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## Belowground impacts of alpine woody encroachment are determined by plant traits, local climate, and soil conditions

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2 DR. COURTNEY GRACE COLLINS (Orcid ID : 0000-0001-5455-172X)

3 DR. HUI GUO (Orcid ID : 0000-0001-6347-5976)

4 PROF. JASON E. STAJICH (Orcid ID : 0000-0002-7591-0020)

5 DR. JEFFREY M. DIEZ (Orcid ID : 0000-0002-4279-1838)

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11 ***Belowground Impacts of Alpine Woody Encroachment are determined by Plant Traits, Local***  
12 ***Climate and Soil Conditions***13 Courtney G. Collins<sup>1,2</sup>, Marko J. Spasojevic<sup>3</sup>, Concepción L. Alados<sup>4</sup>, Emma L. Aronson<sup>5</sup>, Juan C.  
14 Benavides<sup>6</sup>, Nicoletta Cannone<sup>7</sup>, Chatrina Caviezel<sup>8</sup>, Oriol Grau<sup>9,10</sup>, Hui Guo<sup>11</sup>, Gaku Kudo<sup>12</sup>, Nikolas J.  
15 Kuhn<sup>8</sup>, Jana Müllerová<sup>13</sup>, Michala L. Phillips<sup>14,2</sup>, Nuttapon Pombubpa<sup>5</sup>, Frédérique Reverchon<sup>15</sup>, Hannah  
16 B. Shulman<sup>5</sup>, Jason E. Stajich<sup>5</sup>, Alexia Stokes<sup>16</sup>, Sören E. Weber<sup>17,3</sup>, Jeffrey M. Diez<sup>2</sup>17 <sup>1</sup>Institute of Arctic and Alpine Research, University of Colorado Boulder, USA18 <sup>2</sup>Department of Botany and Plant Sciences, University of California Riverside, USA19 <sup>3</sup>Department of Evolution, Ecology, and Organismal Biology, University of California Riverside, USA20 <sup>4</sup>Instituto Pirenaico de Ecología (CSIC), Zaragoza, Spain21 <sup>5</sup>Department of Microbiology and Plant Pathology, University of California Riverside, USA22 <sup>6</sup>Pontificia Universidad Javeriana, Bogotá, Colombia23 <sup>7</sup>Università degli Studi dell'Insubria, Como, Italy24 <sup>8</sup>Department of Environmental Sciences, Physical Geography and Environmental Change, University of  
25 Basel, Switzerland

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26 <sup>9</sup> CREAM, Global Ecology Unit, Campus de Bellaterra (UAB), Edifici C, Cerdanyola del Vallès, 08193,  
27 Barcelona, Catalonia, Spain  
28 <sup>10</sup> Cirad, UMR EcoFoG (AgroParisTech, CNRS, Inra, Univ Antilles, Univ Guyane), Campus Agronomique,  
29 97310 Kourou, French Guiana  
30 <sup>11</sup> College of Resources and Environmental Sciences, Nanjing Agricultural University, China  
31 <sup>12</sup> Environmental Earth Science, Hokkaido University, Sapporo, Japan  
32 <sup>13</sup> Institute of Botany of the Czech Academy of Sciences, Průhonice, Czech Republic  
33 <sup>14</sup> US Geological Survey, Southwest Biological Science Center, Moab, UT, USA  
34 <sup>15</sup> Instituto de Ecología (INECOL), Red de Estudios Moleculares Avanzados, Pátzcuaro, Mexico  
35 <sup>16</sup> University Montpellier, AMAP, INRAE, CIRAD, IRD, CNRS, France  
36 <sup>17</sup> Institut für Evolutionsbiologie und Umweltwissenschaften, Universität Zürich, Switzerland

37  
38 Corresponding author: Courtney G. Collins [courtney.collins@colorado.edu](mailto:courtney.collins@colorado.edu) (407) 620-3062  
39 <https://orcid.org/0000-0001-5455-172X>

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41 Running Title: *Alpine Woody Encroachment Impacts Soil Microbes*

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50 **Abstract**

51 Global climate and land use change are causing woody plant encroachment in arctic, alpine, and  
52 arid/semiarid ecosystems around the world, yet our understanding of the belowground impacts of this  
53 phenomenon is limited. We conducted a globally distributed field study of 13 alpine sites across 4

54 continents undergoing woody plant encroachment and sampled soils from both woody encroached and  
55 nearby herbaceous plant community types. We found that woody plant encroachment influenced soil  
56 microbial richness and community composition across sites based on multiple factors including woody  
57 plant traits, site level climate, and abiotic soil conditions. In particular, root symbiont type was a key  
58 determinant of belowground effects, as Nitrogen-fixing woody plants had higher soil fungal richness,  
59 while Ecto/Ericoid mycorrhizal species had higher soil bacterial richness and symbiont types had distinct  
60 soil microbial community composition. Woody plant leaf traits indirectly influenced soil microbes  
61 through their impact on soil abiotic conditions, primarily soil pH and C:N ratios. Finally, site level climate  
62 affected the overall magnitude and direction of woody plant influence, as soil fungal and bacterial  
63 richness were either higher or lower in woody encroached versus herbaceous soils depending on mean  
64 annual temperature and precipitation. All together, these results document global impacts of woody  
65 plant encroachment on soil microbial communities, but highlight that multiple biotic and abiotic  
66 pathways must be considered to scale up globally from site and species level patterns. Considering both  
67 the aboveground and belowground effects of woody encroachment will be critical to predict future  
68 changes in alpine ecosystem structure and function and subsequent feedbacks to the global climate  
69 system.

70 Keywords: Woody encroachment, plant-soil interactions, alpine, global change, soil microbes, leaf traits

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## Introduction

Global climate and land use change are altering the distributions of organisms worldwide (Chen, Hill, Ohlemüller, Roy, & Thomas, 2011; Parmesan, 2006; Walther et al., 2002) and this is particularly true in arctic and alpine tundra ecosystems where warming is accelerated (Elmendorf et al., 2012; Walker et al., 2006; Wilson & Nilsson, 2009). One prevalent change in tundra ecosystems is the encroachment of woody plants (shrubs and dwarf trees) into areas previously dominated by non-woody grasses, sedges and forbs (Myers-Smith & Hik, 2018; Rundqvist et al., 2011; Sturm et al., 2005). Woody plant encroachment can strongly impact aboveground productivity, the redistribution of snow by wind, and water and nutrient cycling in the tundra (Demarco, Mack, & Bret-Harte, 2014; Myers-Smith et al., 2011; Myers-Smith & Hik, 2013; Weintraub & Schimel, 2005). However, few studies have considered the biotic impacts of woody encroachment, particularly belowground effects on soil microbial communities (Myers-Smith et al., 2011). Some case studies, primarily from the Arctic, show that encroachment alters soil microbial community structure and function via woody litter inputs, leading to increased soil organic matter mineralization and soil carbon C:N ratios (Eskelinen, Stark, & Männistö, 2009; K. Rousk, Michelsen, & Rousk, 2016; Wallenstein, McMahon, & Schimel, 2007). However, we lack a general understanding of how woody encroachment affects soil microbial communities at the global scale, or whether observed impacts are species and site specific (Donhauser & Frey, 2018; Myers-Smith et al., 2011).

To fill this knowledge gap, we conducted a coordinated global study of alpine woody encroachment on soil microbial communities. We assessed a diverse set of pathways by which plants can impact soil microbes, including changes in the quality and quantity of litter inputs (J. H. C. Cornelissen et al., 2007;

115 Santonja et al., 2017), alteration of soil abiotic conditions such as soil chemistry, moisture and pH  
116 (Eskelinen et al., 2009; Schimel, Bilbrough, & Welker, 2004; Yannarell, Menning, & Beck, 2014), or  
117 through interactions with rhizospheric microbes such as dinitrogen (N<sub>2</sub>)-fixing bacteria or mycorrhizae  
118 (Bengtson, Barker, & Grayston, 2012). Due to fluctuating environmental conditions and extreme spatial  
119 heterogeneity, alpine soil microbial communities are highly specialized, and can vary greatly across  
120 vegetation types, soil properties, and microclimates (Donhauser & Frey, 2018). Also, the effects of  
121 woody plant encroachment may interact with the direct effects of climate change (e.g. soil warming or  
122 drought) on soil microbes, making net outcomes difficult to predict (Classen et al., 2015; Kardol,  
123 Cregger, Company, & Classen, 2010). Thus understanding how woody plant encroachment directly and  
124 indirectly influences soil microbial communities is key to predicting long-term changes in the structure  
125 and function of alpine ecosystems (Hagedorn, Gavazov, & Alexander, 2019).

126 Direct effects of woody plant encroachment on soil microbial communities include shifts in both  
127 the quality and quantity of leaf and root litter (Wardle et al., 2004, Eldor Alvin Paul, 2007;) as well as  
128 interactions with microbial symbionts in their roots for nutrient and resource uptake (Smith & Read,  
129 1997a; Wookey et al., 2009). A shift from primarily herbaceous (grasses, sedges, forbs) to woody plant  
130 cover generally increases the quantity and decreases the quality of litter inputs, and may result in slower  
131 decomposition of organic matter (J. H. C. Cornelissen et al., 2007). However this pattern can differ  
132 across woody plant species based on chemical and morphological litter traits such as leaf carbon:  
133 nitrogen ratio (C:N), leaf dry matter content (LDMC) and specific leaf area (SLA) (Cornwell et al., 2008;  
134 Gavazov, 2010; Urbina, Grau, Sardans, Ninot, & Peñuelas, 2020). Litter mixing between woody and  
135 herbaceous plants can increase the chemical complexity of the substrate pool, enhancing both microbial  
136 niche space and diversity (Chapman & Newman, 2010; McGuire, Zak, Edwards, Blackwood, & Upchurch,  
137 2010). Additionally, different types of microbial symbionts engage in distinct resource use strategies,  
138 and can greatly influence the resource economy of their plant host (J. Cornelissen, Aerts, Cerabolini,  
139 Werger, & van der Heijden, 2001; Gerz, Guillermo Bueno, Ozinga, Zobel, & Moora, 2018; Smith & Read,  
140 1997b, 1997c). For example, Ecto- and Ericoid mycorrhizal fungi (ECM, ERM) have a higher affinity for  
141 organic forms of N and phosphorus (P) than arbuscular mycorrhizal fungi (AMF) which primarily  
142 scavenge inorganic nutrients (Read, 2003; Wookey et al., 2009), while N<sub>2</sub>-fixing bacteria directly convert  
143 elemental N<sub>2</sub> into plant available forms of N (van der Heijden, Bardgett, & van Straalen, 2008).  
144 Differences in leaf litter chemistry across plant symbiont types may further select for faster (Cheeke et  
145 al., 2017; M. K. Taylor, Lankau, & Wurzbarger, 2016) or slower (McGuire et al., 2010) decomposition by  
146 saprotrophic soil microbes. Furthermore, root symbionts can directly interact in numerous ways with

147 saprotrophic fungi and bacteria in the rhizosphere. For example, mycorrhizal fungi release organic acids,  
148 hyphal exudates and provide hyphal necromass, which can enhance bacterial growth and serve as a  
149 food source for free-living soil biota (Bending, Aspray, & Whipps, 2006; Liang, Schimel, & Jastrow, 2017).  
150 Alpine soils usually have very low organic matter, and therefore changes in the quantity and quality of  
151 litter inputs, hyphal exudates, and microbial necromass as a result of woody encroachment have the  
152 potential to create major changes in free-living soil microbial communities and belowground ecosystem  
153 functioning (Donhauser & Frey, 2018; Körner, 2003).

154 Woody plant encroachment can also indirectly influence soil microbes through changes in the  
155 abiotic soil environment (Collins, Carey, Aronson, Kopp, & Diez, 2016; Grau et al., 2019) and via  
156 interactions with local climate (Classen et al., 2015). Woody encroachment can alter C and nutrient  
157 cycling, water availability and pH, and can also drastically alter the spatial distribution of resources  
158 across a landscape (Eldridge et al., 2011; Myers-Smith et al., 2011). Shading under woody plant  
159 canopies retains soil moisture higher in the soil profile in addition to physical trapping of snow, that  
160 concentrates snowmelt (Gómez-Aparicio, Gómez, Zamora, & Boettinger, 2005; Sturm et al., 2005).  
161 Enhanced soil moisture and thermal insulation from snow can promote decomposition and  
162 biogeochemical cycling (Schimel et al., 2004), while leaching of organic acids from woody litter can  
163 directly influence soil pH (Jobbagyl & Jackson, 2003), which is a key driver of microbial community  
164 composition (Lauber, Hamady, Knight, & Fierer, 2009; J. Rousk et al., 2010). Overall, resource  
165 accumulation below woody plant canopies can lead to increased microbial biomass (Cable, Ogle, Tyler,  
166 Pavao-Zuckerman, & Huxman, 2009; Liao & Boutton, 2008), diversity (Hollister, Schadt, Palumbo, James  
167 Ansley, & Boutton, 2010) and shifts in community composition (Yannarell et al., 2014). In addition,  
168 impacts of woody plant encroachment may be more or less severe depending on ambient temperature  
169 and precipitation, which are changing rapidly in alpine environments (Rammig, Jonas, Zimmermann, &  
170 Rixen, 2010). Interactions between plant growth form (i.e. woody or herbaceous) and experimental  
171 shifts in air temperature, soil moisture and CO<sub>2</sub> influenced soil microbial enzyme production and  
172 nematode community composition (Kardol et al., 2010). Similarly, soil temperature and moisture  
173 determined whether arctic soils became net sources or sinks of CO<sub>2</sub> in woody but not herbaceous plant  
174 communities (Cahoon, Sullivan, Shaver, Welker, & Post, 2012). Because of these complexities, we lack a  
175 clear understanding of how specific abiotic conditions or climate patterns will influence woody plant-soil  
176 interactions. Thus, assessing woody plant encroachment across multiple sites spanning diverse climates  
177 and environmental conditions is crucial (Wookey et al., 2009).

