

Interrelations of nutrient and water transporters in plants under abiotic stress

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Environmental changes cause abiotic stress in plants, primarily through alterations in the uptake of the nutrients and water they require for their metabolism and growth and to maintain their cellular homeostasis. The plasma membranes of cells contain transporter proteins, encoded by their specific genes, responsible for the uptake of nutrients and water (aquaporins). However, their inter-regulation has rarely been taken into account. Therefore, in this review we identify how the plant genome responds to abiotic stresses such as nutrient deficiency, drought, salinity, and low temperature, in relation to both nutrient transporters and aquaporins. Some general responses or regulation mechanisms can be observed under each abiotic stress such as the induction of plasma membrane transporter expression during macronutrient deficiency, the induction of tonoplast transporters and reduction of aquaporins during micronutrients deficiency. However, drought, salinity and low temperatures generally cause an increase in expression of nutrient transporters and aquaporins in tolerant plants. We propose that both types of transporters (nutrients and water) should be considered jointly in order to better understand plant tolerance of stresses.

Introduction

As they are essential for plants, the maintenance of the optimal concentrations of certain mineral nutrients within the plant tissues is highly important for proper growth. Therefore, to complete the life

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cycle, and for optimal development of morphology and anatomy, nutrient uptake should be rationalized according to the need of each plant (Barker and Pilbeam 2016). But, beside their involvement in primary metabolism, these mineral nutrients are the basis of the secondary metabolism, defense, signal transduction, hormone reception, and energy and molecular regulation of the plant (Maathuis and Diatloff 2013). Therefore, deficiencies in one or more of them produce a dramatic effect on plant physiology.

Root hydraulic conductivity is one of the main parameters that describe the capacity of the root to uptake water, conferring the ability to adapt to changes in environment (Armand et al. 2019). In this way, the plasticity of the changes of root hydraulic conductivity has been related to the presence and functionality of aquaporins, since they allow water to pass freely across cellular membranes, following osmotic or hydrostatic pressure gradients (Wang et al. 2019a).

There is a strong interaction between mineral uptake and water status in plants. Although both ions and water are taken up by specific membrane transporters (channels, antiporters, and specific transporters for ions, and aquaporins for water), the regulation of these transporters must be connected to ensure the cellular homeostasis. The apparently simple water transporters, aquaporins, are in fact highly complicated due to the wide number of families and isoforms. Therefore, the multiplicity of aquaporins isoforms, the interaction between isoforms and lipid bilayer and their response under different abiotic stress is still under study (Martínez-Ballesta and Carvajal 2016). Aquaporins can be classified into five families depending on their cellular membrane localization and amino acid sequence. Thus, they are classified as PIPs, if located in the plasma membrane; TIPs, in the tonoplast; NIPs, if they are nodulin-26-like; SIPs, if they are small and basic; and XIPs, if they are uncharacterized intrinsic proteins (for a review, see Martínez-Ballesta and Carvajal 2014). Reverse genetics and overexpression are effective tools for investigating the physiological functions of each aquaporin isoform in plants and for understanding their roles in water transport and abiotic stress responses. In this way, successful examples have been reviewed by Martínez-Ballesta and Carvajal (2014) as the expression of *Vicia faba* PIP1 in transgenic *Arabidopsis thaliana* and over-expression of PIP1 in *Oriza sativa* improved drought resistance by increasing root hydraulic conductivity.

In this sense, as vital regulators of plant short-distance cell to cell transport and homeostasis, the study of the response of aquaporins to abiotic stress has been implemented in recent years (reviewed by Afzal et al. 2016, Kapilan et al. 2018). Also, changes in nutrient transporters under different abiotic stresses have been studied, highlighting some relationship with tolerance (Hasanuzzaman et al. 2018).

In the context of the abiotic stresses that crops suffer, and with regard to climate change scenarios, attention has been focused on nutrient deficiency, salinity, drought, and sudden low temperatures. The impacts of these stresses on nutrient and water uptake have been studied, but rarely in an integrated way. In this review, we establish the relationship between nutrient transporters and aquaporins in abiotic stress situations, to reinforce the importance of studying their integrated regulation under environmental changes. Also, we will point out the need to complete our knowledge of nutrient transporters and aquaporins for a better interpretation of their key role under abiotic stress.

The influence of macronutrient deficiencies on the interaction of their transporters and aquaporins

The concentration of macronutrients required for plant optimal growth is above 0.1% on a dry matter in plant tissue (Karthika et al. 2018). Therefore, as macronutrients are required at high concentrations, it is not common to find macronutrient toxicity stress in field conditions. However, macronutrient deficiency is an important problem for crop productivity, affecting many plant physiological features (Pessaraki 2015) involving transporters and aquaporins (Fig. 1).

Nitrogen

Nitrogen (N) is taken up either as the nitrate ion (NO_3^-), the prevalent form of uptake, or as the ammonium ion (NH_4^+), depending on the plant species and the soil conditions regarding factors like pH and the redox state (Karthika et al. 2018). The principal transporters described for NO_3^- belong to the NRT family, a large protein family. They include high-affinity transporters such as NRT2 and low-affinity transporters such as NRT1 (Forde 2002). But, among the NRT1s, some transporters have been described that present a dual affinity for NO_3^- , such as AtNRT1;1 (or CHL1) (Gojon et al. 2011). Therefore, under low- NO_3^- conditions the NRT2 transporters (NRT2;1, NRT2;2, NRT2;4, and NRT2;5) take up approximately 95% of the total amount of this anion, NRT2;1 and NRT2;2 being the main contributors (Lezhneva et al. 2014). While it has been reported that *NRT2;5* is the only one up-regulated under NO_3^- starvation in wheat (*Triticum durum* L.) plants, in sorghum (*Sorghum vulgare* Pers, syn), N deficiency caused higher abundance of NRT2;2, NRT2;3, NRT2;5, and NRT2;6 transcripts (Gelli et al. 2014, Curci et al. 2017).

The root hydraulic conductivity (L_p , $\text{m}^{-1} \text{s}^{-1} \text{MPa}^{-1}$), which defines the intrinsic ability of roots to conduct water across a water potential gradient between the root surface and the xylem in the stem (Eissenstat

1997), is affected by N deficiency, showing a significant reduction in N-deficient plants. In this sense, the high contribution of aquaporins to the roots L_p value (Carvajal et al. 1996a, Gorska et al. 2008) suggests that N deficiency produces a reduction in aquaporins activity or expression (Clarkson et al. 2000). Ding et al (2018) showed, in rice (*Oryza sativa* L.) plants, that the expression of PIPs in roots was reduced under low-N conditions. Also, previous studies in *Arabidopsis thaliana* L. found a decrease in root plasma membrane aquaporins (*PIP2;1*, *PIP2;2*, *PIP2;4*, *PIP1;2*, and *PIP1;3*) expressions in response to N starvation for 6 days (Di Pietro et al. 2013). These results suggest that *NRT2;1*, that acts as a NO_3^- sensor, could trigger complex transcriptional and post-transcriptional regulations of aquaporins, leading to possible N-dependent root L_p regulation. Despite these results, the regulatory mechanism still remains unclear and further investigation is needed (Little et al. 2005, Tyerman et al. 2017).

Besides, NH_4^+ uptake by roots occurs mainly via NH_4^+ transporters (AMT) localized in the plasma membrane (Yuan et al. 2007). This ion is transported from the cytosol to the vacuole for N storage and to avoid its toxicity to the plant (Wang et al. 2008). It has been reported that this transport is probably facilitated by the tonoplast aquaporins *AtTIP2;1* and *AtTIP2;3* in *A. thaliana* cells (Loqué et al. 2005). Therefore, when N is needed, it could be remobilized by passive transport. In this way, the described low-affinity transport pathway may generally involve aquaporins of type TIP (Wang et al. 2016). In fact, several TIPs, such as *ZmTIP1;1* and *ZmTIP1;2*, have been described as participating in NH_4^+ transport in corn plants (*Zea mays* L.) (Bárcana et al. 2014).

Members of the plasma membrane PIP and NIP and the tonoplast TIP subfamilies have been reported to facilitate urea transport through membranes (Liu et al. 2003). Accordingly, under N starvation, the expression of *ZmTIP4;4* has been observed to increase significantly in roots and expanded leaves, suggesting that *ZmTIP4;4* is essential for urea efflux to the cytoplasm (Gu et al. 2012). This indicates that this aquaporin is a urea transporter involved in the mobilization of reserve pools in the vacuole under N deficiency (Figure 1).

Phosphorus

Normally, phosphorus (P) is taken up from soil mainly as its inorganic form (Pi), and its uptake by plants is an energy-consuming, co-transport process. In this sense, we can find high- and low-affinity Pi transporters whose activities mostly depend on the rhizosphere concentrations of P (Schachtman et al. 1998). Thereby, in *A. thaliana* and rice plants, five high-affinity Pi transporters (PHT1, PHT2, PHT3, PHT4, and PHT5) have been identified (Sun et al. 2017). In particular, members of the PHT1 group

have been shown to be predominant under Pi deficiency. This has been proven in *A. thaliana* and wheat, where *AtPHT1;4* could become predominant, being up-regulated under Pi deficiency (Liu et al. 2013, Ayadi et al. 2015). However, in soybean (*Glycine max* L.) plants, most of the *PHT1* genes had elevated transcript levels under low-P conditions (Qin et al. 2012).

