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Mercury Levels and Potential Methylation/ Demethylation Rates in Canadian High Arctic Sea Ice

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Sea Ice Decline in the High Arctic



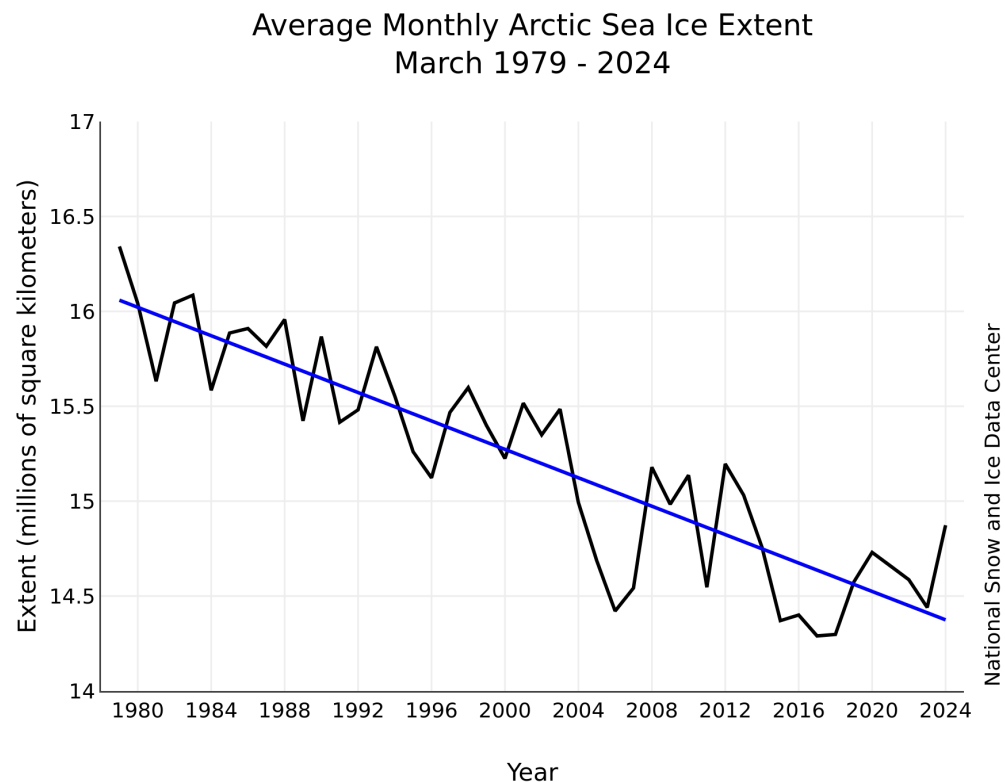


Fig. 1. Declining monthly Arctic sea ice extent from 1979-2024 (National Snow and Ice Data Center)

Due to warmer temperatures, multi year ice (MYI) is melting and being replaced by shorter lived first year ice (FYI)!

