Transcriptional Regulation of Al Tolerance in Plants

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Abstract Great progresses have been made in understating of molecular mechanisms of Al tolerance in plants during last decade. A number of Al-tolerance genes have been functionally characterized, especially in rice and Arabidopsis. Several transcription factors including a C2H2 zinc finger-type ART1/STOP1 have been identified, but only a few downstream genes regulated by ART1 and STOP1 are similar, indicating different regulation mechanism of Al tolerance in rice and Arabidopsis. Transcriptional regulation of the Al-tolerance genes also differs with plant species and genes. Four different patterns have been reported including increase of gene copy number in the genome, insertion of transposon-like sequences, tandem repeat sequences, and increase of cis-acting element of transcription factor in the promoter region. All these alternations in the genome enhance the expression of Al-tolerance genes.

1 Al-Tolerance Genes

Plants have developed strategies to cope with Al toxicity. During last decade, great progresses have been made in understanding molecular mechanisms of aluminum (Al) tolerance in plants, especially in Arabidopsis and rice (Delhaize et al. 2012; Ma et al. 2014; Kochian et al. 2015). Since the first Al-tolerance gene, *ALMT1* (Aluminum-activated malate transporter), which is responsible for the Al-induced malate secretion, was identified in wheat (Sasaki et al. 2004), a number of Al-tolerance genes have been identified in different plant species (Figs. 1 and 2). For example, homologs of *ALMT1* have been identified in Arabidopsis (Hoekenga et al. 2006), oilseed rape (Ligaba et al. 2006), rye (Collins et al. 2008), soybean (Liang et al. 2013), yorkshire fog (Chen et al. 2013) in addition to wheat. Genes responsible for Al-induced secretion of citrate, *AACT1/MATE/FRDL* (Aluminum-activated citrate transporter 1/Multidrug and toxic compound extrusion/Ferric

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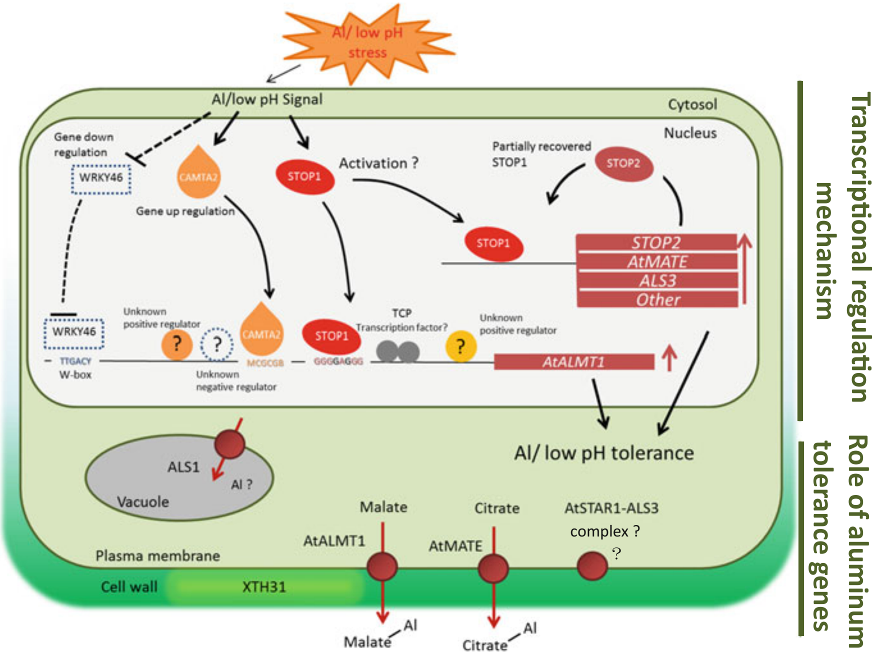

Fig. 1 Aluminum tolerance genes and their transcriptional regulation mechanisms in Arabidopsis. *AtALMT1*, *ATMATE*, and *ALS3* are involved in Al-induced secretion of malate, citrate, and redistribution of Al from sensitive region, respectively. They are induced by low pH and Al and regulated by the transcription factor, STOP1. By contrast, *AtSTAR1* and *ALS1* do not respond to low pH and Al, and their exact role is unknown. On the other hand, XTH31 is involved in cell wall modification. In addition to STOP1, other transcription factors for Al tolerance have also been identified including STOP2, WRKY46 as a negative regulator, and CAMTA2 as an activator. For details, refer to the text

reductase defective3 like), have also been identified in barley (*HvAACT1*) (Furukawa et al. 2007), sorghum (*SbMATE*) (Magalhaes et al. 2007), rice (*OsFRDL4*) (Yokosho et al. 2011), *Arabidopsis* (Liu et al. 2009), rye (Yokosho et al. 2010), wheat (Ryan et al. 2009), maize (Maron et al. 2010), river red gum (Sawaki et al. 2013), and cabbage (Wu et al. 2014).