Also, P starvation could cause combined changes in root *Lp* and aquaporins gene expression together with the formation of endodermal apoplastic barriers in roots (Li et al. 2019a). In fact, recently, Li et al. (2019) showed a decrease in the gene expression of six PIPs aquaporins (*LcPIP1;1*, *LcPIP1;4*, *LcPIP2;1*, *LcPIP2;4*, *Put-LcPIP2;2*, and *Put-LcPIP2;5*) in *Leymus chinensis* L. under low P availability. Indeed, P starvation may also modulate aquaporins activity, due to changes in their phosphorylation status (Wang et al. 2016). A study in corn plants showed correlation between the expression patterns of the high-affinity Pi transporters *ZmPHT4;2* and *ZmPHT4;6* and that of the NIP-type aquaporin *ZmNIP2;1* (Yue et al. 2012), thus revealing the possible existence of a direct or indirect mechanism that regulates their expression under this mineral-deficiency stress.

Potassium

Most potassium ion (K^+) channels in plant cells can be considered as passive transporters. Although, other K^+ transporters usually behave as carriers, and function as co-transporters coupled with H^+ or sodium ion (Na^+) transport (Chen et al. 2008). In *A. thaliana*, a total of 71 K^+ transporters, channels and carrier proteins, have been identified. Also, they are divided into three channel families (the Shaker, TPK, and Kir-like families) and four transporter families (the KUP, KT/KUP/HAK-type, HKT, and CPA families) (Chen et al. 2008). Studies carried out with *A. thaliana* indicated that *AtHAK5*, *AtKEA5*, *AtKUP3*, *AtCHX13*, and *AtCHX17* were up-regulated and induced by potassium (K) starvation (Ahn et al. 2004, Cellier et al. 2004, Gierth et al. 2005, Zhao et al. 2008). In rice plants, Liu et al. (2006) found that K starvation induced the expression of *OsAKT1*, *OsHAK1*, and *OsPIP2;7*. The same authors also showed that the rice root *Lp* dramatically increased in response to K starvation, which could be the result of an increase in either the density or the activity of aquaporins. In addition, other authors reported that aquaporin genes were strongly up-regulated after K^+ resupply; in this sense, 12 aquaporins genes were identified in the shoots of *A. thaliana* plants and 15 in the roots (Armengaud et al. 2004). In contrast, Coffey et al. (2018) observed both increases, but mainly, decreases in gene transcript abundance in barley plants under low K conditions; in particular, the expression of *HvPIP2* in roots decreased. They also found a decrease in root *Lp*. These contradictory results could be due to the PIP isoforms-specific responses or the different experimental designs. While Coffey et al. (2018) grew the plants under K

starvation from the beginning, Liu et al. (2006) only grew the plants for a maximum time of 24 h in a K-deficient solution. Therefore, different plant responses might reflect, on the one hand, a long-term effect of K starvation and, on the other, a rapid response of the plant to changes in K availability. The results of Liu et al. (2006) suggest that aquaporins and K channels were functionally co-regulated during cell turgor regulation; this could reflect the co-regulation of both transporters in roots, leading to the possibility of discovering an unknown regulatory factor for both ion and water channels.

Calcium

Calcium (Ca) deficiency is rare in nature since Ca is usually abundant and available in soils. However, in cases of severe weathering and extreme leaching of soil, deficiency of Ca may occur (Karthika et al. 2018). Calcium ion (Ca^{2+}) channels - that could be Ca^{2+} -selective or non-selective ion channels - allow the entry of Ca into the roots. The influx of Ca^{2+} into the cytosol is carried out by three different types of channels classified on the basis of their voltage-dependence: depolarization-activated (DACC), hyperpolarization-activated (HACC), and voltage-independent (VICC) cation channels (White and Broadley 2003). Meanwhile, Ca^{2+} efflux from the cytosol, that requires energized active transport, is accomplished by either Ca^{2+} -ATPases, divided into two families (P-type ATPase IIA and IIB), or $\text{H}^+/\text{Ca}^{2+}$ -antiporters (Sharma et al. 2017). Among the latter, the CAXs (Cation/ H^+ exchangers) are a group of high-capacity, low-affinity transporters that export cations out of the cytosol to maintain ion homeostasis across biological membranes (Cheng et al. 2003). In particular, under Ca deficiency, amaranth (*Amaranthus hypochondriacus* L.) plants showed an up-regulation of the *AhCAX* and *calmodulin* (*CaM*, a protein that functions as a Ca sensor) genes, as described by Aguilar-Hernández et al. (2011).

On the other hand, Ca starvation generally produces down-regulation of aquaporin genes expression, despite the fact that Ca deprivation does not have a great impact on water relations at the whole plant level (Maathuis et al. 2003). Indeed, White (2001) described trans-root movement of Ca^{2+} as mainly apoplastic. For this reason, it was proposed that, when Ca is limiting, in order to ensure its adequate delivery, a shift to apoplastic water movement might be required through a decrease in symplastic water permeability, which relies on aquaporins activity (Maathuis et al. 2003). In fact, protoplasts extracted from pepper (*Capsicum annuum* L.) plants grown under Ca starvation showed no aquaporin functionality, while, when Ca^{2+} was added to the protoplasts, an increase in the aquaporin functionality of the plasma membrane was observed. In addition, when a Ca^{2+} channel blocker was added, no aquaporin functionality was observed (Cabañero et al. 2006).

Moreover, the gene of *ACA4* (calmodulin-regulated Ca^{2+} pump in endoplasmic reticulum) showed the same expression pattern as *NIP2;2* in corn (Yue et al. 2012). In addition, Kapilan et al. (2018) reported that aquaporins activity could be directly modulated by divalent cations like Ca^{2+} . Furthermore, Ca^{2+} seems to be involved in plasma membrane aquaporins regulation via a chain of processes within the cell but not by alteration of the stability of the plasma membrane (Carvajal et al. 2000, Cabañero et al. 2006). Although a relationship among the Ca^{2+} transporters and aquaporins has not been demonstrated, these findings could suggest an interrelation between aquaporins and Ca^{2+} transporters that needs to be investigated in further studies.

Magnesium

Although it is difficult to find magnesium (Mg) deficiency in soils, its bioavailability is decreased by acidic soils, high rainfall in tropical regions (Gransee and Führs 2013, Sun et al. 2013), aluminum toxicity (Chen and Ma 2013), heat stress (Mengutay et al. 2013), drought-affected soils, and high levels of competing elements (K, Ca, NH_4^+ , and Na) (Guo et al. 2016). The homeostasis of Mg in *A. thaliana* cells is maintained by Mg transporters such as AtMHX (magnesium ion (Mg^{2+})/ H^+ exchanger) (Berezin et al. 2008, Gaash et al. 2013). Another well-known family of Mg transporters is the CorA family; this superfamily groups together high-, low-, and dual-affinity types of transporters. They are considered the primary Mg^{2+} -transport system in plants and play major roles in Mg^{2+} uptake, distribution, and homeostasis in cells (Shaul 2002). In particular, under Mg-starvation conditions, BnMGT1;2 and BnMGT6;1 transporters, associated with Mg^{2+} translocation from root to shoot, were up-regulated in *Brassica napus* L. plants (Sun et al. 2019). There is some evidence that suggests a relationship between Mg deficiency and aquaporins activity since Yue et al. (2012) found that the CorA-like family protein (*MRS2-2*) has the same expression patterns as *ZmPIP1;5* in corn plants. However, there is no clear evidence of a direct relationship between Mg deficiency and aquaporins activity.

Sulfur

Sulfur (S) is taken up and transported as the sulfate ion (SO_4^{2-}), by a family of high-affinity transmembrane SO_4^{2-} transporters that includes SULTR1;1, SULTR1;3, SULTR1;2, SULTR3;1, SULTR3;2, SULTR3;4, SULTR3;5, SULTR4;1, and SULTR4;2 (Yue et al. 2012). Under S deprivation, the expression of the SO_4^{2-} transporter genes *AtSultr1;1*, *AtSultr1;2*, and *AtSultr4;1* is up-regulated in *A. thaliana*, showing the importance of these high-affinity transporters under S deficiency (Buchner et al. 2004). Although there is no evidence of a direct relationship between PIP aquaporins activity or

expression and S transporters, Yue et al. (2012) found that *ZmSULTR2;1* exhibited the same expression patterns as *ZmTIP2;2*, while *ZmSULTR3;4* exhibited the same expression patterns as *ZmTIP3;2*. This suggests the involvement of aquaporins in S transfer from the S pool in the vacuole to the cytoplasm. This could be the starting point for future studies focused on the cooperation of S transporters and aquaporins in stressed plants.

The influence of deficiencies of micronutrients on the interaction of their transporters and aquaporins

Micronutrient deficiencies are extensive in crop soils. Although the total concentration of micronutrients in soil may be optimal, their bioavailability is determined by soil factors such as pH, microorganisms, and water status (Mikula et al. 2020). However, as pointed out below, the interrelation of transporters and aquaporins need investigation (Fig. 1).

The micronutrients are transported by big transporters families as ZRT-IRT-like Protein (ZIP), CAX, natural resistance-associated macrophage protein (NRAMP), heavy metal transporters (HMA) and yellow stripe like (YSL). ZIP, NRAMP and YSL are mainly influx transporters while CAX and HMA are mainly efflux ones, but their specific function depend on nutrient concentration and cellular localization (Dalcorso et al. 2014). Although, all families have members that could transport several micronutrient, the isoforms are highly specific (Haydon and Cobbett 2007). However, under deficient conditions, some overexpressed transporters can transport other similar cations, increasing their concentration (Williams et al. 2000).

