

ABSTRACT

Oxidation and reduction of methionine (Met) in proteins is thought to play important roles in scavenging reactive oxygen species (ROS) and signaling in living organisms. To visualize possible impacts of Met oxidation and reduction in plant during adaptation to stresses, we surveyed the genomes of two dicots, *Arabidopsis* and soybean (*Glycine max* L.), for genes encoding Met-rich proteins (MRPs). We found 121 and 213 genes encoding MRPs in *Arabidopsis* and soybean, respectively. Gene ontology analyses indicated that the functions of half of these genes are to be elucidated. Of the remaining half, the major parts involved in vital cellular processes, such as transcription control, calcium signaling, protein modification and metal transport. Next, to identify if MRPs are involved in stress adaptation in the plants, we analyzed their transcript levels under normal and stress conditions. We found that 57 AtMRPs were

either responsive to drought or high salinity stress in *Arabidopsis*; whereas 35 GmMRPs were responsive to drought in the leaf of late vegetative or early reproductive stages of soybean. Interestingly, among the MRP genes with a known function, the majority of these abiotic stress-responsive genes are involved in two “master switches”, the transcription control and calcium signaling. Furthermore, we found that Met residues were highly conserved in the HMM profiles of several MRPs whose genes were transcriptionally responsive to stress. Taken together, our report indicated that MRPs participate in various vital processes of plants under normal and stress conditions. Thus, the oxidation and reduction of Met in these MRPs may modulate their functions.

