A curated list of genes that control elemental accumulation in plants.

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Abstract-
Knowledge of the genes and alleles underlying elemental composition will be required to understand how plants interact with their environment. Modern genetics is capable of quickly, and cheaply indicating which regions of DNA are associated with the phenotype in question, but most genes remain poorly annotated, hindering the identification of candidate genes. To help identify candidate genes underlying elemental accumulations, we have created the known ionome gene (KIG) list: a curated collection of genes experimentally shown to change elemental uptake. We have also created an automated computational pipeline to generate lists of KIG orthologs in other plant species using the PhytoMine database. The current version of KIG consists of 96 known genes covering 4 species and 23 elements and their 596 orthologs in 8 species. Most of the genes were identified in the model plant \textit{Arabidopsis thaliana} and transporter coding genes as well as genes that affect the accumulation of iron and zinc are overrepresented in the current list.

Intro-
Understanding the complex relationships that determine plant adaptation will require detailed knowledge of the action of individual genes and the environment. One of the fundamental processes that plants must accomplish is to manage the uptake, distribution and storage of elements from the environment. Many different physiological, chemical, biochemical and cell biology processes are involved in moving elements, implicating thousands of genes in every plant species. Modern genetic techniques have made it easy and inexpensive to identify hundreds to thousands of loci for traits such as the elemental composition (or ionome) of plant tissues. However, moving from loci to genes is still difficult as the number of possible candidates is still extremely large and the ability of researchers to identify a candidate gene by looking at annotations is limited by our current knowledge and inherent biases about what is worth studying (Stoeger et al. 2018).

The most obvious candidates for genes affecting the ionome in a species are orthologs of genes that have been shown to affect elemental accumulation in another species. Indeed, there are multiple examples of orthologs affecting elemental accumulation in distantly related species,
such as Arabidopsis thaliana and rice (Oryza sativa), including Na+ transporters from the HKT family (Ren et al. 2005, Baxter et al. 2010); the heavy metal transporters AtHMA3 and OsHMA3 (Chao et al. 2012, Yan et al. 2016); E3 ubiquitin ligase BRUTUS and OsHRZs that regulate degradation of iron uptake factors (Selote et al. 2015, Hindt et al. 2017, Kobayashi et al. 2013) and the K+ channel AKT1 (Lagarde et al. 1996, Ahmad et al. 2016). To our knowledge, no comprehensive list of genes known to affect elemental accumulation in plants exists. To ameliorate this deficiency, we sought to create a curated list of genes based on peer reviewed literature along with a pipeline to identify orthologs of the genes in any plant species and a method for continuously updating the list. Here we present version 0.1 of the known ionomic gene (KIG) list.

Materials and Methods
Criteria for inclusion in the primary KIG list were as follows: we included functionally characterized genes from the literature that are linked to changes in the ionome. For being considered, the phenotype of knockout or knock-down plants for the specific gene needs to show consistent changes in at least one element in at least one experimental condition. Thus, we have not included genes that are linked to metal tolerance or sensitivity but do not alter the ionome. For double mutants, both genes are listed. In order to identify the KIG genes, we created a Google survey that was distributed to members of the ionomicshub research coordinators, as well as advertising on Twitter and in oral presentations by the authors. We asked submitters to provide the species, gene name (or names where alleles of two genes were required for a phenotype), gene ID(s), tissue(s), element(s) altered and a DOI link for the primary literature support.

Creating the inferred orthologs list: The known-ionomics gene list contains known genes from the primary list and their orthologous genes inferred by inParanoid (v4.1) pairwise species comparisons. The inParanoid files were downloaded from Phytozome for each organism-to-organism combination of species in the primary list, plus Glycine max, Sorghum bicolor, Setaria italica, and S. viridis. Orthologs of the primary genes were labeled as “inferred” genes. If a primary gene was also found as an ortholog to a primary gene in another species, the status was changed to “Primary/Inferred” in both species. It is important to note that only primary genes can infer genes; inferred genes cannot infer other genes. The pipeline for transforming the primary list into the known-ionomics gene list can be found at github.com/baxterlab/KIG.

Gene Enrichment analysis: Overrepresentation analysis was performed on the primary and inferred genes in A. thaliana using the GO Consortium’s web-based GO Enrichment Analysis tool powered by PANTHER (GO ontology database, released 09/08/2018) classification system tool (Ashburner et al. 2000, The Gene Ontology Consortium 2017, Mi et al. 2017). We restricted overrepresentation analysis to A. thaliana because of its dominance in the known ionome list and our lack of confidence in the functional annotation of the other species in the list. An analysis performed by Wimalanathan et al. (2018) found that maize gene annotations in
databases like Gramene and Phytozome lacked GO annotations outside of automatically assigned, electronic annotations (IEA). IEA annotations are not curated and have the least amount of support out of all the evidence codes (Harris et al. 2004). *A. thaliana* annotations come from a variety of evidence types, showing a higher degree of curation compared to maize (Wimalanathan et al. 2018).

We tested both the PANTHER GO-Slim and the GO complete datasets for biological processes, molecular function and cellular component. The enriched terms (fold enrichment > 1 and with a false discovery rate <0.05) were sorted into five specific categories relating to the ionome based annotation terms:

1. Ion homeostasis - terms include homeostasis, stress, detoxification, regulation of an ion
2. Ion transport - terms specifically states transport, export, import or localization of ion(s). Does not include hydrogen ion transport
3. Metal ion chelation - terms relating to phytochelatins, other chemical reactions or pathways of metal chelator synthesis
4. Response to ions - vaguely states a response to ions, but does not have any child annotation terms that offer any more clarification (ie. stress response). Broadly this is referring to any change to the state or activity of cell secretion, expression, movement, or enzyme production (Carbon et al. 2009).
5. Other transport - annotation stating the transfer of anything that is not an ion (glucose, peptides, etc.)

Genes may belong to more than one category, but if they belong to a parent and child term in the same category, they were only counted once.

Results

The current primary list (v0.1) consists of 96 genes from *A. thaliana*, *O. sativa*, *Medicago truncatula*, and *Z. mays* with the majority coming from *A. thaliana* and *O. sativa* (Table 1)(Figure 1).

