

Short-term effects of non-grazing on plants, soil biota and aboveground-belowground links in Atlantic mountain grasslands

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Supplementary Table S1. Summary of the linear mixed-effect models on the 20 most abundant taxa in the plant, prokaryotic and fungal communities. Statistically significant results (p-value < 0.05) appear in bold.

Plants			Prokaryotes			Fungi		
Species	t-value	p-value	Order	t-value	p-value	Order	t-value	p-value
<i>Agrostis capillaris</i>	-0.095	0.925	Acidobacteriales	-1.838	0.078	Archaeorhizomycetales	-0.710	0.484
<i>Festuca gr. rubra</i>	0.282	0.781	Planctomycetales	0.297	0.769	Mortierellales	0.474	0.639
<i>Agrostis curtisii</i>	-3.145	0.004	Chthoniobacterales	0.273	0.787	Agaricales	0.010	0.992
<i>Galium saxatile</i>	-0.614	0.545	Rhizobiales	0.533	0.598	Pezizales	0.170	0.867
<i>Holcus lannatus</i>	1.749	0.092	Ktedonobacterales	-0.224	0.825	Filobasidiales	-0.812	0.424
<i>Potentilla erecta</i>	-0.432	0.670	Frankiales	-0.185	0.855	Hypocreales	0.791	0.436
<i>Brachypodium pinnatum</i>	2.598	0.015	Xanthomonadales	-0.976	0.338	Helotiales	-0.336	0.740
<i>Trifolium repens</i>	-3.165	0.004	Sphingobacteriales	-0.226	0.823	Sordariales	-0.746	0.462
<i>Danthonia decumbens</i>	-3.290	0.003	Rhodospirillales	1.736	0.094	Glomerales	-0.260	0.797
<i>Ranunculus repens</i>	2.039	0.052	WD2101 soil group	-0.016	0.987	Saccharomycetales	-0.352	0.728
<i>Lotus corniculatus</i>	1.769	0.089	Myxococcales	0.454	0.653	Pleosporales	-1.504	0.145
<i>Potentilla montana</i>	-1.165	0.255	Bacillales	0.401	0.691	Trichosporonales	1.098	0.282
<i>Carex caryophillea</i>	-3.582	0.001	WD272	1.723	0.097	Dothideales	-0.008	0.994
<i>Erica vagans</i>	2.057	0.050	GR-WP33-30	1.002	0.326	Paraglomerales	0.286	0.777
<i>Rumex acetosella</i>	-1.107	0.278	Solirubrobacterales	0.527	0.602	Chaetothyriales	2.110	0.045

<i>Glechoma hederacea</i> L.	-0.832	0.413	Burkholderiales	0.371	0.714	Eurotiales	2.292	0.030
<i>Carex</i> sp.	-1.227	0.231	AKIW543	0.654	0.519	Cantharellales	-0.646	0.524
<i>Plantago lanceolata</i>	-1.118	0.274	Corynebacteriales	-0.126	0.901	Xylariales	-1.369	0.183
<i>Veronica persica</i>	1.305	0.203	Cytophagales	1.029	0.313	Trechisporales	-0.925	0.364
<i>Ranunculus acris</i> L.	1.656	0.110	Nitrosomonadales	-0.329	0.745	Geoglossales	0.570	0.573

Supplementary Table S2. Mantel's correlations (R statistic) and corresponding p-values, comparing community composition across datasets.

		Plants	Prokaryotes	Fungi	Glomeromycota	CLPPs bacteria	AM spore morphotypes	p-value
All plots	Mantel's correlation		0.000	0.000	0.000	0.037	0.000	
	Plants							
	Prokaryotes	0.70		0.000	0.000	0.000	0.000	
	Fungi	0.58	0.62		0.000	0.001	0.003	
	Glomeromycota	0.52	0.63	0.39		0.137	0.005	
	CLPPs bacteria	0.15	0.31	0.22	0.13		0.139	
	AM spore morphotypes	0.34	0.37	0.17	0.26	0.09		
Only grazed	Mantel's correlation		0.000	0.000	0.001	0.002	0.001	
	Plants							
	Prokaryotes	0.78		0.000	0.001	0.002	0.001	
	Fungi	0.81	0.53		0.005	0.022	0.009	
	Glomeromycota	0.42	0.56	0.23		0.336	0.035	
	CLPPs bacteria	0.35	0.39	0.21	0.07		0.168	
	AM spore morphotypes	0.44	0.49	0.26	0.27	0.11		
Only non-grazed	Mantel's correlation		0.000	0.000	0.000	0.061	0.010	
	Plants							
	Prokaryotes	0.83		0.000	0.000	0.008	0.020	
	Fungi	0.51	0.66		0.004	0.011	0.538	
	Glomeromycota	0.64	0.72	0.27		0.057	0.038	
	CLPPs bacteria	0.21	0.35	0.24	0.28		0.168	
	AM spore morphotypes	0.29	0.25	-0.01	0.28	0.14		

Supplementary Table S3. UTM coordinates of the 16 sampling sites.

