Genetic mapping of natural variation for a shade avoidance response in *Arabidopsis thaliana: ELF3* is a candidate gene for *EODINDEX1* QTL

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Supplementary material

Table S1: List of primer sequences used for qRT-PCR expression analysis.

Primer	**Sequence (5’ – 3’)**
PP2A-F	TAACGTGGCCAAAATGATGC
PP2A-R	GTTCTCCACAACCGCTTGGT
CCA1-F	CCAGATAAGAAGTCACGCTCAGAA
CCA1-R	GTCTAGCGCTTGACCCATAGCT
LHY-F	GACTCAAACACTGCCCAGAAGA
LHY-R	CGTCACTCCCTGAAGGTGTATTT
TOC-F	TCTTCGCAGAATCCCTGTGAT
TOC-R	GCTGCACCTAGCTTCAAGCA
PRR7-F	CTAACCCTGAGTTTCCAAGTAATC
PRR7-R	CCCATTGTGACATCTTCAAATT
PRR9-F	GCCAGAGAGAAGCTGCATTGA
PRR9-R	CCTGCTCTGGTACCGAACCTT
ELF3- F	CATTCGCAGCCGTTGATGAGG
ELF3-R	TGTTCTTGTCGTCGTTGTGGTTG
TZP- F	GGCTCGGGAAATGGGAAGAAG
TZP-R	ACTCAACAAGGCAAGTCACACC

Table S2: Summary statistics for hypocotyl length under WL, WL+EOD and EOD index. Data are means ± SE.

	WL	WL+EOD	EOD index [(WL+EOD) – WL] / (WL+EOD)
Bay	3.93 ± 0.74	7.08 ± 0.84	0.40 ± 0.04
Sha	6.78 ± 0.66	7.80 ± 0.56	0.10 ± 0.04
RIL mean	5.58 ± 1.65	8.09 ± 1.56	0.31 ± 0.01
RIL max – min	2.33 – 10.70	4.43 – 11.53	0.05 – 0.61
H^2	0.88	0.81	0.73

H^2 is defined as broad sense heritability calculated as σG2/σz2. H^2 is the proportion of the total phenotypic variance that is genetic (Vg/(Vg+Ve)).

Table S3: QTL mapping for hypocotyl length under WL, WL+EOD and EOD index in Bay x Sha RIL population.

			WL				WL + EOD				EOD index [(WL+EOD) – WL] / (WL+EOD)			
QTL	Closest marker (# Chrom)	Position (cM)	LOD	Interval (cM)	2xADD (mm)	Variab. (%)	LOD	Interval (cM)	2xADD (mm)	Variab. (%)	LOD	Interval (cM)	2xADD	Variab. (%)
WL1	MSAT5.9 (CV)	44.4	17.80	39-49	-2.19	44								
WL2	MSAT2.41 (CII)	36.5	9.44	33-40	-1.98	19								
*WL3****	NGA248 (CI)	26.9	2.82	15-38	0.81	6								
EOD1	MSAT5.9 (CV)	45.4					17.57	40-49	-2.15	47				
EOD2	NGA248 (CI)	30.9					4.66	20-38	1.18	14				
EODINDEX1*	MSAT2.41 (CII)	35.5									14.94	31-40	0.13	31
*EODINDEX2***	MSAT5.9 (CV)	44.9									8.67	38-49	0.10	19
EODINDEX3	MSAT1.13 (CI)	81.4									3.21	70-84	0.06	6.9
EODINDEX4	NGA128 (CI)	50.1									2.84	43-64	0.06	6.0

**EODINDEX1* colocalized with *WL2* QTL.

***EODINDEX2* colocalized with *WL1* and *EOD1* QTL.

****WL3* colocalized with *EOD2* QTL.

Figure S1: Polymorphisms found in *ELF3* sequence of Bay and Sha accessions. Exon sequences in upper case, introns in lower case and nucleotide changes highlighted in grey.

Genomic sequence

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    508                          1171
Bay ctt atg att gcc ctg ......... ATG GCA GTC CTG AAG
Sha ctt gtg att gcc ctg ......... ATG GTA GTC CTG AAG
    1594                         1609
Bay cac tct cct tca tat ......... ttt ttt tca tga tta
Sha cac gct cct tca tat ......... ttt ttt -ca tga tta
    1819                         2170
Bay aca ttg gat cat gtt ......... gat tgt agg ctt cat
Sha acg ttg gat cat gtt ......... gat tat agg ctt cat
    2635                         2710
Bay tat gct tcc atg agt ......... CTT ATT GCT GCA TCA
Sha tat gtt tcc atg agt ......... CTT ATT GTT GCA TCA
    3283                         3298
Bay CAA CAA CAA CAA CAA ......... CAA CAA CAA CCC AAT
Sha CCC AAT GAG CAA ATG ......... AAC CAG TTT GGA CAT
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