178 The objectives of this research were to determine: 1) Is there a consistent global signature of  
179 woody plant encroachment on soil microbial communities in alpine ecosystems? and 2) What are the  
180 major abiotic and biotic drivers mediating the observed changes in soil microbial communities? We  
181 conducted this study across 13 alpine sites all undergoing woody plant encroachment, spanning four  
182 continents and ten mountain ranges (Table 1). We hypothesized that woody plant encroachment will: 1)  
183 alter soil microbial diversity and microbial community composition via changes in litter quality. Such  
184 changes are likely driven by differences in leaf functional traits and their influence on soil abiotic  
185 conditions; 2) impact soil microbial communities differently depending on root symbiont types (AMF,  
186 ECM and, N<sub>2</sub>-fixers) and associated resource use strategies; 3) influence soil microbial communities  
187 indirectly through changes in abiotic soil conditions; 4) have climate-dependent effects on soil microbial  
188 communities due to high microbial sensitivity to temperature and moisture.

189

## 190 **Materials and Methods**

### 191 *Site selection*

192 This study took place at 13 sites (Fig 1, Table 1) across North and South America, Europe and Asia.  
193 We selected sites based on the following criteria: 1) woody plant encroachment into alpine plant  
194 communities dominated by herbaceous species, was observed within the last 50 years. We confirmed  
195 that woody plants were not previously present using aerial photography, historical records, and  
196 personal knowledge or information from local groups. See citations in Table 1 for further details  
197 regarding woody encroachment at each site. 2) Sites were alpine or subalpine (close to or above  
198 treeline), not Arctic (one site in Abisko, Sweden was considered 'subarctic' alpine). 3) Sites were not  
199 actively grazed or managed for agriculture (low intensity grazing did occur at our sites on the Tibetan  
200 Plateau in China and in the Swiss Alps and pine (*Pinus mugo*) silviculture occurred historically around our  
201 site in the Czech Republic). 4) International shipping speeds allowed samples to arrive in 72 hours or  
202 less on dry ice so that soils would stay frozen (this requirement affected our choice of study sites that  
203 excluded the Southern Hemisphere, Africa, and remote parts of Asia in our study). Finally, while we use  
204 the term 'woody' to describe primarily shrubs and dwarf trees at our study sites, one site (Japan) has a  
205 dwarf bamboo species (*Sasa kurilensis*) which is technically a 'woody graminoid.' This and other species  
206 of bamboo are common woody encroachers across Asia (Xu et al., 2020).



207 *Soil sampling*

208 We sampled soils from both directly under and outside woody plant canopies (~1.5-3.0 m outside) in  
209 the herbaceous plant interspace in areas where woody shrubs and dwarf trees were newly established  
210 (not present > 50 years). Soils were sampled during the growing season in either 2017 or 2018  
211 (depending on site). All soils were sampled using an aseptic technique and sampling protocol as  
212 described in the USEPA/USGS Sample Collection Protocol for Bacterial Pathogens in Surface Soil (EPA,  
213 2014). We collected ten soil samples from each vegetation type (woody and herbaceous) at each site for  
214 a total of 20 samples per site (20 x 13=260 soil samples). For each soil sample, three replicate soil cores  
215 were taken at a depth of 10-15 cm, combined into one sample with all excess rocks, roots, leaves or  
216 twigs removed and placed in sterile Whirlpak bags (Uline, Pleasant Prairie, WI, USA). Sampling locations  
217 within sites (individual woody plants and paired herbaceous soils) were at least 5 m apart. Soils were  
218 frozen within 24 hrs after sampling and remained in the freezer (-20° C) until being shipped. Soils were  
219 shipped on dry ice via expedited shipping to the University of California, Riverside, USA. All soils were  
220 sampled from within the same parent material and 100 m elevation differential or less at each site.

221 *Soil abiotic parameters*

222 At each soil sampling location (N=10 woody + 10 herbaceous=20 per site), we measured soil  
223 volumetric water content (VWC %) and soil pH *in situ* using handheld probes (Vegetronix VG-Meter-200  
224 basic or equivalent; EXTECH Model PH100 or equivalent). For soil chemistry, shipped soils were thawed  
225 at room temperature (half of each sample, other half remained frozen for microbial analyses) sifted  
226 through a 2mm mesh sieve and ground via mortar and pestle. Soils were then oven dried at 60 °C for 72  
227 hours, weighed into tin capsules and measured for total C and N on a Flash EA 112 analyzer at the  
228 University of California Riverside Environmental sciences research laboratory, U.S.A.

229 *Leaf sampling and traits*

230 Ten leaves were sampled from the encroaching woody species at each study site (n=10 x 13 sites=  
231 130 leaves). Leaves were kept moist and weighed within 24 hours of sampling on a microbalance to  
232 obtain fresh weight (g). Leaves were then placed in paper envelopes and left to air dry until shipping.

233 We measured the following leaf functional traits for each woody plant species: leaf dry matter  
234 content LDMC (g/g), specific leaf area SLA (cm<sup>2</sup>/g), leaf N (%), leaf C (%), δ<sup>13</sup>C, and δ<sup>15</sup>N. Leaves were  
235 scanned on a flatbed scanner to calculate leaf area (cm<sup>2</sup>) using ImageJ software  
236 (<https://imagej.nih.gov/ij/>). Leaves were dried (60° C, 72 hours) and then weighed for dry weight (g).  
237 LDMC was calculated as the ratio of fresh weight (g) to dry weight (g) and SLA was calculated as leaf area

238 (cm<sup>2</sup>) to dry weight (g). Leaf chemical (C, N) and isotope ( $\delta^{13}\text{C}$ , and  $\delta^{15}\text{N}$ ) content were measured from  
239 dried leaf subsamples at the University of Wyoming Stable Isotope Facility (Laramie, WY, USA.).

#### 240 *Soil microbial analyses*

241 We extracted microbial DNA from 0.25 g of soil ( $\pm 0.025$  g) of each sample using a Qiagen DNeasy  
242 PowerSoil Kit (Qiagen Inc., Germantown, MD, USA) and quantified the extracted DNA using a NanoDrop  
243 2000 (Thermo Fisher Scientific Inc., Wilmington, DE, USA). After quantification, we standardized DNA  
244 extracts to 10 ng/ $\mu\text{L}$ . We performed PCR amplification using the 515F/806R primer set targeting V4  
245 region of the 16S rRNA gene for bacteria (Caporaso et al., 2011) and the 5.8S-Fun/ITS4-Fun primer set  
246 targeting the ITS-2 region for Fungi (D. L. Taylor et al., 2016). PCR was run in 25  $\mu\text{L}$  reactions including  
247 1.25  $\mu\text{L}$  of 1  $\mu\text{M}$  for each primer (forward and reverse), 1  $\mu\text{L}$  DNA template, 12.5  $\mu\text{L}$  of Phusion Green Hot  
248 Start 2X Master Mix (Thermo Fisher Scientific Inc., USA), 1.5  $\mu\text{L}$  of 3  $\mu\text{M}$   $\text{MgCl}_2$  and 7.5  $\mu\text{L}$  PCR grade  
249 water. Thermocycler settings were 95°C for 2 minutes, followed by 35 cycles of 95°C for 30 seconds,  
250 55°C for 30 seconds, and 60°C for 4 minutes (ITS2) or 2:30 minutes (16S) with a 10°C hold. We then did  
251 PCR clean-up using Agencourt AMPure XP beads (Beckman Coulter, Inc., Indianapolis, USA, IN 46268).  
252 Purified PCR products (2.5  $\mu\text{L}$ ) were mixed with 2.5  $\mu\text{L}$  of 100 nm custom universal tails indexing primers  
253 (forward and reverse) developed at EnGGen Laboratory, Northern Arizona University (Flagstaff, AZ,  
254 USA)(Colman et al., 2015) 12.5  $\mu\text{L}$  of Phusion Green Master Mix, 1.5  $\mu\text{L}$  of 3  $\mu\text{M}$   $\text{MgCl}_2$  and 3.5  $\mu\text{L}$  PCR  
255 grade water and were amplified using thermocycler settings of 95°C for 2 minutes, followed by 15 cycles  
256 of 95°C for 30 seconds, 60°C for 30 seconds, and 72°C for 1 minute with a 10°C hold. We then ran  
257 another round of cleanup and quantified PCR products using the Quant-iT PicoGreen dsDNA assay kit  
258 (Life Technologies Inc., Grand Island, NY, USA). As a final step, the samples were pooled in equimolar  
259 concentrations and sequenced in a multiplexed 2- x 300-bp paired-end sequencing run on the Illumina  
260 MiSeq platform (Illumina Inc., San Diego, CA, USA) at the Genomics Core Facility, University of California  
261 Riverside (USA).

#### 262 *Bioinformatics*

263 ITS-2 sequences were analyzed using AMPtk: Amplicon Toolkit for NGS data (Palmer, Jusino, Banik,  
264 & Lindner, 2018) (<https://github.com/nextgenusfs/amptk>). Demultiplexed paired-end sequences data  
265 were pre-processed by trimming primer sequences, trimming forward and reverse reads to 250 bp  
266 (reads length less than 100 bp were dropped), and merging paired-end reads using USEARCH v9.1.13  
267 (Edgar, 2010). A total of 8,310,353 reads passed the preprocessing steps and reads were filtered based  
268 on quality scores with a cutoff of an expected error less than 0.9 (Edgar & Flyvbjerg, 2015) to produce

269 6,441,443 reads which passed quality filtering. The quality filtered reads were clustered into 19,790  
270 Operational Taxonomic Units (OTUs) using UPARSE (Edgar, 2013) at 97% identity threshold. The OTUs  
271 were further processed with VSEARCH (v 2.3.2)(Rognes, Flouri, Nichols, Quince, & Mahé, 2016) to  
272 identify and remove 569 chimeras based on comparison to the UNITE database v8.0(Nilsson et al., 2019)  
273 leaving 19,221 OTUs . We assigned taxonomy with the AMPtk “hybrid” approach which uses Global  
274 Alignment, SINTAX, and UTX. Lastly, sequences were rarefied to 10,000 sequences per sample and  
275 processed with QIIME Core Diversity pipeline (Caporaso et al., 2010) to estimating Alpha (OTU richness)  
276 and Beta diversity (Bray-Curtis dissimilarity).

277 16S sequences were analyzed using QIIME2 (Bolyen et al., 2018) (<https://qiime2.org>) following the  
278 ‘Atacama soil microbiome’ pipeline for demultiplexed paired-end sequences. We truncated sequences at  
279 220 bp and trimmed the first 25 bp based on the interactive quality plots in QIIME2 and then denoised  
280 sequences using DADA2 after truncating all sequences Chimeras were removed using the default method  
281 in DADA2 (Callahan, Mcmurdie, Rosen, Han, & A, 2016). A total of 12,669,635 sequences passed quality  
282 filtering. Unique sequences were aligned using MAFFT (Katoh & Standley, 2013), filtered using the masked  
283 alignment file, and used to construct a Maximum Likelihood phylogeny with FastTree (Price, Dehal, &  
284 Arkin, 2010). Alpha (OTU richness) and Beta diversity measures (Weighted UniFrac distance) (Lozupone &  
285 Knight, 2005) were estimated using a subsampled feature table containing 10,000 sequences per sample.  
286 Taxonomy was assigned to 34,417 unique sequences using a Naïve Bayes classifier trained on the  
287 GreenGenes database (McDonald et al., 2012) (version 13\_8) using trimmed sequences pre-clustered at  
288 99% similarity. After all sequence processing we retained N=224 unique samples for fungi and N=215  
289 unique samples for bacteria.

#### 290 *Climate data*

291 To test the interaction between site specific changes in climate and the influence of woody  
292 plant encroachment, we acquired climate data for each site through the WorldClim v 2.1 database at 30  
293 second resolution (Fick & Hijmans, 2017). We tested the influence of multiple climate parameters at  
294 each site including: Mean Annual Temperature (MAT), Temperature Seasonality (standard deviation  
295 x100), Maximum Temperature of Warmest Month, Minimum Temperature of Coldest Month, Mean  
296 Annual Precipitation (MAP), and Precipitation Seasonality (Coefficient of Variation). We chose to use the  
297 30-year climate normals (WorldClim) rather than annual climate data because our analyses aimed at  
298 understanding climatic control over broad geographic variation in microbial communities. We found  
299 substantial climate variability across sites and symbiont types (Fig S1), but found that overall MAT was

300 the best univariate predictor of microbial diversity (Fig S2). Therefore, we included MAT, and for  
301 consistency MAP, as the primary climate variables in subsequent models.

## 302 *Statistical methods*

### 303 *Leaf traits*

304 We used Principal Components Analysis (PCA) to collapse the values of the six measured leaf traits  
305 into two PC axes to be used in hierarchical models (below). Prior to the PCA, we infilled missing leaf trait  
306 data (LDMC and leaf chemistry) for one site where only SLA could be measured (China) and any NA  
307 values using the package *mice* in R (R Core Team, 2019; van Buuren & Groothuis-oudshoorn, 2011),  
308 taking the average of 100 imputed values for each trait estimate. All data were logged prior to PCA. Leaf  
309 traits and principal components scores were averaged by (woody) plant species at each site.

310 We also tested for a difference in leaf N between root symbiont types, due to frequently higher N  
311 in tissues of N<sub>2</sub>-fixing plants. We used one way ANOVA with leaf N (%) (logged) as the response and  
312 symbiont type (N<sub>2</sub>-fix, ECM/ERM, AMF) as the predictor, followed by a Tukey's HSD test.