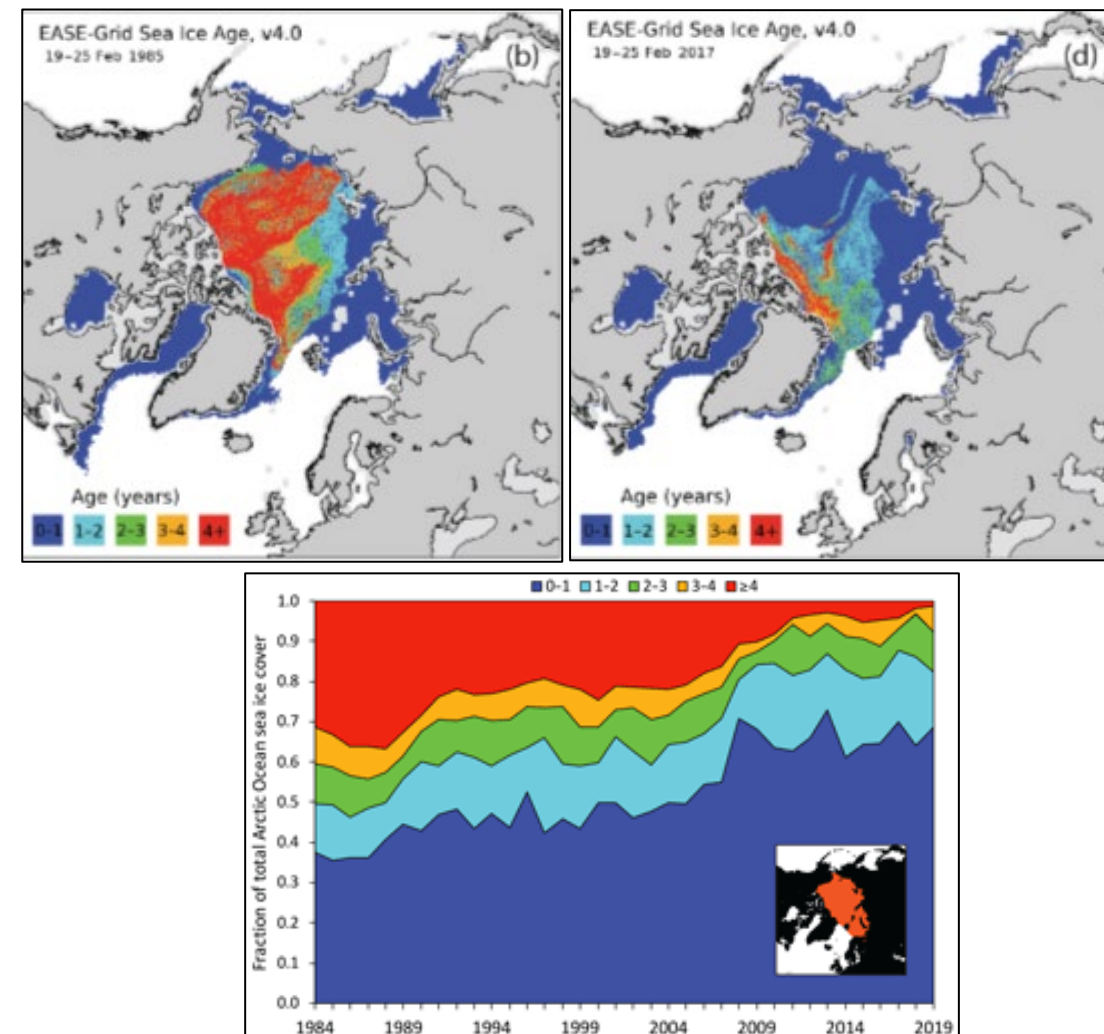


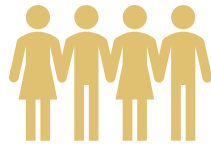
Fig. 2. The shift from MYI to FYI. (Tschudi et al., 2019b; Perovich et al., 2019)



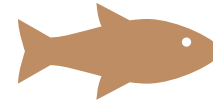
Significance of Research



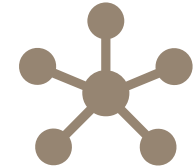
The effects of the climate driven shift from MYI to FYI will impact net MeHg production and bioaccumulation in local marine food webs



Arctic Indigenous peoples who rely on a marine diet



Species at Risk (SAR) or endangered species in the area



Increase the need for more biomonitoring networks



Knowledge Gaps

- Major geographic limitations and representation of the Canadian High Arctic
- Need to know more about the ions, water isotopes, and DOM to help us understand Hg trends in sea ice
- Concentrations are often reported (Schartup et al., 2020; Beattie et al., 2014), but no methylation/ demethylation (K_m , K_d) potentials are reported in literature for sea ice

Total and Methylated Mercury in Arctic Multiyear Sea Ice

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Supporting Information

ABSTRACT: Mercury is one of the primary contaminants of concern in the Arctic marine ecosystem. While considerable efforts have been directed toward understanding mercury cycling in the Arctic, little is known about mercury dynamics within Arctic multiyear sea ice, which is being rapidly replaced with first-year ice. Here we report the first study on the distribution and potential methylation of mercury in Arctic multiyear sea ice. Based on three multiyear ice cores taken from the eastern Beaufort Sea and McClure Strait, total mercury concentrations ranged from 0.65 to 60.8 pM in bulk ice, with the highest values occurring in the topmost layer (~40 cm) which is attributed to the dynamics of particulate matter. Methylated mercury concentrations ranged from below the method detection limit (<0.1 pM) to as high as 2.64 pM. The ratio of methylated to total mercury peaked, up to ~40%, in the mid to bottom sections of the ice, suggesting the potential occurrence of in situ mercury methylation. The annual fluxes of total and methylated mercury into the Arctic Ocean via melt of multiyear ice are estimated to be 420 and 42 kg yr⁻¹, respectively, representing an important and changing source of mercury and methylmercury into the Arctic Ocean marine ecosystem.



Influence of the Arctic Sea-Ice Regime Shift on Sea-Ice Methylated Mercury Trends

Amina T. Schartup,^{*} Anne L. Soerensen, and Lars-Eric Heimbürger-Boavida

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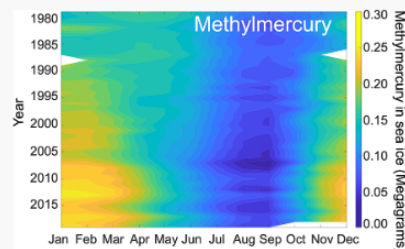
ACCESS |