Site	Replicate	X coordinate	Y coordinate
Oderiaga	1	511426	4768058
Oderiaga	2	510893	4766822
Oderiaga	3	511421	4766920
Oderiaga	4	511579	4766921
Usotegieta	1	514633	4765144
Usotegieta	2	514589	4765222
Usotegieta	3	514289	4765311
Usotegieta	4	514632	4765363
Arimegorta	1	519423	4766255
Arimegorta	2	519810	4766101
Arimegorta	3	519973	4765910
Arimegorta	4	519976	4765821
Ipiñaburu-Urigoiti	1	520671	4768648
Ipiñaburu-Urigoiti	2	520778	4768493
Ipiñaburu-Urigoiti	3	512463	4770543
Ipiñaburu-Urigoiti	4	512405	4770469

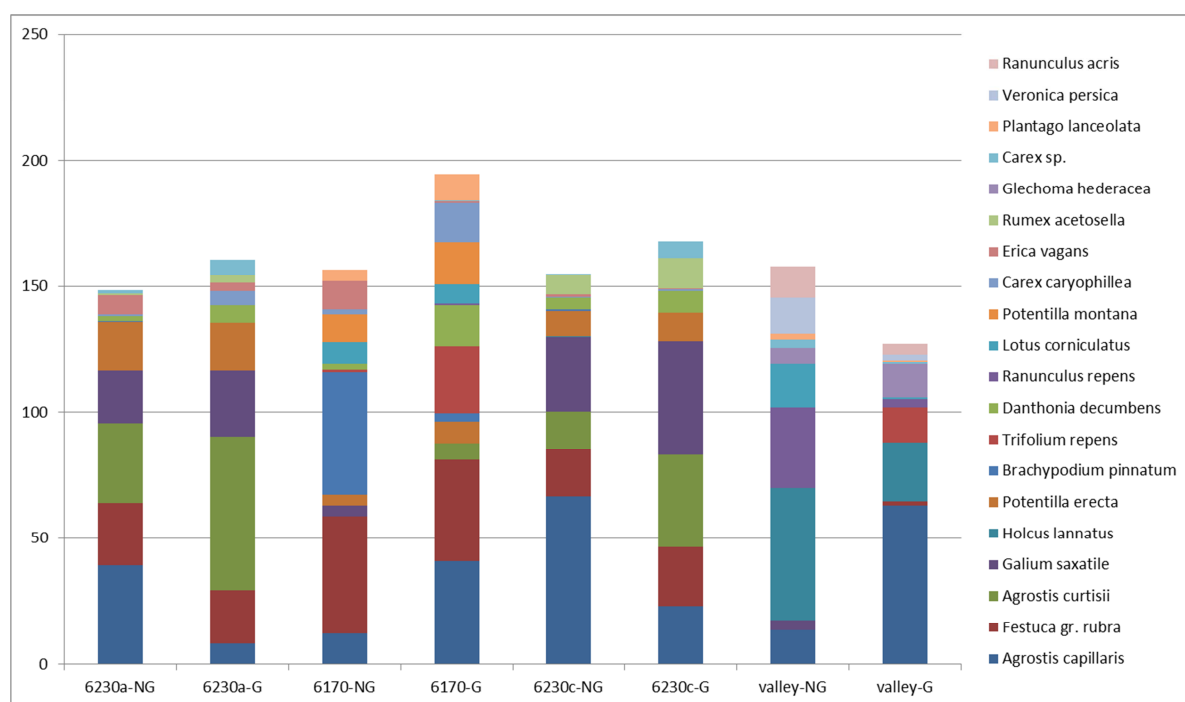
Supplementary Figure Legends

Supplementary Figure S1. Barplots representing the distribution of the 20 most abundant taxa. A: plant community, species level, percentage cover; B: prokaryotic community, order level, relative abundance; C: fungal community, order level, relative abundance. Average values ($n = 4$).

