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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 *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,

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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

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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	GeneID	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	AtNRT1.5 / AtNPF7.3	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)

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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	AtHMA4	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	Mo	Leaf	(Baxter et al. 2008)
A.thaliana	AT2G28670	ESB1	Ca,Mn,Zn,Na,S,K,As, Se,Mo	Leaf	(Baxter et al. 2009)
A.thaliana	AT2G38460	FPN1	Co	Leaf	(Morrissey et al. 2009)
A.thaliana	AT2G39450	AtMTP11	Mn	Shoots,Roots	(Peiter et al. 2007)
A.thaliana	AT2G46430	CNGC3	K	Leaf	(Gobert et al. 2006)
A.thaliana	AT2G46800	AtMTP1	Zn	Shoots	(Desbrosses-Fonrouge et al. 2005)
A.thaliana	AT3G06060	TSC10a	Na,K,Rb,Mg,Ca,Fe,Mo	Leaf	(Chao et al. 2011)
A.thaliana	AT3G06100	NIP7	As	NA	(Lindsay and Maathuis 2016) (Isayenkov and Maathuis 2008)
A.thaliana	AT3G12820	myb10	Fe,Cd,Zn,Co,Mo	Leaf	(Palmer et al. 2013)
A.thaliana	AT3G14280		S	seeds	(McDowell et al. 2013)
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	Shoos	(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	AT4G02780	GA1	Fe	Root	(Wild et al. 2016)
A.thaliana	AT4G10310	AtHKT1;1	Na	Leaf	(Baxter et al. 2010)
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	AtHMA2	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)

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A.thaliana	AT5G03570	FPN2	Co	Leaf	(Morrissey et al. 2009)
A.thaliana	AT5G15410	CNGC2/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	CNGC1	Pb	Leaf	(Sunkar et al. 2000).x
A.thaliana	AT5G53550	YSL3	Fe,Zn,Cu	NA	(Waters et al. 2006)
A.thaliana	AT5G57620	AtMYB36	Li, B, Na, Mg, K, Ca, Mn, Fe, Co, Ni, Cu, Zn, Rb, Sr, Mo, Cd	Shoots	(Kamiya et al. 2015)
A.thaliana	AT5G64930	CPR5	K	Leaf	(Borghi et al. 2011)
A.thaliana	AT5G67330	AtNRAMP3	Fe,Mn,Zn	Shoots	(Lanquar 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	MtMOT1.2	Mo	Nodules	(Gil-Díez et al. 2018)
M.truncatula	Medtr3g088460	MtNramp1	Fe	Nodules	(Tejada-Jiménez et al. 2015)
M.truncatula	Medtr3g464210	MtMOT1.3	Mo	Nodules	(Tejada-Jiménez et al. 2017)
M.truncatula	Medtr4g019870	MtCOPT1	Cu	Nodules	(Senovilla et al. 2018)
M.truncatula	Medtr4g064893	MtMTP2	Zn	Nodules	(León-Mediavilla et al. 2018)
M.truncatula	Medtr4g083570	MtZIP6	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	Seed	(Xu et al. 2017)
O.sativa	LOC_Os02g10290	OsHMA4	Cu	Roots, shoots, 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, seeds	(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, seeds	(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)

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O.sativa	LOC_Os06g48720	OsHMA2	Zn	Shoots,Roots	(Takahashi et al. 2012)x
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	(Zhang et al. 2017)
O.sativa	LOC_Os08g10480	OsATX1	Cu	Shoots, Roots, 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	OsHORZ1	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 Wiren et al. 1994)
Z.mays	GRMZM2G063306	YS3	Fe	Leaf	(Chan-Rodriguez and Walker 2018)

