

# Chapter 15

## Arsenic Tolerance and Signaling Mechanisms in Plants



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**Abstract** Arsenic (As) contamination is now prevalent in large areas of a number of countries. Arsenic stress during vegetative and reproductive phases of plant growth affects the growth, flowering, and fruit/grain development due to a number of physiological, biochemical, and molecular effects. The metabolism of carbon, nitrogen, and sulfur is affected along with changes in photosynthetic and respiratory processes. The avoidance of As toxicity requires fine-tuning of several processes starting from uptake and transport of As to As detoxification and prevention of stress manifestation. Thus, the regulatory processes promoting concerted action of several pathways become an important determinant of As stress tolerance of a plant. These include various phytohormones (auxins, jasmonates, ethylene, abscisic acid, salicylic acid, etc.), transcription factors, microRNAs, reactive oxygen and reactive nitrogen species, and kinases. It is also important to note that an early perception of arsenic entry into plants and signaling of the information to distant parts (leaves) ensure that plants remain prepared to tackle the As stress. Although the research on signaling aspects of arsenic stress is yet in the primary stage, the information available is of potential application and future research. The present work describes current knowledge on perception and signaling of As stress in plants.

**Keywords** Arsenic · MicroRNAs · Nitric oxide · Phytohormones · Reactive oxygen species · Transcription factors

### 1 Introduction

Arsenic (As) is a highly toxic metalloid having an array of toxic manifestations and carcinogenicity on various organisms, including humans (Duker et al. 2005). Arsenic is present in nature due to its use in agricultural and industrial sectors as well as due to natural biogeochemical factors leading to a large amount of As being

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released in the environment (Shukla et al. 2017). Arsenic is posing serious health concerns specifically in West Bengal in India and Bangladesh. Exposure to As for a long time leads to the development of some serious symptoms such as skin lesions and different types of cancers (Kumar et al. 2015). There are many forms of As present in nature. These can be categorized into inorganic [arsenite: As(III) and arsenate: As(V)] and organic [monomethylarsonic acid: MMA, dimethylarsinic acid: DMA]. It is known that mono-, di-, and tri-methylated forms of As are produced in the soil by microbial processes (Mestrot et al. 2011). The entry of toxic As species in plants also occurs via competitive uptake through transporters of essential metals by the mechanism of ionic mimicry (Verbruggen et al. 2009; Ye et al. 2010). The influx of As(III) occurs primarily via nodulin 26-like intrinsic proteins (NIPs) class of aquaglyceroporins (Verbruggen et al. 2009; Bienert et al. 2008; Roychowdhury et al. 2018, 2019), whereas that of As(V) is driven by phosphate transporters (Wu et al. 2011).

The plants suffer toxicity when the As accumulation passes a certain level called threshold level (Srivastava et al. 2007). Arsenic exposure to plants affects several physiological, biochemical, and morphological processes which include germination, growth, and biomass production (Finnegan and Chen 2012). Arsenic toxicity impacts photosynthesis by reducing chlorophyll content in the leaves and by altering photosynthetic efficiency, electron transport rate, transpiration, etc. (Srivastava et al. 2013a). Arsenic, although a non-redox-active metalloid, also induces the production of reactive oxygen species (ROS) by inter-conversion of one ionic form to another and by overconsumption of reduced glutathione (GSH) in the process (Mylona et al. 1998). The oxidative stress conditions in the presence of As cause lipid peroxidation of membranes, damage proteins and DNA, and induce toxicity (Srivastava et al. 2011). Arsenic exposure also causes genotoxic effects like mitotic index depression, increased chromosomal aberrations like a break, fragments, c-metaphase, and multipolar arrangements (Gupta et al. 2018). By translocation to the shoot, the plant growth can be severely inhibited by As by arresting cellular expansion and biomass accumulation as well as by compromising plant reproductive capacity resulting in loss of yield and fruit production (Garg and Singla 2011).

