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HELMHOLTZ-ZENTRUM FÜR POLAR- UND MEERESFORSCHUNG

Iceflux: Ice-Ecosystem Carbon Flux in Polar Oceans

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Objective 1:
Characterize bio-physical sea ice properties

Methods: Conducted Surface and Under-Ice Trawls (SUIT) with a mounted sensor array (Fig. 1) consisting of: *i)* CTD with an upward-looking altimeter for ice draft/thickness and fluorometer for chl *a*; *ii)* ADCP for tilt, roll, and water inflow and; *iii)* Two spectroradiometers for light transmission and ice algae biomass. Fig. 2 shows a SUIT profile of the sensor array data. Spectral-derived ice algae biomass estimates will be determined by relating ice core algae biomass (HPLC) with coincident ROV and L-arm spectral measurements (Fig. 4; e.g. Mundy et al., 2007) which will then be up-scaled to the larger scale ROV and SUIT measurements (Nicolaus et al., 2013).

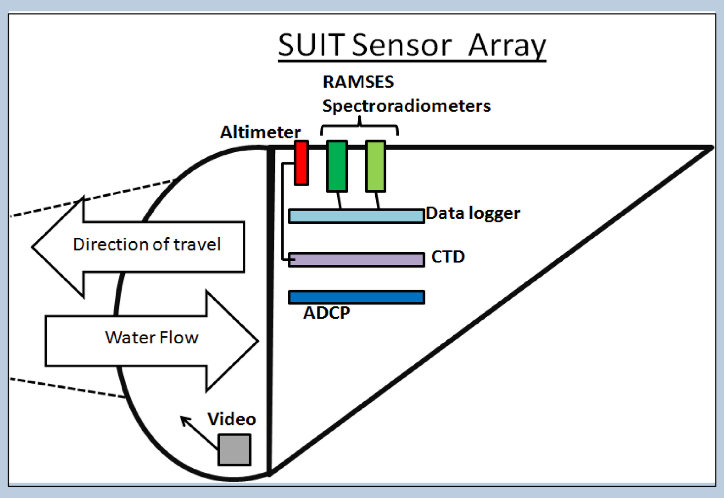
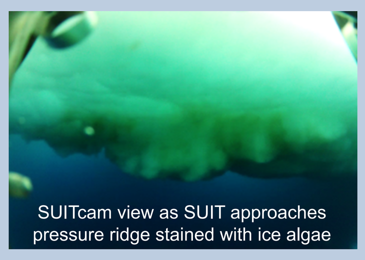


Figure 1: Generalized rendition of the SUIT (vertical cross-section) sensor array setup.



Results from a summer expedition to the Central Arctic Ocean in 2012 (PS80 "IceArc")