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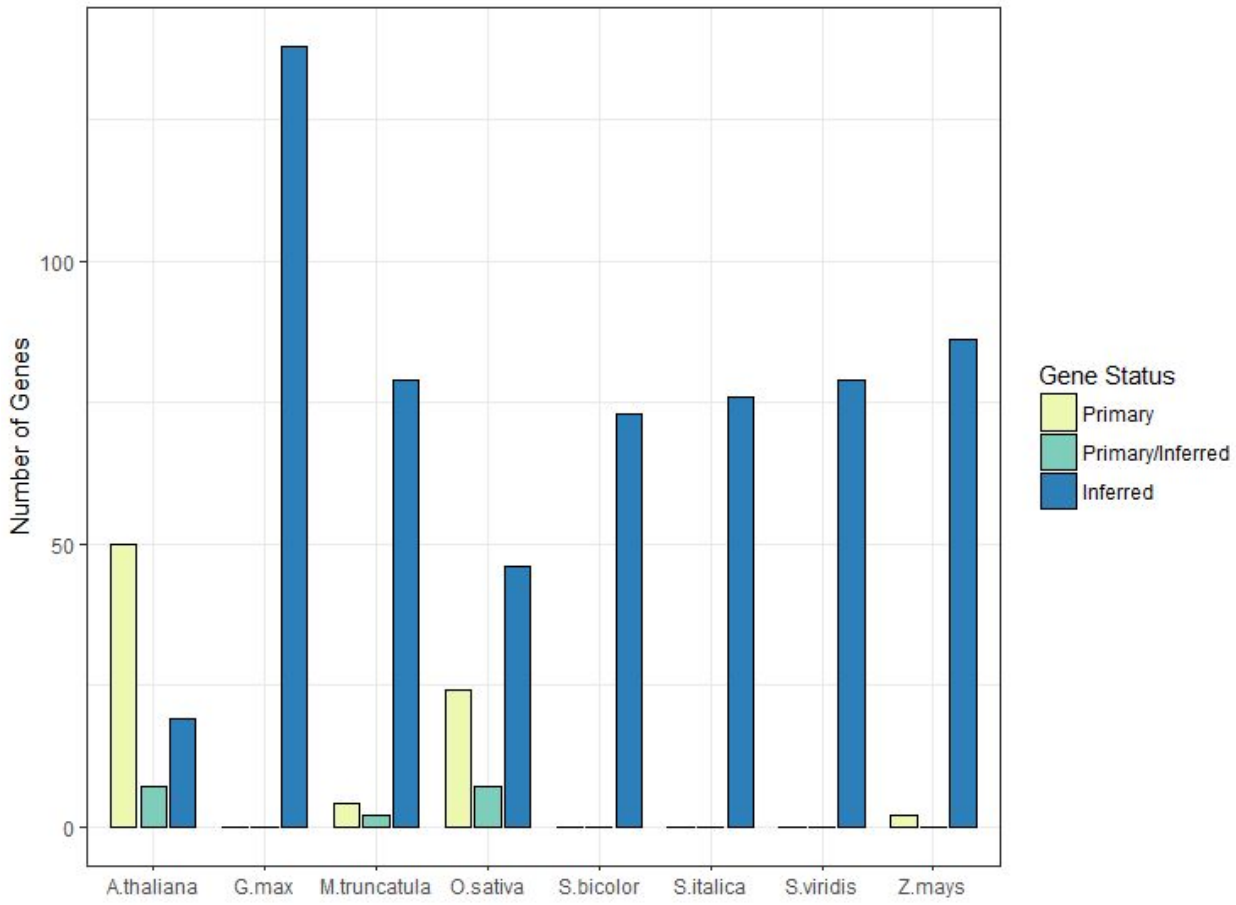

Figure 1. Number of genes for each species that are primary, inferred from other primary genes in other species, or both.

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 #	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 orthologs	10.53%	0.00%	0.00%	0.00%	10.39%	1.18%	0.00%	0.00%

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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).