Metrics & More

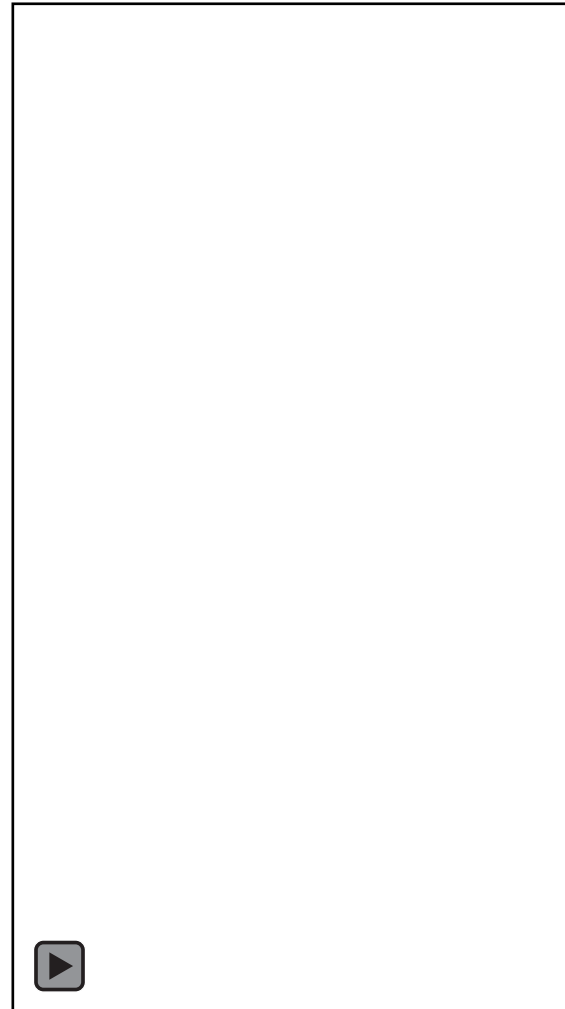
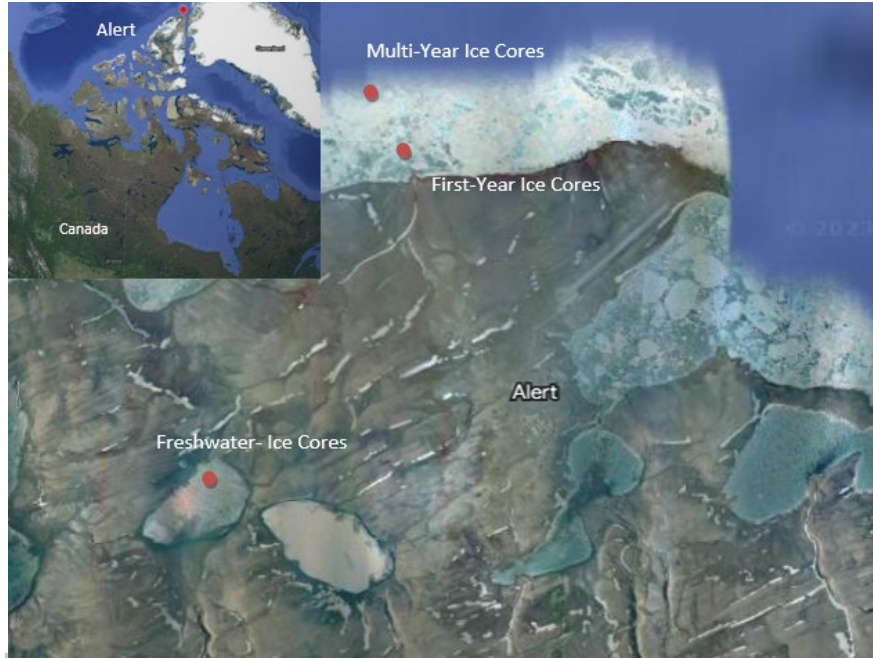
Article Recommendations

Supporting Information

ABSTRACT: Arctic sea ice regulates the air–sea exchange of volatile mercury (Hg) species like dimethylmercury (DMHg) or elemental Hg and is known to host Hg methylating microbes that produce neurotoxic and biomagnifying monomethylmercury (MMHg). Arctic sea ice accounts for 57% of the total primary production in the Arctic Ocean, suggesting that it could be the main source of MMHg to arctic food webs. Despite this, little is known about Hg concentrations and speciation in arctic sea ice. Here, we report Hg species and show the importance of sea-ice composition on sea-ice methylmercury (MeHg = DMHg + MMHg) budgets. We propose that the shift from older sea ice (lower MeHg) to younger sea ice (higher MeHg) resulted in a 40% increase in MeHg (per square meter of sea ice) since 1979 despite a 45% decline in the total sea-ice volume. Approximately



