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## Plant microRNAs and Stressors: A Commentary on Stress-responsive miRNAs in *Glycine max* (L.) Merrill

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### Editorial

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### INTRODUCTION

Small non-coding RNAs (sncRNAs) are potent regulators of indispensable biological functions such as gene expression, maintenance of chromatin status, defence against invading nucleic acids like viruses, transposons etc in plants and animals. sncRNA repertoire of plants comprises small interfering RNAs (siRNAs) and microRNAs (miRNAs) as ultimate regulators of gene expression pathways. First small ncRNA (*lin-4*) with a role in post-transcriptional gene silencing (PTGS) was discovered way back in 1993 in *C. elegans* [1]. Nonetheless, it was not until 1998 the basic phenomenon of sequence dependent RNA based gene silencing or RNA interference (RNAi) itself was uncovered. Later on, the significance of sRNAs especially, miRNAs and their role in multitude of host developmental and growth activities including response to biotic and abiotic stresses were reported. miRNAs downregulate expression of cognate mRNAs that exhibit sequence complementary thereby functions as negative regulators of such genes. Hence under the influence of stress, miRNAs that are upregulated lead to repression of cognate mRNAs whereas miRNAs whose levels are suppressed result in abundant target mRNAs which may assist the plants tide over adverse stress conditions.

Initial reports of plant derived miRNAs were based on the computational identification of sRNAs using the sequence and secondary structural features derived from model organisms and extrapolating it to other non-model species [2]. However, advent of next generation sequencing (NGS) and miRNA microarray based detection methodologies have unearthed voluminous sequence information with regard to sRNAs and computational analysis further complemented it in characterizing the molecular functions of such sRNAs. In addition deep sequencing approaches identified many non-conserved miRNAs along with information of spatio-temporal regulations in miRNA expression patterns [3-7]. Soybean is an important grain legume where the significance of sRNAs and their utility in crop improvement programmes have been very well recognized. At present the sRNA database miRBase hosts 573 miRNA precursors and 639 mature miRNAs derived from soybean (<http://www.mirbase.org/>). Some of the stress responsive miRNAs reported in soybean has been portrayed in the Table 1.

Among these stress responsive sRNAs, it was discerned that conserved plant miRNAs are very commonly represented. Conserved miRNAs share sequence homology with other miRNAs in plant kingdom. It is tempting to speculate that these conserved genes encoding miRNAs might have been selected and preserved in plant genomes in the course of evolution. Besides their principal role in stress responsiveness, these miRNAs have been known to play or acquired other ancillary functions in the cellular milieu [7]. The theory on plant miRNA gene evolution also accounts for the observed little sequence variations in the miRNA genes and acquisition of supplementary roles by miRNAs in course of evolution. Furthermore conserved miRNAs with antiviral potential is desired in engineering virus resistance in crops based on artificial miRNA (amiRNA) based viral gene silencing. Mature miRNAs

derived from conserved or legume specific miRNAs generally cleave a set of conserved target transcripts compared to soybean derived miRNAs [14]. In addition genome organization of soybean specific miRNAs reveal that they are actively evolving and their functional categorization divulge continuous diversification [14].

**Table 1:** Stress responsive miRNAs in soybean.

S.No	Stress responsive miRNAs	Reference
1	<i>B. japonicum</i> responsive miRNAs: miR168 and miR172	[3]
2	EST, genome database screening and qRT-PCR validated 69 miRNAs belonging to 33 families	[8]
3	Drought and rust responsive miRNAs 256 miRNAs representing 24 families	[9]
4	Drought, salinity and alkalinity stress 133 miRNAs belonging to 95 families	[10]
5	Soybean cyst nematode infection 101 miRNAs belong to 40 families	[11]
6	Salt-stress responsive 104 miRNAs	[12]
7	Begomovirus resistance	[13]

Importance of miRNAs in overall growth and development of plants is emphasized considering the following observations: Plants with impaired sRNA metabolism or miRNA biogenesis mutants are vulnerable for external stresses like pathogens especially viral infections; miRNAs have been observed to target mRNAs that encode transcriptional factors (TFs) thus miRNAs are vital to the main gene regulatory networks; miRNAs derived from Leguminous and Solanaceous plants have been implicated in innate immune response system as they are known to alter the expression levels of NBS-LRR genes; In the absence of viral genome encoded RNA silencing suppressors, small RNAs effectively repress the expression of virus genes; On application front, artificial miRNA (amiRNA) based gene silencing platforms are widely employed in engineering desired crop phenotypes [7].