**Table 1. Primary known ionome genes**

| Species    | GenelID   | GeneName   | Elements   | Tissue  | Citation(s)                     |
|------------|-----------|------------|------------|---------|---------------------------------|
| A.thaliana | AT1G01580 | FRO2       | Fe         | Root    | (Robinson et al. 1999)          |
| A.thaliana | AT1G18910 | BTSL2      | Fe,Mn,Zn   | Leaf    | (Hindt et al. 2017)             |
| A.thaliana | AT1G20110 | FYVE1      | Fe,Zn,Co,Mn| Root    | (Barberon et al. 2014)          |
| A.thaliana | AT1G30450 | CCC        | Ca,K,Na,S  | seeds   | (McDowell et al. 2013)          |
| A.thaliana | AT1G32450 | AINRT1.5 / AINPF7.3 | K, NO3- | Shoots, Roots | (Li et al. 2017) |
| A.thaliana | AT1G36370 | AtMSA1     | S, Se      | Shoots  | (Huang et al. 2016)             |
| A.thaliana | AT1G56160 | myb72      | Fe,Cd,Zn,Co,Mo | Leaf | (Palmer et al. 2013)            |
| A.thaliana | AT1G56430 | NAS4       | Fe,Cd,Co,Mo| Leaf    | 10.1371/journal.pgen.1003953   |
| A.thaliana | AT1G62180 | AtAPR2     | S, Se      | Shoots  | (Loudet et al. 2007), (Chao et al. 2014) |
| A.thaliana | AT1G71200 | AtCITF1    | Cu         | Shoots, Anthers | (Yan et al. 2017) |
| A.thaliana | AT1G74770 | BTSL1 | Fe,Mn,Zn | Leaf | (Hindt et al. 2017) |
| A.thaliana | AT1G80830 | AtNRAMP1 | Mn | Shoots,roots | (Cailliatte et al. 2010) |
| A.thaliana | AT2G01770 | VIT1 | Fe | Seed | (Kim et al. 2006) |
| A.thaliana | AT2G13540 | ABH1 | S | seeds | (McDowell et al. 2013) |
| A.thaliana | AT2G16770 | AtbZIP23 | Zn | Shoots, roots | (Assunção et al. 2010) |
| A.thaliana | AT2G19110 | AlHMA4 | Zn | Shoots, seeds | (Hussain et al. 2004) (Olsen et al. 2016) |
| A.thaliana | AT2G21045 | AtHAC1 | As | Shoots | (Chao et al. 2014) |
| A.thaliana | AT2G23150 | AtNRAMP4 | Fe,Mn,Zn | Shoots | (Lanquar et al. 2010) |
| A.thaliana | AT2G25680 | MOT1 | Ca,Mn,Zn,Na,S,Se,Mo | Leaf | (Baxter et al. 2009) |
| A.thaliana | AT2G28670 | ESB1 | Mn | Shoots, Roots | (Peiter et al. 2007) |
| A.thaliana | AT2G39450 | AtMTP11 | Mn | Shoots, Roots | (Gobert et al. 2006) |
| A.thaliana | AT2G46430 | CNGC3 | K | Leaf | (Desbrosses-Fonrouge et al. 2005) |
| A.thaliana | AT2G46800 | AtMTP1 | Zn | Shoots | (Chao et al. 2011) |
| A.thaliana | AT3G06060 | TSC10a | Na,K,Rb,Mg,Fe,Mo | Leaf | (Lindsay and Maathuis 2016) (Isayenkov and Maathuis 2008) |
| A.thaliana | AT3G06100 | NIP7 | As | NA | (Palmer et al. 2013) |
| A.thaliana | AT3G12820 | myb10 | Fe,Cd,Zn,Co,Mo | Leaf | (McDowell et al. 2013) |
| A.thaliana | AT3G14280 | S | S | seeds | (Isayenkov and Maathuis 2008) |
| A.thaliana | AT3G15380 | AtCTL1 | Na,Fe,Zn,Mn,Mo | Shoots, Roots | (Gao et al. 2017) |
| A.thaliana | AT3G18290 | BTS | Fe,Zn,Mn | Leaf | (Hindt et al. 2017) |
| A.thaliana | AT3G22890 | AtATPS1 | S | Shoots | (Koprivova et al. 2013) |
| A.thaliana | AT3G43790 | ZIFL2 | Cs | Leaf | (Remy et al. 2015) |
| A.thaliana | AT3G47640 | PYE | Fe,Zn,Mn,Co | Root | (Long et al. 2010) |
| A.thaliana | AT3G47950 | AHA4 | Na | Root | (Vitart et al. 2001) |
| A.thaliana | AT3G58060 | AtMTP8 | Mn | Shoots, seeds | (Eroglu et al. 2016), (Eroglu et al. 2017) |
| A.thaliana | AT3G58810 | AtMTP3 | Zn | Shoots | (Arrivault et al. 2006) |
| A.thaliana | AT4G16370 | OPT3 | Fe,Cd | Leaf | (Zhai et al. 2014) |
| A.thaliana | AT4G19690 | IRT1 | Fe,Mn,Co,Cd,Zn | Root | (Eide et al. 1996) |
| A.thaliana | AT4G24120 | YSL1 | Fe,Zn,Cu | NA | (Waters et al. 2006) |
| A.thaliana | AT4G30110 | AlHMA2 | Zn | Shoots, seeds | (Hussain et al. 2004); (Olsen et al. 2016) |
| A.thaliana | AT4G30120 | HMA3 | Cd | Leaf | (Chao et al. 2012) |
| A.thaliana | AT4G35040 | AtbZIP19 | Zn | Shoots, roots | (Assunção et al. 2010) |
| A.thaliana | AT5G02600 | NaKR1 | Na,K,Rb | Leaf | (Tian et al. 2010) |
| Species   | Accession | Gene   | Metals | Tissue          | Reference                 |
|-----------|-----------|--------|--------|-----------------|---------------------------|
| A. thaliana | AT5G03570 | FPN2   | Co     | Leaf            | (Morrissey et al. 2009)   |
| A. thaliana | AT5G15410 | CNSGC2/DND1 | Ca,Mg | seeds           | (McDowell et al. 2013)    |
| A. thaliana | AT5G18830 | AtSPL7 | Cu     | Shoots, roots   | (Bernal et al. 2012)      |
| A. thaliana | AT5G35410 | SOS2   | Na     | seeds           | (McDowell et al. 2013)    |
| A. thaliana | AT5G44070 | PCS1   | Zn,Cd  | Leaf            | (Kühnlenz et al. 2016)    |
| A. thaliana | AT5G53130 | CNSGC1 | Pb     | Leaf            | (Sunkar et al. 2000)      |
| A. thaliana | AT5G53550 | YSL3   | Fe,Zn,Cu | NA               | (Waters et al. 2006)      |
| A. thaliana | AT5G57620 | AtMYB36 | Zn, Rb, Sr, Mo, Cd | Shoots | (Kamiya et al. 2015) |
| A. thaliana | AT5G64930 | CPR5   | K      | Root, shoot     | (Li et al. 2016)          |
| A. thaliana | AT5G67330 | AtNRAMP3 | Fe,Mn,Zn | Shoots         | (Languar et al. 2010)     |
| A. thaliana | AT3G23210 | bHLH34 | Fe     | Root, shoot     | (Li et al. 2016)          |
| A. thaliana | AT4G14410 | bHLH104 | Fe     | Root, shoot     | (Li et al. 2016)          |
| M. truncatula | Medtr1g010270 | MMOT1.2 | Mo     | Nodules        | (Gil-Díez et al. 2018)    |
| M. truncatula | Medtr3g088460 | MtNramp1 | Fe     | Nodules        | (Tejada-Jiménez et al. 2015) |
| M. truncatula | Medtr3g464210 | MMOT1.3 | Mo     | Nodules        | (Tejada-Jiménez et al. 2017) |
| M. truncatula | Medtr4g019870 | MCOPT1 | Cu     | Nodules        | (Senovilla et al. 2018)   |
| M. truncatula | Medtr4g064893 | MtMTP2 | Zn     | Nodules        | (León-Mediavilla et al. 2018) |
| M. truncatula | Medtr4g03570 | MZIP6 | Zn     | Nodules        | (Abreu et al. 2017)       |
| O. sativa   | LOC_Os01g03914 | OsMTP9 | Mn     | Shoots         | (Ueno et al. 2015)        |
| O. sativa   | LOC_Os01g45990 | AKT1   | K      | NA             | (Ahmad et al. 2016)       |
| O. sativa   | LOC_Os02g06290 | OsHAC4 | As     | Root, shoots,  | (Xu et al. 2017)          |
| O. sativa   | LOC_Os02g10290 | OsHMA4 | Cu     | seeds          | (Huang et al. 2016)       |
| O. sativa   | LOC_Os02g43370 | OsYSL2 | Fe,Mn  | Seeds          | (Ishimaru et al. 2010)    |
| O. sativa   | LOC_Os02g43410 | OsYSL15 | Fe     | Roots, shoots,  | (Lee et al. 2009)         |
| O. sativa   | LOC_Os02g53490 | OsMTP8.2 | Mn     | Shoots, Roots  | (Takemoto et al. 2017)    |
| O. sativa   | LOC_Os03g12530 | OsMTP8.1 | Mn     | Shoots, Roots  | (Chen et al. 2013)        |
| O. sativa   | LOC_Os03g18550 | OsMIT  | Fe     | Shoots         | (Bashir et al. 2011)      |
| O. sativa   | LOC_Os04g32920 | OsHAK1 | Cs     | Shoots, seeds  | (Rai et al. 2017)         |
| O. sativa   | LOC_Os04g38940 | OsVIT1 | Fe,Zn  | Shoots, seeds  | (Zhang et al. 2012)       |
| O. sativa   | LOC_Os04g45860 | OsYSL9 | Fe     | Shoots, seeds  | (Senoura et al. 2017)     |
| O. sativa   | LOC_Os04g45900 | OsYSL16 | Cu     | Roots, shoots,  | (Zheng et al. 2012)       |
| O. sativa   | LOC_Os04g46940 | OsHMA5 | Cu     | Roots, shoots  | (Deng et al. 2013)        |
| O. sativa   | LOC_Os04g52310 | OsZIP3 | Zn     | Shoots         | (Sasaki et al. 2015)      |
| O. sativa   | LOC_Os04g52900 | OsABCC1 | As     | Seeds          | (Song et al. 2014)        |
| O. sativa   | LOC_Os05g34290 | OsPCS1* | As     | Seeds          | (Hayashi et al. 2017)     |
| O. sativa   | LOC_Os05g39560 | OsZIP5 | Zn     | Leaf           | (Lee et al. 2010)         |
| O. sativa   | LOC_Os06g01260 | OsPCS2* | As, Cd | Seeds          | (Uraguchi et al. 2017)    |
| Species | Gene ID | Gene | Metal | Tissue | Reference |
|---------|---------|------|-------|--------|-----------|
| *O. sativa* | LOC_Os06g48720 | OsHMA2 | Zn | Shoots, Roots | (Takahashi et al. 2012) |
| *O. sativa* | LOC_Os07g01810 | TPKb | K | Leaf, root | (Ahmad et al. 2016) |
| *O. sativa* | LOC_Os07g12900 | OsHMA3 | Cd | Shoots, seeds | (Tanaka et al. 2016) |
| *O. sativa* | LOC_Os08g04390 | OsPRI1 | Fe | Shoots, roots, Shoots, Roots, Seeds | (Zhang et al. 2017) |
| *O. sativa* | LOC_Os08g10480 | OsATX1 | Cu | Shoots, seeds | (Zhang et al. 2018) |
| *O. sativa* | LOC_Os09g23300 | OsVIT2 | Fe, Zn | Shoots, seeds | (Zhang et al. 2012) |
| *O. sativa* | LOC_Os12g18410 | OsMIR | Fe | Shoots, roots, seeds | (Ishimaru et al. 2009) |
| *O. sativa* | Os01g0689300 | OsHRZ1 | Fe | Shoots, seeds | (Kobayashi et al. 2013) |
| *O. sativa* | Os01g0861700 | OsHRZ1 | Fe | Shoots, seeds | (Kobayashi et al. 2013) |
| *O. sativa* | Os05g0551000 | OsHRZ2 | Fe | Shoots, seeds | (Kobayashi et al. 2013) |
| *O. sativa* | Os06g0143700 | SPDT | P | Seed | (Yamaji et al. 2017) |
| *O. sativa* | Os07g0257200 | NRAMP5 | Fe, Mn, Cd | Leaf | (Sasaki et al. 2012) |
| *Z. mays* | GRMZM2G060952 | YS1 | Fe | Root | (Von Wirén et al. 1994) |
| *Z. mays* | GRMZM2G063306 | YS3 | Fe | Leaf | (Chan-Rodriguez and Walker 2018) |
Figure 1. Number of genes for each species that are primary, inferred from other primary genes in other species, or both.