Sample Collection and Preparation



PART 1:
Characterizing Ice
Cores



PART 2: Hg Analysis



PART 1: Characterizing Ice Cores with Stable Water Isotopes

MYI Core

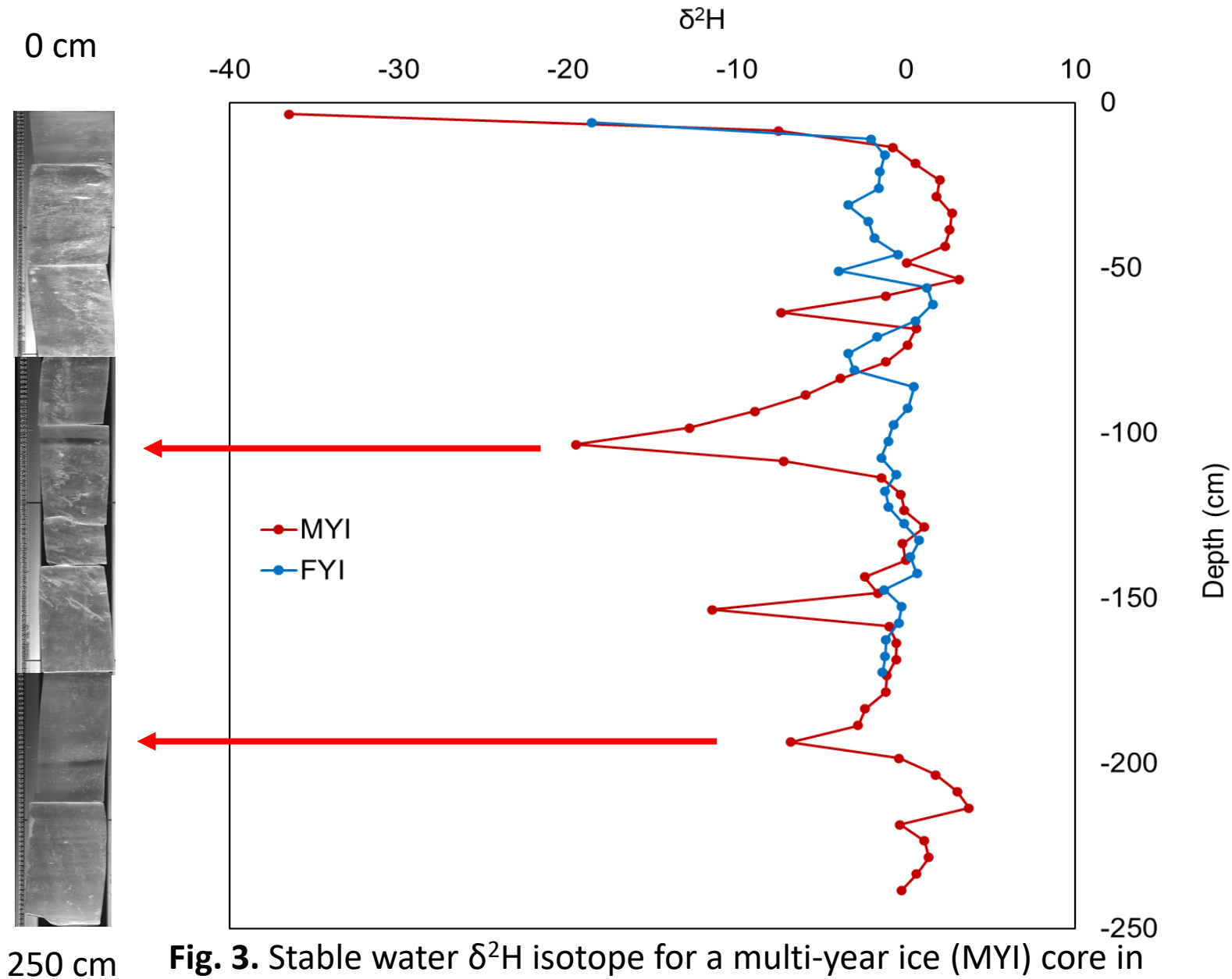
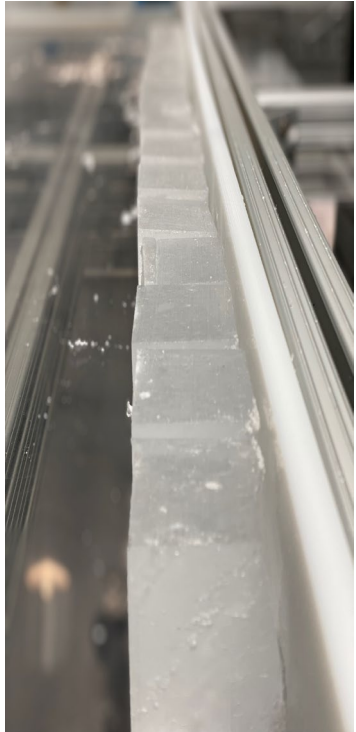


Fig. 3. Stable water $\delta^2\text{H}$ isotope for a multi-year ice (MYI) core in **red** and a first-year ice (FYI) core in **blue**.

How can we differentiate between MYI and FYI cores?