SUIT Sensor Array Profile

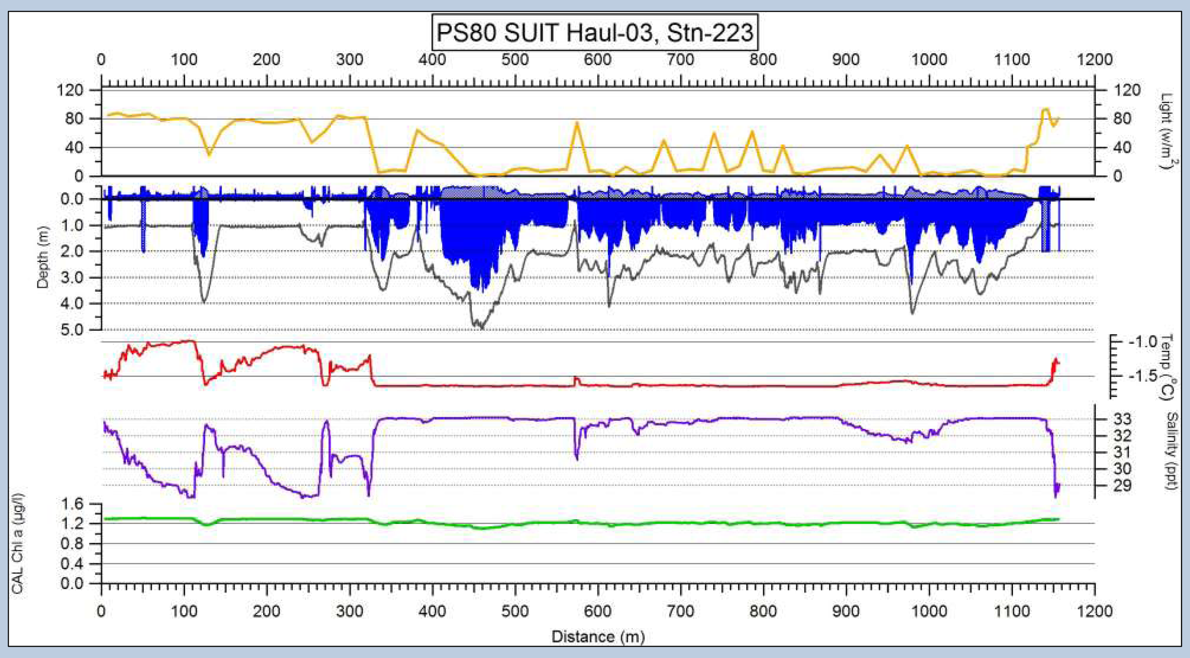


Figure 2: SUIT sensor array profiles, station 223 (summer 2012, Arctic Ocean), of light transmission, draft, freeboard, depth of SUIT, Temperature, Salinity and chl *a* (uncalibrated).

Sea Ice Thickness Distributions (SUIT and EM-31)

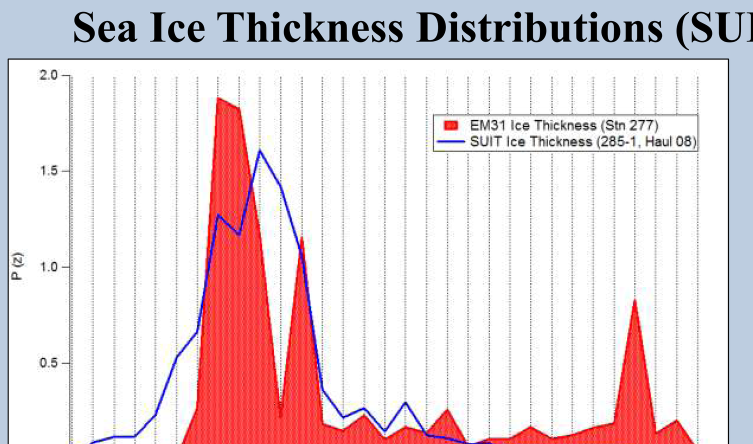


Figure 3: Sea ice thickness distributions comparing SUIT haul 285 and an EM-31 survey of a nearby ice floe.

