26. PHYLOGENY AND PHYLOGEOGRAPHY OF DEEP-SEA AMPHIPODS: CONNECTIVITY WITHIN AND BETWEEN ANTARCTIC, SUB-ANTARCTIC AND ATLANTIC REGIONS

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Objectives

With over 600 described species, amphipods are the most specious group in Antarctic shelf regions, with a high percentage of endemic species. Even if Antarctic shelf species have been extensively investigated, recent studies showed that many species are inadequately described and several morphospecies are composed of genetically heterogeneous species complexes (Havermans et al. 2011). In contrast, the Antarctic deep sea remained virtually unknown until the ANDEEP and SYSTCO I cruises. These expeditions revealed an overwhelming abundance and diversity of amphipods.

By molecular analyses, we investigate for several amphipod species the link between (i) Antarctic and sub-Antarctic regions and (ii) Antarctic regions and Atlantic abyssal basins. We will test how phylogeographic patterns differ between shelf and deep-sea species and whether deep-sea species are genetically less variable than shallow water species. By phylogenetic analyses, the relationships between Antarctic shelf and deep-sea fauna (submergence *vs*. emergence hypothesis) will be examined as well as the relationships between Antarctic and Atlantic species. Former analyses on lysianassoid species demonstrated the presence of identical haplotypes between Atlantic abyssal basins and the Antarctic Peninsula which can be explained by the existence of the Antarctic bottom water, connecting these basins. Furthermore, there are indications for several independent colonizations of these Atlantic abyssal basins from the Antarctic deep sea (Havermans et al. in prep.). More deep-sea samples are needed to confirm these hypotheses.

Specific topics to investigate include: (1) To document faunistical and zoogeographical of amphipod taxocoenoses from different abyssal areas; (2) To contribute to the description of the Antarctic amphipod biodiversity, with a special focus on the Lysianassoidea; (3) To use fast evolving genetic markers to measure the intra- and interpopulation genetic variability and to compare the phylogeography of target taxa; (4) To use more slowly evolving genetic markers to identify colonization patterns between different abyssal basins; (5) To contribute to the SCAR-MarBIN database (www.scarmarbin.be) in bringing a new dataset of distributional, ecological and photographic information on Antarctic amphipods.

Work at sea

Sampling was carried out using three different gears: Agassiz trawl, epibenthic sledge and Rauschert dredge. The epibenthic sledge and Agassiz trawl were deployed at seven stations, the Rauschert dredge only at the last four stations. Amphipods were identified to family, genus or species level and photographed. Specimens were fixed in 96 % pre-cooled undenatured ethanol and stored at 20°C. DNA was extracted from 129 specimens from the deep-sea stations and 14 specimens collected in the shallow-water station.

Preliminary results

All specimens collected were sorted out and identified until species, genus or family level and the different species were photographed. The number of species and individuals per amphipod family for each deep-sea station is represented in Table 26.1, 26.2 and 2.63 according to the different gears. However, the numbers for the last stations (St. PS79/141 and 175) are likely to increase when all samples will be sorted, which has not been done yet onboard due to time limitations. The most abundant taxa found in the Agassiz trawl belonged to the Hyperiidea, a group of pelagic amphipods, most probably caught in the net when the trawl was retrieved through the water column. This group was much less abundant in the epibenthic sledge samples. The second most abundant and diverse group in the AGT samples is the superfamily Lysianassoidea, of main interest for our studies. This group also appeared to be the most diverse and abundant in the EBS samples. Surprisingly, we observed a higher diversity within this group in the low productivity area (St. PS79/81, 84, 85) than in the high chlorophyll area (St. PS79/86, 141), both for EBS and AGT samples.

DNA extractions were carried out for 143 specimens (129 from the deep-sea stations and 14 from the shallow station) of which 60 belong to the Lysianassoidea, 45 to the Hyperiidea and the remaining specimens belonging to Eusiroidea, Liljeborgiidae, Stegocephalidae. In addition, DNA was extracted of a large number of specimens of the bathypelagic species *Cyphocaris richardi*, *Parandania boecki*, *Eurythenes obesus*, *Themisto gaudichaudii* and Eusiroid sp. for future phylogeographic and population genetic studies. At the RBINS, mitochondrial (cytochrome oxidase I, 16S rRNA) and nuclear (28S rRNA) gene fragments will be amplified and sequenced for all these specimens.