Most primary genes have orthologs in other species- which we call inferred genes. Less than 11% of primary genes in *A. thaliana* and *O. sativa*, and less than 2% in *M. truncatula*, lack orthologs (Table 2). *G. max*, *S. bicolor*, *S. italica*, and *S. viridis* currently contain only inferred genes (Table 2, Figure 1).

| Table 2. Break down of primary/inferred genes in each species |
|-------------------------------------------------------------|
|                   | A.thaliana | Z.mays | G.max* | S.bicolor* | O.sativa | M.truncatula | S.italica* | S.viridis* | Gene # |
| Gene #             | 76         | 88     | 138    | 73         | 77       | 85           | 76         | 79         |
| Primary            | 65.79%     | 2.27%  | 0.00%  | 0.00%      | 31.17%   | 4.71%        | 0.00%      | 0.00%      |
| Primary/Inferred   | 9.21%      | 0.00%  | 0.00%  | 0.00%      | 9.09%    | 2.35%        | 0.00%      | 0.00%      |
| Inferred           | 25.00%     | 97.73% | 100.00%| 100.00%    | 59.74%   | 92.94%       | 100.00%    | 100.00%    |
| Genes w/o          | 10.53%     | 0.00%  | 0.00%  | 0.00%      | 10.39%   | 1.18%        | 0.00%      | 0.00%      |
| orthologs          |            |        |        |            |          |              |            |            |
The YSL genes in *A. thaliana* and *O. sativa* are an example that provides evidence for the validity of the KIG list pipeline: AtYSL3, OsYSL9 and OsYSL16 were listed in their respective species as primary genes (Table 1) and after the ortholog search are annotated as primary/inferred genes, referencing each other (STable1). However, AtYSL2 in *A. thaliana*, which was not listed as primary gene, was inferred through both OsYSL9 and OsYSL16. Additionally, AtYSL1 in *A. thaliana* is not a paralog of AtYSL3 or an ortholog of OsYSL9 and OsYSL16 according to PhytoMine, and is not listed as an ortholog to either of the *O. sativa* YSL genes in the KIG list. Other examples include AtVIT1 and OsVIT1/OsVIT2 (Kim et al. 2006, Zhang et al. 2012) and AtMTP8 and OsMTP8.1 (Eroglu et al. 2016, Chen et al. 2013). Thus, we can reliably generate inferred genes for and create a species specific KIG list for any species in PhytoMine.

The primary list covers 23 elements (Figure 2) according to the reported elements from authors in the primary list, which is more elements than predicted by the GO term annotations for those genes. Some GO annotations for these genes mention only a portion of elements listed by the literature in the primary list. This may be due to GO annotation evidence codes lacking curation or biological data (IEA,ND,NAS) (Wimalanathan et al. 2018), or it may be due to alterations in one element leading to alterations in other elements (Baxter et al. 2008).
A. thaliana studies seem to be driving the elements included in the list, as it is the only species to have a gene listing each primary element. There is a bias towards elements like Manganese, Zinc and Iron which have 2, 3.5 and 4.5 times more associated genes than the average 8±9 genes of other elements. Iron is also the only element to contain genes from all four species in the primary list. In addition to biases towards certain elements, our primary list is also skewed towards an overrepresentation of ionome genes in above ground tissue studies (Figure 3). This is likely due to the difficulties in studying the elemental content of below ground tissues. All of our M. truncatula genes come from nodule studies, most likely because it is a model legume species.

Figure 3. Number of primary genes each type of tissue contributes to the known ionomics list. Above ground is a summary of anther, leaf, seed and shoot, while below ground is a summary of root and nodule.

