

The Versatile Role of Plant Aquaglyceroporins in Metalloid Transport 7

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Abstract

Metalloids are elements with intermediate chemical properties between metals and nonmetals. The metalloids are biologically important elements, ranging from essential to extremely toxic elements with contrasting effects on organisms. Plants deal with a considerable imbalance of metalloids in the environment. Plants must acquire adequate amounts of essential metalloids for metabolism or contrarily exclude toxic metalloids to avoid cellular toxicity. The process of uptake and exclusion is guided by channel proteins, which transport metalloids across cellular membranes. Major intrinsic proteins (MIPs) are a family of selective channels that includes aquaporins (water channels) and aquaglyceroporins (glycerol and other solute channels). Aquaglyceroporin facilitates the transport of small solutes, including glycerol, small uncharged solutes, and gasses across biological membranes. Plant MIPs are grouped into five subfamilies based on sequence similarity and subcellular localization. Plant MIPs are mainly categorized into five subfamilies – plasma membrane intrinsic proteins (PIPs), nodulin-26-like intrinsic proteins (NIPs), tonoplast intrinsic proteins (TIPs), small basic intrinsic proteins (SIPs), and uncharacterized intrinsic proteins (XIPs). The uptake of environmental metalloids by aquaglyceroporins explains how beneficial elements such as silicon are taken up in plants. Conversely, toxic elements such as arsenic and antimony also enter the food chain via these channel proteins. The present

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review summarizes the role of various MIP homologs for transporting metalloids into and out of plant cells. This review discusses the detailed mechanism of MIPs for acquiring essential metalloids and their role in the influx and efflux in plant cells.

Keywords

Metalloids · Major intrinsic proteins · Aquaglyceroporins · Homeostasis · Toxicity

7.1 Introduction

Abiotic stress conditions such as salinity, drought, temperature extremes, nutrient deficiency, metalloid toxicity, flooding, etc. cause serious damage to plants in terms of growth, development, and productivity (Singh et al. [2020](#page-16-0); Zulfiqar et al. [2020\)](#page-17-0). For instance, tainting the soil and water bodies with metals, their unfavorable effects on plants, and retransmission to the consuming populations creates significant worries worldwide. Heavy metals and metalloid stress contribute to adverse effects on the health of plants and consumers. Metalloids are semimetals that share some common properties of metals and nonmetals. Metalloid boron (B) acts as a micronutrient. At the same time, silicon (Si) is viewed as a useful component for providing mechanical strength and protection from abiotic and biotic stresses to certain crop plants.

On the other hand, arsenic (As) is an extreme ecological danger to most living forms, including plants, while the less plentiful metalloids germanium (Ge), antimony (Sb), and tellurium (Te) show variable levels of harm (Angulo-Bejarano et al. [2021;](#page-12-0) Sharma et al. [2021](#page-16-1)). Plants in small amounts require the metalloids B, Si, and Se, while some are toxic and nonessential, namely As, Ge, Sb, and Te. Cereals like wheat, rice, maize, and barley are major sources of biomagnification of metalloid (s) in consumers (Deng et al. [2019\)](#page-13-0). B is conjectured to exist as an all-important micronutrient in soil; even so, its role as an essential trace element is being questioned (Pereira et al. [2021\)](#page-15-0). The boric acid (BA) form of B, which possesses no charge at acidic or neutral pH, gets transported in cells by passive transport (Hrmova et al. [2020](#page-14-0)); however, that is a half story, and there exist regulated transport mechanisms that help retain B equilibrium in plants (Miwa and Fujiwara [2010;](#page-15-1) Pereira et al. [2021](#page-15-0)). The requirement of B varies among the plant species. Some plant species like cotton, beet, and *Brassica* require B during the entire plant development cycle. On the other hand, soybean, pea, wheat, and barley need relatively low B levels and that too during the development of seeds and initiation of flowering (Pommerrenig et al. [2015\)](#page-15-2).

Arsenic is considered a potent group I carcinogen and the leading cause of health issues related to cardiovascular, neurological, hematological, renal, and respiratory systems. Various natural and anthropogenic activities release As into the