In addition to these genes related to organic acid anion secretion, several important genes involved in the external and internal detoxification of Al have also been identified. In rice, a highly Al-tolerant species, seven genes have been functionally demonstrated to be required for high Al tolerance in rice (Fig. 2). *STAR1* and *STAR2* (Sensitive to Al rhizotoxicity 1 and 2) encode an ATP-binding domain and a transmembrane domain, respectively, of a bacterial-type ATP binding cassette (ABC) transporter. The complex of STAR1 and STAR2 transports UDP-glucose (Huang et al. 2009), which is used for cell wall modification, resulting in Al fixation in the root cell wall. *Nrat1* (Nramp aluminum transporter 1) encodes an Al transporter localized at the plasma membrane, which transports trivalent Al

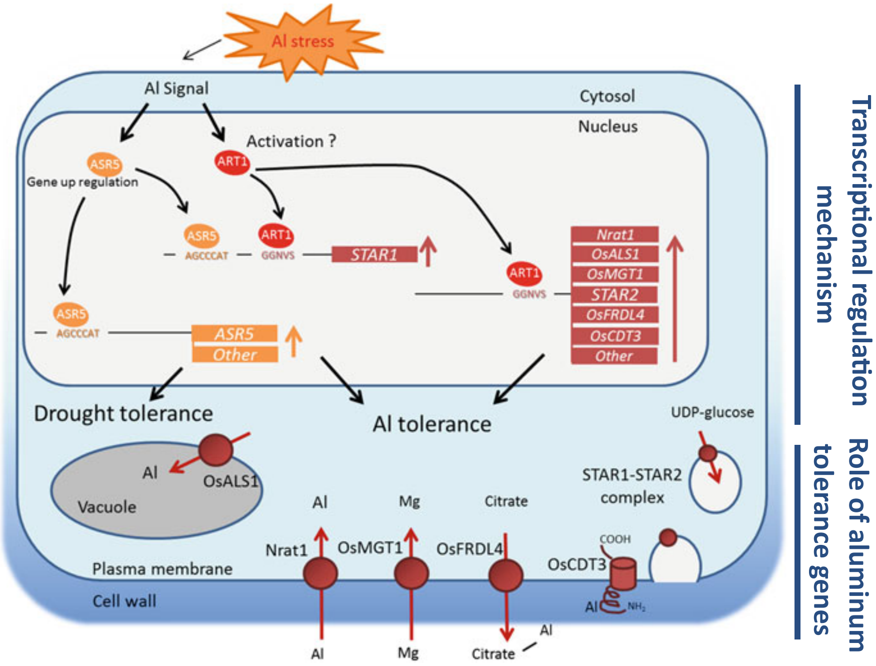

Fig. 2 Aluminum tolerance genes and their transcriptional regulation mechanisms in rice. Al-tolerance genes including *STAR1*, *STAR2*, *Nrat1*, *OsALS1*, *OsFRDL4*, *OsMGT1*, and *OsCDT3* function in Al detoxification at different cellular levels. All of them are regulated by the transcription factor, ART1. ASR5 is another transcription factor, which regulates STAR1 expression. For details, refer to the text

into the cells (Xia et al. 2010) for subsequent sequestration of Al into the vacuoles by OsALS1 (Aluminum sensitive 1). OsALS1 is a half-size ABC transporter and localized to tonoplast of root cells (Huang et al. 2012). On the other hand, a plasma membrane-localized Mg transporter, OsMGT1 (Magnesium transporter 1), also plays an important role in Al tolerance by increasing Mg uptake (Chen et al. 2012). Recently, *OsCDT3*, which encodes a small peptide rich in cysteine, was also demonstrated to be involved in Al tolerance in rice (Xia et al. 2013). It is anchored to the plasma membrane and confers Al probably by binding Al, therefore stopping entry of Al into the root cells. All these genes are rapidly and specifically induced by Al (Huang et al. 2009, 2012; Xia et al. 2010, 2013; Yokosho et al. 2011; Chen et al. 2012). The proteins encoded by these genes are similarly localized at all root cells. Knockout of either gene results in decreased Al tolerance although the contribution to Al tolerance differs with genes.