### 314 *Alpha diversity (OTU richness)*

315 We fit linear mixed-effects (hierarchical) models in a Bayesian SEM framework to test the impacts  
316 of woody plant encroachment on soil fungal and bacterial richness. First, we estimated the effects of  
317 vegetation type, climate, abiotic soil conditions, root symbiont type and their interactions on OTU  
318 richness. Next, we ran a second set of models to estimate the effects of woody plant leaf traits on soil  
319 abiotic conditions (soil C:N and soil pH), as we predicted that leaf traits would influence microbial  
320 richness via shifting abiotic soil conditions (Hypothesis 1). Thus, soil abiotic conditions were a predictor  
321 in the first set and a response in the second set of models (see General Model, Table S1). We did not  
322 hypothesize a relationship between leaf traits and soil moisture, however, so we simply used vegetation  
323 type as a predictor of soil moisture. Additionally, for the root symbiont type by vegetation interaction,  
324 we grouped symbiont types at the site level based on each woody plant species (see Table 1, Table S1),  
325 and thus we only estimate the effect of root symbionts for woody plants.

326 We fit Bayesian models using the *brms* package in R (Bürkner, 2017). All data were standard  
327 normalized prior to modeling to improve model convergence and we logged the bacterial response  
328 variable (16S OTU richness) for normality. All models contained a site level random intercept and  
329 hierarchical structure as described below and in Table S1. The Bayesian framework was convenient here  
330 due to the somewhat uneven design and multilevel structure of the data (Table S1), and was useful for

331 predicting relationships with reasonable estimates of uncertainties. We used the posterior distributions  
332 of each parameter to calculate the probabilities that it was different from zero, and three probability  
333 levels are reported (85, 90 and 95% probabilities, respectively, that the parameter estimate is different  
334 from zero). We also used these parameter distributions to calculate pairwise post-hoc comparisons  
335 between root symbiont types.

336 General Model:

337  $\text{Alpha Diversity} = (1 | \text{site}) + \text{Vegetation type} * \text{Root symbiont Type} + \text{Vegetation type} * \text{Climate} + \text{Soil abiotic}$

338  $\text{Soil abiotic} = (1 | \text{site}) + \text{Woody leaf traits}$

339 BRMS model syntax =

340  $\text{OTU richness} \sim (1 | \text{site}) + \text{Symbiont} * \text{Vegetation type} + \text{MAT} * \text{Vegetation type} + \text{MAP} * \text{Vegetation type} +$

341  $\text{VWC} + \text{pH} + \text{soilC:N}$

342  $\text{soilC:N} \sim (1 | \text{site}) + \text{PC Axis1 (leaf traits)} + \text{PC Axis2 (leaf traits)}$

343  $\text{pH} \sim (1 | \text{site}) + \text{PC Axis1 (leaf traits)} + \text{PC Axis2 (leaf traits)}$

344  $\text{VWC} \sim (1 | \text{site}) + \text{Vegetation type}$

345 *Beta diversity (Community composition)*

346 To assess the impacts of woody plant encroachment on bacterial and fungal community  
347 composition, we used non-metric multidimensional scaling (NMDS) of the Bray-Curtis (fungi) and  
348 weighted Unifrac (bacteria) dissimilarity metrics and permutational multivariate analysis of variance  
349 (perMANOVA) with the 'adonis' function in the *Vegan* package in R (Oksanen, Blanchet, Kindt, Legendre,  
350 & O'Hara, 2016) (999 permutations). We ran three perMANOVA models, first with vegetation type  
351 (woody versus herbaceous) as a predictor and site as a strata variable to restrict permutations within  
352 sites; next we used root symbiont type, climate, and soil abiotic parameters as predictors with  
353 vegetation type as a strata; third we ran a leaf trait model for woody soils only using leaf trait PCA axes 1  
354 and 2 as predictors and no strata variable. All perMANOVA models had either bacterial or fungal  
355 community composition as the response variable.

356 General Model:

357  $\text{Beta Diversity} = \text{Vegetation type}$

358  $\text{Beta Diversity} = \text{Root symbiont Type} + \text{Climate} + \text{Soil abiotic}$

359 *Beta Diversity = Woody leaf traits*

360 Adonis model syntax =

361 Bray Curtis/Unifrac distance ~ Vegetation type, strata=site

362 Bray Curtis/Unifrac distance ~ Symbiont + MAT + MAP + VWC + pH + soilC:N , strata=vegetation type

363 Bray Curtis/Unifrac distance ~ PC Axis1 (leaf traits) + PC Axis2 (leaf traits)

364 Taxonomic analyses

365 To assess differences in the relative read abundance of microbial taxa between woody and non-  
366 woody vegetation, we used linear mixed effects models (for normally distributed data) or generalized  
367 linear models with a Gamma distribution in the 'lmer' and 'glmer' functions in the *lme4* package in R  
368 (Bates, Mächler, Bolker, & Walker, 2014). Read abundances (logged, zeroes removed) of microbial phyla  
369 were the response variable, vegetation type (woody/herbaceous) was a fixed effect and site was  
370 included as a random effect.

371 General Model:

372 *Phylum reads* ~ (1|site) + *Vegetation type*

373 We also used indicator species analysis to determine which taxa characterized soils from different  
374 vegetation types (woody versus herbaceous) using the function 'multipatt' in the *indicspecies* package in  
375 R (De Cáceres, Legendre, Wiser, & Brotons, 2012). We calculated Indicator Values (Indvalg) based on  
376 species (OTU) abundance and considered indicator taxa significant at  $\alpha=0.05$  based on permutation tests  
377 ( $n=999$ ) and an indicator value (stat) of 0.2 or greater.

378

## 379 **Results**

### 380 *Leaf Traits*

381 PCA analysis showed that SLA, leaf N,  $\delta^{15}\text{N}$ , and LDMC loaded on PC1 which explained 37.3% of the  
382 variation among species, and high PC1 values were associated with low SLA, leaf N and  $\delta^{15}\text{N}$  and high  
383 LDMC. Leaf C and  $\delta^{13}\text{C}$  loaded on the second axis (PC2), which explained 17.5% of the variation among  
384 species, and high PC2 values were associated with high leaf C and low  $\delta^{13}\text{C}$  (Fig S3).

385 ANOVA and post hoc analysis revealed N<sub>2</sub>-fixing woody plants had the highest leaf N content (%)  
386 overall, and significantly higher leaf N than AMF and ECM/ERM symbiont types (Fig S5).

387

### 388 *Alpha diversity (OTU richness)*

389 Woody plant encroachment influenced the richness of soil microbial communities, but  
390 interestingly, these impacts differed across sites, with woody plant soils having higher, lower or similar  
391 richness as herbaceous soil microbial communities (Fig 2 a, b). Bayesian hierarchical models showed that  
392 N<sub>2</sub>-fixing woody plants had higher soil fungal richness and lower soil bacterial richness than herbaceous  
393 plant communities within sites (Fig 3, Table S2). Additionally, ECM/ERM woody plants had higher soil  
394 bacterial richness and lower soil fungal richness than herbaceous plant communities within sites (Fig 3,  
395 Table S2). Post-hoc comparisons also revealed that N<sub>2</sub>-fixing woody plants had higher soil fungal  
396 richness than AMF and ECM/ERM woody plants across sites, while ECM/ERM plants had higher soil  
397 bacterial richness than AMF and N<sub>2</sub>-fixing woody plants across sites (Table S2, FigS6).

398 Soil abiotic conditions also predicted fungal and bacterial richness, including a positive relationship  
399 between pH and both fungal and bacterial richness, a negative relationship between soil C:N and fungal  
400 richness (Fig 4, Table S2), and a positive relationship between soil water content (VWC) and bacterial  
401 richness (Table S2). Woody plant soils had lower VWC than herbaceous soils and woody plant leaf traits  
402 predicted soil abiotic conditions (Table S2). The first axis of a principal components analysis (PC1) of  
403 multiple leaf traits was negatively related to soil pH and soil C:N, while PC2 was negatively related to soil  
404 pH in the Bayesian hierarchical model (Fig 4, Table S2).

405 Finally, there were interactions between woody encroachment and climate, including a negative  
406 interaction between mean annual precipitation (MAP) and vegetation type on fungal richness, a positive  
407 interaction between mean annual precipitation (MAP) and vegetation type on bacterial richness and a  
408 negative interaction between mean annual temperature (MAT) and vegetation type on bacterial and  
409 fungal richness (Fig 3, Table S2).

410

### 411 *Beta diversity (Community composition)*

412 Microbial beta diversity was generally higher between rather than within sites, as communities  
413 clustered strongly by sampling site (Fig 2 c, d). Within sites, microbial community composition differed  
414 among vegetation types and this pattern was stronger for bacterial than fungal communities based on  
415 perMANOVA results and NMDS overlap (Fig 5 a, d, Table S3.). Within vegetation types, plant traits,  
416 climate and soil abiotic conditions were significantly related to both fungal and bacterial community

417 composition (Table S3). Environmental variables such as climate and soil abiotic conditions explained up  
418 to an order of magnitude more variation in bacterial than fungal community composition (maximum  $R^2$   
419 0.135 vs 0.012; mean  $R^2$  0.06 vs 0.01, Table S3). Root symbiont type was a significant predictor of both  
420 fungal and bacterial communities, with the highest community similarity within  $N_2$ -fixing soil fungal  
421 communities (Fig 5 b,e). Mean annual precipitation (MAP) and soil pH were the best abiotic predictors of  
422 fungal and bacterial community composition, respectively (Fig 5 c, f, Table S3). Woody plant leaf traits  
423 were also significant predictors of microbial community composition with PC2 being most predictive of  
424 fungal and bacterial communities (Table S3).

425

#### 426 *Taxonomic analyses*

427 The soil fungal community comprised 10 phyla, with Ascomycota dominating (40.1%), followed by  
428 Basidiomycota (26.6%) and Mortierellomycota (13.9%), Glomeromycota (0.8%) and Chytridiomycota  
429 (0.5%) (Fig S4 a,b) . Six percent of the total ITS-2 sequences could not be assigned taxonomically, while  
430 two percent were assigned as unknown Fungi (i.e. only to Kingdom level) (red color-Fig S4). The soil  
431 bacterial community comprised 43 phyla with Proteobacteria making up the largest percentage (29.1%),  
432 followed by Acidobacteria (16.4%), Actinobacteria (12.9%), Bacteroidetes (8.7%), Planctomycetes (6.5%),  
433 Verrucomicrobia (6.5%), Chloroflexi (5.6%), unidentified bacteria (3.8%) and Firmicutes (1.5%) (Fig S4  
434 c,d). Less than one percent of the total 16S sequences could not be assigned a taxonomy, while four  
435 percent were assigned as unknown Bacteria (red color-Fig S4).

436 Taxa abundance models of the dominant microbial phyla showed a lower abundance of  
437 Basidiomycota in woody versus herbaceous soils (Table S4, Fig S4 a,b). For bacterial phyla, soils from  
438 herbaceous communities had a higher abundance of Acidobacteria, Actinobacteria, Proteobacteria,  
439 Verrucomicrobia, and Planctomycetes than woody soils (Table S4, Fig S4 c,d).

440 Fifty-one fungal indicator OTUs (assigned to the species level) were found in woody plant soils and  
441 23 indicator OTUs were in soils from herbaceous communities from Indicator species analysis. The six  
442 most prevalent indicator species were from the *Mortierella*, *Penicillium*, *Vishniacozyma*, *Herpotrichia*,  
443 and *Metapochonia* genera (OTUs 1585, 16274, 1203, 938, 101 and 1386) and were associated with soils  
444 beneath woody plants from at least ten sites (Table S5a). Species in the *Penicillium*, *Clavaria*, and  
445 *Pyrenochaetopsis* genera (OTUs 1611, 808, and 1271) were associated with soils from herbaceous  
446 communities at seven sites (Table S5a). There were only nine bacterial indicator OTUs assigned to the  
447 species level overall, but at the genus level, there were 32 bacterial indicator taxa (20 genera) for woody  
448 soils and 35 indicator taxa (22 genera) for herbaceous soils. Members of the genus *Herminiimonas*



449 (Proteobacteria) and *Segetibacter* (Bacteroidetes) were strongly associated with woody plant soils while  
450 the DA101 (Verrucomicrobia), *Rhodoplanes* (Proteobacteria), and GOUTA19 (Nitrospirae) genera were  
451 associated with soils from herbaceous communities. Indicator taxa from *Flavobacterium*, *Candidatus*  
452 *Koribacter*, *Candidatus Solibacter*, *Kaistobacter*, and *Pseudonocardia* genera were common in soils from  
453 both woody and herbaceous plants (Table S5b).

454

## 455 **Discussion**

456 One of the most striking ways that global change is restructuring alpine tundra plant communities is  
457 through the replacement of herbaceous plants by woody shrubs and dwarf trees (Brandt, Haynes,  
458 Kueemmerle, Waller, & Radeloff, 2013; Formica, Farrer, Ashton, & Suding, 2014; Hallinger, Manthey, &  
459 Wilmking, 2010). For example, conversion rates of alpine meadows to woody shrublands were  
460 estimated between 39-72% in the large portions of the southern Himalayas (Brandt et al., 2013). Here,  
461 using a global, coordinated field study we found that woody plant encroachment is influencing both  
462 richness and composition of soil microbial communities but that these changes depend on a  
463 combination of abiotic soil conditions, climate, root symbiont types and plant functional traits. This is an  
464 important first step in building a more predictive, functional understanding of how climate-driven shifts  
465 in woody plant cover will affect soil microbial communities and ecosystem processes worldwide.

466 Broadly, we did not find one 'global signature' of woody encroachment, but rather that woody  
467 encroachment was associated with increased, decreased, and no change in microbial alpha diversity  
468 (OTU richness) when comparing with soils of nearby herbaceous plant communities (Fig 2). This likely  
469 reflects the broad taxonomic and functional diversity of the woody plant species across these sites,  
470 leading to variable litter quality (Table 1, Fig S3). For example, study species included evergreen conifers,  
471 deciduous hardwoods, legumes and woody graminoids, highlighting the diversity of woody species  
472 expanding into different alpine ecosystems worldwide. However, when accounting for easily measurable  
473 characteristics, such as woody plant leaf traits and root symbiont types, consistent patterns emerged for  
474 effects of woody plants on both bacterial and fungal richness and community composition.

