



OPEN ACCESS

EDITED AND REVIEWED BY
Luisa M. Sandalio,
Spanish National Research Council (CSIC),
Spain

*CORRESPONDENCE

Jing Zhang
✉ zhangjing12306@163.com
Jin-Lin Zhang
✉ jlzhang@izu.edu.cn

RECEIVED 18 October 2023
ACCEPTED 17 November 2023
PUBLISHED 23 November 2023

CITATION

Zhang J, Chen Y, Chai M-F, Shabala S,
Wang K-H and Zhang J-L (2023)
Editorial: Adaptation mechanisms
of grass and forage plants to stressful
environments, volume II.
Front. Plant Sci. 14:1323841.
doi: 10.3389/fpls.2023.1323841

COPYRIGHT

© 2023 Zhang, Chen, Chai, Shabala, Wang
and Zhang. This is an open-access article
distributed under the terms of the [Creative
Commons Attribution License \(CC BY\)](#). The
use, distribution or reproduction in other
forums is permitted, provided the original
author(s) and the copyright owner(s) are
credited and that the original publication in
this journal is cited, in accordance with
accepted academic practice. No use,
distribution or reproduction is permitted
which does not comply with these terms.

Editorial: Adaptation mechanisms of grass and forage plants to stressful environments, volume II

Jing Zhang^{1*}, Yu Chen¹, Mao-Feng Chai², Sergey Shabala³,
Ke-Hua Wang⁴ and Jin-Lin Zhang^{5*}

¹College of Agro-grassland Science, Nanjing Agricultural University, Nanjing, China, ²Key Laboratory of National Forestry and Grassland Administration on Grassland Resources and Ecology in the Yellow River Delta, College of Grassland Science, Qingdao Agricultural University, Qingdao, China, ³Tasmanian Institute of Agriculture, University of Tasmania, Hobart, TAS, Australia, ⁴Department of Turfgrass Science and Engineering, College of Grassland Science and Technology, China Agricultural University, Beijing, China, ⁵State Key Laboratory of Herbage Improvement and Grassland Agro-ecosystems, Key Laboratory of Grassland Livestock Industry Innovation, Ministry of Agriculture and Rural Affairs; College of Pastoral Agriculture Science and Technology, Lanzhou University, Lanzhou, China

KEYWORDS

grass and forage plants, stress tolerance, gene functional characterization, organic acid, host-microbe interactions, nutrient uptake

Editorial on the Research Topic

[Adaptation mechanisms of grass and forage plants to stressful environments, volume II](#)

1 Introduction

In nature, plants encounter various challenges from stressful environments, including high and low temperatures, drought, salinity, heavy metals, and nutrient deficiency, which adversely affect plant growth and development (Zhang et al., 2022). It is well-established that global warming is occurring, leading to frequent and extreme climate fluctuations, resulting in frequent natural disasters and environmental problems. Additionally, the increasing global population presents greater challenges for food and ecological security (Gupta et al., 2020). Therefore, cultivating more stress-resistant crop varieties and increasing crop yield and quality are essential for addressing global food security and sustainable development issues.

Grass and forage plants with relatively more powerful stress resistance fulfill numerous functions, including beautifying landscapes, protecting the environment, enhancing recreational activities, and providing fodder for livestock and wildlife (Huang, 2021). In comparison to crops, grass and forage plants display a diverse range of breeding mechanisms, including cross-pollination, self-pollination, and hybridization between different species. This diversity contributes to a wide genetic variation within these plants and enables them to thrive in more stressful environments (Huang, 2021). Therefore, there is an imperative necessity to investigate the underlying stress-tolerant

mechanisms that might feedback grass, forage and crop plant breeding for stress tolerance improvement.

Despite significant advances in understanding the mechanisms of grass and forage plants to stressful environments, there remain knowledge gaps in these areas, and this Research Topic aims to address these gaps. In this Research Topic, 11 articles written by 75 researchers were published.

2 Functional characterization of genes relevant to stress tolerance

The Full-length cDNA overexpression (FOX) system is a molecular biology technique used for gene mining by overexpressing full-length complementary DNA (cDNA) in cells or organisms (Ichikawa et al., 2006). The FOX hunting system has been successfully applied for stress-tolerant genes screening in *Arabidopsis* and rice. For example, *TsHsfA1d* and *OsREX1-S* identified via FOX hunting system functioned as positive regulators of heat stress and cadmium stress, respectively (Higashi et al., 2013; Kunihiro et al., 2014). In this Research Topic, Zheng et al. identified eleven salt-tolerant genes using FOX hunting system in *Zoysia matrella*. They particularly focused on a novel salt-inducible candidate gene called *ZmGnTL*. Their findings revealed that *ZmGnTL* improves salt tolerance by regulating ion homeostasis, scavenging reactive oxygen species, and adjusting osmotic balance.