In Arabidopsis, in addition to *AtALMT1* and *AtMATE*, two other genes (*ALS1* and *ALS3*) confer Al tolerance (Fig. 1). *ALS3* in Arabidopsis is a homolog of rice *STAR2*, encoding a half-size ATP-binding cassette (ABC) transporter (Larsen et al. 2005). It may form a complex with AtSTAR1 to confer Al tolerance (Huang et al. 2010), which is probably involved in the redistribution process of

Al from sensitive region (Larsen et al. 2005). ALS1, a homolog of rice OsALS1, is a tonoplast-localized ABC transporter in Arabidopsis (Larsen et al. 2007). It may be involved in internal detoxification of Al by sequestering Al into the vacuoles like rice OsALS1 (Larsen et al. 2007; Huang et al. 2012).

Recently, genes involved in xyloglucan metabolism in the cell wall are also reported to be involved in Al tolerance in Arabidopsis (Fig. 1; Zhu et al. 2012, 2014). For example, knockout of *XTH31* resulted in an increased Al tolerance (Zhu et al. 2012). *XTH31* probably encodes xyloglucan endotransglucosylase/hydrolases (XTHs), which cleaves and rejoins hemicellulosic xyloglucan polymers during cell expansion. It seems that reduction of production of cleaved xyloglucans in the cell wall increases Al tolerance.

2 Transcription Factors for Al Tolerance

Several transcription factors controlling Al tolerance have been reported. STOP1 (Sensitive to proton rhizotoxicity 1), a C2H2-type zinc finger transcription factor, was identified from an Arabidopsis mutant sensitive to low pH and Al (Fig. 1; Iuchi et al. 2007). Microarray analyses of *stop1* mutant revealed that STOP1 regulates 43 genes including *AtALMT1*, *AtMATE*, and *ALS3* (Sawaki et al. 2009). The expression of *STOP1* is not induced by low pH and Al, although regulated downstream genes rapidly respond to low pH and Al (Sawaki et al. 2009; Liu et al. 2009), suggesting that posttranslational process is required.

Recently, a STOP1 homolog in Arabidopsis, STOP2, was identified (Kobayashi et al. 2014). STOP1 and STOP2 shared 40 % identity at amino acids level (Kobayashi et al. 2014). The expression level of *STOP2* is much lower than that of *STOP1*, but the expression of *STOP2* is regulated by STOP1 (Fig. 1; Sawaki et al. 2009; Kobayashi et al. 2014). Over-expression of *STOP2* in *stop1* mutant resulted in enhanced tolerance to low pH (Kobayashi et al. 2014). Introduction of *STOP2* in *stop1* mutant under the control of *STOP1* promoter also complemented the expression level of *ALS3* and *AtMATE* (Kobayashi et al. 2014). It seems that STOP2 is a minor isoform, but it can activate transcription of some genes regulated by STOP1 (Fig. 1; Kobayashi et al. 2014).

ART1 (Al resistance transcription factor 1) is a transcription factor for Al tolerance identified in rice (Fig. 2; Yamaji et al. 2009). Similar to STOP1 in Arabidopsis, ART1 is also a C2H2-type zinc finger transcription factor in rice. However, different from STOP1, ART1 does not confer low pH (Yamaji et al. 2009). ART1 regulates the expression of at least 31 genes (Yamaji et al. 2009). Among these genes, seven genes, including *STAR1*, *STAR2*, *Nrat1*, *OsALS1*, *OsFRDL4*, *OsMGT1*, *OsCDT3*, have been functionally characterized as described above (Fig. 2). Comparison of downstream genes showed that only two genes (*AtMATE*/*OsFRDL4*, *ALS3*/*STAR2*) are common between STOP1- and ART1-regulated genes, indicating different Al tolerance regulation mechanisms between Arabidopsis and rice. The core *cis*-acting element of ART1 is [GGN(T/g/a/C)V(C/A/g)S(C/G)], which can be found in the promoter region of 29 genes among 31 ART1-regulated genes (Fig. 2; Tsutsui et al. 2011). Similar to STOP1, the expression of *ART1* is also not induced by Al, but the mechanism underlying activation of ART1 is unknown.

The homologs of *STOP1*/*ART1* homologs were also found in other plant species including monocots, dicots, woody plants, and a bryophyte (Ohyama et al. 2013; Garcia-Oliveira et al. 2013; Chen et al. 2013). Knockout or knockdown of *STOP1*/*ART1* homolog showed Al sensitive phenotype in tobacco and *Moss* (Ohyama et al. 2013). Interestingly, TaSTOP1 in wheat is involved in Al tolerance, but not through regulating *TaALMT1* (Garcia-Oliveira et al. 2013), since *TaALMT1* expression is not induced by Al.