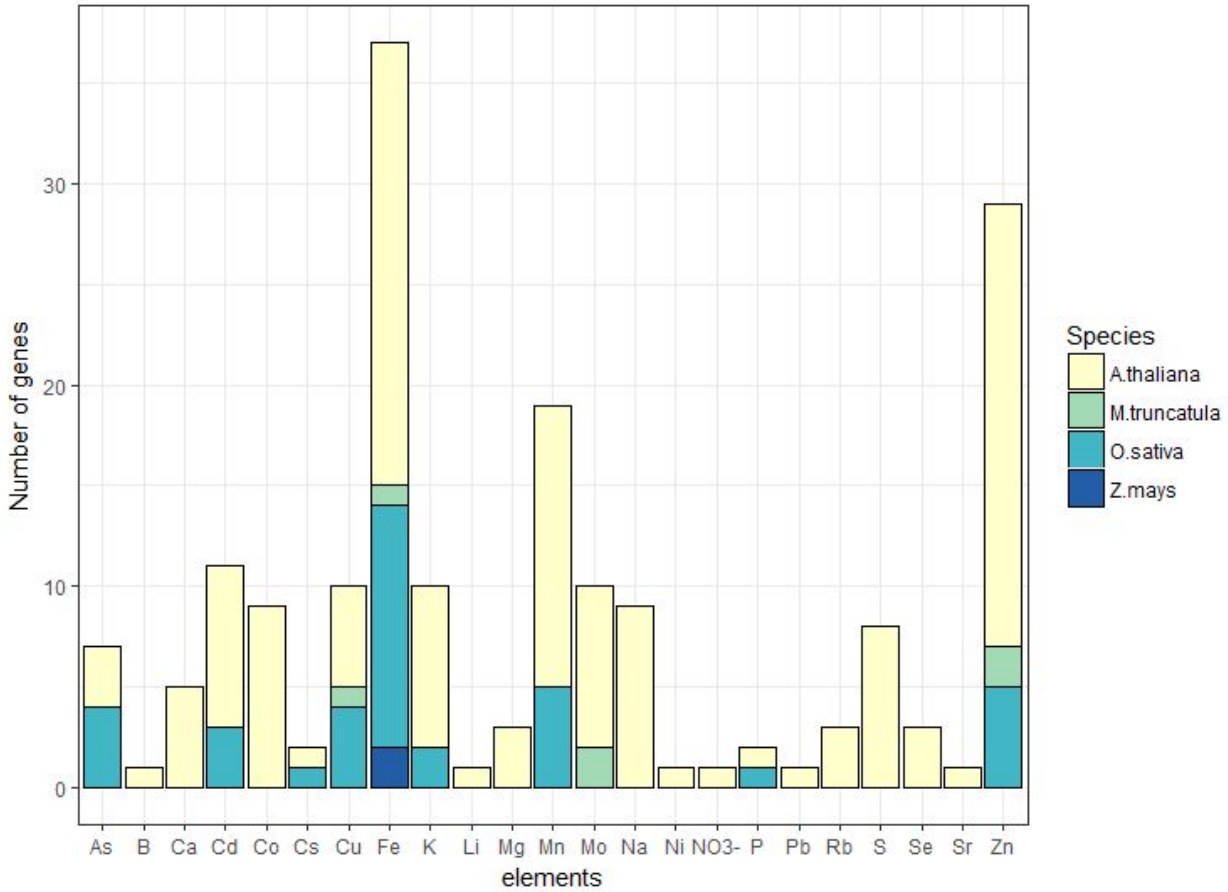

Figure 2. Number of primary genes from each species listing each element.

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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.

