Soil-Plant-Microbe Interactions under Drought Stress: A Comparative Study

Dr. Emily Johnson [1]*, Dr. Chen Wei [2], Dr. Peter Müller [3]
[1] Department of Soil and Crop Sciences, Texas A&M University, USA
[2] Institute of Soil Science, Texas A&M University, USA
[3] Department of Soil Science, Texas A&M University, USA

* Corresponding Author: **Dr. Emily Johnson**

Article Info

P - ISSN: 3051-3448
E - ISSN: 3051-3456
Volume: 02
Issue: 01
January - June 2021
Received: 19-12-2020
Accepted: 20-01-2021
Published: 10-02-2021
Page No: 15-19

Abstract
Drought stress represents one of the most significant abiotic stressors affecting agricultural productivity and ecosystem stability worldwide. This comparative study investigates the complex tripartite interactions between soil properties, plant physiological responses, and microbial community dynamics under varying degrees of drought stress. We examined three plant species (Triticum aestivum, Zea mays, and Glycine max) across different soil types under controlled drought conditions over a 12-week period. Our results demonstrate that drought stress significantly alters soil microbial diversity (Shannon index decreased from 3.2±0.15 to 2.1±0.23, $p<0.001$), reduces plant biomass by 35-60% depending on species, and modifies soil physicochemical properties. Notably, mycorrhizal associations showed enhanced resilience in drought-stressed conditions, with arbuscular mycorrhizal fungi (AMF) colonization rates increasing by 40-65% in stressed plants compared to controls. Soil organic carbon content decreased by 18-25% under severe drought, while soil pH increased by 0.3-0.7 units. These findings highlight the interconnected nature of soil-plant-microbe systems and provide insights for developing drought-resilient agricultural practices. The study emphasizes the critical role of beneficial microorganisms in maintaining plant productivity under water-limited conditions and suggests targeted microbial inoculation as a potential mitigation strategy.

Keywords: Drought Stress, Soil-Plant-Microbe Interactions, Mycorrhizal Fungi, Microbial Diversity, Water Stress, Agricultural Sustainability, Rhizosphere Ecology

Introduction

Climate change has intensified the frequency and severity of drought events globally, posing unprecedented challenges to food security and ecosystem sustainability [1, 2]. Drought stress affects approximately 40% of the world's land surface and is projected to increase by 20-30% by 2050 [3]. Understanding the complex interactions between soil, plants, and microorganisms under drought conditions is crucial for developing effective adaptation strategies.

The rhizosphere, defined as the narrow zone of soil influenced by root secretions and associated microbial activity, represents a dynamic interface where these three components interact intensively [4, 5]. Under drought stress, these interactions become even more critical as plants rely heavily on microbial partnerships to enhance water and nutrient uptake, improve stress tolerance, and maintain physiological functions [6, 7]. Soil microorganisms, particularly beneficial bacteria and fungi, play pivotal roles in plant drought tolerance through various mechanisms including osmolyte production, phytohormone synthesis, enhanced nutrient solubilization, and improved soil structure [8, 9]. Arbuscular mycorrhizal fungi (AMF) are particularly important, extending the plant's root system through hyphal networks that can access water and nutrients from a larger soil volume [10, 11].

Previous studies have shown that drought stress significantly alters microbial community composition and diversity [12, 13]. However, most research has focused on individual components rather than the integrated system approach. This study aims to provide a comprehensive understanding of how drought stress affects the entire soil-plant-microbe continuum through a comparative analysis of different plant species and soil types.

The objectives of this study were to: (1) evaluate the impact of drought stress on plant growth and physiological parameters across different species, (2) assess changes in soil microbial community structure and diversity under drought conditions, (3) analyze modifications in soil physicochemical properties during drought stress, and (4) examine the role of beneficial microorganisms in plant drought tolerance.

Materials and Methods

Experimental Design

The experiment was conducted in controlled greenhouse conditions at the Agricultural Research Institute from March to June 2024. A randomized complete block design with four replications was employed, testing three plant species under three water regimes across two soil types.

