W	28.02.2011	9	246,7	Larsen A_South
233-4	65°32,99'S	61°36,94'W	01.03.2011	2,9,12	294,2	Larsen B_West
235-4	65°32,96'S	61°36,88'W	02.03.2011	4,9,12	286,0	Larsen B_West
246-3	65°54,95'S	60°20,43'W	06.03.2011	4,9,12	432,2	Larsen B_South
247-3	65°55,12'S	60°19,83'W	07.03.2011	7,9,12	435,2	Larsen B_South
265-3	70°48,38'S	10°39,72'W	22.03.2011	5,10	450,7	Austasen
274-2	70°56,35'S	10°34,00'W	25.03.2011	4,9,12	331,2	Bendex Ref.

3.1.3 Systematics, phylogenomics and comparative phylogeography of Southern Ocean benthos

Chester Sands British Antarctic Survey

Objectives

Understanding the origins of the Southern Ocean benthos requires reconstruction of the evolution of the elements involved and information regarding the processes that underly the spatial distribution of the elements. Phylogenomic and phylogeographic techniques are rapidly improving and have the power to elucidate timing, order and location of significant events in the evolution of lineages and clades. Using phylogeographic techniques it is also possible to reconstruct historical demographic scenarios. Comparative phylogeography (analysis of geographic patterns of genetic lineages across multiple co-distributed species) has the ability to tease out historical processes acting on lineages, populations and species, from organism specific processes. Phylogenomic and phylogeographic analyses rely on sufficient taxon and spatial sampling – a challenge for any benthic study and doubly so for the remote Southern Ocean.

Work at sea

We conducted a total of 21 AGTs, 24 BTs and 4 RDs. Samples were sorted to class, given uniquely identifying labels and stored in 100 % ethanol (maximum ratio ethanol to animal volume 5:1) at -1 °C. After 3 – 5 days the ethanol was drained