In the presence of As, it becomes important for the plants to prepare and be equipped with mechanisms to tolerate the stress so as to survive and propagate. Plants tolerate As stress by an array of metabolic processes such as binding of As to thiol (-SH) containing ligands, glutathione (GSH), and phytochelatins (PCs) followed by As–thiol sequestration in vacuoles (Srivastava et al. 2007; Song et al. 2014; Tang et al. 2019), reduction of As(V) to As(III) (Chao et al. 2014; Shi et al. 2016), decrease in uptake of As by altered expression of transporters (Srivastava et al. 2014), protection against oxidative stress via activation of antioxidant enzymes and molecules (Srivastava et al. 2007; Roychowdhury et al. 2018, 2019), anatomical and morphological changes allowing plants to bind As to cell walls and to maximize nutrient uptake and translocation (root phenotype), etc. There are a large number of metabolites such as cysteine, glutathione, proline,  $\alpha$ -tocopherol,  $\gamma$ -aminobutyric acid (GABA), and carotenoids which have a role in As tolerance (Pathare et al. 2013; Singh et al. 2016). The physiological and biochemical experiments to omics

approach like transcriptomics, metabolomics, and proteomics have been employed to unravel the response networks for As tolerance in plants (Yu et al. 2012; Dixit et al. 2015; Srivastava et al. 2015; Roychowdhury et al. 2018, 2019). It is clear that a complex interplay of various mechanisms and their concerted response is important for tackling As stress. This necessitates the involvement of a number of regulatory and signaling processes to operate for the early perception and signaling of As stress and for coordinating various physiological, biochemical, molecular, and metabolic responses (Pathare et al. 2013). This chapter presents the knowledge gained in the field of As stress perception and signaling in plants.

## 2 Perception and Signaling of Arsenic Stress

The perception and signaling involve sensing the entry of As in plants and transfer this information among various plant cells and tissues from receptor systems to effector ones. The timely perception of the stress allows plants to respond appropriately to the incoming stress. Apart from the perception of the stress, the signal must reach to all cells, tissues, and organs so as to prepare them for stress that might reach to them sooner or later. In the case of As stress, a few studies have been conducted that provide valuable insights into the perception and signaling of As stress. Some of the well-known signaling mechanisms constitute mitogen-activated protein kinases (MAPKs), reactive oxygen species (ROS) and reactive nitrogen species (RNS), hormones [abscisic acid (ABA), jasmonic acid (JA) and other jasmonates, salicylic acid (SA), ethylene, brassinosteroids, etc.], microRNAs, and transcription factors. In the following sections, the available knowledge is presented to showcase the aspects of perception and signaling of As stress in plants (Roychowdhury et al. 2018, 2019).

## 3 Phytohormones

Phytohormones regulate crucial physiological responses of plants during growth, such as cell division, cell differentiation, organ formation, leaf senescence, flowering, and grain development, and also in response to various abiotic and biotic stresses (Shukla et al. 2017). Auxins play the role of key regulators of phenotypic changes that directly affect responses of plants to the stresses (Nibau et al. 2008). The auxin accumulation takes place at the root tip, and the plant apical tissues are a place of auxin synthesis. Therefore, auxins are transported downward via phloem toward the tip of the root (Benkova et al. 2003). The exogenous supply of an auxin, indole-3-acetic acid (IAA), was found to improve the growth of *Brassica juncea* and enhance tolerance of plants under As stress. The effects were found to be mediated through changes in the expression of microRNAs like miR167, miR319, and miR854 (Srivastava et al. 2013b). Selenium (Se) is known to ameliorate As toxicity

in rice plants (Chauhan et al. 2017). The exogenous supply of auxin along with Se further augments As tolerance of rice plants in comparison to that achieved through Se alone supply (Pandey and Gupta 2015). In *A. thaliana*, mutants of auxin transporters *aux1*, *pin1*, and *pin2* have been found to be more sensitive to As(III) as compared to WT plants. Further, the supply of auxin transport inhibitors also compromised plants' tolerance to As(III) of WT plants, while exogenous IAA supply improved As(III) tolerance of *aux1* mutants (Krishnamurthy and Rathinasabapathi 2013).