475 Woody plant leaf traits modulated shifts in soil microbial communities supporting our first  
476 hypothesis. Leaf traits predicted the community composition of both bacteria and fungi in woody plant  
477 soils and influenced soil microbial richness indirectly through changes in soil abiotic conditions (pH, soil  
478 C:N). Two distinct trait axes influenced microbial community structure. The first axis of the principal  
479 components analysis (PC1) was primarily characterized by low SLA, leaf N and  $\delta^{15}\text{N}$  and high LDMC and  
480 the second axis (PC2) was primarily characterized by high leaf C and low  $\delta^{13}\text{C}$  (Fig S3). Thus PC1

481 represents variation in leaf economic traits and nitrogen acquisition strategies with low PC1 scores  
482 representing more resource-acquisitive species with higher N content and SLA (Wright et al., 2004).  
483 Moreover, PC2 represents variation in leaf C and water use with high PC2 scores representing species  
484 with resource-conservative strategies including high leaf C content and water use efficiency (Moreno-  
485 Gutiérrez, Dawson, Nicolás, & Querejeta, 2012). There was a negative relationship between PC2 and soil  
486 pH (Fig 4), suggesting that woody plants with higher C content in leaves reduced soil pH, likely due to  
487 leaching of organic acids into soil solution via recalcitrant litter (Eldridge et al., 2011; Jobbagy & Jackson,  
488 2003). Consistent with other studies, we also found that soil pH was a strong predictor of both bacterial  
489 and fungal richness (Lauber et al., 2009; J. Rousk et al., 2010), providing a clear mechanism for how  
490 woody plant litter chemistry can influence soil microbial diversity. Plant traits also influenced bacterial  
491 and fungal community composition, but PC2 was a stronger predictor than PC1 (Table S3), further  
492 suggesting that leaf C content is an important determinant of woody encroachment impacts on soil  
493 microbial communities.

494 Woody plants with different root symbiont types (AMF, ECM/ERM, N<sub>2</sub>-fixers) had distinct impacts  
495 on soil microbial communities, supporting our second hypothesis. In particular, N<sub>2</sub>-fixing woody species  
496 had higher soil fungal richness and lower bacterial richness than both herbaceous soils (within sites) and  
497 AMF, ECM/ERM woody plant soils (across sites)(Fig 3a, FigS6a, Table S2). Conversely, ECM-ERM  
498 symbionts had higher soil bacterial richness but lower fungal richness than both herbaceous soils (within  
499 sites) and N<sub>2</sub>-fixing, AMF woody plant soils (across sites)(Fig 3a, FigS6b, Table S2). Root symbiont type  
500 was also an important predictor of both fungal and bacterial community composition (Fig 5b,e, Table  
501 S3). Root symbiont types can greatly influence plant resource use strategies, as well as litter chemistry  
502 and thus the impact of woody plants on soil microbial communities (Cheeke et al., 2017; Wookey et al.,  
503 2009). For example, N<sub>2</sub>-fixing woody plants had higher leaf N content (%) than AMF symbiont types in  
504 our study (Fig S5) and thus may be altering soil microbial richness through high N leaf litter. Previous  
505 work has shown invasion of N<sub>2</sub>-fixing woody species reduces soil microbial diversity (Lorenzo, Pereira, &  
506 Rodríguez-Echeverría, 2013; Lorenzo, Rodríguez-Echeverría, González, & Freitas, 2010), which we find to  
507 be true for bacteria, however we see the opposite response in fungi. Root symbionts, especially extra-  
508 radical hyphal forming ecto- and ericoid mycorrhizas, may also interact directly with free-living microbes  
509 (Bending et al., 2006). Woody plants utilizing ECM and ERM fungi had higher soil bacterial richness and  
510 distinct soil microbial community composition (Fig 3a, 5b,e). ECM and ERM fungi release extracellular  
511 enzymes and organic acids for decomposition into the rhizosphere which can select for specific bacterial  
512 communities (Churchland & Grayston, 2014). In addition, mycorrhizal helper bacteria (MHB) (Frey-Klett,

513 Garbaye, & Tarkka, 2007) and/or chitinophagous species that feed on dead fungal hyphae may be  
514 enhanced in the rhizosphere of ECM and ERM woody plants (Brabcová, Nováková, Davidová, & Baldrian,  
515 2016), and several of these taxa were indicator species of woody plant soils in our analysis (Table S5).

516 While we designated root symbiont types based on current literature and site-specific information,  
517 several of the woody plant species in our study can utilize multiple types of root symbionts. For  
518 example, *Salix* spp. (Teste, Jones, & Dickie, 2019) and *Juniperus communis* (Thomas, El-Bargathi, &  
519 Polwart, 2007) can be dually colonized by ECM and AMF, and the relative abundance of each  
520 mycorrhizal type often differs across habitats, with alpine *Salix* varieties being more ECM dominant  
521 (Dhillion, 1994). In addition, Nitrogen fixers may utilize different bacterial symbionts; for example, *Alnus*  
522 *alnobetula* is an actinorhizal species which associates with bacteria in the genus *Frankia* (Richardson,  
523 Allsopp, D'antonio, Milton, & Rejmánek, 2000), while *Echinopartum horridum* is a legume which  
524 associates with bacterial species in the genus *Rhizobium* (Komac, Alados, & Camarero, 2011). Rhizobial  
525 strains are considered more host-specific than *Frankia*, and N<sub>2</sub>-fixing plant species may also have co-  
526 occurring AMF or ECM fungi (Teste et al., 2019). Despite these discrepancies, these very broad  
527 categories still proved to be useful predictors of complex soil microbial communities undergoing woody  
528 plant encroachment.

529 Soil abiotic conditions influenced microbial communities, supporting our third hypothesis, and soil  
530 pH was the most consistent driver of soil microbial richness (Fig 3, Table S2) and community  
531 composition (Table S3). Further, abiotic conditions were influenced by woody plant leaf traits,  
532 suggesting that woody plants affect soil microbial communities indirectly through changes in abiotic soil  
533 conditions (Fig 4). For example, soil pH had a positive effect on both fungal and bacterial richness and  
534 was the best predictor of bacterial community composition (Fig 3a, 5f). As described previously, there  
535 was also a negative relationship between woody plant leaf traits, particularly leaf C content, and pH (Fig  
536 4). Soil pH is a consistently strong predictor of microbial community structure (Lauber et al., 2009; J.  
537 Rousk et al., 2010), however it is often framed as an abiotic driver decoupled from plant litter chemistry.  
538 Soil C:N had a negative effect on fungal richness and also influenced fungal and bacterial community  
539 composition (Fig 3a, Table S3). On the other hand, Soil C:N was negatively associated with N related leaf  
540 traits (PC1), however the direction of this relationship was the opposite of what we predicted (Fig 4).  
541 This may be due to the fact that in low N environments such as the alpine, N mineralization is very low  
542 and direct microbial uptake of organic N from is high (Schimel & Bennett, 2004), potentially weakening  
543 the link between leaf N traits and soil C:N. Finally, VWC had a positive effect on bacterial richness, and  
544 influenced microbial and fungal community composition (Fig 3a, Table S3), however unlike our initial

545 prediction, soils from beneath woody plants had slightly lower VWC (Table S2). Thus, woody plants may  
546 be depleting soil moisture as compared to herbaceous vegetation through deeper roots, or via accessing  
547 water later into the growing season (Acharya, Kharel, Zou, Wilcox, & Halihan, 2018; Awada et al., 2013).  
548 Overall, these patterns highlight that woody plant effects on abiotic soil conditions are an important  
549 indirect pathway between woody plant encroachment and soil microbial community structure.

550 While changing climate is among the major drivers of woody plant encroachment, our results  
551 demonstrate that woody encroachment may also modulate climate effects on soil microbes. In support  
552 of our fourth hypothesis, the effects of woody plants interacted with climate at the site level, including  
553 interactions between vegetation type and MAP, MAT on fungal and bacterial richness (Fig 3, Table S2).  
554 This suggests that soil microbial communities undergoing woody encroachment are more distinct from  
555 those of herbaceous plants at the more extreme ends of temperature and precipitation gradients (Fig 3  
556 b, c). Fungal richness was more sensitive to the precipitation by vegetation type interaction, which is  
557 consistent with previous work showing MAP to be the best predictor of fungal richness worldwide  
558 (Tedersoo et al., 2014). Bacterial richness was more sensitive to the temperature by vegetation type  
559 interaction, likely because bacteria tend to be less cold tolerant than fungi, and fewer strains can  
560 maintain their biomass under winter snowpack (Lazzaro, Hilfiker, & Zeyer, 2015; Zinger, Shahnava,  
561 Baptist, Geremia, & Choler, 2009). Furthermore, MAT was one of the best predictors of fungal richness  
562 overall and MAP was among the top predictors of both fungal and bacterial community composition (Fig  
563 3a, Fig 5c, Table S3), emphasizing the strong influence of climate on soil microbial communities in alpine  
564 environments. All together, we find that woody encroachment can significantly influence how soil  
565 microbial communities respond to temperature and precipitation and may alter both the magnitude and  
566 influence of the climate driver. Thus, future predictions of climate impacts on alpine soil microbial  
567 communities must also consider co-occurring shifts in plant community structure.

568 Due to this study's observational rather than experimental approach, we cannot conclusively state  
569 that observed differences in soil microbial communities are in *response* to woody plant encroachment  
570 rather than a potential *cause* of woody plant establishment. However, there are several reasons why we  
571 believe the former to be true. First, soil microbial communities were highly correlated with attributes of  
572 the woody plants themselves, including leaf traits, root symbiont type, and soil abiotic conditions  
573 related to litter chemistry. In addition, we selected sites where woody plant encroachment began within  
574 the last 50 years, and at most sites, woody encroachment has been present for between 30-40 years. In  
575 a previous study, alpine soil microbial communities reflected the transition from a woody to herbaceous  
576 plant community in under 5 years (Collins et al., 2016) and thus we believe our sampling interval

577 provides sufficient time for woody plants to have cultivated distinct soil communities. Next, our analysis  
578 of soil microbial community composition has focused on the saprotrophic, generalist species which are  
579 most abundant in bulk soil and unlikely to directly influence plant community composition (Fierer,  
580 2017). This analysis does not test for species-specific soil mutualists or pathogens, the taxa which most  
581 strongly influence the success of plant establishment and range expansion (Mccarthy-Neumann &  
582 Ibáñez, 2012; Nuñez, Horton, & Simberloff, 2009; Tomiolo & Ward, 2018). Finally, while all soils were  
583 collected during the growing season (alpine summer), sampling times varied among sites due to  
584 differences in growing season length and snowmelt timing. Differences in sampling time can influence  
585 site-specific patterns in soil microbial communities (Bjork, Bjorkman, Andersson, & Klemedtsson, 2008;  
586 Lazzaro et al., 2015; Lipson & Schmidt, 2004), yet despite this, we observed many consistent patterns  
587 across sites in response to woody encroachment, suggesting that vegetation strongly influences soil  
588 microbial community structure in alpine ecosystems.

589 This study documents the global impacts of woody plant encroachment on soil microbial  
590 communities, but we emphasize that multiple pathways must be considered to disentangle these  
591 impacts. Specifically, divergent functional trait strategies and functional groups of woody plants based  
592 on root symbionts have consistent impacts belowground regardless of woody plant species or site. In  
593 addition, the influence of woody plants on soil microbes can be indirect through changes in the soil  
594 abiotic environment, such as reduced soil pH driven by high C content of woody plant litter. Finally,  
595 woody encroachment can influence both the direction and magnitude of direct climate effects on  
596 microbial richness, and bacteria and fungi respond to distinct climate and woody plant drivers. Our work  
597 highlights the complexity of plant-soil interactions in rapidly changing alpine ecosystems, an  
598 understanding that will influence our ability to predict feedbacks to terrestrial ecosystem function and  
599 climate, particularly the global C cycle, where soil microbes play an integral role.

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## **Data Availability**

632 All raw data and analysis scripts for this study may be found at the following repository:  
633 <https://github.com/cour10eygrace/woody-encroachment-microbes.git>. Raw Sequences may be found in  
634 the NCBI Short Read Archive (SRA) accession # PRJNA659596.

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960 **Figure legends**

961 **Fig 1.** Map and images of 13 alpine woody encroachment sites included in this study. Sites span 10  
962 countries and 4 continents. See Table 1 for further information.

963 **Fig 2.** Box and whisker plots of soil a) fungal and b) bacterial OTU richness (logged) and NMDS ordination  
964 plots of soil c) fungal (stress =0.13) and d) bacteria (stress =0.11) beta diversity (community  
965 composition) at each site. For richness, box fill color designates whether the soil was sampled in woody  
966 encroached or herbaceous plant community and box outline color designates the root symbiont type of  
967 the woody plant at each site. Here both fungal and bacterial richness are plotted on the log scale for  
968 consistency but we only logged bacterial richness in Bayesian models. For beta diversity, colored ovals  
969 represent 95% confidence intervals of sample ordination grouped by sampling site and shapes represent  
970 the vegetation community (woody or herbaceous) of each soil sample.

971 **Fig 3.** a) Parameter estimates (points) and 95% credible intervals (lines) from Bayesian hierarchical  
972 models for the effects of root symbiont type (woody plants only), climate, and soil abiotic conditions  
973 associated with woody plant encroachment on alpha diversity (OTU richness) of fungi and bacteria.  
974 Asterisks denote probabilities that the effect of a parameter is greater or less than zero based on  
975 credible intervals (\*\* = probability > 95%; \* = probability > 90%; \* = probability > 85%). Parameter  
976 estimates and credible intervals are listed in Table S2. All values are standard normalized as was done  
977 prior to modeling. b,c) Interactions between vegetation type and mean annual precipitation (MAP) and  
978 mean annual temperature (MAT) on fungal and bacterial richness. Points are raw data, lines are fitted  
979 model estimates, and all values are standard normalized. Interactions showed that encroachment by  
980 woody plants lead to increased, decreased fungal richness in sites with lower, higher precipitation and  
981 increased, decreased bacterial richness in sites with lower, higher temperature as compared to  
982 herbaceous plant communities. All values are standard normalized as was done prior to modeling

983 **Fig 4.** Diagram of impacts of woody plant leaf traits on bacterial and fungal richness via changes in soil  
984 abiotic conditions based on the Bayesian SEM. Red lines show significant negative relationships and blue  
985 lines show significant positive relationships. Slope coefficients (standardized) show the magnitude and  
986 line thickness reflects the associated credible interval of each relationship (85%, 90%, 95%). Leaf traits  
987 shown in each corner reflect loadings on each Principal coordinates (PC) axis. Parameter estimates and  
988 credible intervals are listed in table S2 and trait loadings are shown in Fig S3.