High-affinity K^+ transporters (HKTs) are transmembrane cation transporters that play a pivotal role in Na^+ or Na^+-K^+ co-transport, thereby regulating salt tolerance in plants (Horie et al., 2007). Therefore, HKTs represent valuable gene resources for enhancing plant salt tolerance. In this Research Topic, Haxim et al. characterized a novel HKT gene named *SeHKT1;2* from a halophyte *Salicornia europaea*. *SeHKT1;2* selectively transports Na^+ rather than K^+ and is an important target for understanding the mechanisms of salt tolerance in plants.

Plant plasma membranes (PMs) serve important functions in maintaining intracellular stability and exchanging information with the external environment. Studying the dynamics of the PM proteome is crucial for elucidating cellular regulation in response to various stimuli. However, analyzing the PM proteome poses challenges due to the low abundance of PM proteins in the total cellular protein pool (Chen and Weckwerth, 2020). To enhance the separation and enrichment of PM proteins, Yang et al. developed a simplified method that combines differential centrifugation and Brij-58 treatment. This method increased the abundance of PM proteins in the enriched fraction while reducing contamination from other organellar proteins.

3 Regulations of natural metabolites or synthetic chemicals on stress tolerance

The remediation of saline-alkali and heavy metal-contaminated lands plays a crucial role in protecting the ecological environment,

improving land availability, and promoting sustainable agriculture (Khan and Bhatt, 2023). Chemical substances, such as organic acids and biochar, have the potential to react with pollutants, neutralizing or transforming them into less harmful forms. In this Research Topic, Yang et al. discovered that the exogenous application of citric acid reduced soil salinity and increased soil nutrient content, root vigor, and photosynthesis in sweet sorghum. As a result, the stress tolerance of sweet sorghum was improved, leading to higher biomass yield. Additionally, Meng et al. found that the use of 5% corn straw biochar effectively alleviated the toxicity of Pb to red clover and the associated soil. Above findings contribute to sustainable development and foster the harmonious coexistence between humans and nature.

4 Omics-related studies

Recent significant progress in omics techniques, such as transcriptomics, genomics, proteomics, and metabolomics, has significantly contributed to the profound understanding of the molecular mechanisms underlying plant stress tolerance (Singhal et al., 2021). In this Research Topic, Wang et al. found that application of P fertilizer resulted in improved root structure and increased levels of soluble sugar and soluble protein. The integration of the transcriptome and metabolome revealed the impact of P on the biosynthesis of N-acetyl-L-phenylalanine, L-serine, lactose, and isocitrate during the cold acclimation period.

Strong ultraviolet radiation and low temperature environments can induce the synthesis of specific secondary metabolites in plants as a defense mechanism against severe environmental stresses. To understand the adaptive mechanism of *Draba oreades Schrenk* at high altitude, Lei et al. conducted a comprehensive evaluation of the metabolome in plants at 3800 m, 4000 m, and 4200 m, respectively. Based on the metabolome data, ten crucial metabolites were identified as potential biomarkers. The levels of L-phenylalanine, L-histidine, naringenin-7-O-Rutinoside-4'-O-glucoside, and apigenin, which are associated with flavonoid biosynthesis and plant disease resistance, increased with the increase of altitude.

5 Cross stress tolerance

In natural environments, plants frequently encounter various simultaneous stresses, leading to the occurrence of cross-tolerance phenomena (Zhang et al., 2023). Climate change exposes plants to multiple abiotic stresses simultaneously. While the responses of plants to individual stresses have been extensively studied, it is challenging to speculate and infer the effects of stress combinations based on solely these studies. In this Research Topic, Zhou et al. examined the responding mechanism of bermudagrass to combined low temperature and salt treatments. It was observed that low temperature treatment reduced the relative growth rate, chlorophyll fluorescence transient curve, biomass, and crude fat content. Conversely, mild salt addition alleviated cold stress-induced damage by enhancing photosynthesis and improving the

enzymatic activity of antioxidant. This study provides a comprehensive understanding of the probable interaction mechanism between low temperature and salt stress in grass plants, offering valuable insights for fodder growth in cold regions.

