

Editorial

System Resilience in Plant Stress Responses: From Memory Shaping to Transgenerational Adaptation

Panfeng Yao 

State Key Laboratory of Aridland Crop Science, Gansu Agricultural University, Lanzhou 730070, China; yaopf@gsau.edu.cn

Traditional research in plant stress biology has predominantly focused on physiological and molecular response mechanisms under single stressors. However, in natural environments, stresses typically occur as complex combinations with spatiotemporal dynamics. Recent studies have revealed that plants develop multi-level stress response systems through the establishment of stress memory, systemic signaling networks, and epigenetic regulation, thereby enhancing their system resilience [1]. This review proposes a core framework centered on stress memory-guided ecosystem adaptability to re-evaluate plant stress response strategies.

Stress Memory: From Cellular Epigenetic Marks to Organismal Information Integration

Plants form stress memory via epigenetic mechanisms (e.g., DNA methylation, histone modifications), enabling faster activation of defense genes upon re-exposure to stress [2,3]. For example, in *Arabidopsis thaliana*, repeated drought exposure increases H3K4me3 modifications at the promoter regions of genes such as *RD29A*, accelerating their expression by 50% under secondary stress [4]. Lie et al. further showed that heat induces heritable phenotypes via a coordinated epigenetic network involving histone demethylases, transcription factors, and tasiRNAs, ensuring reproductive success and transgenerational stress adaptation [5]. Importantly, stress memory is not merely the retention of molecular marks but an ecological adaptation strategy constructed by plants through epigenetic plasticity, allowing for the optimization of resource allocation in fluctuating environments.

Systemic Signaling Networks: Root-Shoot Communication and Microbiome Synergy

Plants coordinate systemic responses through long-distance signals (e.g., Ca^{2+} waves, reactive oxygen species, peptide hormones) and recruit beneficial microorganisms to enhance stress resistance. Under drought, roots secrete strigolactones (SLs) to induce stomatal closure, while leaves regulate phosphorus redistribution to roots via miR399 [6]. Strain FB-14, isolated from the rice rhizosphere, reduces ethylene levels by producing ACC deaminase. Under 25 mM salt stress, rice inoculated with FB-14 exhibits 55.54% and 26.53% higher fresh weights in roots and shoots, respectively, compared to non-inoculated plants [7]. The “holobiont response unit” (comprising plants, microorganisms, and soil) redefines the boundaries of stress responses, with the microbiome functioning as the plant’s “extended genome”.

Ecological Trade-Offs in Stress Response Strategies

Natural selection has shaped a precision activation strategy—rapid responses via memory mechanisms instead of continuous defense, balancing stress resistance and growth demands [8]. For instance, in the case of plants adapting to drought stress, some species may prioritize growth during periods of relative water availability, while quickly switching to a defense-oriented mode when drought sets in [9]. In a study on the intertidal copepod *Tigriopus californicus*, lines selected for increased heat tolerance showed greater heat tolerance but lower fecundity, indicating an energetic cost to tolerance [10]. These findings



Received: 22 October 2025

Accepted: 1 November 2025

Published: 2 November 2025

Citation: Yao, P. System Resilience in Plant Stress Responses: From Memory Shaping to Transgenerational Adaptation. *Agronomy* **2025**, *15*, 2550. <https://doi.org/10.3390/agronomy15112550>

Copyright: © 2025 by the author. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

highlight that across different species, both in plants and animals, there are trade-offs in resource allocation during stress responses.

Future Directions: Integration of Smart Breeding and Ecological Simulation

Recent advancements in genome-editing technologies have opened up new possibilities for precisely manipulating plant epigenomes. Similar to how CRISPR-Cas9 has been used to modify genes directly, the CRISPR-dCas9 system can be harnessed to target specific epigenetic marks. This approach has the potential to revolutionize plant breeding by creating plants with enhanced stress memory capabilities while maintaining normal growth and development, as proposed in Targeted editing of epigenetic regulators (e.g., HDA6, ROS1) to enhance stress memory without impairing growth [11].

Development of synthetic microbial community (SynComs) inoculants to improve plant resilience to combined stresses [12]. The importance of the plant microbiome in stress tolerance has become increasingly evident. By engineering synthetic microbial communities, researchers aim to create tailored inoculants that can enhance plant resilience to multiple stressors simultaneously. This concept is in line with the growing understanding of the “holobiont” concept, where plants and their associated microorganisms function as a unified entity.

Construction of plant–environment interaction models by integrating machine learning and multi-omics data to predict the dynamics of stress responses. The era of big data and artificial intelligence has provided powerful tools for predicting plant responses to stress. By integrating multi-omics data, such as genomics, transcriptomics, and metabolomics, with machine-learning algorithms, researchers can build sophisticated models that simulate plant–environment interactions. These models, often referred to as “digital twins,” can predict how plants will respond to different stress scenarios in real time, as described in [13]. This predictive ability can greatly aid in the development of more effective stress management strategies in agriculture and forestry.

