SCAR Fellowship Report 2007/08

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Institution visited

British Antarctic Survey (BAS), Cambridge, UK Host: Dr. Katrin Linse & Dr. David K. A. Barnes

Dates

February–April 2008: BIOPEARL 2 cruise (Field work, Amundsen Sea, Antarctic)

October-November 2008: laboratory work, BAS

December 2008: lab work and BIOPEARL-2 workshop (Natural History Museum, London)

Work towards scientific objectives of the fellowship:

Quantification of Southern Ocean biodiversity in space: richness and distribution of Isopoda (Crustacea, Malacostraca) in the Amundsen and Bellingshausen Seas

Objectives

The aim of this project was to study richness and abundance patterns in space on the Bellingshausen and Amundsen Sea shelves (i.e. Pacific sector of the Southern Ocean [SO]) using isopod crustaceans as a model group. These represent one of the least known shelf areas on the planet and biggest biogeographic gap of SO shelf benthos. Comparison with complementary sampling from the Scotia Sea (during the BIOPEARL 2 expedition) should help to elucidate how much we know about Antarctic shelf biodiversity, and how richness and composition changes with distance (across sites and seas) and depths

The key questions addressed in this project were:

- 1) How many species or genera found are potentially new to science in well studied (Scotia Sea), and unsampled areas (i.e. Amundsen Sea)
- 2) How fast are species accumulated with increased sampling in each area
- 3) How does genetic variability/ diversity change in space on Antarctic shelves

Methods

Benthic samples were collected in four different areas of the eastern Amundsen Sea shelf and slope using an epibenthic sledge (EBS) at 500, 1000 and 1500 m. Unfortunately, no sampling could have been carried out in the Bellingshausen Sea due to bad weather conditions and unsuitability of bottom structure. In the Amundsen Sea, two sets of three replicates each were taken at 500 m, whilst two replicates were sampled at 1000 and 1500 m respectively. Additionally, three deep-sea samples were taken at 3500 m depth, resulting in a total of 36 EBS stations. Initial sorting of the samples into taxonomic groups was started onboard, and this work has been continued in the laboratories of BAS, the Natural History Museum, London and the Zoological Museum of Hamburg. Isopods have been identified to family level, and in two model taxa (Desmosomatidae and Nannoniscidae) to generic and species level. Onboard, DNA was partly extracted from 45 specimens of desmosomatids and nannoniscids. For this, three legs (pereopods) were dissected per specimen, transferred into extraction buffer (using QIAamp® DNA Mini Kit) and kept there at -80°C until extraction was completed at BAS.

Data analyses integrated systematic, ecological, biogeographic and molecular genetic approaches in order to assess biodiversity patterns and how these changed with depth, spatial and taxonomic scale. Initial analyses started during visits to BAS, and this work will be continued in the following few years.

Results

The first results included an assessment of macrobenthic richness and abundance patterns on the Amundsen Sea shelf (see Kaiser et al 2009). Based on five 500 m samples from the Amundsen Sea and 15 from the Scotia Sea (sampled during BIOPEARL 1 in 2006), isopod richness, abundance and composition were compared between an unstudied (i.e. the Amundsen Sea) and a well-known (i.e. the Scotia Sea) Antarctic continental shelf. Faunal richness and (species) composition in two families (Desmosomatidae and Nannoniscidae) differed greatly between Amundsen and Scotia Sea assemblages. In contrast to the Scotia Sea, the Amundsen Sea samples showed high faunal richness across taxonomic levels (family, genus, and species) and a high proportion of species were potentially new to science (96%). Prior to this study only 13 (described) nannoniscid and desmosomatid species in six genera had been recorded from the Antarctic continental shelf. Thus, this study increased the number of taxa known from the shelf, within these two families, to 47 species in 14 genera.

Abundance levels in isopod crustaceans were consistently high across all stations in the Amundsen Sea, and in contrast highly variable across Scotia Sea sites. I suggest that this probably reflects environmental variability (e.g. differing topography/rugosity, sediment types or overlying productivity) there. The dominance structure at family level though was similar in the Scotia and Amundsen Sea in that one or two families dominated samples. This usually implies high levels of disturbance of the fauna (e.g. by deep ice scouring).

Unfortunately, the molecular genetic analyses have not been entirely successful, that is DNA could only be extracted from three specimens (out of 45).

Future work

Future work will include further analyses of the structure of biodiversity in the Amundsen Sea, i.e. assessing richness and abundance patterns across different spatial (i.e. between stations being 10⁰-10³ km apart) and taxonomic scales. Therefore the identification of all isopods to species level will be continued and this data will be compared with other taxa (i.e. those displaying different reproduction modes such as some polychaete, mollusc and bryozoan groups)

The identification of Agassiz trawl samples from the Scotia and Amundsen seas, which were collected during BIOPEARL 1 and 2 cruises, is currently being in progress. By comparing AGT and EBS data, the similarity of results can be compared across size spectra and apparatus in terms of e.g. rate of novelty or differences in species/generic composition between the Scotia and Amundsen Sea.

Collaboration

This work, which has been funded by the SCAR fellowship, has led to a strong collaboration with scientist from BAS and has been already published and presented on two international conferences. Some question could have been answered; many more remain open, though led to the development of further ideas, which will be integrated into already existing projects.

What SCAR funds were allocated?

€6629.45 / \$9,500 US\$ were awarded to the fellow.

How were the SCAR funds spent?

- a) Travel costs to/ from the ship (UK-Falkland Is.-Chile-UK): 1563.08€
- b) Consumables for DNA extractions: 587.42€
- c) Accommodation and living costs in Cambridge 1508.62€
- d) BIOPEARL workshop London, December 2008: 150€
- e) Transport of benthic material to Hamburg: 310.13€
- f) Flights to Stansted (Cambridge): 71.55€
- g) Conference fees and accommodation at the SCAR conference in St. Petersburg: 863.35€

Total spent: 5054.15€*.

*I did not spend all the money, as the molecular analyses have not been as successful as I hoped. The remaining fund will be spent on conference fees and publication costs.

Publications

Kaiser S, Barnes DKA, Sands CJ, Brandt A (2009) Biodiversity of an unknown Antarctic sea: isopod richness and abundance in the first benthic survey of the Amundsen continental shelf. *Marine Biodiversity*, DOI:10.1007/s12526-009-0004-9.

Three further manuscripts in progress.

Talks

- Kaiser S, Barnes DKA, Griffiths HJ, Sands CJ (2008) Biodiversity of the big known unknown; isopod richness across scale in the Amundsen Sea. SCAR/IASC IPY Open Science conference, St. Petersburg (Russia).
- Enderlein P, Barnes DKA, Griffiths HJ, Hillenbrand DC, Kaiser S, Linse K, Larter R, Sands CJ, Strugnell J (2008) The unknown Antarctic benthos: Discoveries in the southern Bellingshausen and Amundsen Seas. SCAR/IASC IPY Open Science conference, St. Petersburg (Russia).
- Barnes DKA, Griffiths HJ, Kaiser S, Allen C, Danis B, Linse K, Clarke A (2008) Range shift responses to climate change by Antarctic biodiversity: where should we look? SCAR/IASC IPY Open Science conference, St. Petersburg (Russia).
- Kaiser S (2008) Southern Ocean biogeography: An abyssal perspective on macrobenthic distributions. World Conference of Marine Biodiversity, Valencia (Spain).
- Barnes, DKA, Kaiser, S., Griffiths HJ, Linse K (2008) First cross realm compendium for a polar locality: The South Orkney Island, Antarctica. World Conference of Marine Biodiversity, Valencia (Spain).