Iron

Although iron (Fe) is an abundant element in soil, most of it is present as non-available (insoluble) forms (Ricachenevsky et al. 2013). Plants possess different strategies of Fe uptake from soil, involving reduction of insoluble Fe³⁺ to soluble Fe²⁺ (Strategy I) or direct chelation in the rhizosphere (Strategy II) (Briat et al. 2015).

Thus far, the relationship between Fe and water flow has not been directly studied. Under Fe deficiency, plants seem to produce a signal that could influence the water movement through the plant. Lei et al. (2014) concluded that in Fe-deficient *A. thaliana* plants the contents of some hormones, such as abscisic acid (ABA) increase, as well as the expression of tonoplast *AtNRAMP3*, leading to the removal of Fe from vacuolar pools. Also, the expression of plasma membrane transporters localized mainly in pericycle and vascular cells - namely, *AtFRD3*, *AtYSL2*, and *AtNAS1* - was increased to

enhance long-distance transport of Fe. In addition, a study performed by Hopff et al. (2013), in maize roots, showed a decrease in PIP2.2 abundance under Fe deficiency, but no relationship has been found between the two types of transporter (Fe-transporters and aquaporins). Now, Fe uptake and transport have been studied in depth, but the roles of aquaporins as plasma membrane proteins could be a starting point for future investigation of Fe movement.

Manganese

Deficiencies of manganese (Mn) often appear in plants growing in alkaline soils or in soils with a high concentration of other minerals, such as Fe, Mg, Ca, or P, which decreases Mn bioavailability (Marschner 2011). Manganese could be a substrate of many membrane transporters that have been reported to contribute to the influx and efflux of this element. In this regard, the transporter families can be separated according to their participation in Mn efflux or influx. Then, NRAMP, ZIP, and YSL are considered Mn influx transporters. NRAMP is a big family of transporters localized in the plasma membrane, NRAMP1 being the main member that contributes to Mn uptake. Also, other members, such as NRAMP3 and 4, have been found in the tonoplast, where they regulate the Mn homeostasis in cells (Thomine et al. 2003). Besides, members of the ZIP family are known to transport metals in plants; they are localized mainly in the plasma membrane and are composed of eight transmembrane domains (Rogers et al. 2000). Studies in *A. thaliana* have demonstrated that many members - such as AtZIP1, AtZIP2, AtZIP5, AtZIP6, AtZIP7, and AtZIP9 - are involved in Mn uptake, mainly under Mn deficiency (Milner et al. 2013); AtZIP1 is localized in the tonoplast, suggesting that it is involved in Mn movement from vacuole to cytoplasm. In addition, some YSL transporters, which are proteins involved in the long-distance and intracellular transport of metals, have been shown to be involved in Mn influx. In *A. thaliana*, YSL 4 and 6 have been localized in the membranes of the vacuole and chloroplast, moving Mn from these organelles to the cytosol. Also, in rice plants, these transporters were found in the plasma membrane, involved in Mn uptake from the apoplast (Socha and Guerinot 2014).

Also, there are many protein families involved in Mn efflux - such as the cation exchanger (CAX), Ca cation exchanger (CCX), and vacuolar Fe transporter (VIT) families - together with Ca-permeable channels (Gollhofer et al. 2011, Zhang et al. 2012). Thus, CAX and CCX have been localized in the tonoplast and they are involved in Mn movement from cytosol to vacuole in *A. thaliana*. Also, VITs were found in the tonoplast of rice and *A. thaliana*. Under Mn deficiency, Mn can pass through the plasma membrane via Ca-permeable channels, from apoplast to cytoplasm (White et al. 2002).

Although there has been no investigation that relates water flow, aquaporins, and Mn nutrition status, the fact that there is a relationship with other micronutrients supports some unknown interrelations.

Copper

Copper (Cu) is moved by membrane transporters of several families, such as COPT, ZIP, HMA, and YSL. Under Cu deficiency, there is up-regulation of *COPT 1 and 2* and *ZIP 2 and 4*, which encode proteins localized in the plasma membrane, mainly in root tips and the zone of differentiation. Also, COPT5, localized in the tonoplast, mediates influx transport to increase the Cu concentration in the cytosol. In addition, under Cu deficiency, the abundance of YSL 2 increases since it is involved in long-distance transport of Cu, from the xylem to sink cells. However, there are other important transporters, like HMA5, that have a contrary role depending on the plant. So, in rice, HMA5 is up-regulated to facilitate long-distance Cu transport since it mediates Cu efflux across the plasma membrane. While, in *A. thaliana*, HMA5 is localized in the tonoplast, mediating Cu efflux to the vacuole; under Cu deficiency its expression is down-regulated (Bernal et al. 2012, Aguirre and Pilon 2016, Printz et al. 2016).

Few studies have demonstrated the relationship of Cu stress with water uptake and transport. It has been reported that in the leaves of Cu-deficient plants of safflower (*Carthamus tinctorius* L.) and cotton (*Gossypium hirsutum* L.) the water flow was decreased, since these plants had low stomatal conductivity (Sharma 2006). However, an excess of Cu could affect aquaporins functioning in the plasma membrane, inhibiting their water transport. In this way, the blue copper-binding protein (GhBCP2) has been reported to inhibit the cotton GhPIP2;6 activity, suggesting that Cu levels could regulate the function of this aquaporin decreasing the water flow across it (Li et al. 2013). Recently, Landa et al. (2017) reported that excess Cu provoked the down-regulation of genes involved in metal homeostasis and aquaporins synthesis in *A. thaliana* plants. A high Cu concentration provoked a decrease in the transcription of aquaporins genes, such as *PIP1C*, *DELTA TIP*, *TIP2*, and *PIP2;4*, reducing water uptake. Also, these authors indicated that the reduction of water flow was due to damage to the membrane structure caused by the low content and expression of aquaporins under this condition.

In addition, Noronha et al. (2016) described a XIP in grapevine (*Vitis vinifera* L.), VvXIP1, that transports Cu and Ni, but an excess of Cu provoked a down-expression of this aquaporin. The mechanism by which cations cross the aquaporins pore is unknown at this time. But, these authors suggested similarities with the results found in human aquaporins. They pointed out that PIP1 is formed by four subunits having one pore each, and water should be transported by each individual pore, but the central pore could facilitate the diffusion of charged solutes in response to cyclic nucleotide binding.

Previously, Yool and Weinstein (2002) found similarities between the carboxy tail domains of cyclic nucleotide gated (CNG) channels and PIP1. This could open the way to future studies that help us to understand the possible role of aquaporins in the transport of cations.

Molybdenum

Molybdenum (Mo) uptake is mediated by a plasma membrane transporter known as MOT1, described in *A. thaliana*; due to its analogy with S transport it was known previously as SULTR5;2 (Mendel and Kruse 2012). Also, there is another Mo transporter localized in the vacuolar membrane, known as MOT2; normally, it accumulates and its activity increases in senescing leaves, suggesting that MOT2 could transport Mo from vacuole to cytosol (Vatansever et al. 2017).

In relation to Mo and water status, there are no studies that found a direct relationship between them. However, under Mo deficiency, nitrate reductase is inactive and the NO_3^- concentration increases in cells and tissues. This could enhance TIPs activity since these aquaporins are involved in NO_3^- efflux to the vacuole (Little et al. 2005), which would avoid NO_3^- toxicity as the first step under Mo deficiency. Therefore, although there are no studies relating transporters of Mo and aquaporins, the indirect evidence for such a relationship supports the need for mutual regulation.

Zinc

Zinc (Zn) uptake by plants is carried out by six families of transporters that include: ZIP, cation diffusion facilitator proteins (CDF), P-type ATPase, NRAMP, ATPase, HMA, and CAX (Kobae et al. 2004). Members of the ZIP family move Zn from apoplast to cytosol, so they are considered the main transporters involved in Zn uptake from soil (Lin et al. 2009). However, Zn movement at the vacuolar level is controlled by CDF (efflux) and NRAMP (influx) (Oomen et al. 2009), so that the cytosolic Zn concentration is highly controlled. Under Zn deficiency, many ZIP transporters are strongly induced, mainly ZIP4, which is localized in the plasma membrane of root tip and epidermal cells (Assunção et al. 2010). Also, it seems that there is a general response to Zn deficiency in higher plants, since the transcription factors involved in the increase in these ZIP transporters are found in several species (Assunção et al. 2010; Kabir et al. 2014). In addition, NRAMP transporters in the tonoplast are up-regulated while CDF are down-regulated, to transfer vacuolar Zn to the cytosol (Kabir et al. 2014). Furthermore, HMA transporters, mainly HMA2, are found in the plasma membrane of root vascular cells and affect the loading of Zn into the xylem for transport to the shoot in times of deficiency. Also,

these transporters permit Zn to cross the plasma membrane of root cells, reaching the xylem and finally the shoots (Hussain et al. 2004).

Zinc deficiency has been shown to provoke changes in water relations in plants similar to those observed under drought stress, but aquaporins have not been studied in this regard. However, Jain et al. (2008) showed that excess Zn acted as an inhibitor of PIPs functions in seeds of tomato (*Solanum lycopersicum* L.). Also, Devi et al. (2016) studied the effect of excess Zn in soybean plants, observing no increase in aquaporins transcription, but there was inhibition of aquaporins function, with reduced water flow across cells. In this way, Gitto and Fricke (2018) showed decreased plant water flow together with a decrease in aquaporins functionality (14-80%), mainly for PIP1;3, PIP2;4, and PIP2;5 that are involved in water flux. But, a recent work in poplar (*Populus trichocarpa* L.) reported that excess Zn not only down-regulated *PIP1*, but also provoked post-translational changes - since it was observed that PIP1 was co-localized in the vacuolar membrane together with TIP1, in *A. thaliana* protoplasts (Ariani et al. 2019) - which could be involved in the control of water fluxes to maintain the cell homeostasis under excess Zn. Future investigations are needed to understand the Zn-water flux relationship, but reports on the relationship between Zn deficiency and aquaporins are scarce.