Correlation Surfaces for Ice Algae Biomass with NDIs

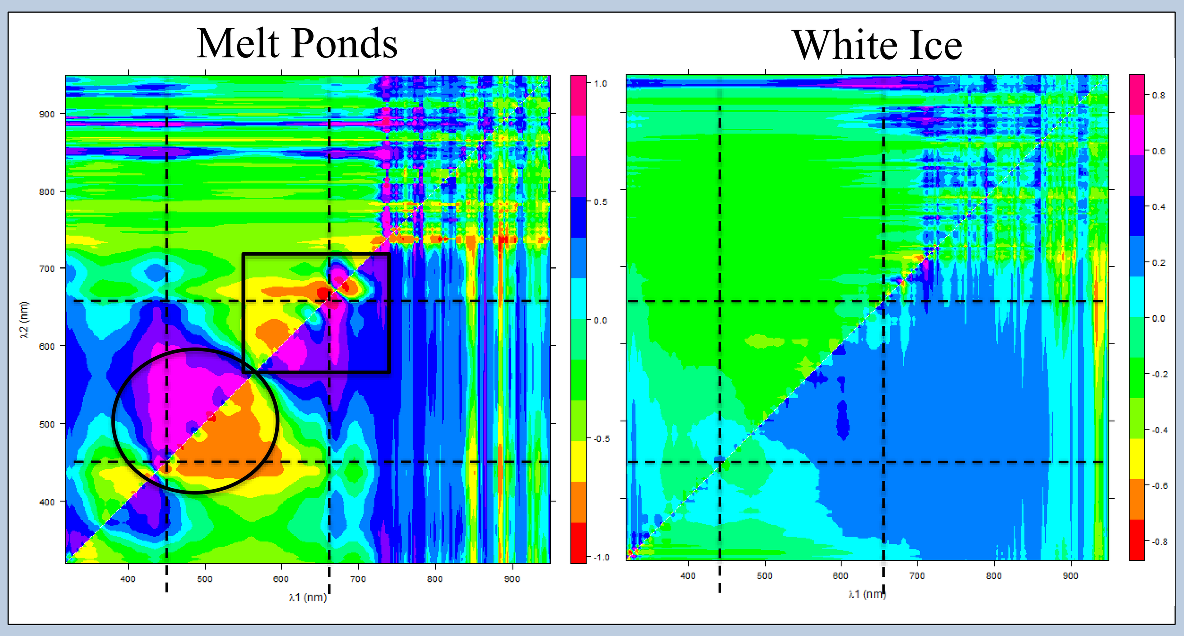


Figure 4: Correlation surfaces for ice algae with NDIs. Spectral measurements conducted under melt ponds only (left) and under white ice only (right). Dashed lines highlight the absorption peaks of chl *a* at 440 and 670 nm.

Results & Conclusions:

- SUIT sensor array data are good quality and are **ideal for relating to under-ice communities** (see Objective 2).
- Spectral-derived algae biomass models (NDIs) show **good correlations for melt ponds** in 2 spectral regions of highest chl*a* absorption: 400-550 nm (Fig. 4 circle) and 600-690 nm (Fig.4 square).
- **No clear correlation for white ice** but this could be due to variable ice properties (e.g. thickness, snow, scattering layer). Further analysis and model development will be conducted to improve accuracy of the model(s) before up-scaling to ROV and SUIT spectral measurements.

Introduction

Polar sea ice habitats are undergoing rapid change. Because Polar sea ice ecosystems thrive significantly on carbon produced by **ice-associated microalgae**, these changes have a significant impact on ecosystem functioning. Species dwelling at the ice-water interface (e.g. **Antarctic krill** *Euphausia superba* and **Polar cod** *Boreogadus saida*) play a key role in transferring carbon from sea ice into pelagic food webs. Understanding the association of under-ice fauna with sea ice habitat properties is therefore essential to understanding future changes of sea ice ecosystems. Until now, the dependency of Polar food webs on carbon produced by ice algae is barely understood in quantitative terms. Recent progress in **biomarker analysis** makes it possible to quantify the significance of ice algal production along food chains. On this poster we present the progress of our group in linking biological and physical sea ice data, and first results from trophic biomarker studies from the Arctic Ocean.

Under-ice sampling in the Arctic Ocean

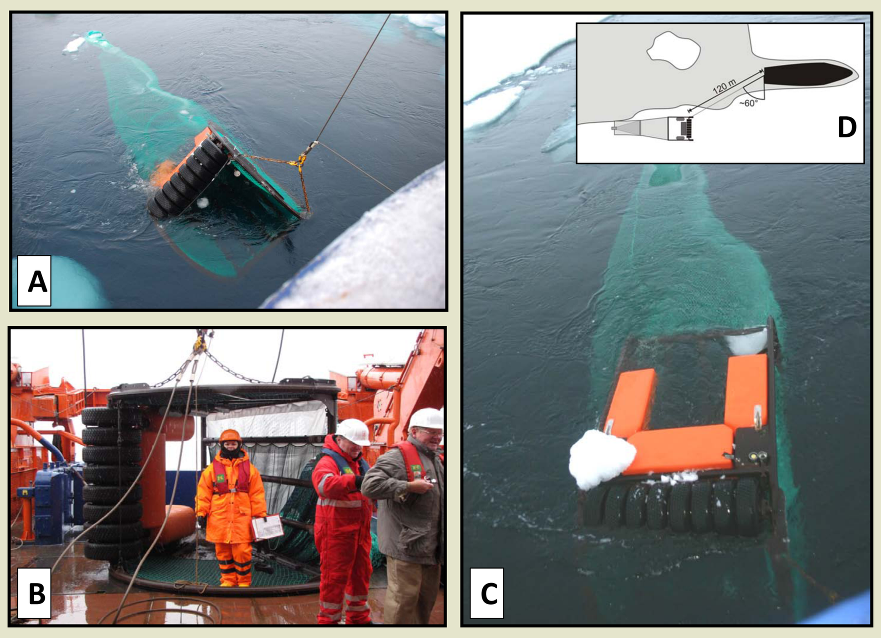


Figure 4: SUIT net system A) being winched out of water after deployment; B) on deck of the Polarstern laying on its side, with Carmen David and crew members, and; C) in the water just before being hauled in; D) birdeye sketch of SUIT shearing behind vessel.