PART 1: Characterizing Ice Cores with PARAFAC

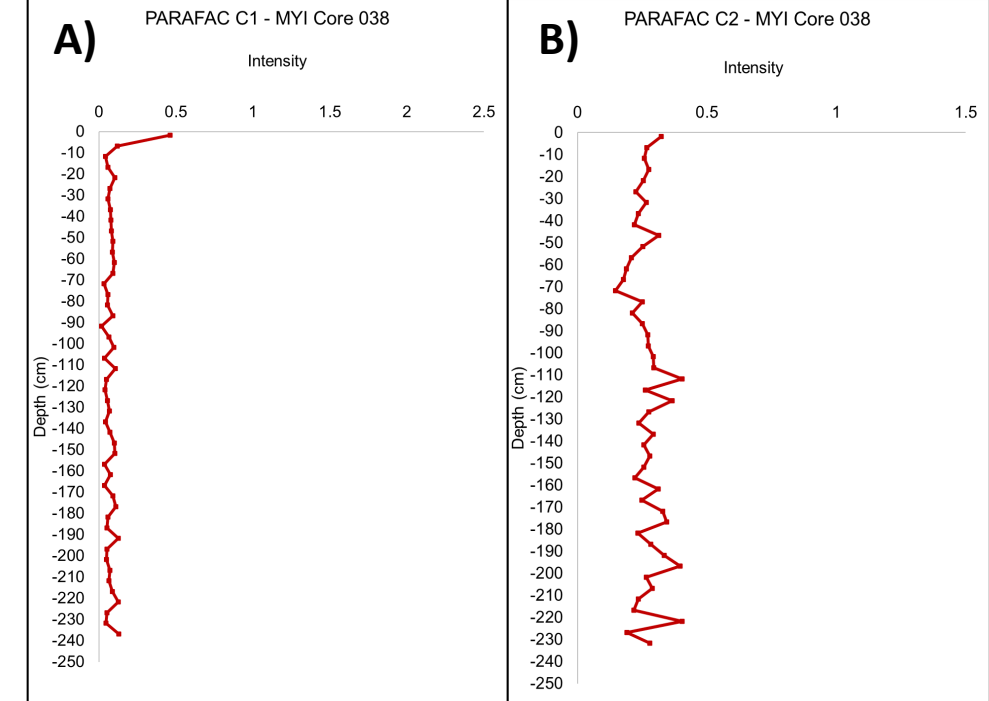
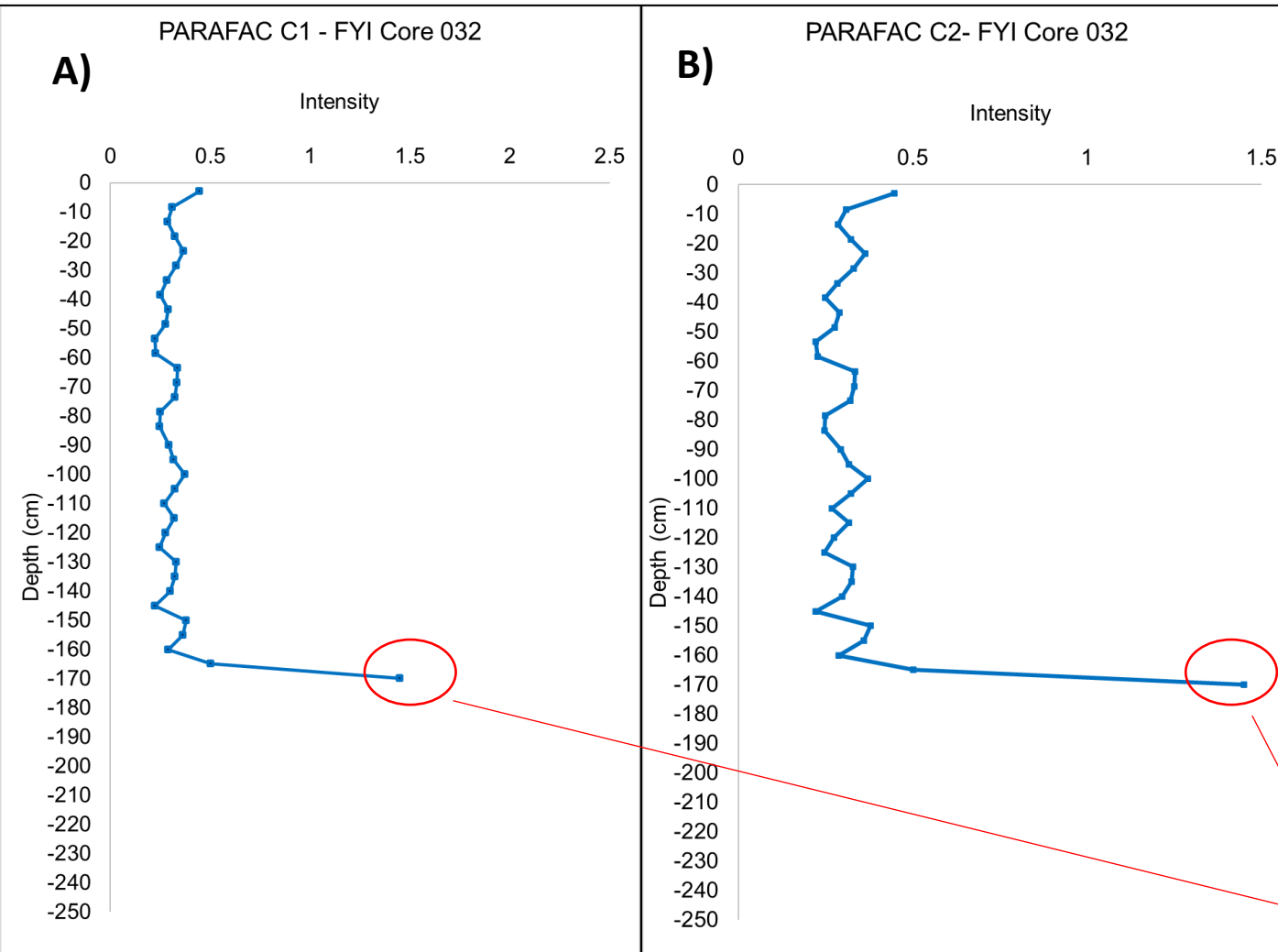


Fig. 4. Parallel Factor Analysis (PARAFAC) for **amino acid like component (A)** and **protein like component (B)** in a multi-year ice (MYI) core.



