AM fungi and pathogen dissimilarity predicting plant-microbial interactions strength in graminoids and forbs

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Abstract

Plant-microbial interactions (PMI) play a crucial role in plant growth, fitness and productivity, primarily through the mutualism and antagonism interactions between plants and soil microorganisms. The colonization of arbuscular mycorrhizal (AM) fungi and pathogen are often used to speculate on the effects of microorganisms on plant growth, i.e. plant-microbial interactions (PMI). However, empirical studies demonstrate the relationship between AM fungi or pathogen and PMI effects remains limited, especially under different biotic and abiotic conditions. Here, we evaluated the colonization rates of AM fungi and pathogen across 13 grassland species under individual or communal conditions, in both overgrazed and restored soil. Furthermore, we investigated the relationship between AM fungi or pathogen and PMI. Our results showed that forbs exhibited significantly higher rates of AM fungal colonization compared to graminoids in community condition and overgrazed soil while graminoid roots showed higher pathogen infestation compared to forbs in individual condition and overgrazed soil. Generally, there was a positive correlation between PMI and AM fungal colonization but a negative correlation between PMI and pathogen disease. The PMI of graminoids exhibited a negative correlation with pathogen disease in individual condition and overgrazed soil, but showed no correlation with AM fungal colonization. On the other hand, the PMI of forbs showed a positive correlation with AM colonization in both restored and overgrazed soil, as well as in both individual and community experiments. However, there was no correlation between PMI of forbs and pathogen disease. The PMI of graminoids and forbs in grassland ecosystems can be driven by distinct soil microorganisms. These insights enable us to better understand how soil mutualists and pathogen mediate PMI effects on plant growth, with implications for grassland management and restoration.

Introduction

Soil microbial communities play key roles in facilitating host nutrient absorption, growth, and physiological processes (Li et al. 2019a), ultimately shaping plant community structure (Rasmussen et al. 2020). The plant-soil feedback (PSF) theory provides a powerful framework for understanding how plants respond to soil microbial communities that are modified by plants growing in that soil (Crawford et al. 2019). Accumulating evidence supports the contribution of PSF in ecological processes, such as interspecific competition (Xue et al. 2018a, b), community succession (Zhang et al. 2021, Yandi et al. 2023), species coexistence (Li et al. 2020, in 't Zandt et al. 2021), and so on.

PSF can range from positive to negative. Positive PSF occurs when plants perform better in soils conditioned by themselves vs another species or sterilized soil, and negative PSF occurs if plants influence soil communities to suppress conspecific plants (Bever 2003). Positive and negative PSF are commonly linked to plant species co-existence, since dominant plants in a stable community often suffer from negative PSF, while other rare species benefit from positive plant-soil microbial feedbacks (Li et al. 2020). In PSF framework, symbionts, enemies and decomposers are considered as the main biotic mechanisms of PSF effects (van der Putten et al. 2016). Mutualists such as mycorrhizal fungi are often essential for plant nutrition and contribute to plant drought tolerance and pathogen resistance (Stevens et al. 2018, Tedersoo et al. 2020). This mutualistic interaction can lead to positive feedback such that reduce plant diversity, as the competitive ability of the plant species with strong mycorrhizal responses will be increased, suppressing other plant species in the community (Johnson et al. 2013). Conversely, mycorrhizal fungi can also increase plant diversity by promoting subdominant plant species. For example, mycorrhizal inoculation enhances community diversity during a short term succession process (Koziol and Bever 2019). Enemies, such as pathogen, are the main factors responsible for the negative PSF, as they reduce plant performance at multiple life history stages (Bennett and Klironomos 2019). The PSF driven by soil-borne pathogen is regarded as an important driver of species abundance (Mangan et al. 2010, Kempel et al. 2018), plant species coexistence (Bever et al. 2015), plant community diversity (Mommer et al. 2018), and community succession (Pfennigwerth et al. 2018). Most speculations of arbuscular mycorrhizal (AM) fungi and pathogen driving PSF were illustrated in some reviews (Bennett and Klironomos 2019), and few researches illustrated the positive role of AM fungi in PSF by treating soil with the fungicide triadimenol (García-Parisi and Omacini 2017). To date, few empirical studies have quantitatively considered the role of both AM fungi and pathogen in mediating the strength of PSF.