989 **Fig 5.** NMDS plots of community dissimilarity using Bray-Curtis and Weighted Unifrac distance for soil  
990 fungi (a-c) and bacteria (d-f) respectively. Colored ovals represent 95% confidence intervals of sample  
991 ordination grouped by vegetation and root symbiont type. The strongest abiotic predictor of each

992 microbial group (MAP-Fungi and soil pH-Bacteria) is plotted on the right with a color ramp for  
993 continuous values. Model parameter estimates are listed in Table S3.

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## 999 Tables and Figures

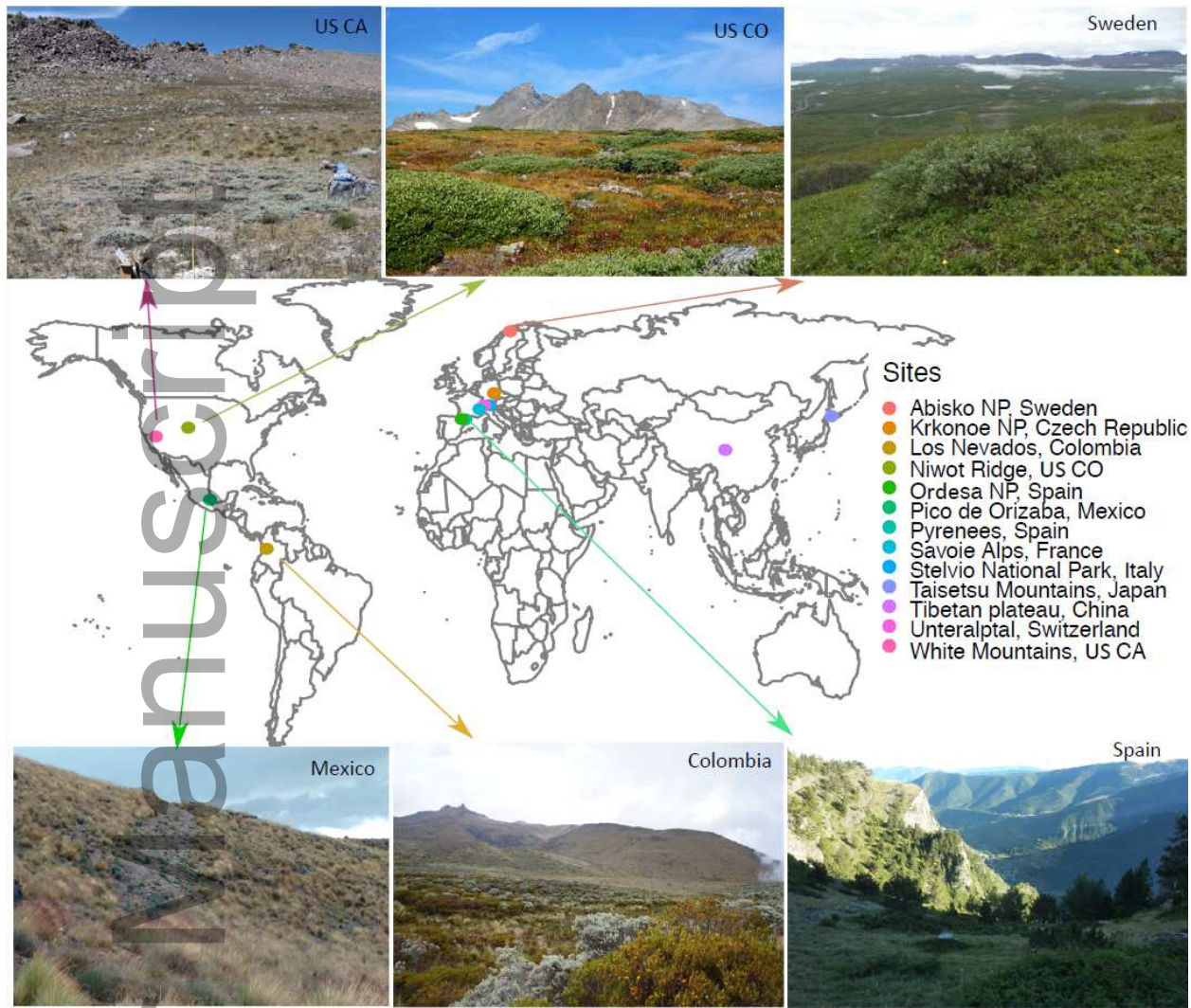
1000 **Table 1.** Woody Encroachment study sites included in this synthesis and corresponding information.  
1001 Symbiont type refers to root microbial symbionts of woody plant species Arbuscular mycorrhizal (AMF),  
1002 Ecto- or Ericoid mycorrhizal (ECM.ERM) and N<sub>2</sub>-fixing bacterial (Nfix). Reference manuscripts describe  
1003 woody encroachment patterns at each site.

Site	Latitude	Longitude	Elevation (m)	Symbiont type	Woody species	Reference
China	33.66536	101.8663515	3506.000	AMF	<i>Potentilla fruticosa</i>	Klein et al. 2007
Colombia	4.792977	-75.4254868	4024.000	AMF	<i>Hesperomeles obtusifolia</i>	Matson and Bart 2013
Czech Rep	50.768887	15.5398797	1343.749	ECM.ERM	<i>Pinus mugo</i>	Soukupová et al. 1995
France	45.421500	6.1780400	1797.946	Nfix	<i>Alnus alnobetula</i>	Anthelme et al. 2007
Italy	46.673611	10.5919444	2357.600	ECM.ERM	<i>Rhododendron ferrugineum</i>	Cannone et al. 2007
Japan	43.563258	142.9011030	1771.600	AMF	<i>Sasa kurilensis</i>	Kudo et al 2011

Mexico	19.064165	-97.2669115	4110.500	AMF	<i>Chionolaena lavandulifolia</i>	Ramírez-Amezcu et al. 2016
Spain	42.575821	1.3667150	2100.000	AMF	<i>Juniperus communis</i>	Montané et al. 2007
Spain Ordesa	42.602807	0.0332073	1942.007	Nfix	<i>Echinopartum horridum</i>	Komac et al. 2011
Sweden	68.360658	18.7368890	740.000	ECM.ERM	<i>Salix lapponum</i>	Rundqvist et al. 2011
Switzerland	46.621100	8.6349430	1598.800	Nfix	<i>Alnus alnobetula</i>	Caviezel et al. 2014
US CA	37.576447	-118.240913	3750.000	AMF	<i>Artemisia rothrockii</i>	Kopp and Cleland 2014
US CO	40.153600	-105.670750	3530.000	ECM.ERM	<i>Salix glauca</i>	Bueno de Mesquita et al. 2018

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1011 **Fig 1.**

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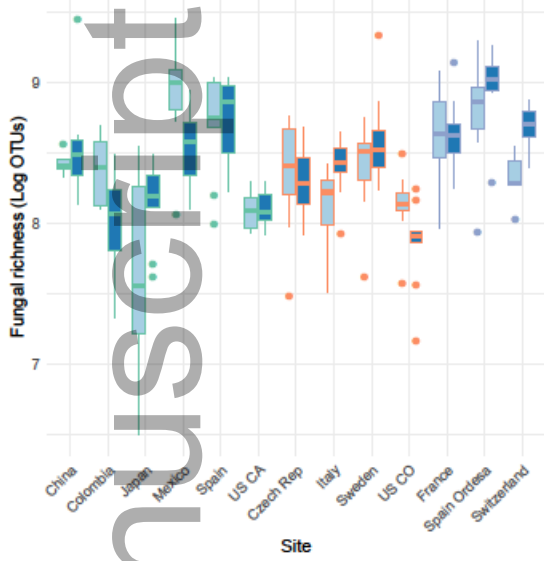
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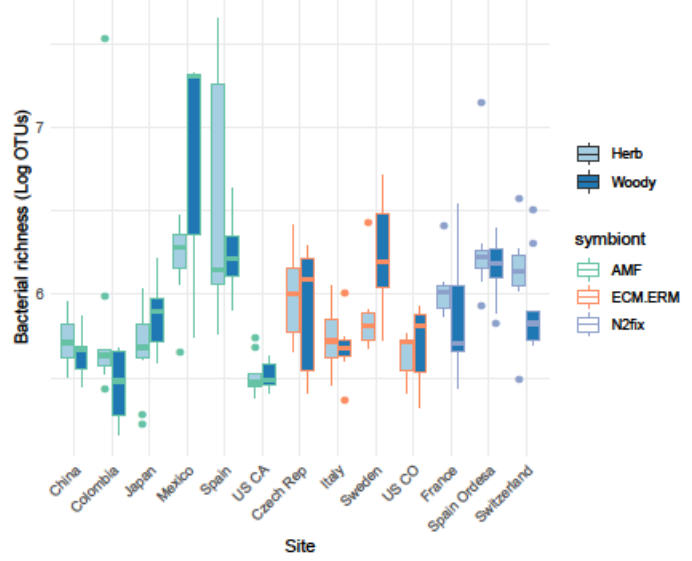
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(c)

(a)

(b)



(d)

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1024 Fig 2.

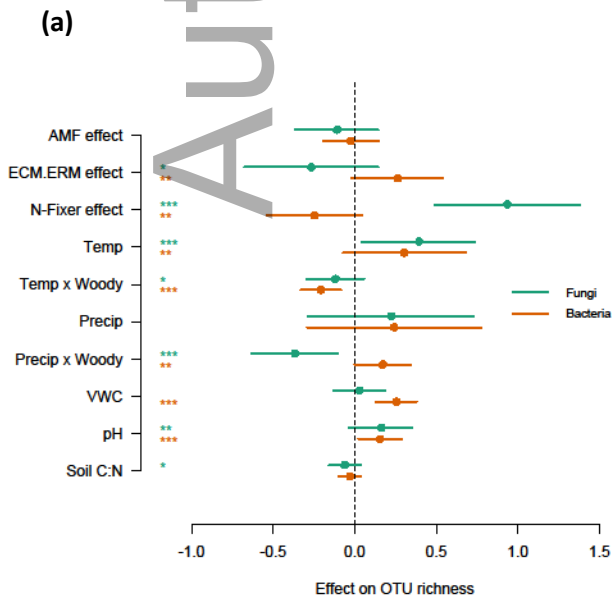
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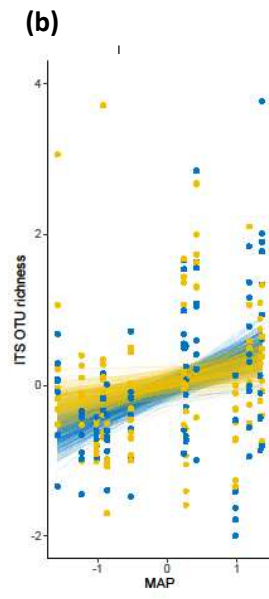
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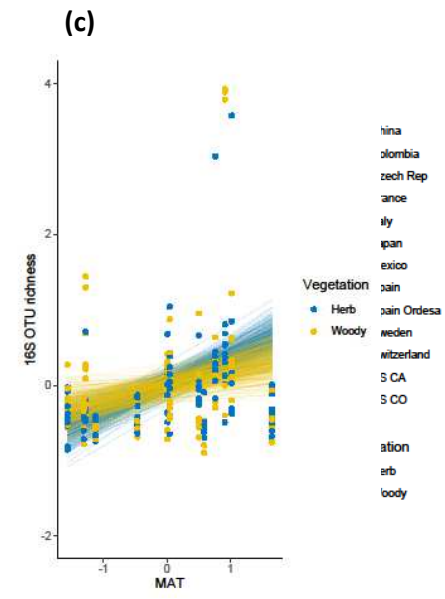
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(a)



(b)



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1030 Fig 3.

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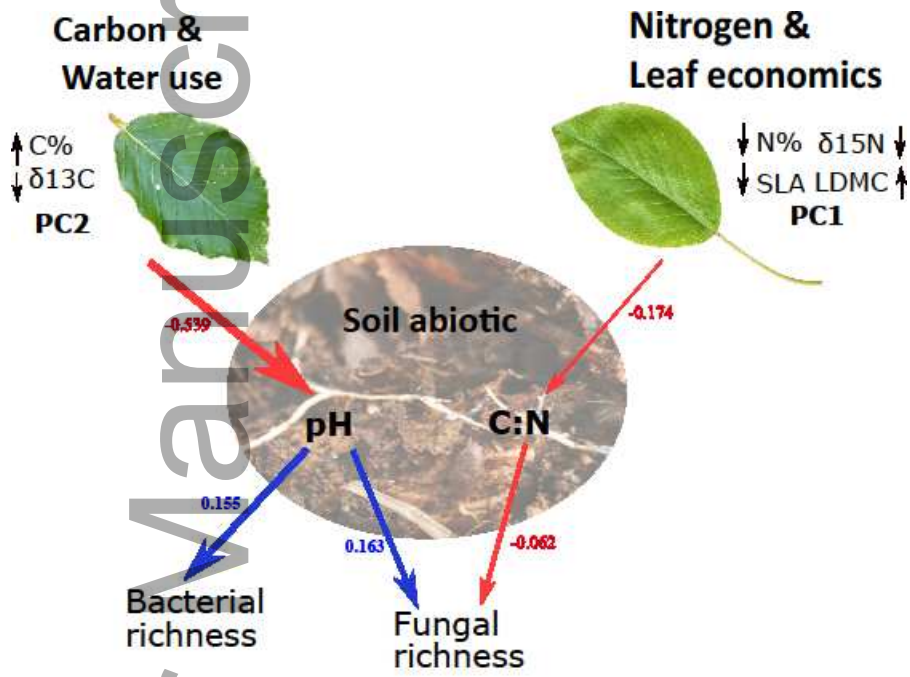


Fig 4.