Querying the manually curated PANTHER GO-Slim biological process database, with the A. thaliana KIG list returned no terms significantly overrepresented. However, all of the A. thaliana genes in the known ionomics list were mapped to significantly (false discovery rate <0.05) overrepresented annotation terms within the GO biological processes complete database and thus categorized into the five groups listed in the methods (Figure 4).
Even though some genes were annotated as associated in the “other transport” of glycoside, glucose, oligopeptides, or phloem transport, the citations that have added them into our primary list show that their mutant alleles altered elemental accumulation. AtBCC1 and AtBCC2 are annotated as glycoside transporters, but were inferred orthologs through an *O. sativa* gene in the primary list from a paper finding that OsABCC1 was contributing to the reduction of arsenic in rice grains (Song et al. 2014). The YSL genes and OPT3 are annotated as genes encoding oligopeptide transporters, but more specifically they are encoding predicted phloem-localized metal-nicotianamine complex and iron/cadmium transporters, respectively (Waters et al. 2006, Zhai et al. 2014). Lastly, NRT1.5/NPF7.3 is also annotated as encoding an oligopeptide transporter, but Li et al. (2017) identifies it as a xylem loading potassium ion antiporter.

The PANTHER GO-Slim molecular function annotation database did show a significant overrepresentation for cation transmembrane transporter activity. The results using the GO complete molecular function database supported this, with the addition of metal ion binding and cyclic nucleotide binding annotations. The cyclic nucleotide binding annotation genes were more specifically cyclic nucleotide ion gated channel genes (Gobert et al. 2006). The PANTHER GO-Slim cell component and GO complete cell component annotation database both returned
significant overrepresentation for vacuoles and the plasma membrane, both known to be critical for elemental movement and storage (need refs). The molecular function and cell component results are further evidence that our list is dominated by ion transporters.

To test how complete our list is in its current state, we searched PANTHER's biological processes annotations for the number of *A. thaliana* genes encoding predicted elemental transporters predicted to transport elements. We found 634 genes predicted to encode elemental transport, and only 18 of these PANTHER genes are listed in the known ionomics list. We checked these results against ThaleMine genes with the term “ion transport” in the gene name, description, or GO annotation and found only 376 genes, with 53 of these genes listed in the known ionomics list. Interestingly, 219 of the genes from ThaleMine were not found in the 634 from PANTHER.

**Discussion**

Here we have produced a curated list of genes known to alter the elemental composition of plant tissues. We envision several possible uses for this list:

1. Researchers can use the list to identify candidate genes in loci from QTL and GWAS experiments.
2. This list can serve as a gold standard for computational approaches.
3. The list can serve as a reading list for those interested in learning about elemental accumulation.

The list is highly enriched for transporters, genes that affect elemental accumulation in above ground tissues and genes that affect the accumulation of Fe and Zn. All of these factors, however, could be the result of human bias towards research topics. For example, transporter genes became obvious candidates for studying plant material nutrition when disruption allele collections were produced ([McDowell et al. 2013](https://doi.org/10.1101/456384)). Fe and Zn are both important nutrients and of considerable interest to the community where the ionomics approach was developed. Additionally, above ground tissues are easier to study without contamination from the soil, and such studies are therefore more prevalent.

Most entries on this list are derived from model organisms which reflects the fact that most of our knowledge about genes that affect elemental accumulation comes from these species. *A. thaliana* and *M. truncatula* account for 65.63% of the primary genes list, and several of the genes in crop plants were found due to being orthologs of genes in the model organisms ([Ahmad et al. 2016](https://dx.doi.org/10.1093/jxb/erw416), [Xu et al. 2017](https://dx.doi.org/10.1093/jmej/dix156)).

We conducted all of our analyses of GO terms in Arabidopsis, as it had the highest number of high confidence annotations. The lack of good annotations in other species highlights the value of creating curated lists like this one.
Call for more submissions: While we believe that the current list is useful, we are likely missing genes due to our lack of comprehensive knowledge of the literature. Currently, the list contains entries from only 9 people. We ask readers who know of genes that we are missing to contribute by submitting them here: https://docs.google.com/forms/d/e/1FAIpQLSdmS_zeOIxTOLmq2wB45BuSQml1LMKtKnWSatmFRGR2Q1o0Ew/viewform?c=0&w=1 or email corresponding author. KIG lists 0.1v for each of the species can be seen in STable1, and future updates to the list can be found at https://docs.google.com/spreadsheets/d/1XI2l1vtVjiHrlXLeOS5yTQQnLYq7BOHmpjuC-kUejUU/edit?usp=sharing.

Contributions:
Contributed genes: IB, FKR, FM, SC, EW, PK
Analyzed data: LW, GZ
Wrote paper: LW, FKR, IB
Edited paper: FKR, FM, SC, EW, PK, GZ, LW, IB

References
Abreu, Isidro, Ángela Saéz, Rosario Castro-Rodríguez, Viviana Escudero, Benjamín Rodríguez-Haas, Marta Senovilla, Camille Larue, et al. 2017. “Medicago Truncatula Zinc-Iron Permease6 Provides Zinc to Rhizobia-Infected Nodule Cells.” Plant, Cell & Environment 40 (11): 2706–19.

Ahmad, Izhar, Jean Devonshire, Radwa Mohamed, Michael Schultze, and Frans J. M. Maathuis. 2016. “Overexpression of the Potassium Channel TPKb in Small Vacuoles Confers Osmotic and Drought Tolerance to Rice.” The New Phytologist 209 (3): 1040–48.

Ahmad, Izhar, Afaq Mian, and Frans J. M. Maathuis. 2016. “Overexpression of the Rice AKT1 Potassium Channel Affects Potassium Nutrition and Rice Drought Tolerance.” Journal of Experimental Botany 67 (9): 2689–98.

Arrivault, Stéphanie, Toralf Senger, and Ute Krämer. 2006. “The Arabidopsis Metal Tolerance Protein AtMTP3 Maintains Metal Homeostasis by Mediating Zn Exclusion from the Shoot under Fe Deficiency and Zn Oversupply.” The Plant Journal: For Cell and Molecular Biology 46 (5): 861–79.

Ashburner, M., C. A. Ball, J. A. Blake, D. Botstein, H. Butler, J. M. Cherry, A. P. Davis, et al. 2000. “Gene Ontology: Tool for the Unification of Biology. The Gene Ontology Consortium.” Nature Genetics 25 (1): 25–29.

Assunção, Ana G. L., Eva Herrero, Ya-Fen Lin, Bruno Huettel, Sangita Talukdar, Cezary Smacziński, Richard G. H. Immink, et al. 2010. “Arabidopsis Thaliana Transcription Factors bZIP19 and bZIP23 Regulate the Adaptation to Zinc Deficiency.” Proceedings of the National Academy of Sciences of the United States of America 107 (22): 10296–301.

Barberon, Marie, Guillaume Dubeaux, Cornelia Kolb, Erika Isono, Enric Zelazny, and Grégory Vert. 2014. “Polarization of IRON-REGULATED TRANSPORTER 1 (IRT1) to the Plant-Soil Interface Plays Crucial Role in Metal Homeostasis.” Proceedings of the National Academy of Sciences of the United States of America 111 (22): 8293–98.

Bashir, Khurram, Yasuhiro Ishimaru, Hugo Shimo, Seiji Nagasaka, Masaru Fujimoto, Hideki Takanashi, Nobuhiro Tsutsumi, Gynheung An, Hiromi Nakashima, and Naoko K. Nishizawa. 2011. “The Rice Mitochondrial Iron Transporter Is Essential for Plant Growth.” Nature Communications 2: 322.

Baxter, Ivan, Jessica N. Brazelton, Danni Yu, Yu S. Huang, Brett Lahner, Elena Yakubova, Yan Li, et al. 2010. “A Coastal Cline in Sodium Accumulation in Arabidopsis Thaliana Is Driven by Natural Variation of the Sodium Transporter AtHKT1;1.” PLoS Genetics 6 (11): e1001193.
Baxter, Ivan, Prashant S. Hosmani, Ana Rus, Brett Lahner, Justin O. Borevitz, Balasubramaniam Muthukumar, Michael V. Mickelbart, Lukas Schreiber, Rochus B. Franke, and David E. Salt. 2009. “Root Suberin Forms an Extracellular Barrier That Affects Water Relations and Mineral Nutrition in Arabidopsis.” PLoS Genetics 5 (5): e1000492.

