

Supplementary data

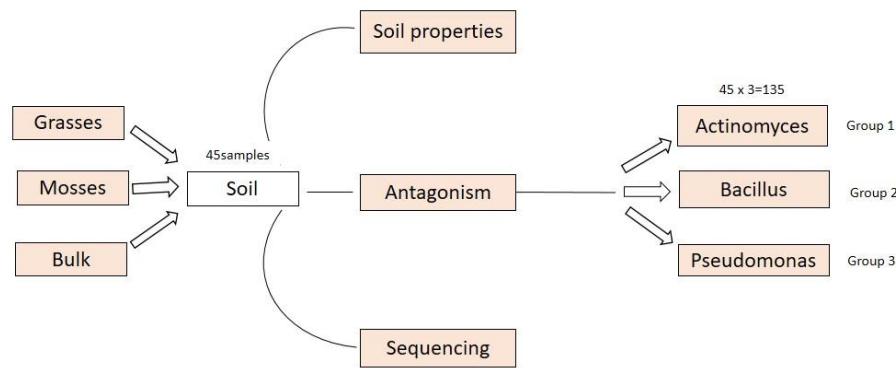


FIGURE S1 Flow chart for soil distribution (n=135)

Table S1 Hypothesis liable for the structural equation model (Pathways referred to Figure S2).

Number	Reference
Pathway 1	(Mendes et al. 2011), (Latz et al. 2016), (Latz et al. 2012)
Pathway 2	(Janvier et al. 2007)
Pathway 4-3	(Bueno et al. 2016), (Benavent-González et al. 2018)
Pathway 4-6	(Tian and Li 2017), (Opelt and Berg 2004)
Pathway 5-3	(Latz et al. 2016), (Lange et al. 2014), (Pérès et al. 2013)
Pathway 5-6	(Latz et al. 2012), (Eisenhauer et al. 2010), (Latz et al. 2016)

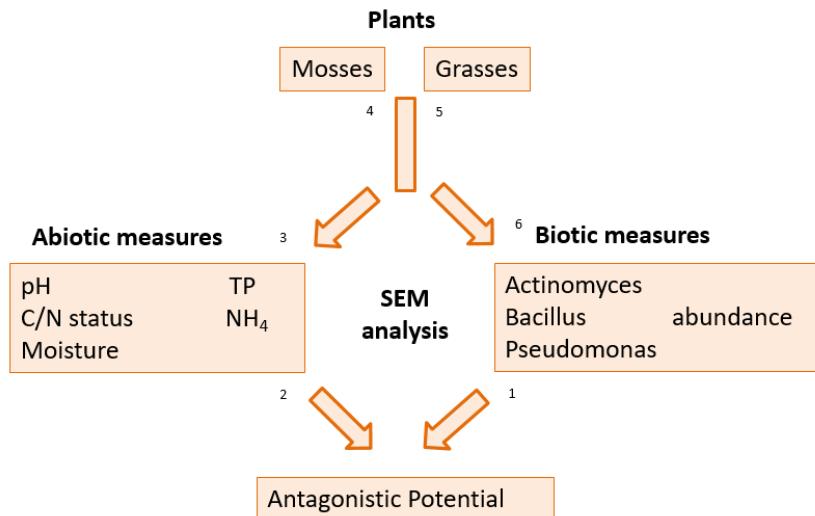


FIGURE S2 The conceptual figure of structural equation models shows that plant community composition may affect bacterial antagonistic potential via soil abiotic and biotic measures. Numbers (1,2,3...) near each arrow represent pathways. Abbreviations: C/N, carbon/nitrogen ratio; TP, total phosphorus; NH₄⁺, ammonium; SEM, structure equation modeling

