

1 **Running Head: Plant structure drives soil functions**

2 **The functional structure of plant communities drives soil functioning via**  
3 **changes in soil abiotic properties**

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22 **Abstract**

23 While biodiversity is expected to enhance multiple ecosystem functions (EFs), the different  
24 roles of multiple biodiversity dimensions remain difficult to disentangle without carefully  
25 designed experiments. We sowed plant communities with independent levels of functional  
26 (FD) and phylogenetic diversities (PD), combined with different levels of fertilization, to  
27 investigate their direct and indirect roles on multiple EFs, including plant-related EFs (plant  
28 biomass productivity, litter decomposability), soil fertility (organic carbon and nutrient pool  
29 variables), soil microbial activity (respiration and nutrient cycling), and an overall  
30 multifunctionality. We expected an increase in most EFs in communities with higher values  
31 of FD and/or PD via complementarity effects, but also the dominant plant types (using  
32 community weighted mean, CWM, independent of FD and PD) via selection effects on  
33 several EFs. The results showed strong direct effects of different dimensions of plant  
34 functional structure parameters on plant-related EFs, through either CWM or FD, with weak  
35 effects of PD. Fertilization had significant effects on one soil microbial activity and indirect  
36 effects on the other variables via changes in soil abiotic properties. Dominant plant types and  
37 FD showed only indirect effects on soil microbial activity, through litter decomposition and  
38 soil abiotic properties, highlighting the importance of cascading effects. This study shows the  
39 relevance of complementary dimensions of biodiversity for assessing both direct and  
40 cascading effects on multiple EFs.

41 **Keywords:** biodiversity effect, ecosystem functioning, functional diversity, litter  
42 decomposition, multifunctionality, phylogenetic diversity, plant–soil interaction, soil abiotic  
43 properties.

## 44 **1. Introduction**

45 Despite multiple studies on the effects of biodiversity on ecosystem functioning (Naeem et  
46 al. 1994, Tilman and Downing 1994), such a relationship is still unclear due to a high degree  
47 of complexity in assessing multiple biodiversity effects. On the one hand, biodiversity can be  
48 characterized by different, often non-independent dimensions, e.g. taxonomical, functional  
49 and phylogenetic (de Bello et al. 2017), where each can play different roles (Cadotte 2017).  
50 On the other hand, the fact that many ecosystem functions (EFs) are also non-independent  
51 with respect to each other increases the complexity of the relationship between EFs and  
52 biodiversity (Zavaleta et al. 2010, Lavorel and Grigulis 2012, Meyer et al. 2018, van der Plas  
53 et al. 2019). Finally, the effect of a given trophic level on certain EFs can be mediated,  
54 through cascade effects, by other trophic levels or other ecosystem properties (Valencia et al.  
55 2018). Thus, to improve our understanding of the complex biodiversity–ecosystem  
56 functioning (BEF) relationships it is necessary separate the effects of biodiversity dimensions  
57 across multiple types of EF.

58         Among the different dimensions of biodiversity, awareness is increasing that the  
59 distribution of functional trait values in a community, rather than taxonomical diversity  
60 (usually species richness), chiefly controls EFs (Hooper et al. 2005, Díaz et al. 2007,  
61 Cernansky 2017, Cadotte 2017). Recently, the effect of plant species richness on EFs was  
62 shown to be mediated by different parameters of the community functional structure  
63 (Eisenhauer et al. 2018). At the community level, community weighted mean (CWM) and  
64 functional diversity (FD; Díaz et al. 2007) are likely to be among the main parameters of the  
65 trait distribution affecting EFs (Valencia et al. 2018). CWM is expected to mainly reflect the  
66 selection effect driven by traits of dominant species, while FD reflects the complementarity

67 effect, or non-additive effects in general (Dias et al. 2013, Cadotte 2017). Since available and  
68 measured trait information might only reflect a subset of functionally relevant traits,  
69 researchers have further considered phylogenetic relatedness between species as a proxy (or  
70 complement) of trait differences, under the assumption that more closely related species are  
71 more likely to have similar trait values (Cadotte et al. 2013). If closely related species are  
72 similar in their traits, then FD and PD (phylogenetic diversity) should be related at least to  
73 some degree. Then, the independence of PD from FD depends on the identity of traits used to  
74 compute FD and the level of conservatism of those traits in the phylogeny (Webb et al. 2002,  
75 Flynn et al. 2011, de Bello et al. 2017). While many biodiversity experiments have aimed to  
76 evaluate the role of species richness on ecosystem functioning (Tilman and Downing 1994,  
77 Roscher et al. 2004, Fargione and Tilman 2005), we know much less about the independent  
78 and combined role of functional and phylogenetic structure (but see Pichon et al. 2020).  
79 Therefore, to test the relative roles of different dimensions of biodiversity on EFs,  
80 manipulative designs that avoids the non-independence of potential predictors (e.g. FD and  
81 PD) would provide a step forward in the understanding of the complex nature of BEF  
82 relationships.

83         Another open issue in understanding BEF relationships is that given communities  
84 provide a variety of EFs, often interrelated between them. However BEFs have been  
85 primarily studied through individual functions such as biomass productivity (Hector et al.  
86 2002), resistance to weed invasion (Fargione and Tilman 2005) or nutrient loss (Scherer-  
87 Lorenzen et al. 2003). Over the past decade, quantitative tests for evaluating  
88 multifunctionality, i.e. the provision of multiple functions simultaneously (Zavaleta et al.  
89 2010), have been developed (see Byrnes et al. 2014 for a review). EFs are often not entirely

90 independent from each other but rather covary in bundles of related functions (Lamarque et  
91 al. 2014). In fact, trade-offs among different EFs (Meyer et al. 2018) may cause the absence  
92 of biodiversity effects on multifunctionality, highlighting the interest of evaluating each  
93 individual function both separately and in combination. This can be achieved by  
94 investigating direct and indirect effects between the functions and their drivers. For example,  
95 plant communities, as primary producers, are a strong driver of local environmental  
96 conditions, affecting directly or indirectly (so-called cascading effects) the EFs controlled by  
97 other trophic levels (Lavorel et al. 2013). Previous experimental work showed that the plant-  
98 species-richness effect on soil multifunctionality was mediated by changes in plant  
99 community functional structure and soil microbial communities (Valencia et al. 2018).  
100 Effects on soil ecosystem properties can occur via litter decomposability, which is strongly  
101 related to species trait syndromes (Garnier et al. 2004, Pérez-Harguindeguy et al. 2013,  
102 Pichon et al. 2020) and particularly to species positions on the acquisitive–conservative  
103 strategy continuum (Wright et al. 2004, Díaz et al. 2016). Differences in litter  
104 decomposability trigger different rates in soil processes such as mineralization of organic  
105 matter and C sequestration (Hättenschwiler et al. 2005, Hobbie 2015). Plant traits related to  
106 nutrient content and decomposability of leaves, shoots and roots, as well as root architecture  
107 or nutrient uptake efficiency, can thus influence soil microbial community composition and  
108 functions by changing resource availability and local microclimatic conditions (de Vries et  
109 al. 2012, Moreau et al. 2015, Colin et al. 2019, De Long et al. 2019). Given the strong links  
110 between plant communities and ecosystem functioning, we argue that assessments of the role  
111 of plant community functional structure on EFs would improve if they consider possible

112 cascading effects via changes in litter decomposition and /or in abiotic properties (Figure 1  
113 summarizing possible direct and indirect drivers over multiple EFs).

