**Supplementary Information**  
**Title:** Drivers of C cycling in three arctic-alpine plant communities

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**Authors:** Mia Vedel Sørensen\*, Bente Jessen Graae, Aimee Classen, Brian J. Enquist, Richard Strimbeck  
**CORRESPONDING AUTHOR phone and email:**  
\*Mia Vedel Sørensen, +47 46653944, email: [miavedelsorensen@gmail.com](mailto:miavedelsorensen@gmail.com)



**Figure S1**: Sampling design and location of study area. In Dovre Mountains, Central Norway, we sampled in six blocks within each of a shrub, meadow and heath community. The sampling design of this study was part of a larger experiment that included herbivore exclosure (E) and willow transplant (T) treatments. Carbon fluxes, microclimate, and leaf traits were measured on control plots, above-ground C to N ratio was measured in harvest plots, and root biomass, microbial activity and pH was measured in samples from a separate soil pit.

**Table S1**: Effects (µmol m-2 s-1) SD-1of each variable in full models within community. Explanatory variables were z-standardized (x- mean(x))/sd(x)) so one unit change corresponds to one SD. Models were run without log transformation to ease understanding of the effects. Sum of squares (ꭓ2) and *p*-values were derived from a likelihood-ratio test (Chi square test) performed on backward model selection (drop1 function in R). Significant effects are bold.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  | **Heath (n = 6)** | | | | **Meadow (n = 6)** | | | | **Shrub (n = 5)** | | | |
| **Response** | **Explanatory variable** | **Effect**  **(µmol m-2 s-1) SD-1** | **SE** | **ꭓ2(1)** | ***p*-value** | **Effect**  **(µmol m-2 s-1) SD-1** | **SE** | **ꭓ2(1)** | ***p*-value** | **Effect**  **(µmol m-2 s-1) SD-1** | **SE** | **ꭓ2(1)** | ***p*-value** |
| GEP600 | (Intercept) | 10.16 | 6.65 |  |  | -4.76 | 21.86 |  |  | 7.98 | 2.65 |  |  |
| zSLACWM | 3.32 | 5.86 | 1.33 | 0.345 | 1.37 | 3.27 | 0.99 | 0.478 | 5.74 | 2.28 | 2.41 | **0.002** |
| zMoisture | 1.01 | 3.17 | 0.42 | 0.586 | 6.91 | 8.95 | 3.38 | 0.211 | 3.49 | 1.42 | 2.29 | **0.002** |
| zBiomassabove | -5.24 | 5.18 | 4.24 | 0.116 | -16.23 | 22.80 | 2.88 | 0.244 | 0.85 | 1.90 | 0.08 | 0.340 |
| Rabove | (Intercept) | 2.25 | 1.34 |  |  | 1.02 | 0.64 |  |  | 2.98 | 0.74 |  |  |
| zSLACWM | 0.93 | 1.14 | 0.11 | 0.276 | 0.04 | 0.11 | 0.00 | 0.604 | 0.70 | 0.77 | 0.19 | 0.190 |
| zBiomassabove | -1.57 | 0.99 | 0.43 | **0.057** | 0.62 | 0.62 | 0.015 | 0.190 | -0.71 | 0.56 | 0.38 | 0.085 |
| Rbelow | (Intercept) | 4.17 | 2.56 |  |  | 6.54 | 2.06 |  |  | 2.38 | 0.09 |  |  |
| zSLACWM | 1.22 | 2.37 | 0.06 | 0.389 | -0.16 | 1.49 | 0.05 | 0.853 | 1.94 | 0.11 | 4.28 | **< 0.001** |
| zBiomassroots | 0.20 | 0.22 | 0.18 | 0.157 | 0.62 | 1.23 | 0.99 | 0.401 | -0.12 | 0.09 | 0.03 | **0.022** |
| zMicrobessum | 0.10 | 0.51 | 0.01 | 0.742 | -1.01 | 1.05 | 3.72 | 0.129 | -0.87 | 0.15 | 0.48 | **< 0.001** |



**Figure S2:** Mean enzyme activity ± SD (a, c) in organic and (b, d) in mineral horizons for alpine *Empetrum*-dominated heath, meadow and *Salix*-shrub plant communities in Dovre Mountains, Central Norway. Activity for each enzyme is the sum across the total soil pit with mean depth 56 ± 8 cm (n = 17). Note different units top: (nmol h-1 m-2), and bottom: mol h-1 gC-1 m-2. Mineral soil is defined as LOI < 20 %. See statistical differences in Table 6 and Table S2.

**Table S2:** F-value, degrees of freedom and *p*-value from one-way ANOVA tests of differences among enzyme activities (nmol h-1 gC-1 m-2) between communities. The enzymes were from organic and mineral horizons, and total across the soil pit. The significant differences are bold.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Horizon** | **Enzyme** | **F-value** | **dfnum** | **dfden** | ***p*-value** |
| Organic | a-gluc | 0.67 | 2 | 13 | 0.53 |
| b-gluc | 0.24 | 2 | 13 | 0.79 |
| cbh | 2.73 | 2 | 13 | 0.10 |
| xylo | 1.94 | 2 | 13 | 0.18 |
| nag | 0.11 | 2 | 13 | 0.89 |
| Mineral | a-gluc | **4.36** | **2** | **15** | **0.03** |
|  | b-gluc | 3.44 | 2 | 15 | 0.06 |
|  | cbh | 1.12 | 2 | 15 | 0.35 |
|  | xylo | 1.41 | 2 | 15 | 0.28 |
|  | nag | 2.49 | 2 | 15 | 0.12 |
| Total | a-gluc | **3.99** | **2** | **15** | **0.04** |
|  | b-gluc | 3.35 | 2 | 15 | 0.06 |
|  | cbh | 1.43 | 2 | 15 | 0.27 |
|  | xylo | 0.56 | 2 | 15 | 0.58 |
|  | nag | 1.23 | 2 | 15 | 0.32 |

**Figure S3**

**Figure S3:** Enzyme activity (nmol h-1 m2) sampled over depth from surface (m). The data point of a-gluc in the red circle was removed (from block 4 in the heath) since it was driving the pattern in the PCA and because it was inexplicably high. We decided not to remove other outliers, due to the small sample sizes.