

A**Predicted target genes of DEmiRNA at 21 dpi (TYLCV/mock)**

PANTHER GO Slim Biological Process	GO terms	Ref-list (34652)	Genes	Expect.	Fold Enrich.	raw P-value	FDR
Response to stress	GO:0006950	662	43	6.78	6.34	5.09E-21	9.45E-19
Defense response	GO:0006952	188	38	1.93	19.73	8.45E-35	1.79E-32
Defense response to other organism	GO:0098542	146	38	1.50	25.41	2.21E-38	8.19E-36
Multicellular organism development	GO:0007275	121	9	1.24	7.26	7.69E-06	5.71E-04
System development	GO:0048731	95	9	0.97	9.25	1.21E-06	9.97E-05
Shoot system development	GO:0048367	69	9	0.71	12.73	1.01E-07	8.83E-06
Developmental process	GO:0032502	196	9	2.01	4.48	2.66E-04	1.72E-02
Anatomical structure morphogenesis	GO:0009653	65	9	0.67	13.52	6.34E-08	5.89E-06
Multicellular organismal process	GO:0032501	124	9	1.27	7.08	9.25E-06	6.55E-04
Morphogenesis of a branching structure	GO:0001763	18	8	0.18	43.38	1.38E-10	1.71E-08

B**Predicted target genes of DEmiRNA at 21 dpi (TYLCV/mock)****Mapman ontology**

BIN	BIN name	DEGs	p-value
20	stress	43	0.006
20.1	stress.biotic	41	0.001
30	signalling	18	0.029
30.2	signalling.receptor kinases	15	0.009
30.2.11	signalling.receptor kinases.leucine rich repeat XI	14	0.009

Additional file 9: Fig. S9. Functional enrichment of the predicted target genes from the DEmiRNAs in response to TYLCV infection at 21 dpi. A) Gene ontology (GO) analysis using the PANTHER GO-Slim biological process (statistical overrepresentation test) of all the predicted targets from DEmiRNAs at 21 dpi (684 miRNAs-targets pairs, 470 unique targets). Selected statistically significant biological processes are shown (FDR adjusted p-value ≤ 0.05). B) MapMan ontology of predicted DE targets of DEmiRNAs at 21 dpi (352 miRNAs-targets pairs, 235 unique targets). Selected statistically significant MapMan BINs are shown (Wilcoxon test and Benjamini-Hochberg FDR adjusted p-values ≤ 0.05).