114         In the present study, we used a grassland BEF experiment designed with fixed species  
115 richness and independent levels of both FD and PD to investigate the role of ecological  
116 differences between species on multiple EFs. We used two levels of fertilization, which is a  
117 key driver of plant communities and EFs (Bobbink et al. 2010) and may modulate the  
118 relationship between plant traits and soil. We ask the following questions: i) what are the  
119 relative effects of different parameters of plant community functional and phylogenetic  
120 structure and fertilization levels on individual ecosystem functions/properties and  
121 multifunctionality? ii) to which extent these effects are directly affecting soil microbial  
122 activity (respiration and enzymatic activities related to carbon, nitrogen and phosphorous  
123 cycling) or are indirectly mediated by plant-related EFs (plant aboveground biomass  
124 production, litter decomposability), soil abiotic conditions (acidity, salinity and moisture)  
125 and soil fertility (organic carbon and nutrient pools)? We hypothesized that i) higher EF  
126 values are associated with higher values of FD and/or PD, i.e. higher ecological  
127 differentiation between species, due to niche complementarity and non-additive biodiversity  
128 effects; ii) the dominant plant types, i.e. as reflected by CWMs, is expected to drive selection  
129 effects on different EFs. For instance, communities dominated by species with conservative  
130 strategies are associated with lower litter decomposability and productivity (Wardle et al.  
131 2004, Lavorel and Grigulis 2012); iii) functional and phylogenetic structure might explain  
132 the activity of decomposers either directly or indirectly via changes in plant-related EFs that  
133 affect soil abiotic conditions; and iv) fertilization affects soil microbial activity, since this

134 treatment might directly impact several soil related EFs, but also indirectly via its effects on  
135 plant communities (Barnard et al. 2006, Sardans et al. 2008).

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## 137 **2. Material and Methods**

### 138 **2.1. Experimental site and design**

139 A field experiment was established in 2015 on a mesic meadow in the Czech Republic at an  
140 elevation of 660 m (Vysočina region, 49.331N, 15.003E). The mean annual temperature is  
141 6.7°C and average annual rainfall is 759 mm (data from Černovice meteorological station, 4  
142 km from the site). The study site is an abandoned crop field used for organic farming, last  
143 cultivated in 2001 and ploughed in 2014 prior to the experiment.

144 We selected a species pool of 19 species that naturally occur in similar habitats. Prior  
145 to the experimental setup, five quantitative traits and three qualitative (categorical) traits  
146 related to the competitive ability and niche occupation of the species were obtained from the  
147 LEDA trait database (Kleyer et al. 2008) and BioFlor (Kühn et al. 2004) and used to design  
148 the experiment. The quantitative traits were canopy height (m), seed mass (mg), specific leaf  
149 area (SLA, mm<sup>2</sup>/mg), leaf dry matter content (LDMC, mg/g) and length of flowering period  
150 (month 1–12), and the categorical traits were lifespan (annual/perennial), growth form  
151 (erosulate/hemirosette/rosette) and nitrogen-fixing ability (present/absent).

152 The experimental design was completely randomized and was based on plant  
153 communities with a constant sown species richness (six species) but contrasting levels  
154 (high/low) of FD and PD resulting in four combinations. We did this by simulating all  
155 potential combinations of six species from the pool and estimating their values of FD and  
156 PD. As measures of FD and PD, we used the Rao diversity index (Rao 1982) based on the

157 trait average differences (Gower distance, for FD) and evolutionary distance (for PD)  
158 between species. Out of the possible mixtures, 10 communities were randomly selected from  
159 each of the four combinations of high and low values of FD and PD. While we focus closely  
160 on disentangling FD and PD roles, we also made sure the resulting communities did not  
161 include any unimodal or linear relationship between FD, or PD and CWM. Such relationships  
162 would stem from the fact that communities with extreme CWM values are generally  
163 composed by species with similar trait values (i.e., most species have either high or low trait  
164 values), and hence the FD values of these communities will always be small (as discussed in  
165 Dias et al. 2013). To avoid this, we excluded potential communities with extreme CWM, FD  
166 and PD values, resulting in communities in the experiment having independent CWM values  
167 from both FD and PD (see Galland et al. [2019] for a more detailed description of  
168 community selection). In addition to the 40 communities with six species combinations, three  
169 monoculture replicates of the 19 species were sown (sowing densities to all species used in  
170 Appendix S1: Table S1). Finally, the entire setup was replicated on fertilized and unfertilized  
171 plots, resulting in a total of 196 plots. Two extra monoculture plots were sown: unfertilized  
172 *Lotus corniculatus* and fertilized *Plantago media*. On each fertilized plot, fertilization was  
173 applied as dried, composted cow manure (2.2 t/ha, 33 kg N/ha, 55 kg P<sub>2</sub>O<sub>5</sub>/ha, 33 kg K<sub>2</sub>O/ha)  
174 every year at the beginning of the growing season (March).

175         In the spring and fall of 2015, all the communities were sown with seeds from a local  
176 commercial supplier (Planta Naturalis). The experiment was designed as a fully randomized  
177 factorial design, with three treatments: functional diversity (high/low), phylogenetic diversity  
178 (high/low) and fertilization (with/without). Each of the 196 plots was 1.5 × 1.5 m, with a

179 buffer zone of 0.5 m between them to avoid a possible edge effect (more information in  
180 Galland et al. [2019]).

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## 183 **2.2. Plant trait and diversity**

184 We measured *in situ* traits after the experiment was established in order to obtain the  
185 functional trait information from both the general environmental conditions of our  
186 experimental field and intraspecific variability within our experiment. The functional traits  
187 were measured following standard protocols (Pérez-Harguindeguy et al. 2013). Height, SLA  
188 and LDMC were measured in June 2016 for each of the 19 species on two individuals (one  
189 leaf per individual) per plot where the species were sown (22 to 40 samples per species per  
190 fertility level). Leaf nutrient content (carbon [C], nitrogen [N], phosphorus [P], C:N and N:P  
191 ratios) was measured in September 2016 on five samples per species per fertilization level:  
192 one monoculture and one of each of the four diversity levels. Total C and N concentrations  
193 were measured by dry combustion (Nelson and Sommers 1996) using a CHNS Elemental  
194 Analyzer vario MICRO cube (Elementar Analysensysteme GmbH, Germany). Total P was  
195 obtained by flow injection analysis (FIA). All quantitative trait values (except ratio) were ln  
196 transformed. For the analyses, all functional structure indices were recomputed with *in situ*  
197 trait values and observed biomass (g), which was obtained from ln transformed ( $\ln[x+1]$ )  
198 biomass measurement of July 2017 (see below).