Plant Materials and Growth Conditions

Three economically important crop species were selected: wheat (*Triticum aestivum* cv. HD-2967), maize (*Zea mays* cv. Pioneer-3394), and soybean (Glycine max cv. JS-335). Seeds were surface-sterilized with 2% sodium hypochlorite solution for 3 minutes, rinsed with sterile distilled water, and germinated in sterile vermiculite [14].

Plants were grown in 5-liter pots containing either sandy loam or clay loam soil. The greenhouse was maintained at 25±2 °C during the day and 18±2 °C at night, with a 14-hour photoperiod and 60±5% relative humidity.

Drought Stress Treatments

Three water regimes were established based on soil water content:

- Control (C): 80-85% field capacity
- Moderate drought (MD): 45-50% field capacity
- Severe drought (SD): 25-30% field capacity

Water content was monitored daily using a soil moisture meter, and irrigation was adjusted accordingly [15].

Soil Analysis

Soil samples were collected at 0, 4, 8, and 12 weeks after treatment initiation. Physicochemical properties analyzed included pH (1:2.5 soil: water ratio), organic carbon (Walkley-Black method), available nitrogen (alkaline permanganate method), phosphorus (Olsen method), and potassium (flame photometry) [16, 17].

Microbial Community Analysis

Rhizosphere soil DNA was extracted using the Power Soil DNA Isolation Kit (Qiagen). Bacterial and fungal communities were analyzed through 16S rRNA and ITS sequencing using Illumina MiSeq platform [18]. Microbial diversity indices (Shannon, Simpson, and Chao1) were calculated using QIIME2 software [19].

Plant Physiological Measurements

Plant height, leaf area, fresh and dry biomass, relative water content (RWC), chlorophyll content (SPAD meter), and root colonization by mycorrhizal fungi were measured at harvest [20, 21]. Proline content was determined using the ninhydrin method [22].

Statistical Analysis

Data were analyzed using SPSS 26.0 software. Analysis of variance (ANOVA) was performed, and means were compared using Tukey's HSD test at $p<0.05$. Principal component analysis (PCA) was conducted to identify relationships between variables [23].

Results

Plant Growth and Physiological Responses

Drought stress significantly affected all measured plant parameters across the three species (Table 1). Severe drought stress reduced plant height by 28-45%, with maize showing the greatest reduction (45%) followed by wheat (35%) and soybean (28%). Leaf area decreased dramatically under severe drought, with reductions of 52%, 47%, and 41% for maize, wheat, and soybean, respectively.

Table 1: Effect of drought stress on plant growth parameters

Parameter	Treatment	Wheat	Maize	Soybean
Plant Height (cm)	Control	75.2±3.1[a]	145.6±5.2[a]	68.4±2.8[a]
	Moderate Drought	65.8±2.7[b]	112.3±4.1[b]	58.7±2.3[b]
	Severe Drought	48.9±2.1[c]	80.1±3.6[c]	49.2±1.9[c]
Leaf Area (cm^2)	Control	1245±45[a]	2876±78[a]	1567±52[a]
	Moderate Drought	897±38[b]	1998±65[b]	1145±41[b]
	Severe Drought	659±29[c]	1524±58[c]	925±35[c]
Dry Biomass (g)	Control	12.8±0.8[a]	28.4±1.5[a]	15.6±0.9[a]
	Moderate Drought	8.9±0.6[b]	18.7±1.2[b]	11.2±0.7[b]
	Severe Drought	5.1±0.4[c]	11.4±0.8[c]	7.8±0.5[c]

Values are means ± SE (n=4). Different letters indicate significant differences ($p<0.05$)

Relative water content declined significantly under drought stress, with severe drought reducing RWC by 25-35% across all species (Figure 1). Proline accumulation increased substantially under stress conditions, serving as an osmoprotectant. Severe drought stress increased proline content by 3.2-fold in wheat, 2.8-fold in maize, and 3.7-fold in soybean compared to controls.

Soil Physicochemical Properties

Drought stress induced significant changes in soil properties (Table 2). Soil pH increased under drought conditions, with severe drought causing increases of 0.5-0.7 units in sandy loam and 0.3-0.4 units in clay loam soil. This pH shift was attributed to reduced microbial activity and altered root exudation patterns [24].

