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Labo Pr Laforest-Lapointe, Co-dir. Pr Sebastien Roy

Of Microbiomes and Mosses

Exploring the functional diversity of the boreal moss microbiome from the Eeyou Istchee region of Québec





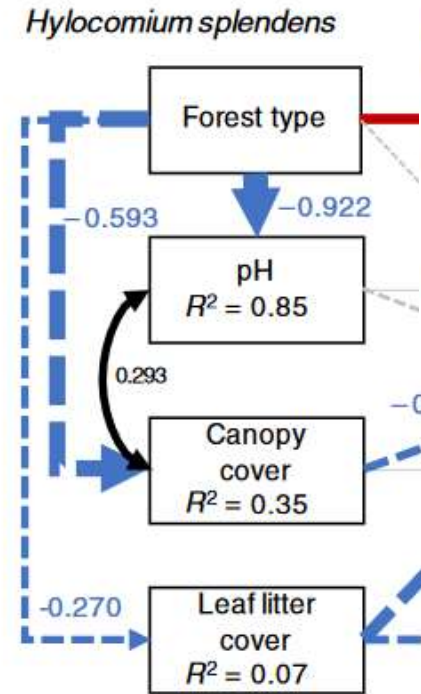
Boreal Mosses

- ❖ 20% of forest net primary productivity
- ❖ Contribute up to 50% of nitrogen inputs
- ❖ Contribute to carbon cycling
- ❖ Slow decomposers
- ❖ Major C + N element sink
- ❖ Moss-associated microbial communities

Moss Microbiomes

Experimental assessment of tree canopy and leaf litter controls on the microbiome and nitrogen fixation rates of two boreal mosses

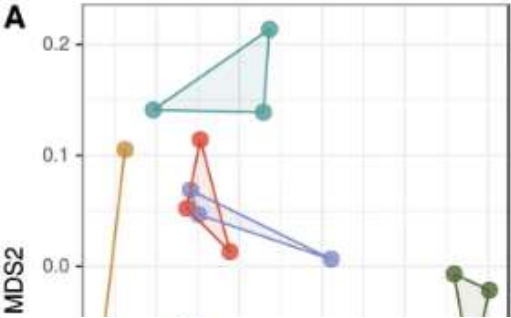
Mélanie Jean^{1,2}, Hannah Holland-Moritz¹, Michelle C. Mack¹



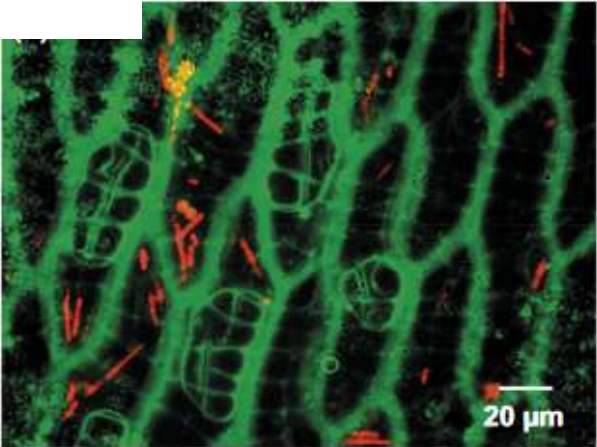
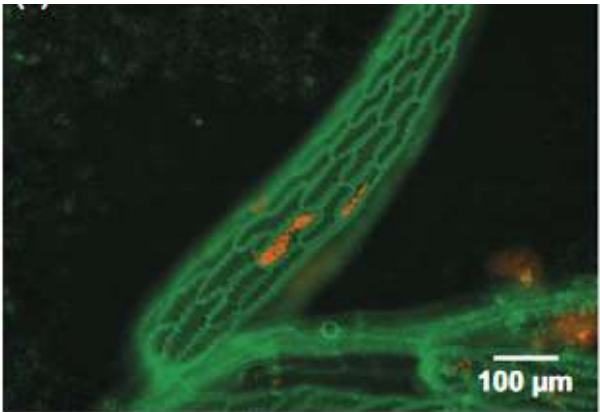
The bacterial communities of Alaskan mosses and their contributions to N₂-fixation

Hannah Holland-Moritz^{1*}, Julia E. M. Stuart², Lily R. Lewis³, Samantha N. Miller², Michelle C. Mack², Jose Miguel Ponciano⁴, Stuart F. McDaniel⁴ and Noah Fierer^{1,5}

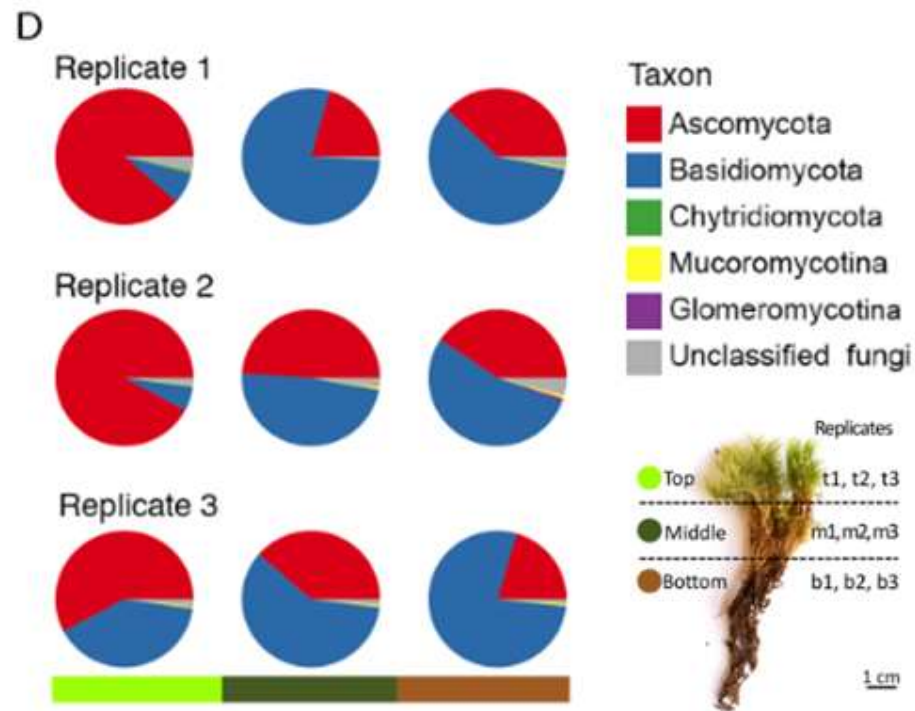
2628 H. Holland-Moritz et al.



MANOVA
= 63%,
p-value = <0.001



Moss compartments



Chen, et al. (2019)

- ❖ Green zones: photosynthetically active, frequent dry-wet cycles, cyanobacteria
- ❖ Brown zones: More consistently wet, saprotrophic fungi for organic decomposition

Mosses in mine sites

- ❖ Mine sites: harsh and dry, acidic, poor soil substrate
- ❖ Mosses can survive and tolerate this environment
- ❖ Pioneer species ?

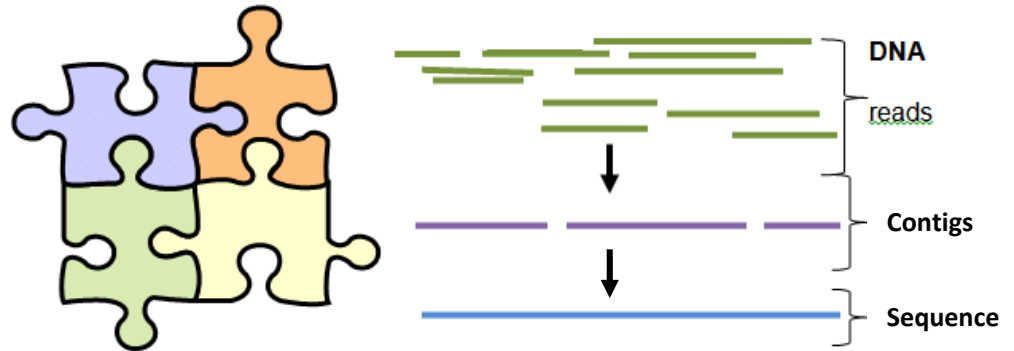
? Moss microbiome ?