Baxter, Ivan, Balasubramaniam Muthukumar, Hyeong Cheol Park, Peter Buchner, Brett Lahner, John Danku, Keyan Zhao, et al. 2008. “Variation in Molybdenum Content across Broadly Distributed Populations of Arabidopsis Thaliana Is Controlled by a Mitochondrial Molybdenum Transporter (MOT1).” PLoS Genetics 4 (2): e1000004.

Bernal, María, David Casero, Vasantika Singh, Grandon T. Wilson, Arne Grande, Huijun Yang, Sheel C. Dodani, et al. 2012. “Transcriptome Sequencing Identifies SPL7-Regulated Copper Acquisition Genes FRO4/FRO5 and the Copper Dependence of Iron Homeostasis in Arabidopsis.” The Plant Cell 24 (2): 738–61.

Borghi, Monica, Ana Rus, and David E. Salt. 2011. “Loss-of-Function of Constitutive Expressor of Pathogenesis Related Genes5 Affects Potassium Homeostasis in Arabidopsis Thaliana.” The Plant Cell 22 (3): 904–17.

Carbon, Seth, Amelia Ireland, Christopher J. Mungall, Shengqiang Shu, Brad Marshall, Suzanna Lewis, AmiGO Hub, and Web Presence Working Group. 2009. “AmiGO: Online Access to Ontology and Annotation Data.” Bioinformatics 25 (2): 288–89.

Chan-Rodriguez, David, and Elsbeth L. Walker. 2018. “Analysis of Yellow Striped Mutants of Zea Mays Reveals Novel Loci Contributing to Iron Deficiency Chlorosis.” Frontiers in Plant Science 9 (February): 157.

Chao, Dai-Yin, Patrycja Baraniecka, John Danku, Anna Kopriwova, Brett Lahner, Hongbing Luo, Elena Yakubova, Brian Dilkes, Stanislav Kopriwa, and David E. Salt. 2014. “Variation in Sulfur and Selenium Accumulation Is Controlled by Naturally Occurring Isoforms of the Key Sulfur Assimilation Enzyme ADENOSINE 5’-PHOSPHOSULFATE REDUCTASE2 across the Arabidopsis Species Range.” Plant Physiology 166 (3): 1593–1608.

Chao, Dai-Yin, Yi Chen, Jiugeng Chen, Shulin Shi, Ziru Chen, Chengcheng Wang, John M. Danku, Fang-Jie Zhao, and David E. Salt. 2014. “Genome-Wide Association Mapping Identifies a New Arsenate Reductase Enzyme Critical for Limiting Arsenic Accumulation in Plants.” PLoS Biology 12 (12): e1002009.

Chao, Dai-Yin, Kenneth Gable, Ming Chen, Ivan Baxter, Charles R. Dietrich, Edgar B. Cahoon, Mary Lou Guerinot, et al. 2011. “Sphingolipids in the Root Play an Important Role in Regulating the Leaf Ionomere in Arabidopsis Thaliana.” The Plant Cell 23 (3): 1061–81.

Chao, Dai-Yin, Adriano Silva, Ivan Baxter, Yu S. Huang, Magnus Nordborg, John Danku, Brett Lahner, Elena Yakubova, and David E. Salt. 2012. “Genome-Wide Association Studies Identify Heavy Metal ATPase3 as the Primary Determinant of Natural Variation in Leaf Cadmium in Arabidopsis Thaliana.” PLoS Genetics 8 (9): e1002923.

Chen, Zonghui, Yumi Fujii, Naoki Yamaji, Sakine Masuda, Yuma Takemoto, Takehiro Kamiya, Yusufiujiang Yusuyin, et al. 2013. “Mn Tolerance in Rice Is Mediated by MTP8.1, a Member of the Cation Diffusion Facilitator Family.” Journal of Experimental Botany 64 (14): 4375–87.

Deng, Fenglin, Naoki Yamaji, Jixing Xia, and Jian Feng Ma. 2013. “A Member of the Heavy Metal P-Type ATPase OsHMA5 Is Involved in Xylem Loading of Copper in Rice.” Plant Physiology 163 (3): 1353–62.

Desbrosses-Fonrouge, Anne-Garlonn, Katrin Voigt, Astrid Schröder, Stéphanie Arrivault, Sébastien Thomine, and Ute Krämer. 2005. “Arabidopsis Thaliana MTP1 Is a Zn Transporter in the Vacuolar Membrane Which Mediates Zn Detoxification and Drives Leaf Zn Accumulation.” FEBS Letters 579 (19): 4165–74.

Eide, D., M. Broderius, J. Fett, and M. L. Guerinot. 1996. “A Novel Iron-Regulated Metal Transporter from Plants Identified by Functional Expression in Yeast.” Proceedings of the National Academy of Sciences of the United States of America 93 (11): 5624–28.

Eroglu, Seckin, Ricardo F. H. Giehl, Bastian Meier, Michiko Takahashi, Yasuko Terada, Konstantin Ignatyev, Elisa Andresen, Hendrik Küpper, Edgar Peiter, and Nicolaus von Wirén. 2017. “Metal Tolerance Protein 8 Mediates Manganese Homeostasis and Iron Reallocation during Seed Development and Germination.” Plant Physiology 174 (3): 1633–47.

Eroglu, Seckin, Bastian Meier, Nicolaus von Wirén, and Edgar Peiter. 2016. “The Vacuolar Manganese Transporter MTP8 Determines Tolerance to Iron Deficiency-induced Chlorosis in Arabidopsis.” Plant Physiology 170 (2): 1030–45.

Gao, Yi-Qun, Jiu-Geng Chen, Zi-Ru Chen, Dong An, Qiao-Yan Lv, Mei-Ling Han, Ya-Ling Wang, David E. Salt, and Dai-Yin Chao. 2017. “A New Vesicle Trafficking Regulator CTL1 Plays a Crucial Role in Ion Homeostasis.” PLoS Biology 15 (12): e2002978.
Gil-Díez, Patricia, Manuel Tejada-Jiménez, Javier León-Mediavilla, Jiangqi Wen, Kirankumar S. Mysore, Juan Imperial, and Manuel González-Guerrero. 2018. “MMOT1.2 is Responsible for Molybdate Supply to Medicago Truncatula Nodules.” Plant, Cell & Environment, June. https://doi.org/10.1111/pce.13388.

Gobert, Anthony, Graeme Park, Anna Amtmann, Dale Sanders, and Frans J. M. Maathuis. 2006. “Arabidopsis Thaliana Cyclic Nucleotide Gated Channel 3 Forms a Non-Selective Ion Transporter Involved in Germination and Cation Transport.” Journal of Experimental Botany 57 (4): 791–800.

Harris, M. A., J. Clark, A. Ireland, J. Lomax, M. Ashburner, R. Foulger, K. Eilbeck, et al. 2004. “The Gene Ontology (GO) Database and Informatics Resource.” Nucleic Acids Research 32 (Database issue): D258–61.

Hayashi, Shimpei, Masato Kuramata, Tadashi Abe, Hiroki Takagi, Kenjirou Ozawa, and Satoru Ishikawa. 2017. “Phytochelatin Synthase OsPCS1 Plays a Crucial Role in Reducing Arsenic Levels in Rice Grains.” The Plant Journal: For Cell and Molecular Biology 91 (5): 840–48.