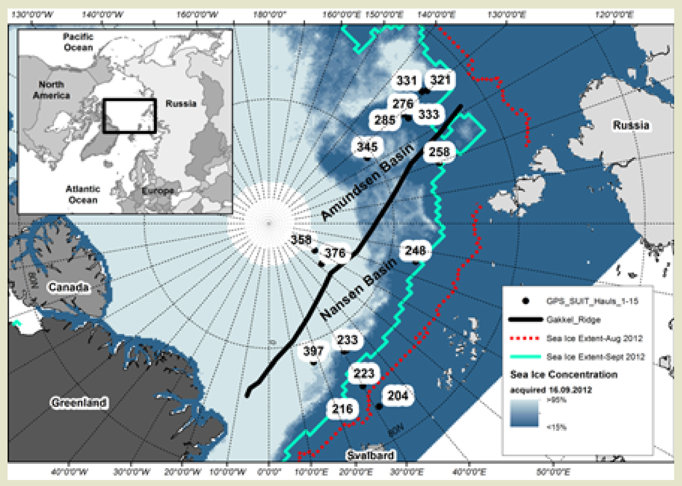


Figure 5: Stations map during RV Polarstern Expedition PS80 "*IceArc*".

Under-ice fauna was sampled with a Surface and Under-Ice Trawl (**SUIT**[3]). The SUIT consists of a sideward-shearing steel frame equipped with floaters enabling the net to glide along the underside of sea ice (Fig. 4). An environmental **sensor array** was mounted in the SUIT frame, consisting of an Acoustic Doppler Current Profiler (ADCP), a CTD probe with built-in fluorometer and altimeter, two spectral radiometers, and a GoPro underwater camera. The 12 SUIT stations were distributed over the Nansen and Amundsen Basins of the central Arctic Ocean (Fig. 5).