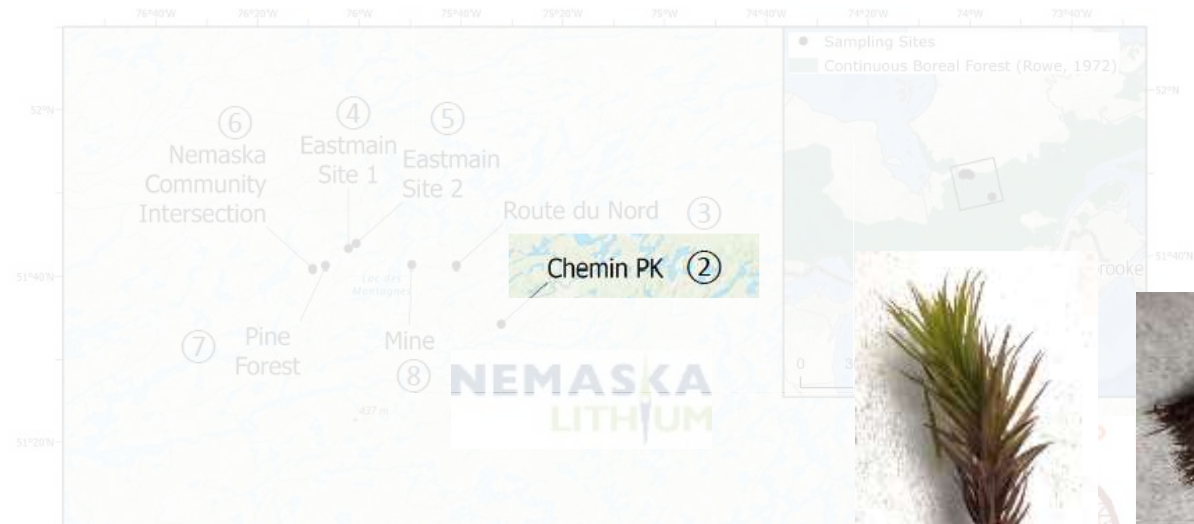


Objective

❖ Using **shotgun sequencing** to assess moss microbiome function and taxonomy

- ❖ Moss compartments
- ❖ Site types
- ❖ Host moss species





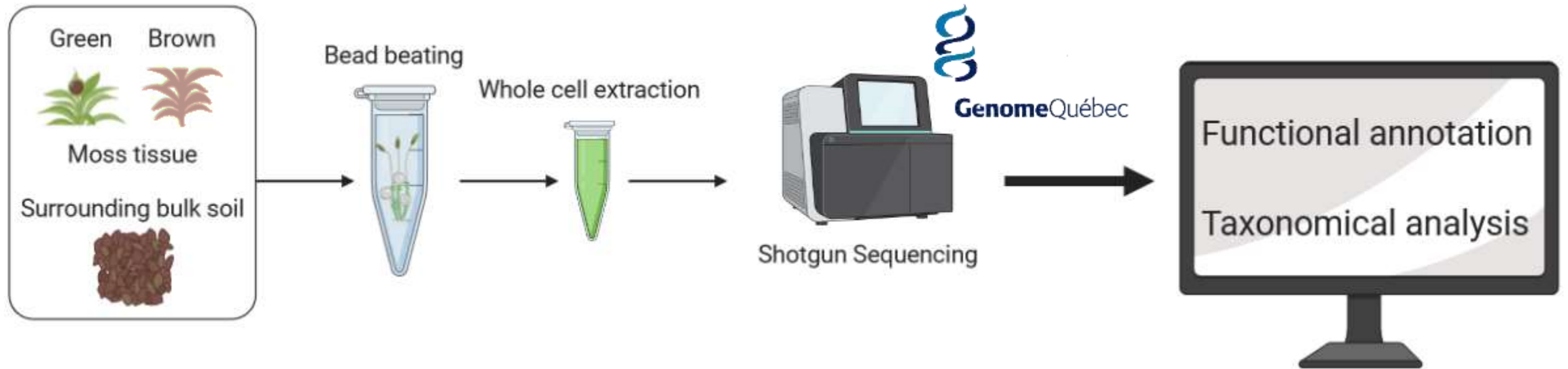
3 microsites

3 replicates

**2 moss zones
(green and brown)**



Lab extraction and sequencing procedure



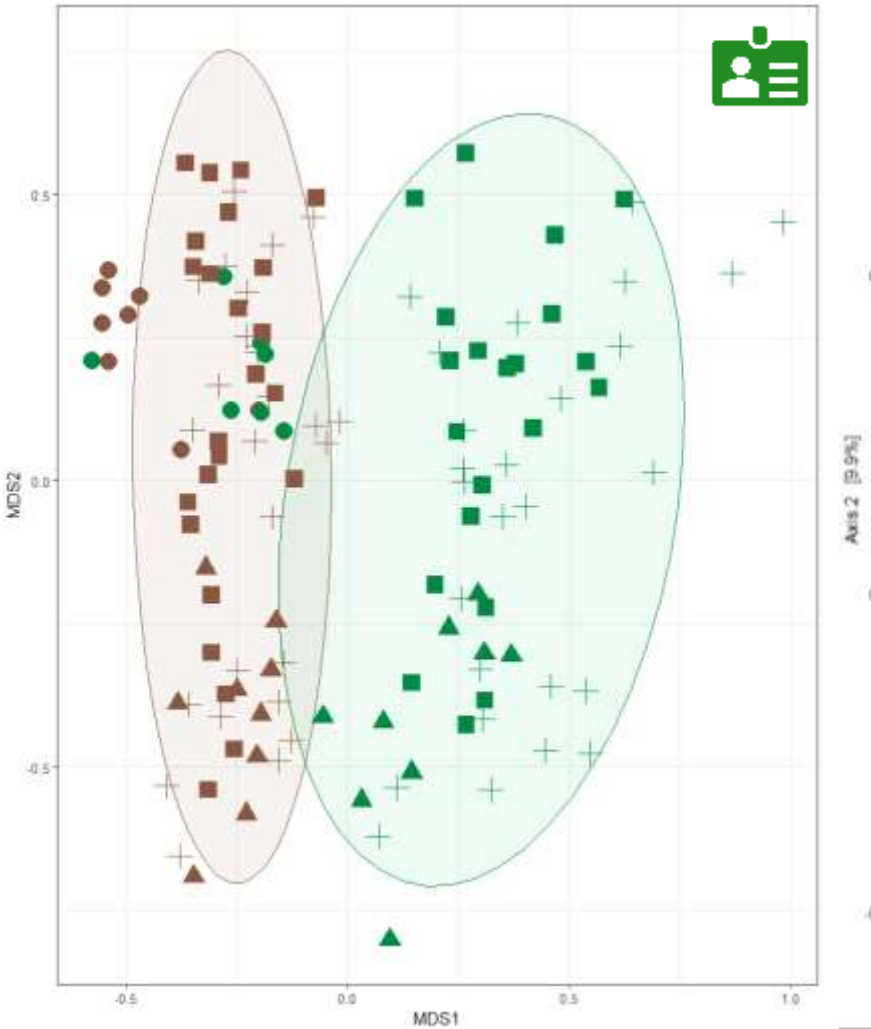
186 samples sequenced



A photograph of a forest landscape. The ground is covered in a thick layer of green moss, with some patches of bare earth or low-lying vegetation visible. The background is filled with tall, thin trees, likely pines or firs, with dense green foliage. The lighting is soft, suggesting a shaded forest environment. The word "Results" is overlaid in the center in a bright green, sans-serif font.

