



Plant–Soil Microbial Interactions Under Contrasting Moisture Conditions: Implications for Plant Fitness and Environmental Adaptation

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ABSTRACT

The integrated responses of the microbial communities, the soil processes and the root biomass to variable water availability are not sufficiently resolved and plant–soil microbial interactions play a central role in plant performance. The effect of contrasting soil moisture conditions on soil microbial composition, biochemical activity, respiration, nutrient status and below-ground plant performance was investigated. Soil moisture, microbial groups (based on phospholipid fatty acids), arbuscular mycorrhizal fungi (AMF), soil respiration components, enzyme activities, carbon and nitrogen variables and species-specific root biomass were used to analyze 40 experimental plots. Soil moisture, total PLFAs, abundance of bacteria and fungi, some groups of bacteria, AMF, heterotrophic respiration and LC root biomass were significantly influenced by moisture treatments. Generally, bacterial abundance, AMF, heterotrophic respiration and root biomass decreased with lower moisture conditions and fungal dominance increased. The amount of biomass of LC root was correlated positively with soil moisture, bacterial abundance, AMF and inorganic nitrogen, and negatively with fungal abundance and total organic carbon. Other microbial and plant parameters were also affected by nitrogen treatment. Coordinated gradients were suggested by multivariate analysis of the environmental, microbial and plant responses. Overall, the results indicate that moisture availability alters below-ground ecological interactions and affects plant performance because of complex microbial and soil processes.

Keywords: soil moisture; plant-microbe interactions; soil microbiome; arbuscular mycorrhizal fungi; root biomass

1. Introduction

Soil moisture is an environmental driver of plant growth, nutrient availability, microbial activity and ecosystem function. When water availability changes, the aeration, diffusion of substrates, root metabolism and microbial turnover will also change, thus modifying the biological relationship between plants and the soil environment around them. In drought-stressed plants, water uptake is decreased, nutrient uptake is impaired, photosynthesis is reduced, and root development is altered; while in the soil microbes, reduced mobility of resources and osmotic stress are experienced. These coupled responses highlight the importance of plant–soil microbial interactions in studying the resilience of ecosystems under moisture conditions that vary from dry to wet. Good rhizosphere management has consequently been recognized as a keyway of maintaining plant performance when water is scarce (Zia et al. 2021).

The rhizosphere harbours a wide variety of bacteria and fungi that can affect plant nutrition, hormone balance, root architecture and stress response. Phytostimulation by plant growth-promoting rhizobacteria may be possible to increase their drought resistance by producing a variety of plant growth hormones, accumulating osmolytes, mobilizing nutrients, and promoting better root growth (Ahmad et al., 2022). Under drought conditions, drought-tolerant rhizobacteria are also gaining importance in stabilizing the biological functions in soil and consequently enhancing soil health (El-Saadony et al., 2024). As a more general principle, the functional role of plant-associated microbiomes is now recognized as extending the phenotype of the plant, influencing both nutrient acquisition and stress signalling and environmental responsiveness (Compant et al., 2025).

Another important factor of plant adaptation below ground is the arbuscular mycorrhizal fungi. These fungi are in a symbiotic association with roots and increase the absorptive surface of the roots by extraradical hyphae, which enhance the ability to absorb water and nutrients. Its role in plant water relations is especially critical during drought stress; during such periods, mycorrhizal colonization can enhance the hydraulic function and water status of plants (Abdalla et al., 2023). In addition to plant responses, arbuscular mycorrhizae play a role in nutrient exchange, aggregation and ecosystem stability (Kuyper & Jansa, 2023). The associations can facilitate establishment and persistence of plants under dry conditions by increasing plant water acquisition and stress tolerance (Madouh & Quoreshi, 2023). Their significance in plant nutrition, soil health, and resilience in stress conditions has also been highlighted in recent studies (Bhosale et al., 2026).

In the case of moisture limitation, however, microbial communities can be reorganized in complex ways. Drought can have a negative effect on overall microbial biomass but can also select for taxa that are physiologically able to cope with drought. These changes may impact the ratio of bacteria to fungi, nutrient conversion, enzyme activity and soil respiration, which can influence carbon and nitrogen cycling (De Silva et al., 2025). Root–soil–microbiota interactions are thus being increasingly recognized as drivers of drought resilience as the response of plants is influenced by their intrinsic physiology but also by the functional composition of the microbial community they surround (Gholizadeh et al., 2024). Microbial regulation of drought and heat stress can also impact plant survival, biomass yield and resource-use efficiency (Parasar et al., 2024).