Recently, WRKY46, a member of the WRKY domain-containing family of transcription factors, was identified as a negative regulator of expression of *AtALMT1*, a key Al-tolerance gene in Arabidopsis (Ding et al. 2013). It could be bound to the *AtALMT1* promoter region as a repressor (Fig. 1; Ding et al. 2013), because there are several putative W-box domains in the *AtALMT1* promoter region. Knockout of *AtWRKY46* resulted in increased expression of *AtALMT1*, root malate secretion, and Al tolerance (Fig. 1; Ding et al. 2013). More recently, a study by Tokizawa et al. (2015) showed that CAMTA2 (Calmodulin binding transcription activator 2) may function as an activator of *AtALMT1* expression (Fig. 1).

ASR5 (Abscisic acid, stress and ripening 5) is another transcription factor for Al tolerance identified in rice (Fig. 2; Arenhart et al. 2013, 2014). ASR5 is localized in the chloroplast, cytoplasm, and nucleus (Arenhart et al. 2013). Its transcript levels increase in response to Al in the roots and shoots, and ASR5-silenced plants are extremely sensitive to Al (Arenhart et al. 2013). ASR5 is the Al-activated factor that binds to the STAR1 promoter to enhance its expression (Fig. 2). Among ASR5-regulated genes, there are three genes (*STAR1*, *Nrat1*, *OsFRDL4*), which are regulated by ART1 (Arenhart et al. 2014). The requirement of both ASR5 and ART1 for Al-induced STAR1 expression suggests that ASR5 and ART1 may interact with each other directly and function cooperatively although further work is required.

Different from STOP1 and ART1, WRKY46 and ASR5 are also involved in tolerance to other abiotic stresses.

3 Transcriptional Regulation of Al-Tolerance Genes

Recent several studies have shown that some Al-tolerance genes undergo transcription regulation although unknown translational and posttranslational regulation may also be involved. There are four different patterns for the transcriptional regulation depending on plant species (Fig. 3). In pattern I, the expression of Al-tolerance genes is enhanced through increasing gene copy number in the genome. This is seen in *ScALMT1* in rye and *ZmMATE1* in maize. Rye (*Secale cereale* L.), one of the most

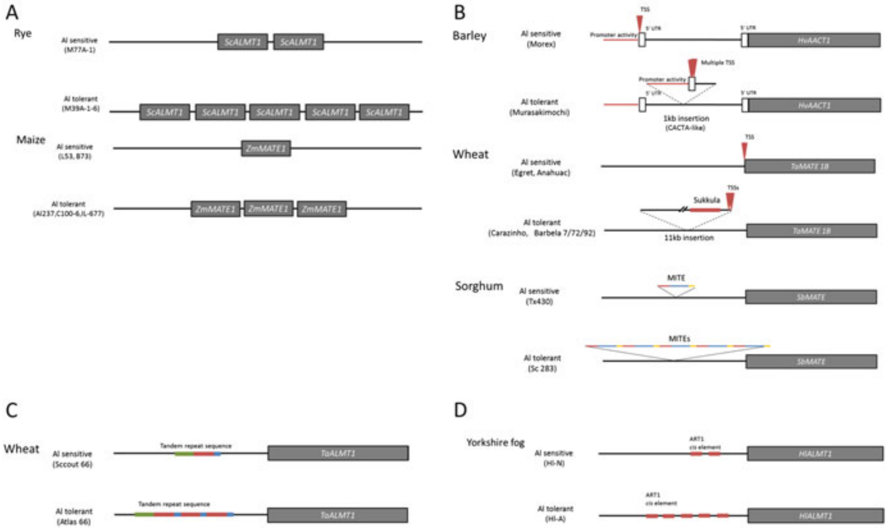

Fig. 3 Transcriptional regulation of Al-tolerance genes involved in Al-induced organic acid anion secretion in different plant species. (**A**) Pattern I: Increase of gene copy number in the genome. The copy number of *ScALMT1* in rye and *ZmMATE1* in maize are more in the Al-tolerant cultivars than in the Al-sensitive cultivars. (**B**) Pattern II: Transposon-like insertion in the genome. A transposon-like sequence is inserted upstream of *HvAACT1* in barley, *TaMATE1B* in wheat, and *SbMATE* in sorghum, which enhance the expression of these genes. (**C**) Pattern III: Tandem repeat sequences in the promoter region. Tandem repeat sequences are located at upstream of *TaALMT1* in wheat and increase its expression. (**D**) Pattern IV: Increase of ART1 *cis*-acting elements in the promoter region. The number of *cis*-acting element of ART1 is increased in the promoter region of *HlALMT1* in Al-tolerant accession of Yorkshire Fog (*H. lanatus*), resulting in increased expression of *HlALMT1*. Modified according to Delhaize et al. (2012), Ma et al. (2014)