Results

Taxonomy



PERMANOVA

Comp: $R^2=21.9\%$, $p = 0.001$

Species: $R^2 = 17.2\%$, $p = 0.001$

Species

- *Dicranum undulatum*
- ▲ *Polytrichum commune*
- *Polytrichum juniperinum*
- + *Polytrichum piliferum*

Compartment

- Brown
- Green



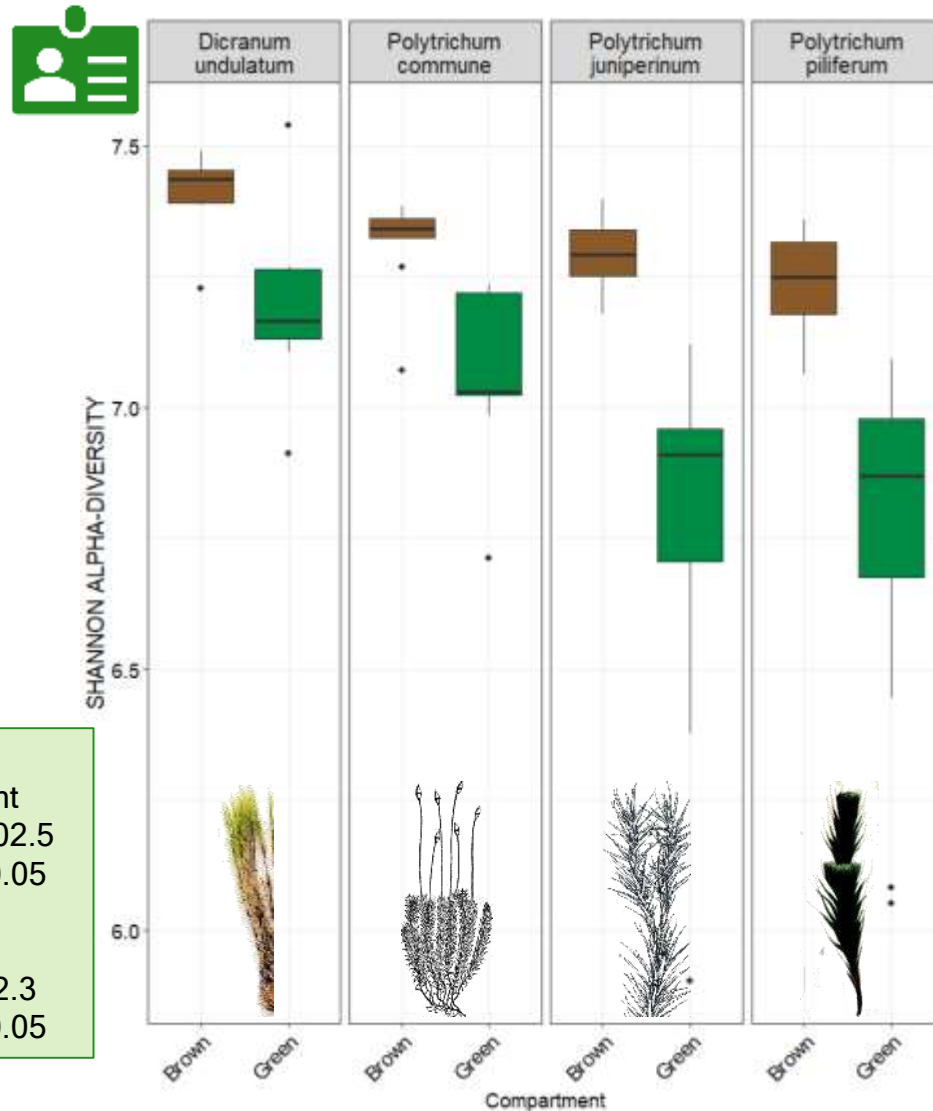
MOSS COMPARTMENT

is the main driver of both

taxonomical and

functional beta-diversity

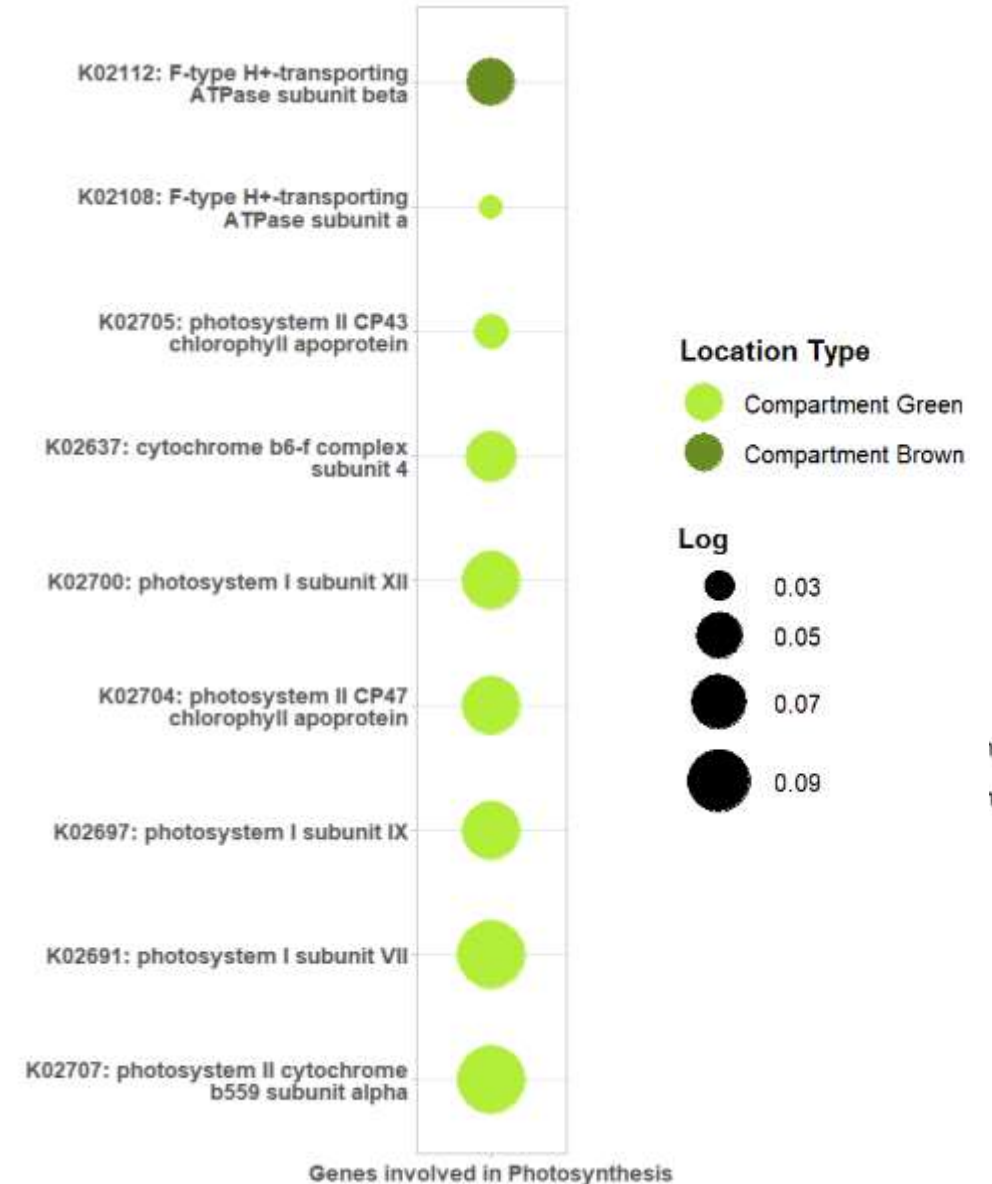
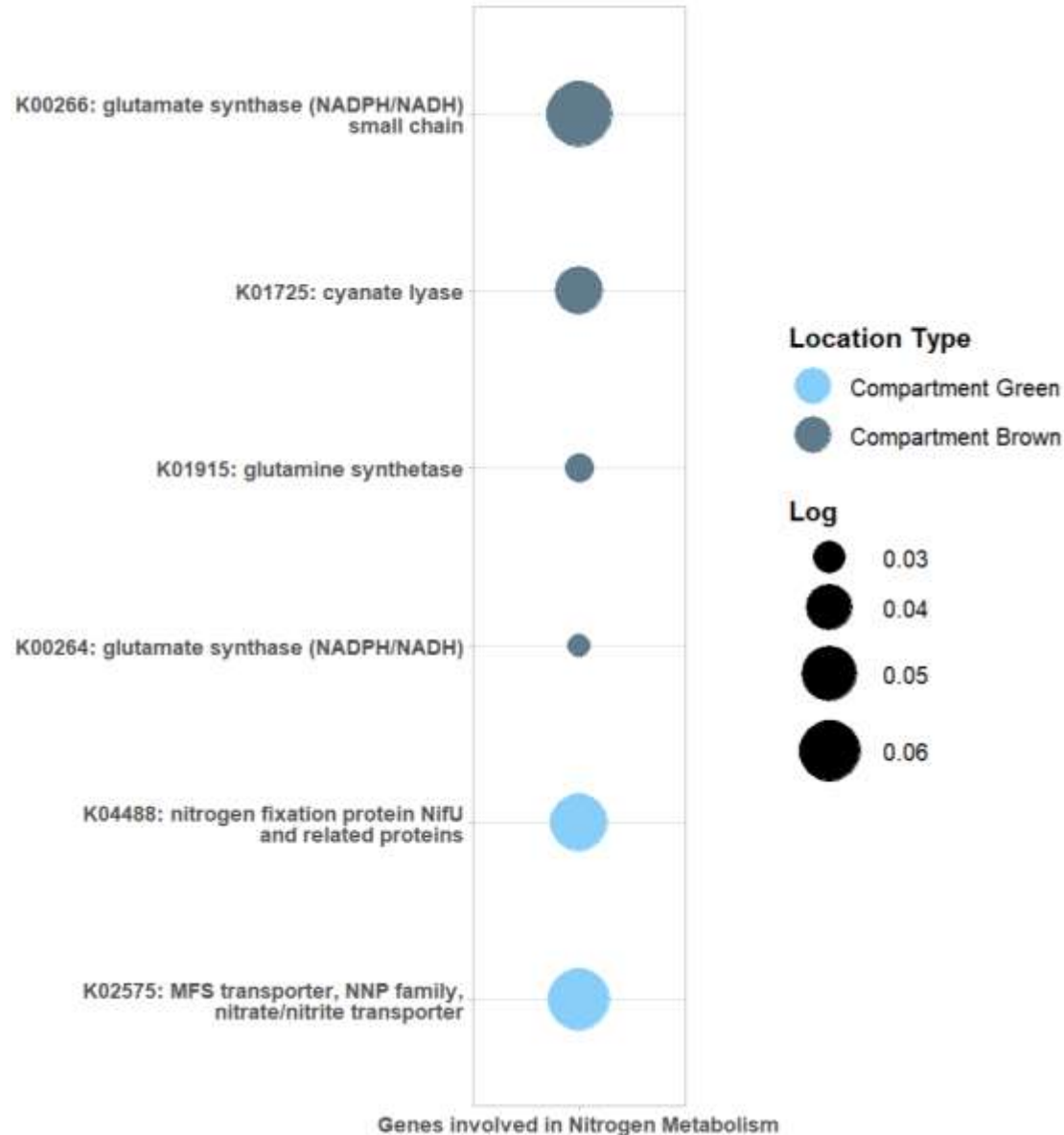
Less taxonomic and functional diversity within green compartments compared to brown compartments