Chemical signaling and metabolite exchange affect the root–microbiome interface as well. The rhizosphere can be altered by plants via rhizosphere exudates, and the plant's response can also be altered by rhizosphere microorganisms through metabolic pathways and signaling. These interactions can lead to the development of microbial communities that are resilient to drought, improving resource uptake and ensuring plant resilience (Pantigoso et al., 2025). Recent studies also suggest that combined ecological filtering, host regulation and microbial functional selection are responsible for the formation of drought resistant rhizospheres, directly connecting soil moisture with plant-associated microbial adaptation (Wang et al., 2026).

Despite the advances, however, there are key knowledge gaps regarding the interactions among contrasting moisture regimes and their effects on soil microbial community composition, biochemical activity, soil respiration, soil nutrient status, and plant performance within a common analytical framework. The majority of studies focus on microbial changes or plant responses separately, and fail to interpret the complex interactions linking soil moisture to the ecological processes below ground. A more comprehensive evaluation is consequently required to define the relationships between the microbial community structure and soil processes with plant performance under varying moisture regimes.

This study aims to explore how plant–soil microbial interactions differ under various water conditions and their effect on plant fitness-related function and adaptation to the environment.

Objectives:

- Determine the effects of contrasting moisture conditions on soil microbial community characteristics, enzyme activity, respiration, and soil carbon and nitrogen properties.
- To compare plant root biomass as an indicator of plant performance below-ground under various moisture levels.
- To evaluate the relationship between soil moisture, microbial properties, soil processes, and plant performance based on correlation, regression and multivariate analysis.

2. Materials and Methods**2.1 Study Design and Data Source**

The research design for this study was a quantitative secondary data analytical design, using the Rs_data dataset to analyze the plant-soil microbial relationship under contrasting moisture conditions. The analysis was confined to the 2021 observations, as this year would have concurrent measurements representing the soil moisture, microbial community characteristics, soil biochemical properties, respiration, and plant root biomass. Following the removal of repeated plots, the final analytical data set comprised 40 unique plots in five experimental blocks. These moisture-treatment categories (CK, ID, RF, and CD) and nitrogen-treatment categories (C and N) were kept as they were first defined in the original dataset (Xu & Du, 2025).

2.2 Environmental and Soil Variables

Environmental conditions were characterized by soil moisture and soil temperature over the experimental treatments. Chemical properties of soils included total organic carbon, dissolved organic carbon, dissolved organic nitrogen and inorganic nitrogen. The following variables were measured to determine if there was any relationship between soil moisture and the soil physicochemical environment, which is important for microbial activity and plant performance.

2.3 Microbial Community and Enzyme Activity

Microbial characteristics of the soil were measured by means of phospholipid fatty acids (PLFAs) such as total PLFAs, bacteria, fungi, Gram-positive bacteria, Gram-negative bacteria, Actinobacteria and arbuscular mycorrhizal fungi (AMF). To characterize changes in microbial community structure, fungal-to-bacterial ratios were also added, as were ratios of Gram-positive to Gram-negative bacteria. Microbial and nutrient-cycling activity under contrasting moisture conditions was quantified with the activities of soil biochemicals, represented by β -glucosidase and acid phosphatase.

2.4 Soil Respiration and Plant Performance

Below-ground biological activity was measured by total soil respiration, heterotrophic respiration and autotrophic respiration. The following variables from the Rs_data were used to measure plant performance, each specific to one species: Below-ground plant performance was measured by root biomass instead of as a direct measure of reproductive fitness. Where there were a significant number of missing observations, input variables were treated as supplementary species-level responses, and the variables with more complete root-biomass data were the ones used primarily in the analysis.

2.5 Data Preparation and Quality Control

Data were checked for completeness, consistency and duplication prior to statistical analysis. Duplicate plot-level records were removed to prevent pseudoreplication. No zero values were inserted for missing values. The core microbial variables were complete for the entire analytical data set, while the variables with fewer observations missing were run through available-case procedures.

2.6 Statistical Analysis

Environmental, microbial, biochemical properties of the soil and respiration and plant response variables were calculated. The appropriate treatment based inferential models were used for differences across moisture treatments, where relevant, nitrogen treatment and block effects were considered. The relationships between soil moisture, microbial properties, soil properties, respiration and root biomass were analysed with correlation analysis. Moisture conditions, microbial characteristics and plant performance were evaluated with a multivariable regression. A multivariate analysis was also used to provide a summary of soil and microbial co-ordinated variability. The criterion of statistical significance was set at $p < 0.05$.