Boron

Boron (B) deficiency is one of the most widespread micronutrient deficiencies in crops. Boron can be taken up by plants in different ways. For a long time, passive diffusion was considered the only way of entry of B into roots and cells. This probably is the main mechanism under optimal or high B conditions (Miwa and Fujiwara 2010). But, at low external B concentrations, this element can be taken up by an active process mediated by the specific efflux transporter BOR1 localized in the inner domain of root cells (Dannel et al. 2000). In addition, some aquaporins - such as NIP5;1 - are able to transport B (Kato et al. 2009). Takano et al. (2006) reported that, under B deficiency, damage to the xylem could reduce water transport to leaves, affecting the distribution of other elements: in this situation, aquaporin NP5;1 was highly expressed in *A. thaliana* plants, with an increase of almost 15-fold. Also, the expression of *NIP6;1*, which is expressed mainly in the phloem of stems, doubled under B-deficient conditions (Tanaka et al. 2008). Such increases in expression have also been observed for other NIPs, such as *NIP3;1* in rice and *NIP2;1* in barley (*Hordeum vulgare* L.); the latter was described as participating in B transport, indicating the important roles of this channel protein in B uptake and transport (Hanaoka and Fujiwara 2007, Schnurbusch et al. 2010). In addition, other B transporters, like BOR1, should be activated under these conditions to increase the B movement across root cells to the stele, due to the

opposite localizations of NIP and BOR in the plasma membrane that facilitates B movement. Another transporter, known as BOR2, is involved in the efflux of B from symplast to apoplast, to maintain the formation in root cells of the cell wall, due to the importance of this structure to plant cells.

Although, under B toxicity, normally BOR1 is quickly degraded to avoid excessive transport of B to the shoot (Poschenrieder et al. 2019), in rice an enhancement of other aquaporins, such as OsPIP2,4 and OsPIP2,7 (Kumar et al. 2014), to augment B movement to the leaves, was observed. Sutton et al. (2007), in barley plants, demonstrated an enhanced expression of efflux transporters in cells of leaves and roots; the key to tolerance lies in an increase in B efflux from the sensitive symplast to the apoplast, with later efflux of this B from hydathodes to the leaf surface, mediated by BOR1 (Reid and Fitzpatrick 2009). In addition, a member of the TIP aquaporins family localized in the tonoplast, AtTIP5,1 has been described as participating in B transport, effluxing it to the vacuole and thereby increasing the tolerance of B toxicity in *A. thaliana* plants (Pang et al. 2010). Finally, due to the importance of B to plants, a large number of aquaporins, of distinct types, participate in its homeostasis, mediating both influx and efflux processes. Thus, its movement is highly regulated, to maintain optimal B concentrations in cells and tissues.

Effect of drought on the interaction of nutrient transporters and aquaporins

The main effect of drought stress is the reduction of crop growth and yield, which ranges from 10 to 90% depending on the severity and the phenological stage of the plant when subjected to water deficit. The reduced water availability leads to a reduction in cell turgor, inhibiting cell elongation and promoting stomatal closure. The latter inhibits CO₂ absorption and photosynthetic efficiency, but also reduces water and nutrients uptake (Akinci and Lösel 2012).

In general, most of the genes encoding nitrate transporters and the enzymes responsible for NO₃⁻ assimilation and remobilization are down-regulated under drought stress (Goel and Singh 2015). However, in *Brassica juncea* L. plants, the expression of *BjNRT1;1* and *BjNRT1;5* was found to be up-regulated after 1 h of exposure to different abiotic stresses, indicating an early reaction of N accumulation upon detection of the onset of stress, but down-regulation occurred after 24 h, affecting most of the N transporters, including *BjNRT2;1* (Goel and Singh 2015). However, there are differences in the regulation of NRTs among different species and varieties of the same plant species. As an example, Duan et al. (2016) showed that a N-inefficient variety of winter wheat (*Triticum aestivum* L.) up-regulated *NRT1;1*, *NRT1;2*, and *NRT2;2* in the reproductive stage and had strong down-regulation

of *NRT2;1*, *2;2*, and *2;3* (high-affinity transporters) in vegetative tissues after 30 days of drought stress (long-term stress). Meanwhile, a N-efficient variety maintained the expression of almost all the NO_3^- transporters, including the fundamental sensor *NRT1;1* and the *NRT2;1* and *NRT2;2*, at the same levels (Duan et al. 2016), demonstrating a better NO_3^- uptake capacity. Curiously, the N-efficient variety also showed an up-regulation of *AMT1;2* (NH_4^+ transporter), that points to a fine sensing of changes in the availability of N forms in the soil and to better resource utilization under such long periods of drought stress.

Under drought conditions, Pi uptake in plants is likely associated with alterations in the expression of the PHT family of transporters, and reflects the degree of drought tolerance in plants. In poplar *PtPHO9* and *PtPHT1;2* were up-regulated under drought (Zhang et al. 2016a); in apple (*Malus domestica* L.) *MdPHT1;5*, *MdPHT1;7*, and *MdPHT4;7* were up-regulated in roots, and *MdPHT3;7* and *MdPHT4;3* in leaves (Sun et al. 2017); and in *B. napus* only three genes, *BnaPT11*, *BnaPT34*, and *BnaPT38* (BnPHT1 family), were up-regulated in roots while 18 genes of the BnPHT1 family were up-regulated in the leaves under drought stress, and, in addition, no genes were down-regulated (Li et al. 2019c).

Regarding the K^+ transporters, it has been reported that the grapevine K^+ transporter *VvK1.1*, the counterpart of the *A. thaliana* *AKT1* channel, has a major role in K^+ uptake from the soil solution and its expression is strongly sensitive to drought stress. Nevertheless, the highest expression of *VvK1;1* has been shown in berries, where it is localized in the phloem vasculature, pointing to a major role in K^+ loading into berry tissues, especially upon drought stress (Cuéllar et al. 2010). Also, in chickpea (*Cicer arietinum* L.), the *CarAKT1,2* influx K^+ transporter and *CarGORK* (putatively involved in the K^+ efflux directly related to stomatal closure (Osakabe et al. 2013)) were both up-regulated in response to drought stress (Azeem et al. 2018). However, decreased expression of *CarKATI,1* in chickpea and of *HvAKT1* in barley indicates that the change in the transcript level of some members of the *AKT1* family might not be related to drought tolerance (Azeem et al. 2018, Cai et al. 2019). The results demonstrate that a fine regulation of K^+ transporters is essential to develop a strategy to cope with drought stress, although the response seems to be time- and genotype-dependent (Cai et al. 2019).

Calcium plays a key role as signaling molecule. When plants are exposed to abiotic stress, transient peaks of Ca^{2+} in cytoplasm regulate the response of different genes and proteins activity depending on the intensity and duration of the stress (Choi et al. 2014, Jing et al. 2019). For this reason, there is high variability in the regulation of calcium transporters under drought stress depending on tissues and specific functions. Plant Ca^{2+} pumps are involved in Ca^{2+} efflux from the cytosol. The

transcript level of P-IIB Ca-ATPase PCA1 rose in *Physcomitrella patens*, B&S. were up-regulated in response to dehydration and abscisic acid (Qudeimat et al. 2008), and some auto-inhibited calcium ATPases (ACAs) and ER-type ATPases (ECAs) pumps have shown to be regulated by short-term dehydration stress in rice, *ACA5* and *ACA7* being strongly up-regulated in roots and seedlings, while *ECA1* and *ACA4* were strongly down-regulated and *ACA3*, *ACA5*, and *ACA7* were up-regulated in mature leaves (Singh et al. 2014). In *Brassica oleracea* L., the *BoACA4* and *BoACA11* levels remained high for 24 h in leaves under dehydration stress (Lee et al. 2013). For *A. thaliana* and rice CAX (exchangers of Ca²⁺), transcripts levels increased or decreased in abundance in response to water deficit (Bickerton and Pittman 2015). A wide-ranging analysis in rice showed differences in the patterns of regulation between tissues, almost all the CAX exchangers being down-regulated in roots but not in leaf tissues (Singh et al. 2014). Also, in *B. oleracea* the expression level of *BoCAX1* in leaf tissues gradually increased with the drought stress imposed (Lee et al. 2013), probably indicating a link to drought tolerance.

Under drought stress, differences in the response of aquaporins have been shown between different aquaporin homologs in diverse plant species (Gambetta et al. 2017), cultivars of the same plant species with differing drought tolerance strategies (Vandeleur et al. 2009), and between tissues (Martins et al. 2015) or even between portions of the same tissue (Knipfer et al. 2011). Indeed, root transcriptome analysis showed both up and down-regulation of different PIPs, TIPs, and NIPs homologs under drought stress (Molina et al. 2008, Aroca et al. 2012, Afzal et al. 2016) and different homologs responded differently depending on the intensity and nature of the stress applied (Aroca et al. 2012, Bárzana et al. 2014). Among the aquaporin groups, PIPs are the most responsive to drought stress, undergoing a general transcriptional down-regulation, particularly in roots (Jang et al. 2004, Alexandersson et al. 2005, Mahdiah et al. 2008, Ruiz-Lozano et al. 2009, Šurbanovski et al. 2013, Bárzana et al. 2014). Only a few PIP genes (mostly from the PIP1 subgroup) were found to be up-regulated - in specific tissues and drought conditions, especially in leaves (Jang et al. 2004, Lian et al. 2004, Aroca et al. 2007, Mahdiah et al. 2008, Li et al. 2009, Ruiz-Lozano et al. 2009, Vandeleur et al. 2009, Bárzana et al. 2014, Martins et al. 2015). This up-regulation of specific isoforms of the PIP1 subgroup in leaves implies their involvement in gas and water exchange and stomatal behavior under stress conditions (Flexas et al. 2006, Cui et al. 2008, Uehlein et al. 2012, Wang et al. 2016, Zwiazek et al. 2017).