RESULTS

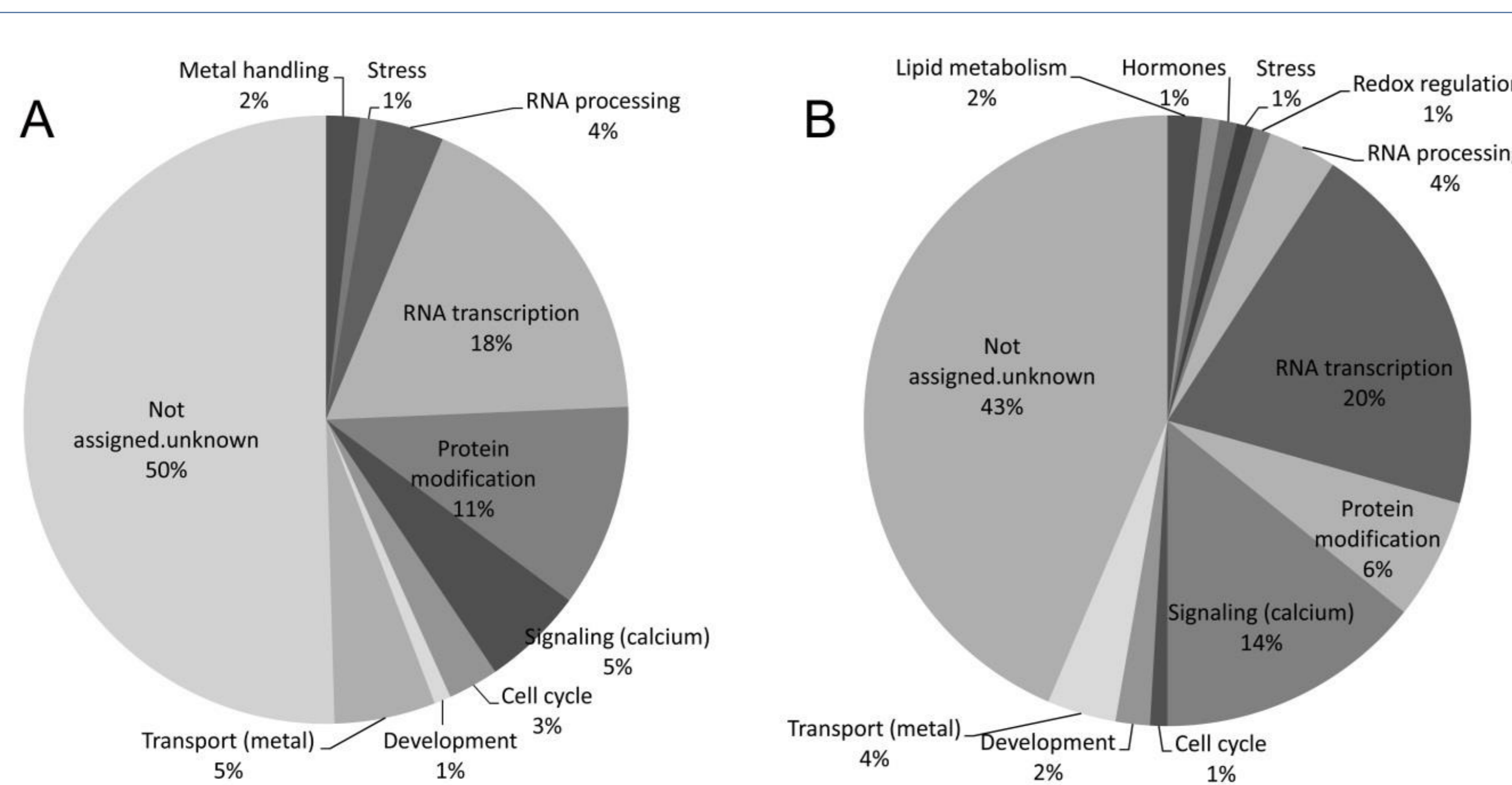


Figure 1. Distribution of genes encoding MRPs into various biological processes in *Arabidopsis* (A) and soybean (B)

Figure 2. Venn diagram analyses of the expression of MRP-coding genes in *Arabidopsis* and soybean under abiotic stresses (A), and HMM profile of *Arabidopsis* and soybean homologs share common responsiveness to drought (B) and their sequence alignment (C).