Jasmonates play a vital role in mediating several processes involved in the overall development of plants and abiotic and biotic stress response. Some of the developmental processes include senescence, tuber formation, pollen maturation, root growth, and interactions with other organisms (Carvalhais et al. 2015). The activation of jasmonic acid (JA) signaling pathway happens due to the conjugation of JA to the amino acids, i.e., L-isoleucine (Ile), which produces an active hormone called as (3R, 7S)-jasmonoyl-L-isoleucine (JA-Ile). The F-box protein Coronatine-Insensitive 1 (COI1) is a co-receptor of JA-Ile, which binds with JA-Ile, for ubiquitin-mediated degradation of JAZs (jasmonate ZIM-domain) proteins. This releases transcription factors, i.e., MYC2, which activate or repress gene expression associated with JA (Carvalhais et al. 2015). JAs can regulate sulfur metabolism and the level of GSH and PCs to ameliorate the toxic effects of metals (Maksymiec et al. 2007). Jasmonates are suggested to play the primary role in sensing the entry of As in plants via an indirect perception of As-induced stress to sulfur metabolism (Srivastava et al. 2009). The significant changes in the level of JA and methyl jasmonate (MeJA) were observed in As-stressed *B. juncea*. Further, the exogenous supply of JA was found to improve the growth of *B. juncea* plants as well as tolerance under As stress (Srivastava et al. 2013b). An involvement of JA in the responses to As stress in rice and *B. juncea* was also suggested when the transcriptome analysis showed significant upregulation of genes of JA biosynthesis and JAZs (Yu et al. 2012; Srivastava et al. 2015).

Abscisic acid (ABA) is a derivative of carotenoid and is an essential phytohormone, which plays a vital role against various kinds of stresses like low temperature, heat stress, drought, salinity, and metals (Vishwakarma et al. 2017). In transcriptomic analyses in rice and *B. juncea* under As(III) and/or As(V) stress, a change in ABA metabolism genes was noticed (Chakrabarty et al. 2009; Srivastava et al. 2015). It has been found that there is an increase in ABA synthesis under As stress in *B. juncea*. An evidence of interaction between ABA and miR159 was also found to have an impact on As stress response (Srivastava et al. 2013b). Salicylic acid (SA), a phenolic compound, is synthesized from phenylalanine in cytoplasm and chorismate in chloroplast by two different pathways (Vlot et al. 2009). The main functions of SA include seed germination, respiration, and thermal tolerance. It plays a vital role in plant response to a variety of abiotic stresses (Vlot et al. 2009). A reversion in the plant growth and oxidative stress upon the exogenous application of SA in the rice has been found under As stress. It could also reduce As translocation to shoots through changes in As transporter genes (Singh et al. 2015). SA also acts as a direct scavenger of ROS and affects oxidative metabolism and increases

antioxidant potential (Singh et al. 2015). An interplay of SA and nitric oxide (NO) in the regulation of As stress is also demonstrated. In rice plants exposed to As(III), a decline in the level of NO and SA was noticed. Upon exogenous supply of SA, the level of SA, as well as NO, was found to increase through the increase in the activity of nitrate reductase. The supplementation of SA was found to reduce As concentrations while increasing that of nutrient elements like Zn, Mn, and Fe in rice shoots (Singh et al. 2017). Ethylene is the only plant hormone present in a gaseous state. This hormone is involved in processes like fruit ripening and abscission and root hair formation (Lewis et al. 2011). An increase in ethylene levels under metal stress has been found, and the role of ethylene in the regulation of metal stress responses of plants is demonstrated (Masood et al. 2012; Khan and Khan 2014). However, the role of ethylene in As stress responses of plants is not yet elucidated. Nonetheless, ethylene biosynthesis and ethylene-responsive genes have been observed to upregulated during transcriptome analysis of rice plants upon As exposure (Chakrabarty et al. 2009; Yu et al. 2012).