The interaction between plants and microorganisms is significantly influenced by biotic or abiotic factors (Smith-Ramesh and Reynolds 2017, Lekberg et al. 2018). Increased soil nutrient availability can shift plantmycorrhizal interaction from mutualistic to parasitic (Jiang et al. 2017) and favor pathogen (Wedekind et al. 2010), thus reducing positive plant-microbial interactions (van der Putten et al. 2016). Conversely, higher soil fertility may result in less negative PSF by increasing plant defenses (Smith-Ramesh and Reynolds 2017). Generally, the modification of PSF by soil nutrient availability is likely linked to the competitive ability of plant species (Larios and Suding 2015). Higher soil nutrient levels can weaken negative PSF effects of high nutrient-demanding species, which tend to become superior competitors after nutrient enrichment (Klinerová and Dostál 2020). In addition, interspecific competition can also affect PSF by shaping resource availability (Beals et al. 2020). Dostál (2021) demonstrated the effects of nutrient availability and competition type on the PSF strength (Dostál 2021), but so far, the combined effects of soil nutrient availability and interspecific competition on PSF are still poorly explored in a high diversity community. Further, the role of AM fungi and pathogen in this process are incompletely understood. Here, we conducted a fully reciprocal experiment to explore the relationship between AM fungi or pathogen and PSF, and how they are associated with the responses of soil nutrient availability, in both no-competition or competition conditions. To this end, we cultivated plants of 13 grass species in live and sterilized soil, which were grown alone and together with interspecific competitor plants two different nutrient levels of soil. Soil microorganism inoculation was carried out by introducing sterile or unsterilized field soil in situ into sterile field soil. This approach allows us to investigate the impact of soil microorganism variations resulting from diverse steppe plant communities on plant growth. Given the absence of a standard training process for plant-soil feedback tests, we will use the term plant-microorganism interaction (PMI) to refer to this phenomenon. We aimed to answer the following specific questions: (1) How do interspecific competition and soil nutrient availability impact PMI. AM fungal colonization, and root disease severity? (2) Whether AM fungal colonization and root disease severity of plants modulate plant-soil microbial interaction? Are these relationships changed by interspecific competition and soil nutrient availability?

Methods

STUDY SYSTEM

The experiments described here are based on our previous study (Li et al. 2020). We selected 13 grass species (4 graminoids and 9 forbs) commonly found in the steppe of China, with Leymus chinensis as the dominant species. Graminoids include Leymus chinensis, Elymus dahuricus, Stipa capillata and Agropyron cristatum, and forbs include Thermopsis lanceolata, Taraxacum mongolicum, Heteropappus hispidus, Saussurea japonica, Lepidium apetalum, Allium mongolicum, Sanguisorba officinalis, Erodium stephanianumand Plantago asiatica. Soil for inoculation and substrates were collected from the National Field Station of Grassland Ecosystem (Guyuan, Hebei province, China, 41°46' N, 115deg40'E) in July 2017. We used soil collected from overgrazed grassland (>30 years) as a low-nutrient condition substrate, and soil obtained from restored

grassland (>10 years) as a high-nutrient condition substrate. The inoculation soil was collected from restored grassland. The restored soil exhibited relatively higher soil nutrient levels compared to the overgrazed soil (Li et al. 2020). All soils were excavated from the top 20 cm, and the substrate soil and the inoculum soil used as controls were sterilized in an autoclave (120 min, 121degC, 103 kPa).

PLANT-MICROBIAL INTERACTIONS

All seeds were collected in the field in autumn and surface-sterilized by 75% ethanol and then 10% '84 disinfector'. We use wet filter paper or sterilized soil to germinate the seeds, and transplant them when the roots reach about 2 cm in length. In individual experiment, one seed from each species was transplanted into a single pot containing a 500 ml mixture of sterilized substrate and living or sterilized inoculum (6:1 V: V). Sterilized substrate is composed of sterilized field soil and sterilized fine vermiculite (2:1 V: V). In a community experiment, 13 species were established together in a pot containing 4500 ml of soil mixture. In general, we set two soil nutrient levels and two soil microbial conditions, with 3 replicates per treatment, resulting in a total of 156 individual pots (2 soil substrates x 2 soil microbial conditions x 3 replicates).