Hindt, Maria N., Garo Z. Akmakjian, Kara L. Pivarski, Tracy Punshon, Ivan Baxter, David E. Salt, and Mary Lou Guerinot. 2017. “BRUTUS and Its Paralogs, BTS LIKE1 and BTS LIKE2, Encode Important Negative Regulators of the Iron Deficiency Response in Arabidopsis Thaliana.” Metallomics: Integrated Biometal Science 9 (7): 876–90.

Huang, Xin-Yuan, Dai-Yin Chao, Anna Koprivova, John Danku, Markus Wirtz, Steffen Müller, Francisco J. Sandoval, et al. 2016. “Nuclear Localised MORE SULPHUR ACCUMULATION1 Epigenetically Regulates Sulphur Homeostasis in Arabidopsis Thaliana.” PLoS Genetics 12 (9): e1006298.

Huang, Xin-Yuan, Fenglin Deng, Naoki Yamaji, Shannon R. M. Pinson, Milho Fuji-Kashino, John Danku, Alex Douglas, Mary Lou Guerinot, David E. Salt, and Jian Feng Ma. 2016. “A Heavy Metal P-Type ATPase OsHMA4 Prevents Copper Accumulation in Rice Grain.” Nature Communications 7 (July): 12138.

Hussain, Dawar, Michael J. Haydon, Yuwen Wang, Edwin Wong, Sarah M. Sherson, Jeff Young, James Camakaris, Jeffrey F. Harper, and Christopher S. Cobbett. 2004. “P-Type ATPase Heavy Metal Transporters with Roles in Essential Zinc Homeostasis in Arabidopsis.” The Plant Cell 16 (5): 1327–39.

Isayenkov, Stanislav V., and Frans J. M. Maathuis. 2008. “The Arabidopsis Thaliana Aquaglyceroporin AtNIP7;1 Is a Pathway for Arsenite Uptake.” FEMS Letters 582 (11): 1625–28.

Ishimaru, Yasuhiro, Khurram Bashir, Masaru Fujimoto, Gyunheung An, Reiko Nakanishi Itai, Nobuhiro Tsutsumi, Hiromi Nakanishi, and Naoko K. Nishizawa. 2009. “Rice-Specific Mitochondrial Iron-Regulated Gene (MIR) Plays an Important Role in Iron Homeostasis.” Molecular Plant 2 (5): 1059–66.

Ishimaru, Yasuhiro, Hiroshi Masuda, Khurram Bashir, Haruhiko Inoue, Takashi Tsukamoto, Michiko Takahashi, Hiromi Nakanishi, et al. 2010. “Rice Metal-Nicotianamine Transporter, OsYSL2, Is Required for the Long-Distance Transport of Iron and Manganese.” The Plant Journal: For Cell and Molecular Biology 62 (3): 379–90.

Kamiya, Takehiro, Monica Borghi, Peng Wang, John M. C. Danku, Lothar Kalmbach, Prashant S. Hosmani, Sadaf Naseer, Toru Fujinawa, Niko Geldner, and David E. Salt. 2015. “The MYB36 Transcription Factor Orchestrates Casparian Strip Formation.” Proceedings of the National Academy of Sciences of the United States of America 112 (33): 10533–38.

Kim, Sun A., Tracy Punshon, Antonio Lanzieri, Liangtao Li, José M. Alonso, Joseph R. Ecker, Jerry Kaplan, and Mary Lou Guerinot. 2006. “Localization of Iron in Arabidopsis Seed Requires the Vacuolar Membrane Transporter VIT1.” Science 314 (5803): 1295–98.

Kobayashi, Takanori, Seiji Ishimaru, Takeshi Senoura, Reiko Nakanishi Itai, Hiromi Nakanishi, and Naoko K. Nishizawa. 2013. “Iron-Binding Haemerythrin RING Ubiquitin Ligases Regulate Plant Iron Resonances and Accumulation.” Nature Communications 4: 2792.

Koprivova, Anna, Marco Giovannetti, Patrycja Baraniecka, Bok-Rye Lee, Cécile Grondin, Olivier Loudet, and Stanislav Kopriva. 2013. “Natural Variation in the ATPS1 Isoform of ATP Sulfurylase Contributes to the Control of Sulfate Levels in Arabidopsis.” Plant Physiology 163 (3): 1133–41.

Kühnlenz, Tanja, Christian Hofmann, Shimpei Uraguchi, Holger Schmidt, Stefanie Schempp, Michael Weber, Brett Lahner, David E. Salt, and Stephan Clemens. 2016. “Phytochelatin Synthesis Promotes Leaf Zn Accumulation of Arabidopsis Thaliana Plants Grown in Soil with Adequate Zn Supply and Is Essential for Survival on Zn-Contaminated Soil.” Plant & Cell Physiology 57 (11): 2342–52.

Lagarde, Delphine, Mireille Basset, Marc Lepetit, Geneviève Conjeero, Frédéric Gaymard, Suzette Astruc, and Claude Grignon. 1996. “Tissue-Specific Expression of Arabidopsis AKT1 Gene Is Consistent with a Role in K+ Nutrition.” The Plant Journal: For Cell and Molecular Biology 9 (2): 195–203.
Lanquar, Viviane, Magali Schnell Ramos, Françoise Lelièvre, Hélène Barbier-Brygoo, Anja Krieger-Liszkay, Ute Krämer, and Sébastien Thomine. 2010. “Export of Vacuolar Manganese by ATPRAMP3 and ATPRAMP4 Is Required for Optimal Photosynthesis and Growth under Manganese Deficiency.” Plant Physiology 152 (4): 1966–99.

Lee, Sichul, Jeff C. Chiecko, Sun A. Kim, Elsbeth L. Walker, Youngsook Lee, Mary Lou Guerinot, and Gynheung An. 2009. “Disruption of OsYSL15 Leads to Iron Inefficiency in Rice Plants.” Plant Physiology 150 (2): 786–800.

Lee, Sichul, Hee Joong Jeong, Sun A. Kim, Joohyun Lee, Mary Lou Guerinot, and Gynheung An. 2010. “OsZIP5 Is a Plasma Membrane Zinc Transporter in Rice.” Plant Molecular Biology 73 (4-5): 507–17.

León-Mediavilla, Javier, Marta Senovilla, Jesús Montiel, Patricia Gil-Díez, Ángela Saez, Igor S. Kryvoruchko, María Reguera, Michael K. Udvardi, Juan Imperial, and Manuel González-Guerrero. 2018. “MnMTP2-Facilitated Zinc Transport Into Intracellular Compartments Is Essential for Nodule Development in Medicago Truncatula.” Frontiers in Plant Science 9 (July): 990.

Li, Hong, Miao Yu, Xin-Qiao Du, Zhi-Fang Wang, Wei-Hua Wu, Francisco J. Quintero, Xue-Hua Jin, Hao-Dong Li, and Yi Wang. 2017. “NRT1.5/NPF7.3 Functions as a Proton-Coupled H+/K+ Antiporter for K+ Loading into the Xylem in Arabidopsis.” The Plant Cell 29 (8): 2016–26.

Li, Xiaoli, Huimin Zhang, Qin Ai, Gang Liang, and Diqiu Yu. 2016. “Two bHLH Transcription Factors, bHLH34 and bHLH104, Regulate Iron Homeostasis in Arabidopsis Thaliana.” Plant Physiology 170 (4): 2478–93.

Lindsay, Emma R., and Frans J. M. Maathuis. 2016. “Arabidopsis Thaliana NIP7;1 Is Involved in Tissue Arsenic Distribution and Tolerance in Response to Arsenate.” FEBS Letters 590 (6): 779–86.

