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miRNA/phasiRNA mediated regulation of plant defense response against P. syringae

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Gene silencing is a mechanism of regulation of gene expression where the small RNAs (sRNAs) are key components for giving specificity to the system. In plants, two main types of noncoding small RNA molecules have been found: microRNAs (miRNAs) and small interfering RNAs (siRNAs). DCL proteins acting on large RNA precursors produce the mature forms of sRNAs (20-24nt) that can act as negative regulators of gene expression. In recent years, the role of miRNAs in regulation of gene expression in plant responses against bacterial pathogens is becoming clearer. Comparisons carried out in our lab between expression profiles of different *Arabidopsis thaliana* mutants affected in gene silencing, and plants challenged with *Pseudomonas syringae* pathovar tomato DC3000, led us to identify a set of uncharacterized R genes, belonging to the TIR-NBS-LRR gene family, as differentially expressed in these conditions. Through the use of bioinformatics tools, we found a miRNA* of 22 nt putatively responsible for down-regulating expression of these R genes. We have validated this regulation, and have also established that the corresponding pri-miRNA is down-regulated upon PAMPs or bacteria perception. Using GUS reporters, we have characterized the expression pattern of both pri-miRNA and its best target R genes. We demonstrate that plants with altered levels of miRNA* (knockdown or overexpression lines) exhibit altered PTI-associated phenotypes, supporting a role for this miRNA* in the defence response against this bacterial pathogen. Finally, we identify phasiRNAs that arise from the transcript of one of the R target genes in a miRNA*-RDR6-DCL4-dependent manner.