environment as a potentially toxic, ubiquitous entity in soil and water bodies (Deng et al. [2019\)](#page-13-0). The inorganic form of As in the form of arsenite As(III) and arsenate As (V) predominantly exists in soil and is taken up by the plants (Panda et al. [2010\)](#page-15-3). Roots usually take up the excess concentrations of metalloids by various transporters, including phosphate transporters, sulfate transporters, aquaglyceroporins, nodulin-26-like proteins, Si influx transporter, hexose transporter, etc. (Deng et al. [2019](#page-13-0)). The detoxification of such metalloids via conjugation with glutathione (GSH) and phytochelatins (PCs) and vacuolar sequestration in roots could be a primary strategy for reducing the metalloid contents in cereal grains (Deng et al. [2019](#page-13-0)). Si in the form of silicates is the second most plentiful component after oxygen in the environment. The expanding proofs have shown that this metalloid is advantageous to plants, particularly under stress conditions such as salinity, drought, and biotic stresses (Yan et al. [2018](#page-16-2)). The plant accessibility of Si in soil (as monosilicic acid, H_4SiO_4) differs between 0.1 and 0.6 mM (Yan et al. [2018\)](#page-16-2). Si is taken up and moved through the plant to be saved as $SiO₂$ phytoliths (Epstein [2001;](#page-13-1) Ma and Yamaji [2008;](#page-15-4) Deshmukh et al. [2017a;](#page-13-2) Luyckx et al. [2017](#page-14-1); Pavlovic et al. [2021\)](#page-15-5). The main Si species accessible to living beings is uncharged orthosilicic acid. Like Si, the most bio-accessible Ge type is the uncharged germanic acid (Pommerrenig et al. [2015\)](#page-15-2).

Plants have transporters that keep the required degree of metal and metalloid ion homeostasis inside the cells to perform distinctive functions. These transporters facilitate the entry, multi-organ, and subcellular distribution and exit of various metal(loids) ions. These transporters involve aquaporins, phosphate and sulfate transporters, hexose transporters, etc. (Pandey et al. [2019\)](#page-15-6). Major intrinsic proteins (MIPs) are the membrane proteins that facilitate the transport of small polar molecules across membranes (Johanson et al. [2001\)](#page-14-2). The plant MIP superfamily is highly conserved, with members ranging in size from 23 to 31 kDa (Gomes et al. [2009;](#page-13-3) Venkatesh et al. [2013;](#page-16-3) Maurel et al. [2015](#page-15-7)). The MIPs are divided into five main aquaporin subfamilies based on their sequence similarities and localization: plasma membrane intrinsic protein (PIPs), tonoplast membrane intrinsic proteins (TIPs), nodulin-26-like intrinsic membrane proteins (NIPs), uncharacterized intrinsic proteins (XIPs), and the small basic intrinsic proteins (SIPs) (Maurel et al. [2008;](#page-15-8) Sakurai et al. [2005;](#page-16-4) Kumar et al. [2018](#page-14-3)). Structurally, MIP tetramer is functional, and each monomer comprises six transmembrane alpha-helices (H1–H6) and five loops (LA–LE), of which loops B and E are hydrophobic. In contrast, loops A, C, and D are hydrophilic. The conserved motifs among all MIPs include two highly conserved NPA (asparagine–proline–alanine) motifs in loops B and E. The NPA motifs are known to regulate the substrate selectivity of the AQPs (Deshmukh et al. [2015\)](#page-13-4). Moreover, the aromatic/arginine (ar/R) selectivity filter of MIPs is a tetrad in which each residue is located in H2 and H5 helices and loops LE1 and LE2. The ar/R filter forms a central pore and contributes to substrate selectivity (Afzal et al. [2016;](#page-12-1) Deshmukh et al. [2016,](#page-13-5) [2017b](#page-13-6); Shivaraj et al. [2017](#page-16-5)).

The members of the TIP subfamily are mainly localized to the vacuole and facilitate the transport of water, glycerol, hydrogen peroxide, urea, and ammonia by different ar/R selectivity filters (Deshmukh et al. [2015](#page-13-4)). According to the current

Fig. 7.1 Diagrammatic representation of different MIP localizations in plant cells and their role as various metalloid transporters

consensus, aquaporins have been major contributing entities in plant metalloid stress response and adaptations. The localization of MIPs and their role as potential metalloids (As, B, Si, Se, and Sb) are represented in Fig. [7.1](#page-3-0). The possible mechanisms reported so far include changes in the activities of ROS-scavenging enzymes, the altered expression level of certain stress marker genes through the cross talk, hormone-mediated response, and so on (Sun et al. [2017\)](#page-16-6). This chapter will discuss the role of different classes of MIPs in metalloid transport and stress responses.