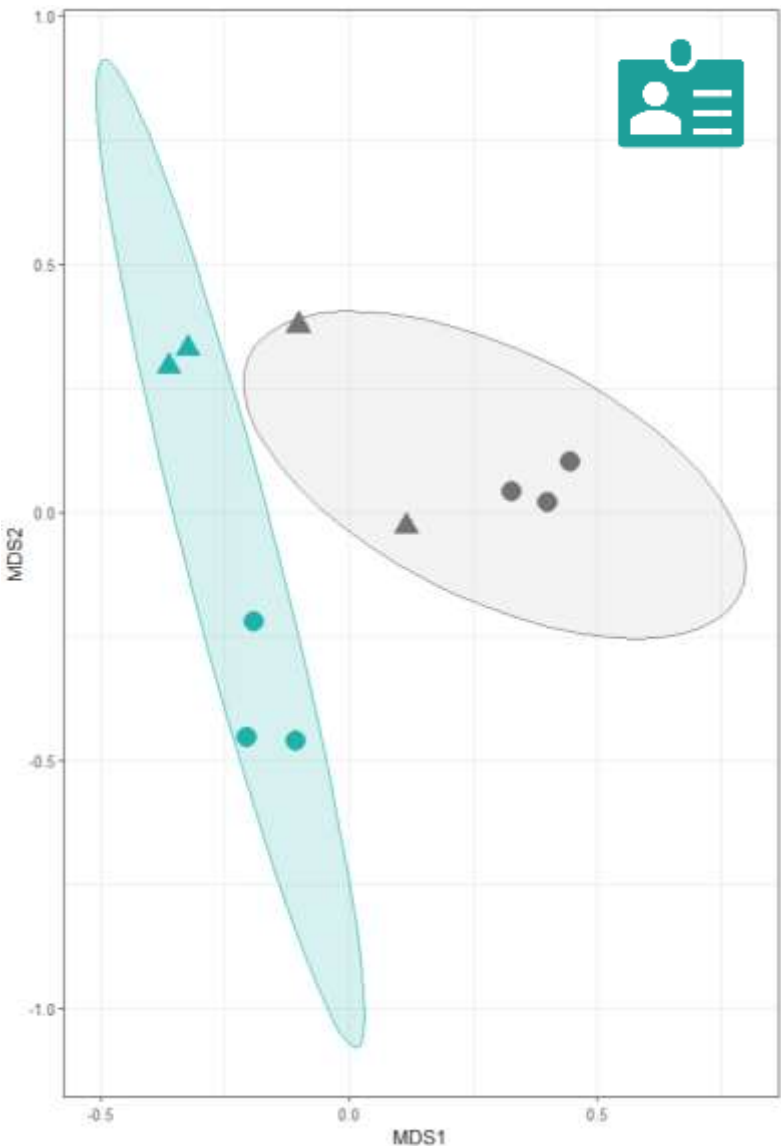


ANOVA
Compartment
Sum Sq = 102.5
p-value = <0.05

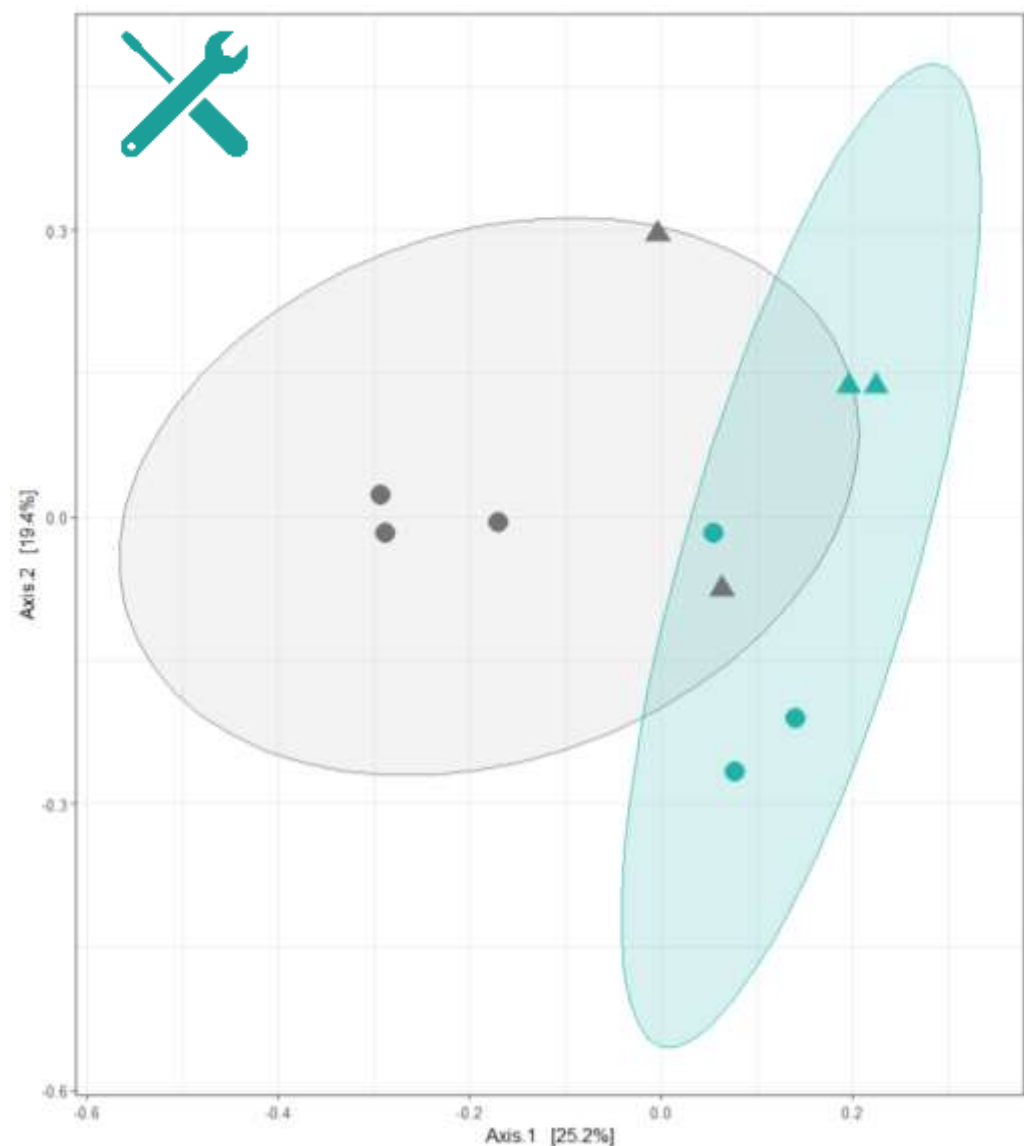
Species
Sum Sq = 22.3
p-value = <0.05

Different nitrogen metabolism processes between the different moss compartments, more