Studies with transgenic plants overexpressing PIP aquaporin genes have also yielded complex outcomes, sometimes with increased plant resistance (Lian et al. 2004, Cui et al. 2008, Ayadi et al. 2011, Sreedharan et al. 2013, Xu et al. 2014, Zhuang et al. 2015), but not in other cases (Aharon et al. 2003,

Katsuhara et al. 2003, Jang et al. 2007), while silencing of PIP genes commonly increases the susceptibility of the plants to drought stress (Martre et al. 2002, Siefritz et al. 2002, Yu et al. 2005).

Besides PIPs, also TIPs and NIPs could be involved in the response of plants to drought stress. However, studies involving the overexpression of TIP and NIP homologs in different plants are scarce and also provide contradictory results. The constitutive expression of *SITIP2;2* converted tomato plants from isohydric to anisohydric drought-tolerance behavior (Sade et al. 2009). Overexpression of *Panax ginseng*, C.A.Mey. *PgTIP1* in *A. thaliana* plants was detrimental to drought resistance under limited water supply due to rapid drying of the rooting medium and faster water loss through leaves by enhanced transpiration, but may be beneficial under slight drought stress and favorable growing conditions (Peng et al. 2007). Transgenic *A. thaliana* plants expressing *TaNIP* showed much longer roots and higher salt tolerance (Gao et al. 2010), while the tolerance of drought was not directly tested.

The regulation of aquaporins by different N forms provides an effective mechanism to increase plant water stress tolerance and water use efficiency. Aquaporins are tightly linked with N metabolism in higher plants, and members of the PIP, NIP, and TIP subfamilies have been shown to transport NH_3 and urea, and are directly involved in maintenance of the cytoplasm-vacuole balance (Gaspar et al. 2003, Liu et al. 2003, Jahn et al. 2004, Loqué et al. 2005, Wallace and Roberts 2005, Bertl and Kaldenhoff 2007, Gu et al. 2012, Bárzana et al. 2014, Yang et al. 2015, Zhang et al. 2016b). Moreover, NO_3^- and NH_4^+ are critical signaling factors for radial water fluxes in the roots (Gorska et al. 2008, Ding et al. 2015). PIP expression has been shown to be controlled by both exogenous and internal NO_3^- concentrations and the increased root hydraulic conductivity stimulated by NO_3^- correlated with up-regulation of PIP expression (Li et al. 2016). Under water stress, NH_4^+ increased the drought tolerance of rice plants by inducing aquaporin expression and activity, which corresponded with increased root water uptake (Ding et al. 2015). In relation to urea, while DUR3 was identified as a high-affinity urea transporter, members of the PIP, NIP, and TIP sub-groups of aquaporins were identified as low-affinity transporters (Liu et al. 2003, Gu et al. 2012, Yang et al. 2015, Zhang et al. 2016b). The uptake or reutilization of urea as a N source could be extremely useful to the plant under drought conditions, when the NO_3^- availability in soil decreases considerably. In *Cucumis sativus* L., CsNIP2;1 has a function in root urea uptake (Zhang et al. 2016b), and both CsNIP2;1 and DUR3 are up-regulated under conditions of N limitation such as under drought stress (Wang et al. 2016). Indeed, an up-regulation of maize ZmTIP1.1 and ZmTIP1.2 with a direct link to water, NH_4^+ , and urea transport, and a possible role in the remobilization of N under severe drought stress, has been described (Bárzana et al. 2014), while

ZmTIP4;4 has been related to vacuolar unloading under N-deprivation (Gu et al. 2012). We cannot rule out, therefore, that DUR3 and AMT1 are equally involved in such redistribution under drought stress.

There are several studies that relate Pi uptake with water flow. The fact that Pi accumulation was reduced under drought conditions indicates that aquaporins expression was also reduced (Carvajal et al. 1996b, Lovelock et al. 2006, Wang et al. 2016). Similarly, it has been reported that augmented Pi uptake is related to increased aquaporins expression and/or activity during the recovery of plant water status after drought stress (Shangguan et al. 2005).

There is also a close relationship between water and K under drought stress. Both are transported throughout the plant by channels/transporters which share regulatory mechanisms under drought stress. Transmembrane channels for water and K⁺ channels/transporters are co-regulated and function in a coordinated manner to maintain the cytosolic osmolality. The first evidence of this coordination was obtained with K⁺-channel inhibitors that produce a diminution in the hydraulic conductivity of the roots (Tazawa et al. 2001) and down-regulation of both water channels (*PIP1;2*, *PIP2;2*, and *TIP1;2*) and the K transporter *HAK5* (Sahr et al. 2005). Similar co-regulation has been observed under drought stress in rice plants, where water deficiency strongly affects PIPs aquaporins and the OsAKT1, OsHAK1, and OsHKT1 K⁺ channel and transporters in a coordinated manner that directly affects hydraulic conductance (Liu et al. 2006). These authors suggested that a common factor should exist for ion and water channels regulation in plants, ABA being the suggested candidate.

The interaction between Ca²⁺ and water channels/transporters under drought stress has not been directly measured, but it is well known that Ca²⁺ can indirectly and directly regulate the water transport in plants. The first clues of an indirect regulation of the closure of aquaporin channels by phosphorylation mediated by Ca²⁺ were provided in the 1990s for PIPs, TIPs, and NIPs isoforms, and the relationship of this aquaporin gating with a diminished water conductance of membranes mediated by Ca²⁺ and, to a lesser degree, by Mg²⁺ is well established (Johnson and Chrispeels 1992, Weaver and Roberts 1992, Johansson et al. 1996, Gerbeau et al. 2002). In roots, *AtPIP2;1*, *AtPIP2;2*, and *AtPIP2;7* are important for the regulation of water flow through plants, and *AtPIP2;1* is also implicated in signaling for stomatal closure; these aquaporins are Ca²⁺-regulated, by direct interaction (Byrt et al. 2017, Kourghi et al. 2017).

Effect of salinity on the interaction of nutrient transporters and aquaporins

Salinity is one of the most widespread plant abiotic stresses around the world. Around 6% of the total land area is affected by salinity, which corresponds to 800 million hectares (Munns and Tester 2008). Soil is considered saline when the EC is greater than 4 dS m⁻¹ and the osmotic pressure is ~ 0.2 MPa (USDA-ARS 2008). This stress entails large losses in agriculture, since moderate levels of environmental salt cause important decreases in the yield of crops because the most important crops are glycophytes (sensitive to saline stress) (Cheeseman 2015). This problem has arisen firstly due to natural causes and secondly through human-induced changes, and soil salinization is expected to increase further owing to climate change (Munns and Tester 2008, Zaman et al. 2018). Therefore, there has been an increase in the scientific research with the objective of understanding mechanisms of salt tolerance in plants. Different ways to solve the salinity problem have been proposed, such as the establishment of halophytic plants (resistant to saline stress) as new crops or the improvement of the tolerance of the main crop species by crossing or transferring genes from halophytes (Cheeseman 2015).

The accumulation of salt in the soil results in a plant stress that can be divided in two phases: (1) a rapid osmotic and water stress, caused by a decrease in water uptake (Sharma et al. 2012) and (2) a slower ionic and nutritional stress, due to the competition among saline ions (Na⁺, Cl⁻) and ionic forms of nutrients and/or the toxicity of saline ions (Munns and Tester 2008). Therefore, primary C and N metabolism in plant cells is altered (Ashraf et al. 2018) especially, NO₃⁻ uptake and transport through roots is disrupted (Gallegos-Cedillo et al. 2016), the levels of many signalling molecules are modified (Zhang et al. 2016c), protein synthesis is reduced (and the transmembrane movement of water is altered (Patankar et al. 2019). Regarding tolerance mechanisms to deal with this stress, there are three types of plant response or tolerance (Munns and Tester 2008): (1) tolerance of osmotic stress with a primary response, namely the inhibition of root water uptake and a decrease in *Lp* (Boursiac et al. 2005), (2) Na⁺ exclusion from leaf blades, to ensure that Na does not reach a toxic concentration, and (3) intracellular compartmentalization of Na, to avoid a toxic accumulation within the cytoplasm. These tolerance mechanisms vary or are more or less efficient depending on whether the plant is a halophyte or glycophyte (Munns 2002, Himabindu et al. 2016).

Therefore, saline stress is associated with nutritional stress caused by a deficit in the uptake of essential nutrients from the soil, because excessive concentrations of Na⁺ and Cl⁻ impair the uptake of beneficial ions (K⁺ and Ca²⁺) (Acosta-Motos et al. 2017). Furthermore, a balanced K⁺/Na⁺ ratio inside metabolically-active tissue and an adequate Ca²⁺ status, which is part of the signalling mechanism of Na⁺ exclusion (Chakraborty et al. 2018), are important factors for salt tolerance. Hence, nutrient transporters have a key role in the response and tolerance mechanisms employed against saline stress.