An additional sampling was carried out at a shallow-water shelf station (54°S 52°W, 336 m). More than 115 specimens were sorted out alive during the sieving of the material; 80 specimens from the Rauschert dredge and 35 specimens from the Agassiz trawl. Due to time limitations, the sieved fractions of the sample will be sorted out back home. The dominant species in the Agassiz trawl sample was *Leucothoe* sp. (26 specimens), of which some individuals were found inside a sponge, indicating a possible commensally life style. This could explain the high abundance of this species in the catch, which was dominated by sponges. The other abundant taxa included several lysianassoid, liljeborgiid and eusiroid species. The most important taxa found in the Rauschert dredge sample were: *Schraderia gracilis* (Eusiroidea), *Liljeborgia* sp. (Liljeborgiidae), oedicerotids, stenothoids and several lysianassoid species of the family Tryphosinae. Afterwards, DNA was extracted of 14 specimens belonging to the families Liljeborgiidae and Lysianassoidea for further molecular studies.

Data management

Refer to page 75.

References

Havermans, C., Nagy, Z.T., Sonet, G., De Broyer, C., Martin, P. 2011: DNA barcoding reveals new insights into the diversity of Antarctic species of *Orchomene sensu lato* (Crustacea: Amphipoda: Lysianassoidea). Deep-Sea-Research II, 58, 230-241.

Tab. 26.1.: Number of species and individuals per amphipod family sampled at each deep-sea station with the AGT.

	PS79/81-19	PS79/84-26	PS79/85-16	PS79/86-21	PS79/86-23	PS79/141-7	PS79/141-8	PS79/175-3	PS79/175-4
Caprellidea							1 sp. (N=1)		
Chuneolidae						1 sp. (N=1)			
Eusiroidea	1 sp. (N=1)			1 sp. (N=1)					
Hyperiidea	8 spp. (N=16)	5 spp. (N=18)	4 spp. (N=15)	2 spp. (N=94)	6 spp. (N=52)	9 spp. (N=33)	5 spp. (N=29)	4 spp. (N=9)	1 sp. (N=2)
Hyperiopsidae				1 sp. (N=1)					
Liljeborgiidae						1 sp. (N=1)		1 sp. (N=1)	
Lysianassoidea	2 spp. (N=4)	2 spp. (N=3)	1 sp. (N=2)	6 spp. (N=6)		3 spp. (N=5)	3 spp. (N=3)	1 sp. (N=1)	1 sp. (N=1)
Melphidippidae				1 spp. (N=1)					
Phoxocephalidae								2 spp. (N=2)	2 spp. (N=2)
Stegocephalidae	2 sp. (N=5)	1 sp. (N=3)		2 spp. (N=10)	1 sp. (N=8)	1 sp. (N=9)	1 sp. (N=4)		
Indet.	1 sp. (N=1)	3 spp. (N=3)		4 spp. (N=4)				1 sp. (N=1)	1 sp. (N=1)

Tab. 26.2.: Number of species and individuals per amphipod family sampled at each deep-sea station with the RD.

	PS79/141-7	**PS79/141-8**	**PS79/175-3**	**PS79/175-4**
Epimeridae			1 spp. (N=1)	
Lysianassoidea			1 spp. (N=2)	1 spp. (N=1)
Eusiroidea				
Hyperiidea	4 spp. (N=4)	2 spp. (N=4)	4spp. (N=5)	3 spp. (N=5)
Oedicerotidae			1 sp. (N=1)	
Stegocephalidae	1 sp. (N=1)	1 sp. (N=1)		
Indet.	1 sp. (N=1)			

Tab. 26.3.: Number of species and individuals per amphipod family sampled at each deep-sea station with the EBS

	PS79/81-17	PS79/81-18	PS79/84-25	PS79/85-15	PS79/86-20	PS79/86-24	PS79/86-25
Aoridae						1 sp. (N=1)	
Calliopiidae		1 sp. (N=1)					
Corophioidea	1 sp. (N=1)	2 spp. (N=2)				2 spp. (N=2)	
Hyperiidea	2 spp. (N=2)		3 spp. (N=3)	2 spp. (N=3)	1 sp. (N=1)	1 sp. (N=2)	1 sp. (N=1)
Lysianassoidea	9 spp. (N=10)	11 spp. (N=12)	5 spp. (N=6)	2 spp. (N=3)	4 spp. (N=4)	2 spp. (N=3)	
Pardaliscidae						1 sp. (N=2)	
Phoxocephalidae		2 spp. (N=2)	2 spp. (N=4)	1 sp. (N=1)		2 spp. (N=8)	
Oedicerotidae		1 sp. (N=1)	1 sp. (N=1)	2 spp. (N=7)			1 sp. (N=1)
Stegocephalidae			1 sp. (N=1)			1 sp. (N=1)	1 sp. (N=1)
Indet.		3 spp. (N=4)	5 spp. (N=5)	3 sp. (N=3)	1 sp. (N=1)	2 spp. (N=2)	1 sp. (N=1)