Al-tolerant cereal crops, secretes both malate and citrate from the roots in response to Al (Li et al. 2000). The expression level of *ScALMT1* in the Al-tolerance cultivar is higher than that in the Al-sensitive cultivar, which is derived from the difference in the genomic copy number of *ScALMT1* (Fig. 3A; Collins et al. 2008). Five *ScALMT1* genes are clustered together on chromosome 7R in the tolerance cultivar, of which two are highly expressed in the root tip. On the other hand, only two copies are found in the sensitive cultivar, of which only one copy is highly expressed in the root tip (Collins et al. 2008). In maize, Al-tolerant cultivars have three functional copies of *ZmMATE1* in the genome, which are identical and part of a tandem triplication (Maron et al. 2013). This copy number variation is associated with both gene expression of *ZmMATE1* and Al tolerance (Fig. 3A). Interestingly, maize cultivars carrying the three-copy allele share the same geographical origin in acid-soil regions of the South American tropics, suggesting that copy number increase is an adaptation to acid soil.

By contrast, in pattern II, the expression level of Al-tolerance genes is enhanced through an insertion of transposon-like elements in the upstream region of ORF (Fig. 3B), which can be found in barley, wheat, and sorghum. In barley, the higher expression of *HvAACT1* in the root tips of Al-tolerant cultivars is associated with a 1-kb transposon insertion (CACTA-like transposon) in the upstream of the ORF region (Fujii et al. 2012). This insertion acts as a promoter to enhance the expression level of *HvAACT1* (Fig. 3B). Furthermore, this insertion also alters the expression location of *HvAACT1* from mature root region to the root tips, the site of Al toxicity (Fujii et al. 2012). Interestingly, *HvAACT1* at the mature root region is originally involved in the translocation of Fe from the roots to the shoots, which have similar role as OsFRDL1 in rice (Yokosho et al. 2009). The 1-kb insertion was only found in barley accessions cultivated in Japan, China, and Korea, where acid soils distribute.

In wheat, a Sukkula-like transposable element (11 kb) was found to be inserted at the promoter region of *TaMATE* gene in several Brazilian wheat cultivars, which secrete citrate constitutively in response to Al (Tovkach et al. 2013). This insertion also enhances the expression of the *TaMATE1* gene (Fig. 3B; Tovkach et al. 2013). Furthermore, this insertion was also found in other Al-tolerance bread wheat cultivars (Garcia-Oliveira et al. 2014).

In sorghum, tourist-like miniature inverted repeat transposable elements (MITEs) occur at upstream of the *SbMATE* gene, and the number of these repeats is broadly correlated with the level of *SbMATE* expression (Fig. 3B; Magalhaes et al. 2007). Recent study showed that introduction of *SbMATE* into different background resulted in different expression level, suggesting that *SbMATE* expression is regulated at multiple levels (Melo et al. 2013). It seems that both *cis*- and *trans*-acting elements are involved in regulating *SbMATE* expression.

In pattern III as seen in wheat, the expression level of *TaALMT1* is controlled by tandem repeated elements in the promoter region (Fig. 3C; Sasaki et al. 2006; Ryan et al. 2010). The expression level of *TaALMT1* is not induced by Al, but the expression level is higher in Al-tolerant cultivars than Al-sensitive cultivars (Sasaki et al. 2006). The constitutively greater expression of *TaALMT1* in Al-tolerant genotypes has a series of *cis* mutations in the promoter (Ryan et al. 2010). Among these, alleles with duplications and triplications are associated with enhanced expression of *TaALMT1*, increased malate efflux, and greater Al tolerance compared with alleles that lack these repeats (Ryan et al. 2010).

In pattern IV, expression level is associated with the number of *cis*-acting element of transcription factor, ART1. In an accession of yorkshire fog (*Holcus lanatus*) grown on highly acidic soils, the expression of *HlALMT1* was twice as high as in the accession grown on neutral soil (Chen et al. 2013). The number of *cis*-acting elements of *HlART1* in the promoter region of *HlALMT1* was more in the accession grown on acid soil due to nucleotide substitution (Fig. 3D), indicating that the adaptation of *H. lanatus* to acidic soils may be achieved by increasing number of *cis*-acting elements for *ART1* in the promoter region of the *HlALMT1* gene, enhancing the expression of *HlALMT1* and the secretion of malate.

Genotypic difference in the expression of *Nrat1* was also found in rice (Li et al. 2014; Xia et al. 2014). Promotor analysis detected five unique SNPs, which are not related to the *cis*-acting element of ART1. It remains to examine whether these SNPs are involved in the transcriptional regulation of *Nrat1* in rice.

There is also a positive correlation between *OsFRDL4* expression level and the amount of citrate secretion in rice cultivars that are differing in Al tolerance (Yokosho et al. 2011), but the mechanism for regulating the expression of *OsFRDL4* is also unknown.

