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## SPECIALTY SECTION

This article was submitted to  
Plant Abiotic Stress,  
a section of the journal  
Frontiers in Plant Science

RECEIVED 17 October 2022

ACCEPTED 31 October 2022

PUBLISHED 15 November 2022

## CITATION

Wu H and Hill C (2022) Editorial: New insights into salinity sensing, signaling and adaptation in plants, volume II. *Front. Plant Sci.* 13:1072658. doi: 10.3389/fpls.2022.1072658

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# Editorial: New insights into salinity sensing, signaling and adaptation in plants, volume II

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## KEYWORDS

nano-biotechnology, nanomaterials, salt sensor, transcription factors, glycine betaine, genome-wide expression

## Editorial on the Research Topic

[New insights into salinity sensing, signaling and adaptation in plants, volume II](#)

## Plants perceive salt through plant salinity sensors

In the past decade, much progress has been made in identifying the sensors involved in salt-induced stress signaling in plants. Plant roots are the first organs to detect changes in the osmotic potential induced by salt stress. Wang et al. have summarized the recent progress in identifying osmotic and Na<sup>+</sup> sensors and their signal transduction pathways, specifically in plant roots. Different types of putative sensors in the plasma membrane of root cells exist, including mechanosensory channels (MSCs), which respond to turgor pressure changes of plant cells, plasma membrane-bound protein kinases, which can phosphorylate signaling proteins, and Ca<sup>2+</sup>-mediated ion transporters, such as non-selective cation channels (NSCCs) and cyclic nucleotide-gated channels (CNGCs) which, upon activation, allowing Ca<sup>2+</sup> to flow into cells. They have further performed bioinformatic analyses of transmembrane domains of receptor-like kinases (RLKs), which are considered as candidate ionic sensors.

## Nano-biotechnological approaches for improving plant salt stress tolerance

Plant nano-biotechnology is an emerging tool to improve plant growth and salt stress tolerance. Nano-enabled plant salt tolerance has been widely reported in many plant species. Li *et al.*, presented a review paper to illustrate how nanomaterials can be used to improve plant salt tolerance. In this review paper, the mechanisms behind nano-enabled plant tolerance were summarized. It includes maintaining ROS and ion ( $\text{Na}^+$  and  $\text{K}^+$ ) homeostasis, increasing  $\alpha$ -amylase activities, producing gas signaling molecules such as nitric oxide and reducing oxidative damage in membranes *via* decreasing lipoxygenase activities. They highlighted that alleviating oxidative stress damage and maintaining ion homeostasis are commonly employed mechanisms for nano-enabled salt tolerance in plants. Moreover, they also discussed the possible role of phytohormones and the molecular mechanisms in nano-enabled plant salt tolerance.

## Transcription factors involved in salinity stress tolerance in plants

Transcription factors (TFs) play roles in many biological processes, including the regulation of salinity stress tolerance, and have been a target of engineering crops with improved stress tolerance. TFs are well-characterized in the model plant *Arabidopsis* and major crop species such as wheat, but only little is known in pearl millet, a staple food crop grown in the arid and semi-arid regions of Africa and Asia. Awan *et al.* performed transcriptome profiling of a pearl millet genotype grown under salt stress at three different time points (1, 3, and 7 h after salt treatment). Their study identified TFs mostly upregulated at 1 and 7 h of salt treatment which belonged to different families, including APETALA2/ethylene-responsive element binding factors (AP2-ERF), Basic helix-loop-helix (bHLH), MYB, NAC, and WRKY. Additionally, TFs related to the biosynthesis of phytohormones including abscisic acid (ABA), jasmonic acid (JA), and gibberellic acid (GA) were among the identified differentially expressed genes, and also mostly upregulated at 1 and 7 h of salt treatment. The availability of the transcriptome profiling data sets is a valuable resource to the pearl millet research community and may help identify valuable traits to improve salinity stress tolerance in pearl millet.

Han *et al.* showed that LbMYB48, an R1-type MYB TF, was strongly induced under salt stress in *Limonium bicolor*, a dicotyledonous recretahalophyte with several multicellular salt glands on the leaves. Salt gland density and salt secretion capacity were impaired in LbMYB48-silenced lines, resulting in reduced salt resistance. RNA-seq analysis showed that LbMYB48 modulates genes related to epidermal cell development, such as *LbCPC-like* and *LbDIS3*, and salt stress-related genes, i.e. *LbSOSs*, *LbRLKs*, and *LbGSTs* to regulate salt gland development and thus salt tolerance in

*Limonium bicolor*. Further, heterologous over-expression of *LbMYB48* improved salt tolerance in *Arabidopsis thaliana*. The authors conclude that *LbMYB48* regulates the salt gland development and salt tolerance by regulating the expression of epidermal cell development-related genes in *Limonium bicolor*.

## Maintaining $\text{Na}^+$ homeostasis is important for plant salt tolerance

Over-accumulation of  $\text{Na}^+$  is toxic to most plants. Zhu *et al.* investigated the mechanisms underlying glycine betaine-improved maize salt tolerance *via* the maintenance of  $\text{Na}^+$  homeostasis. Non-invasive micro-test technology (NMT) and confocal microscope imaging showed that glycine betaine application can increase leaf and root  $\text{Na}^+$  efflux and alleviate cytosolic  $\text{Na}^+$  over-accumulation in maize under salt stress. Glycine betaine significantly upregulated the expression of plasma membrane  $\text{H}^+$ -ATPase genes *ZmMHA2*, and *ZmMHA4* as well as  $\text{Na}^+/\text{H}^+$  antiporter gene *ZmNHX1*, and also improved vacuolar activity of *NHX*. However, no significant effect of glycine betaine on V type  $\text{H}^+$ -ATPases was detected. Taken together, their results showed that glycine betaine modulated PM  $\text{H}^+$ -ATPase to help to maintain cellular  $\text{Na}^+$  homeostasis, ultimately showing improved salt tolerance in maize.

Salt Overly Sensitive 1 (*SOS1*) is a well-characterized  $\text{Na}^+$  efflux transporter, but only limited knowledge exists of its role in soybean salt stress responses. To understand *SOS1* gene function in soybean, Zhang *et al.* created three *gmsos1* mutants using the CRISPR-Cas9 gene editing system. *gmsos1* mutants were hypersensitive to salt stress and accumulated higher root  $\text{Na}^+$  levels but much lower levels of root  $\text{K}^+$  under salt stress compared to the wild-type. The transcriptomic profiles of the *gmsos1* mutant roots showed that many differentially expressed genes encode proteins with functions in ion transport and response to abiotic stress. In summary, the authors provide evidence that *SOS1* function is conserved across eudicots such as *Arabidopsis* and soybean, as well as monocots such as rice.

## Author contributions

All authors listed have made a substantial, direct and intellectual contribution to the work, and approved it for publication.

## Funding

This work was supported by the NSFC grant (No. 32071971, 31901464), Hubei Agricultural Science and Technology Innovation Center Program (2021-620-000-001-032), project 2662020ZKPY001 supported by the Fundamental Research Funds for the Central Universities, and joint project SZYJY2021008 from Huazhong

Agricultural University and Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences to HW.

## Conflict of interest

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