Good conditions for methylators to thrive?

Fig. 4. Parallel Factor Analysis (PARAFAC) for **amino acid like component (A)** and **protein like component (B)** in a first-year ice (FYI) core.

PART 2: Total Mercury (THg) and Methyl Mercury (MeHg) Depth Profiles

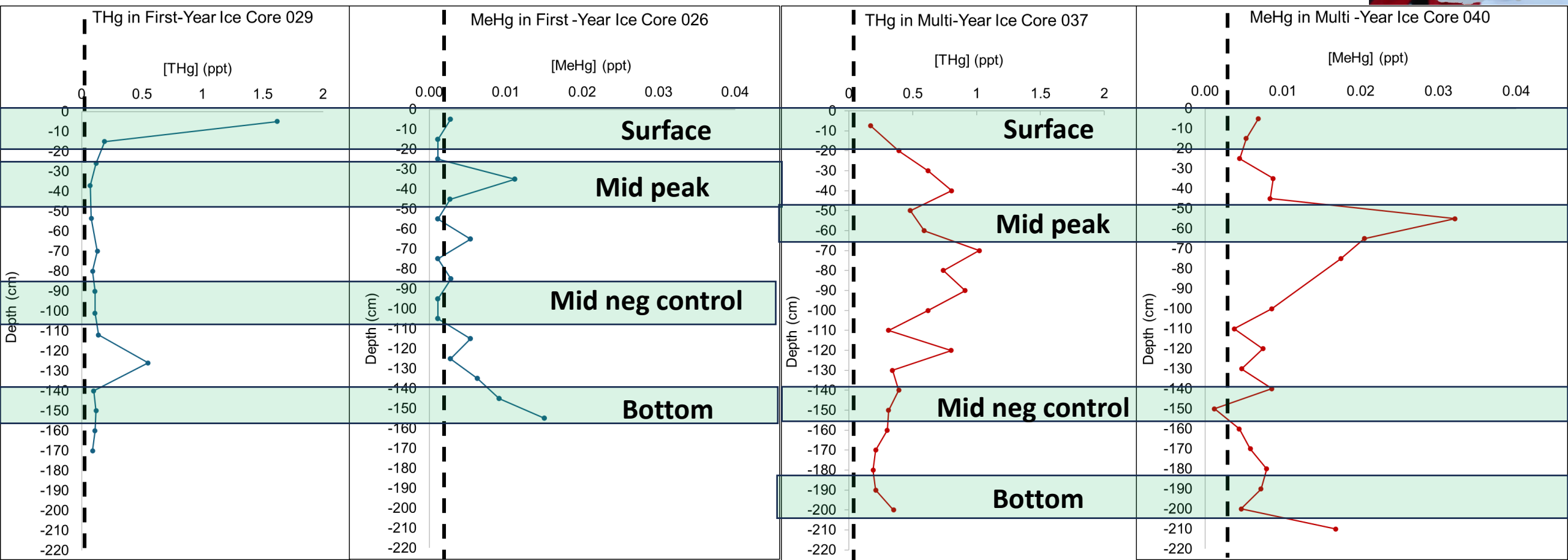


Fig. 6. Total mercury and methyl mercury profiles in first-year (left two panes) and multi-year (right two panes) ice cores. Green bands represent depths used for methylation and demethylation experiments. Dashed line represents the method detection limit.