Conclusion: A Paradigm Shift from “Passive Response” to “Active Environment Shaping”

Plant stress responses are no longer viewed as isolated physiological reactions but as a systemic resilience-building process that integrates memory, signaling, and microbial interactions. Future research should transcend “plant centrism” by incorporating the microbiome, soil environment, and climate fluctuations into a holistic analytical framework, and synergize smart breeding with ecological management to enhance the sustainability of agricultural systems.

Funding: We are grateful to the supports from the funding support from the General Project of the Joint Scientific Research Fund of Gansu Province (24JRR838); the China Agricultural University Corresponding Support Research Joint Fund (GSAU-DKZY-2024-005); the National Natural Science Foundation of China (32560446).

Data Availability Statement: Not applicable.

Conflicts of Interest: The author declares that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

References

1. Hilker, M.; Schwachtje, J.; Baier, M.; Balazadeh, S.; Kopka, J. Priming and memory of stress responses in organisms lacking a nervous system. *Biol. Rev. Camb Philos. Soc.* **2015**, *91*, 1118–1133. [[CrossRef](#)] [[PubMed](#)]
2. Rahman, M.M.; Keya, S.S.; Bulle, M.; Ahsan, S.M.; Rahman, M.A.; Roni, M.S.; Al Noor, M.M.; Hasan, M. Past trauma, better future: How stress memory shapes plant adaptation to drought. *Funct. Plant Biol.* **2025**, *52*, FP24355.
3. Liu, J.; He, Z. Small DNA methylation, big player in plant abiotic stress responses and memory. *Front. Plant Sci.* **2020**, *11*, 595603. [[CrossRef](#)] [[PubMed](#)]
4. Ding, Y.; Fromm, M.; Avramova, Z. Multiple exposures to drought ‘train’ transcriptional responses in *Arabidopsis*. *Nat. Commun.* **2012**, *3*, 740. [[CrossRef](#)] [[PubMed](#)]

5. Liu, J.; Feng, L.; Gu, X.; Deng, X.; Qiu, Q.; Li, Q.; Zhang, Y.; Wang, M.; Deng, Y.; Wang, E. An H3K27me3 demethylase-HSFA2 regulatory loop orchestrates transgenerational thermomemory in *Arabidopsis*. *Cell Res.* **2019**, *29*, 379–390. [[CrossRef](#)] [[PubMed](#)]
6. Wang, X.; Yuan, D.; Liu, Y.; Liang, Y.; He, J.; Yang, X.; Hang, R.; Jia, H.; Mo, B.; Tian, F.; et al. INDETERMINATE1 autonomously regulates phosphate homeostasis upstream of the miR399-ZmPHO2 signaling module in maize. *Plant Cell* **2023**, *35*, 2208–2231. [[CrossRef](#)] [[PubMed](#)]
7. Muhammad, S.; Asad Ali, S.; Farwa, B.; Muhammad, N.; Muhammad, Z.; Temoor, A.; Tahir, N.; Irfan, M.; Awais, M. *Achromobacter* sp. FB-14 harboring ACC deaminase activity augmented rice growth by upregulating the expression of stress-responsive CIPK genes under salinity stress. *Braz. J. Microbiol.* **2020**, *51*, 719–728.
8. Fallon, B.; Cavender-Bares, J. Leaf-level trade-offs between drought avoidance and desiccation recovery drive elevation stratification in arid oaks. *Ecosphere* **2018**, *9*, e02149. [[CrossRef](#)]
9. Li, X.; Piao, S.; Wang, K.; Wang, X.; Wang, T.; Ciais, P.; Chen, A.; Lian, X.; Peng, S.; Peuelas, J. Temporal trade-off between gymnosperm resistance and resilience increases forest sensitivity to extreme drought. *Nat. Ecol. Evol.* **2020**, *4*, 1075–1083. [[CrossRef](#)] [[PubMed](#)]
10. Kelly, M.W.; Debiase, M.B.; Villela, V.A.; Roberts, H.L.; Cecola, C.F. Adaptation to climate change: Trade-offs among responses to multiple stressors in an intertidal crustacean. *Evol. Appl.* **2016**, *9*, 1147–1155. [[CrossRef](#)]
11. Moradpour, M.; Abdulah, S.N.A. CRISPR/dCas9 platforms in plants: Strategies and applications beyond genome editing. *Plant Biotechnol. J.* **2020**, *18*, 32–44. [[CrossRef](#)] [[PubMed](#)]
12. Ke, J.; Wang, B.; Yoshikuni, Y. Microbiome Engineering: Synthetic biology of plant-associated microbiomes in sustainable agriculture. *Trends Biotechnol.* **2021**, *39*, 244–261. [[CrossRef](#)]
13. Li, G.; An, L.; Yang, W.; Yang, L.; Wei, T.; Shi, J.; Wang, J.; Doonan, J.H.; Xie, K.; Fernie, A.R. Integrated biotechnological and AI innovations for crop improvement. *Nature* **2025**, *643*, 925–937. [[CrossRef](#)] [[PubMed](#)]

Disclaimer/Publisher’s Note: The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.