199 The final functional dissimilarity between species values used in the analyses were  
200 computed using the Traits Probability Density (TPD) framework (Carmona et al. 2016). The  
201 TPD approach can accommodate intraspecific trait variability between species in a

202 multivariate space. To compute TPD, we first selected the traits which had correlation  
203 coefficients between them below 0.7 (Appendix S1: Figure S1) in order to avoid specific  
204 traits having a large effect on the combined functional diversity. Note that  $r$  values over 0.7  
205 are often associated with levels of collinearity that cause problems with parameter estimation  
206 in statistical modelling (Dormann et al. 2013). The final traits selected to describe the  
207 functional differences between species were height, SLA, LDMC, leaf P and C:N ratio. For  
208 each fertilization level, using individual species means and standard deviations for each trait  
209 together with the correlation structure between the traits, we simulated trait combinations for  
210 a population of 100 individuals for each species based on a multivariate normal distribution  
211 (function *mvnorm* in package MASS, Venables and Ripley 2002). Then a PCA was computed  
212 based on those five selected traits for the 19 populations, and the scores of individuals on the  
213 two first axes were used as “trait” values to compute the TPD functions of each species  
214 (variance explained: 68.3%, Figure 2A). The functional pairwise dissimilarity between  
215 species was calculated based on the TPD overlap between species (Carmona et al. 2019) and  
216 used to compute the Rao diversity index for functional diversity (FD). Moreover, we used  
217 PCA axis scores of species centroids and observed biomass ( $\ln[x+1]$ ) in each community to  
218 compute CWM indices. For each community, higher values of CWM-PCA1 represent  
219 communities dominated by taller species with higher LDMC and low leaf P. Higher values of  
220 CWM-PCA2 represent communities dominated by species with higher leaf C:N ratio and  
221 lower SLA. This axis separates a group of legumes from the other plants, as these have  
222 particularly low C:N and tend to cluster at the negative pole (Figure 2A).

223         Phylogenetic relationships between species were extracted from an ultrametric  
224 supertree of European plant species, ‘Daphne’ (Durka and Michalski 2012), which was

225 pruned to obtain a subtree with our 19 species. The phylogenetic distances between species  
226 were computed based on branch length information included in the Daphne supertree. These  
227 distances were used together with observed  $\ln$  transformed ( $\ln[x+1]$ ) biomass (see below) to  
228 compute the Rao phylogenetic diversity (PD) of each community. We largely achieved the  
229 desired independence between FD, PD, and CWM (see Pearson correlation among the  
230 variables in Appendix S1: Table S2), so that this is ideal for disentangling the effects of these  
231 facets on EFs.

### 232 **2.3. Vegetation biomass, diversity effect and weed colonization resistance**

233 In the first week of July 2017 (i.e. two years after sowing), at the peak of the vegetative  
234 season, the aboveground biomass of each plot was clipped (2 cm aboveground) in a 50 x 50  
235 cm quadrat. The biomass was sorted into individual sown species, while potential colonizing  
236 species were pooled into another sample. The samples were dried at 70°C for 48 h before  
237 weighing. The colonizing species biomass was used as a proxy of the sown community  
238 vulnerability to colonization. Note that the biomass of colonizing species was always limited  
239 (Galland et al. 2019) and its effect on EFs was then considered to be secondary with respect  
240 to the sown species.

241         The experimental design with biomass sampling of individual sown species in  
242 monocultures and mixtures allowed us to evaluate the net diversity effect and its partitioning  
243 into complementarity and selection effects as proposed by Loreau and Hector (2001). The net  
244 diversity effect is estimated by the difference between the observed and the expected  
245 community yield based on species performances in monoculture. Specifically, the expected  
246 yield is the weighted (by the initial relative abundance of species in the community) average  
247 yield from the monocultures of species that compose the community. In the present

248 experiment, the initial sowing density aimed to approximate equal abundance between  
249 species by adjusting both sowing density (seed number) and sowing mass (seed mass) (see  
250 details in Galland et al. 2019), so the expected yield was equivalent to a non-weighted  
251 average yield. The partitioning of the net diversity effect into complementarity and selection  
252 effects is based on the formula of Loreau and Hector (2001).

#### 253 **2.4. Litter decomposability**

254 We conducted a litterbag experiment to evaluate plant community decomposability,  
255 following a similar protocol to Cornelissen (1996) and Finerty et al. (2016). On each plot, we  
256 collected senescent leaves at the end of the 2016 growing season (from the end of September  
257 until the end of November) from all species present (sown and colonizing species). We filled  
258 three replicate litter bags with 3 g of dried material and kept the litterbags on a homogenized  
259 sand bed for 5 months (see Appendix S2 for methodological details on the decomposition  
260 experiment). Finally, for each plot we estimated the averaged complement of the ratio  
261 between the final weight and the initial weight (decomposition =  $1 - [\text{Weight}_{\text{FINAL}} /$   
262  $\text{Weight}_{\text{INITIAL}}]$ ) from the three replicate samples, and used it as an indicator of community  
263 litter decomposability.

#### 264 **2.5. Soil sampling and analysis**

265 After the biomass sampling in July 2017, we collected one soil sample per plot, which was  
266 composed of three soil cores (3 cm in diameter and 10 cm in depth) evenly distributed in the  
267 central square meter of the plot to account for spatial heterogeneity while avoiding edge  
268 effects. The pooled samples were sieved on a 2 mm mesh and split into two: a 20 g sample  
269 was frozen at -20°C while the rest was oven dried (60°C, 48 h). Dried samples were used to  
270 measure pH and electrical conductivity (EC,  $\mu\text{S cm}^{-1}$ ). Frozen samples were stored, and

271 subsequently thawed at 5°C to measure soil gravimetric humidity as the weight loss after  
272 oven drying (105°C) (GH, %). Total organic carbon (TOC, g kg<sup>-1</sup> dw), total nitrogen (TN, g  
273 kg<sup>-1</sup> dw), total potassium (K, g kg<sup>-1</sup> dw) and total phosphorus (P, g kg<sup>-1</sup> dw) were analyzed in  
274 ground samples following standard protocols as in Navarro-Cano et al. (2015). In the same  
275 root-free sieved samples, we measured microbial CO<sub>2</sub>-C production during aerobic  
276 incubation in the dark (ca. 12 g soil, 60% water-holding capacity, 28°C, 28 days) using a  
277 6700 Headspace CO<sub>2</sub> analyzer (Illinois Instruments). We fitted the curve of cumulative CO<sub>2</sub>-  
278 C production over time to a sigmoidal equation with three parameters ( $y = a/(1 +$   
279  $\exp -(\frac{x-x_0}{b}))$ );  $R^2 \geq 0.95$ , in all cases) in SigmaPlot v10.0. We estimated the kinetic  
280 parameters of soil microbial respiration (a, maximum degree of CO<sub>2</sub>-C production; b, slope  
281 of CO<sub>2</sub>-C production) and used the slope as a proxy for microbial productivity. Enzymatic  
282 activities related to C ( $\beta$ -glucosidase, GA) and P (acid phosphatase, PA) cycling were  
283 quantified as the amount of p-nitrophenol (PNP) that 0.5 g of soil produced under controlled  
284 conditions (temperature 37°C, 1 h and pH 6) (Tabatabai and Bremner 1969, Eivazi and  
285 Tabatabai 1988). Enzymatic activity related to the N cycle (urease, UA), which catalyzes the  
286 conversion of urea into carbon dioxide and ammonia, was quantified colorimetrically as the  
287 NH<sub>4</sub><sup>+</sup> produced after incubating (37°C, 2 h) 1 g of soil in 4 ml borate buffer (pH 10) and 0.5  
288 ml of 0.48% urea (Kandeler and Gerber 1988).

