Expression profiling of genes encoding Methionine Sulfoxide Reductase in soybean plants under normal and stress conditions[1]

Ha Duc Chu,[1] Kim-Lien Nguyen,[1] Lam-Son Phan Tran,[2] Dung Tien Le[1,2,]*

[1]National Key Laboratory of Plant and Cell Technology, Agricultural Genetics Institute, Vietnam Academy of Agricultural Sciences, Pham Van Dong Road, Hanoi, Vietnam

[2]Signaling Pathway Research Unit, RIKEN Center for Sustainable Resource Science, Yokohama, Japan

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ABSTRACT

Plant protein can be oxidized at its methionine residues to form methionine sulfoxide (MetO). Met-R-O, one of the two MetO isomers, can be reduced by 5 methionine-R-sulfoxide reductases (GmMSRBs). In this work, we determined transcript levels of GmMSRBs in various tissues treated or untreated with abiotic stress. Under normal conditions, expression levels were highest in leaves followed by roots, and lowest in pod and seeds. Transcripts of GmMSRB1 in the leaves were the highest; at the same time, GmMSRB5 was shown to express the lowest levels. In seedling shoots, GmMSRB2 and GmMSRB5 were induced upon dehydration. In V6 trifolia, only GmMSRB3 was induced under drought. In R2 trifolia, the expression of GmMSRB2 and 5 was induced by drought treatment. Under salt stress, GmMSRB1was down-regulated in seedling shoots and GmMSRB5 was up-regulated in seedling roots. Treatment with ABA did not affect the transcript levels of any GmMSRBs in seedling shoots. However, this treatment up-regulates GmMSRB2 in seedling roots. Taken together, our data suggested that GmMSRBs may play a role in the adaptation of soybean plants to multiple environmental stress, providing useful candidate genes for further characterization toward engineering improved stress-tolerant crops.

MATERIALS & METHODS

Dehydration stress treatment and samples collection of seedling plants were performed as described earlier (Le et al., 2011). The sample collections of V6 vegetative and R2 reproductive stages were described elsewhere (Le et al., 2012). For salt stress and abscisic acid (ABA) treatments, seeds were germinated in 6-litre pots containing vermiculite and were allowed to grow in greenhouse conditions (continuous 30ºC temperature, photoperiod of 12 h/12 h). At 12th-day old, the seedlings were carefully pulled out and washed to remove excess soil, then transferred to either distilled water (water control treatment), 250 mM NaCl or 100 µM ABA for 2 hr and 10 hr. After exposure to treatments for indicated durations, the roots and shoots of soybean plants were collected separately and immediately frozen in liquid nitrogen until RNA isolation was performed.

The isolation of RNA, DNAse I treatment and cDNA synthesis as well as qPCR experiment and data analyses were performed exactly as reported earlier (Le et al., 2011).

Soybean used in this study was *Glycine max* L. var. Williams 82.