photosynthetic genes in green compartments

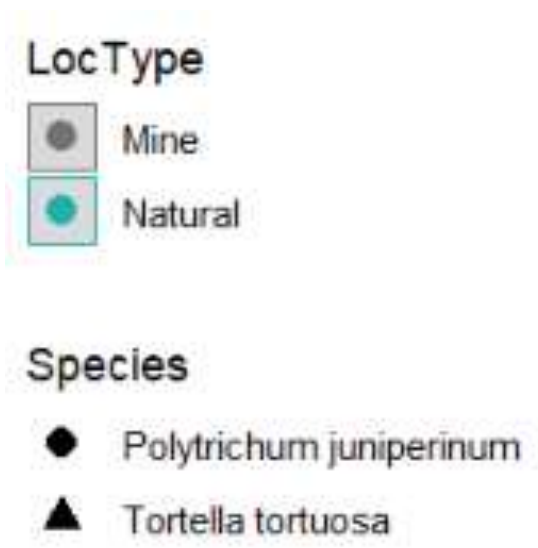




PERMANOVA:
 Site Type: $R^2=32.7\%$, $p=0.001$
 Species: $R^2=23.0\%$, $p=0.002$

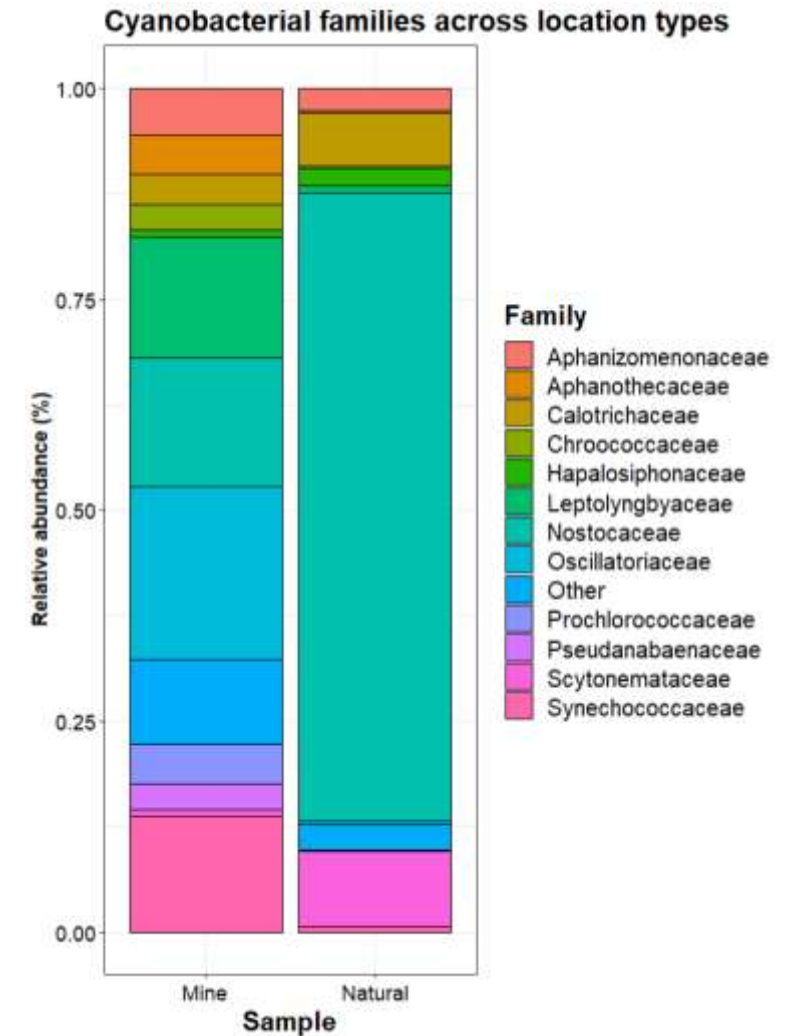
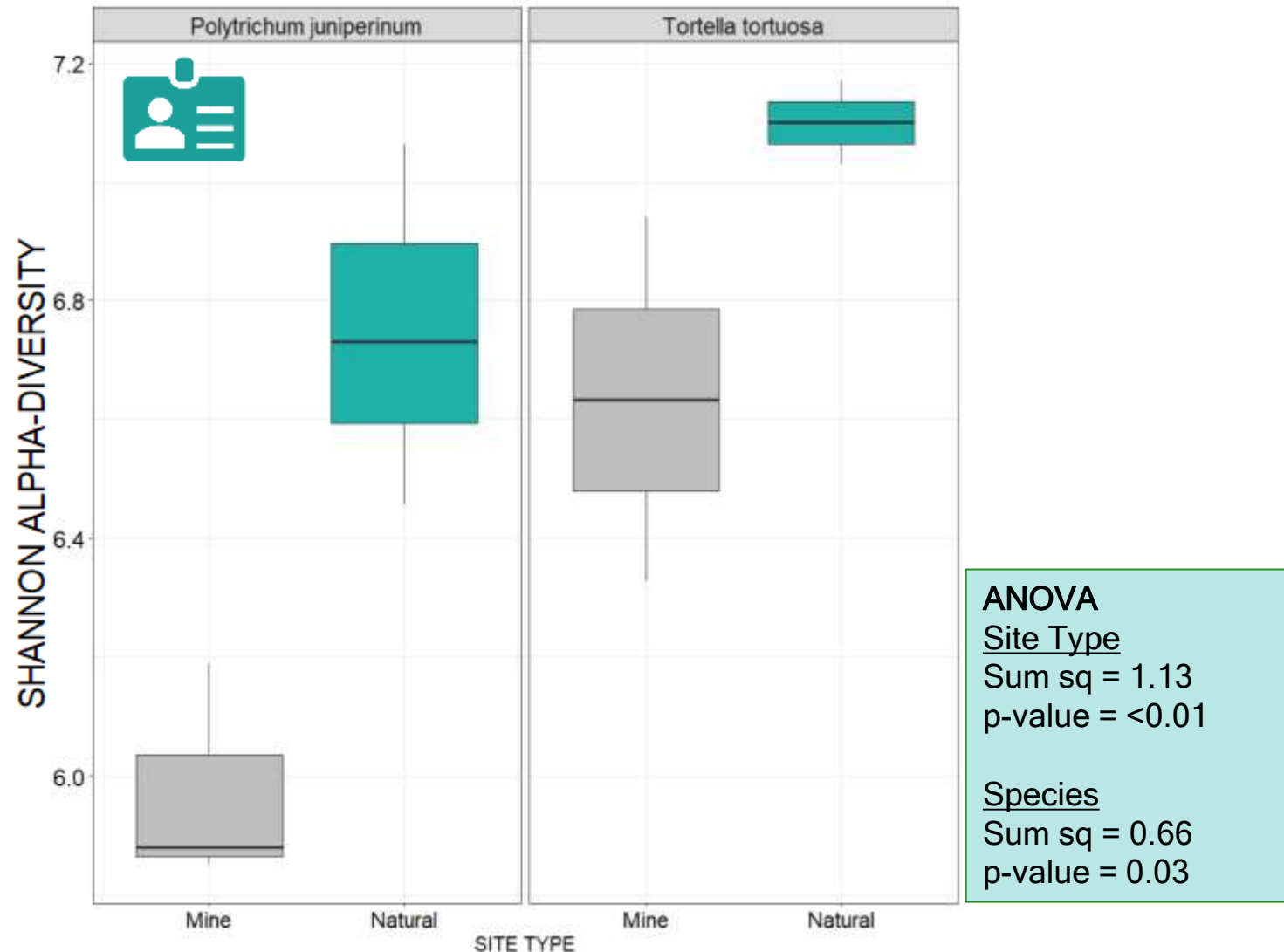


