Supplementary Material

Monitoring a changing Arctic: Recent advancements in the study of sea ice microbial communities

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Supplementary Material

S.1 References of primary and bacterial production

Data from the following references are represented in Figure 1:

General Movement of Surface Waters

Stein, R., and R.W. Macdonald. 2004. The Organic Carbon Cycle in the Arctic Ocean. Springer.

Nutrient Fluxes

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Primary Production

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Kaartokallio, H. (2004), Food web components, and physical and chemical properties of Baltic Sea ice, *Mar. Ecol. Prog. Ser.* 273, 49-63, doi:10.3354/meps273049.

Lee, S.H., de Mora, S.J., Gosselin, M., Levasseur, M., Bouillon, R.-C., Nozais, C., and C. Michel (2001), Particulate dimethylsulfoxide in Arctic sea-ice algal communities: the cryoprotectant hypothesis revisited, *J. Phycol.* 37, 488-499, doi: 10.1046/j.1529-8817.2001.037004488.x.

Mock, T., and R. Gradinger (1999), Determination of Arctic ice algal production with a new in situ incubation technique, *Mar. Ecol. Prog. Ser.* 177, 15-26, doi: 10.3354/meps177015.

Smith, R.E.H., and A.W. Herman (1992), In situ patterns of intracellular photosynthate allocation by sea ice algae in the Canadian High Arctic, *Polar Biol.* 12, 545-551, doi: 10.1007/BF00236978.

Bacterial Production

Bunch, J.N., and R.C. Harland (1990), Bacterial production in the bottom surface of sea ice in the Canadian subarctic, *Can. J. Fish. Aquat. Sci*. 43, 1986-1995, doi: 10.1139/f90-223.

Haecky, P., and A. Anderson (1993), Primary and bacterial production in sea ice in the northern Baltic Sea, *Aquat. Microbiol. Ecol.* 20, 107-118, doi: 10.3354/ame020107.

Kaartokallio, H., Søgaard, D.H., Norman, L., Rysgaard, S., Tison, J.L-., Delille, B., and D.N. Thomas (2013), Short-term variability in bacterial abundance, cell properties, and incorporation of leucine and thymidine in subarctic sea ice, *Aquat. Microbiol. Ecol.* 71, 57-73, doi:10.3354/ame01667.

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S.2 Northwestern Hudson Bay dataset

Data collected during the The Coral Harbour Oceanographic Observation and Sea ice Experiments (CHOOSE) from May 1 – June 7, 2019, took place in northwestern Hudson Bay, offshore from the community of Coral Harbour. Sampling focused on the bottom 10 cm of ice cores collected from three study sites along a transect orientated perpendicular to the flow edge a polynya and the Canadian coastline. Specific location and dates of sampling are detailed in Table S.1. Three sites (A, C, and F) situated increasingly offshore from the community of Coral Harbour, Nunavut were sampled in 2019 during the spring bloom period on 4 May (Site C), 17 May

(sites A, C & F) and 29 May (Site C). The >10 µm size fraction was chosen to reduce the signal of the algal bloom, allowing for amplicons of larger grazers to be detected.

Table S.1 Location of ice cores drilled for 18S rRNA gene analysis.

Site	Location	Date	Snow depth (cm)	18S rRNA sequences
A	64°06'52.6"N 83°04'45.8"W	17/5/19	15	18-21K
C	63°59'39.1"N 83°20'19.1"W	05/05/19 17/5/19 30/5/19	9 23.5 13	14-16K 14-20K 14-21k
F	63°54'36.7"N 83°18'24.6"W	17/5/19	19	16-20k

18S rRNA gene analysis: From each ice core, the bottom 10cm of core was melted and filtered onto triplicate 47mm, 10 µm filters. DNA was extracted from the filters using a DNeasy Plant Mini Kit (Qiagen). We amplified the V4 region of the 18S rRNA gene as previously described (Stoeck et al., 2010), yielding 500 basepair fragments. PCR products were sequenced on an Illumina MiSeq (Nano V2, 2 × 250bp paired end reads) by the Bristol Genomics Facility. Amplicons were denoised using DADA2 (Callahan et al 2016) in the QIIME2 package (Estaki et al., 2020). Sequences were assigned a taxonomy using the QIIME2 classifier pretrainted on Silva 138 99% OTUs (Bokulich et al., 2018; Quast et al., 2013).

Metagenomic assembled genome analysis: Metagenomes were generated as previously described, from a pooled sample across all sites (Table S.1) (Bellas et al., in prep). Briefly, the bottom 10cm of ice core was melted, prefiltered through a 10 µm filter before being filtered onto a 90mm, 0.2um polycarbonate filter to collect prokaryotes. This filter was frozen and stored at -80℃. DNA was extracted from the filtered with a DNeasy PowerWater Kit (Qiagen) before being sequenced on an Illumina NextSeq 500 at the Bristol Genomics Facility. Reads were assembled using MEGAHIT (Li et al., 2015), binned using METABAT2 (Kang et al., 2019) and taxonomically classified using GTDB-Tk (Chaumeil et al., 2020). Functional annotation of the individual MAGs was carried out by searching against the Kyoto Encyclopedia of Genes and Genomes (KEGG), using the GhostKOALA (Kanehisa et al., 2016) (www.genome.jp/kegg/).

References for S.2

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Stoeck, T., Bass, D., Nebel, M., Christen, R., Jones, M. D. M., Breiner, H.-W., & Richards, T. A. (2010). Multiple marker parallel tag environmental DNA sequencing reveals a highly complex eukaryotic community in marine anoxic water. Molecular Ecology, 19(s1), 21–31. doi.org/10.1111/j.1365-294X.2009.04480.x

S.3 Lincoln Sea dataset

Data were collected as part of the *Multidisciplinary Arctic Program - Last Ice (MAP- Last ice)* in the Lincoln Sea (82.576°N -62.471°W), located off-shore from the Canadian Forces Station *Alert.* This was done between 7 and 23 May, 2018. Additional information can be found in:

Campbell, K., Lange, B., Landy, J.C., Katlein, C., Nicolaus, M., Anhaus, P., Matero, I., Gradinger, R., Charette, J., Duerksen, S., Tremblay, P., Rysgaard, S., Tranter, M., Haas, C., and C. Michel (*in review*). Widespread net heterotrophy in High Arctic first-year and multi-year sea ice. *Elementa*.

S.4 Lowermost Northwest Passage dataset

Data were collected in Spring 2014 on 12 discrete sampling occasions between 21 April and 9 June from landfast first-year sea ice. The sampling site in Dease Strait (69.017°N 105.317°W) was near Cambridge Bay, Nunavut, Canada. The data used in this study is a subset of the more comprehensive dataset described in Campbell et al. (2016).