

Citizen Science ^{in the} High Arctic





Benefits of Citizen Science for research in remote regions Janne E. Søreide, Prof. in marine biology UNIS

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UQAR



De-icing of Arctic Coasts: Critical or new opportunities for marine biodiversity and Ecosystem Services?

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Global warming

Permafrost

thaw



Loss of habitat, increased sea tempertures and stronger land to sea interactions

Melting

glaciers

Changes in

precip/runoff

THE REAL PRIME TO A PR

Will impact timing, magnitude and quality of primary and secondary producers with implications for the coastal marine food web

Coastal

erosion

An increase in air temperature (4-7°C) and in precipitation (45-65%) are expected in near future in Svalbard



Gjermundsen et al. 2021, SESS report 2020

Nowak et al. 2021, SESS report 2020

Landfast ice extent and duration in Svalbard

In future if +4°C increase in air temp.



The maps show how long the fast ice lasted . Map (a) and (c) were created using a geographically weighted random forest model, map (b) using observational data.

Ecological losers include cold-adapted species that rely on sea ice

pepod nauplii

Sympagohydr

Polychaete juvenile

Wheel animal

Trochophore arvae

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Photos V. Pitusi, UNIS

How sea ice loss impact the many microorganisms living inside the sea ice is largely unknown

Photo M. Daase

Sea ice biology

Sympagic meiofauna – "ice-associated" animals - 20 to 500 µm



UNIS PhD student

Sea Ice Algae





Hearts in the Ice – UNIS cooperation

 Frequent sampling of ice cores from February to June to study seasonal colonization and development of algae and tiny animals living inside the sea ice.





Van Keulen March 2021

Contraction of the second



March sampling







Van Keulen May 2021





Figure 3.4: Timing and magnitude of algal chl a biomass grouped into respective fjords and according to Julian day (i.e. day of year/date of sampling)

Physical data on:

Sea ice thickness Snow depth Freeboard



Remote sensing: Important tool for monitoring BUT calibration/validation needed for better precision



The next decade's greatest environmental changes are expected in northeastern Svalbard. Time series from N and E Svalbard important!



years ; on average from 5 months sea ice duration to only 1 month (Weslawski et al. 2017)



Spatial and temporal sampling in Svalbard



Figure 3. Map of common routes during the 2018 and 2019 trips with Hurtigruten (broken blue lines), and sampling stations in 2018 (blue points) and 2019 (red points)

Water and plankton sampling



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3.4 DNA-based analysis of protist and zooplankton communities

DNA extracted from the filtered seawater was sequenced using a metabarcoding approach. In this analysis, a marker gene (in this case either the 18S ribosomal RNA gene or the CO1 barcoding gene) is scanned and compared to a database of sequences belonging to known organisms. The end result is a semi-



quantitative overview of which organisms are present in the sample, and thus a measure of biodiversity. The 2018 samples have been processed and sequenced, and the 18 S rDNA data is currently being analyzed. Preliminary results from analyses of the CO1 barcoding gene are shown in Fig. 7. Here it can be seen that the high chlorophyll values observed at Kvitøya were due to a haptophyta bloom (black in Fig. 7), while the late algal community in Smeerenburg was dominated by diatoms (Bacillariophyta, cyan in Fig. 7) and green algae (Chlorophyta, red in Fig. 7). Zooming in we can investigate which organisms are abundant (data not shown). Dominant zooplankton included the copepods *Calanus, Pseudocalanus* and especially *Oithona* (Maxillopoda). Barnacles (Maxillopoda) were abundant at some stations in June and July, probably larval stages that drift with the water.



Figure 7. Community composition of protist and zooplankton from the 2018 samples. Stacked bar chart showing the relative gene abundance of the indicated taxonomic groups (mostly phyla), based on metabarcoding of the mitochondrial CO1 gene. The group "others" is made up of various taxonomic groups with low abundance, as well as DNA with uncertain taxonomic assignment. The percentage of each taxonomic group gives us information about the relative abundance of these organisms in the sampled community, and cannot be directly converted to biomass. Such data are linked with the algae biomass and nutrients (Fig. 6) in the different water masses around Svalbard (Fig. 5). Thanks a lot to Hearts in the ice team!

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