Long, Terri A., Hironaka Tsukagoshi, Wolfgang Busch, Brett Lahner, David E. Salt, and Philip N. Benfey. 2010. “The bHLH Transcription Factor POPEYE Regulates Response to Iron Deficiency in Arabidopsis Roots.” The Plant Cell 22 (7): 2219–36.

Loudet, Olivier, Vera Saliba-Colombani, Christine Camilleri, Fanny Calenge, Virginie Gaudon, Anna Koprivova, Kathryn A. North, Stanislav Kopriva, and Françoise Daniel-Vedele. 2007. “Natural Variation for Sulfate Content in Arabidopsis Thaliana Is Highly Controlled by APR2.” Nature Genetics 39 (7): 896–900.

McDowell, Stephen C., Garo Akmakjian, Chris Sladek, David Mendoza-Cozatl, Joe B. Morrissey, Nick Saini, Ron Mittler, et al. 2013. “Elemental Concentrations in the Seed of Mutants and Natural Variants of Arabidopsis Thaliana Grown under Varying Soil Conditions.” PLoS One 8 (5): e63014.

Mi, Huaiyu, Xiaosong Huang, Anushya Muruganujan, Haiming Tang, Caitlin Mills, Diane Kang, and Paul D. Thomas. 2017. “PANTHER Version 11: Expanded Annotation Data from Gene Ontology and Reactome Pathways, and Data Analysis Tool Enhancements.” Nucleic Acids Research 45 (D1): D183–89.

Morrissey, Joe, Ivan R. Baxter, Joohyun Lee, Liangtao Li, Brett Lahner, Natasha Grotz, Jerry Kaplan, David E. Salt, and Mary Lou Guerinot. 2009. “The Ferrroportin Metal Efflux Proteins Function in Iron and Cobalt Homeostasis in Arabidopsis.” The Plant Cell 21 (10): 3326–38.

Olsen, Lene Irene, Thomas H. Hansen, Camille Larue, Jeppe Thulin Østerberg, Robert D. Hoffmann, Johannes Liesche, Ute Krämer, et al. 2016. “Mother-Plant-Mediated Pumping of Zinc into the Developing Seed.” Nature Plants 2 (5): 16036.

Palmer, Christine M., Maria N. Hindt, Holger Schmidt, Stephan Clemens, and Mary Lou Guerinot. 2013. “MYB10 and MYB72 Are Required for Growth under Iron-Limiting Conditions.” PLoS Genetics 9 (11): e1003953.

Peiter, Edgar, Barbara Montanini, Anthony Gobert, Pai Pedas, Sören Husted, Frans J. M. Maathuis, Damien Blaudez, Michel Chalot, and Dale Sanders. 2019. “A Secretory Pathway-Localized Cation Diffusion Facilitator Confers Plant Manganese Tolerance.” Proceedings of the National Academy of Sciences of the United States of America 104 (20): 8532–37.

Rai, Hiroki, Saki Yokoyama, Namiko Satoh-Nagasawa, Jun Furukawa, Takiko Nomi, Yasuka Ito, Shigeto Fujimura, et al. 2017. “Cesium Uptake by Rice Roots Largely Depends Upon a Single Gene, HAK1, Which Encodes a Potassium Transporter.” Plant & Cell Physiology 58 (9): 1486–93.

Remy, Estelle, Tânia R. Cabrito, Rita A. Batista, Miguel C. Teixeira, Isabel Sá-Correia, and Paula Duque. 2015. “The Major Facilitator Superfamily Transporter ZIFL2 Modulates Cesium and Potassium Homeostasis in Arabidopsis.” Plant & Cell Physiology 56 (1): 148–62.

Ren, Zhong-Hai, Ji-Ping Gao, Le-Gong Li, Xu-Ling Cai, Wei Huang, Dai-Yin Chao, Mei-Zhen Zhu, Zong-Yang Wang, Sheng Luan, and Hong-Xuan Lin. 2005. “A Rice Quantitative Trait Locus for Salt Tolerance Encodes a Sodium Transporter.” Nature Genetics 37 (10): 1141–46.
Robinson, Nigel J., Catherine M. Procter, Erin L. Connolly, and Mary Lou Guerinot. 1999. “A Ferric-Chelate Reductase for Iron Uptake from Soils.” *Nature* 397 (February): 694.

Sasaki, Akimasa, Naoki Yamaji, Namiki Mitani-Ueno, Miho Kashino, and Jian Feng Ma. 2015. “A Node-Localized Transporter OsZIP3 Is Responsible for the Preferential Distribution of Zn to Developing Tissues in Rice.” *The Plant Journal: For Cell and Molecular Biology* 84 (2): 374–84.

Sasaki, Akimasa, Naoki Yamaji, Kengo Yokosho, and Jian Feng Ma. 2012. “Nramp5 Is a Major Transporter Responsible for Manganese and Cadmium Uptake in Rice.” *The Plant Cell* 24 (5): 2155–67.

Selote, Devarshi, Rozalyynne Samira, Anna Matthiadis, Jeffrey W. Gillikin, and Terri A. Long. 2015. “Iron-Binding E3 Ligase Mediates Iron Response in Plants by Targeting Basic Helix-Loop-Helix Transcription Factors.” *Plant Physiology* 167 (1): 273–86.

Senoura, Takeshi, Emi Sakashita, Takanori Kobayashi, Michiko Takahashi, May Sann Aung, Hiroshi Masuda, Hiromi Nakanishi, and Naoko K. Nishizawa. 2017. “The Iron-Chelate Transporter OsYSL9 Plays a Role in Iron Distribution in Developing Rice Grains.” *Plant Molecular Biology* 95 (4-5): 375–87.

Senvillla, Marta, Rosario Castro-Rodríguez, Isidro Abreu, Viviana Escudero, Igor Kryvoruchko, Michael K. Udvardi, Juan Imperial, and Manuel González-Guerrero. 2018. “Medicago Truncatula Copper Transporter 1 (MtCOPT1) Delivers Copper for Symbiotic Nitrogen Fixation.” *The New Phytologist* 218 (2): 696–709.

Song, Won-Yong, Tomohiro Yamaki, Naoki Yamaji, Donghi Ko, Ki-Hong Jung, Miho Fujii-Kashino, Gynheung An, Enrico Martinoa, Youngsook Lee, and Jian Feng Ma. 2014. “A Rice ABC Transporter, OsABCC1, Reduces Arsenic Accumulation in the Grain.” *Proceedings of the National Academy of Sciences of the United States of America* 111 (44): 15699–704.

Stoeeger, Thomas, Martin Gerlach, Richard I. Morimoto, and Luis A. Nunes Amaral. 2018. “Large-Scale Investigation of the Reasons Why Potentially Important Genes Are Ignored.” *PLoS Biology* 16 (9): e2006643.

Sunkar, R., B. Kaplan, N. Bouché, T. Arazí, D. Dolev, I. N. Talke, F. J. Maathuis, D. Sanders, D. Bouchez, and H. Fromm. 2000. “Expression of a Truncated Tobacco NtCBP4 Channel in Transgenic Plants and Disruption of the Homologous Arabidopsis CNGC1 Gene Confer Pb2+ Tolerance.” *The Plant Journal: For Cell and Molecular Biology* 24 (4): 533–42.

Takahashi, Ryuichi, Yasuhiro Ishimaru, Hugo Shimo, Yuko Ogo, Takeshi Senoura, Naoko K. Nishizawa, and Hiromi Nakanishi. 2012. “The OsHMA2 Transporter Is Involved in Root-to-Shoot Translocation of Zn and Cd in Rice.” *Plant, Cell & Environment* 35 (11): 1948–57.