2.7 Ethical Considerations

The study did not include direct experiments on humans or animals and was conducted using only secondary environmental data (Rs_data). Thus, there was no need to seek new human or animal ethical approval for the current secondary analysis. The dataset has been used only for research, and the treatment labels, and the measured observations were not fabricated or changed.

3. Results

3.1 Environmental Conditions and Soil Respiration

There were 10 observations for CK moisture treatment, 10 for ID, 10 for RF and 10 for CD moisture treatment. The 40 experimental plots were equally distributed among the moisture treatments. The moisture-treatment effect was significant ($p = 0.021$); after the effects of nitrogen treatment and block effects had been removed from the data, mean soil moisture was significantly different among the moisture treatments. RF showed the highest mean soil moisture at 11.33 ± 2.42 , followed by CK at 10.92 ± 1.99 , whereas ID and CD had lower mean values of 9.50 ± 1.04 and 9.53 ± 1.84 , respectively. Soil temperature did not vary significantly as affected by the moisture treatments, but a significant ($p = 0.009$) treatment effect due to nitrogen was detected, as shown in Table 1.

The overall moisture effect was not significant at $p = 0.058$, but the total soil respiration exhibited a decreasing trend from CK to RF to CD. Heterotrophic respiration, on the other hand, was significantly different among moisture treatments ($p = 0.002$). The heterotrophic respiration rate was the highest in RF and the lowest in CD, with values of 2.03 ± 0.34 and 1.59 ± 0.20 , respectively. Tukey comparisons showed that RF was significantly greater than CD and ID. The moisture treatment had no significant effect on autotrophic respiration, while the nitrogen treatment effect was significant at $p < 0.001$.

Table 1. Environmental conditions and soil respiration across moisture treatments

Variable	CK	ID	RF	CD	Moisture p	Nitrogen p	Interaction p
Soil moisture	10.92 $\pm$ 1.99	9.50 $\pm$ 1.04	11.33 $\pm$ 2.42	9.53 $\pm$ 1.84	0.021	0.153	0.543
Soil temperature	19.81 $\pm$ 2.85	19.28 $\pm$ 2.25	19.07 $\pm$ 1.35	19.25 $\pm$ 2.46	0.566	0.009	0.439
Soil respiration, R_s	3.08 $\pm$ 0.37	2.91 $\pm$ 0.37	3.01 $\pm$ 0.43	2.58 $\pm$ 0.50	0.058	0.166	0.977
Heterotrophic respiration, R_h	1.83 $\pm$ 0.19	1.72 $\pm$ 0.23	2.03 $\pm$ 0.34	1.59 $\pm$ 0.20	0.002	0.128	0.997
Autotrophic respiration, R_a	1.27 $\pm$ 0.42	1.21 $\pm$ 0.26	1.01 $\pm$ 0.27	1.09 $\pm$ 0.38	0.240	<0.001	0.656

Values are mean $\pm$ SD. P -values were obtained from factorial linear models including moisture treatment, nitrogen treatment, their interaction, and block.

Figure 1 shows the distribution of the measured soil moisture across the 4 treatments. In the individual treatments, there was variation, but RF, in general, had higher soil moisture levels and ID and CD had lower soil moisture levels.

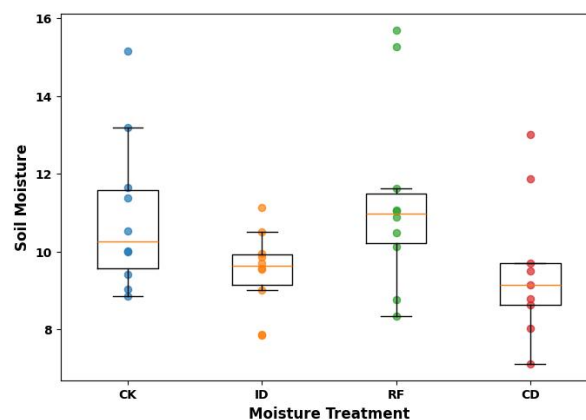


Figure 1. Distribution of measured soil moisture across CK, ID, RF, and CD moisture treatments. Boxes indicate the interquartile range, central lines represent medians, and individual points show plot-level observations

3.2 Moisture-Related Changes in Soil Microbial Communities

There were significant differences in the microbial community characteristics between the four moisture treatments. Treatment means had a significant difference at $p < 0.001$ and the highest mean was observed in the RF at 14.03 ± 0.92 and the lowest mean was observed in the CD at 12.34 ± 0.43 for total PLFAs. Bacterial abundance exhibited an even stronger treatment response, declining from 10.76 ± 0.74 in RF and 10.43 ± 0.62 in CK to 9.38 ± 0.50 in ID and 8.58 ± 0.32 in CD. Effect of moisture treatment on bacteria was highly significant ($p < 0.001$).