7.2 PIP Members as Metalloid Transporters

PIP members are the largest subfamilies of plant MIPs and are localized to the plasma membrane. PIPs mainly regulate water homeostasis, and they are also known to be the transporters of urea, H_2O_2 , CO_2 , and metalloids such as, B, Sb, and Si (Kumar et al. [2018\)](#page-14-3). PIPs are further grouped in two subgroups, namely PIP1 and PIP2 (Chaumont et al. [2001\)](#page-13-7). Plant roots absorb essential mineral nutrients such as B and Si from the soil and transport them to other parts of the plants via various transporters, including PIPs. PIPs also provide sensitivity/tolerance to metalloids, particularly As, via uptake/influx/efflux and compartmentalization of toxic metalloids in different plant tissues. PIPs form channel-like structures that act differently in plants under various environmental conditions during metalloid transport. PIPs are involved in B uptake and support the plants to survive under B limitations. In barley (Hordeum vulgare), PIP members such as HvPIP1;3 and $HvPIP1;4$ act as B transporters, confirmed in the heterologous system by complementation studies (Fitzpatrick and Reid [2009](#page-13-8)). The overexpression of ZmPIPs, HvPIP1;3 and HvPIP1;4, in yeast showed B influx and channel activities (Zangi and Filella [2012](#page-16-7)). Several studies in rice demonstrated that OsPIP1;3, OsPIP2;4, OsPIP2;6, and OPIP2;7 are involved in B transport and lead to influx and efflux activities in rice (Kumar et al. [2014;](#page-14-4) Mosa et al. [2016](#page-15-9)). The heterologous expression of OsPIPs genes, namely, OsPIP1;2, OsPIP1;3, OsPIP2;4, OsPIP2;7, and OsPIP2;8, in deficient strain $(\Delta f \rho s I \Delta acr 3 \Delta y c f I)$ of yeast resulted in enhanced B transport and sensitivity (Mosa et al. [2016\)](#page-15-9). Heterologous overexpression of OsPIP1;3 and OsPIP2;6 in Arabidopsis exhibited enhanced tolerance under higher B concentration (Mosa et al. [2016](#page-15-9)). Transcript accumulation of several PIP members in Arabidopsis roots was decreased under higher B concentrations (Aquea et al. [2012\)](#page-12-2). The expression of $PIP1;2$, $PIP2;1$, and $PIP2;2$ was higher in shoots compared to roots of Arabidopsis at increased B concentration (Macho-Rivero et al. [2018\)](#page-15-10). In non-AM (arbuscular mycorrhizal) plants like maize, the transcript of ZmPIP2;2 was upregulated at a higher concentration of B under drought stress, showing its role in enhancing water flow in plant roots and decreasing excessive B levels (Quiroga et al. [2020\)](#page-15-11). In contrast, the AM plants under excessive B levels showed reduced ZmPIP2;2 expressions. The authors hypothesized that AM plants might have a different process to regulate excess B. Higher phosphorous (P) concentration in tissues and interplay of boron and phosphorous reduces B toxicity (Quiroga et al. [2020\)](#page-15-11). These studies concluded strongly that B toxicity caused water flux reduction to the shoot and caused reduced hydraulic conductance of shoot tissue, resulting in downregulation of aquaporin genes in roots and shoots. However, further studies suggested that repression of these PIP genes in the shoot is due to the excessive B accumulation, or excess B leads to activation of signaling cascades (Macho-Rivero et al. [2018](#page-15-10)). Studies involving RNA sequencing transcriptional profiling of the Brassica napus BnaAQPs in contrasting B-resistant genotype (Qingyou10) and B-sensitive genotype (Westar10) under sufficient and deficient B conditions suggested that BnaPIPs are highly expressed in roots, old leaves, and juvenile leaves (Yuan et al. [2017](#page-16-8)). In both the cultivars, BnaPIP1;1s, BnaPIP1;2s, and BnaPIP2;2/2;3s showed elevated transcript abundance in roots under the B-sufficient condition, whereas the same PIPs transcripts were downregulated in minimal B stress (Yuan et al. [2017](#page-16-8)).

To subside the metalloid toxicity, the various plants have developed potential strategies, including downregulation of the specialized transporters, metalloid exclusion through efflux channel proteins, and metalloid complexation with thiols such as GSH and PCs, followed by vacuolar sequestration. Most of the NIP subfamilies of aquaporins are identified as As(III) transporters; however, fewer studies also revealed the role of the PIP subfamily in providing metalloids such as B tolerance in plants. To reduce the metalloid accumulation in plant cells and cope with the metalloid stress in rice, PIPs act as a bidirectional pump (Kumar et al. [2014;](#page-14-4) Mosa et al. [2016\)](#page-15-9). Members of rice PIPs play a potential role in As(III) and B transport pathways (Mosa et al. [2012,](#page-15-12) [2016;](#page-15-9) Kumar et al. [2014\)](#page-14-4). Several studies also demonstrated downregulation of transcripts of five rice PIPs (OsPIP1;2, OsPIP1;3, OsPIP2;4, OsPIP2;6, and OsPIP2;7) and 13 PIPs of Brassica juncea under arsenite

