

Geochemical and microbiological gradients along Arctic chronosequences

ROBIN WOJCIK^{1*}, JOHANNA DONHAUSER^{2*}, STINE HOLM¹, LUCIE MALARD³, ALEXANDRA HOLLAND⁴, BEAT FREY², DIRK WAGNER¹, DAVID PEARCE³, ALEX ANESIO⁴, JÖRN HÖVELMANN¹ AND LIANE G. BENNING^{1,5*}

¹ GFZ, German Research Centre for Geosciences, Potsdam, Germany (* correspondence: robin.wojcik@gfz-potsdam.de; liane.g.benning@gfz-potsdam.de)

² WSL, Zurich, Switzerland (johanna.donhauser@wsl.ch)

³ Northumbria University, Newcastle, United Kingdom

⁴ University of Bristol, Bristol, United Kingdom

⁵ Dept. Earth Sci., Free Univ. Berlin, Germany

The link between carbon cycling and weathering in recently deglaciated areas may result in important feedbacks on global warming and biogeochemical element cycles, particularly since glaciers are predicted to retreat at increasing rates in the future. In addition, recently deglaciated areas are also unique environments to study the initial and successional development stages of soil formation. Such soils are also prime targets for evaluating processes linked to the initial colonization of pioneer microorganisms, which in turn can both be influenced and impact nutrient and organic carbon bioavailability.

The processes regulating carbon and nutrient cycling in such environments are however poorly known. To close this gap, we aim to link carbon and nutrient availability with microbial community structures activity and evaluate the effects on abiotic and biotic parameters on weathering rates in Arctic soils. This study is based on samples collected in winter season along a chronosequence in the proglacial area of Longyearbreen, Svalbard.

Our results show that soils particle size, conductivity and pH decrease with soil age (e.g., pH and conductivity were 8.8 and 380 mS.cm⁻¹ in the young sites and 7.4 and 86 mS.cm⁻¹ in the older sites). The variation in chemical index of alteration (CIA), calculated using on X-ray fluorescence data, indicate an increase in weathering with decreasing size-fraction and increasing age. In additions, sequencing result show clear differences in microbial diversity between the younger and older soils along the chronosequence.