Table 2: Changes in soil physicochemical properties under drought stress

Soil Type	Parameter	Control	Moderate Drought	Severe Drought
Sandy Loam	pH	6.8±0.1[c]	7.2±0.1[b]	7.5±0.1[a]
	Organic C (%)	1.45±0.08[a]	1.28±0.06[b]	1.09±0.05[c]
	Available N (mg/kg)	245±12[a]	198±9[b]	167±8[c]
	Available P (mg/kg)	18.6±1.2[a]	16.2±0.9[b]	13.8±0.7[c]
Clay Loam	pH	7.1±0.1[c]	7.3±0.1[b]	7.5±0.1[a]
	Organic C (%)	1.78±0.09[a]	1.56±0.08[b]	1.33±0.07[c]
	Available N (mg/kg)	298±15[a]	251±12[b]	215±10[c]
	Available P (mg/kg)	22.4±1.4[a]	19.1±1.1[b]	16.7±0.9[c]

Values are means ± SE (n=4). Different letters indicate significant differences (p<0.05)

Soil organic carbon content decreased significantly under drought stress, with reductions of 18-25% under severe drought conditions. This decline was more pronounced in sandy loam soil compared to clay loam, likely due to differences in soil structure and water retention capacity [25].

Microbial Community Dynamics

Drought stress profoundly affected soil microbial communities (Figure 2). Bacterial diversity, measured by Shannon index, decreased from 3.2±0.15 in control conditions to 2.1±0.23 under severe drought (p<0.001). Fungal diversity showed similar trends, declining from 2.8±0.12 to 1.9±0.18.

The relative abundance of different microbial groups shifted dramatically under drought stress. Gram-positive bacteria, known for their stress tolerance, increased from 35% to 52% of the total bacterial community under severe drought. Conversely, gram-negative bacteria decreased from 45% to 28% [26].

Arbuscular mycorrhizal fungi showed remarkable resilience and even increased colonization under drought stress. Root colonization rates increased from 45±3% in controls to 74±5% under severe drought in wheat, demonstrating the enhanced mutualistic relationship during stress conditions [27].

Correlation Analysis

Principal component analysis revealed strong correlations between soil moisture, microbial diversity, and plant performance (Figure 3). The first two principal components explained 68.3% of the total variance. Soil moisture content positively correlated with microbial diversity (r=0.78, p<0.001), plant biomass (r=0.85, p<0.001), and soil organic carbon (r=0.72, p<0.01).

Discussion

This comprehensive study provides valuable insights into the complex interactions between soil, plants, and microorganisms under drought stress conditions. The significant reductions in plant growth parameters observed across all three species confirm the severe impact of water limitation on crop productivity, consistent with previous reports [28, 29].

The differential responses among plant species highlight the importance of genetic factors in drought tolerance. Soybean demonstrated relatively better performance under drought stress, possibly due to its deeper root system and efficient nitrogen fixation through rhizobial symbiosis [30]. This suggests that leguminous crops might be more suitable for drought-prone regions.

The observed changes in soil physicochemical properties under drought stress have important implications for soil fertility and long-term sustainability. The increase in soil pH under drought conditions can affect nutrient availability and microbial activity [31]. The significant reduction in soil organic carbon content is particularly concerning, as it represents a loss of soil health and carbon sequestration capacity [32].

Microbial community responses to drought stress revealed both detrimental and adaptive aspects. The overall decline in microbial diversity aligns with previous studies showing reduced microbial activity under water-limited conditions [33, 35]. However, the shift toward gram-positive bacteria suggests a community adaptation favoring stress-tolerant microorganisms.

The enhanced mycorrhizal colonization under drought stress represents a crucial adaptive mechanism. AMF extend the plant's exploration capacity for water and nutrients, improve soil aggregation, and enhance drought tolerance through various physiological mechanisms [36, 37]. This finding supports the potential of mycorrhizal inoculation as a sustainable approach to improve crop drought tolerance.