In contrast, abundance of fungi exhibited the opposite general pattern. Fungi were higher in CD and ID, with means of 3.76 ± 0.12 and 3.73 ± 0.22 , respectively, than in RF at 3.27 ± 0.24 . As a result, the fungal-to-bacterial ratio was found to be significantly raised under ID and CD. The ratio ranged from 0.30 ± 0.02 in RF to 0.44 ± 0.01 in CD, with an overall moisture-treatment effect of $p < 0.001$.

All three groups of bacteria were highly moisture-treatment specific: Gram-positive, Gram-negative and Actinobacteria. The means of their highest levels were usually present in either RF or CK, whereas CD was the bacterial group with the lowest means. Moisture treatment also evoked a positive response from AMF with a value of 0.69 ± 0.07 in RF while it was 0.44 ± 0.02 in CD. A highly significant moisture $\times$ nitrogen interaction was also found for the AMF response at $p < 0.001$. These microbial patterns have been summarized in Table 2.

Table 2. Soil microbial community characteristics across moisture treatments

Variable	CK	ID	RF	CD	Moisture <i>p</i>	Nitrogen <i>p</i>	Interaction <i>p</i>
Total PLFAs	13.90 $\pm$ 0.77	13.12 $\pm$ 0.70	14.03 $\pm$ 0.92	12.34 $\pm$ 0.43	<0.001	<0.001	0.192
Bacteria	10.43 $\pm$ 0.62	9.38 $\pm$ 0.50	10.76 $\pm$ 0.74	8.58 $\pm$ 0.32	<0.001	<0.001	0.106
Fungi	3.46 $\pm$ 0.16	3.73 $\pm$ 0.22	3.27 $\pm$ 0.24	3.76 $\pm$ 0.12	<0.001	0.001	0.796
Gram-positive bacteria	6.28 $\pm$ 0.34	5.60 $\pm$ 0.29	6.47 $\pm$ 0.39	5.12 $\pm$ 0.19	<0.001	<0.001	0.561
Gram-negative bacteria	2.13 $\pm$ 0.15	1.91 $\pm$ 0.12	2.20 $\pm$ 0.17	1.74 $\pm$ 0.07	<0.001	<0.001	0.030
Actinobacteria	1.38 $\pm$ 0.07	1.22 $\pm$ 0.04	1.45 $\pm$ 0.08	1.10 $\pm$ 0.03	<0.001	0.016	0.304
AMF	0.57 $\pm$ 0.06	0.55 $\pm$ 0.05	0.69 $\pm$ 0.07	0.44 $\pm$ 0.02	<0.001	0.005	<0.001
Fungi:bacteria ratio	0.33 $\pm$ 0.01	0.40 $\pm$ 0.01	0.30 $\pm$ 0.02	0.44 $\pm$ 0.01	<0.001	0.028	0.550
GP:GN ratio	2.95 $\pm$ 0.08	2.93 $\pm$ 0.09	2.94 $\pm$ 0.11	2.94 $\pm$ 0.06	0.923	0.061	0.010

The microbial community's restructuring is graphically illustrated in Figure 2 as a result of the treatment. Under CD, bacterial abundance noticeably decreased, while fungal abundance was comparatively high, which resulted in an apparent shift towards increased fungal representation under the comparatively lower moisture treatments.

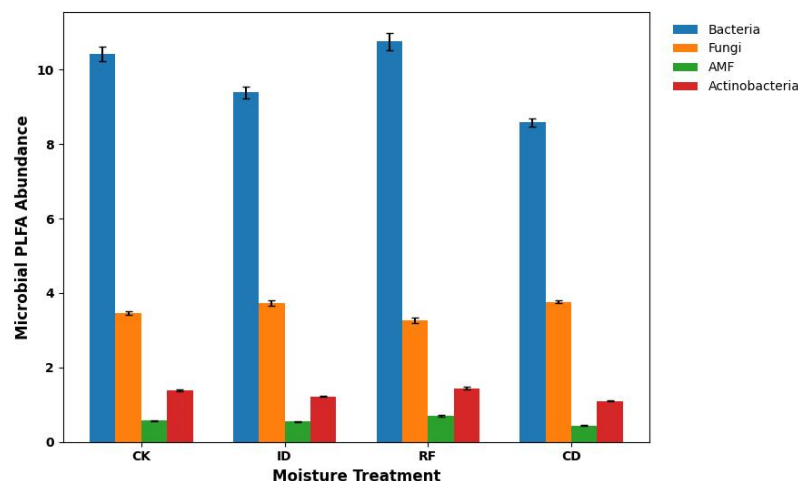


Figure 2. Mean abundance of major microbial groups across contrasting moisture treatments. Error bars represent standard errors of the mean