Objective 2:
Relate environmental properties to under-ice communities

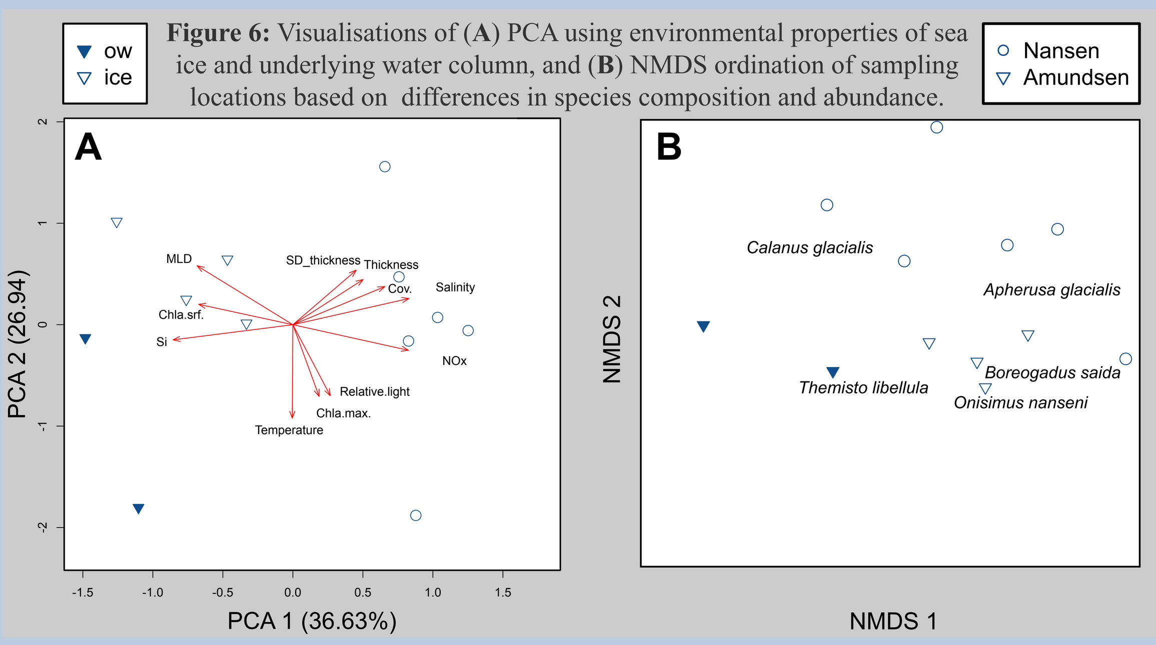


Figure 6: Visualisations of (**A**) PCA using environmental properties of sea ice and underlying water column, and (**B**) NMDS ordination of sampling locations based on differences in species composition and abundance.

Results & Conclusions:

- The **first basin-wide trawl survey** of under-ice fauna in the Arctic Ocean provided a unique dataset.
- Principal Component Analysis (PCA) of physical parameters revealed **two different environmental regimes**, which were broadly consistent with the two basins (Fig. 6A).
- **Sea ice properties and nutrient concentrations were the major factors** separating the two regimes.
- This environmental seperation was **mirrored in the community structure** (Fig. 6B).
- In **open water**, ice amphipods and Polar cod were replaced by pelagic amphipods, causing a pronounced difference with the under-ice community.

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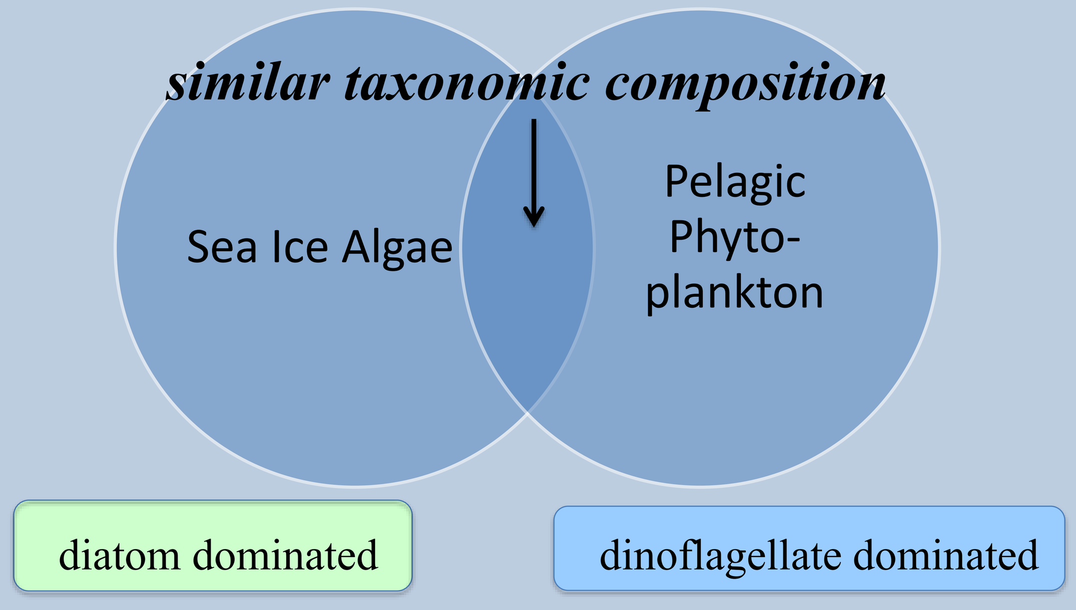
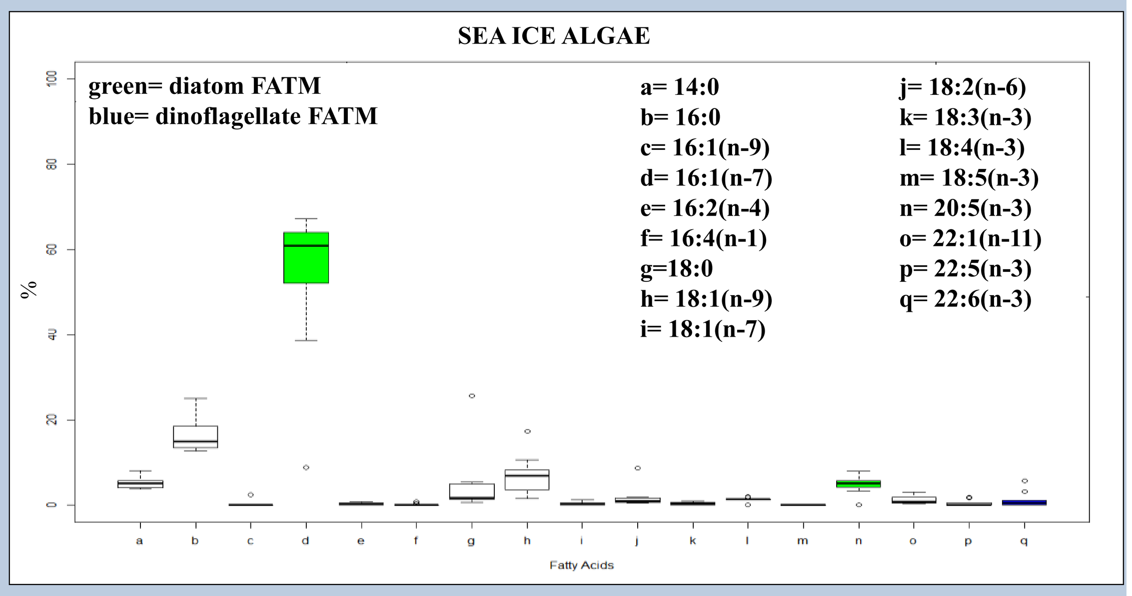
Objective 3:
Quantify the contribution of sea ice algae derived carbon in polar foodwebs