Takemoto, Yuma, Yuta Tsunemitsu, Miho Fujii-Kashino, Namiki Mitani-Ueno, Naoki Yamaji, Jian Feng Ma, Shin-Ichiro Kato, Kozo Iwasaki, and Daisei Ueno. 2017. “The Tonoplast-Localized Transporter MTP8.2 Contributes to Manganese Detoxification in the Shoots and Roots of Oryza Sativa L.” *Plant & Cell Physiology* 58 (9): 1573–82.

Tanaka, Nobuhiro, Sho Nishida, Takehiro Kamiya, and Toru Fujiwara. 2016. “Large-Scale Profiling of Brown Rice Ionome in an Ethyl Methanesulphonate-Mutagenized Hitomebore Population and Identification of High- and Low-Cadmium Lines.” *Plant and Soil* 407 (1-2): 109–17.

Tejada-Jiménez, Manuel, Rosario Castro-Rodríguez, Igor Kryvoruchko, M. Mercedes Lucas, Michael Udvardi, Juan Imperial, and Manuel González-Guerrero. 2015. “Medicago truncatula Natural Resistance-Associated Macrophage Protein1 Is Required for Iron Uptake by Rhizobia-Infected Nodule Cells.” *Plant Physiology* 168 (1): 258–72.

Tejada-Jiménez, Manuel, Patricia Gil-Díez, Javier León-Mediavilla, Jiangqi Wen, Kirankumar S. Mysore, Juan Imperial, and Manuel González-Guerrero. 2017. “Medicago truncatula Molybdate Transporter Type 1 (MtMOT1.3) Is a Plasma Membrane Molybdenum Transporter Required for Nitrogenase Activity in Root Nodules under Molybdenum Deficiency.” *The New Phytologist* 216 (4): 1223–35.

The Gene Ontology Consortium. 2017. “Expansion of the Gene Ontology Knowledgebase and Resources.” *Nucleic Acids Research* 45 (D1): D331–38.

Tian, Hui, Ivan R. Baxter, Brett Lahner, Anke Reinders, David E. Salt, and John M. Ward. 2010. “Arabidopsis NPC6/NaKR1 Is a Phloem Mobile Metal Binding Protein Necessary for Phloem Function and Root Meristem Maintenance.” *The Plant Cell* 22 (12): 3963–79.

Ueno, Daisei, Akimasa Sasaki, Naoki Yamaji, Takaaki Miyaj, Yumi Fujii, Yuma Takemoto, Sawako Moriyama, et al. 2015. “A Polarly Localized Transporter for Efficient Manganese Uptake in Rice.” *Nature Plants* 1 (November): 15170.

Uraguchi, Shimpei, Nobuhiro Tanaka, Christian Hofmann, Kaho Abiko, Naoko Ohkama-Ohtsu, Michael Weber, Takehiro Kamiya, et al. 2017. “Phytochelatin Synthase Has Contrasting Effects on Cadmium and Arsenic Accumulation in Rice Grains.” *Plant & Cell Physiology* 58 (10): 1730–42.
Vitart, Veronique, Ivan Baxter, Peter Doerner, and Jeffrey F. Harper. 2001. “Evidence for a Role in Growth and Salt Resistance of a Plasma Membrane H+-ATPase in the Root Endodermis: Salt Sensitive H+-ATPase Mutant.” *The Plant Journal: For Cell and Molecular Biology* 27 (3): 191–201.

Von Wiren, N., S. Mori, H. Marschner, and V. Romheld. 1994. “Iron Inefficiency in Maize Mutant ys1 (Zea Mays L. Cv Yellow-Stripe) Is Caused by a Defect in Uptake of Iron Phytosiderophores.” *Plant Physiology* 106 (1): 71–77.

Waters, Brian M., Heng-Hsuan Chu, Raymond J. Didonato, Louis A. Roberts, Robynn B. Eisle, Brett Lahner, David E. Salt, and Elsbeth L. Walker. 2006. “Mutations in Arabidopsis Yellow Stripe-like1 and Yellow Stripe-like3 Reveal Their Roles in Metal Ion Homeostasis and Loading of Metal Ions in Seeds.” *Plant Physiology* 141 (4): 1446–58.

Wild, Michael, Jean-Michel Davière, Thomas Regnault, Lali Sakvarelidze-Achard, Esther Carrera, Isabel Lopez Diaz, Anne Cayrel, Guillaume Dupeaux, Grégory Vert, and Patrick Achard. 2016. “Tissue-Specific Regulation of Gibberellin Signaling Fine-Tunes Arabidopsis Iron-Deficiency Responses.” *Developmental Cell* 37 (2): 190–200.

Wimalanathan, Kokulapalan, Iddo Friedberg, Carson M. Andorf, and Carolyn J. Lawrence-Dill. 2018. “Maize GO Annotation—Methods, Evaluation, and Review (maize-GAMER).” *Plant Direct* 2 (4): e00052.

Xu, Jiming, Shulin Shi, Lei Wang, Zhong Tang, Tingting Lv, Xinli Zhu, Xiaomeng Ding, Yifeng Wang, Fang-Jie Zhao, and Zhongchang Wu. 2017. “OsHAC4 Is Critical for Arsenate Tolerance and Regulates Arsenic Accumulation in Rice.” *The New Phytologist* 215 (3): 1090–1101.

Yamaji, Naoki, Yuma Takemoto, Takaaki Miyaji, Namiki Mitani-Ueno, Kaoru T. Yoshida, and Jian Feng Ma. 2017. “Reducing Phosphorus Accumulation in Rice Grains with an Impaired Transporter in the Node.” *Nature* 541 (7635): 92–95.

Yan, Jiali, Peitong Wang, Meng Yang, Xingming Lian, Zhong Tang, Chao-Feng Huang, David E. Salt, and Fang Jie Zhao. 2016. “A Loss-of-Function Allele of OsHMA3 Associated with High Cadmium Accumulation in Shoots and Grain of Japonica Rice Cultivars.” *Plant, Cell & Environment* 39 (9): 1941–54.

Yan, Jiapei, Ju-Chen Chia, Huajin Sheng, Ha-II Jung, Tetiana-Olena Zavodna, Lu Zhang, Rong Huang, et al. 2017. “Arabidopsis Pollen Fertility Requires the Transcription Factors CITF1 and SPL7 That Regulate Copper Delivery to Anthers and Jasmonic Acid Synthesis.” *The Plant Cell* 29 (12): 3012–29.

Zhai, Zhiyang, Sheena R. Gayomba, Ha-Il Jung, Nanditha K. Vimalakumari, Miguel Piñeros, Eric Craft, Michael A. Rutzke, et al. 2014. “OPT3 Is a Phloem-Specific Iron Transporter That Is Essential for Systemic Iron Signaling and Redistribution of Iron and Cadmium in Arabidopsis.” *The Plant Cell* 26 (5): 2249–64.

Zhang, Huimin, Yang Li, Xiani Yao, Gang Liang, and Diqiu Yu. 2017. “POSITIVE REGULATOR OF IRON HOMEOSTASIS1, OsPRI1, Facilitates Iron Homeostasis.” *Plant Physiology* 175 (1): 543–54.

Zhang, Yu, Yong-Han Xu, Hong-Yin Yi, and Ji-Ming Gong. 2012. “Vacuolar Membrane Transporters OsVIT1 and OsVIT2 Modulate Iron Translocation between Flag Leaves and Seeds in Rice.” *The Plant Journal: For Cell and Molecular Biology* 72 (3): 400–410.

Zhang, Yuanyuan, Naoki Yamaji, Kengo Yokosho, and Jian Feng Ma. 2012. “YSL16 Is a Phloem-Localized Transporter of the Copper-Nicotianamine Complex That Is Responsible for Copper Distribution in Rice.” *The Plant Cell* 24 (9): 3767–82.