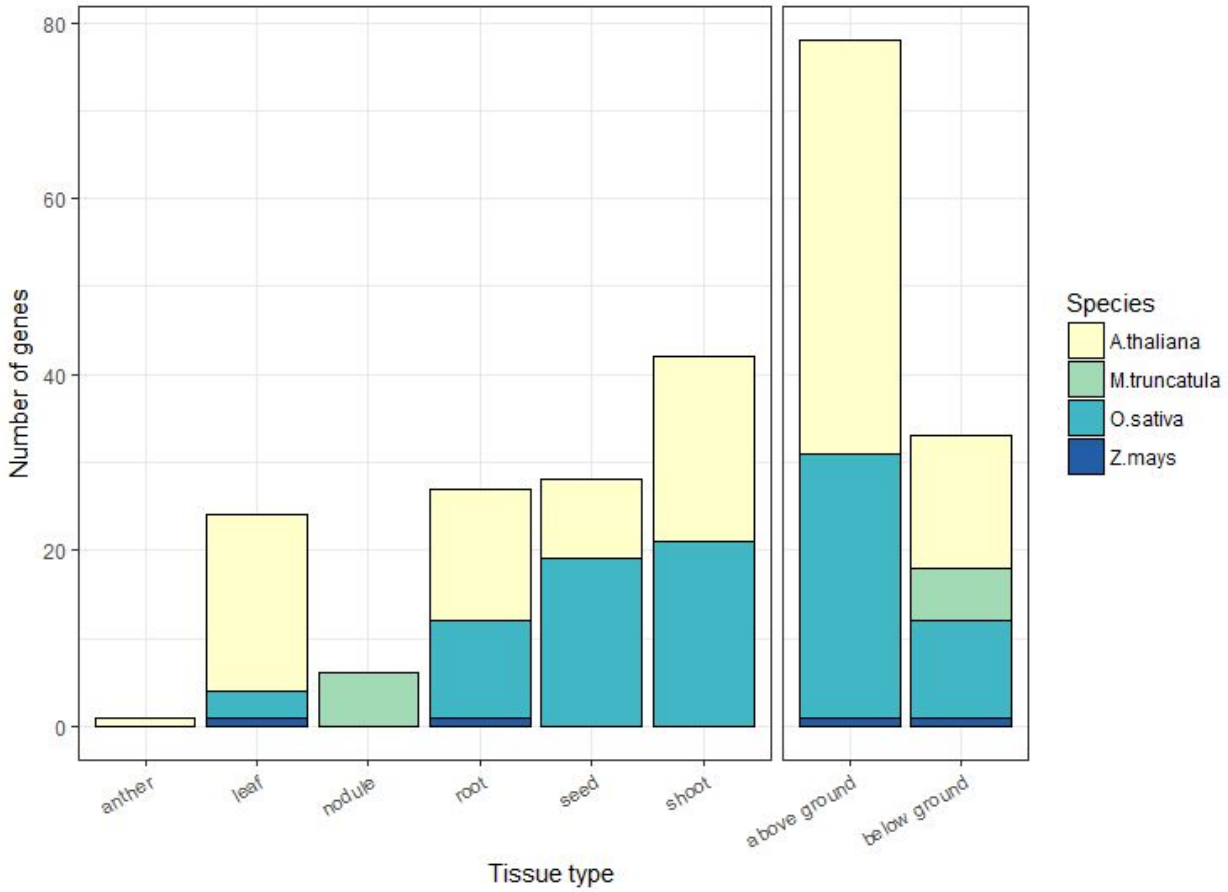

Figure 3. Number of primary genes each type of tissue contributes to the known ionomics list. Above ground is a summary of anther, leaf, seed and shoot, while below ground is a summary of root and nodule.

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).

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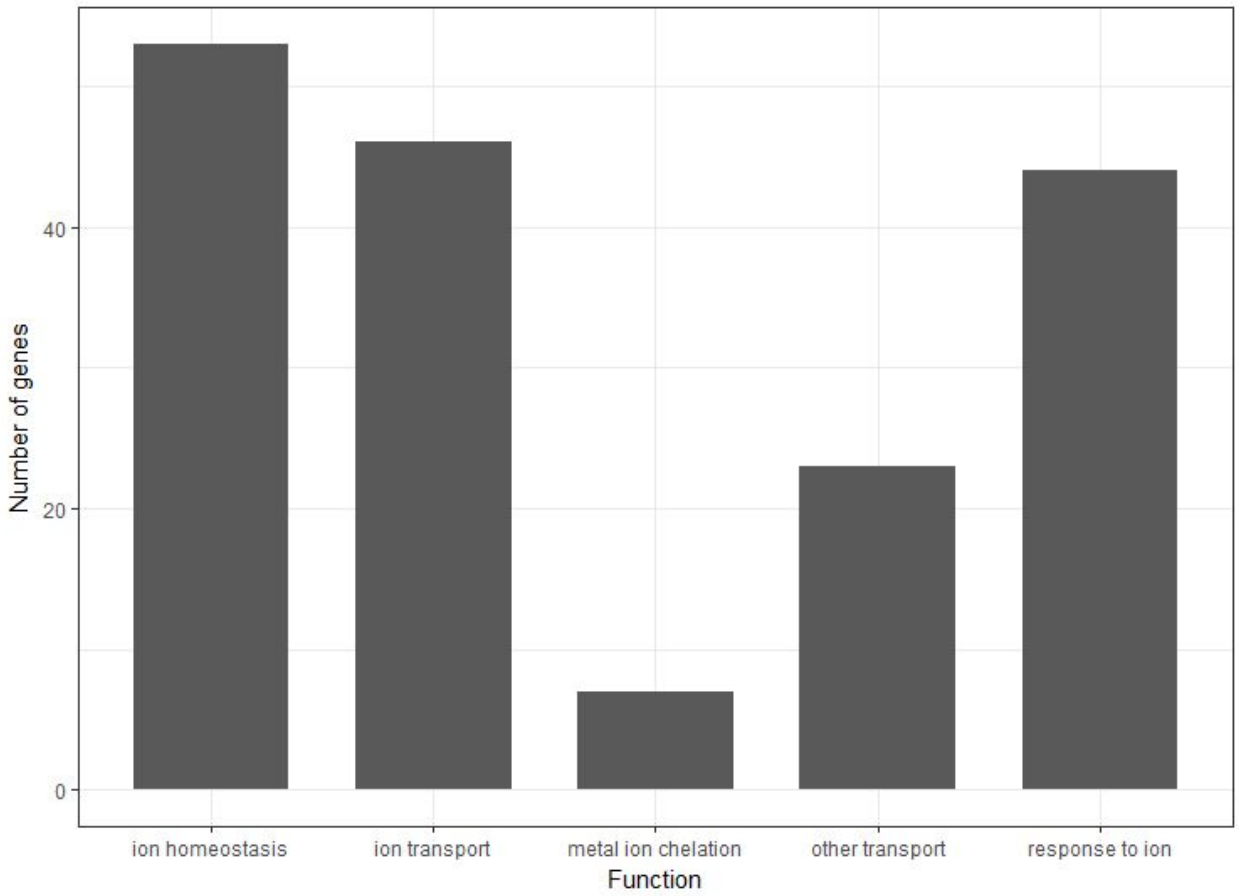

Figure 4. Known ionome genes relating to different biological processes. Ontology groups of GO Enrichment Analysis from PANTHER.

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

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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). 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, Xu et al. 2017).

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.

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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_zeOlxTOLmq2wB45BuSQml1LMKtKnWSatmFRGR2Q1o0Ew/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/1XI2l1vtVJiHrlXLeOS5yTQQnLYq7BOHpmjuC-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

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