stress (Mosa et al. [2012](#page-15-12); Srivastava et al. [2013\)](#page-16-9). In heterologously expressed rice, PIPs (OsPIP2;4, OsPIP2;6, and OsPIP2;7) in Xenopus oocytes showed enhanced As (III) transport. Studies of transgenic Arabidopsis with constitutive expression of $OSPIP2;4,OSPIP2;6,$ and $OSPIP2;7$ exhibit enhanced tolerance under As(III) stress without affecting the levels of As in root and shoot tissues. To underpin the role of PIPs as bidirectional As(III) transporters, heterologous overexpression of OsPIPs in Arabidopsis roots displayed both arsenite influx and efflux processes (Mosa et al. [2012\)](#page-15-12). The other members of rice PIPs need to be characterized at the plant level, and their prominent role needs to be identified. AtPIP2;2 is largely expressed with cell division-related protein (NtCyc07) and demonstrated to provide higher tolerance toward As(III) in Arabidopsis (Lee and Hwang [2012](#page-14-5)). Arabidopsis atpip2;2 exhibited decreased As(III) tolerance without difference in As(III) concentration, whereas the overexpressed AtPIP2;2 exhibited increased As(III) tolerance and decreased As(III) levels in yeast and *Arabidopsis* (Modareszadeh et al. [2021](#page-15-13)). The studies potentiate the role of AtPIP2;2 in bidirectional transporter of As(III). The enhanced As(III) efflux in *Arabidopsis* is due to the higher As(III) exporter activity compared to the importer activity indicating that AtPIP2;2 provides As(III) tolerance by reducing As(III) accumulation (Modareszadeh et al. [2021\)](#page-15-13).

The various transporters present in the roots help regulate Si uptake and, therefore, act as a major element to cope with biotic and abiotic stresses in plants (Rios et al. [2017\)](#page-16-10). The Si-treated roots exhibited enhanced expression of PIP genes. In saltstressed cucumber (Cucumis sativus), Si enhances root water uptake via upregulation of aquaporin gene expression. The expression of PIPs (PIP1;2, PIP2;1, PIP2;4, PIP2;5) was upregulated on treatment with Si in cucumber (Zhu et al. [2015\)](#page-17-1). Similarly, Si supplementation in leaves of bottle gourd (Lagenaria siceraria) decreased transcript accumulation of LsiPIP1-5 at 24 h, while at 72 h, LsiPIP1-5 expression was enhanced (Kumawat et al. [2021\)](#page-14-6). In stem, Si treatment enhanced transcript accumulation of $LsiPIP1-5$, $LsiPIP2-4$, and $LsiPIP4-1$ at 24 h with a decrease at 72 h. The root Si application exhibits enhanced transcript accumulation of LsiPIP1-5 and LsiPIP2-4 (Kumawat et al. [2021\)](#page-14-6). The transcript levels of Sorghum bicolor PIPs (SbPIP1;6, SbPIP2;2, and SbPIP2;6) show upregulation upon Si treatment in limited time salt stress (Liu et al. [2014](#page-14-7)). The improvement in root water uptake under dehydration stress may be due to the upregulation of PIP genes (Liu et al. [2014](#page-14-7)). These reports highlight that the manipulation of PIPs in many plant species exhibits an enhanced level of B and Si and controls and limits the toxic As concentration. However, further studies are needed to demonstrate the role of PIPs in metalloid transport and tolerance at the field level under natural environmental and soil conditions.

7.3 NIP Members as Metalloid Transporters

NIPs allow the diffusion of metalloids through membranes and facilitate their cellular transport in different parts of the plants (Wallace et al. [2006](#page-16-11); Pommerrenig et al. [2015\)](#page-15-2). Different forms of metalloids transported by NIPs include B, Si, As, Ge,

selenium (Se), and Sb (Pommerrenig et al. [2015\)](#page-15-2). For instance, Ma and Yamaji (2006) (2006) showed that Si transporter Lsi1 $(OSNIP2;1)$ also transported As(III) and facilitated the entry of As(III) into rice roots. In addition to Lsi1, three other rice NIPs (OsNIP1;1, OsNIP2;2, and OsNIP3;1) were also able to mediate As(III) influx when expressed in *Xenopus laevis* oocytes; however, these genes were expressed at significantly low levels in rice roots (Li et al. [2009](#page-14-9)). The expression of Lsi1 in X. laevis oocytes also significantly increased the uptake of the methylated As species MMAV (monomethylarsonic acid) but not DMAV (dimethylarsonic acid) (Li et al. [2009\)](#page-14-9). Lsi1 helped increase As(III) efflux in rice roots exposed to AsV (Zhao et al. [2010\)](#page-17-2). Additionally, the heterologous expression of OsNIP2;1 and OsNIP3;2 in yeast increased sensitivity to As(III) and As accumulation (Bienert et al. [2008\)](#page-13-9). Arabidopsis thaliana NIP1;1, NIP2;1, NIP3;1, NIP5;1, NIP6;1, and NIP7;1 were permeable to As(III) in the yeast expression system (Isayenkov and Maathuis [2008;](#page-14-10) Bienert et al. [2008](#page-13-9)), and AtNIP1;1 was capable of transporting As(III) when expressed in X. laevis oocytes (Kamiya and Fujiwara [2009](#page-14-11)). Other NIPs such as LjNIP5;1 and LjNIP6;1 from Lotus japonicas are also permeable to As(III) (Bienert et al. [2008](#page-13-9)). It is clear that members of NIP aquaporins are metalloid channels that transport Si, As, and Sb.