6 Future research

The articles presented in this Research Topic make a significant contribution to addressing gaps in our understanding of the role of complex signaling transduction pathways in grass and forage plants in response to various stressful environments. These articles also highlight the identification of stress-tolerant genes, beneficial natural metabolites, and root-associated microbes, which serve as valuable resources not only for grass and forage plants, but also for other crops. CRISPR/Cas is a valuable biotechnological approach for breeding crops with increased tolerance to stressful environments (Zhu et al., 2020), while no CRISPR/Cas-related research has been included in this Research Topic. We look forward to more articles to be published exploring the application of CRISPR/Cas and further advancements in creating stress-tolerant grass and forage germplasms without transgenic elements.

Author contributions

JZ: Funding acquisition, Supervision, Writing – original draft, Writing – review & editing. YC: Funding acquisition, Writing – review & editing. M-FC: Writing – review & editing. SS: Writing – review & editing. K-HW: Writing – review & editing. J-LZ: Writing – original draft, Writing – review & editing.

References

- Chen, Y., and Weckwerth, W. (2020). Mass spectrometry untangles plant membrane protein signaling networks. *Trends Plant Sci.* 25, 930–944. doi: 10.1016/j.tplants.2020.03.013
- Gupta, A., Rico-Medina, A., and Caño-Delgado, A. I. (2020). The physiology of plant responses to drought. *Science* 368 (6488), 266–269. doi: 10.1126/science.aaz7614
- Higashi, Y., Ohama, A., Ishikawa, T., Katori, T., Shimura, A., Kusakabe, K., et al. (2013). HsfA1d, a protein identified via FOX hunting using *Thellungiella salsuginea* cDNAs, improves heat tolerance by regulating heat stress responsive gene expression. *Mol. Plant* 6, 411–422. doi: 10.1093/mp/sst024
- Horie, T., Costa, A., Kim, T. H., Han, M. J., Horie, R., Leung, H. Y., et al. (2007). Rice OsHKT2;1 transporter mediates large Na⁺ influx component into K⁺-starved roots for growth. *EMBO J.* 26, 3003–3014. doi: 10.1038/sj.emboj.7601732
- Huang, B. (2021). Grass research for a productive, healthy and sustainable society. *Grass Res.* 1, 1. doi: 10.48130/GR-2021-0001
- Ichikawa, T., Nakazawa, M., Kawashima, M., Iizumi, H., Kuroda, H., Kondou, Y., et al. (2006). The FOX hunting system: an alternative gain-of-function gene hunting technique. *Plant J.* 48, 974–985. doi: 10.1111/j.1365-3113X.2006.02924.x
- Khan, M. M., and Bhatt, P. (2023). Editorial: Environmental pollutants in agroecosystem: toxicity, mechanism, and remediation. *Front. Plant Sci.* 14, 1208405. doi: 10.3389/fpls.2023.1208405
- Kunihiro, S., Kowata, H., Kondou, Y., Takahashi, S., Matsui, M., Berberich, T., et al. (2014). Overexpression of rice *OsREX1-s*, encoding a putative component of the core general transcription and DNA repair factor IIH, renders plant cells tolerant to cadmium- and UV-induced damage by enhancing DNA excision repair. *Planta* 239, 1101–1111. doi: 10.1007/s00425-014-2042-1
- Singhal, R. K., Saha, D., Skalicky, M., Mishra, U. N., Chauhan, J., Behera, L. P., et al. (2021). Crucial cell signaling compounds crosstalk and integrative multi-omics techniques for salinity stress tolerance in plants. *Front. Plant Sci.* 12, 670369. doi: 10.3389/fpls.2021.670369
- Zhang, H., Zhu, J., Gong, Z., and Zhu, J. K. (2022). Abiotic stress responses in plants. *Nat. Rev. Genet.* 23 (2), 104–119. doi: 10.1038/s41576-021-00413-0
- Zhang, J., Chai, M.-F., Shabala, S., Wang, K.-H., and Zhang, J.-L. (2023). Editorial: Adaptation mechanisms of grass and forage plants to stressful environments. *Front. Plant Sci.* 14, 1132198.
- Zhu, H., Li, C., and Gao, C. (2020). Applications of CRISPR-Cas in agriculture and plant biotechnology. *Nat. Rev. Mol. Cell Biol.* 21 (11), 661–677. doi: 10.1038/s41580-020-00288-9

Funding

The author(s) declare financial support was received for the research, authorship, and/or publication of this article. This work was financially supported by the Fundamental Research Funds for the Central Universities (XUEKEN2022020 and YDZX2023001).

Acknowledgments

We greatly appreciate all authors and reviewers for their contribution to this Research Topic.

Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

The author(s) declared that they were an editorial board member of Frontiers, at the time of submission. This had no impact on the peer review process and the final decision.

Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.