289         The soil abiotic properties are those parameters not directly linked to fertility but  
290 which affect soil microbial community composition and activity or access to organic  
291 substances: pH, EC and GH. The soil fertility variables were the pools of TOC and  
292 macronutrients (total N, P and K), which are basic resources for the majority of heterotrophic  
293 soil microorganisms. Finally, we used microbial respiration (the slope of the CO<sub>2</sub>-C

294 accumulation curve of microbial respiration, rslope) and enzymatic activities related to C  
295 (GA), P (PA) and N (UA) cycling as indicators of soil microbial activity (Navarro-Cano et  
296 al. 2015). A PCA combining these variables showed a direct correlation between soil fertility  
297 and soil moisture, with the decomposition of organic matter, and the hydrolysis of C and P  
298 (positive pole, Dim 1; Figure 2B). Similarly, EC was positively correlated with the previous  
299 variables as typically occurs under carbon and nutrient enriched conditions due to a higher  
300 amount of ions in the soil solution. Soil pH was inversely related to TOC, as expected based  
301 on the acidic character of organic matter (negative pole, Dim 1; Figure 2B).

## 302 **2.6. Assessing multiple ecosystem functions/properties**

303 The evaluation of multiple EFs simultaneously has been a central goal of methodological  
304 development concerning multifunctionality (see Byrnes et al. [2014] for a review of different  
305 methodologies). Two of the most common approaches are the averaging method (Hooper and  
306 Vitousek 1998, Maestre et al. 2012) and the multiple threshold method (Byrnes et al. 2014);  
307 both are considered in the present study. The averaged multifunctionality takes the mean of a  
308 set of standardized EF values per plot using Z-score transformation. High values of this  
309 index mean high values for the different EFs evaluated, providing an easily interpretable  
310 summary of the measurements. We used the averaging methodology to estimate two  
311 averaged multifunctionality indices. The first one (MultF. soil) is a soil multifunctionality  
312 index and focuses on soil functions (fertility, respiration and nutrient cycling). The second  
313 one (MultF. all) combines soil and plant functions (biomass of sown community, resistance  
314 to colonization, litter decomposability).

315 Additionally, a multiple threshold approach was used to compare the results among  
316 the indices, as this approach performs well even in the presence of trade-offs among EF

317 variables (Byrnes et al. 2014). We plotted the slope of the relationship between a predictor  
318 and multifunctionality across a range of thresholds from 5 to 95%. In the curve obtained,  
319 when there is no overlap between the 95% confidence interval and the zero line for a given  
320 threshold, it means a significant relationship between the multifunctionality at that threshold  
321 and the predictor. Therefore, this indicates the percentage of functioning at which the  
322 changes in the predictor has influenced multifunctionality.

## 323 **2.7. Statistical analysis**

324 We first explored how the functional and phylogenetic structure of plant communities  
325 together with the fertilization treatment affected individual ecosystem functions/properties  
326 and averaged multifunctionality indices. We used linear models and predictor selection  
327 procedure based on the Akaike information criterion (AIC) to obtain the best model for each  
328 response variable. Fertilization, CWM-PCA1, CWM-PCA2, FD and PD were the predictors  
329 in these models.

330 In a second step, we included functional and phylogenetic structure parameters, plant  
331 biomass productivity, decomposability and fertilization as predictors before running the  
332 selection procedure. The aim of this step was to investigate if the plant EFs (biomass and  
333 decomposability) are better predictors of individual soil ecosystem functions/properties and  
334 multifunctionality than plant functional and phylogenetic structure. Also, we conducted a  
335 similar model selection including soil abiotic properties and soil fertility as additional  
336 potential predictors of individual soil EFs (soil microbial activity) and multifunctionality  
337 indices. Since soil nutrient pool variables were well correlated with each other (Figure 2B)  
338 we computed a fertility summary variable for the nutrient pool using the average  
339 multifunctionality method (i.e. MultF-NutPool is the mean of the four Z-transformed carbon

340 and nutrient pool variables TOC, TN, P and K) to reduce the number of mediator variables.  
341 Note that we also tested whether the inclusion of the interactions between fertilization and  
342 the predictors considered improved the models described above (i.e. whether the explained  
343 variance increased). However, we removed such interactions since they did not explain much  
344 additional variation.

345 Furthermore, we tested i) the full model with fertilization and all functional and  
346 phylogenetic structure parameters as predictors, and ii) the best model selected for averaged  
347 multifunctionality with the multiple thresholds approach (Appendix S1: Figure S2). Since the  
348 results were consistent with the averaged multifunctionality method, we present the results of  
349 the multiple threshold analysis only in the appendix (Appendix S1: Figures S3 and S4).

350 To test the direct effects of fertilization and plant community functional and  
351 phylogenetic structure on soil microbial activity, and also the indirect effects on this activity  
352 mediated by decomposability and soil abiotic parameters, we conducted a confirmatory path  
353 analysis using the d-sep approach (Shipley 2013) and the piecewise SEM package (Lefcheck  
354 2016). This approach has certain characteristics that differentiate it from standard structural  
355 equation models. For example, it allows for the inclusion of non-linear relationships among  
356 variables, non-normal data distributions and small sample sizes (Grace 2006, Shipley 2009).  
357 We selected the most appropriate predictors for each soil microbial activity variable (rslope,  
358 GA, PA, UA) using the selection procedure described above. For instance, biomass  
359 productivity of sown species reduced microbial respiration (Appendix S1: Figure S2).  
360 However, after considering the partial effect of soil nutrient pool (Appendix S1: Figure S5),  
361 the effect of biomass on microbial respiration ceased to be significant. Therefore, plant  
362 biomass productivity was removed from the piecewise SEM to simplify the model (i.e.

363 reducing the number of variables). The total effect of each predictor was calculated as the  
364 sum of direct and indirect effects on each soil microbial activity variable. Additionally,  
365 standardized path coefficients were used to measure the direct and indirect effects of  
366 fertilization, and community functional and phylogenetic structure (CWMs, FD, PD), plant  
367 community EFs (plant biomass and litter decomposability), and the summary variable for the  
368 nutrient pool (MultF-NutPool) on each soil microbial activity variable (Grace and Bollen  
369 2005).

370 All analyses were conducted with R software version 3.3.2 (R Development Core  
371 Team 2018) using different R packages.