3.3 Soil Biochemical Characteristics and Plant Root Responses

The moisture effect p -values for β -glucosidase activity and acid phosphatase were 0.911 and 0.853, respectively, which were not significantly different. Don't forget that there was no significant overall moisture treatment effect for DOC either. In general, moisture effect was not significant, although TOC tended to be higher in CD than in the other treatments. Scale up of TOC, however, was highly significant for N and moisture $\times$ N interactions, suggesting that it was influenced by the factorial treatment design. Inorganic nitrogen was not significantly different between moisture treatments but was strongly affected by nitrogen treatment at $p < 0.001$.

Plant performance was more strongly influenced. There was a significant difference in the amount of LC root biomass between moisture treatments at $p < 0.001$. Mean LC root biomass was 1.56 ± 0.18 in CK and 1.55 ± 0.21 in RF, compared with approximately 1.30 in both ID and CD. There was significantly more LC root biomass in CK than in ID and CD, and significantly more biomass in RF than in ID and CD, as confirmed by Tukey comparisons. Nitrogen treatment also had significant effects on LC root biomass ($p < 0.001$). In contrast, the CS root biomass was non-significantly different among moisture treatments as indicated in Table 3.

Table 3. Soil biochemical variables and principal root-biomass responses

Variable	CK	ID	RF	CD	Moisture p	Nitrogen p	Interaction p
β -Glucosidase	36.92 ± 7.48	36.25 ± 8.22	38.16 ± 5.41	36.20 ± 5.85	0.911	0.377	0.802
Acid phosphatase	62.77 ± 9.55	65.38 ± 5.67	60.47 ± 13.11	62.15 ± 14.40	0.853	0.608	0.191
TOC	19.64 ± 4.82	20.02 ± 5.67	20.91 ± 4.77	22.72 ± 7.83	0.371	0.006	<0.001
DOC	94.52 ± 5.41	96.87 ± 4.84	98.90 ± 7.11	93.31 ± 28.64	0.796	0.270	0.039
DON	32.65 ± 3.48	31.69 ± 3.21	32.83 ± 4.30	32.50 ± 3.71	0.893	0.644	0.089
Inorganic nitrogen	33.27 ± 10.58	35.54 ± 15.68	34.39 ± 11.67	28.27 ± 11.86	0.138	<0.001	0.058
LC root biomass	1.56 ± 0.18	1.30 ± 0.19	1.55 ± 0.21	1.30 ± 0.17	<0.001	<0.001	0.747
CS root biomass	0.42 ± 0.26	0.17 ± 0.10	0.42 ± 0.49	0.38 ± 0.36	0.385	0.209	0.682

The difference in response to treatment of LC root biomass is illustrated in Figure 3. However, below-ground biomass of plants was higher for CK and RF, and lower for ID and CD, suggesting that below-ground plant performance reflected their treatment according to the moisture-related treatments more strongly than did measured enzyme activities.

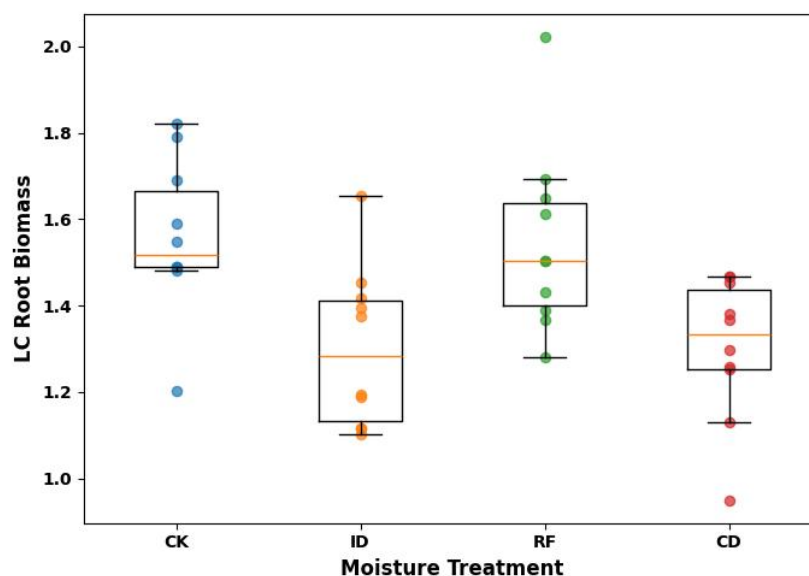


Figure 3. LC root biomass across the four contrasting moisture treatments. Boxes represent interquartile ranges and points represent individual experimental plots