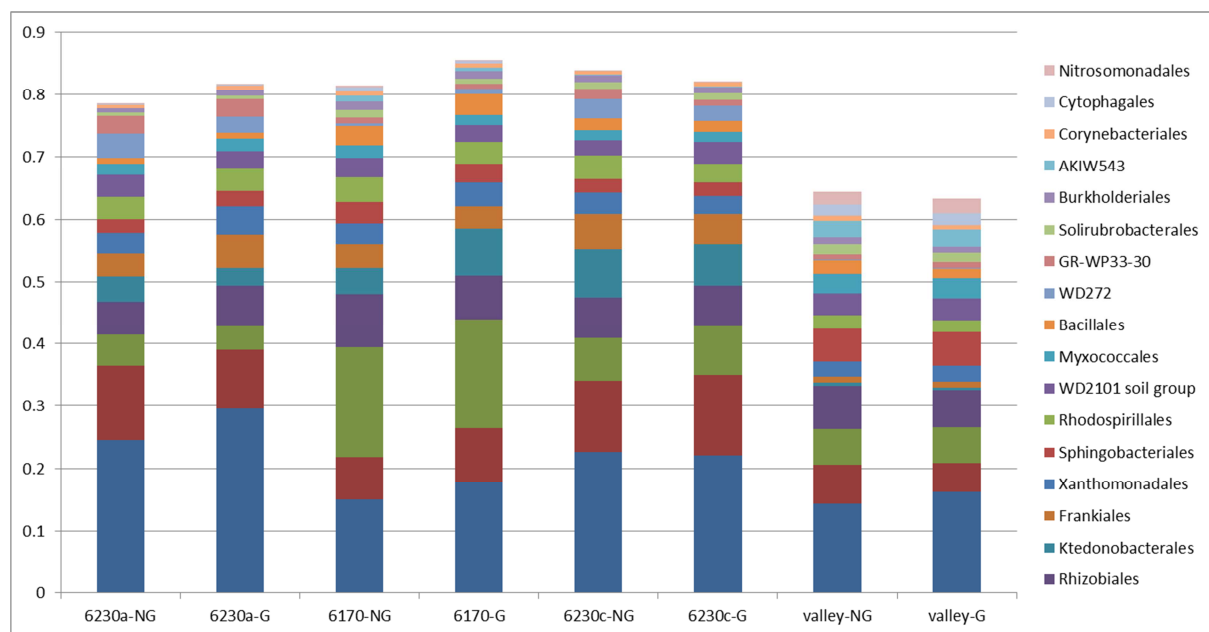
Supplementary Figure S2. Biplot of the partial canonical analysis performed with plant community composition as response variables, grazing as explanatory variable, and site as covariable (pseudo-F = 2.4, p-value = 0.002). Only the 15 response variables with best fit are shown. Variation explained by the first axis is indicated between brackets.

Supplementary Figure S3. Biplot of the redundancy analysis performed with (A) Glomeromycota community composition at the species level (pseudo-F = 5.7, p-value = 0.002), (B) CLPPs of bacteria (pseudo-F = 2.3, p-value = 0.002), and (C) arbuscular mycorrhizal spore morphotype abundances (pseudo-F = 2.6, p-value = 0.002) as response variables, with grazing, bedrock and habitat as explanatory variables. Variation explained by each axis is indicated between brackets. The explanatory variables that appear are those that significantly explained the variation in response data following forward selection; the contribution percentage of each variable is shown between brackets.

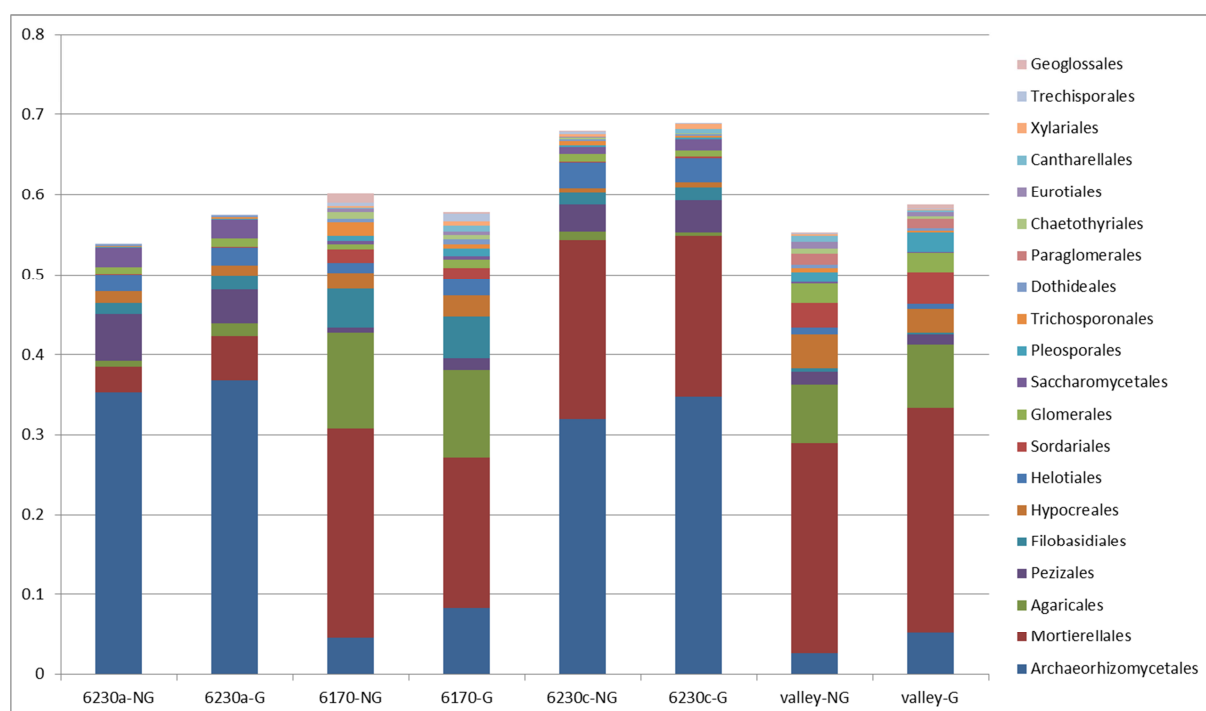
A)



