Biodiversity Monitoring in the Davis-Baffin Division of the Eastern Arctic

Protocols for Benthic Sample Collection and Processing

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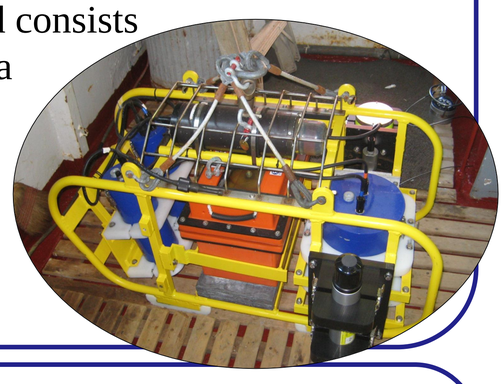
Introduction

As part of the Canadian initiative to collect baseline information on the distribution and abundance of benthic invertebrates for assessing the impacts of climate change, in 2012 Fisheries and Oceans Canada (DFO) conducted benthic sampling in the Greenland Halibut Fishery Closure, Baffin Bay. Data on megafauna, macrofauna, meiofauna, and microbes were collected in accordance with protocols described in the Conservation of Arctic Flora and Fauna (CAFF)'s Circumpolar Marine Biodiversity Monitoring Plan. This poster details the protocols followed for benthic sample collection and post-processing.

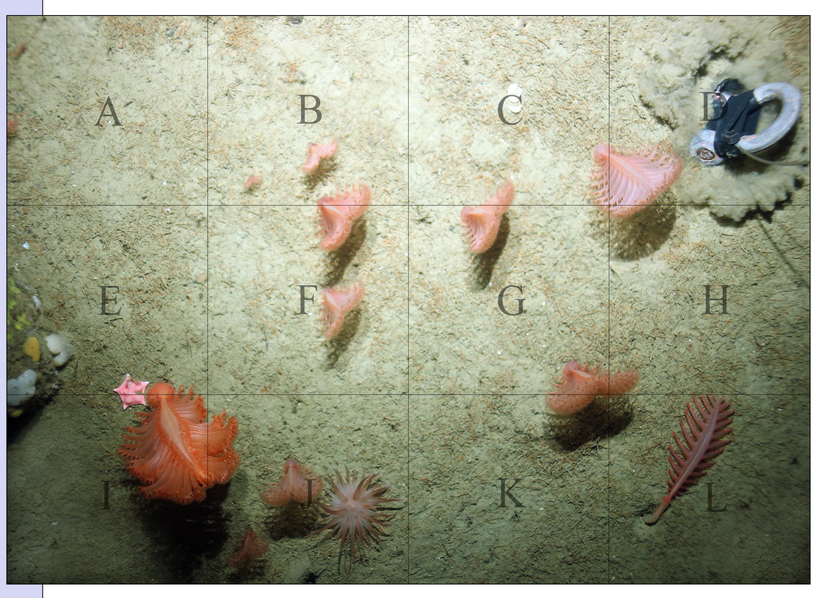
1. Megafauna

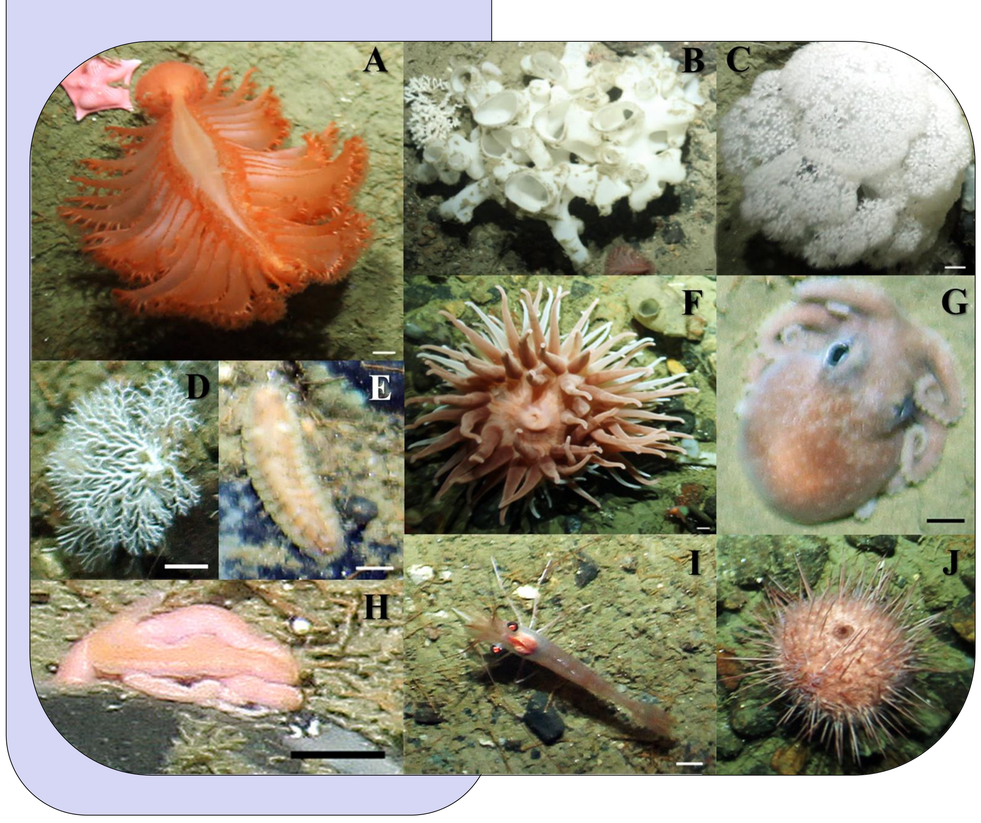
Megafauna (that is epibenthic fauna ≥ 1 cm) were sampled using the '4K' drop-camera system, built by the Geological Survey of Canada. This system is capable down to 4,000 m depth, and consists of a Canon Rebel Eos Ti 12 megapixel camera and two flashes that are housed inside an aluminum roll cage. The system was lowered to the seabed via a winch for photo acquisition every 60 seconds, corresponding roughly to every 10 m on the seabed.