RESULTS

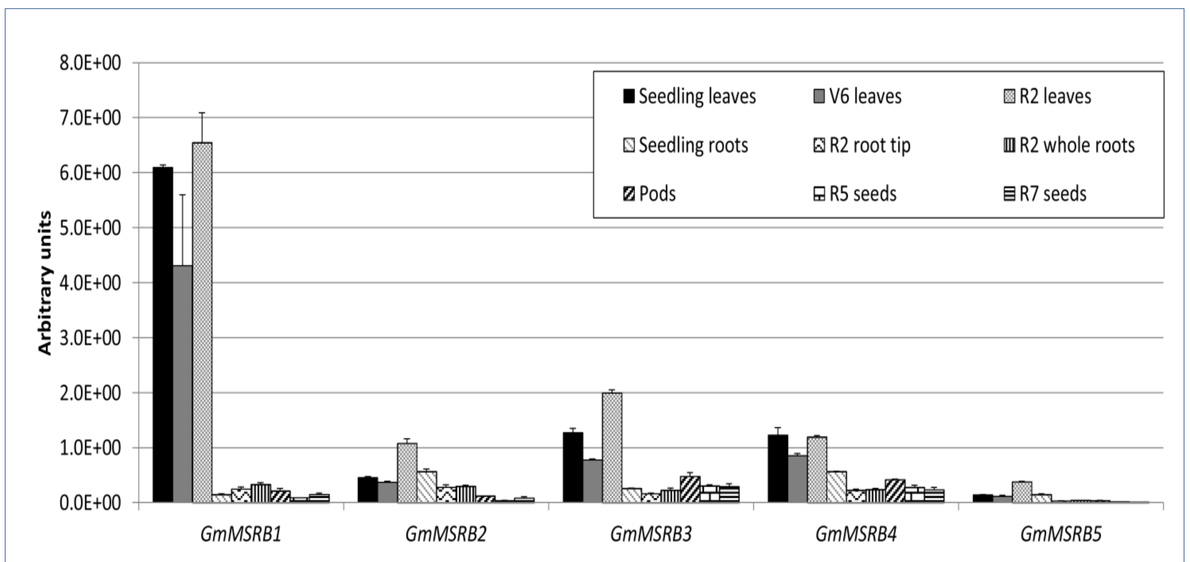

Figure 1. Expression profiles of GmMSRBs in various tissues under normal physiological condition.

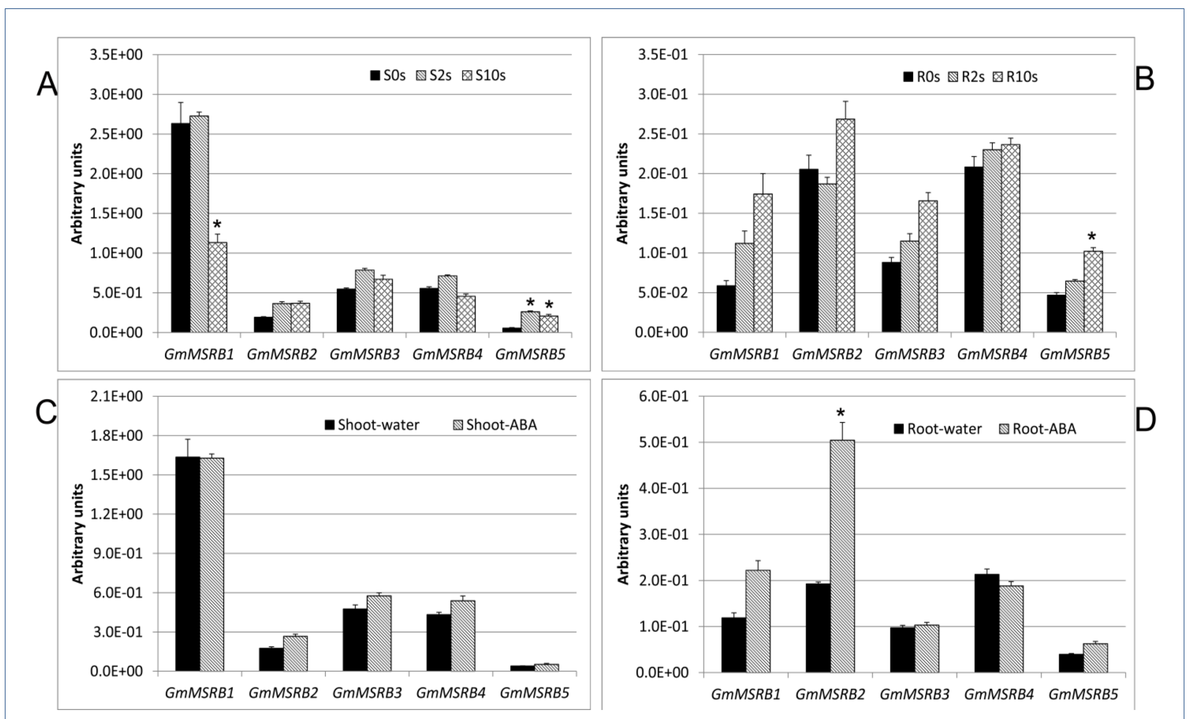

Figure 3. Expression profiles of GmMSRBs in young seedlings under normal and salt (A & B) or ABA (C & D) treatments.