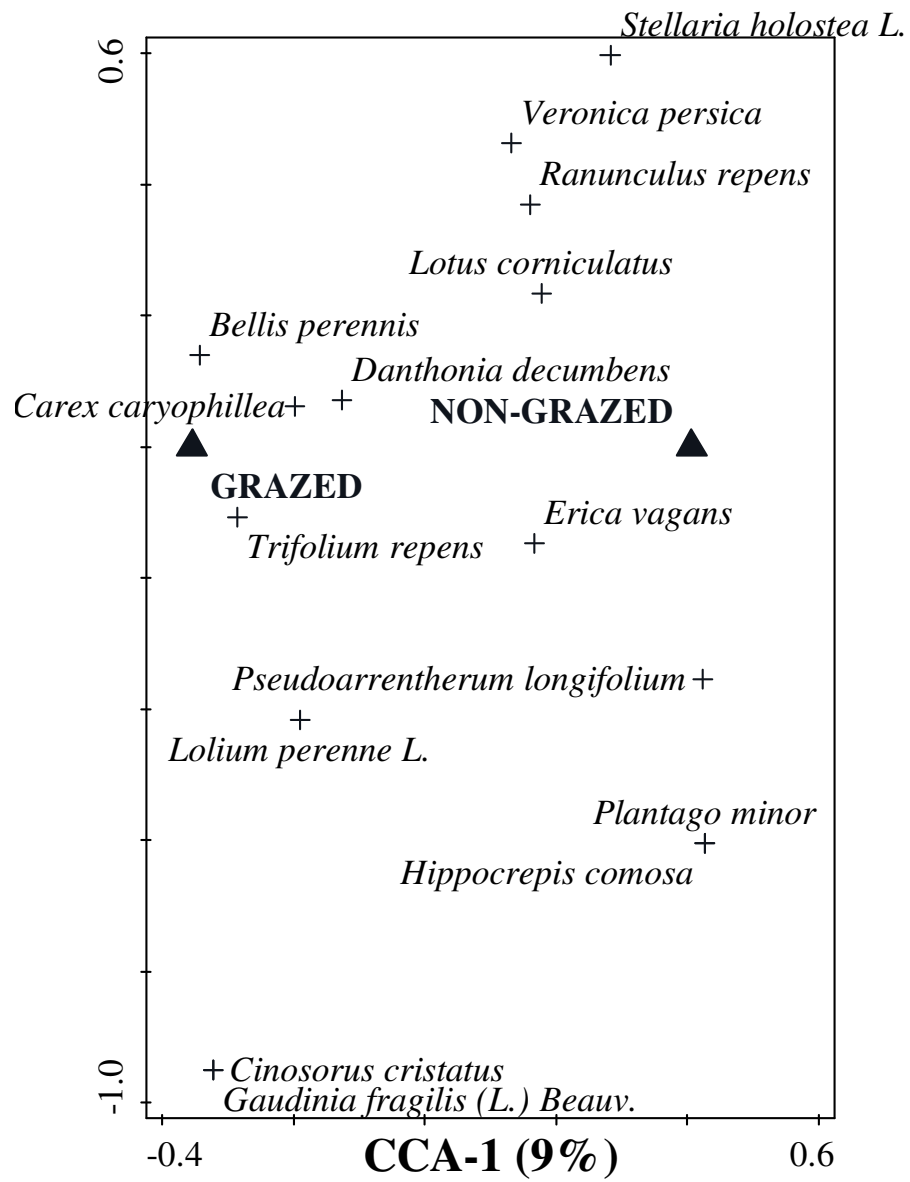
B)



C)



SUPPLEMENTARY FIGURE S1



SUPPLEMENTARY FIGURE S2

