

M-13

The evolutionary novelty of microRNAs and their targets in soybean and other legumes  
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Small RNAs are ubiquitous, versatile repressors and include (a) microRNAs (miRNAs), processed from mRNA forming stem-loops, and (b) small interfering RNAs (siRNAs), the latter derived in plants by a process typically requiring an RNA-dependent RNA polymerase. My lab, with collaborators, has conducted extensive genome-wide analyses of soybean small RNAs; from these data we have found that soybean contains the highest number of loci generating 21-nt 'phased' siRNAs (phasiRNAs, from *PHAS* loci) of any eudicot yet examined - over 500 loci, of which 483 overlapped annotated protein-coding genes. The miRNA triggers for many of these *PHAS* loci were detected, and molecular analyses provides insights into the mechanisms by which these small RNAs are generated. The primary class of *PHAS* loci (>40% of the total) corresponded to NB-LRR genes; some of these small RNAs preferentially accumulate in nodules. Several miRNAs are particularly interesting due to their emergence only in soybean or closely related legumes. For example, one locus demonstrating high abundance of small RNAs in the anthers of soybean is a non-coding *PHAS* locus, triggered by miR4392. The phasiRNAs are predicted to target transposable elements (TEs), with their peak abundance during soybean reproductive development. In addition, the most widespread trigger of phasiRNAs from NB-LRRs in soybean, miR1510, demonstrates recent emergence and an unusual pattern of biogenesis. I will discuss these and other insights into soybean small RNAs.