Cytokinins are derivatives of adenine and are involved in cell division, nutrient metabolism, nodulation, and circadian rhythms (Argueso et al. 2010). Cytokinins act as negative regulators of lateral root formation via interplay with auxins (Laplaze et al. 2007). Srivastava et al. (2009) found that in the presence of As stress, *B. juncea* shows downregulation of cytokinin response 1 (CRE1) gene, which is a cytokinin receptor. The negative effect on cytokinin reception led to an increase in the expression of sulfate transporters. Mohan et al. (2016) developed transgenic *Arabidopsis thaliana* lines having a constitutive expression of cytokinin oxidase/dehydrogenase 1 (CKX1) gene to achieve cytokinin depletion. It was found that cytokinin-depleted lines became As(V) tolerant through efficient suppression of As(V) transporter and PHT1;1 and also due to increase in the expression of As(V) reductase gene as well as due to increase in the level of thiol compounds (GSH and PCs). Gibberellins are a large family of plant growth hormones associated mainly with seed germination, leaf expansion, and floral development (Daviere and Achard 2013). The role of gibberellins in metal stresses like cadmium, nickel, and lead is revealed (Meng et al. 2009; Sharaf et al. 2009). However, the role of gibberellins in As stress responses of plants is suggested only due to observed changes in the expression of gibberellin synthesis and response genes (Chakrabarty et al. 2009). The above discussion implicates that coordinated action of several phytohormones operates under As stress to fine-tune plants' responses. However, more experiments are needed in the future to delineate the in-depth mechanisms.

## 4 Reactive Oxygen and Nitrogen Species (ROS and RNS)

The oxygen-dependent life on Earth also entails the continuous production and dismutation of reactive oxygen species (ROS) due to the transfer of electrons or excess energy to oxygen. The process normally occurs at an optimal rate, and the role of ROS as an essential component of growth and development is known (Mittler 2002).

The ROS include singlet oxygen ( $^1\text{O}_2$ ), hydrogen peroxide ( $\text{H}_2\text{O}_2$ ), superoxide radical ( $\text{O}_2\cdot^-$ ), and hydroxyl radical ( $\cdot\text{OH}$ ) (Foyer and Noctor 2000). However, in the presence of metals including As, the rate of ROS production may surpass that of ROS dismutation leading to an excess of oxygen molecules wandering to react with biomolecules. The excessive ROS production under As stress causes oxidative stress and damages membranes, proteins, and DNA (Srivastava et al. 2011). However, ROS stimulation under As stress can also act as a signaling component. In fact, an increase in the activity of prooxidant enzymes like ascorbate oxidase and NADPH oxidase, involved in ROS generation, has been observed in response to As stress (Srivastava et al. 2011). Research on NADPH oxidase mutant lines of *A. thaliana* demonstrated the role of another prooxidant enzyme, glycolate oxidase, in As-induced stress responses (Gupta et al. 2013). Further, ROS are known to interact with other signaling components like NO and phytohormones (Shukla et al. 2017; Singh et al. 2017).