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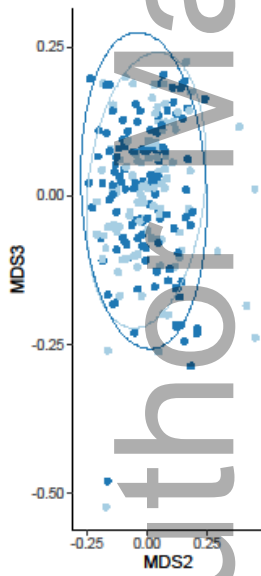
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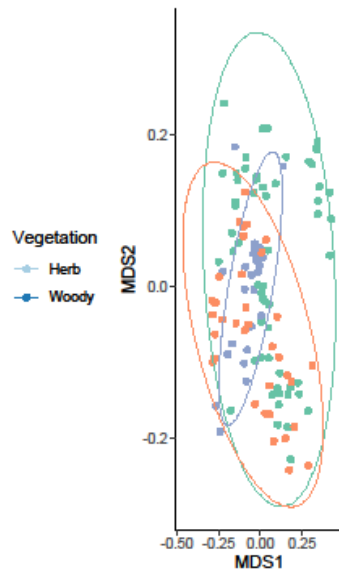
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**Fungi**

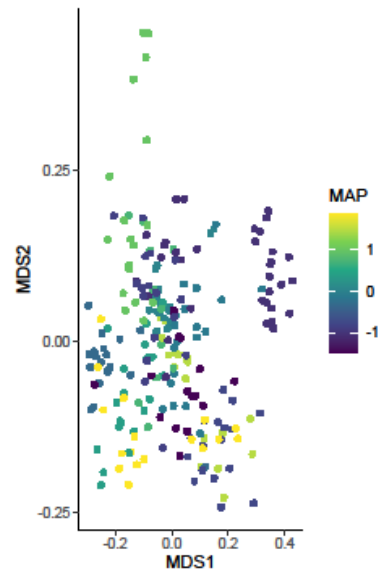
**(a)**



**(b)**



**(c)**



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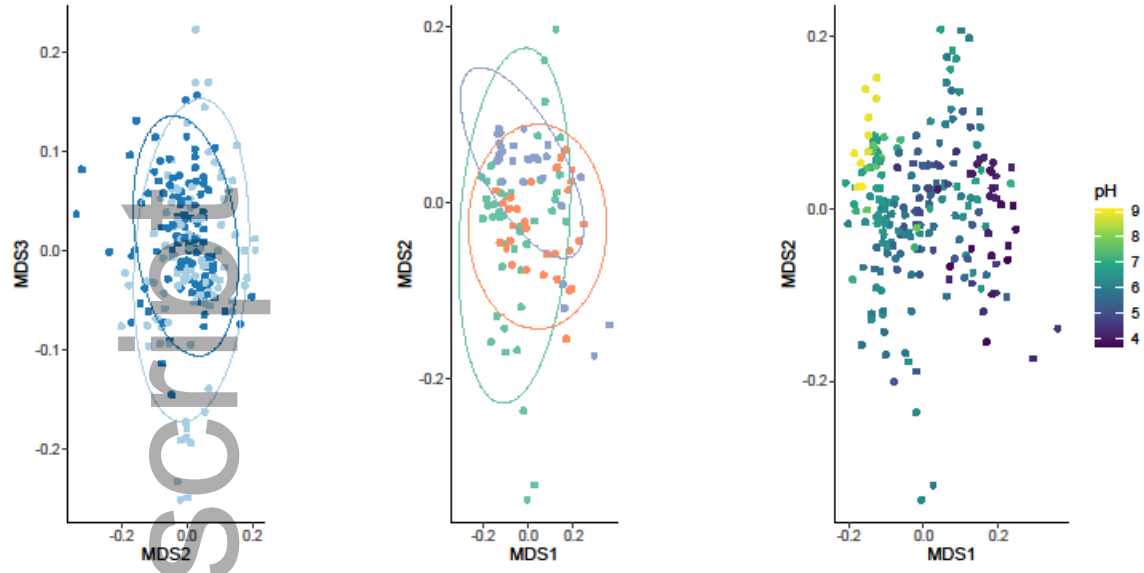
**Bacteria**

**(d)**

**(e)**

**(f)**

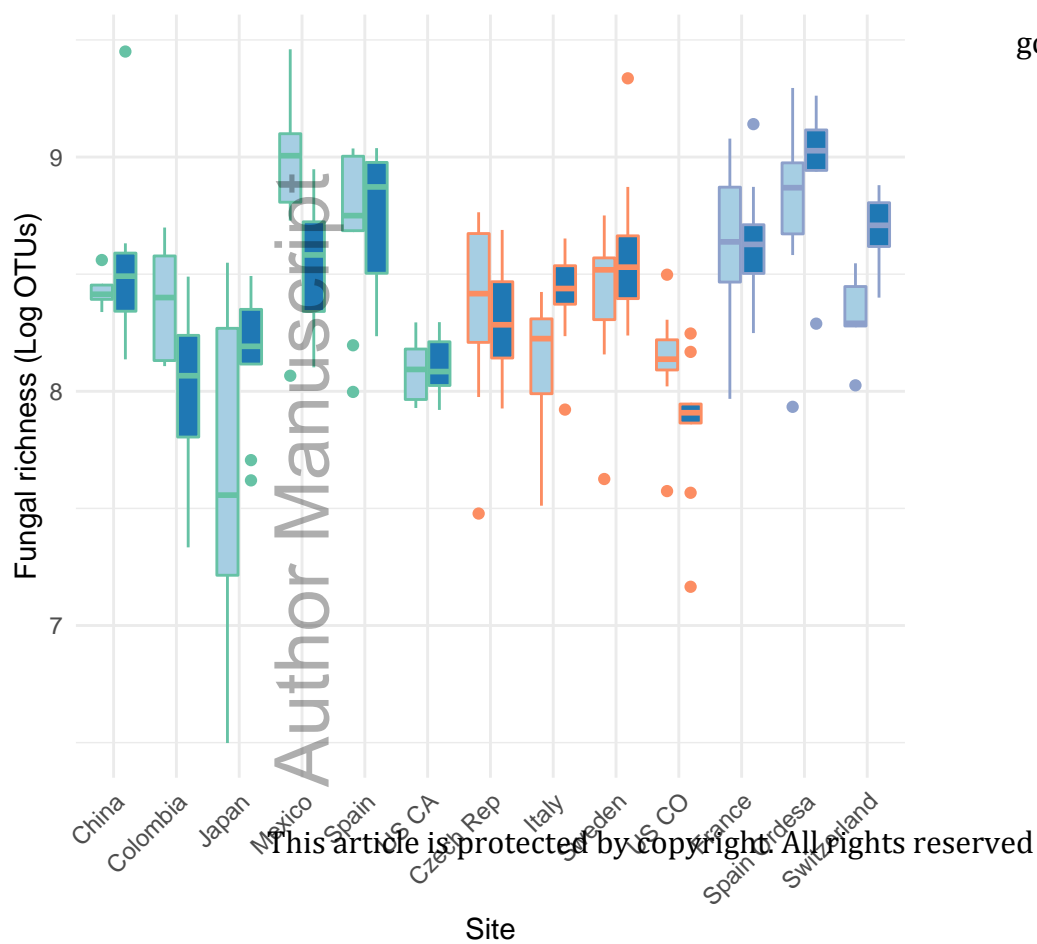
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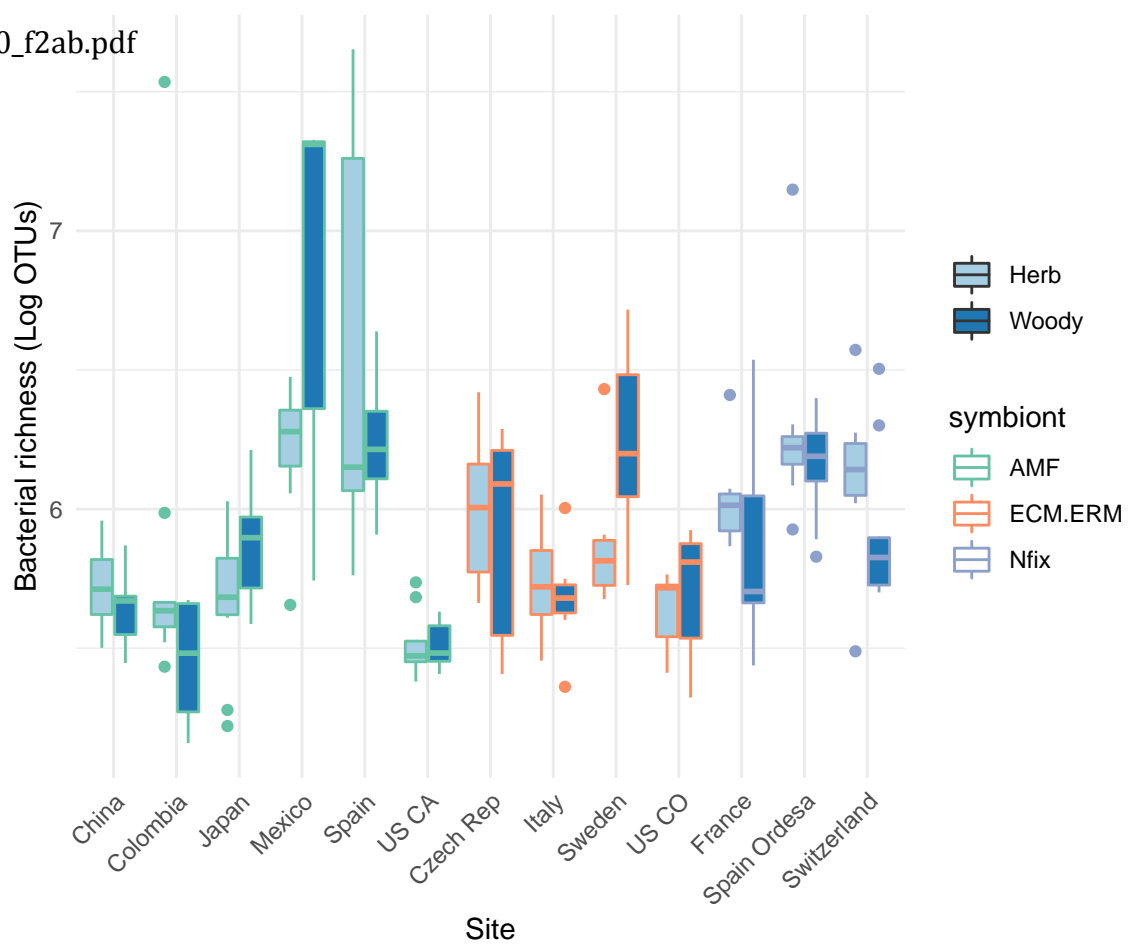
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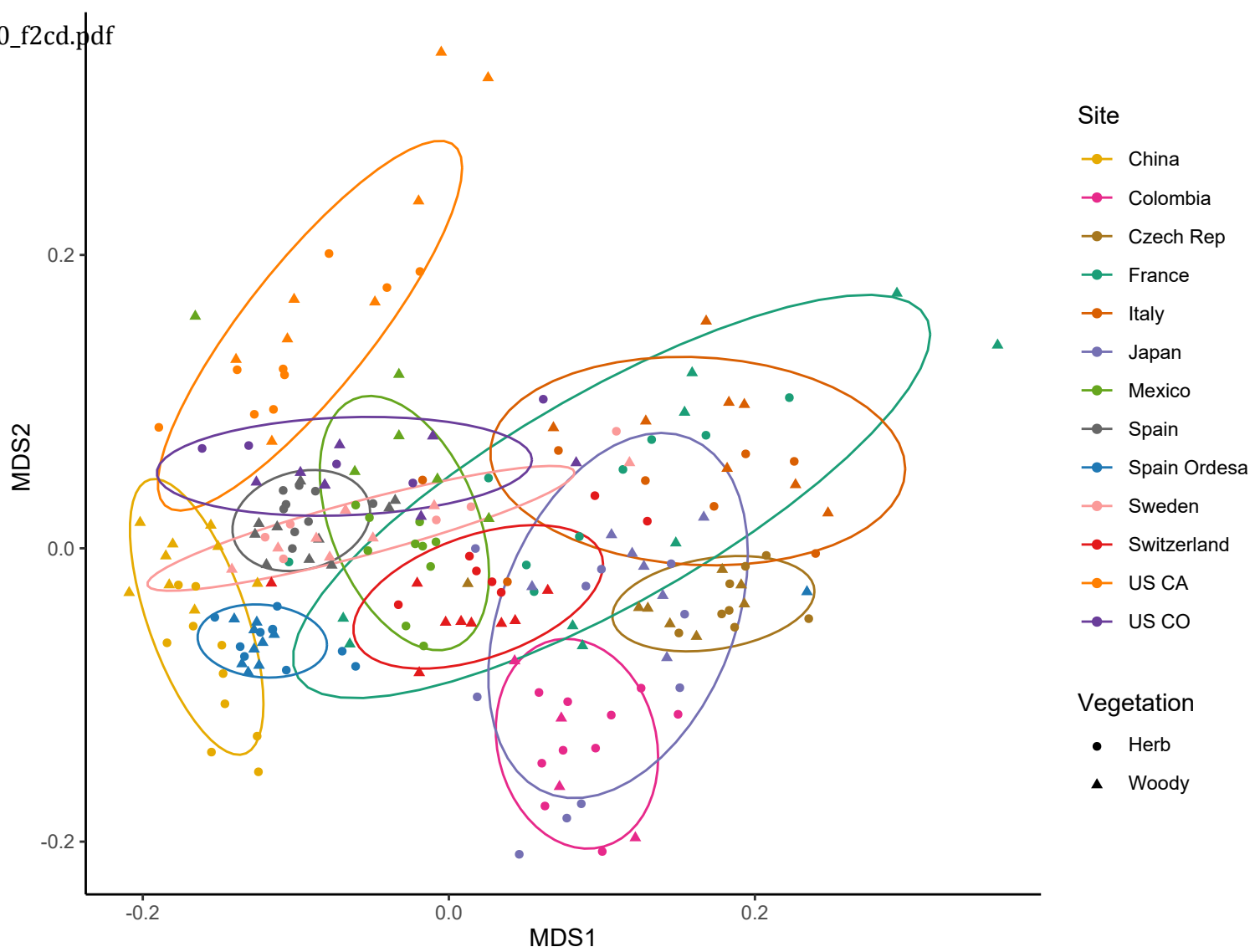
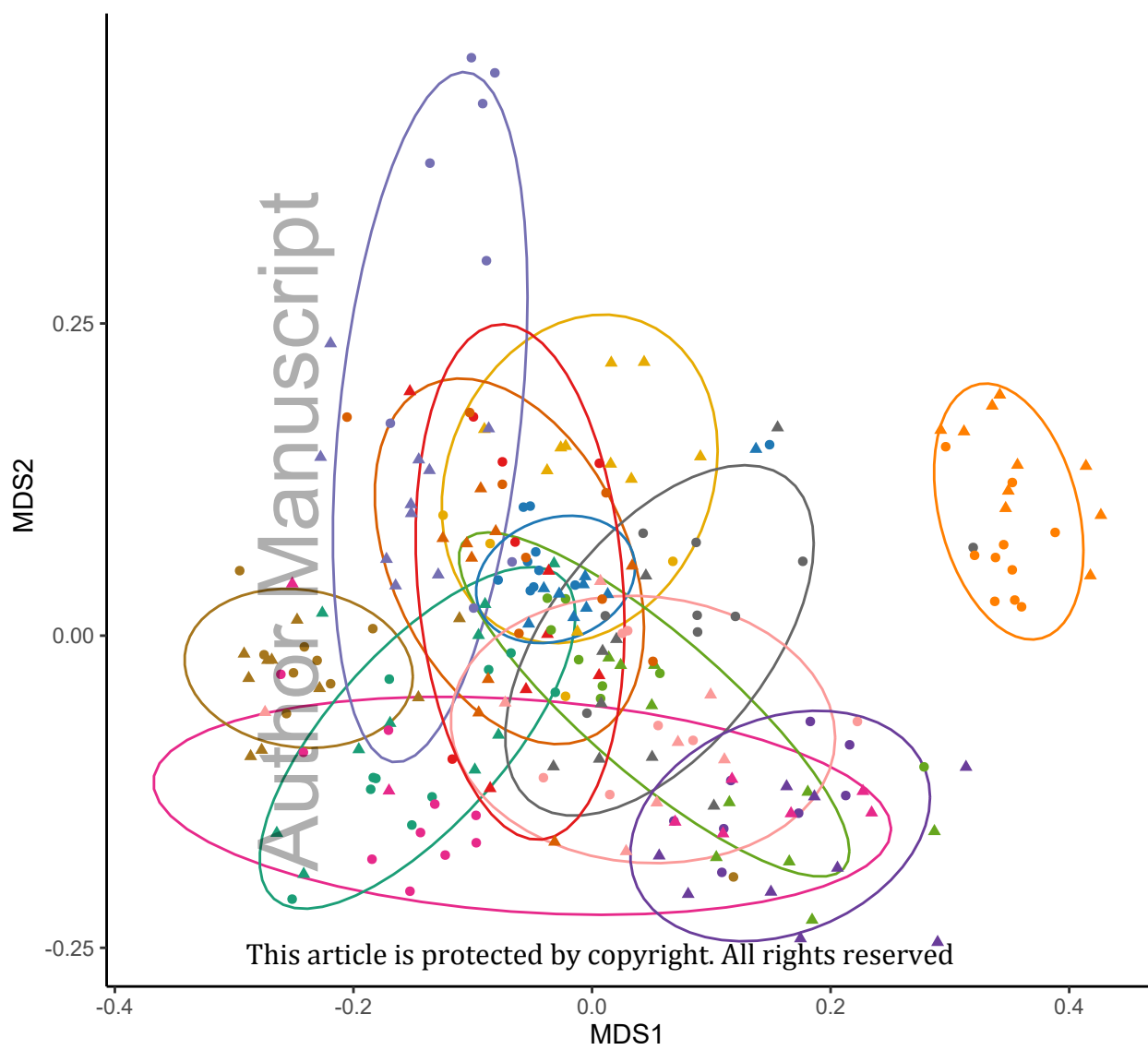
1069 Fig 5.