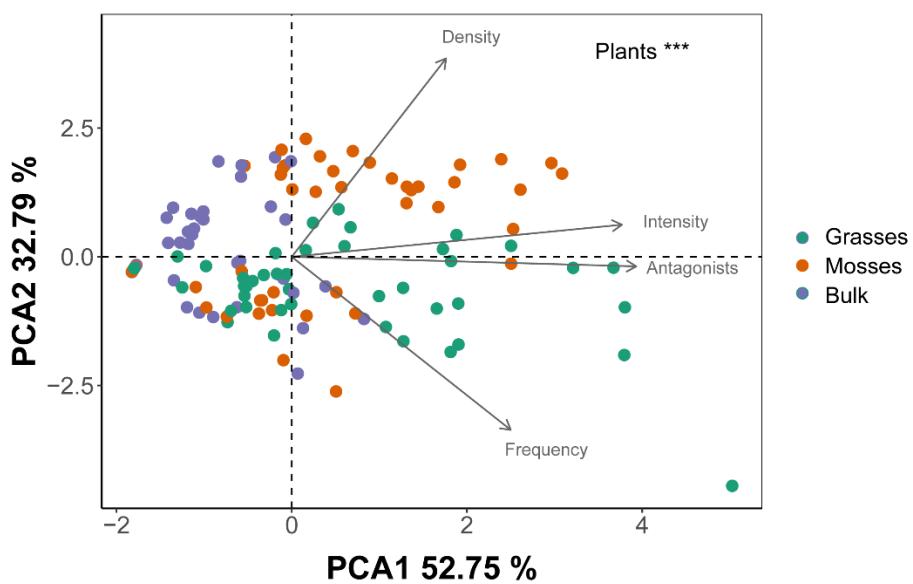


FIGURE S3 Principal component analysis (PCA) using PERMANOVA showing dominant plants effects on combined bacterial antagonism (n=135).

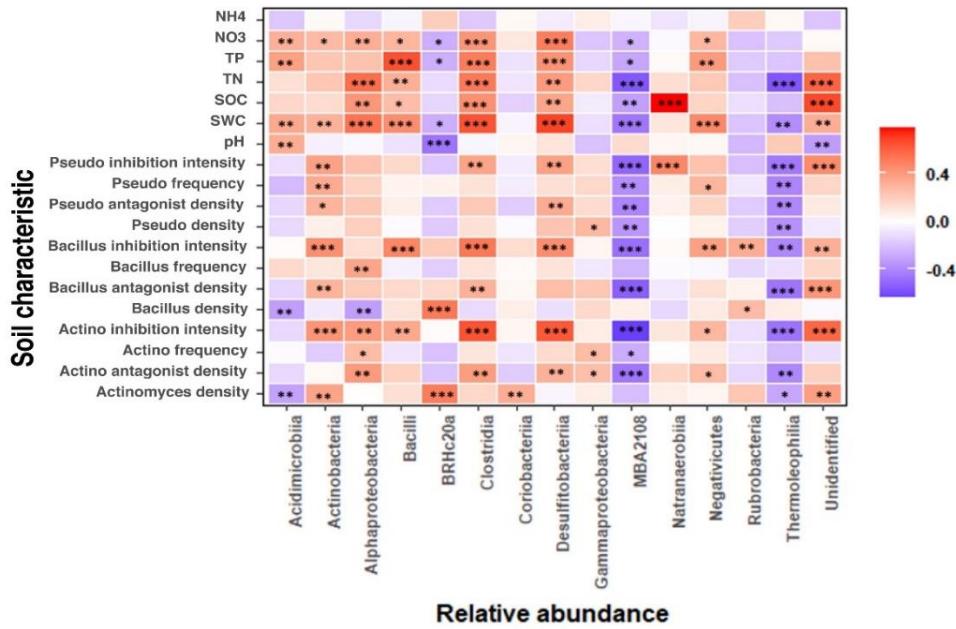


FIGURE S4 Heatmap with Pearson correlation showing the relationship between bacterial relative abundance at the class level and soil characteristics and indices of bacterial antagonism (* $P < 0.1$, ** $P < 0.05$, *** $P < 0.001$)

Table S2 Overview of dominant plant effects on soil edaphic properties (mean \pm SE). The boldface means significant effects of dominant plants ($P < 0.05$). Abbreviation: SWC, moisture; SOC, organic carbon, TN, total nitrogen; TP, total phosphorus; NO_3^- , nitrates; NH_4^+ , ammonium