372

### 373 **3. Results**

#### 374 **3.1. Effects of plant functional structure on individual EFs**

375 Biomass productivity was the EF best explained by plant community functional structure  
376 (Figure 3,  $R^2 = 0.28$ ). Communities with greater values of CWM-PCA1 (higher plant height  
377 and LDMC), CWM-PCA2 (higher C:N and lower SLA) and FD showed greater sown  
378 community biomass (Figure 3). Furthermore, high values in both CWM-PCA1 and CWM-  
379 PCA2 values had a positive effect on the net biodiversity effect, i.e. a larger increase with  
380 respect to the productivity of monocultures. Selection and complementarity effects responded  
381 to different parameters of the community functional structure. The selection effect increased  
382 with fertility and CWM-PCA2 while the complementarity effect increased under the  
383 combined effect of FD and CWM-PCA1.

384 Communities with greater CWM-PCA2 values were more productive and more  
385 resistant to weed colonization. The litter decomposability of the communities was lower

386 when sown communities had higher values of CWM-PCA2 and FD (Figure 3). Interestingly,  
387 the fertilization treatment had no impact on plant biomass productivity, although it had a  
388 significant positive effect on the selection effect (Figure 3).

389 Overall, functional structure was a better predictor of soil abiotic properties (pH, EC,  
390 GH) than soil EFs (Figure 3). In particular the pH of the soil decreased as CWM-PCA2 and  
391 FD increased (Figure 3 and Appendix S1: Figure S6). EC and GH tended to decrease with  
392 higher values of FD and CWM-PCA2, respectively, although those relationships were only  
393 marginally significant (Figure 3). The fertilization treatment had a positive effect on pH and  
394 EC.

395 The soil organic carbon and nutrient pool variables (TOC, TN, K and P) showed, in  
396 our models, no direct relationship with any plant community functional or phylogenetic  
397 structure variables. The variables related to microbial activity (rslope, GA, PA and UA)  
398 showed a weak but significant relationship with the functional structure of plant communities  
399 (Figure 3 and Appendix S1: Figure S7). In particular, soil respiration decreased with  
400 decreases of FD gradient, as phosphatase activity did along the CWM-PCA2 gradient.  
401 Fertilization had opposite effects on glucosidase and urease activities, which increased and  
402 decreased respectively. Neither functional/phylogenetic community structure nor fertilization  
403 treatment had direct effects on either multifunctionality index (MultF. all and MultF. soil).  
404 PD was not selected as a significant predictor for any of the response variables.

### 405 **3.2. Cascading effect of plant community on soil EFs**

406 The results from the path analysis (Figure 4) showed that the effects of plant community  
407 functional and phylogenetic structure on soil EFs are essentially mediated by  
408 decomposability and by soil abiotic variables. The results were consistent with the separate

409 models that add plant community EFs (plant biomass and litter decomposability, Appendix  
410 S1: Figure S2) and soil abiotic parameters (Appendix S1: Figure S5) to the initial model.

411 The main driver of soil microbial activity was the pool of organic carbon and  
412 nutrients (MultF-NutPool), which acted via both direct and indirect effects mediated by the  
413 soil abiotic conditions (EC, pH and GH; Figure 4 and Appendix S1: Figure S8). None of the  
414 functional or phylogenetic structure parameters nor the fertilization treatment were  
415 significant drivers of organic carbon and nutrient pools (neither as an aggregated index,  
416 Figure 4; nor as individual variables, Figure 3 and Appendix S1: Figure S1)

417 Greater FD and CWM-PCA2 were associated with lower levels of litter  
418 decomposability and impacted some abiotic parameters of the soil (Figure 4). Also, the  
419 CWM-PCA2 gradient had a direct negative effect on PA. The effect of CWM-PCA1 on soil  
420 EFs was essentially mediated through its positive, albeit weak, effect on litter  
421 decomposability. High decomposability was related to low GH but had no direct effect on  
422 any of the soil EFs measured (Figure 4). However, the soil EFs were well predicted by the  
423 soil abiotic properties and, also, indirectly via decomposability, CWM-PCA2 and FD (Figure  
424 4 and Appendix 1: Figure S8). PD remained a significant direct predictor of acid phosphatase  
425 activity after the inclusion of soil nutrient pool and other abiotic soil parameters (Figure 4  
426 and Appendix S1: Figure S5).

427

#### 428 **4. Discussion**

429 This study shows the importance of disentangling the potential effects of ecological  
430 differences between species in affecting – directly or indirectly – EFs. The results show the  
431 importance of plant functional structure in predicting biomass productivity- and

432 decomposition-related EFs (biomass of sown community, community resistance to  
433 colonization by weeds and community decomposability), with little additional value from  
434 phylogenetic differences. In return, these changes in plant EFs, and especially in litter  
435 decomposability, can have a direct consequence on soil conditions and EFs. In contrast, the  
436 effects of plant functional and phylogenetic structure on soil ecosystem properties are  
437 limited. Finally, fertilization has direct and indirect effects on soil microbial activity, via  
438 modification of soil abiotic variables but not via litter decomposability nor the organic pool.  
439 Our results support the importance of the cascading effects of plant functional structure and  
440 fertilization on soil EFs, which are mediated through both shifts in litter decomposability and  
441 soil abiotic properties (Figure 4, Appendix S1: Figures S2 and S5).

#### 442 **4.1. Effects on individual EFs and multifunctionality**

443 Theoretical and empirical studies suggest that different dimensions of biodiversity support  
444 different aspects of the BEF relationship. In particular, complementarity is expected to  
445 increase with increasing FD, and the selection effect is expected to be influenced more by  
446 CWMs (Cadotte 2017). Our results provide nuanced support for these hypotheses, with  
447 indeed selection effects driven by CWM-PCA2, reflecting acquisitive-conservative trade-  
448 offs, and complementarity increasing with greater FD. However, complementarity also  
449 depended from the dominant trait values (CWM-PCA1 reflecting size relate traits) and FD  
450 was not related to the net diversity effect. These latter results seems partially counter-  
451 intuitive although they are not isolated in the literature. For example, Mahaut et al. (2020)  
452 reported experimental results where the complementarity effect was essentially related to  
453 CWMs. In light of the relationship between niche differentiation and competitive ability, as  
454 described by Mayfield and Levine (2010), a potential mechanistic explanation as to why

455 CWM-PCA1 is associated with the complementarity effect on biomass production could be  
456 its relation to CWM-height (pearson  $R = 0.71$ ,  $p$ -value  $< 0.001$ ). Because average trait values  
457 are driven by the dominant species and the dominant species is usually the tallest species, the  
458 potential for vertical complementarity in the vegetation layers is greater when the dominant  
459 species of a community is taller. Hence, when the dominant species is tall, then the short  
460 subordinates can coexist under the condition that they tolerate partial shading (e.g. plots with  
461 *Achillea millefolium*, the tallest species in our study, showed more diversity in height among  
462 the other species). Overall, a tall dominant species can also include subordinates, but a short  
463 dominant simply does not leave physical space for vertical complementarity.