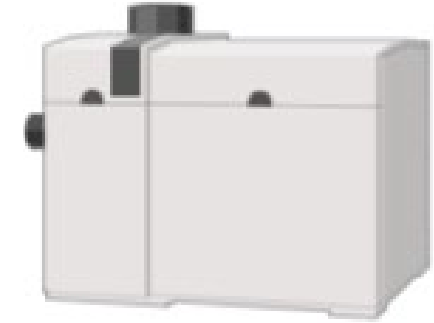


PART 2: Methylation (K_m) and Demethylation (K_d) Incubations

Step 1: Blend 10 cm sections and transfer to jars



Steps 4+5: Distillations and quantification by ICP-MS for MeHg analysis



Step 2: Inject with isotopes and incubate for 48 hours between 0-1 °C



Control

Stimulation

Inhibition

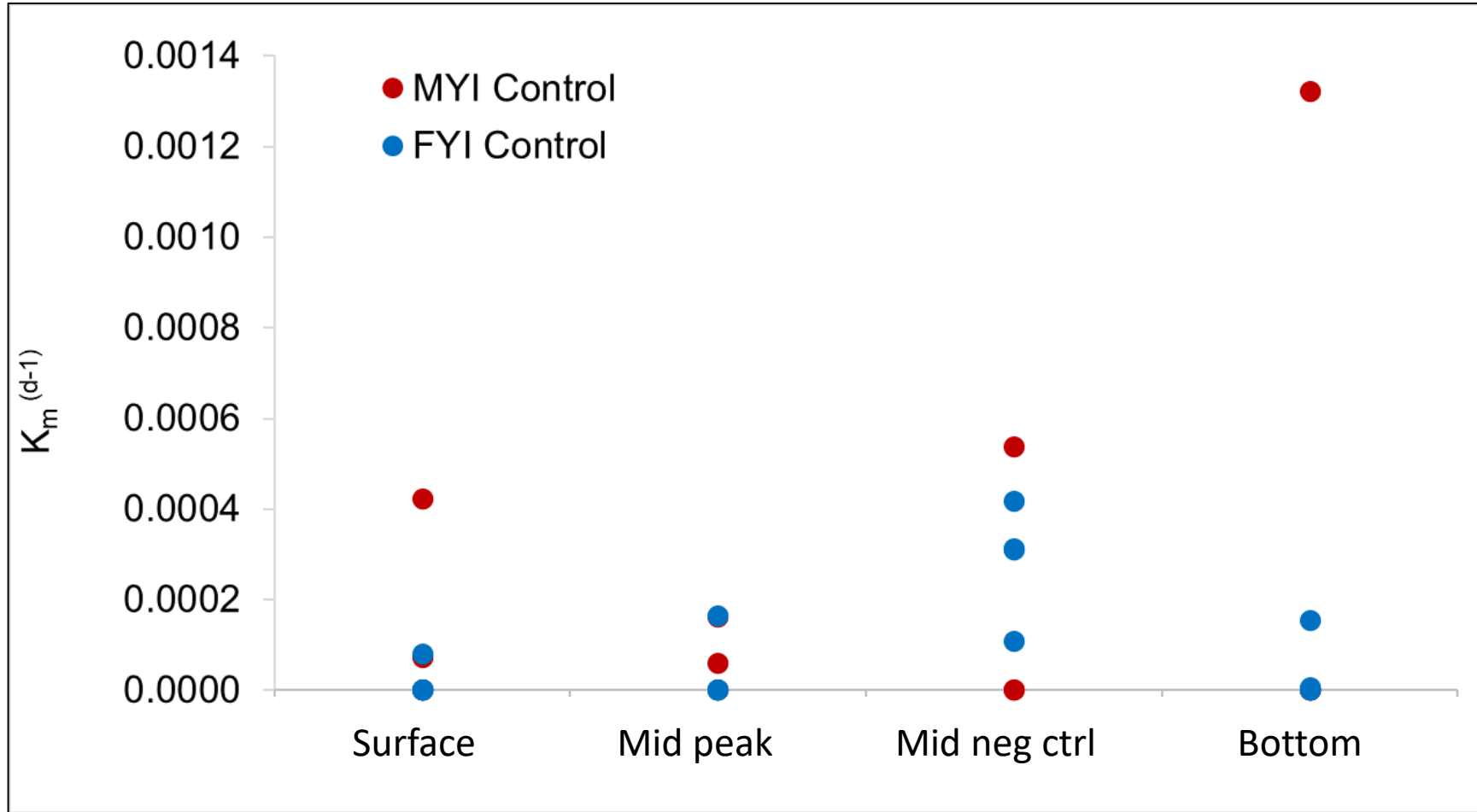


4 MYI cores x 4 depths
4 FYI cores x 4 depths
1 T_0 core x 4 depths

Step 3: Stop the incubation with HCl and separate 25 mL for THg analysis for quantification by Tekran 2600