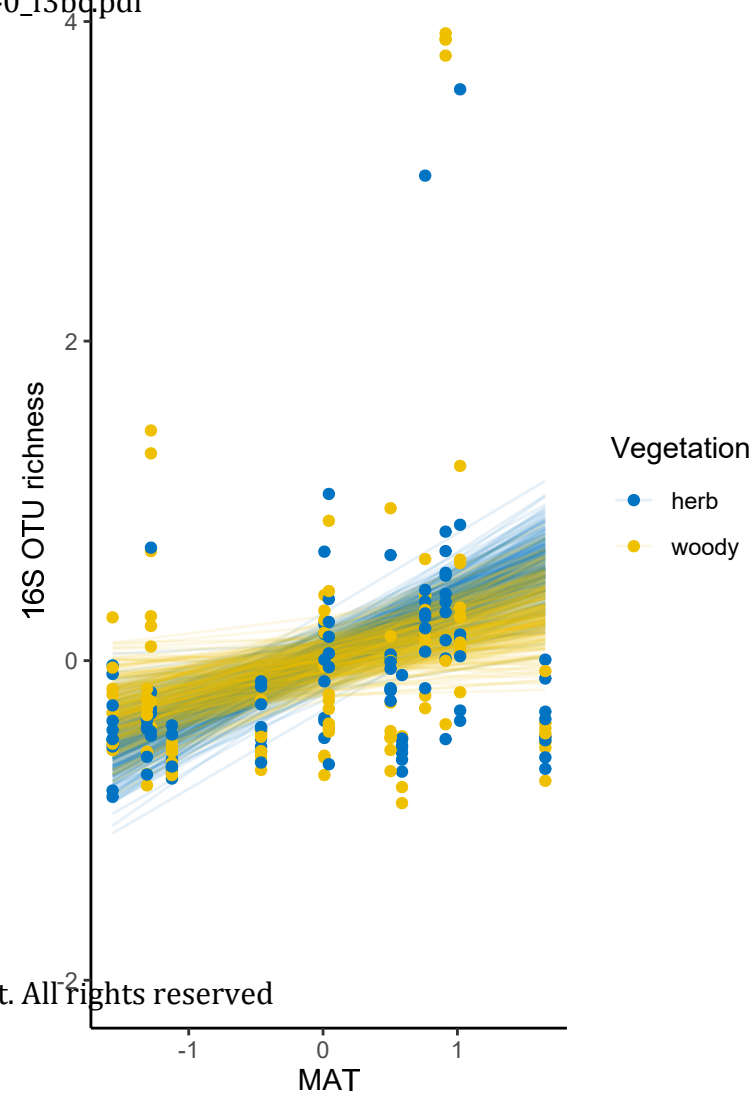
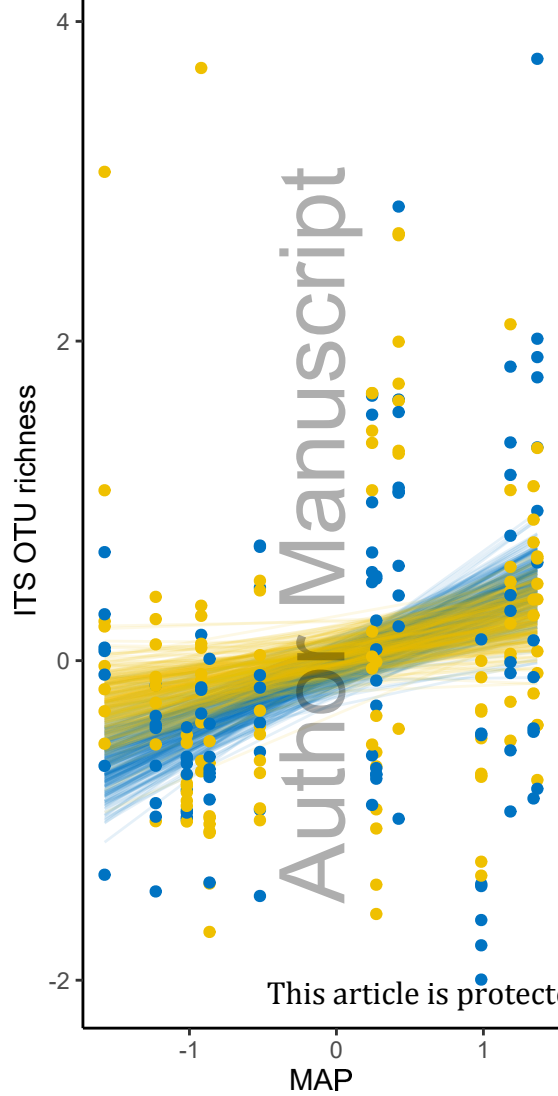
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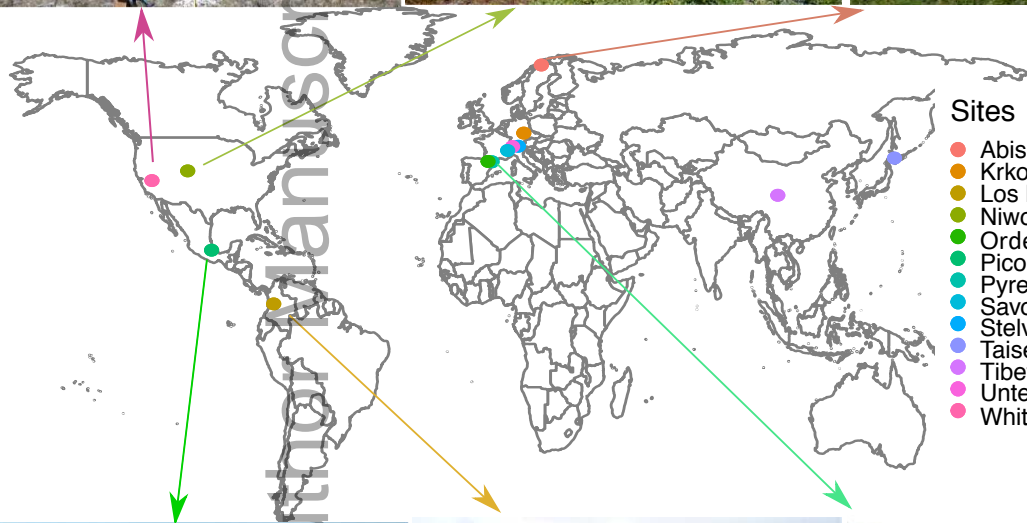


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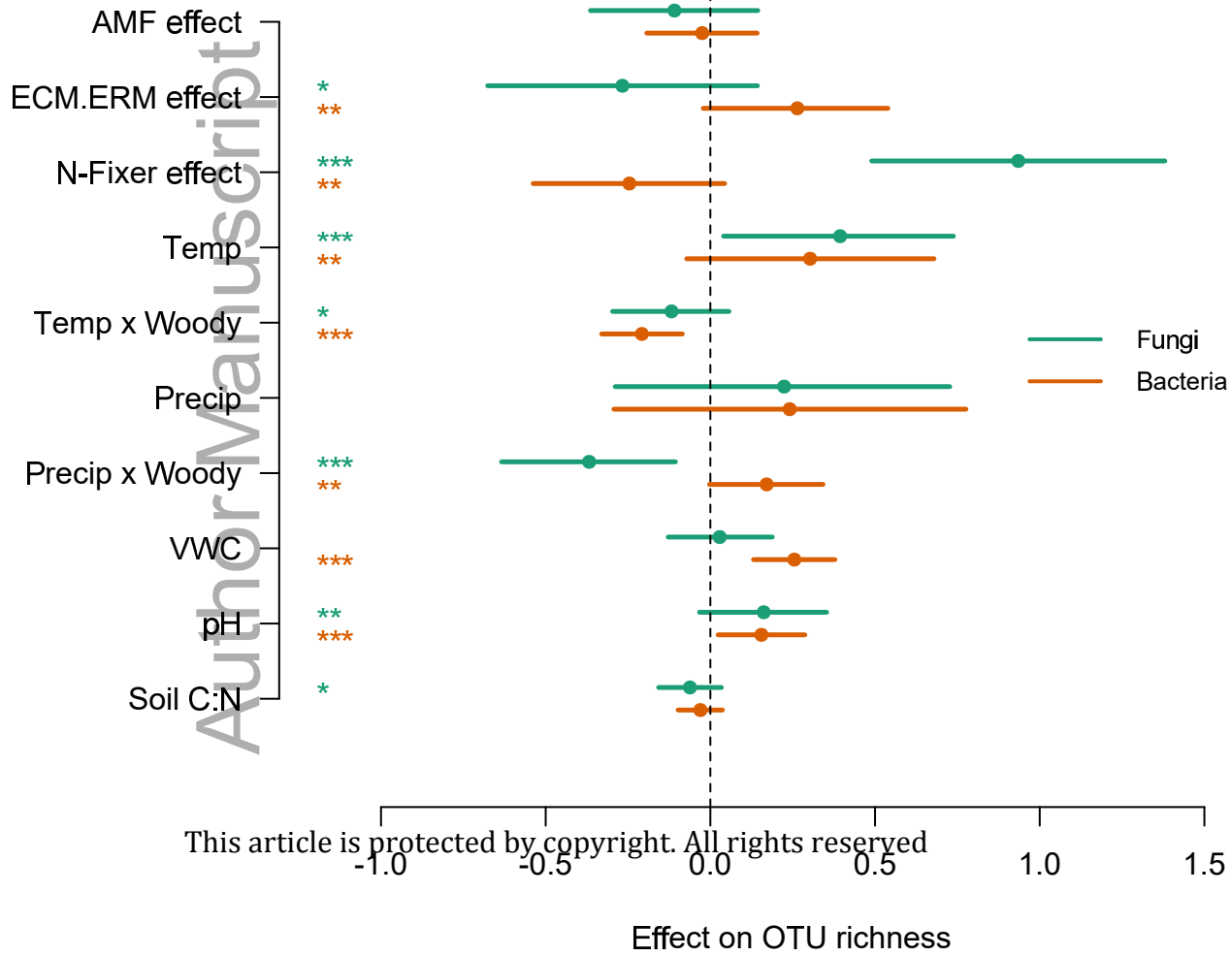