3.4 Associations Between Soil Moisture, Microbial Variables, and Plant Performance

Several significant relationships between LC root biomass and the measured plant–soil variables were found by correlation analysis. There was a positive relationship between soil moisture and LC root biomass (Spearman's $\rho = 0.402$, $p = 0.011$). There were also positive relationships with bacterial abundance, AMF and inorganic nitrogen. However, the number of fungi showed a negative correlation with LC root biomass, $\rho = -0.553$, $p < 0.001$. TOC was also negatively associated with LC root biomass at $\rho = -0.433$ and $p = 0.007$.

There was also a positive but statistically insignificant relation with total PLFAs. Soil respiration was also significantly, but not strongly, predicted by the LC root biomass. There were no significant correlations between the response of the LC and either β -glucosidase or acid phosphatase. The results are summarised in Table 4.

Table 4. Spearman correlations between LC root biomass and selected soil and microbial variables

Predictor	n	Spearman's ρ	p
Soil moisture	39	0.402	0.011
Total PLFAs	40	0.217	0.178
Bacteria	40	0.346	0.029
Fungi	40	-0.553	<0.001
AMF	40	0.344	0.030
β -Glucosidase	37	0.201	0.234
Acid phosphatase	38	-0.158	0.342
Soil respiration	40	0.284	0.076
TOC	37	-0.433	0.007
DOC	40	0.176	0.277
DON	40	0.258	0.108
Inorganic nitrogen	40	0.479	0.002

The integrated correlation structure is shown in Figure 4. The heatmap highlights the positive association between LC root biomass and soil moisture, bacteria, AMF, inorganic N and the negative association with soil fungal abundance and TOC.

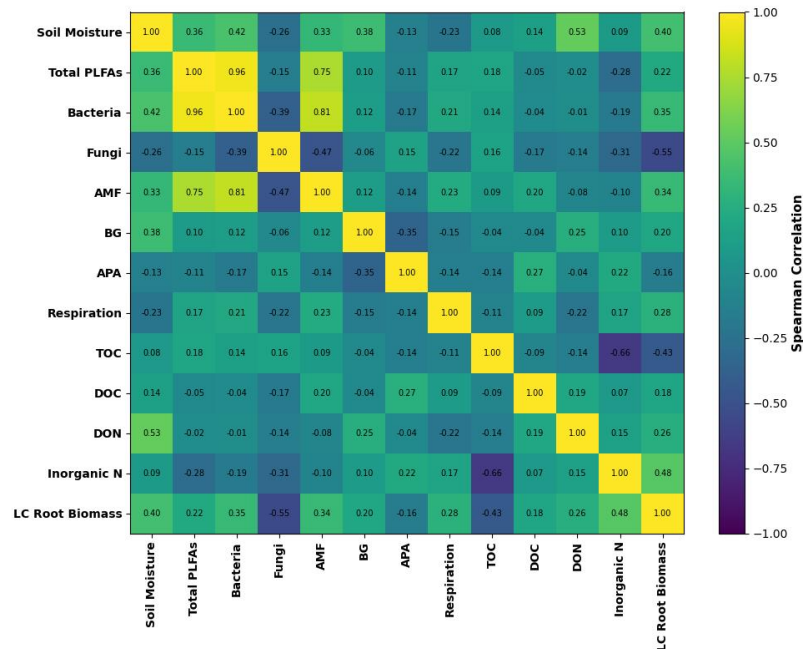


Figure 4. Spearman correlation heatmap showing relationships among soil moisture, microbial characteristics, soil properties, respiration, and LC root biomass

3.5 Multivariable Predictors of LC Root Biomass

A block adjusted multivariable model was fitted to see if individual microbial variables could be significant when the soil moisture and nitrogen treatment was also included. The overall model was significant ($p < 0.001$) and accounted for 58.7% of the variation in observed LC root biomass, and had an adjusted R^2 of 0.458.