PERMANOVA:
 Site Type: $R^2=20.3\%$, $p=0.002$
 Species, $R^2=19.0\%$, $p=0.005$

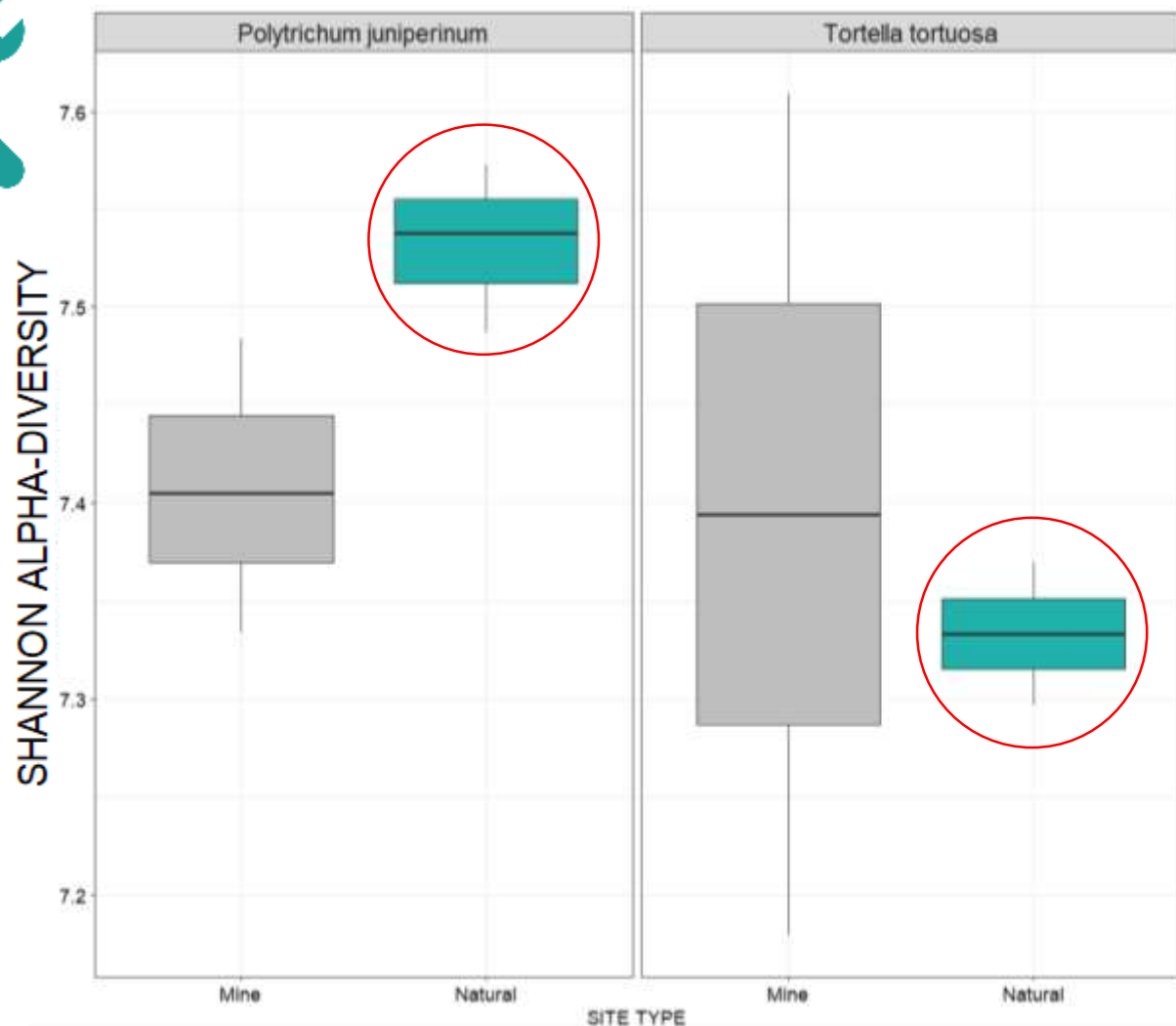


SITE TYPE is the
 main driver of
 both taxonomical
 and functional
 beta-diversity