	Bulk	Mosses	Grasses	P-value
Edaphic properties				
SWC (%)	0.17 ± 0.04	0.23 ± 0.11	0.20 ± 0.06	0.0016
SOC (mg/g)	8.80 ± 4.57	15.7 ± 8.33	19.2 ± 19.9	0.0378
TN (mg/g)	1.05 ± 0.41	1.97 ± 1.00	2.29 ± 1.27	< 0.001
TP (mg/g)	0.76 ± 0.26	0.77 ± 0.24	0.74 ± 0.16	0.8738
$\text{NO}_3^- (\text{mg/g})$	41.3 ± 19.4	48.2 ± 27.9	33.5 ± 17.7	0.1207
$\text{NH}_4^+ (\text{mg/g})$	14.2 ± 7.80	14.9 ± 4.96	14.5 ± 4.87	< 0.001
pH	7.41 ± 0.12	7.38 ± 0.17	7.11 ± 0.16	< 0.001

References

- Benavent-González A, Delgado-Baquerizo M, Fernández-Brun L, et al (2018) Identity of plant, lichen and moss species connects with microbial abundance and soil functioning in maritime Antarctica. *Plant Soil* 429:35–52.
<https://doi.org/10.1007/s11104-018-3721-7>
- Bueno CG, Williamson SN, Barrio IC, et al (2016) Moss Mediates the Influence of Shrub Species on Soil Properties and Processes in Alpine Tundra. *PLoS One* 11:e0164143. <https://doi.org/10.1371/journal.pone.0164143>
- Eisenhauer N, Beßler H, Engels C, et al (2010) Plant diversity effects on soil microorganisms support the singular hypothesis. *Ecology* 91:485–496.
<https://doi.org/10.1890/08-2338.1>
- Janvier C, Villeneuve F, Alabouvette C, et al (2007) Soil health through soil disease suppression: Which strategy from descriptors to indicators? *Soil Biol Biochem* 39:1–23. <https://doi.org/10.1016/j.soilbio.2006.07.001>
- Lange M, Habekost M, Eisenhauer N, et al (2014) Biotic and abiotic properties mediating plant diversity effects on soil microbial communities in an experimental grassland. *PLoS One* 9:e96182. <https://doi.org/10.1371/journal.pone.0096182>
- Latz E, Eisenhauer N, Rall BC, et al (2012) Plant diversity improves protection against soil-borne pathogens by fostering antagonistic bacterial communities. *J Ecol* 100:597–604. <https://doi.org/10.1111/j.1365-2745.2011.01940.x>
- Latz E, Eisenhauer N, Rall BC, et al (2016) Unravelling Linkages between Plant Community Composition and the Pathogen-Suppressive Potential of Soils. *Sci Rep* 6:23584. <https://doi.org/10.1038/srep23584>

Mendes R, Kruijt M, De Bruijn I, et al (2011) Deciphering the rhizosphere microbiome for disease-suppressive bacteria. *Science* (80-) 332:1097–1100.
https://doi.org/10.1126/SCIENCE.1203980/SUPPL_FILE/PAP.PDF

Opelt K, Berg G (2004) Diversity and antagonistic potential of bacteria associated with bryophytes from nutrient-poor habitats of the baltic sea coast. *Appl Environ Microbiol* 70:6569–6579. <https://doi.org/10.1128/AEM.70.11.6569-6579.2004>

Pérès G, Cluzeau D, Menasseri S, et al (2013) Mechanisms linking plant community properties to soil aggregate stability in an experimental grassland plant diversity gradient. *Plant Soil* 373:285–299. <https://doi.org/10.1007/s11104-013-1791-0>

Tian Y, Li YH (2017) Comparative analysis of bacteria associated with different mosses by 16S rRNA and 16S rDNA sequencing. *J Basic Microbiol* 57:57–67.
<https://doi.org/10.1002/jobm.201600358>