The most studied transporters in this regard are K⁺ (HAK, AKT, KT, and KUP families) and Na⁺ (SOS, NHX, and HKT families) specific transporters, which control the cellular ion homeostasis and salt tolerance (Chakraborty et al. 2018). As a response to salt stress, the genes of these transporters are up- (Wang et al. 2017) or down-regulated (Chen et al. 2017a) depending on plant type or in relation to the degree of tolerance.

Apart from these elements, saline stress also affects the homeostasis of other ions, such as Ca²⁺, Mg²⁺, or NO₃⁻, and the plant response in this sense is also important to confer salt tolerance. Hence, different studies, mainly in *A. thaliana*, have shown that CAX transporters (H⁺/Ca²⁺ antiporters located in the tonoplast) are precisely modulated under salt stress - with CAX expression being higher or lower in response to salinity, depending on the isoform - to provide tolerance (reviewed in Bickerton and Pittman 2015). Regarding Mg²⁺, Chen et al. (2017b) reported that a Mg transporter (OsMGT1) was involved in enhancing the activity of OsHKT1;5 in the stelar tissues of the root mature zone; specifically, the Mg²⁺ transported by OsMGT1 was the enhancer of this activity. In the tolerance of this stress, OsHKT1;5 plays an essential role, restricting Na⁺ accumulation in the shoots by excluding Na⁺ from the xylem (Cotsaftis et al. 2012). The exact mechanism of its activation is unknown but Mg²⁺ could be required for the stereo-structure of the OsHKT1;5 protein (Chen et al. 2017b). As for NO₃⁻, there is a family of specific transporters (NRT). As indicated above, NO₃⁻ uptake is altered under saline stress; this will involve these transporters, specifically NRT2, whose genes are mainly expressed in the roots (Wang et al. 2003). For example, *NRT2;1* genes are down-regulated under high salinity in different plants, such as *Solanum pennellii* L., *S. esculentum* L., *B. juncea*, and *A. thaliana* (Yao et al. 2008, Goel and Singh 2015, Taochy et al. 2015, Abouelsaad et al. 2016). Also, as NRT2.1 is involved in promoting lateral root (Remans et al. 2006), a reduction in the mRNA content of NRT2.1 could subsequently reduce nitrate uptake under salt stress.

As indicated above, salinity stress is directly related to the water status of plants; specifically, water transport rates are quickly reduced. Therefore, aquaporins play an important role in the response to this stress (Chaumont et al. 2005, Kapilan et al. 2018) and in the tolerance mechanisms (Afzal et al. 2016). Salinity affects the expression of aquaporins genes and produces biochemical changes in these proteins (Martínez-Ballesta et al. 2006); the changes occur to regulate water transport and to try to maintain the water homeostasis. It is difficult to establish a general pattern for the behaviour of aquaporins under saline stress. In some reports, general conclusions appear, such as that in *A. thaliana* there is a 60 to 75% decrease in the abundance of *PIP* and *TIP* transcripts in the medium-to-long term after salt treatment (100 mM NaCl) (Boursiac et al. 2005, Sutka et al. 2011, Afzal et al. 2016). However,

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this effect varies according to the type of aquaporin, the duration and intensity of the stress, and the tolerance of the plant and tissue (Kapilan et al. 2018). In *A. thaliana* seedlings, clear differences in the response to salt stress, regarding aquaporins expression in aerial parts and roots, were revealed (Jang et al. 2004): for example, in aerial parts, after a short exposure to NaCl, *PIP2;2* and *PIP2;3* were up-regulated and *PIP2;6* down-regulated, and in roots *PIP1;1*, *PIP1;2*, *PIP1;3*, and *PIP2;7* were up-regulated and *PIP1;5* down-regulated. Nevertheless, in other work, Pou et al. (2016) showed that *PIP2;7* expression was repressed in *A. thaliana* seedlings under salt stress; the main difference with respect to the previous work mentioned was the age of the plants, which in the first work was 2 weeks and in the second only 8 days. In the same way, Muries et al. (2011) showed that PIP1 and PIP2 were down-regulated in roots of broccoli plants after NaCl treatment for 15 days, although the amount of PIP1 and PIP2 in PM increased. Nonetheless, the water transport capacity of the roots decreased after 15 days of saline stress.

Overexpression of different aquaporins genes is widespread as a way to elucidate the role of these proteins in the response to salinity. In this sense, different works have shown that transgenic plants overexpressing certain aquaporins genes possessed higher salinity tolerance: for example, *MaPIP2;7* and *MaPIP1;2* in banana plants (*Musa acuminata* L.) (Sreedharan et al. 2013, Xu et al. 2020), *PdPIP1;2* in date palm (*Phoenix dactylifera* L.) (Patankar et al. 2019), or *ScPIP1;1* from jojoba (*Simmondsia chinensis* L.) and *MsPIP2;2* from alfalfa (*Medicago sativa* L.) in *A. thaliana* (Li et al. 2019b, Wang et al. 2019).

In addition to these subfamilies of aquaporins, others - such as the NIP subfamily - have been reported to have a role in salt tolerance. For instance, Gao et al. (2010) showed that the expression of *TaNIP* in winter wheat was up-regulated under salinity, while transgenic *A. thaliana* plants overexpressing *TaNIP* had higher salt tolerance. The greater tolerance of these transgenic plants is due to the role of the overexpressed aquaporins in (1) the accumulation of compatible solutes to improve osmotic adjustment, since previous works have shown the role of certain aquaporins in the permeability of the vacuole membrane to small solutes; for example, NtTIPa in tobacco (Gerbeau et al. 1999), (2) the improvement of the antioxidant defence system, to reduce membrane damage, and the activation of immunity signalling pathways, since some aquaporins transport H₂O₂ into the cytoplasm (Boursiac et al. 2008, Tian et al. 2016), and (3) the decline in Na⁺ and K⁺ contents and the maintenance of a balanced K⁺/Na⁺ ratio, which is in consonance with the evidence that certain aquaporins are involved in Na⁺ uptake by roots (Byrt et al. 2017).

Regardless of the effect of salinity on aquaporins in terms of gene expression, this stress causes changes at the protein level and in the function and status of aquaporins. For example, changes in the cytosolic levels of pH and Ca^{2+} trigger modification in the aquaporins. It has been reported that in salt-sensitive plants the cytosolic pH decreases (Kader et al. 2007), causing aquaporin closure due to a pH-sensitive His residue that helps to maintain the aquaporin in a closed state (Törnroth-Horsefield et al. 2006). Also, the reduction in cytosolic Ca^{2+} caused by salt stress seems to be associated with an inhibition of aquaporins (Martínez-Ballesta et al. 2008).

The importance of nutrient and water transport under saline stress for the correct development of plants suggests that there could be a key relationship between some nutrient transporters and aquaporins in the maintenance of the cell homeostasis and in the improvement of salt tolerance in plants. In *A. thaliana* plants that over-expressed a *NIP* aquaporin, produced more salt-tolerant when the expression of *SOS2* (a Na^+ -specific transporter) was suppressed (Gao et al. 2010). Cheng et al. (2004) found that *SOS2* could regulate *CAX1* (a $\text{H}^+/\text{Ca}^{2+}$ antiporter) negatively, so it is possible that *NIP* is involved in Ca^{2+} homeostasis, which is a salt stress response regulating the cytosolic pH (Pittman and Hirschi 2016). Another example of interaction is that of *NRT2;1* (a NO_3^- transporter) and PIP aquaporins in *A. thaliana*. Li et al. (2016) revealed modification of *Lp* mediated by NO_3^- and *NRT2;1*, there being a positive correlation between *Lp* and NO_3^- . The modification of *Lp* is through regulation of PIP aquaporins, which are mainly responsible for *Lp* and thus there is a direct relationship between PIPs and water transport. As we have indicated above, a reduction in *NRT2;1* abundance in roots under salinity has been reported, which could cause a decrease in the content or functionality of PIP aquaporins, since *NRT2;1* triggers a regulation of aquaporins at the transcriptional and post-transcriptional levels (Li et al. 2016). A lower activity of PIP aquaporins would lead to a decrease in *Lp*, which is a plant response to salt stress (Boursiac et al. 2005). The work cited and the existing knowledge about saline stress and the response of plants to it allow us to conclude that the regulation of *Lp* as a response to salinity could depend on the external and internal NO_3^- concentrations and the *NRT2;1* activity, through regulation of PIP aquaporins. This last aspect would be in accordance with previous knowledge on the correlation between nitrogen and water uptake into plant roots (Clarkson 2000).

Effect of low temperature on the interaction of nutrient transporters and aquaporins

Extreme temperature is a major abiotic stress for plants and one of the main environmental factors that hinder plant growth and development and vegetation distribution (Jeon and Kim 2013). Due to climate

changes, weather punctuated by extreme temperature events will affect future agricultural production. In crop production areas, sudden low temperatures nowadays very often produce yield reduction (Lohani et al. 2019). Therefore, it is vital to understand how temperature can affect the transport of nutrients and water by plants, to optimize the production (Fig. 2).

One of the most important nutrients whose transport is affected by low temperatures is nitrogen, for several reasons. Firstly, low temperatures modify the form (NH_4^+ or NO_3^-) in which nitrogen is found in soil. At low temperatures, nitrifying bacteria become inactivated, increasing the $\text{NH}_4^+/\text{NO}_3^-$ ratio, NH_4^+ being less mobile (Laanbroek 1990, Warren 2009). Also, NH_4^+ uptake via the high-affinity transport system (HATS) has been reported to be reduced by low temperatures (Wang et al. 1993). Also, a study in *B. juncea* reported that low temperatures decrease the expression of the main transporters of NO_3^- (*NRT1;1*, *NRT1;2*, *NRT1;4*, *NRT1;5*, *NRT1;8*, *NRT2;1*) and of an NH_4^+ transporter (*AMT2*) (Goel and Singh 2015). A decrease in the temperature can also modify intracellular transport; for example, through the overexpression of the vacuolar transporter *CAX1*, via abscisic acid, which was found to raise the cytosolic free Ca^{2+} concentration (Catalá et al. 2003).