Overall less taxonomical diversity in mine sites compared to natural sites



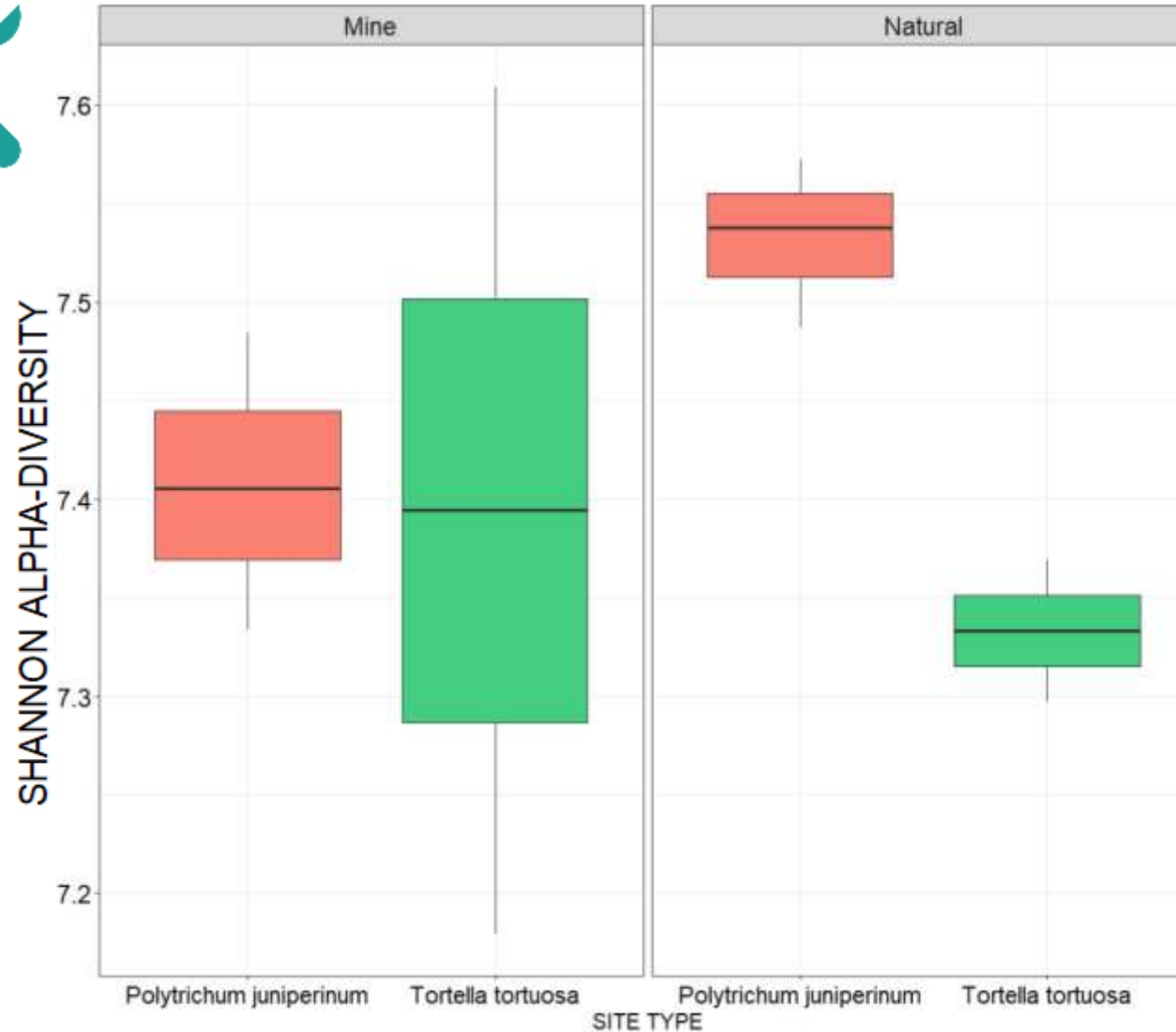
Function: Alpha-diversity differences are more prominent in *P. juniperinum* samples



ANOVA
Site Type
Chi Sq= 0.35
p-value = 0.56

Species
Chi Sq = 1.18
p-value = 0.22

Function: Species differences in functional diversity are more prominent in natural sites

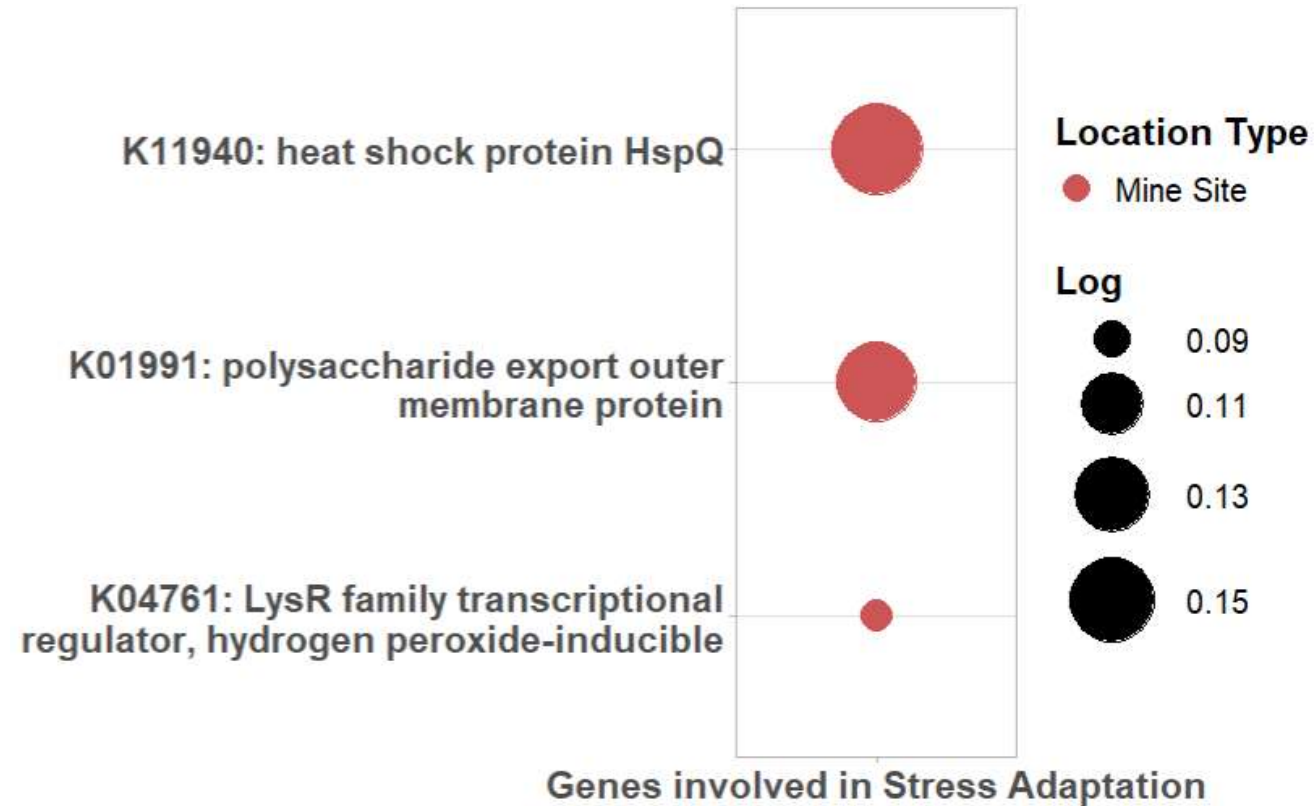


ANOVA
Site Type
Chi Sq = 0.35
p-value = 0.56

Species
Chi Sq = 1.18
p-value = 0.22

Natural sites: nitrogen-fixing genes

Mine sites: Biofilm formation genes - stress adaptation?

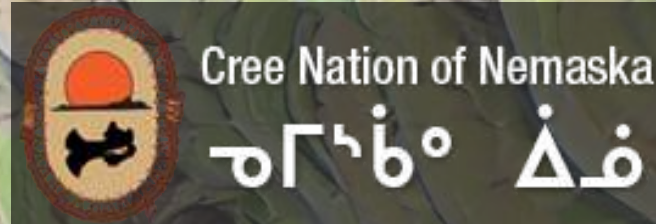


Take home messages

- ❖ Moss compartments and mine sites are very strong drivers of both taxonomic and functional diversity
- ❖ Significant differences in microbial functions between mine sites and natural sites
- ❖ Looking at specific genes can give us a better idea of the moss microbiome contribution to restoration and ecosystem functions

Acknowledgements

- ❖ Laforest-Lapointe Lab
- ❖ Sébastien Roy Lab
- ❖ Jean-Philippe Bellenger Lab



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(University of New Hampshire)
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(Université Laval)



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**Merci
beaucoup!**



Table 1: Moss sample counts for the June sampling period

	Route du Nord	Eastmain Site 1	Eastmain Site 2	Intersection	Mine Site
<i>Polytrichum juniperinum</i>				xxx (n=3)	xxx x (n=4)
<i>Polytrichum piliferum</i>		xxx (n=3)			
<i>Polytrichum commune</i>			xx (n=2)		
<i>Dicranum undulatum</i>			xxx xxx (n=6)		
<i>Racomitrium canescens</i>	xxx (n=3)				
<i>Tortella tortuosa</i>				xxx (n=3)	xxx (n=3)