After adjustment, nitrogen treatment was a key positive predictor of the biomass of roots of LC, with $\beta = 0.244$ and $p = 0.001$. However, soil moisture, bacterial abundance, fungal abundance, and AMF were not significant in the multivariable model. The extent to which this reduction occurs from the bivariate correlations suggests that the soil moisture has a significant amount of common variability with microbial characteristics, rather than the soil moisture and the microbial characteristics being independent of each other. The main model coefficients are reported in Table 5.

Table 5. Block-adjusted multivariable model for LC root biomass

Predictor	β	SE	p	95% CI
Nitrogen treatment, N vs C	0.244	0.068	0.001	0.105 to 0.382
Soil moisture	0.011	0.019	0.578	-0.028 to 0.049
Bacteria	0.066	0.048	0.182	-0.032 to 0.163
Fungi	-0.151	0.136	0.278	-0.429 to 0.128
AMF	0.248	0.420	0.559	-0.610 to 1.107

Model $n = 39$; $R^2 = 0.587$; adjusted $R^2 = 0.458$; overall model $p < 0.001$. Block effects were included as adjustment terms.

3.6 Integrated Multivariate Pattern of Plant–Soil–Microbial Responses

All the environmental, microbial, biochemical, respiration, soil nutrient and LC root biomass variables with complete observations were subjected to principal component analysis. The first two principal components accounted for 46.1% of the total standardized variation, with PC1 accounting for 25.6% and PC2 accounting for 20.5%.

Positive contributions of bacterial abundance, total PLFAs, AMF, LC root biomass, soil respiration and soil moisture dominated PC1, while the negative contribution was from fungal abundance. The relationships between PC2 and inorganic nitrogen, DON, LC root biomass, soil temperature and TOC were stronger. The ordination in Figure 5 illustrates that the variables of the environment, the microorganisms and the response of the plants were not operating in isolation, but as a set of coordinated gradients.

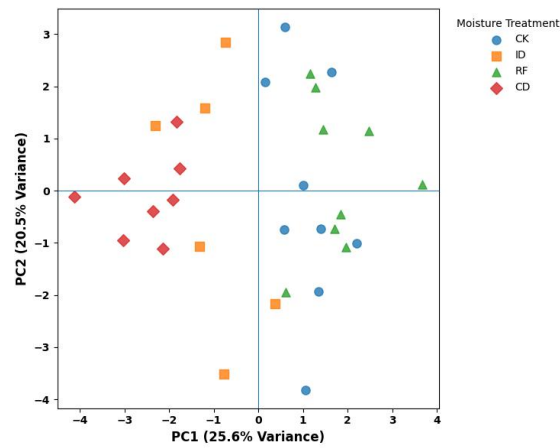


Figure 5. Principal component ordination of integrated soil moisture, microbial, soil biochemical, respiration, nutrient, and LC root-biomass variables. PC1 and PC2 explained 25.6% and 20.5% of total standardized variation, respectively

The overall results indicate that moisture treatments led to significant changes in the soil microbial community and in heterotrophic respiration and LC root biomass. A higher bacterial abundance tended to be correlated with higher below-ground plant performance, while a higher fungal dominance was correlated with lower LC root biomass. The multivariable analysis, however, revealed that these relationships were not independent, highlighting the holistic responses of plant, soil and microbes to different moisture regimes.

4. Discussion

This study revealed that the contrasting moisture conditions were correlated with the coordinated changes in microbial composition of the soil, heterotrophic respiration and plant root performance, whereas several enzyme and soil nutrient variables were comparatively stable. Soil moisture varied significantly between treatments and the lower moisture treatments resulted in lower levels of bacterial abundance, lower total PLFAs, lower abundance of AMF, and decreased LC root biomass. The results here show that a drought does not just alter the above-ground ecological system, but it also reorganizes the below ground one via coupled changes in microbial community, resources availability, and plant performance.

The reduction in the abundance of bacteria in lower-moisture treatments is similar to what has been observed as a water deficit ecological filter on soil microbial communities (Fahey et al., 2020). Drought history may increase the numbers of physiologically stress-tolerant microbial groups and decrease the populations that are moisture-sensitive (Gebauer et al., 2022). The overall reduction in the amount of total PLFAs is thus indicative of a reduction in overall microbial biomass or activity under water limitation. Increased microbial resistance has been described to change in response to the community composition and the environmental context (Gillespie et al., 2020). The higher abundance and fungal-to-bacterial ratio observed under the drier treatments could be due to a relative advantage for fungi in dry conditions, in line with syntheses on drought-induced microbial restructuring (Ramatsitsi & Manyevere, 2026).

