

SHORT COMMUNICATION

The complexity of the rice rhizosphere and endosphere bacterial network is enhanced by drought stress

Lobban Thomas*

College of Horticulture Science, Zhejiang A&F University, Hangzhou 311300, China

*Corresponding author E-mail: thomaslobban@oms.cn

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The rice rhizosphere and endosphere represent critical microbial habitats influencing plant health and productivity. This study investigates how drought stress alters the bacterial communities within these environments, focusing on their complexity and functional dynamics. Using high-throughput sequencing and network analysis, we examined bacterial communities in the rhizosphere and endosphere of rice plants under normal and drought conditions. Our findings reveal that drought stress significantly increases the complexity of bacterial networks in both compartments, characterized by enhanced network connectivity, diversity, and stability. These changes are accompanied by shifts in microbial composition and functional potential, suggesting that drought stress imposes selective pressures that reshape microbial interactions and functionality. Our study underscores the intricate relationship between environmental stressors and microbial communities, providing insights into how drought alters plant-associated bacterial networks and highlighting potential strategies for improving drought resilience in rice cultivation.

Keywords: Rhizosphere, Endosphere, Bacterial Networks, Drought Stress, High-throughput Sequencing, Network Analysis, Plant Microbiome, Environmental Stress.

Introduction

Rice (*Oryza sativa*) is a staple crop that supports over half of the global population. Its productivity is critically affected by environmental stresses, with drought being one of the most severe. Understanding how drought influences the microbial communities associated with rice plants can provide insights into plant stress responses and potential strategies for improving resilience. The rice plant hosts diverse bacterial communities in both the rhizosphere—the soil region adjacent to plant roots—and the endosphere—the interior tissues of the plant. These bacterial communities play pivotal roles in nutrient cycling, disease suppression, and overall plant health (Trivedi, P., et al., 2020). The rhizosphere and endosphere are distinct yet interconnected environments where microbial interactions can significantly impact plant performance. Recent advancements in molecular techniques have enabled detailed profiling of microbial communities, revealing that drought stress can drastically alter their composition and function. However, less is known about how drought impacts the complexity and connectivity of bacterial networks within these environments.

Description

Rice plants were grown under controlled conditions, with half of the plants subjected to drought stress by withholding water for a specified period. The other half were maintained under optimal watering conditions as controls. Soil and plant tissue samples were collected from the rhizosphere and endosphere, respectively. Rhizosphere samples were obtained by washing soil adhering to roots,

while endosphere samples were collected by surface sterilizing roots and extracting interior tissues. High-throughput sequencing of the 16S rRNA gene was employed to profile bacterial communities. DNA extraction, library preparation, and sequencing were

performed according to standard protocols. Bacterial communities were analyzed using network-based approaches to assess community complexity and connectivity. Network metrics such as degree centrality, betweenness centrality, and modularity were calculated to evaluate changes in network structure under drought conditions (de Vries, F. T., et al., 2020).

Drought stress led to significant changes in the bacterial composition of the rhizosphere. Network analysis revealed an increase in network complexity, with greater connectivity between bacterial taxa and higher diversity. Specific bacterial groups known for their stress tolerance and resilience were more prevalent, indicating a shift towards a more robust microbial community capable of withstanding adverse conditions (Xu, L., et al., 2019). In the endosphere, drought stress similarly increased bacterial network complexity. The network metrics indicated enhanced connectivity and stability, suggesting that the endosphere microbiome undergoes adaptive changes in response to drought. Functional predictions based on microbial composition suggested shifts towards pathways related to stress response and resource acquisition. The increased complexity of bacterial networks in response to drought stress reflects a dynamic and adaptive microbial response. In the rhizosphere, the enhanced connectivity may facilitate more efficient nutrient acquisition and stress resilience. In the endosphere, the changes might indicate an adaptive shift in microbial functions to support plant stress tolerance (Xu, L., et al., 2018).

These findings highlight the intricate interplay between environmental stress and microbial communities, suggesting that managing soil and plant microbiomes could be a valuable strategy for enhancing drought resilience in rice. Future research should focus on understanding the functional implications of these network changes and exploring potential applications in crop management and breeding. Drought stress significantly influences the complexity of bacterial networks in the rice rhizosphere and endosphere, leading to increased connectivity and diversity. These changes reflect adaptive responses that may help rice plants cope with water scarcity. Understanding these microbial dynamics provides valuable insights into plant-microbe interactions under stress and could inform strategies for improving crop resilience (Santos-Medellín, C., 2018).

Conclusion

Drought stress significantly reshapes the bacterial networks within both the rhizosphere and endosphere of rice plants. Our study demonstrates that under drought conditions, these microbial communities exhibit increased complexity, characterized by enhanced network connectivity, diversity, and stability. This heightened complexity in bacterial interactions likely reflects adaptive mechanisms employed by microbial communities to support plant survival under water scarcity. In the rhizosphere, the altered bacterial network suggests a shift towards more resilient and functionally diverse communities capable of improving nutrient acquisition and stress resilience. Similarly, in the endosphere, the increased network complexity may enhance the plant's ability to maintain internal stability and support stress responses. These findings underscore the critical role of microbial communities in plant stress responses and highlight the potential for leveraging microbial management strategies to improve drought tolerance in rice. Future research should explore the specific functional contributions of these bacterial networks and investigate how targeted interventions or microbial inoculations could further enhance plant resilience to drought.

Acknowledgement

None.

Conflict of Interest


The authors declare no conflict of interest.

References

- Trivedi, P., Leach, J. E., Tringe, S. G., Sa, T., Singh, B. K. (2020). Plant–microbiome interactions: From community assembly to plant health. *Nature Reviews Microbiology*, 18 :607-621.
- de Vries, F. T., Griffiths, R. I., Knight, C. G., Nicolitch, O., Williams, A. (2020). Harnessing rhizosphere microbiomes for drought-resilient crop production. *Science*, 368 :270-274.
- Xu, L., Coleman-Derr, D. (2019). Causes and consequences of a conserved bacterial root microbiome response to drought stress. *Current Opinion in Microbiology*, 49 :1-6.
- Xu, L., Naylor, D., Dong, Z., Simmons, T., Pierroz, G., Hixson, K. K., Coleman-Derr, D. (2018). Drought delays development of the sorghum root microbiome and enriches for monoderm bacteria. *Proceedings of the National Academy of Sciences*, 115 :E4284-E4293.
- Santos-Medellín, C., Edwards, J., Liechty, Z., Nguyen, B., Sundaresan, V. (2017). Drought stress results in a compartment-specific restructuring of the rice root-associated microbiomes. *MBio*, 8 :10-1128.

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