PLANT MEASUREMENTS

Plants were grown for 4 months after transplant. At harvest, the aboveground plant biomass was clipped flush with the soil, and the weight of the dried shoots for each species was measured separately after drying for 48 hours at 65degC. Fifty1-cm segments of each plant were used to estimate root disease and AM fungal root colonization. We visually quantified the incidence of root disease. The brown area was considered as disease (Schnitzer et al., 2011). For AM fungal colonization analysis, root segments were washed in 10% KOH at 90 until pellucid (about 1-2 h), followed by a rinse in deionized water, soaking in 2% HCl for 5 min, and staining with 0.05% Trypan blue for 90 min. Prior to microscopy, the root segments were soaked in a Glycerol-Lactic Acid solution for over 60 minutes (Trouvelot et al. 1986).

DATA ANALYSIS

Soil microbial effects were quantitatively represented as PMI (PMI = $\ln_{\text{plant biomass in living soil}} - \ln_{\text{plant biomass in sterilized soil}$). An index value greater than zero indicates a positive PMI, while a negative value indicates a negative PMI (Lepinay et al. 2018). We used a three-way ANOVA to analyze the effects of species, interspecific competition, soil substrates and their interactions on PMI, AM fungal colonization, and pathogen diseases. The effects of interspecific competition, and pathogen diseases were assessed between graminoids and forbs, as well as between overgrazed soil and restored soil, or between individual condition and community condition. Pearson correlation was employed to examine the relationship between PMI and AM fungal colonization or pathogen diseases in different treatments. Statistical analyses were performed using the statistical software R ver. 4.3.1 'car', 'pwr' and 'psych'.

Results

PLANT-MICROBIAL INTERACTIONS

The strength of plant-microbial interactions (PMI) had significant difference between plant species, but not modified by interspecific competition and soil nutrient availability (Table 1). Interspecific competition had interaction effects with species (Table 1, P < 0.001), for example, *L.chinensis* and *E. dahuricus* suffered more negative PMI in community experiment, while *T. mongolicum* and *L. apetalum* received more benefits from soil microorganisms in community experiment than individual experiment (Fig. 1). Plant functional group was found to be an important factor influencing the direction of PMI (P < 0.001). Generally, graminoids exhibited a negative response to soil microorganisms, while forbs benefited from them (Fig. 2), interspecific competition strengthen the PMI.

AM FUNGAL COLONIZATION AND ROOT DISEASE SEVERITY

AM fungal colonization rate and percentage of disease roots among species were variable, and not affected by soil substrates origin (Table 1). Interspecific competition had a strong effect on AM fungal colonization rate (Table 1), with A. cris and H. hisp in restored soil and T. mong, H. hisp and S. offi in overgrazed soil showing a significant increased colonization rate in community experiment, while colonization rate decreased for S. japo in overgrazed soil (Fig. 3). Disease roots percentage was not modified by interspecific competition, but the species x interspecific competition interaction was significant (Table 1). Root disease incidence of specific species showed similar changes both in restored and overgrazed soil, with L. chin, S. capi, S. japo, A. mong and P. asia suffering alleviated disease in community experiment, while the others suffered more serious disease.

At the functional group level (Fig. 4), there were significant difference of AM fungal colonization rate (ANOVA, P = 0.03) and percentage of disease roots (ANOVA, P < 0.001) between graminoids and forbs. AM fungal colonization rate of graminoids were not modified by interspecific competition (paired samples test, restored soil P = 0.49, overgrazed soil P = 0.81). In community experiments, forbs showed approximately 18.1% more AMF colonization rate than in individual experiments, both in restored (P = 0.08) and overgrazed soil (P = 0.07). No significant effects of interspecific competition on PDR (percentage of disease roots) of graminoids and forbs were detected, but graminoids suffered from 15.8% and 28.9% less disease incidence in community experiment vs. individual experiment respectively in restored soil and overgrazed soil.

RELATIONSHIPS BETWEEN PMI AND AMF OR PATHOGEN

We tested whether AM fungal colonization rate and percentage of disease roots are associated with the strength of PMI, and if these relationships were influenced by interspecific competition under varying soil nutrient availability. In general, the strength of PMI positively related with AM fungal colonization rate, especially in overgrazed soil or in community experiment (Table 2, Fig.5). Specific to functional groups, AM fungal colonization rate had no significant effects on the PMI of graminoids, but it played key and positive roles in forbs-microbial interactions. Both lower soil nutrient availability and interspecific competition reinforce this relationship.