### Sites

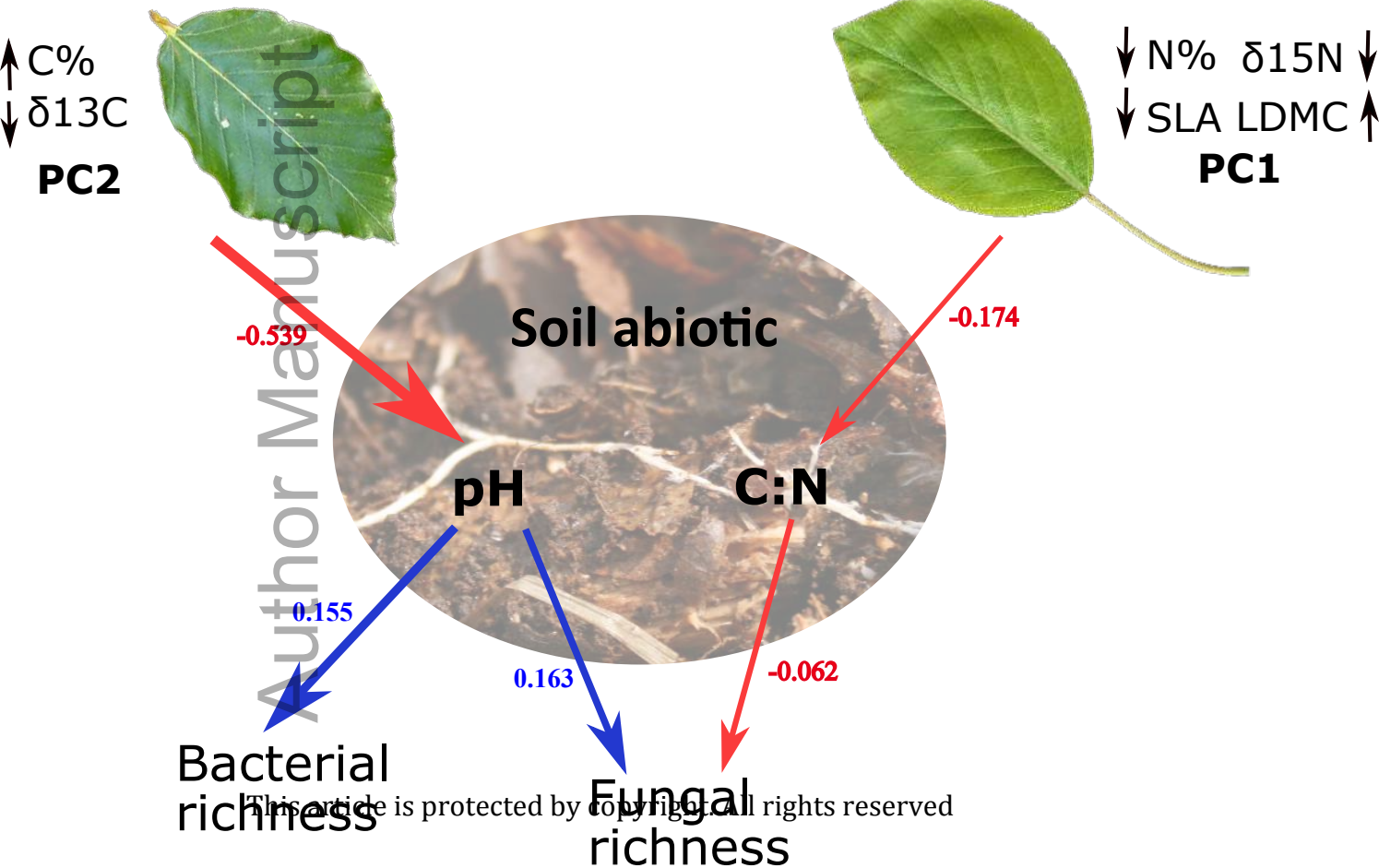
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- Krkonoe NP, Czech Republic
- Los Nevados, Colombia
- Niwot Ridge, US CO
- Ordesa NP, Spain
- Pico de Orizaba, Mexico
- Pyrenees, Spain
- Savoie Alps, France
- Stelvio National Park, Italy
- Taisetsu Mountains, Japan
- Tibetan plateau, China
- Unteralptal, Switzerland
- White Mountains, US CA



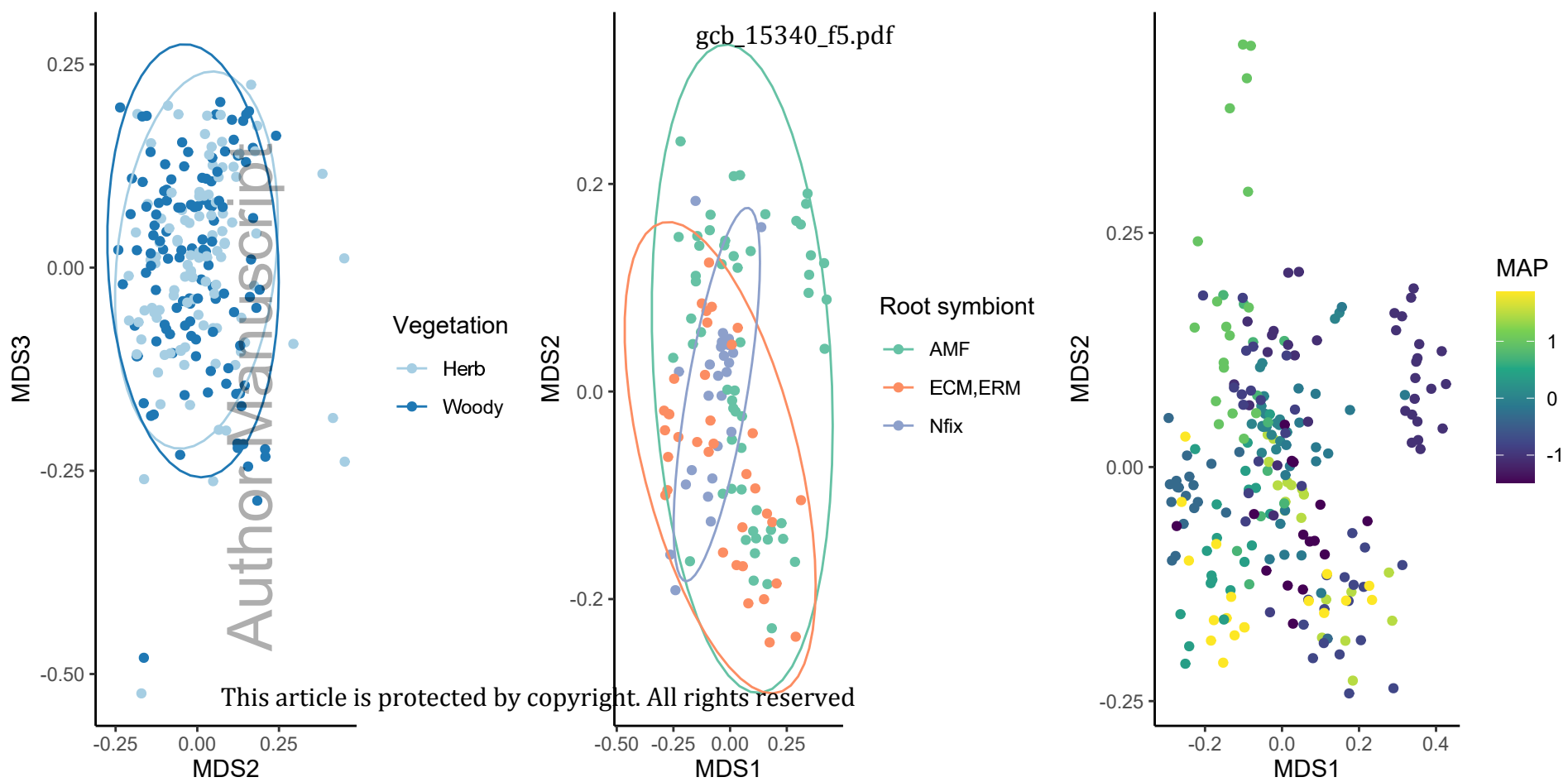


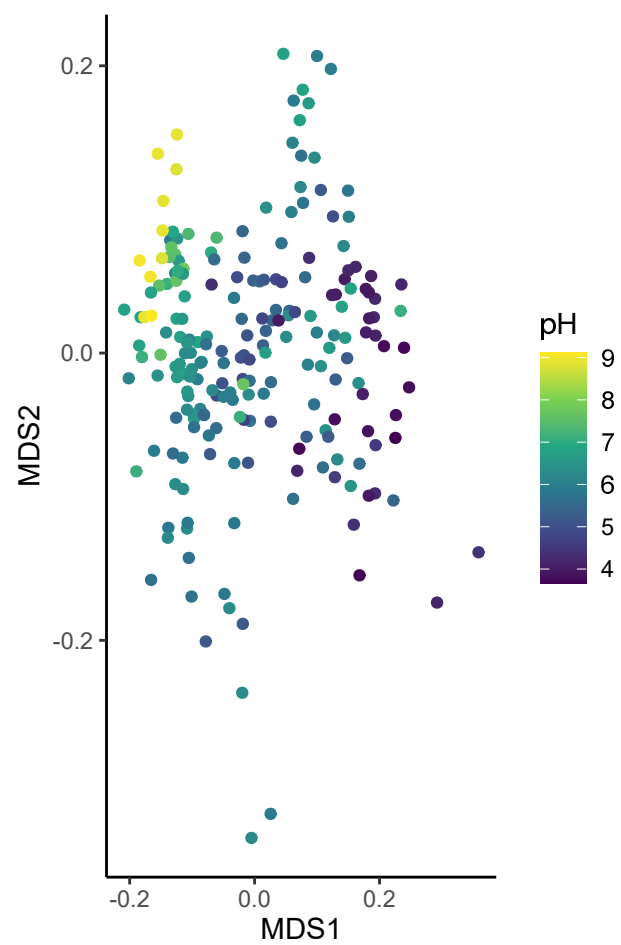
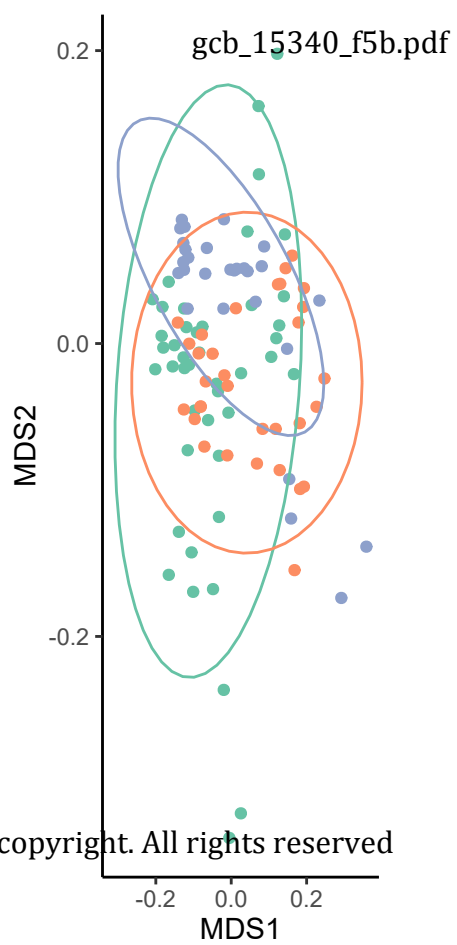
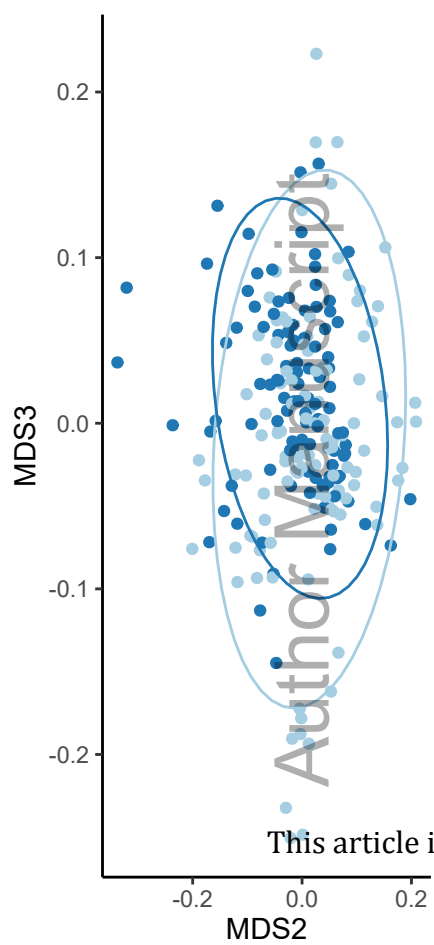
# Carbon & Water use

# Nitrogen & Leaf economics









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