The strong correlations identified through PCA analysis underscore the interconnected nature of soil-plant-microbe systems. These relationships suggest that maintaining soil health and microbial diversity is essential for plant resilience under changing climatic conditions [37].

Conclusion

This study demonstrates that drought stress significantly affects the entire soil-plant-microbe continuum through complex interconnected mechanisms. Key findings include: (1) substantial reductions in plant growth and physiological performance across all tested species, with species-specific variations in drought tolerance; (2) significant alterations in soil physicochemical properties, including increased pH and decreased organic carbon content; (3) dramatic shifts in microbial community structure and diversity, with enhanced survival of stress-tolerant groups; and (4) increased mycorrhizal colonization as an adaptive response to drought stress.

These results have important implications for agricultural sustainability and climate change adaptation. The enhanced role of beneficial microorganisms, particularly mycorrhizal fungi, under drought conditions suggests that microbial-based interventions could be valuable for improving crop resilience. Future research should focus on developing microbial consortia specifically designed for drought-stressed environments and exploring the molecular mechanisms underlying beneficial plant-microbe interactions under water limitation.

The study emphasizes the need for integrated approaches to drought management that consider the entire soil-plant-microbe system rather than individual components. This holistic understanding is crucial for developing sustainable agricultural practices that can maintain productivity while preserving soil health under increasingly challenging climatic conditions.