Taking all 13 species into account, negative relationship between percentage of disease roots and PMI was found in individual experiments (Table 2, Fig.6). Further, negative PMI of graminoids was enhanced significantly with increased root disease severity (P = 0.008), but only in the individual experiment and low soil nutrient context. Forbs suffered less root disease severity than graminoids, while no relationship between percentage of disease roots and PMI was found.

Discussion

AM fungi can contribute positively to PMI due to their role in resource access and disease resistance, whereas pathogen give rise to negative PMI by causing root diseases (Schroeder et al. 2020). Our empirically results showed a statistical positive correlation between AM fungal colonization and PMI, as well as a negative correlation between pathogen disease and PMI. These observed relationships were largely caused by the difference between graminoids and forbs. Moreover, the correlativity between AM fungal colonization or pathogen disease and PMI varied for graminoids and forbs, indication that the relationship between PMI and its driving factors may vary depending on the plant functional group being considered. Additionally, interspecific competition and soil nutrient availability also play significant roles in this dynamic interaction. For example, the disease severity of graminoids was statistically negative related to their PMI effects in individual experiments in overgrazed soil, while the colonization of AM fungi was more positively related to the PMI of forbs in community experiment. Overall, we found that graminoids were suppressed by harmful microorganisms, particularly in resource limited context, whereas forbs benefited from AM fungi. These linkages between soil microorganisms and PMI can aid in the management and restoration of grassland vegetation by targeting specific plant function groups.

Various plant-microbial interactions among different plant species contribute fundamentally to community diversity (Stein and Mangan 2020). Our findings reveal that *L. chin*, which is overwhelmingly dominant in steppe grassland of northern China, suffered from a negative PMI, suggesting that soil microorganisms sup-

press the growth of L. chin. This suppression may facilitate community richness by creating low-competitive conditions for other plant species. This phenomenon aligns with the concept of negative PMI, also known as PSF, frequently occurs when plant seedlings grow in conspecific soil (Mangan et al. 2010). Considering that our soil samples were collected from a grassland perennially dominant by L. chin (biomass accounting for >40%), it is an unsurprising result that strong negative PMI would be exerted on L. chin. For other graminoids, E. dahu and A. cris exhibited a propensity for experiencing negative PMI, whereas the biomass of S. capi appeared to be simply reduced by soil microorganisms in overgrazed soil. According to previous studies, plant species that are closely related are more likely to have natural enemies (Kamble et al. 2024) and show more similar feedback effects due to their longer shared evolutionary history (Munzbergova and Šurinová 2015). Moreover, graminoids generally release similar semi-polar metabolites to each other (Dietz et al. 2019, 2020). which are related to shaping soil microbial communities (Badri and Vivanco 2009). Our results showed that E. dahu and A. crisgenerally experienced a more comparable PMI with L. chin as compared to S. capi, possibly due to their close relation. Specifically, E. dahu, A. cris and L. chin were categorized as Triticeae while S. capi was classified as Stipeae. In contrast, eight plant forbs, with the exception of L. apet, exhibited a tendency to experience positive PMI, indicating that they were able to derive benefits from soil microorganisms. At the level of plant functional group, forbs suffered a more pronounced positive PMI compared to graminoids. This phenomenon could be attributed to the absence of specific pathogen that target forbs in the soil, as well as the relatively weaker nutrient competition ability of forbs (Li et al. 2020). which result in a greater reliance on mutualistic microorganisms for nutritional support.