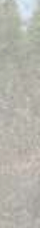
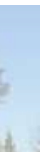
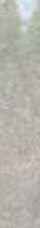
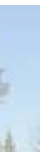
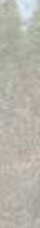
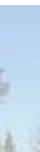
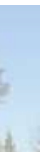
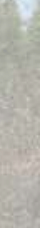
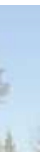
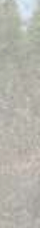
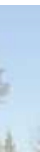
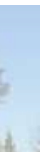
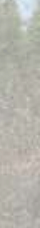
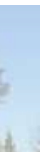
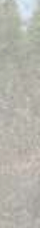
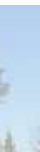
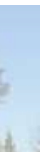
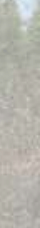
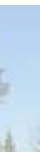
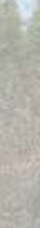
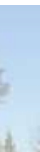
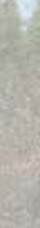
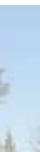
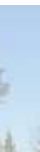
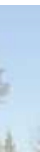
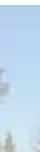
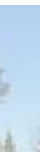
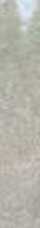
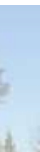
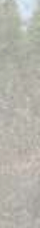
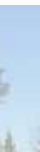
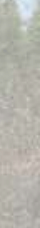
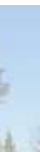
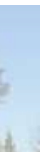
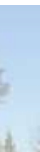
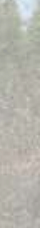
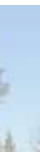
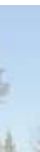
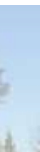
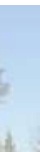
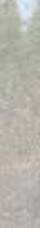
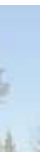
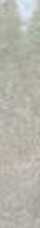
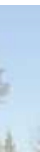
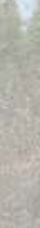
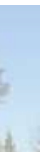
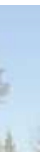
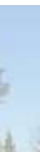
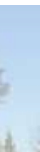
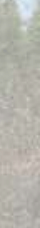
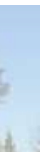
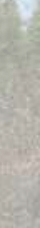
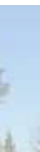
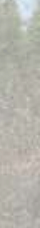
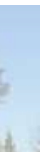
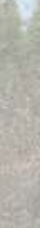
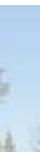
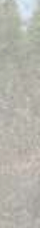
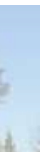
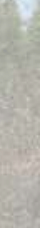
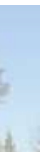
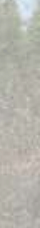
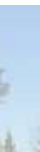
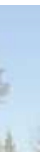
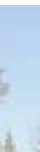
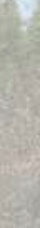
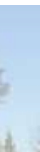
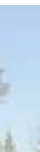
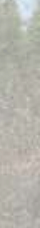
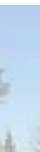
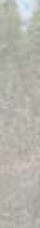
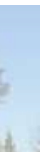
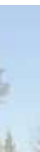
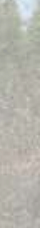
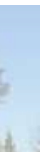
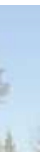
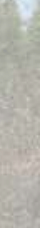
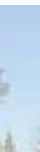
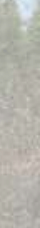
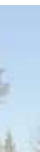
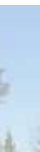
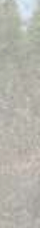
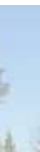
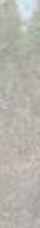
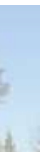
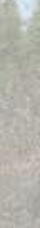
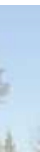
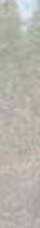
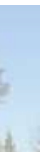
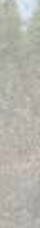
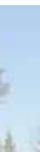
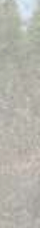
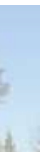
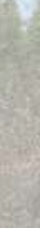
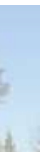
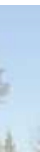
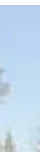
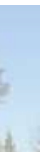
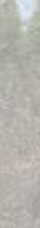
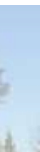
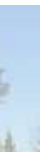
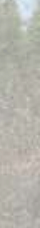
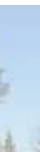
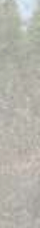
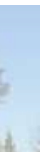
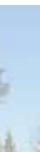
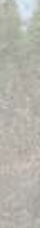
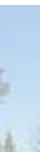
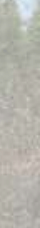
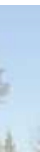
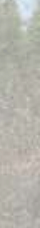
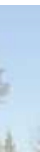
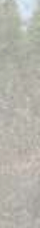
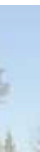
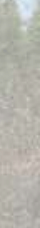
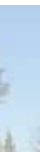
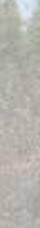
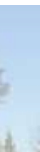
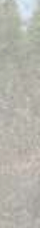
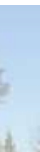
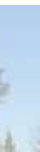
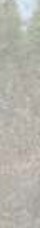
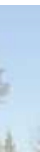
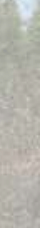
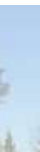
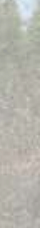
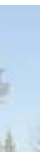
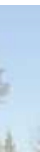
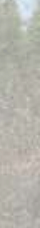
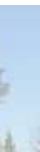
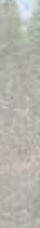
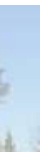
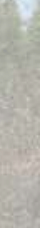
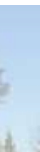
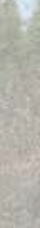
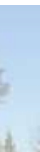
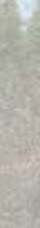
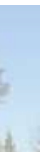
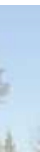
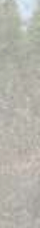
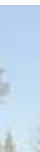
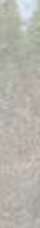
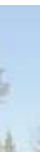
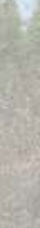
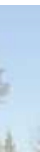
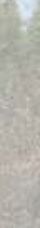
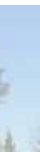
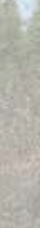
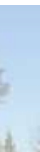
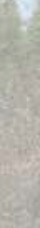
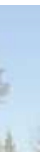
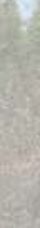
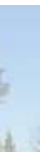
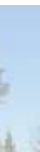
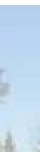
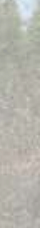
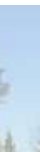
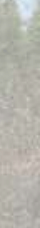
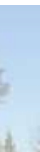
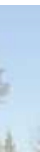
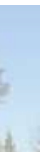
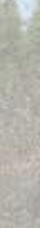
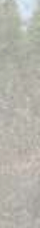
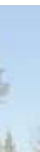
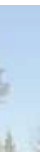
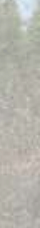
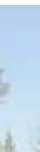
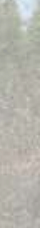
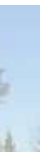


Table 2: Moss sample counts for the September sampling period.

	<i>Populus balsamifera</i> Plantation	Chemin PK	Route du Nord	Eastmain Site 1	Eastmain Site 2	Intersect	Pine Forest
Polytrichum juniperinum				xxx xxx (n=6)		xxx xxx xxx (n=9)	xxx xxx xxx (n=9)
Polytrichum piliferum		xxx xxx xxx (n=9)		xxx xxx xxx (n=9)			xxx xxx xxx (n=9)
Polytrichum commune					xxx xxx xxx (n=9)		
Dicranum undulatum					xxx xxx xxx (n=9)		
Racomitrium canescens	xxx xxx xxx (n=9)		xxx xxx xxx (n=9)				
Racomitrium ericoides			xxx xxx xx (n=8)				

Nitrogen fixation
Photosynthesis-related genes are
higher