Reactive nitrogen species constitute NO and compounds derived from NO reaction with biomolecules like S-nitrosothiols (Shukla et al. 2017). NO plays a critical part in abiotic and biotic stress responses of plants due to its ability to interact with several biomolecules, proteins, ROS, and phytohormones (Mengel et al. 2013; Grun et al. 2016). NO interacts with biomolecules in three types of mechanisms: S-nitrosylation, metal nitrosylation, and tyrosine nitration (Lamotte et al. 2014). S-nitrosylation is the reaction of NO with thiol-containing molecules and proteins. Metal nitrosylation is the binding of NO to transition metals to form metalloproteins. In tyrosine nitration, a nitro group is added to tyrosine residues. Nitric oxide supplementation has been found to play a vital role in the reduction of As accumulation in rice (Singh et al. 2015). Involvement of NO and SA interaction in As stress responses of rice was also demonstrated (Singh et al. 2017). As induced, nitro-oxidative stress occurs due to the effect of As on the activity of glutathione reductase and S-nitrosoglutathione reductase. This, in turn, decreases GSH and GSNO content (Letierrier et al. 2012). NO-mediated protection against As toxicity has also been noticed in *Luffa acutangula* (Singh et al. 2013), *Hordeum vulgare* (Shukla et al. 2015), and *Pistia stratiotes* (Farnese et al. 2017). NO supplementation improved plant physiology and maintained the organellar structure. In rice plants, NO supplementation has been found to reduce As-induced oxidative stress and improve thiol metabolism and expression of genes (Praveen and Gupta 2018). In *B. juncea*, exogenous supply of sodium nitroprusside (NO donor) was found to reduce As accumulation and improve growth and mineral nutrient status of plants. The supply of NO was also found to affect nitrogen metabolism and the expression of auxin transporter genes (Praveen et al. 2019).

## 5 MicroRNAs (miRNAs)

Posttranscriptional regulation of mRNAs by other small RNAs is an important component of gene expression regulation (Axtell 2013; Bej and Basak 2014). MicroRNAs (miRNAs) are highly conserved small RNAs of 20–24 nucleotides that regulate the expression of genes by targeting specific mRNAs. The miRNAs either cleave the target mRNA or decrease translation of mRNA into protein (Xie et al. 2015; Stepien et al. 2017; Srivastava and Pathare 2017). These miRNAs regulate several processes of growth and development of plants, metabolic pathways, and enzymatic reactions. In the case of abiotic and biotic stresses, including metals, the role of miRNAs has been revealed and has emerged as a crucial component (Srivastava and Pathare 2017). A few As-responsive miRNAs like miR168, miR169, miR319, miR416, miR444, miR820, miR1430, miR1437, etc. were computationally identified by Tuli et al. (2010). In another study comparing high and low As-accumulating varieties of rice, miRNA profiling identified a number of As(III)- and As(V)-responsive miRNAs. These miRNAs either demonstrated a common response to both As species and/or in both varieties or showed variety and As(III)/As(V)-specific response (Sharma et al. 2015). The miR164, miR171, miR395, miR529, miR820, and miR1432 showed downregulation in both As(III) and As(V) stress, whereas miR408, miR1861, miR2102, and miR2907 showed upregulation. miR396 and miR528 showed a variable response in As(III) and As(V) stress, while miR399 and miR1846 demonstrated rice variety-specific response (Sharma et al. 2015). In *B. juncea*, As(V) stress-induced changes in the miRNA profile were evaluated for variable time points of 1 h and 4 h. The study identified a total of 69 miRNAs of 18 miRNA families that showed changes in expression pattern in time- and organ-dependent manner (Srivastava et al. 2013b). The upregulated miRNAs, miR426, miR472, and miR390, at 1 h depicted downregulation at 4 h, while the reverse trend was true for miR395. The time-dependent (6 h, 24 h, 72 h) and organ-dependent (root, shoot) real-time RT PCR analysis of few miRNAs (miR156, miR159, miR162, miR167, miR838, and miR854) further confirmed that expression of miRNAs changes dynamically and differentially in various tissues in response to As(V) stress in *B. juncea* (Srivastava et al. 2013b). The response of miRNAs also varies from plant to plant as seen in *O. sativa* and *B. juncea* (Liu and Zhang 2012, Srivastava et al. 2013b) where, for example, miR164 and miR172 were upregulated in *B. juncea* but showed downregulation in *O. sativa*. Further, the varying concentration of As(III) from low to high also has an influence on the miRNA profile of rice plants (Yu et al. 2012). In elemental interactions of As and selenium (Se) also, the role of miRNAs has been demonstrated Pandey et al. (2015). It is evident that miRNAs constitute a dynamic component of regulatory processes involved in As stress responses of plants, and the profile of miRNAs is an As concentration, As species, plant species, plant organ, and time-dependent process. Through dynamic changes, miRNAs affect crucial processes of metal detoxification (sulfur metabolism), metal uptake and distribution (transporters), metal stress (anti-oxidant mechanisms), and metal stress response (transcription factors, hormones)