Although the genetic regulation of the B accumulation is less known, a recent study demonstrated that HvNIP2;2/HvLsi6 appear within quantitative trait loci (QTL) largely responsible for B-level dynamics in barley. Further, complementation studies in yeast Δ *atrl* mutant (B efflux transporter deficient) showed that the expression of HvNIP2;2/HvLsi6 induces growth suppression in Δ atr1 yeast cells, indicating that these NIPs function as B transporters. Also, its heterologous expression in X. laevis oocytes showed a high rate of B uptake (Jia et al. 2021). As HvNIP2;2/HvLsi6 is previously reported to function as Si transporter, studies with B transport system show the versatile role of NIP aquaporins in the metalloid transport. The rapeseed's QTL mapping and differential gene expression (DGE) analysis has identified putative NIP transporters that may transport B (Hua et al. [2016\)](#page-14-13). The QTL mapping approach encouraged the identification of the B-efficient gene BnaA3.NIP5;1 which induces the root tip growth under B deficiency in *Brassica napus.* Additionally, the 5'-untranslated region (UTR) of $BnaA3.NIP5;1$ contains "CTTTC" repeats which contribute to the differential expression of the genes involved in plant growth and seed setting (He et al. [2021\)](#page-14-14). Hence, not only the key functional residues but the untranslated regions of the NIPs may also function in the regulatory mechanisms involved in metalloid transport-associated mechanisms in plants. The increased expression of CiNIP5 under B-deficient conditions has been reported in trifoliate orange and Carrizo citrange; in this case, the gene's predominant expression was found in root tissues. The function of CiNIP5 has similarities with AtNIP5;1 gene from the *Arabidopsis* (An et al. [2012](#page-12-3)). Thus, the tissue-specific NIP expression reflects their particular roles in plants.

Moreover, certain functions can be seen conserved among different plant species. The site-directed mutagenesis in the H2 and H5 regions of AtNIP5;1 and OsLsi1 (OsNIP2;1) shows that the amino acid residues in the H5 region of the ar/R filter are critical for the transport of B and Si (Mitani-Ueno et al. 2011). The QTL analysis revealed HvNIP2;1 marker gene associated with B and Ge toxicity in barley. Further site-directed mutagenesis in the amino acid residues of H2 and H5 regions and yeast complementation assay showed that the mutant's B, Ge, and As transport activity was altered (Hayes et al. [2013](#page-14-15)). Thus, the conserved structural features are important in deciding the transport substrates for NIP aquaporins.

The transcriptome analysis has shown that *Arabidopsis NIP5*; *1* gene expression increases under B-deficient conditions. Studies with the promoter-GUS fusion showed that NIP5;1 expression is upregulated in the root extension and the root hair zone under B-deficient conditions. Heterologous expression in X. laevis oocytes showed that NIP5;1 transported boric acid. Further, T-DNA mutants of NIP5;1 exhibited impaired boric acid uptake by roots, less growth of plants, and overall increased sensitivity to B inadequacy in both roots and shoots. Thus, it may be stated that under B-deficient stress conditions, NIPs could notably influence plant growth and also influence the transport processes in plants (Takano et al. [2006\)](#page-16-12). Similarly, Gómez-Soto et al. [\(2019](#page-13-10)) proposed that the AtNIP5;1 promoter is largely regulated by phytohormones, including abscisic acid (ABA) and ethylene. When applied exogenously, the influence of ABA and ethylene results in the induced expression of the $AtNIP5$; 1 gene. Further, the $AtNIP5$; 1 exhibits ABA-induced B uptake and induces root growth.

Sb is toxic to all living beings, including plants, if taken up by plants in the rhizosphere system (Bienert et al. [2008;](#page-13-9) Kamiya and Fujiwara [2009\)](#page-14-11). The toxicity and tolerance studies in yeast showed that the $AtNIP1;1$ transport antimonite (SbIII) and determine consequent sensitivity. Although selenium (Se) is not essential for plants, selenocysteine in plants is involved in the defense against oxidative stress. Vegetables and fruits are the rich sources of Se (Arnér [2010\)](#page-12-4). Examples of the Se transporters in plants include sulfate transporters and OsNIP2;1 (Sors et al. [2005;](#page-16-13) Zhang et al. [2010](#page-17-3), [2012](#page-17-4); Zhao et al. [2010](#page-17-2)). Geranium and silica share similarities in their chemical properties. Ge has been proposed as a biomarker and has been useful for identifying OsNIP2;1 responsible for the silica accumulation (Ma and Yamaji [2006\)](#page-14-8). Also, the radiolabeled Ge has been shown to trace silica accumulation in heterologous expression systems. A similar biomarker principle has been applied to assess B uptake in barley mediated by NIP aquaporins (Takahashi et al. [1976;](#page-16-14) Mitani-Ueno et al. [2011;](#page-15-14) Bárzana et al. [2014\)](#page-13-11).