References

Arenhart RA, Lima JC, Pedron M, Carvalho FE, Silveira JA, Rosa SB, Caverzan A, Andrade CM, Schünemann M, Margis R, Margis-Pinheiro M (2013) Involvement of *ASR* genes in aluminum tolerance mechanisms in rice. Plant Cell Environ 36:52–67

Arenhart RA, Bai Y, Valter de Oliveira LF, Neto LB, Schunemann M, Maraschin Fdos S, Mariath J, Silverio A, Sachetto-Martins G, Margis R, Wang ZY, Margis-Pinheiro M (2014) New insights into aluminum tolerance in rice: the ASR5 protein binds the *STAR1* promoter and other aluminum-responsive genes. Mol Plant 7:709–721

Chen ZC, Yamaji N, Motoyama R, Nagamura Y, Ma JF (2012) Up-regulation of a magnesium transporter gene *OsMGT1* is required for conferring aluminum tolerance in rice. Plant Physiol 159:1624–1633

Chen ZC, Yokosho K, Kashino M, Zhao FJ, Yamaji N, Ma JF (2013) Adaptation to acidic soil is achieved by increased *cis*-acting element numbers regulating *ALMT1* expression in *Holcus lanatus*. Plant J 76:10–23

Collins NC, Shirley NJ, Saeed M, Pallotta M, Gustafson JP (2008) An *ALMT1* gene cluster controlling aluminum tolerance at the *Alt4* locus of rye (*Secale cereale L.*). Genetics 179: 669–682

Delhaize E, Ma JF, Ryan PR (2012) Transcriptional regulation of aluminium tolerance genes. Trends Plant Sci 17:341–348

Ding ZJ, Yan JY, Xu XY, Li GX, Zheng SJ (2013) WRKY46 functions as a transcriptional repressor of *ALMT1*, regulating aluminum-induced malate secretion in Arabidopsis. Plant J 76:825–835

Fujii M, Yokosho K, Yamaji N, Saisho D, Yamane M, Takahashi H, Sato K, Nakazono M, Ma JF (2012) Acquisition of aluminium tolerance by modification of a single gene in barley. Nat Commun 3:713

Furukawa J, Yamaji N, Wang H, Mitani N, Murata Y, Sato K, Katsuhara M, Takeda K, Ma JF (2007) An aluminum activated citrate transporter in barley. Plant Cell Physiol 48:1081–1091

Garcia-Oliveira AL, Benito C, Prieto P, Menezes RA, Rodrigues-Pousada C, Guedes-Pinto H, Martins-Lopes P (2013) Molecular characterization of TaSTOP1 homoeologues and their response to aluminium and proton (H^+) toxicity in bread wheat (*Triticum aestivum* L.). BMC Plant Biol 13:134

Garcia-Oliveira AL, Martins-Lopes P, Tolrá R, Poschenrieder C, Tarquis M, Guedes-Pinto H, Benito C (2014) Molecular characterization of the citrate transporter gene *TaMATE1* and expression analysis of upstream genes involved in organic acid transport under Al stress in bread wheat (*Triticum aestivum*). Physiol Plant 152:441–452

Hoekenga OA, Maron LG, Cancado GMA, Piñeros MA, Shaff J, Kobayashi Y, Ryan PR, Dong B, Delhaize E, Sasaki T (2006) *AtALMT1*, which encodes a malate transporter, is identified as one of several genes critical for aluminum tolerance in Arabidopsis. Proc Natl Acad Sci U S A 103:9734–9743

Huang CF, Yamaji N, Mitani N, Yano M, Nagamura Y, Ma JF (2009) A bacterial-type ABC transporter is involved in aluminum tolerance in rice. Plant Cell 21:655–667

Huang CF, Yamaji N, Ma JF (2010) Knockout of a bacterial-type ATP-binding cassette transporter gene, *AtSTAR1*, results in increased aluminum sensitivity in Arabidopsis. Plant Physiol 153: 1669–1677

Huang CF, Yamaji N, Chen ZC, Ma JF (2012) A tonoplast-localized half-size ABC transporter is required for internal detoxification of aluminum in rice. Plant J 69:857–867

Iuchi S, Koyama H, Iuchi A, Kobayashi Y, Kitabayashi S, Kobayashi Y, Ikka T, Hirayama T, Shinozaki K, Kobayashi M (2007) Zinc finger protein STOP1 is critical for proton tolerance in Arabidopsis and coregulates a key gene in aluminum tolerance. Proc Natl Acad Sci U S A 104: 9900–9905

Kobayashi Y, Ohyama Y, Kobayashi Y, Ito H, Iuchi S, Fujita M, Zhao CR, Tanveer T, Ganesan M, Kobayashi M, Koyama H (2014) STOP2 activates transcription of several genes for Al- and low pH-tolerance that are regulated by STOP1 in Arabidopsis. Mol Plant 7:311–322