We conducted measurements of AM fungal colonization and the percentage of root disease in order to evaluate the mutualistic or antagonistic relationships between plant and soil microorganisms, as previously mentioned. The results revealed a significantly higher colonization rate of AM Fungi in forbs compared to graminoids in community experiments conducted under low nutrient level. Furthermore, forbs showed a significant positive correlation between PMI and AM fungal colonization in all biological (individual and community experiments) and abiotic treatments (restored and overgrazed soil), whereas the PMI of graminoids was not affected by AM Fungi. These results statistically suggested a weak effect of AM fungi on the growth of graminoids, correspond to the patterns that C3 grasses exhibited smaller responses to mycorrhizal inoculation than C4 grasses and non-N-fixing plants (Hoeksema et al. 2010), with the graminoids selected in this experiment following the C3 photosynthetic pathway. This weak effect of AM fungi on the growth of graminoids could also potentially be attributed to differences in root structures and physiology (Güsewell 2004), and the resulting nutrient uptake strategies. Specifically, AM fungi could benefit plants by enhancing their nutrient access through the exploration of hyphae in plant-fungal symbiosis (Bueno de Mesquita et al. 2018, Li et al. 2019b). The lush root system of graminoids, particularly their fibrous root system, enables them to rapidly occupy soil space and efficiently absorb nutrients, whereas the root system of forbs is comparatively smaller in size, potentially limiting their nutrient uptake. Within the confined microcosmic system of our experiment, the expansive distribution of graminoids across a considerable soil has the potential to hinder the involvement of AM fungi in nutrient uptake processes. Conversely, forbs with their more restricted root range might exhibit a more pronounced increase in plant nutrient absorption facilitated by the hyphae.

In individual experiments, it was observed that graminoids exhibited a higher percentage of root diseases caused by pathogen compared to forbs. This could be attributed to the legacy of a grassland plant community that was dominated by *L. chin*, which made the graminoids more susceptible to these diseases. We detected a significant negative linear relationship between the PMI of graminoids and the percentage of pathogen-induced diseases under overgrazed soil conditions. However, the PMI of forbs did not show any changes with respect to diseases percentage. This finding suggested that the PMI of graminoids was more reliant on their resistance to pathogen, particularly when these plants were unable to obtain sufficient nutrients. Gramineous plants in our research could be regarded as being 'fast' species with a high root length (Cortois et al. 2016). When nutrients in the soil are insufficient, their growth may be limited, resulting in a weakened immune system and increased susceptibility. On the other hand, 'slow' species such as forbs showed slower growth but higher disease resistance, which explains the lack of correlation between the PMI of forbs and pathogen diseases. Further, we did not observe significant effects of soil nutrients on AM fungal coloniza-

diseases. In our research, restored soil was consider to be more resource-rich than overgrazed soil, with the presents of interspecific competition allowed graminoids to obtain more resources. On the other hand, forbs were subject to greater resource competition influenced by variations in plant competitiveness, supporting the notion that the intensity of competition is similar along a resource gradient. These findings contradict the expectations of Lekberg et al. (2018), who predicted that plant-soil microbial interaction would be more negative in high resource environments (Lekberg et al. 2018). Additionally, these finds do not align with the results of *Klinerova and Dostal* (2019), who suggested that nutrient-demanding species would experience less negative plant-soil feedback (Klinerová and Dostál 2020). Nevertheless, we did find that the relationship between PMI and AM fungi or pathogen, which indicates the dependence of plant growth on specific microorganisms, could be influenced by soil nutrients and interspecific competition. In the case of plants grown in overgrazed soil and with interspecific competitors, the relationship between the PMI of forbs and AM fungi became even stronger compared to plants grown in restored soil and grown alone. We attributed this result in Plant's dependence to mycorrhizal fungi is enhanced in low-nutrient environments (Schultz et al. 2001). Parallelly, the relationship between the PMI of graminoids and root diseases was found to be significantly only in overgrazed soil and in individual experiment. This suggests that plant resistance to pathogen is enhanced by higher nutrient levels. Conclusion The interactions among plants, mutualists, and antagonists within the plant-soil microorganism system are highly intricate, posing a challenge in identifying the primary driving factor of plant-soil microorganism interactions (PMI). In this study, we propose an empirical approach to shed light on the outcomes of PMI by examining the relationship between PMI strength and colonization by AM fungi or pathogen. By considering

the diversity of 13 grass species, two soil contexts, and two community conditions, we found that graminoids experienced a higher incidence of pathogen diseases, while forbs benefitted more from AM fungi. The PMI of graminoids appeared to be influenced by antagonists, whereas forbs relied on mutualists. We observed that these relationships were enhanced by low soil nutrient levels and interspecific competition. We argue that this conceptual framework could offer a more mechanistic understanding of plant-soil microorganism interactions. Additionally, we propose that colonization by AM fungi or pathogen may serve as key predictors of the direction and strength of PMI, but vary depending on the plant functional groups.

tion and pathogen diseases, nor did we observe significant effects of interspecific competition on pathogen

Table 1 Three-way analysis of variance (ANOVA) for the effects of species, competition, soil substrates and their interactions on PMI, colonization rate of AM fungi (CAM) and percentage of disease roots (PDR). Statistically significant sources of variation are in bold.