7.4 XIP Members as Metalloid Transporters

In the genome of different plant species, including Physcomitrella patens, Nicotiana benthamiana, grape, cotton, tomato, and poplar, various XIP subfamilies were identified (Shelden et al. [2009](#page-16-15); Park et al. [2010](#page-15-15); Lopez et al. [2012;](#page-14-16) Ampah-Korsah et al. [2016](#page-12-5)). The XIPs are absent in monocots and found only in diversified dicot species, except Brassicaceae (Danielson and Johanson [2008\)](#page-13-12). The NPARC motif, the signature sequence for XIPs, showed cysteine residue, followed after the second NPA motif (Danielson and Johanson [2008;](#page-13-12) Gupta and Sankararamakrishnan [2009\)](#page-13-13). XIPs exhibit discrepancies in amino acids of the first NPA motif and ar/R filter. XIPs

are subdivided into four subclasses based on demarcating ar/R filters. In some plants, NIPs showed similarity with the two subclasses having an ar/R signature; instead, the other two subclasses had hydrophobic signature amino acids (Noronha et al. [2016\)](#page-15-16). The XIP cDNA was cloned from morning glory, potato, tobacco, and tomato and showed to be localized in the plasma membrane (Bienert et al. [2011\)](#page-13-14).

Bienert et al. ([2011\)](#page-13-14) showed that in a yeast mutant (δfps1), XIPs belonging to Solanales species transport boric acid. In the Solanales' XIPs mutants, the expression of the various splice variants showed impaired and no growth at 10 mM and 20 mM boric acid, respectively. The role of XIPs to facilitate B transport was proved by increased sensitivity to boric acid (Bienert et al. [2011\)](#page-13-14). Overexpression of NtXIP1;1 in Nicotiana tabacum with Nicotiana plumbaginifolia PMA4 promoter fused with 35S enhancer (En2pPMA4) resulted in severe B deficiency symptoms. Overexpression of NtXIP1;1 in Arabidopsis, which does not contain any XIP gene, by CaMV 35S promoter, resulted in severe B deficiency symptoms. The expression of the two splice variants $NtXIP1; \alpha$ and $NtXIP1; \beta$ in *Xenopus* oocytes showed increased boric acid uptake (Bienert et al. [2019](#page-13-15)). However, heterologous expression of NtXIP1;1 with Arabidopsis AtNIP5;1 promoter rescued the B deficiency symptoms of $Atnip5;1$ mutant, indicating that NtXIP1;1 is a functional boric acid channel in N. tabacum and provides B homeostasis and its distribution in tobacco through the tissue-specific expression (Bienert et al. [2019\)](#page-13-15). Some studies on the heterologous expression of grapevine *Vitis vinifera* VvXIP1 in yeast showed their inclusion in metalloids (B and As) and heavy metals (copper and nickel) transport and reduced yeast cell growth in the presence of 40 mM B, 0.5 mM nickel, and 5 mM copper, whereas the growth of the transformed yeast was improved in the presence of 0.45 mM As (Noronha et al. [2016\)](#page-15-16). The knowledge of XIPs and their role in metals and metalloid transport in plants is very limited. Further studies are needed to decipher the exact role of the XIP subfamily in plants.

