

Supplementary Tables

Table S1. Temperature values (average $\pm$ standard deviation) in $^{\circ}\text{C}$, taken from the leaf surface of plants grown under high and low light conditions. Fifty temperature measurements were performed in each case.

Light conditions	Leaf temperature ($^{\circ}\text{C}$)
High Light	21.542 $\pm$ 1.597
Low Light	21.747 $\pm$ 1.549

Table S2. Number of plants exhibiting spontaneous systemic silencing or spontaneous short-range silencing (SSRS) under high and low light conditions over the total number of plants examined (5.1 and 5.3 line).

Light conditions	Number of plants exhibiting systemic silencing / total number of plants examined (%) 5.1 line		
	(≤ 10)#	(11-20)#	(21-30)#
High Light	20/179 (11%)	41/179 (23%)	42/179 (24%)
Low Light	7/191 (4%)	18/191 (9%)	20/191 (11%)
Light conditions	Number of plants exhibiting SSRS / total number of plants examined (%) 5.1 line		
	(≤ 10)#	(11-20)#	(21-30)#
High Light	48/179 (27%)	127/179 (71%)	129/179 (72%)
Low Light	38/191 (20%)	83/191 (44%)	99/191 (52%)
Light conditions	Number of plants exhibiting SSRS / total number of plants examined (%) 5.3 line		
	(≤ 10)#	(11-20)#	(21-30)#
High Light	56/90 (62%)	78/90 (87%)	84/90 (93%)
Low Light	25/126 (20%)	92/126 (73%)	101/126 (80%)

Number of leaves indicative of the growth stage.

Table S3. Number of silencing spots (SSRS events) over cm² of leaf area (average ± standard deviation) appeared on plants grown under high and low light conditions (6.4 line).

Light conditions	Number of spots / cm ²
High Light	0.087 ± 0.014
Low Light	0.107 ± 0.009

Table S4. Sequence homology values (%) between *N. benthamiana* DCL gene fragments and the corresponding *A. thaliana* DCL orthologue.

<i>N. benthamiana</i> DCL gene fragment	Nucleotide identity	Amino-acid identity	Amino-acid similarity
<i>DCL1</i>	76.7 %	89.9 %	93.7%
<i>DCL2</i>	64.6 %	63.8 %	75.9%
<i>DCL3</i>	58.5 %	51.5 %	72.2%
<i>DCL4</i>	63.6 %	51.7%	65.5%

Table S5. Amino-acid identity and similarity values (%) between *N. benthamiana* DCL fragments and *A. thaliana* DCL1-4.

<i>N. benthamiana</i> DCL gene fragment	Amino-acid identity/similarity with the <i>A. thaliana</i> DCL			
	AtDCL1	AtDCL2	AtDCL3	AtDCL4
DCL1	89.9%/93.7%	55.1%/71.0%	61.2%/77.6%	45.6%/61.8%
DCL2	36.5%/50.2%	63.8%/75.9%	40.2%/54.2%	38.8%/55.5%
DCL3	30.5%/45.3%	30.4%/50.0%	51.5%/72.2%	29.0%/42.0%
DCL4	31.6%/50.4%	25.7%/54.5%	29.3%/46.4%	51.7%/65.5%

The cloned *NbDCL1*, *NbDCL2*, and *NbDCL4* gene fragments encode a part of the second RNaseIII domain, whereas the *NbDCL3* fragment corresponds to a part of the second double-stranded RNA binding domain.

Table S6. Relative expression ratio values (average $\pm$ standard deviation) for high over low light grown plants as determined by real-time qPCR analysis in different types of leaf tissue.

Type of leaf tissue	Gene of Interest					
	<i>DCL1</i>	<i>DCL2</i>	<i>DCL3</i>	<i>DCL4</i>	<i>AGO1</i>	<i>RDR6</i>
GFP silenced (6.4 line)	3.869 $\pm$ 0.792	1.734 $\pm$ 0.201	6.273 $\pm$ 0.069	2.152 $\pm$ 0.723	1.213 $\pm$ 0.182	1.704 $\pm$ 0.200
GFP non-silenced (6.4 line)	0.982 $\pm$ 0.278	1.937 $\pm$ 0.332	1.813 $\pm$ 0.216	1.937 $\pm$ 0.206	1.487 $\pm$ 0.023	2.426 $\pm$ 0.222
GFP stably expressing (16C line)	0.996 $\pm$ 0.216	1.551 $\pm$ 0.072	2.559 $\pm$ 0.229	1.916 $\pm$ 0.290	0.893 $\pm$ 0.225	0.929 $\pm$ 0.062
Wild type	0.945 $\pm$ 0.103	1.158 $\pm$ 0.083	0.920 $\pm$ 0.079	1.785 $\pm$ 0.192	0.802 $\pm$ 0.120	1.019 $\pm$ 0.030

Table S7. Number of plants exhibiting spontaneous systemic silencing under blue and red light conditions over the total number of plants examined (6.4 line, ≤ 5 leaf stage).

Light conditions	Number of plants exhibiting systemic silencing / total number of plants examined (%)
Blue Light	6/27 (22%)
Red Light	4/32 (13%)

Table S8. Number of plants exhibiting spontaneous short-range silencing (SSRS) under blue and red light conditions over the total number of plants examined (6.4 line, ≤ 5 leaf stage).

Light conditions	Number of plants exhibiting SSRS / total number of plants examined (%)
Blue Light	3/27 (11%)
Red Light	0/32 (0%)

Table S9. List of primer sequences used in quantitative real-time PCR assays.

Primer ID	Primer sequence 5' - 3'
DCL1_FOR	TGTGGGTGATGCAGTATT
DCL1_REV	TGAAACCTGGTTTTGATAGT
DCL2_FOR	CGGGATCC-CCGGGATTTATTTCGTAAT
DCL2_REV	CCCTCGAG-AATGACAAAGCCGCTACT
DCL3_FORa	ACTTGTTGAATGCGGTGAAG
DCL3_REVa	CCCCTGTCGTTCTAGCTCAT
DCL3_FORb	GGGGAGGAATTGAATCTTCTG
DCL3_REVb	TCCAGTATGAATGGCCACAA
DCL4_FORa	CGTCCGTGCCCAGAAATCT
DCL4_REVa	AATGCAATTGCCGCTTTGA
DCL4_FORb	GCACTTACTACAGAGAAATGCAATG
DCL4_REVb	ACAATGTTTGAGCGCCTTCT
AGO1_FOR	GCTCTAGAAGATCTGTACAAGACTTGGC
AGO1_REV	CGAATTCTTATTGGCAAACAACCTAGT
RDR6_FOR	CTTTGGATGAGAAGTGCCTA
RDR6_REV	TTTGGGACAAGCTCAAGTC
UBI3_FOR*	GCCGACTACAACATCCAGAAGG
UBI3_REV*	TGCAACACAGCGAGCTTAACC
EF1_FOR*	GATTGGTGGTATTGGAAGTGC
EF1_REV*	AGCTTCGTGGTGCATCTC

*These primers sequences were used in Rotenberg *et al.* (2006).