464 Litter decomposability was strongly and negatively related to CWM-PCA2 (Figure 3),  
465 with leaf related traits associated with it being interpreted as a proxy for litter quality of the  
466 community (high CWM-PCA2 values represent low quality). Litter quality is particularly  
467 associated with low values of C:N ratio in leaf chemical composition (Pérez-Harguindeguy et  
468 al. 2000, Pálková and Lepš 2008). C:N ratio is a trait well represented on the second axis of  
469 the trait PCA (Figure 2A) and CWM-C:N is strongly correlated with CWM-PCA2 (Pearson  
470  $R = 0.85$ ,  $p$ -value  $< 0.001$ ). CWM-PCA2 is also negatively correlated with SLA, so, again,  
471 low litter decomposability is associated with low SLA. These results indicate that  
472 communities dominated by species with conservative strategies (i.e. lower SLA) are  
473 associated with lower litter decomposability (i.e. slower turnover) and lower productivity  
474 (Wardle et al. 2004, Lavorel and Grigulis 2012). No non-additive effects between plant  
475 species seems to be at play in our study system, as litter decomposition was negatively  
476 associated with FD. Those results are consistent with the recent findings of Finerty et al.  
477 (2016) and Pichon et al. (2020) showing that decomposability increased when community

478 functional composition was dominated by species with an acquisitive trait syndrome. Pichon  
479 et al. (2020) also reported a positive, indirect effect of species richness on litter  
480 decomposition, but no statistically significant effect of functional diversity, while Finerty et  
481 al. (2016) found both positive and negative FD effects depending on CWM values.

482         Soil abiotic properties showed a direct response to the experimental treatment in our  
483 models. In particular, fertilization increased pH and EC (Figure 3), as typically occurs with  
484 manure amendments. We did not detect a significant increase in carbon or nutrient pools with  
485 fertilization. However, soil glucosidase activity increased and urease activity concurrently  
486 decreased as a result of supplying this fertilizer which is rich in organic nitrogen. Community  
487 functional structure also impacted soil abiotic properties and microbial activity in the soil  
488 (i.e. respiration and phosphatase activity). On the one hand, the relationships between  
489 community functional structure and soil abiotic properties could be related with root  
490 exudates, ions uptake, vegetation effects via changes in micro-climatic conditions or in  
491 organic matter. However, a new study is needed to explore the ecological mechanism of the  
492 statistical relationships between CWM and FD considered here and soil abiotic properties.  
493 On the other hand, phosphatase activity responded positively to plant community  
494 phylogenetic diversity (Appendix 1: Figure S5), which is consistent with previous findings  
495 (Navarro-Cano et al. 2014) and can result from two mechanisms (Goberna et al. 2016): i)  
496 plant phylogenetic diversity can stimulate soil microbial phylogenetic diversity via niche  
497 differences, stimulating microbial activity via the complementarity effect; ii) plant  
498 phylogenetic diversity can reduce microbial phylogenetic diversity via increased fitness  
499 differences, stimulating microbial activity by selection of highly competitive clades. As for  
500 litter decomposition, CWM-PCA2 and FD had a negative effect on microbial activity

501 variables and, as discussed below, the effect of community functional structure on soil  
502 properties is in fact mediated by litter decomposition.

503         We did not find any strong direct effect of community functional or phylogenetic  
504 structure, or fertilization treatment, on averaged or multi-thresholded multifunctionality  
505 indices. These results can be explained by the lack of synergy, or even trade-offs, either  
506 among individual EFs (Figure 2B and Appendix S1: Figure S9) or in response to plant  
507 community functional structure. Indeed plant-related EFs, biomass productivity and litter  
508 decomposability, all showed the same opposing responses to CWM-PCA2 and FD.  
509 Regarding soil functions, none of the four nutrient pool parameters showed a response to any  
510 treatment, but all four microbial activity measures responded to either fertilization treatment  
511 (GA, UA) or community functional structure (rslope, PA). This observation could be the  
512 result of different timelags in responses to treatments; while the microbial community can  
513 respond relatively quickly, changes in nutrient pools can take longer (Haynes and Naidu  
514 1998). In summary, our results point towards the presence of a trade-off between the EFs  
515 linked to biomass productivity and the other variables, i.e. while the biomass of the sown  
516 communities and their resistance increase along CWM-PCA2 and FD increase, the soil  
517 becomes more acidic, and litter decomposability and soil microorganism respiration reduce  
518 (Figure 3). This lack of synergy or even trade-off among individual EF responses could  
519 explain the absence of significant responses from multifunctionality analysis, as suggested by  
520 Meyer et al. (2018). However, other potential explanations are that the effect may be  
521 mediated by other variables or that some of the EFs do not respond to biodiversity (Allan et  
522 al. 2013).

#### 523 **4.2. Cascading effect on soil EFs**

524 CWM-PCA2 and FD were the variables most often selected in the models predicting  
525 individual ecosystem properties from the plant community functional structure. The soil EFs  
526 were best predicted by a combination of the direct effect of plant community functional  
527 structure and their indirect effect through litter decomposition and soil abiotic properties,  
528 highlighting the need for considering a combination of different parameters to improve  
529 predictions of EFs.

530         Microbial respiration was the soil EF for which the cascading effect of plant  
531 community functional structure was most evident. The most dominant plant species in  
532 communities are located in the upper right corner of the PCA in Figure 2A, and they are  
533 characterized by conservative traits (tall species with high LDMC [PCA1], low SLA and  
534 high C:N ratio [PCA2]). These characteristics mean that communities with high values of  
535 CWM-PCA1 and CWM-PCA2 build up large biomass with slowly decomposing material  
536 (Pérez-Harguindeguy et al. 2000). High biomass productivity and slow litter decomposition  
537 were associated with slight but significant acidification of the soil, which was, in turn,  
538 associated with slower respiration in the soil.

539

## 540 **5. Conclusion**

541 Our study highlights the richness of plant-soil interactions and the necessity to include  
542 different dimensions of plant biodiversity, particularly focusing on plant traits, in the study  
543 of multiple EFs. As expected, the amount of soil organic carbon and the nutrient pool were  
544 the main drivers of rates of microbial decomposition and nutrient cycling. Still, even just two  
545 years after manipulating the functional structure of the plant communities, we observed its  
546 impact on soil functions, particularly through the effect that plant traits exerted on soil

547 abiotic properties. Given the experimental nature of our study, this provides evidence for  
548 cascading effects from primary producers to decomposers.

549

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563

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858

859 **Figure captions**

860 **Figure 1:** Hypothetical relationships between fertilization, plant community functional and  
861 phylogenetic structure (FD = functional diversity, PD = phylogenetic diversity, CWMs =  
862 community weighted means), plant-related ecosystem functions (EFs), soil abiotic conditions,  
863 soil fertility and soil microbial activity. Fertilization treatment and plant structure (FD, PD and  
864 CWMs) could affect directly microbial activity (Malý et al. 2009, Valencia et al. 2018, Le  
865 Bagousse-Pinguet et al. 2019). However, they could also affect indirectly (i.e. cascading effect)  
866 soil microbial activity via changes in plant-related EFs, soil abiotic conditions and soil fertility.  
867 Both fertilization and plant structure may directly alter plant-related EFs, soil abiotic properties  
868 and soil fertility (arrows “c” to “h”; Bobbink et al. 2010, Laliberté and Tylianakis 2012, Sardans  
869 et al. 2012, Navarro-Cano et al. 2014, 2019, Goberna et al. 2016, Li et al. 2017, Eldridge et al.  
870 2020, Pichon et al. 2020, Pei et al. 2020, Valencia et al. 2022). For instance, root exudates,  
871 productivity, litter decomposition, and soil humidity are variables which may depend on the  
872 functional traits of plants inhabiting a given community (de Bello et al. 2010). However,  
873 fertilization and plant structure may also affect soil abiotic properties via changes in plant  
874 aboveground biomass, litter decomposability and / or soil fertility (arrows “i” to “k”;  
875 Hättenschwiler et al. 2005, Sinsabaugh et al. 2008, Blankinship et al. 2011, Eldridge et al. 2020).  
876 Typically, increases in organic matter (through root exudates or litter deposition arrows “h” and  
877 “i”, respectively) lead to concurrent increases in acidity and electrical conductivity (more  
878 organic acids are released into the soil solution) and soil moisture (Hinsinger et al. 2003).  
879 Finally, the right part of the figure shows how the plant-related EFs, soil abiotic conditions  
880 and soil fertility affect soil microbial activity (arrows “h”, to “j”; Sinsabaugh et al. 2008,  
881 Delgado-Baquerizo et al. 2013, Dacal et al. 2022).