7.5 Role of TIPs in Metalloid Transport and Tolerance

TIPs are a subfamily of MIPs and are detected to be predominantly located at the tonoplast membrane (Jauh et al. [1998](#page-14-17), [1999](#page-14-18); Srivastava et al. [2013\)](#page-16-9). However, some TIPs such as AtTIP2;1 and AtTIP1;2 are also localized in endosomal membrane compartments and plasma membrane (Liu et al. [2003](#page-14-19)). GFP fusion experiments confirmed that AtTIP5;1 is localized to mitochondria (Soto et al. [2010\)](#page-16-16). PvTIP4;1 from Pteris vittata, an arsenite hyperaccumulator, has been shown to mediate As(III) transport by yeast functional complementation assay and heterologous expression in Arabidopsis (He et al. [2016\)](#page-14-20). Srivastava et al. [\(2013\)](#page-16-9), through the transcriptomic studies in B. juncea under arsenate $As(V)$ stress, found that the TIP2 gene is responsive to different As(V) treatment periods in both root and shoot parts. The TIP function in the B transport has been investigated either in vivo by utilizing transgenic plants or in vitro by heterologous expression analysis (Bienert and Bienert [2017;](#page-13-16) Bienert et al. [2019](#page-13-15); Pang et al. [2010\)](#page-15-17). AtTIP5;1 overexpression builds the resilience to high B in the transgenic *Arabidopsis* plants, probably occurring through the vacuolar compartmentation (Pang et al. [2010\)](#page-15-17). Porcel et al. [\(2018](#page-15-18)) identified a novel gene, BvCOLD1, in Beta vulgaris whose sequence shares similarities with the TIP aquaporins. However, it was localized to the endoplasmic reticulum during the subcellular localization analysis with the GFP-fused construct. In yeast cells, BvCOLD1 showed B homeostasis. When overexpressed, it exhibited enhanced tolerance against the B deficiency in Arabidopsis. However, mere sequence similarity may not determine its aquaporin type and role, and further structural studies are imperative to determine the same. Pang et al. (2017) (2017) stated that AtTIP5;1 manages elongation of hypocotyl under high convergences of B in A. *thaliana* by unknown mechanisms. Studies with two mutants of AtTIP5;1 showed that the elongation of cells is hampered when given high B or gibberellin (GA3) compared to the wild-type plants. Further, paclobutrazol (GA synthesis inhibitor) hindered the upregulation of AtTIP5;1 expression influenced by high B. In the case of GA3 treatment, the expression of $ATIP5$; *I* was upregulated compared to wild-type plants. Further, treatment with high B stimulated the transcript level increase of the GA biosynthesis genes in WT seedlings. Also, double mutant studies with the DELLA genes showed no upregulation of the AtTIP5;1 gene under high B stress. Altogether, these outcomes recommend that $A tTIP5; l$ function downstream to GA signaling in high B stress (Pang et al. [2017](#page-15-19)). Hence, TIP aquaporins may cross talk with phytohormones and participate in various stress regulatory mechanisms under metalloid stress. Moreover, they may stimulate growth and development under these stress conditions.

Rivera-Serrano et al. ([2012\)](#page-16-17) proposed that the localization of the TIP aquaporins may occur by the vesicular trafficking that involves the Golgi-dependent and Golgiindependent transport through the endoplasmic reticulum. However, the underlying mechanisms are less known; besides, the role of vesicular trafficking under metalloid stress conditions has not been elucidated. Gattolin et al. [\(2011](#page-13-17)) reported the localization of *Arabidopsis* TIP3;1 and TIP3;2 to the tonoplast and the plasma membrane; however, their significance to the metalloid stress response is not known. Some reports suggest the differential localization of the TIPs to the subcellular organelles other than the vacuole (Sudhakaran et al. [2021](#page-16-18)). Further, the localization of the TIPs to other cellular organelles has also been reported; for instance, AtTIP2;1, AtTIP1;2, and AtTIP1;1 localized to the chloroplast membrane (Ferro et al. [2010\)](#page-13-18), GmTIP3;3 and AtTIP5;1 to the mitochondria, GmTIP1;1 to the endoplasmic reticulum, and GmTIP2;6, GmTIP2;7, GmTIP1;7, GmTIP2;3, and GmTIP2;1 to the plasma membrane (Deshmukh et al. [2013\)](#page-13-19). Also, the cytoplasmic localization of the TIPs has been reported in the case of the flax (Shivaraj et al. [2017](#page-16-5)), nonetheless, their importance in the transport of metalloids is yet to be characterized. The representative plant MIPs' role as metalloid transporters determined by functional studies and the studies conducted to determine functionality are listed in Table [7.1](#page-10-0).