For moisture response, the response of AMF was one of the most obvious, with the highest abundance under RF and the lowest under CD. This pattern indicates drought resilience responses because AMF help to acquire water and nutrients and maintain plant physiology under stress conditions (Abdallah et al., 2026). Drought will change AMF communities that are associated with some plant species and may affect their ecological role in plant species (Cao et al., 2020). Although there was no independent significance in the multivariable model for the correlation between AMF and LC root biomass, the positive relationship may indicate that higher AMF representation has a positive effect on below-ground plant performance. Experimental evidence shows that mycorrhizal associations can enhance drought tolerance and survival (Pereira et al., 2021). They may also interact with nitrogen availability due to the ability of AMF to alter drought tolerance and nitrogen-use efficiency (NUE) (Tang et al., 2022).

There was also a large treatment effect on heterotrophic respiration indicating that moisture conditions further altered microbial functioning. The heterotrophic respiration seems to be the highest for RF and the lowest for CD. Under severe water limitation, microbial metabolism has been found to be limited and functional microbial groups changed by reduced heterotrophic respiration (Kang et al., 2022). However, total respiration and autotrophic respiration both were relatively insensitive to moisture treatment, indicating that different respiration components are sensitive. The difference is significant in that total soil respiration may mask differences between the contributions from microbial and root respiration.

The lack of major moisture effects on the activity of both enzymes, β -glucosidase and acid phosphatase, suggests that extracellular enzyme activity is relatively insensitive within the moisture range studied. The moisture history (drying-rewetting) could change the extracellular enzyme activities, but the changes are enzyme-specific and sensitive to both microbial composition and the availability of substrates (Ouyang & Li, 2020). In contrast, stable enzyme activities and significant changes in the microbial community could suggest functional buffering, which is the process of microbial community structure changes to buffer biochemical processes from environmental stress.

Moisture treatment had a significant effect on plant performance (LC root biomass). Less biomass under ID and CD suggests that the growth of the plant was hampered by less water availability resulting in smaller biomass. More biomass under CK and RF suggests that these conditions allowed more growth below ground. Soil microbial communities can impact drought response by affecting root growth, nutrient uptake and stress signaling (Monohon et al., 2021). Synthetic bacterial communities can also be used to modify the responses of plants to drought, thereby providing support for an effect of microbial community on plant performance (Armanhi et al., 2021). Thus, the positive correlations of root biomass with the abundance of bacteria, AMF, soil moisture and inorganic nitrogen are ecologically coherent.

Nitrogen was another factor that appeared to be a big driver that affected several microbial variables and for LC root biomass. Modification of the rhizosphere microbiome can be used to enhance drought tolerance and nitrogen use efficiency, which should not be viewed in isolation (Du et al., 2022; Rui et al., 2026). Some of the bivariate microbial associations that were not present in the multivariable model may be attributed to the importance of nitrogen effects.

An integrated interpretation: moisture availability influences the composition of the microbial community, heterotrophic respiration, and is linked to the variation in plant root performance. Enzymes seem stable in function, and AMF, bacteria, and nitrogen availability seem particularly important. The patterns are consistent with the knowledge that drought resilience of plants is the result of interactions among microorganisms, roots and resources

5. Conclusion

The results of this study show how soil moisture conditions can differently influence the soil–plant–microbial relationships in a coordinated manner, affecting the microbial community composition, microbial respiration, nutrient dynamics and below-ground plant performance. The total PLFAs, the abundance of bacterial and arbuscular mycorrhizal fungi, heterotrophic respiration and LC root biomass were reduced with lower-moisture conditions while the abundance of fungal and fungal-to-bacterial ratio increased. There was a significant change in the soil microbial community under moisture limitation as these responses show. Overall, microbial variation was found to be partly functional with relatively stable activities of β -glucosidase and acid phosphatase. Coordinated biotic and abiotic regulation of plant performance is further underscored by positive relationships of LC root biomass to soil moisture, bacterial abundance, AMF and inorganic nitrogen. Several microbial variables and root biomass were also affected by nitrogen treatment, highlighting the importance of moisture responses in a nutrient context. Analyses of multivariate data revealed that plant, soil and microbial variables were integrated ecological gradients and not independent responses. Overall, the results suggest below-ground ecosystem function is mediated by moisture availability, which in turn alters the structure of the microbial community and plant–microbe interactions. Such interactions can facilitate persistence and adaptation to changing moisture variability and drought stress conditions in plants and thus impact on ecosystem resilience in future climate scenarios.

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