Low temperatures have been reported to affect the uptake of micronutrients via a reduction in the expression of their transporters, as was the case of Mn in *A. thaliana* with the *AtNRAMP1* transporter (Ihnatowicz et al. 2014). However, although there are many studies on micronutrients concentrations in plants grown under low-temperature stress (e.g., a recent study with sweet pepper that showed a decrease in Fe and Zn due to low temperatures; Ropokis et al. 2019), there are no studies about their transporters. Another important aspect affected by low temperatures is the root and leaf hydraulic conductivity, which is directly regulated by aquaporins (Aroca et al. 2005, Ahamed et al. 2012). Thus, many studies revealed a direct correlation among PIP1s and PIP2s abundance, high hydraulic conductance, and low-temperature tolerance (Matsumoto et al. 2009, Lee et al. 2012, Ranganathan et al. 2016). In studies of isoforms, similarities between plants were observed. Thus, when low temperatures were applied to *A. thaliana*, there was down-regulation of root *PIP1;1*, *PIP 1;2*, *PIP1;5*, *PIP2;2*, *PIP2;3*, *PIP2;4*, and *PIP2;7* expression, but *PIP2;5* was up-regulated, while in the aerial part *PIP1;1*, *PIP 1;2*, *PIP1;4*, *PIP1;5*, *PIP2;1*, *PIP2;2*, *PIP2;3*, and *PIP2;4* were down-regulated but *PIP2;5* was up-regulated (Jang et al. 2004). Also, in roots of rice plants, the protein levels of the aquaporins *PIP1;1*, *PIP1;2*, *PIP1;3*, *PIP2;1*, *PIP2;2*, *PIP2;3*, *PIP2;4*, *PIP2;5*, *PIP2;6*, *TIP1;1*, *TIP2;1*, and *TIP2;2* decreased and only *PIP2;5* had an increase in its protein level (Ahamed et al. 2012), indicating an important role of *PIP2;5* in cold-stress acclimation (Ahamed et al. 2012, Lee et al. 2012, Ranganathan et al. 2016).

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There are a number of recent studies about the overexpression of aquaporins to increase the tolerance of low temperatures, such as the over-expression of *TaAQP7*, a PIP2 gene of wheat, in tobacco plants (Huang et al. 2014). Other recent studies have shown how the overexpression of PIP2;7 from *Medicago falcata* L. and banana increased cold tolerance in transgenic tobacco (Zhuo et al. 2016) and banana (Xu et al. 2020), respectively, evincing also the involvement of this aquaporin in the response to cold stress. Finally, studies with rice plants indicate that inhibition of water uptake at low temperatures is not associated directly with the abundance of aquaporins in the root membrane, but with the inhibition of their activity (Murai-Hatano et al. 2008), coming into play not only the decrease/increase in transcription or translation levels, but also a posttranslational regulation of aquaporins (Chaumont and Tyerman 2014).

Nonetheless, the relationship among aquaporins, other nutrient transporters, and abiotic stresses like extreme temperature is poorly understood, notwithstanding the capacity of aquaporins to transport some elements like N (as urea or NH_4^+), B (boric acid), Si (silicic acid), As (arsenite), or H_2O_2 (Bienert et al. 2008; Bienert and Chaumont 2011). Also, a decrease in nutrient transport and the generation of reactive oxygen species (ROS), like H_2O_2 , is a typical response of plants to extreme temperatures (Giri et al. 2017; Hsu and Hsu 2019). There are some recent, pioneering studies of the relationships of aquaporins with other nutrient transporters under low-temperature stress. One of them shows a possible regulation of aquaporins PIP2;1 and PIP2;6 in the response to cold stress, through a calcium-dependent protein kinase, *OsCPK17* (Almadanim et al. 2017); so, an increase in the vacuolar expression of a Ca^{2+} transporter like CAX1 could be related to aquaporins (Catalá et al. 2003). In another example, the tissue B concentration did not change in spite of the decrease in the protein level of BOR1 (a B transporter), while the levels of NIP5;1 remained stable (Giri et al. 2017) - suggesting that the B levels were maintained despite the stress due to the stability of the aquaporin. In a work performed with tomato, it was demonstrated that the P deficit (common in low-temperature situations) can be compensated by a greater concentration of Si (Zhang et al. 2019), which can be transported by some aquaporins in the form of silicic acid (Jian et al. 2006). Other studies related the transport of Si, in the form of silicic acid (Pandey et al. 2016), and Se nutrition (Pandey et al. 2015) to a decrease in the uptake of As through competitive inhibition; Si and Se mitigated its toxicity, because they share the transporter *Lsi1*, an aquaporin (Ma et al. 2007).

Conclusions

The expression of both nutrient transporters and aquaporins genes should be regulated in the response of plants to environmental stress - such as nutrient deficiency, drought, salt stress, and low temperatures - so that they can cope with the stress. Therefore, although the interactions of both type of transporters deserve more investigation, attention should be paid to that the first signal which triggers the rest of the responses must be hydric. In this way, the involvement of aquaporins to the initial stress sensing needs to be taken into account to understand the integrated physiological responses.

The results summarized in this review highlight some general responses. For instance, a deficiency of each macronutrient induces its own transporters expression but reduces the expression of plasma membrane aquaporins. In other way, deficiencies of micronutrients induce their tonoplast transporters for remobilization from the vacuole and also reduce aquaporins presence. Also, the fact that some aquaporins have been reported to transport mineral nutrients - such as NH_4^+ , B, and urea - to ensure nutrient availability under abiotic stress, should be taken into account.

While the response of plants to drought and salinity depends on the specific mechanism and degree of tolerance of each species, for drought we can generalize that higher expression of transporters and aquaporins is observed in tolerant plants (Fig. 3). However, the complexity of salinity in all facets of the stress suggests several transport processes as key to the tolerance, decreasing Na uptake but increasing K and N uptake. Also, under saline stress, some aquaporins have been demonstrated to be important in water transport, for the correct development of plants (Fig. 4). Therefore, the link between nutrient transporters and aquaporins in the maintenance of the cell homeostasis should be studied in each particular case. Under low-temperature stress, a general decrease in the expression of aquaporins has been found but the fact that *PIP2;5* or *PIP2;7* was increased in all the studies assigns them a key role in the response.

Understanding the interactions between aquaporins and mineral nutrients under environmental stress conditions will enable us to modulate the water and mineral nutrient uptake and assimilation to improve the water and nutrient use efficiency in plants. Therefore, much more research is needed to clarify the signaling and regulation of aquaporins and nutrient transport in tandem since only the modification of their joint response will improve tolerance.

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Figure legends

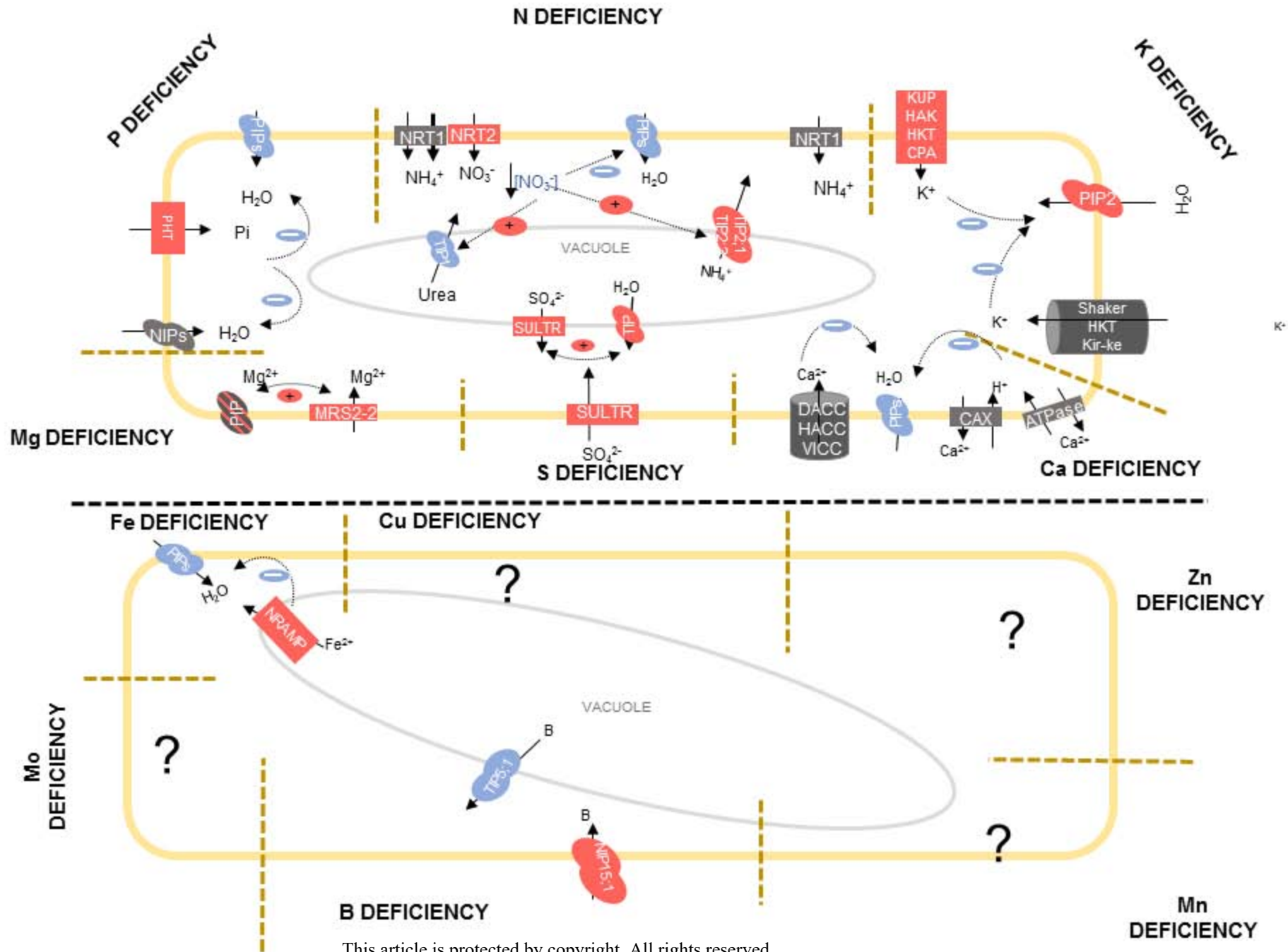
Fig. 1. Scheme of the interregulation of aquaporins and nutrient transporters under nutrients deficiency. Plasma membrane aquaporins PIPs reduced the expressions in response to N deprivation in coordination to NRT transporters. Several TIPs, participate in NH₄⁺ an urea transport under N deficiency. Low-K conditions reduced expression of PIP2. A coordinated response to Ca deficiency reducing aquaporin and Ca²⁺ transporters gene expression is observed. Under S starvation some SULTR transporters exhibited the same expression patterns as some TIPs. Under Mg deficiency, some MRS transporter has the same expression patterns as some PIPs. Low P availability showed a decrease in the gene expression of PHT, PIPs and NIPs. Under Fe deficiency, the inhibition of NRAMP transporters showed is related to some PIPs abundance. Under B deficiency some NIPs and TIPs participate in B transport. The interregulation of Cu, Zn, Mn and Mo transporters and aquaporins under Cu, Zn, Mn and Mo deficiency is unknown.