Kochian LV, Piñeros MA, Liu J, Magalhaes JV (2015) Plant adaptation to acid soils: the molecular basis for crop aluminum resistance. Annu Rev Plant Biol 66:23.1–23.28

Larsen PB, Geisler MJ, Jones CA, Williams KM, Cancel JD (2005) *ALS3* encodes a phloem-localized ABC transporter-like protein that is required for aluminum tolerance in Arabidopsis. Plant J 41:353–363

Larsen PB, Cancel J, Rounds M, Ochoa V (2007) Arabidopsis *ALS1* encodes a root tip and stele localized half type ABC transporter required for root growth in an aluminum toxic environment. Planta 225:1447–1458

Li XF, Ma JF, Matsumoto H (2000) Pattern of aluminum-induced secretion of organic acids differs between rye and wheat. Plant Physiol 123:1537–1543

Li JY, Liu J, Dong D, Jia X, McCouch SR, Kochian LV (2014) Natural variation underlies alterations in Nramp aluminum transporter (*Nrat1*) expression and function that play a key role in rice aluminum tolerance. Proc Natl Acad Sci U S A 111:6503–6508

Liang C, Piñeros M, Tian J, Yao Z, Sun L, Liu J, Shaff J, Coluccio A, Kochian LV, Liao H (2013) Low pH, aluminum and phosphorus coordinately regulate malate exudation through *GmALMT1* to improve soybean adaptation to acid soils. Plant Physiol 161:1347–1361

Ligaba A, Katsuhara M, Ryan PR, Shibasaka M, Matsumoto H (2006) The *BnALMT1* and *BnALMT2* genes from rape encode aluminum-activated malate transporters that enhance the aluminum resistance of plant cells. Plant Physiol 142:1294–1303

Liu J, Magalhaes JV, Shaff J, Kochian LV (2009) Aluminum activated citrate and malate transporters from the MATE and ALMT families function independently to confer Arabidopsis aluminum tolerance. Plant J 57:389–399

Ma JF, Chen ZF, Shen RF (2014) Molecular mechanisms of Al tolerance in gramineous plants. Plant Soil 381:1–12

Magalhaes JV, Liu J, Guimarães CT, Lana UG, Alves VM, Wang YH, Schaffert RE, Hoekenga OA, Piñeros MA, Shaff JE, Klein PE, Carneiro NP, Coelho CM, Trick HN, Kochian LV (2007) A gene in the multidrug and toxic compound extrusion (MATE) family confers aluminum tolerance in sorghum. Nat Genet 39:1156–1161

Maron LG, Piñeros MA, Guimarães CT, Magalhaes JV, Pleiman JK, Mao C, Shaff J, Belicuas SN, Kochian LV (2010) Two functionally distinct members of the MATE (multi-drug and toxic compound extrusion) family of transporters potentially underlie two major aluminum tolerance QTLs in maize. Plant J 61:728–740

Maron LG, Guimarães CT, Kirst M, Albert PS, Birchler JA, Bradbury PJ, Buckler ES, Coluccio AE, Danilova TV, Kudrna D, Magalhaes JV, Piñeros MA, Schatz MC, Wing RA, Kochian LV (2013) Aluminum tolerance in maize is associated with higher *MATE1* gene copy number. Proc Natl Acad Sci U S A 110:5241–5246

Melo JO, Lana UG, Piñeros MA, Alves VM, Guimarães CT, Liu J, Zheng Y, Zhong S, Fei Z, Maron LG, Schaffert RE, Kochian LV, Magalhaes JV (2013) In complete transfer of accessory loci influencing *SbMATE* expression underlies genetic background effects for aluminum tolerance in sorghum. Plant J 73:276–288

Ohyama Y, Ito H, Kobayashi Y, Ikka T, Morita A, Kobayashi M, Imaizumi R, Aoki T, Komatsu K, Sakata Y, Iuchi S, Koyama H (2013) Characterization of *AtSTOP1* orthologous genes in tobacco and other plant species. Plant Physiol 162:1937–1946

Ryan PR, Raman H, Gupta S, Horst WJ, Delhaize E (2009) A second mechanism for aluminum resistance in wheat relies on the constitutive efflux of citrate from roots. Plant Physiol 149: 340–351

Ryan PR, Raman H, Gupta S, Sasaki T, Yamamoto Y, Delhaize E (2010) The multiple origins of aluminium resistance in hexaploid wheat include *Aegilops tauschii* and more recent *cis* mutations to *TaALMT1*. Plant J 64:446–455