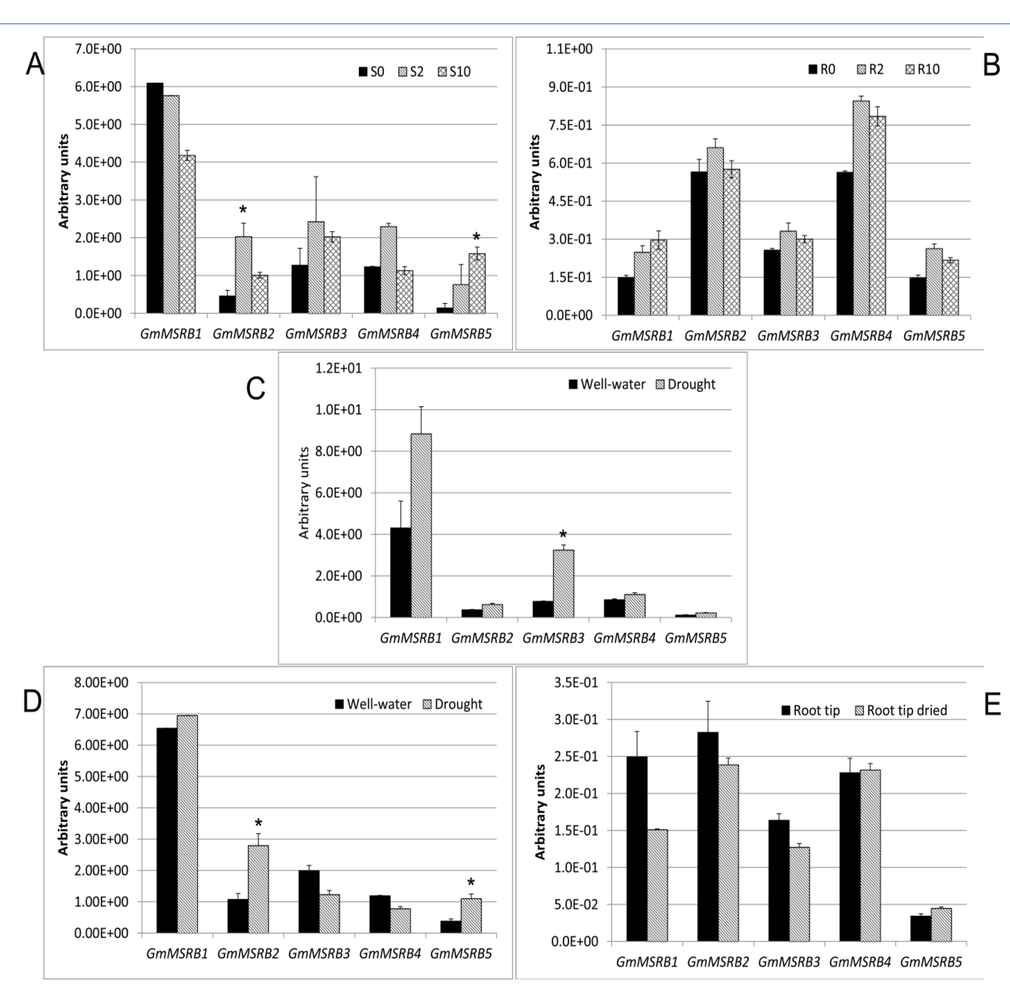

Figure 2. Expression profiles of GmMSRBs in seedlings shoots (A) & roots (B), V6 trifoliate (C) and R2 trifoliate (D) and root tips (E) under normal and drought or dehydration stress.

Table 1. Expression responsiveness to stresses of GmMSRBs

	Drought - Dehydration					Salt		ABA	
	Leaves			Roots		Seedlings		Seedlings	
	Seedlings	V6	R2	Seedlings	R2	Shoots	Roots	Shoots	Roots
GmMSRB1						Down			
GmMSRB2	Up		Up						Up
GmMSRB3		Up							
GmMSRB4									
GmMSRB5	Up		Up			Up	Up		

CONCLUSIONS & REFS.

1. GmMSRB1, GmMSRB3 and GmMSRB4 genes encoding enzymes targeted to chloroplast were highly expressed in the leaf tissues.
2. GmMSRB2 and GmMSRB5 were the most induced genes upon exposure to drought/dehydration, high salinity or ABA treatment.
3. GmMSRB4 gene was unresponsive to the stresses or hormone treatment in this study.

References

1. Le et al., 2011, DNA research, 18:17-29
2. Le et al., 2012a, PLOS ONE, 7:e42411
3. Le et al., 2012b, PLOS ONE 7: e46487
4. Le et al., 2013, PLOS ONE 8:e65637