Fig. 2. Scheme of the interregulation of aquaporins and nutrient transporters under cold stress in order

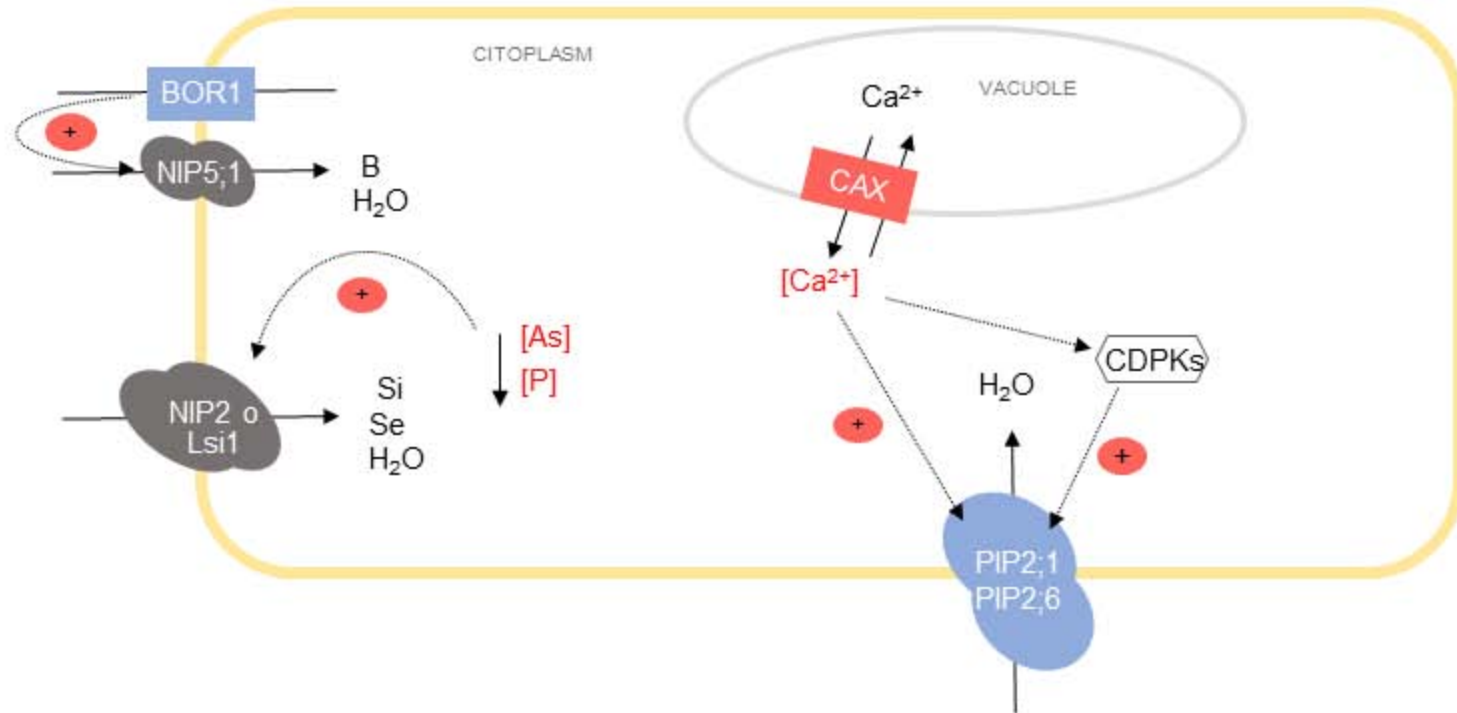
to provide higher tolerance. The regulation of aquaporins PIP2;1 and PIP2;6 in the response to cold stress, through a calcium-dependent protein kinase, OsCPK17 is related to the vacuolar expression of a Ca^{2+} transporter like CAX1. The decrease in the protein level of BOR1 (a B transporter) is replaced by the aquaporin NIP5;1 for maintaining the B levels. The P deficit and low As concentrations that appeared under cold stress can be compensated by higher concentrations of Si and Se transported through the aquaporin NIP2 or Lsi1.

Fig. 3. Scheme of the interregulation of aquaporins and nutrient transporters under drought stress in order to provide higher tolerance. NO_3^- and NH_4^+ are signaling factors for PIP expression. DUR3, high-affinity urea transporter, and PIP, NIP, and TIP identified as low-affinity transporters, up-regulate TIP. Pi transporter is related positively with PIP. Transmembrane channels for K^+ and PIPs are coordinately regulated. Ca^{2+} transporters regulate positively PIPs, TIPs, and NIPs isoforms.

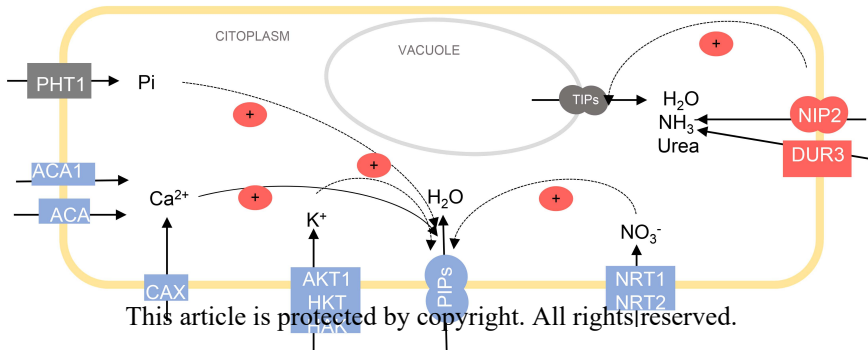
Fig. 4. Scheme of the interregulation of aquaporins and nutrient transporters under salinity stress in order to provide higher tolerance. Over-expressed a *NIP* aquaporin, and suppression of *SOS2* provide higher tolerance. *SOS2* regulate negatively CAX1 reducing cytosolic Ca^{2+} and regulating negatively PIPs aquaporins. But NIPs could reduce cytosolic regulating positively PIPs. Interaction of NRT2;1 and PIP aquaporins is positively correlated.



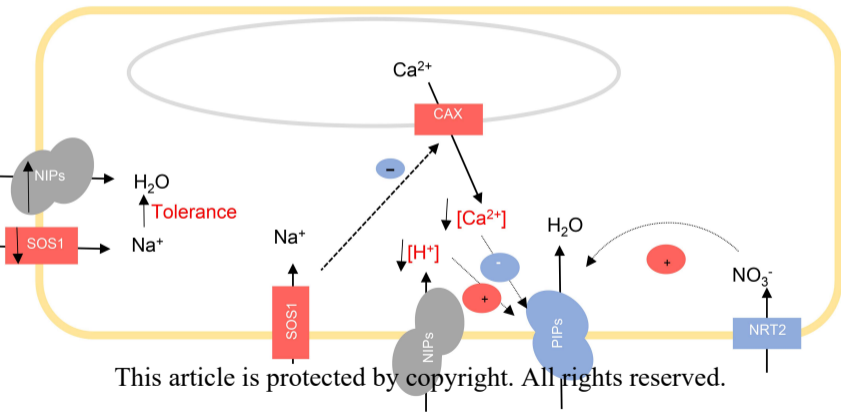
COLD STRESS



DROUGHT STRESS



SALINITY STRESS



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