K_m Results

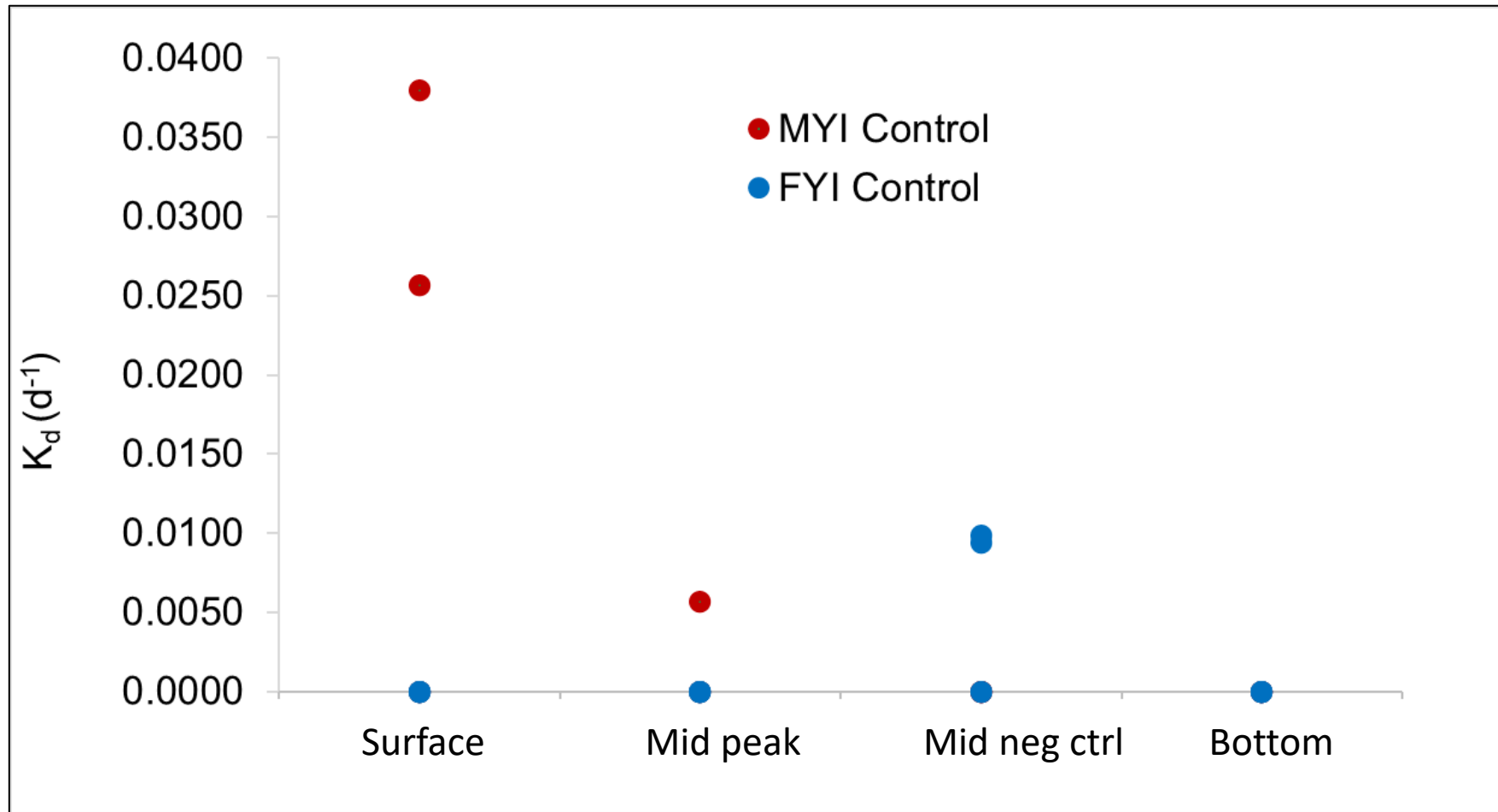


- Methylation was higher for the mid neg control
- No significant differences in methylation rate potential constants at all depths (there is evidence for some methylation activity)
- FYI bottoms did not have higher methylation activity than the rest of the core, but MYI bottom had a higher methylation activity

Fig. 7. Methylation rate potential constant (K_m) for multi-year ice (MYI) in **red** and first year ice (FYI) in **blue**. Dots represent individual measurements with 3-4 replicates per depth.



K_d Results



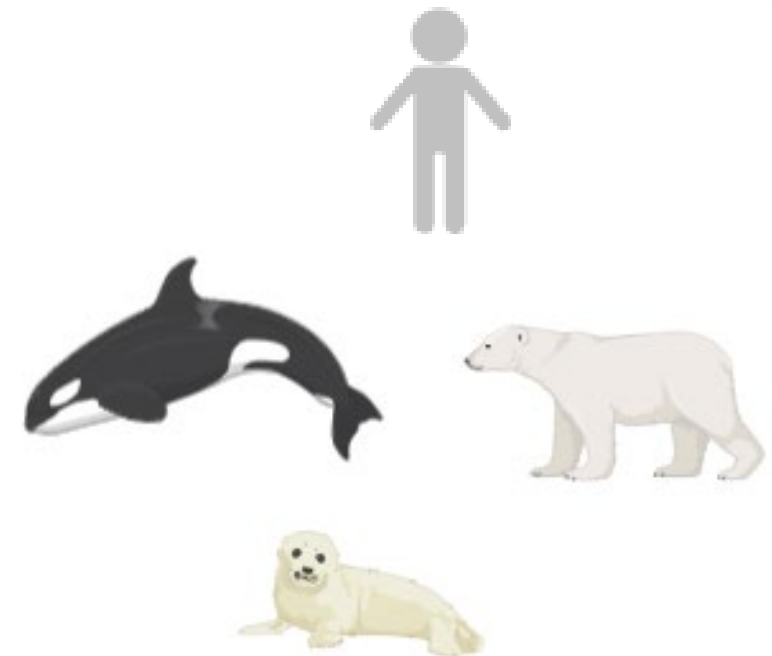
- More demethylation at the surface
- There was no significant differences in demethylation between MYI and FYI at all depths
- There was no demethylation detected in the bottom (last 10 cm of FYI) or MYI cores

Fig. 8. Demethylation rate potential constant (K_d) for multi-year ice (MYI) in **red** and first year ice (FYI) in **blue**. Dots represent individual measurements with 3-4 replicates per depth.



Conclusion

- FYI and MYI cores did not differ significantly in terms of K_m or K_d (both p values >0.05) but there is evidence of methylation in the ice at ice relevant temperatures
- There are clear differences in concentrations at different depths, but no methylation activity was seen on the bottom of FYI cores where biofilms are present
- However, no demethylation was detected on the bottoms of either cores, but some methylation was detected at the bottom of a MYI core
- Longer term storage vs. in-situ production of MeHg



THANK YOU FOR LISTENING!

- Alert Team for sample collection
- Global Atmospheric Watch Lab Alert
- Canadian Forces Station Alert
- MSc Student Erika Bullen and Dr. Katrina MacSween
- All WATER lab members!



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