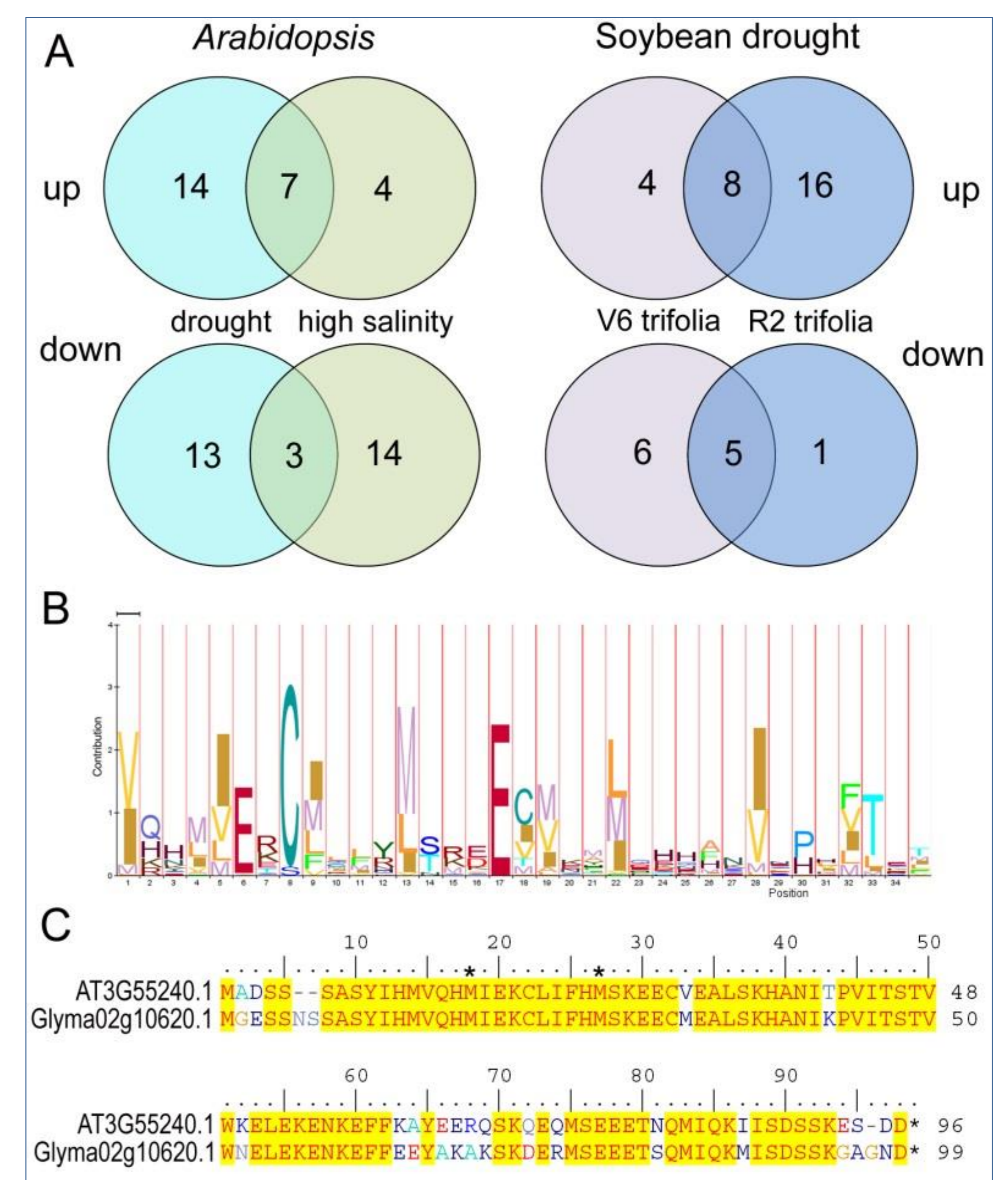


Table 1. Genes encoding AtMRPs whose expression levels were responsive to both drought and high salinity

No	Locus IDs	Met (%)	Length (a.a.)	Drought vs untreated		Salinity vs untreated		Gene descriptions
				Fold change ³	q-value	Fold change ³	q-value	
1	AT1G32560	6.02	134	135.33	0.002	3.31	0.005	LEA group 1 domain-containing protein
2	AT1G33860	8.55	153	2.37	0.092	2.16	0.003	unknown protein
3	AT3G55240	6.12	95	-60.29	0.007	-26.88	0.001	Overexpression leads to Pseudo-Etiolation in Light phenotype
4	AT3G59900	6.20	130	10.70	0.011	-2.57	0.015	(ARGOS); unknown protein [AT3G59900.1]
5	AT3G62090	6.38	346	64.56	0.020	2.28	0.002	PHYTOCHROME INTERACTING FACTOR 3-LIKE 2
6	AT4G12334	6.25	113	-9.79	0.003	-3.04	0.005	Pseudogene of cytochrome P450 family protein
7	AT4G33467	8.91	102	337.51	0.002	6.16	0.023	unknown protein [AT4G33467.1]
8	AT4G34590	6.33	159	8.26	0.004	3.27	0.002	GBF6 (A. thaliana BASIC LEUCINE-ZIPPER 11)
9	AT5G42325	6.03	233	2.70	0.028	2.45	0.049	Transcription elongation factor-related
10	AT5G67390	7.43	176	-4.17	0.015	-4.15	0.001	Similar to unknown proteins (TAIR:AT1G69360.1)

METHODS & REFERENCES

Methods

Protein sequences were downloaded from PHYTOZOME database (<http://www.phytozome.net>) and searched for proteins of 95 residues or more whose sequences contain 6% or more Met by using a java script. Genes satisfied these conditions were named Met-rich proteins (MRP); AtMRPs for genes from *Arabidopsis* and GmMRPs for genes from soybean. Genes encoding MRPs were classified into various functional categories using MAPMAN (Thimm et al., 2004). PFAM database (<http://pfam.xfam.org/>) was used to search for HMM profiles as well as possible protein domains. To obtain transcription levels, microarray data from previous studies were mined, including datasets for *Arabidopsis* under drought and salinity stress (Nishiyama et al., 2012; Nishiyama et al., 2013) and soybean under experimental drought condition (Le et al., 2012).

References

- Le et al., 2012. Differential gene expression in soybean leaf tissues at late developmental stages under drought stress revealed by genome-wide transcriptome analysis. *PIOS ONE*, 7:e49522
- Nishiyama et al., 2012. Transcriptome analyses of a salt-tolerant cytokinin-deficient mutant reveal differential regulation of salt stress response by cytokinin deficiency. *PIOS ONE*, 7:e32124.
- Nishiyama et al., 2013. *Arabidopsis* AHP2, AHP3, and AHP5 histidine phosphotransfer proteins function as redundant negative regulators of drought stress response. *PNAS*, 110:4840-4845.
- Thimm et al., 2004. MAPMAN: a user-driven tool to display genomics data sets onto diagrams of metabolic pathways and other biological processes. *The Plant journal*, 37:914-939

CONCLUSIONS

- 121 and 213 genes encoding methionine-rich proteins in *Arabidopsis* and soybean, respectively.
- Expression data mining indicated 57 and 35 genes encoding MRP in *Arabidopsis* and soybean, respectively, responsive to either drought or high salinity stresses
- HMM profiles of stress-responsive MRP contain several conserved Met residues.
- Among 121 AtMRPs, 21 were predicted to localized in chloroplast, while 9 were targeted to mitochondria, the two cellular organelles with elevated ROS levels