Sasaki T, Yamamoto Y, Ezaki B, Katsuhara M, Ahn SJ, Ryan PR, Delhaize E, Matsumoto H (2004) A wheat gene encoding an aluminum-activated malate transporter. Plant J 37:645–653

Sasaki T, Ryan PR, Delhaize E, Hebb DM, Ogihara Y, Kawaura K, Noda K, Kojima T, Toyoda A, Matsumoto H, Yamamoto Y (2006) Sequence upstream of the wheat (*Triticum aestivum* L.) *ALMT1* gene and its relationship to aluminum resistance. Plant Cell Physiol 47:1343–1354

Sawaki Y, Iuchi S, Kobayashi Y, Kobayashi Y, Ikka T, Sakurai N, Fujita M, Shinozaki K, Shibata D, Kobayashi M, Koyama H (2009) STOP1 regulates multiple genes which protect *Arabidopsis* from proton and aluminum toxicities. Plant Physiol 150:281–294

Sawaki Y, Kihara-Doi T, Kobayashi Y, Nishikubo N, Kawazu T, Kobayashi Y, Koyama H, Sato S (2013) Characterization of Al-responsive citrate excretion and citrate-transporting MATEs in *Eucalyptus camaldulensis*. Planta 237:979–989

Tokizawa M, Kobayashi M, Saito T, Kobayashi M, Iuchi S, Nomoto M, Tada Y, Yamamoto YY, Koyama H (2015) SENSITIVE TO PROTON RHIZOTOXICITY1, CALMODULIN BINDING TRANSCRIPTION ACTIVATOR2, and other transcription factors are involved in ALUMINUM-ACTIVATED MALATE TRANSPORTER1 expression. Plant Physiol 167: 991–1003

Tovkach A, Ryan PR, Richardson AE, Lewis DC, Rathjen TM, Ramesh S, Tyerman SD, Delhaize E (2013) Transposon-mediated alteration of *TaMATE1B* expression in wheat confers constitutive citrate efflux from root apices. Plant Physiol 161:880–892

Tsutsui T, Yamaji N, Ma JF (2011) Identification of a *cis*-acting element of ART1, a C2H2-type zinc-finger transcription factor for aluminum tolerance in rice. Plant Physiol 156:925–931

Wu X, Li R, Shi J, Wang J, Sun Q, Zhang H, Xing Y, Qi Y, Zhang N, Guo YD (2014) *Brassica oleracea MATE* encodes a citrate transporter and enhances aluminum tolerance in *Arabidopsis thaliana*. Plant Cell Physiol 55:1426–1436

Xia JX, Yamaji N, Kasai T, Ma JF (2010) Plasma membrane-localized transporter for aluminum in rice. Proc Natl Acad Sci U S A 107:18381–18385

Xia JX, Yamaji N, Ma JF (2013) A plasma membrane-localized small peptide is involved in rice aluminum tolerance. Plant J 76:345–355

Xia JX, Yamaji N, Che J, Shen RF, Ma JF (2014) Differential expression of *Nrat1* is responsible for Al-tolerance QTL on chromosome 2 in rice. J Exp Bot 65:4297–4304

Yamaji N, Huang CF, Nagao S, Yano M, Sato Y, Nagamura Y, Ma JF (2009) A zinc finger transcription factor ART1 regulates multiple genes implicated in aluminum tolerance in rice. Plant Cell 21:3339–3349

Yokosho K, Yamaji N, Ueno D, Mitani N, Ma JF (2009) OsFRDL1 is a citrate transporter required for efficient translocation of iron in rice. Plant Physiol 149:297–305

Yokosho K, Yamaji N, Ma JF (2010) Isolation and characterization of two *MATE* genes in rye. Funct Plant Biol 37:296–303

Yokosho K, Yamaji N, Ma JF (2011) An Al-inducible MATE gene is involved in external detoxification of Al in rice. Plant J 69:1061–1069

Zhu XF, Shi YZ, Lei GJ, Fry SC, Zhang BC, Zhou YH, Braam J, Jiang T, Xu XY, Mao CZ, Pan YJ, Yang JL, Wu P, Zheng SJ (2012) *XTH31*, encoding an *in vitro* XEH/XET-active enzyme, regulates aluminum sensitivity by modulating in vivo XET action, cell wall xyloglucan content, and aluminum binding capacity in Arabidopsis. Plant Cell 24:4731–4747

Zhu XF, Wan JX, Sun Y, Shi YZ, Braam J, Li GX, Zheng SJ (2014) Xyloglucan endotransglucosylase-hydrolase17 interacts with xyloglucan endotransglucosylase- hydrolase31 to confer xyloglucan endotransglucosylase action and affect aluminum sensitivity in Arabidopsis. Plant Physiol 165:1566–1574