# ICE-Jelly: Influence of sea-ice and sub-mesoscale oceanography on jellyfish distributions and communities during PS131

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## Project summary and goals

Gelatinous zooplankton (GZP, jellies or jellyfish) are a broad group of taxa, comprised of ctenophores, cnidarians and tunicates. They are largely understudied despite their hypothesized recent increase in biomass in many localities of the World's Oceans. This phenomenon, referred to as "ocean jellification", is likely a result of the complex interplay of climate change, overfishing and other anthropogenic factors. Environmental changes are occurring at an unprecedented pace in the Arctic Ocean, urgently highlighting the need for a large-scale understanding of Arctic marine biodiversity. Pioneering work has shown GZP to be particularly abundant in Arctic waters, including under-ice environments. GZP species are also known to aggregate at hydrographic features because of their affinities to certain water masses. However, little is known about GZP diversity, abundances and community structure in the Arctic in general, and even less at the sub-mesoscale. The overarching goal of the ICE-Jelly research programme is to establish a comprehensive baseline knowledge of jelly diversity and distributional patterns and their link to oceanographic patterns and sea ice.

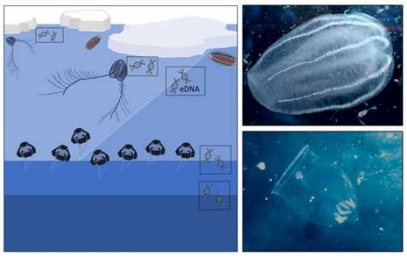


**Figure 1:** A schematic drawing illustrating the small-scale distributions of GZP (left) and GZP species known to be abundant under the ice: the ctenophore *Beroe cucumis* and the hydrozoan *Aglantha digitale* (right)

The objectives of the ICE-Jelly project were:

- Study species richness, community composition and small-scale distributions of GZP and link these to environmental parameters – *environmental DNA (eDNA) metabarcoding, plankton net catches, UVP surveys*;
- Obtain and compare GZP abundance data from different sampling methods across different hydrographic and sea-ice gradients – *eDNA metabarcoding, plankton net catches, UVP surveys*;
- Elucidate the trophic role of dominant jellies in local Arctic food webs and their reliance on sea-ice associated food sources – *plankton net catches, biomarker and molecular diet analyses*;
- Identify GZP "bioregions" based on data from the different sampling methods in the various sampling areas of open water, Marginal Sea-Ice Zone, and pack ice;
- Compare GZP species composition at the same localities over several years and link this to local hydrography and other environmental parameters – *eDNA time series at several LTER-HAUSGARTEN stations (2019-2022), plankton net catches.*

## Sampling and Results

Different types of station work has been carried out:

→ Transect stations based on oceanographic results from the topAWI deployments
→ Ice stations in the Marginal Ice Zone (MIZ)
→ Pelagic stations at the LTER Hausgarten sites and sites in East Greenland waters

During the cruise, eDNA samples from seawater at various depths were taken at 23 pelagic stations and 11 sea-ice stations. The Midi-Multinet was deployed at 13 of these stations, and in total, 58 UVP casts were done.

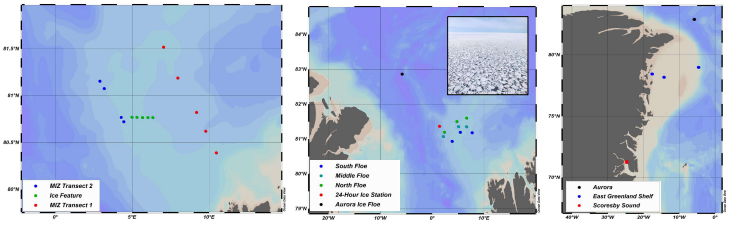


**Figure 2:** Different maps of sampling stations: Left: Transect stations based on Top-AWI deployments across the MIZ; Middle: Ice stations sampled; Right: Pelagic stations sampled in East Greenland including the Aurora Vent Field and Scoresby Sound.

→ The majority of the 580 eDNA samples obtained during PS131 have been extracted and sequenced on a NovaSeq Illumina Sequencer for one or two genetic markers (mitochondrial COI Leray XT fragment and the nuclear 18S V1-V2 fragment).

→ Around 250 jellyfish samples have been preliminary identified on board and stored for further analyses. The majority of these have been DNA barcoded.

→ Several zooplankton species (including *Themisto* amphipods, pteropods) have been DNA barcoded and have been included in ongoing phylogeographic analyses

**Figure 3:** eDNA water sampling with Niskin bottle at an ice station.

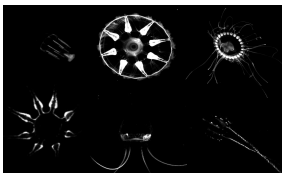

**Figure 4:** GZP taxa captured on the UVP (not to scale). Top left to Bottom right: *Aglantha digitale, Botrynema* sp., *Atolla* sp., *Hydrozoan, Aeginopsis laurentii*, cyddipid ctenophore.

## Focus: Under-ice eukaryotic communities revealed with eDNA

Focus on the MIZ as highly dynamic habitat impacted by ongoing climate warming
→ sub-ice seawater samples were investigated with multi-marker (COI, 18S V1-V2) eDNA metabarcoding


Major outcome:

- Alpha diversity recovered was higher under ice (0m) compared to 5m below it, for both genes
- Metazoan fraction recovered was higher with 18S: mostly arthropod DNA → importance of multi-marker studies
- Lots of unassigned metazoan DNA: unknown species, need for improvement of reference databases
- Eukaryotic communities vary with abiotic factors such as meltwater properties, sea-ice concentration, distance to ice edge

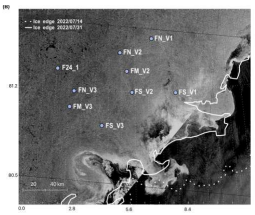


**Figure 5:** Sentinel-1 Synthetic Aperture Radar (SAR) image of the ice floe stations in the MIZ. The dotted white line is a visual estimate of the ice edge at the beginning of the sampling period and the hard-white line the end of the sampling period.

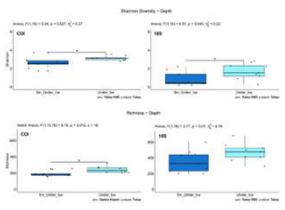

**Figure 6:** Shannon diversity (Top) and Species Richness (Bottom) in relation to sampling depth under the ice (0 vs 5m).

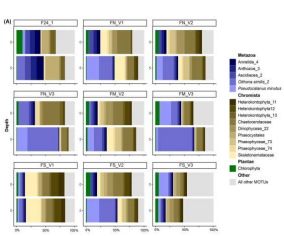

**Figure 7:** The 15 most dominant Molecular Operational Taxonomic Units (MOTUs) at each ice floe station with their relative read abundance in the COI dataset. MOTUs are labelled to the highest taxonomic resolution possible (up to species level). All remaining MOTUs are grouped together as "Other".

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