Methods: Different taxonomic groups of microalgae can be distinguished by the composition of Fatty Acid Trophic Markers (FATM). Investigation of solvent-extracted (Dichloromethane/Methanol 2:1) lipids is carried out via gas chromatography after derivatization into Fatty Acid Methyl Esters (FAME).



FATTY ACID ANALYSIS



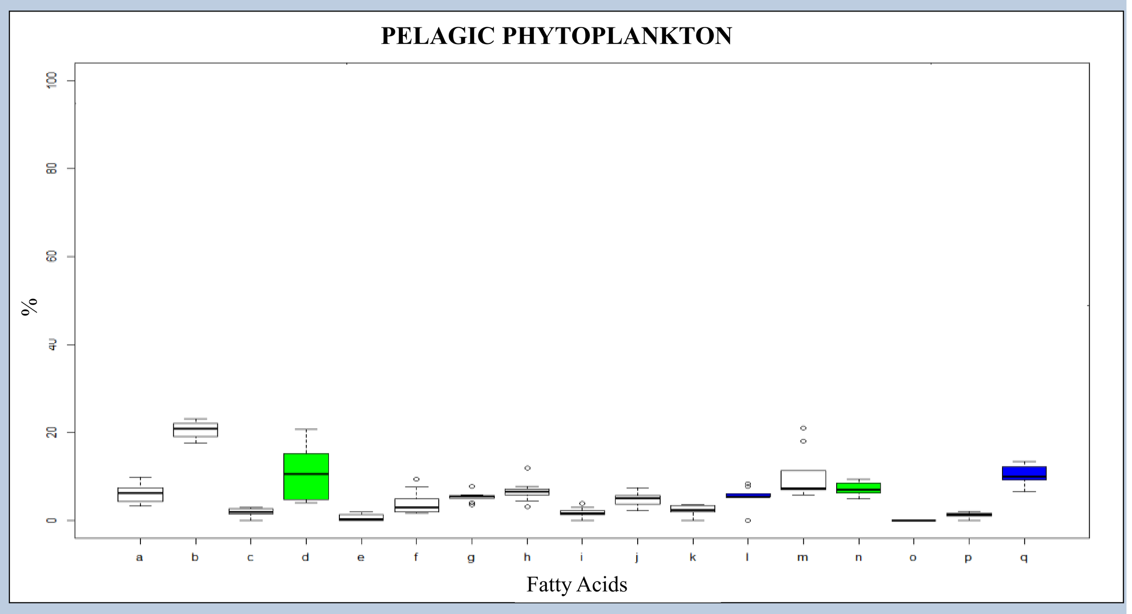


Figure 7 : Fatty Acid Signatures ("fingerprints") of sea ice algae (n=10) and pelagic phytoplankton samples (n=10) taken in August /September 2012 in the Arctic Ocean (PS80 „*IceArc*"). Green bars FATMs originated mostly from diatoms, blue bars FATMs produced by dinoflagellates.