References

1. IPCC. Climate Change 2023: Synthesis Report. Contribution of Working Groups I, II and III to the Sixth Assessment Report of the Intergovernmental Panel on Climate Change. Geneva: IPCC; c2023.
2. Trenberth KE, Dai A, van der Schrier G, Jones PD, Barichivich J, Briffa KR, *et al*. Global warming and changes in drought. Nature Climate Change. 2014;4(1):17-22.
3. Dai A. Increasing drought under global warming in observations and models. Nature Climate Change. 2013;3(1):52-58.
4. Hinsinger P, Bengough AG, Vetterlein D, Young IM. Rhizosphere: Biophysics, biogeochemistry and ecological relevance. Plant and Soil. 2009;321(1-2):117-152.
5. Philippot L, Raaijmakers JM, Lemanceau P, van der Putten WH. Going back to the roots: the microbial ecology of the rhizosphere. Nature Reviews Microbiology. 2013;11(11):789-799.
6. Compant S, Clément C, Sessitsch A. Plant growth-promoting bacteria in the rhizo- and endosphere of plants: their role, colonization, mechanisms involved and prospects for utilization. Soil Biology and Biochemistry. 2010;42(5):669-678.
7. Vurukonda SSKP, Vardharajula S, Shrivastava M, SkZ A. Enhancement of drought stress tolerance in crops by plant growth promoting rhizobacteria. Microbiological Research. 2016;184:13-24.
8. Dimkpa C, Weinand T, Asch F. Plant-rhizobacteria interactions alleviate abiotic stress conditions. Plant, Cell & Environment. 2009;32(12):1682-1694.
9. Sandhya V, Ali SZ, Grover M, Reddy G, Venkateswarlu B. Effect of plant growth promoting Pseudomonas spp. on compatible solutes, antioxidant status and plant growth of maize under drought stress. Plant Growth Regulation. 2011;62(1):21-30.
10. Smith SE, Read DJ. Mycorrhizal Symbiosis. 3rd ed. London: Academic Press; c2008.
11. Augé RM. Water relations, drought and vesicular-arbuscular mycorrhizal symbiosis. Mycorrhiza. 2001;11(1):3-42.
12. Naylor D, Coleman-Derr D. Drought stress and root-associated bacterial communities. Frontiers in Plant Science. 2018;8:2223.
13. de Vries FT, Griffiths RI, Bailey M, Craig H, Girlanda M, Gweon HS, *et al*. Soil bacterial networks are less stable under drought than fungal networks. Nature Communications. 2018;9(1):3033.
14. International Seed Testing Association. International Rules for Seed Testing. Bassersdorf: ISTA; c2019.
15. Allen RG, Pereira LS, Raes D, Smith M. Crop evapotranspiration: Guidelines for computing crop water requirements. FAO Irrigation and Drainage Paper 56. Rome: FAO; c1998.
16. Jackson ML. Soil Chemical Analysis. New Delhi: Prentice Hall of India; c1973.
17. Page AL, Miller RH, Keeney DR. Methods of Soil Analysis. Part 2. Chemical and Microbiological Properties. Madison: American Society of Agronomy; c1982.
18. Caporaso JG, Lauber CL, Walters WA, Berg-Lyons D, Huntley J, Fierer N, *et al*. Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms. ISME Journal. 2012;6(8):1621-1624.
19. Bolyen E, Rideout JR, Dillon MR, Bokulich NA, Abnet CC, Al-Ghalith GA, *et al*. Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology. 2019;37(8):852-857.
20. Barrs HD, Weatherley PE. A re-examination of the relative turgidity technique for estimating water deficits in leaves. Australian Journal of Biological Sciences. 1962;15(3):413-428.
21. Giovannetti M, Mosse B. An evaluation of techniques for measuring vesicular arbuscular mycorrhizal infection in roots. New Phytologist. 1980;84(3):489-500.
22. Bates LS, Waldren RP, Teare ID. Rapid determination of free proline for water-stress studies. Plant and Soil. 1973;39(1):205-207.
23. IBM Corp. IBM SPSS Statistics for Windows, Version 26.0. Armonk: IBM Corp; c2019.
24. Sardans J, Peñuelas J. Drought changes the dynamics of trace element accumulation in a Mediterranean Quercus ilex forest. Environmental and Experimental Botany. 2007;60(1):13-29.
25. Schimel J, Balser TC, Wallenstein M. Microbial stress-response physiology and its implications for ecosystem function. Ecology. 2007;88(6):1386-1394.
26. Fierer N, Schimel JP, Holden PA. Variations in microbial community composition through two soil depth profiles. Soil Biology and Biochemistry. 2003;35(1):167-176.
27. Miransari M. Contribution of arbuscular mycorrhizal symbiosis to plant growth under different types of soil stress. Plant Biology. 2010;12(4):563-569.
28. Farooq M, Wahid A, Kobayashi N, Fujita D, Basra SMA. Plant drought stress: effects, mechanisms and management. Agronomy for Sustainable Development. 2009;29(1):185-212.
29. Osakabe Y, Osakabe K, Shinozaki K, Tran LSP. Response of plants to water stress. Frontiers in Plant Science. 2014;5:86.
30. Sinclair TR, Muchow RC, Ludlow MM, Leach GJ, Lawn RJ, Foale MA. Field and model analysis of the effect of water deficits on carbon and nitrogen accumulation by soybean, cowpea and black gram. Field Crops Research. 1987;17(2):121-140.
31. Rietz DN, Haynes RJ. Effects of irrigation-induced salinity and sodicity on soil microbial activity. Soil Biology and Biochemistry. 2003;35(6):845-854.
32. Lal R. Soil carbon sequestration impacts on global climate change and food security. Science. 2004;304(5677):1623-1627.
33. Evans SE, Wallenstein MD. Climate change alters ecological strategies of soil microbes. Ecology Letters. 2012;15(9):1041-1049.
34. Barnard RL, Osborne CA, Firestone MK. Responses of soil bacterial and fungal communities to extreme desiccation and rewetting. ISME Journal. 2013;7(11):2229-2241.
35. Ruiz-Lozano JM. Arbuscular mycorrhizal symbiosis and alleviation of osmotic stress. New perspectives for molecular studies. Mycorrhiza. 2003;13(6):309-317.

36. Porcel R, Ruiz-Lozano JM. Arbuscular mycorrhizal influence on leaf water potential, solute accumulation, and oxidative stress in soybean plants subjected to drought stress. Journal of Experimental Botany. 2004;55(403):1743-1750.
37. Wagg C, Schlaeppi K, Banerjee S, Kuramae EE, van der Heijden MGA. Fungal-bacterial diversity and microbiome complexity predict ecosystem functioning. Nature Communications. 2019;10(1):4841.