	Plant	MIPS (gene/		
S. no.	species	protein)	Functional studies employed	References
	B oron			
$\mathbf{1}$	Hordeum vulgare	$HvPIPI;3$ and HvPIPI;4	Yeast complementation studies	Fitzpatrick and Reid (2009)
\mathfrak{D}	Oryza sativa	$OsPIP2;4$, OsPIP2;6 OSPIP2;7, and OsPIPI;3	Yeast complementation and overexpression studies in Arabidopsis thaliana	Kumar et al. (2014) and Mosa et al. (2016)
3	Nicotiana tabacum	NtXIP1;1	Xenopus oocyte assay, yeast complementation, and overexpression in Nicotiana and Arabidopsis	Bienert et al. (2011, 2019)
$\overline{4}$	Vitis vinifera	VvXIP1	Overexpression and transformation in yeast	Noronha et al. (2016)
5	Hordeum vulgare	HvNIP2;2	Yeast complementation studies Heterologous expression in X. laevis oocytes	Jia et al. (2021)
6	Arabidopsis thaliana	AtNIP5;1 and OsLsi1 (OsNIP2;1)	Site-directed mutagenesis	Mitani-Ueno et al. (2011)
7	Hordeum vulgare	HvNIP2;1	Site-directed mutagenesis and yeast complementation studies	Hayes et al. (2013)
8	Arabidopsis thaliana	NIP5;1	Heterologous expression in X. laevis oocytes T-DNA mutant analysis	Takano et al. (2006)
	Arsenic			
9	Oryza sativa	OsPIP2;4, $OsPIP2; 6$, and OSPIP2;7	Xenopus oocyte assay and overexpression studies in Arabidopsis thaliana	Mosa et al. (2012)
10	Arabidopsis thaliana	AtPIP2;2	Overexpression studies in yeast and Arabidopsis. Knockout studies in Arabidopsis	Modareszadeh et al. (2021)
11	Oryza sativa	OsNIP2;I OsNIP1;1, OsNIP2;2, and OsNIP3;1	Transport in Xenopus laevis oocytes	Li et al. (2009)
12	Arabidopsis thaliana	NIP1;1, NIP2;1, NIP5;1, $NIP6;1$, and NIP7;1	Transport studies in yeast cells	Isayenkov and Maathuis (2008)
13	Arabidopsis thaliana	AtNIP1:1	Transport in Xenopus laevis oocytes	Kamiya and Fujiwara (2009)
14	Lotus japonicas	$LjNIP5;1$ and LjNIP6;1	Transport studies in yeast cells	Bienert et al. (2008)

Table 7.1 The role of representative MIPs from different plant species acts as metalloid transporters as determined by functional studies

(continued)

Table 7.1 (continued)

7.6 Future Perspectives

Metalloid contamination, its stress to plants, and accumulation in the edible plant parts have emerged as serious food production and safety problems. Cereals like wheat, rice, maize, and barley are major sources of biomagnification of metalloid (s) in consumers. For instance, rice is one of the major sources of As exposure. Compared to other crop plants, the translocation factor (TF) for As is higher in rice (0.8), indicating its ten times higher concentration in rice than in other cereals. Being a staple food in most parts of the world, As accumulation in rice grains poses a great concern to consumers. Thus major efforts are needed to reduce the As content in rice grains up to at least maximum permissible limits (safe for consumption), 200 μg/kg for white rice and 300 μg/kg for brown rice as suggested by the World Health Organization (WHO [2014](#page-16-19)). Brown rice contains 80% more inorganic As than white rice because of the germ layer in brown rice, which retains a considerable amount of As. Hence, it is imperative to reduce the deposition of this metalloid into the edible plant parts. Although notable studies have helped to understand the role of different types of transporters, including MIPs in metalloid transport in plants, many research gaps need to be identified and addressed. As stated above, certain MIPs (e.g., TIPs) have been shown to cross talk with multiple plant hormones in metalloid stress conditions. This indicates that MIPs could directly or indirectly influence plant growth and development. However, the scarcity of knowledge about the underlying signaling mechanisms may limit to employ different MIPs for the crop improvement programs. The selective transport of specific metalloid types by the aquaporins denotes their functions. However, their versatility in transporting other metalloid types directly or indirectly needs to be assessed.

As of now, only PIPs, TIPs, NIPs, and XIPs are involved in metalloid stress tolerance/sensitivity in plants. The literature shows that most of the known metalloids that influence plant growth and productivity are transported by NIP and PIP aquaporins showing their versatile role in metalloid stress response. However, some reports studied their differential regulation at the gene expression level, and functional characterization of them either by homologous or heterologous systems will certainly help uncover many unknown aspects of the NIP- and PIP-mediated metalloid stress signaling in plants. Few reports have proved the metalloid transportability of the MIPs through the heterologous expression studies, which could further be scaled up in many other model systems. When it comes to the function, the sensitivity or tolerance to the metalloid stress responses can be seen as variable among each MIP type from species to species; this discrepancy and dynamic functionality of the MIPs should be addressed at the individual level. Also, distinct MIP signaling pathways regarding the corresponding morphological and physiological modifications in plants are yet to be studied. The inconsistencies among the current data may result from the sort of plant species, the stress treatment systems, etc.

Consequently, the exploratory examinations on the model plant species could give a baseline to future research. It is well known that the MIPs contain significant key amino acid residues in certain conserved regions which take part in the metalloid transport process. Identifying such critical amino acid residues through in silico and mutant analysis approach will help understand the nature of aquaporins to show differential preference to various metalloid substrates for transport. Moreover, it may help engineer modified and improved crop plants exhibiting multimetalloid stress tolerance and biomagnification in permissible limits in the food chain (Mittler and Blumwald [2010](#page-15-20)). Additionally, studies with other biologically significant metalloids/metal-induced stress in plants will be useful to expand the spectrum of functional characterization of the MIPs.

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