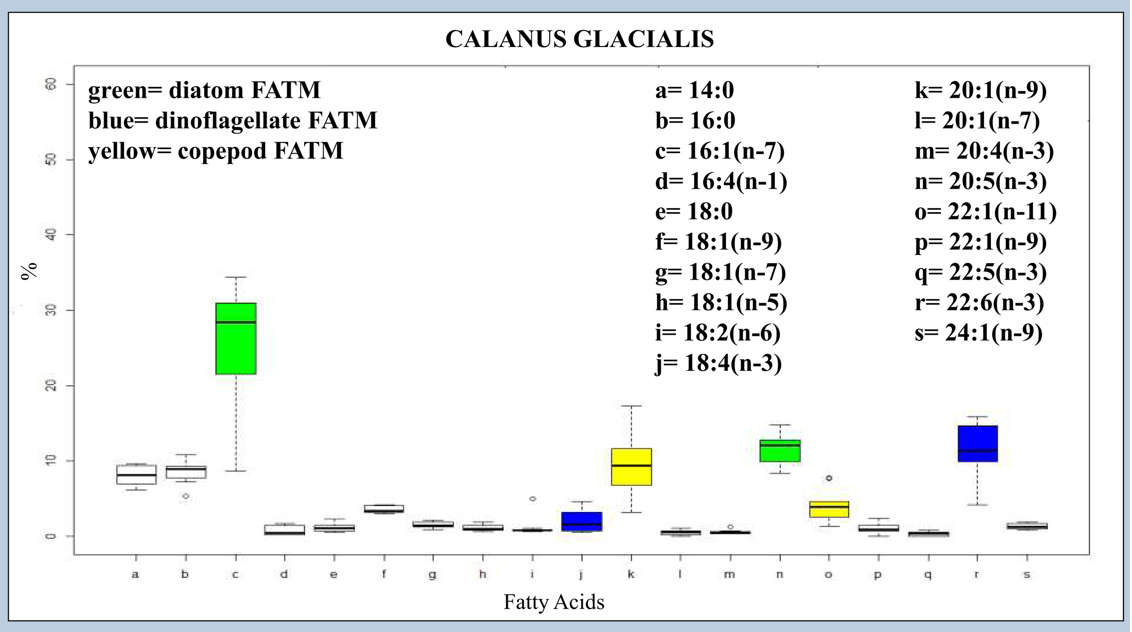


Figure 8 : Fatty Acid Signature of the Arctic copepod *Calanus glacialis* (n= 10). The fatty acid composition shows high amounts of both diatom and dinoflagellate FATM.

Results & Conclusions

- There are FATM exclusively produced by diatoms, representing the main part of the ice algae community, as well as FATM only biosynthesized by dinoflagellates, the main taxonomic group of pelagic phytoplankton (Fig. 7). That allows a **qualitative determination of consumer diets**.
- Regarding to the fatty acid pattern, ***Calanus glacialis*** fed on both, ice algae and phytoplankton (Fig. 8).
- For determining the relative contribution of ice-algae produced carbon, combination with **STABLE ISOTOPE ANALYSIS** is essential.

References
1. Mundy, C.J., et al. 2007, *J Geophys Res.,* 112, C03007, doi:10.1029/2006JC003683.
2. Nicolaus, M. et al. 2013, *Geoph. Res. Let.*, 39, L24501, doi:10.1029/2012GL053738
3. Van Franeker et al. 2009, The Surface and Under-Ice Trawl. In: Flores, H.: *Frozen Desert Alive. The role of sea ice for macrofauna and its predators: implications for the Antarctic pack-ice food web.* PhD thesis, University of Groningen.

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