	PMI	PMI	CAM	CAM	PDR	PDR
Source of variation	F	p	F	p	F	p
Species	12.171	$<\!0.001$	12.063	$<\!0.001$	12.171	< 0.001
Competition	0.002	0.966	7.167	0.009	0.002	0.966
Soil substrates (SS)	1.844	0.178	0.444	0.507	1.844	0.178
Species*Competition	8.203	$<\!0.001$	1.641	0.092	8.203	< 0.001
SS*Species	0.912	0.538	0.981	0.472	0.912	0.538
Competition*SS	0.528	0.469	0.439	0.509	0.528	0.469
Species*Competition*SS	0.607	0.831	0.776	0.674	0.607	0.831

Table 2 Pearson relationship between PMI and colonization rate of AM fungi (CAM) or percentage of disease roots (PDR) among different functional groups. Statistically significant sources of variation are in bold, and r means correlation index.

Individual experiments	Individual experiments	Community experiments
r	p	r
6		

			Individual experiments	Individual experiments	Community experiments
Restored soil	Total	CAM-PMI	0.274	0.096	0.352
		PDR-PMI	-0.302	0.065	-0.229
	Graminoids	CAM-PMI	-0.099	0.76	0.453
		PDR-PMI	0.485	0.11	0.390
	Forbs	CAM-PMI	0.367	0.065	0.406
		PDR-PMI	-0.161	0.433	-0.263
Overgrazed soil	Total	CAM-PMI	0.432	0.006	0.156
		PDR-PMI	-0.472	0.002	-0.215
	Graminoids	CAM-PMI	0.371	0.235	0.204
		PDR-PMI	-0.719	0.008	0.119
	Forbs	CAM-PMI	0.414	0.032	0.516
		PDR-PMI	-0.252	0.205	-0.215



Fig.1 Plant-microbial interactions (PMI) for 13 species grown in restored and overgrazed soil in our individual and community experiments. Species abbreviations are described in Table S1. Positive or negative PMI are determined by subtracting sterile soil plant biomass (ln transformed) from live (inoculated) soil plant biomass (ln transformed). Significant PMI differences between individual and community experiments are indicated by an asterisk (p < 0.05).



Fig.2 Average plant-microbial interactions (PMI) for all plant species in individual (I-T) and community experiments (C-T), for graminoids in individual (I-G) and community experiments (C-G), and for forbs in individual (I-F) and community experiments (C-F) grown in restored and overgrazed soil. Box plots indicate interquartile range in the box area, median is solid line in the box, 25% and 75% percentiles are presented as lower and upper box margins. Significant PMI differences between individual and community experiments are indicated by an asterisk (p < 0.05). Significant PMI differences between graminoids and forbs are indicated by lowercase letter (p < 0.05).



Fig.3 Colonization rate of AM fungi (CAM) and percentage of disease roots (PDR) for 13 species grown in restored and overgrazed soil in our individual and community experiments. Species abbreviations are described in Table S1. Significant MC or PDR differences between individual and community experiments are indicated by an asterisk (p < 0.05).



Fig.4 Colonization rate of AM fungi (CAM) and percentage of disease roots (PDR) for all plant species in individual (I-T) and community experiments (C-T), for graminoids in individual (I-G) and community experiments (C-G), and for forbs in individual (I-F) and community experiments (C-F) grown in restored and overgrazed soil. Box plots indicate interquartile range in the box area, median is solid line in the box, 25% and 75% percentiles are presented as lower and upper box margins. Significant PMI differences between individual and community experiments are indicated by an asterisk (p < 0.05). Significant PMI differences between graminoids and forbs are indicated by lowercase letter (p < 0.05).



Fig.5 Relationship between plant–microbial interactions (PMI) and colonization rate of AM fungi (CAM) in individual and community experiments with two soil substrates. Linear regression model analyses were utilized and the solid line indicates a significant correlation.



Fig.6 Relationship between plant–microbial interactions (PMI) and percentage of disease roots (PDR) in individual and community experiments with two soil substrates. Linear regression model analyses were utilized and the solid line indicates a significant correlation.

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