From Degradation to Disturbance: Pesticide Impacts on Cryoconite Microbial Communities from an Alpine Glacier and the Greenland Ice Sheet.

L.G. van Dijk[1*], A. Cuzzeri[2,3], B. Sattler[2,3], A. Zervas[1] & C.S. Jacobsen[1]

[1] *Aarhus University, Denmark*

[2] *University of Innsbruck, Austria*

[3] *Austrian Polar Research Institute, Austria*

** Corresponding Author (lvd@envs.au.dk, Aarhus University, Frederiksborgvej 39, 4000 Roskilde, Denmark)*

Glaciers and ice sheets are increasingly shaped by global and local pollution sources. For more than a century, pollutants from agricultural and industrial sources have been deposited into these remote regions through short- and long-range atmospheric transport, gradually accumulating in the snow and ice over time. Alpine glaciers situated closer to population centers, like those in the Alps, have received heavier pollution loads than more remote regions such as the Greenland Ice Sheet. Evidence from previous research on glaciers in the Alps shows that some contaminants can drive surface microbial communities to evolve the capacity to degrade them. Yet the broader "side-effects" of pollutants on whole microbial systems, such as shifts in community structure and ecological functioning, remain poorly understood.

To address this gap, we conducted a microcosm experiment with cryoconite from the anthropogenically influenced Forni Glacier (Italian Alps) and from the remote Greenland Ice Sheet near Kangerlussuaq. In this experiment, cryoconite was exposed to two pesticides, the organophosphorus insecticide chlorpyrifos and the phenoxy herbicide 4-chloro-2-methylphenoxyacetic acid (MCPA), at concentrations of 1 and 100 ppm for 170 days. The addition of a trace amount of 14C-labeled pesticide enabled the quantification of the mineralization rate of the pesticides over time using a scintillation counter. Preliminary results show distinct mineralization curves between the two cryoconites, with no mineralization of chlorpyrifos occurring in the cryoconite from the Greenland Ice Sheet. Future quantification of activity levels of functional genes involved in pesticide degradation by qPCR and rt-qPCR will provide insights into the abundance of potential degraders and gene activities over time. Meanwhile, TotalRNA metatranscriptomics combined with metagenomics will be employed to reveal shifts in community structure and functioning caused by pesticide exposure, providing insight into the broader impacts of pollutants on the entire microbial community and potentially revealing distinct local adaptations.

Funding: This study is funded by the European Union under the HORIZON-MSCA-2021-DN-01 program, project number 101072761.