The greatest challenge in the sRNA research is to decipher the definitive role of such stress responsive miRNAs in the cellular milieu and to propose a comprehensive molecular mechanism of plant's response to biotic and abiotic stresses [15]. The foremost step in this direction is to identify the target mRNA that are regulated by the activity of these miRNAs. miRNA arrest, target mimicry approach, decoy miRNAs are valuable functional genomics tool in this endeavour. Development of soybean miRNA functional network (miRFN) on a system-wide level is a valuable addition in defining soybean sRNA transcriptomics (<http://nclab.hit.edu.cn/SoymiRNet>). [16]. Moreover a recently developed sRNA atlas of soybean discloses the role of miRNAs in triggering the expression of phased siRNAs (phasiRNAs from PHAS loci). Interestingly more than one third of PHAS loci encode NBS-LRR genes further corroborating the centrality of miRNAs in triggering plant stress response [17]. Further molecular cross-talk between biotic and abiotic stressors via miRNAs is an active area of research as it provides information regarding molecular fine tuning that occurs in the interface of environmental stress and developmental regulations. Thus to conclude it is suffice to state that function of miRNAs under the influence of stressors is indispensable, diverse, and it warrants complete molecular dissection studies to improve our understanding of gene regulatory networks.

## REFERENCES

1. Lee RC, et al. The *C. elegans* heterochronic gene *lin-4* encodes small RNAs with antisense complementarity to *lin-14*. Cell. 1993; 75: 843-854.
2. Wen J, et al. Computational prediction of candidate miRNAs and their targets from *Medicago truncatula* non-protein coding transcripts. In Silico Biol. 2008; 8: 291-306.
3. Subramanian S, et al. Novel and nodulation-regulated microRNAs in soybean roots. BMC Genomics 2008; 9: 160
4. Shuai P, et al. Identification of drought-responsive and novel *Populus trichocarpa* microRNAs by high-throughput sequencing and their targets using degradome analysis. BMC Genomics. 2013; 14: 233.
5. Gupta OP, et al. MicroRNA mediated regulation of metal toxicity in plants: present status and future perspectives. Plant molecular biology. 2014; 84: 1-18.
6. Xie F, et al. High-throughput deep sequencing shows that microRNAs play important roles in switchgrass responses to drought and salinity stress. Plant Biotechnology Journal. 2014; 12: 354-366.
7. Ramesh SV, et al. Plant miRNAome and antiviral resistance: a retrospective view and prospective challenges. Virus genes. 2014; 48: 1-14.
8. Zhang B, et al. Identification of soybean microRNAs and their targets. Planta. 2008; 229: 161-182.
9. Kulcheski FR, et al. Identification of Novel Soybean MicroRNAs Involved in Abiotic and Biotic Stresses. BMC Genomics. 2011; 12: 307.
10. Li H, et al. Characterization of the stress associated microRNAs in *Glycine max* by deep sequencing. BMC Plant Biol. 2011; 11: 170
11. Li X, et al. Identification of Soybean MicroRNAs Involved In Soybean Cyst Nematode Infection by Deep Sequencing. 2012; PLoS ONE 7.

12. Ding Y, et al. Emerging roles of microRNAs in the mediation of drought stress response in plants. *Journal of Experimental Botany*. 2013; 64: 3077-3086.
13. Ramesh SV and Pappu HR. Plant miRNAome and soybean infecting Begomovirus genomes Identification of innate plant small RNAs in antiviral resistance. *Phytopathology*. 2014; 104: 107.
14. Turner M, et al. Genome organization and characteristics of soybean microRNAs. *BMC genomics*, 2012; 13: 169.
15. Ni Z, et al. Overexpression of gma-MIR394a confers tolerance to drought in transgenic *Arabidopsis thaliana*. *Biochemical and Biophysical Research Communications*. 2012; 427: 330-335.
16. Xu Y, et al. Inferring the soybean (*Glycine max*) microRNA functional network based on target gene network. *Bioinformatics*. 2014; 30: 94-103.
17. Arikat S, et al. An Atlas of Soybean Small RNAs Identifies Phased siRNAs from Hundreds of Coding Genes. *The Plant Cell Online*. 2014; 114.