(Curaba et al. 2014; Srivastava and Pathare 2017). In sulfur metabolism, miR395 regulates sulfur transporter (SULTR2;1) and ATP sulfurylase (APS), while miR838 and miR854 affect SULTR2;1 and SULTR2;2 and serine acetyl transferase (SAT) (Liang et al. 2010, Srivastava et al. 2013b). The regulation of Cu/Zn superoxide dismutase, the important enzyme of antioxidant defense dismutating superoxide ion to hydrogen peroxide, is achieved via miR398 (Bouche 2010). The level and signaling of phytohormones are also regulated by miRNAs, for example, miR160 and miR167 for auxin and miR319, miR168, and miR169 for jasmonates (Schommer et al. 2008).

## 6 Transcription Factors (TFs) and Kinases

The transcription process of mRNA synthesis and hence the gene expression are regulated by a number of transcription factors (TFs) (Anumalla et al. 2016). The role of several TFs is tuned in response to stress so as to achieve desirable expression of the required set of genes. A number of transcriptome studies have revealed the involvement of several families of TFs in As stress responses in plants like rice and *B. juncea*. The important TFs include WRKY, Myb, NAM, ATAF, NF-YA, AP2/EREBP, GATA, heat shock TFs, basic helix–loop–helix, homeobox, C2H2 zinc fingers, DOF zinc finger, etc. (Chakrabarty et al. 2009, Yu et al. 2012, Srivastava et al. 2015, Rai et al. 2015). The role of WRKY TF, WRKY6, was experimentally demonstrated by Castrillo et al. (2013) who found that As(V) stress-induced suppression of As(V)/phosphate transporter, PHT1;1, was regulated by WRKY6 in *A. thaliana*. Recently, the role of another WRKY TF, WRKY28, was studied in rice. WRKY28 was found to be an As(V)-inducible TF, and it regulated As accumulation in rice seedlings through effects on jasmonates (Wang et al. 2018). Mitogen-activated protein kinases (MAPKs) are a group of proteins, which are evolutionarily conserved and play important roles in signal transduction. MAPKs function in a cascade. Generally, the signals are relayed through MAPK kinase kinases (MAPKKKs), MAPK kinases (MAPKKs), and MAPK. In most cases, a single MAPK module transmits more than one signal in plants (Rodriguez et al. 2010). In the case of As, the role of MAPK3, MAPK4, and MKK4 is demonstrated in rice (Rao et al. 2011).

## 7 Conclusion and Future Perspective

The research on arsenic has mostly focused on arsenic chemistry in field and management practices to regulate arsenic levels in rice plant. The research on arsenic–plant interactions demonstrates involvement of various hormones, microRNAs, and kinases in the process of arsenic stress perception, signaling, and tolerance. However, the present picture mostly shows isolated changes in various signaling processes. The future research needs to bring about exact mechanisms of integration



of various signaling molecules, hormones, and proteins so as to construct a holistic picture. There is a need to reveal how arsenic infiltration is perceived by the plants. Hypothetically, arsenic entry might be perceived through interaction with a sensor protein, and this needs to be elucidated in coming years. The regulatory mechanisms involved in transporters' expression in roots, shoot, flag leaves, and seeds need to be understood so as to enable development of low-grain arsenic-accumulating rice varieties. The interconversion of arsenic species from one form to another constitutes an important mechanism of regulation of arsenic stress, its concentration in tissues, and its transport within plant. The process itself needs to be delineated in more detail. In addition, the aim should be to elucidate regulatory processes involved in arsenic metabolism. In conclusion, the research needs to focus on enhancing our knowledge about mechanistic details of arsenic–plant interactions.

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