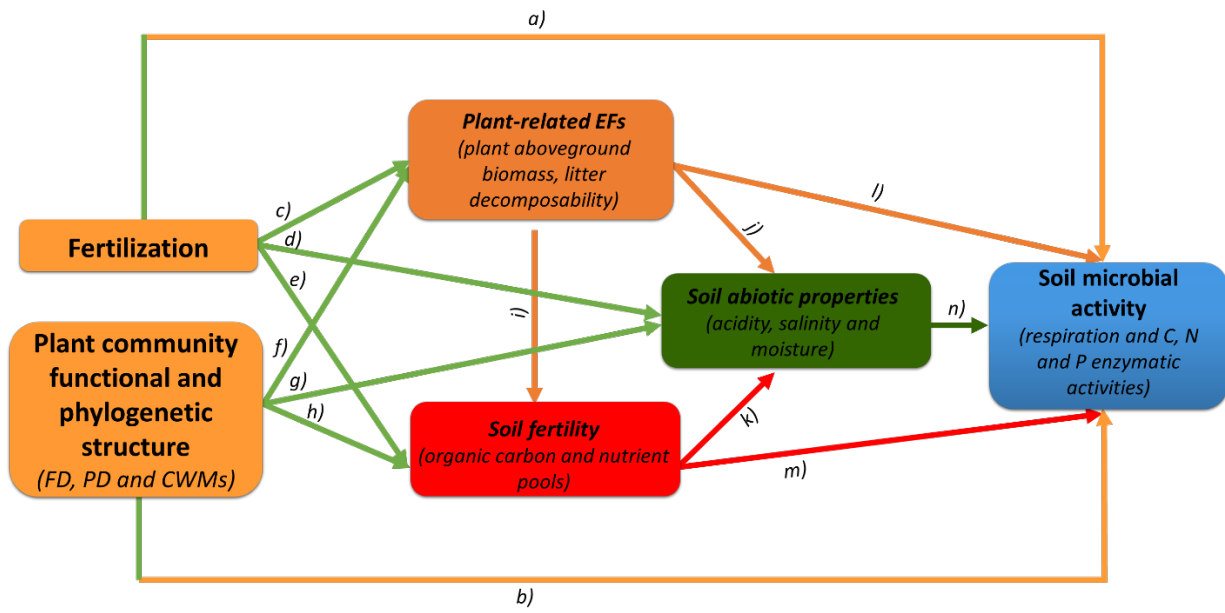
882 **Figure 2: A)** PCA on 19 species pool populations in trait space. Each color represents one  
883 species. Red arrows represent traits: H = plant height, LDMC = leaf dry matter content, SLA =  
884 specific leaf area, P = leaf phosphorus content, CN = carbon to nitrogen ratio in leaves. **B)** PCA  
885 on ecosystem property variables. The colors represent groups of ecosystem property variables:  
886 navy blue for plant biomass (Biomass sown and Biomass weed for sown or invasive species  
887 respectively), turquoise for litter decomposability, red for soil abiotic properties (pH, EC =  
888 electrical conductivity, GH = gravimetric humidity), green for soil fertility (TOC = total organic  
889 carbon, TN = total nitrogen, P = phosphorus and K = potassium) and gold for soil microbial  
890 activity (rslope = slope of the soil CO<sub>2</sub>-C accumulation curve, GA =  $\beta$ -glucosidase activity, PA =  
891 alkaline phosphatase activity, UA = urease activity).

892 **Figure 3:** Effect of fertilization and plant community functional and phylogenetic structure  
893 (CWMs, FD, PD) on individual ecosystem functions/properties and averaged multifunctionality  
894 indices. Each line represents the final linear model for a given response variable after forward  
895 selection. The adjusted coefficient of determination of the models are given in parenthesis next  
896 to each response variable. We show the averaged parameter estimates (standardized regression  
897 coefficients) of model predictors and the associated 95% confidence intervals. The colors  
898 represent groups of ecosystem function variables: navy blue for plant biomass productivity and  
899 its diversity effect decomposition (biom. sown and biom. weed for biomass of sown and invasive  
900 species respectively, NetEffect = net biodiversity effect, Sel = selection effect, Comp =  
901 complementarity effect), turquoise for litter decomposability (Decomp), red for soil abiotic  
902 properties (pH, EC = electro conductivity, GH = gravimetric humidity), green for soil nutrient  
903 pool (TOC = total organic carbon, TN = total nitrogen, P = phosphorus and K = potassium), gold  
904 for soil microbial activity (rslope = slope of the soil CO<sub>2</sub>-C accumulation curve, GA =  $\beta$ -

905 glucosidase activity, PA = alkaline phosphatase activity, UA = urease activity) and black for  
906 averaged multifunctionality indices (MultF. all and MultF. soil). In addition, light grey colors are  
907 coefficients selected in the final model, but not significant. Fert = fertilization treatment, FD =  
908 functional diversity, PD = phylogenetic diversity, CWM-PCA1 = CWM obtained with the PCA  
909 of trait values (axis 1) and the observed biomass; high CWM-PCA1 is related to taller species  
910 and higher LDMC, CWM-PCA2 = CWM obtained with the PCA of trait values (axis 2) and the  
911 observed biomass, high CWM-PCA2 is related to higher leaf C:N ratio, lower SLA and fewer  
912 legume species.

