## Role of cryptogamic covers in metalnitrogen biogeochemical coupling at the edge of the critical zone

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Cryptogamic covers, such as lichens and bryophytes, are nonvascular photoautotrophs that live at biotic and abiotic interfaces of vegetation, rocks, and soils to function as the "skin" of the Earth. Their associated microbiomes are estimated to contribute about half of terrestrial new nitrogen (N) input through biological N fixation [1], as well as 5-10 % of land N<sub>2</sub>O emissions through poorly understood N loss pathways [2]. However, our understanding of the biotic and abiotic controls over these crucial metabolisms is insufficient given the importance of cryptogam holobionts for ecosystem succession and resilience, particularly under global change.

Using hundreds of samples of lichens and mosses collected along large latitudinal gradients in Asia and North America, we will show evidence of (i) the segregation of biological N fixation and N<sub>2</sub>O production metabolisms and discuss the role of exogenous N availability in controlling this dichotomization, and (ii) the strong influence of trace metal bioavailability on cryptogamic cover microbial metabolic activity [3], focusing on molybdenum (Mo) and copper (Cu), which are required in several critical N cycle enzymes.

Overall, our results exemplify the crucial roles of trace metal availability in the biogeochemical cycling of N at the outmost layer of the critical zone. Moreover, the ability of cryptogamassociated microbiomes to modulate N input and N removal processes could constitute a safe-guard from N imbalance in terrestrial ecosystems, helping to buffer the heterogeneity in N inputs from natural and anthropic sources. Whether or not this potential "nitrostat" is actively working to control ecosystemlevel N status remains to be further investigated. Finally, we will discuss the implications of these findings for the contributions of cryptogamic covers to ecosystem services in the pre-industrial era, present, and near future.

References:

[1] Elbert et al., (2012), Nature Geosciences 5, 459-462, [2] Lenhart et al., (2015), Global Change Biology 21(10), 3889-3900, [3] Darnajoux et al., (2019), PNAS 116(49), 24682-24688.