In the lab, a 4 x 3 grid was placed over each photo to aid in consistency during data recording within and among images. Megafauna were identified down to the lowest taxonomic classification possible, following the World Register of Marine Species (WoRMS) as the taxonomic authority. The abundance of large foraminifera (such as *Rhizammina algaeformis*) was qualitatively assessed across each photo using four different categories: absent/rare, sparse, moderate, abundant.

Right image. Seabed photo from the Greenland Halibut Closed Area with 4 x 3 lettered grid overlay. All sessile and motile epibenthic megafauna ≥ 1 cm were recorded from each grid cell. The abundance of large foraminifera was qualitatively assessed across each photo.





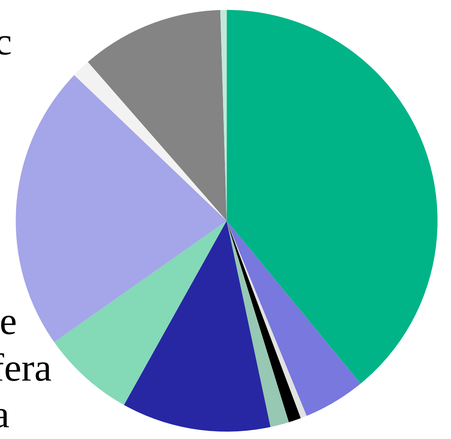
Left panel. Megafauna observed in the Greenland Halibut Closed Area biodiversity stations. A) sea pen *Pennatula borealis* and sea star *Ceramaster granularis*, B) sponge *Asconema foliata*, C) nephtheid soft coral, D) unknown stalked bryozoan, E) scale worm, F) unknown anemone, G) unknown octopus, H) unknown nemertean, I) pandalid shrimp, J) urchin of the genus *Echinus*.

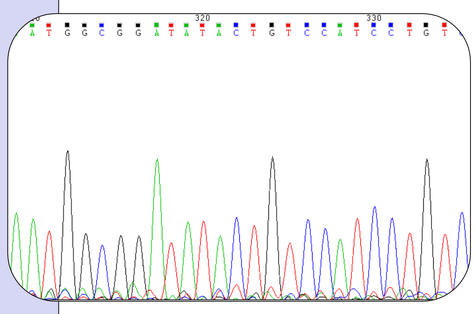
2. Macrofauna

Macrofauna (i.e. those fauna retained on a 1 mm and 0.95 cm mesh) were sampled using a 0.145 m^2 Van Veen grab and 0.25 m^2 mega-box corer. Sediment samples were sorted into three different size fractions (0.5 mm, 1 mm, and 0.95 cm) and preserved in 10% formalin. Some calcareous specimens (e.g., sponges and bryozoans) were preserved in 70% ethanol to prevent degradation of the features used for taxonomic identification.

Macrofauna were identified down to the lowest taxonomic classification possible. Biomass of each specimen, or groups of the same taxon, was measured.

The Annelida, followed by the Mollusca, Cnidaria, and Porifera were the most abundant phyla observed in the 0.95 cm size fraction.



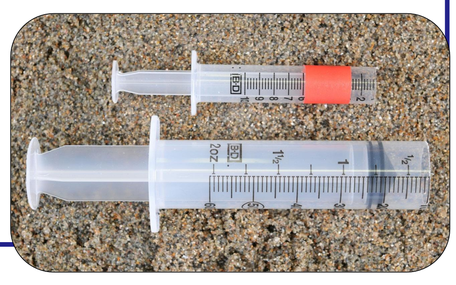


Identification of specimens aided by DNA amplification and sequencing of the mitochondrial cytochrome c oxidase subunit I gene (COI).

Sponge identification aided by comparing their skeletal fragments (spicules) to those of described species. Spicules are visualized by microscopy after dissolving cellular material with bleach.

3. Meiofauna & Microbes

Meiofauna and microbes were sampled from surface sediments collected using the Van Veen and mega-box corer systems. For meiofauna, a modified 60 cc syringe was plunged into the surface sediment of the grab and the top 1 cm (roughly 5 ml of sediment) was extracted. Microbes were sampled in a similar fashion using a 10 cc syringe. The resulting sediment was fixed or frozen for subsequent processing.



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