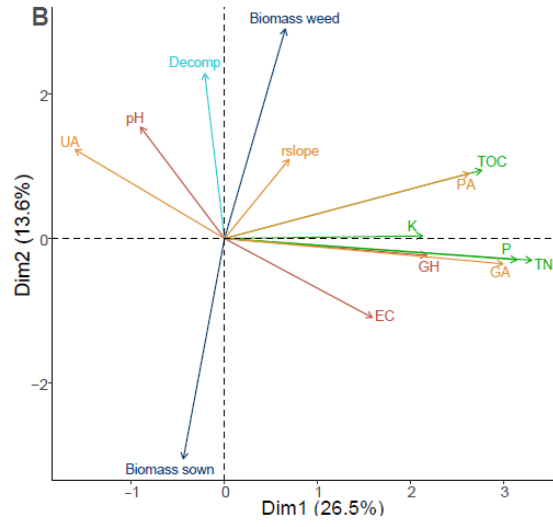
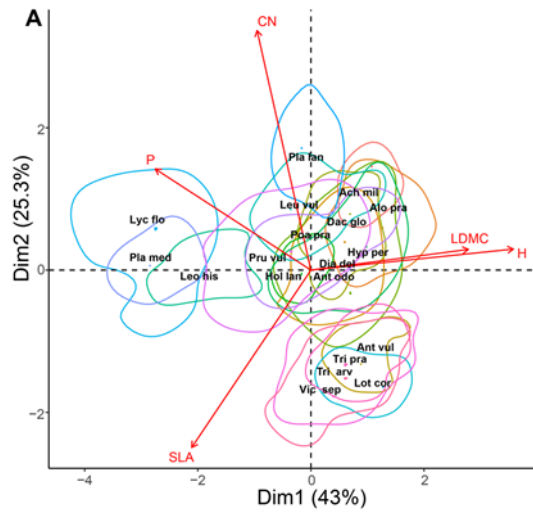
913 **Figure 4:** Structural equation models showing the effects of fertilization and plant  
914 community functional and phylogenetic structure on soil microbial activity, mediated by  
915 decomposability and soil abiotic properties (there are four piecewise SEMs superposed, one  
916 per soil microbial activity variable. See Appendix S1: Figure S10 to visualize each of the  
917 piecewise SEMs separately). The variances explained for each individual model are given in  
918 the response variable boxes. Blue and red arrows describe positive and negative effects  
919 respectively, solid lines are significant paths (p-value < 0.05) and dashed lines are marginally  
920 significant paths (p-value < 0.1). Non-significant paths are not represented for clarity. The  
921 width of the arrows is proportional to the strength of the relationship. See Appendix S1:  
922 Table S3 for all coefficients and global goodness-of-fit measures for individual models. FD =  
923 functional diversity, PD = phylogenetic diversity, CWM-PCA1 = CWM obtained with the  
924 PCA of trait values (axis 1) and the observed biomass; high CWM-PCA1 is related to taller  
925 species and higher LDMC, CWM-PCA2 = CWM obtained with the PCA of trait values (axis  
926 2) and the observed biomass, high CWM-PCA2 is related to higher leaf C:N ratio, lower  
927 SLA and fewer legume species, Litter decomp. = litter decomposability, MultF-NutPool =

928 aggregated soil nutrient pool (Mean of the four Z-transformed nutrient pool variables: total  
929 organic carbon, total nitrogen, phosphorus and potassium), EC = electro conductivity, GH =  
930 gravimetric humidity, GA =  $\beta$ -glucosidase activity, UA = urease activity, PA = alkaline  
931 phosphatase activity, rslope = slope of the soil CO<sub>2</sub>-C accumulation curve.  
932



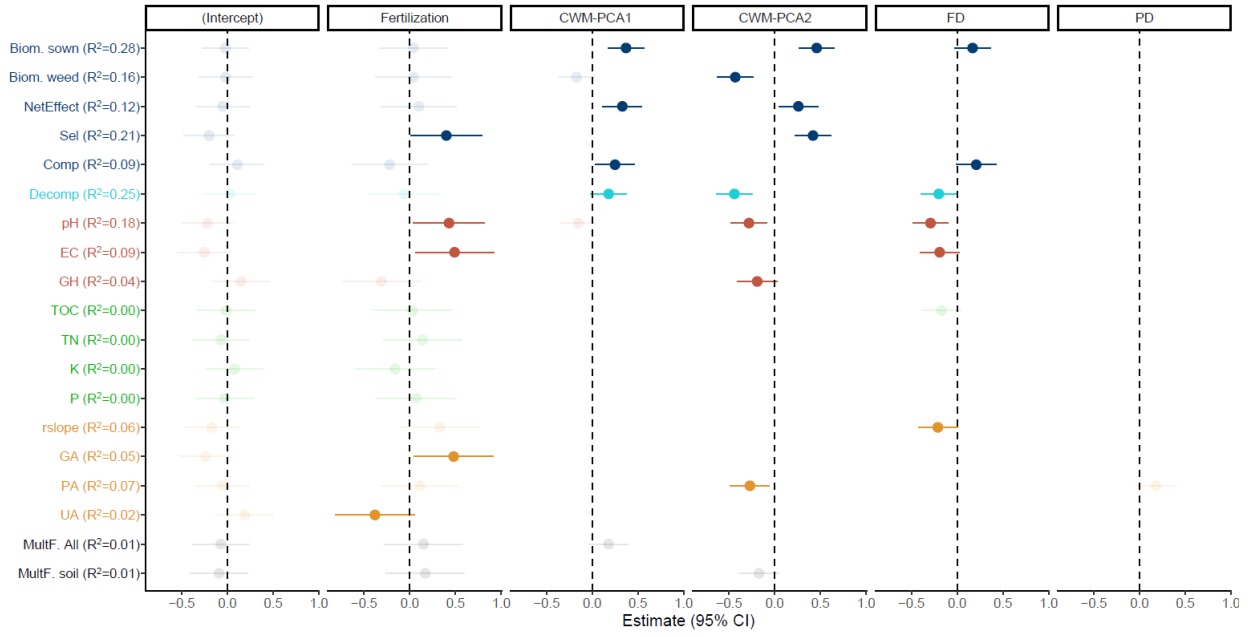
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934 **Figure 1.**



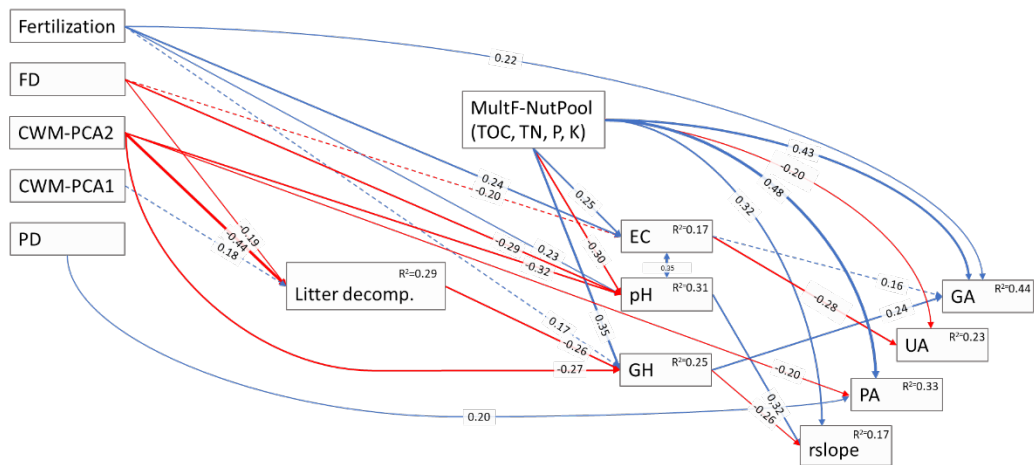
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936 **Figure 2.**



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938 **Figure 3.**



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940 **Figure 4.**

941