

**The Gene *ANTHER DEHISCENCE REPRESSOR (ADR)*
Controls Male Fertility by Suppressing the ROS
Accumulation and Anther Cell Wall Thickening in
*Arabidopsis***

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ADR      : MGGSTSKDERNSSKRRIRKVKANEQ-R-RRETRELEDEKERVILALKMAE
At3g23930 : MGGCTSKQERRGV-RSVKETSKDQSRGRRHLIKERDEREKVMFLQLKEAE

ADR      : TEWRKERKRLREEVKRLRQKMEEEKKEGKA---KQHE-WEWVVEQMCLERA
At3g23930 : REWRKERKRLREEVRLRKLLEEREAKTTTTEEREYWKWVVEEMCVERA

ADR      : VREEAVERWKQLYFAIKNELDDLI-HTTY--GEALRQKP---QEEV---A
At3g23930 : VRDEAVEKWKQLYLAIKNELDHLISHTTSSSGEAIMQRKLEEQEEETEBA

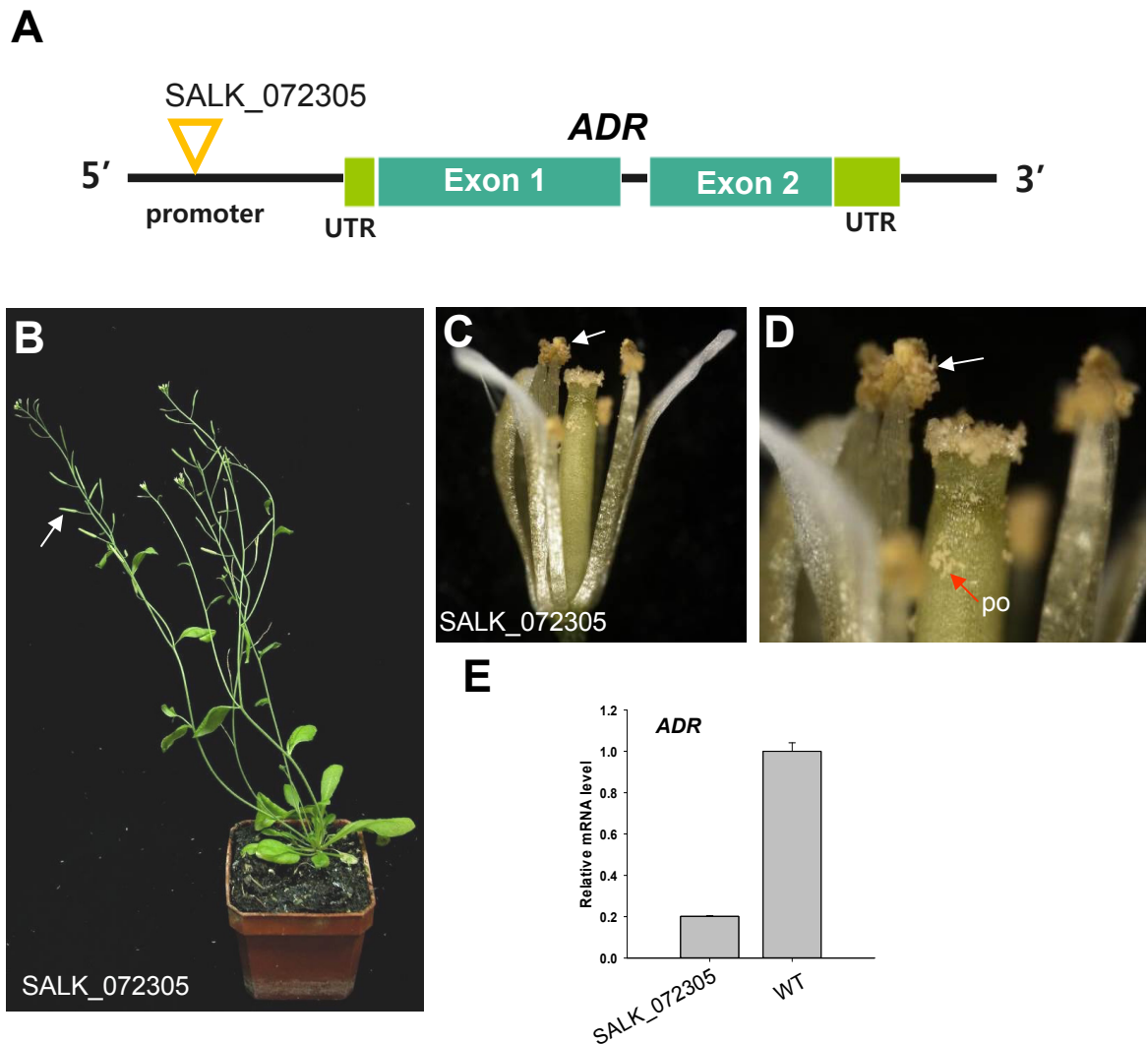
ADR      : KAVQELRKEVKARGETIETLKGRIINLMEKQONGKEREIDLLRQSLRILGG
At3g23930 : KRVEVLRDEVRVKKEETVETLEEQIVLMDRQKYEKEREIDLLRQSLRILG-

ADR      : SSGKNKALSSTTRNLTVFKTKFIGCK
At3g23930 : SKKKKKTGSFASMNLLILKTKCVECT

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Supplementary Figure S1. Protein sequence comparison of *Arabidopsis* ADR and ADR-like gene At3g23930.

Protein sequence comparison of ADR (At4g13540) and other *Arabidopsis* ADR-like proteins (At3g23930). The ADR protein contains a predicted recognition site for N-myristoylase (in the blue box), N-terminal basic residues (in the red box) and a predicted binding site for a peroxisomal targeting signal (in the green box). Dashes were introduced to improve alignment. The amino acid sequences were aligned by the BIOEDIT program (<http://www.mbio.ncsu.edu/BioEdit/bioedit.html>) using CLUSTALW MULTIPLE ALIGNMENT with default parameters.



Supplementary Figure S2. Phenotypic analysis and the detection of gene expression in *ADR* T-DNA insertion line SALK_072305.

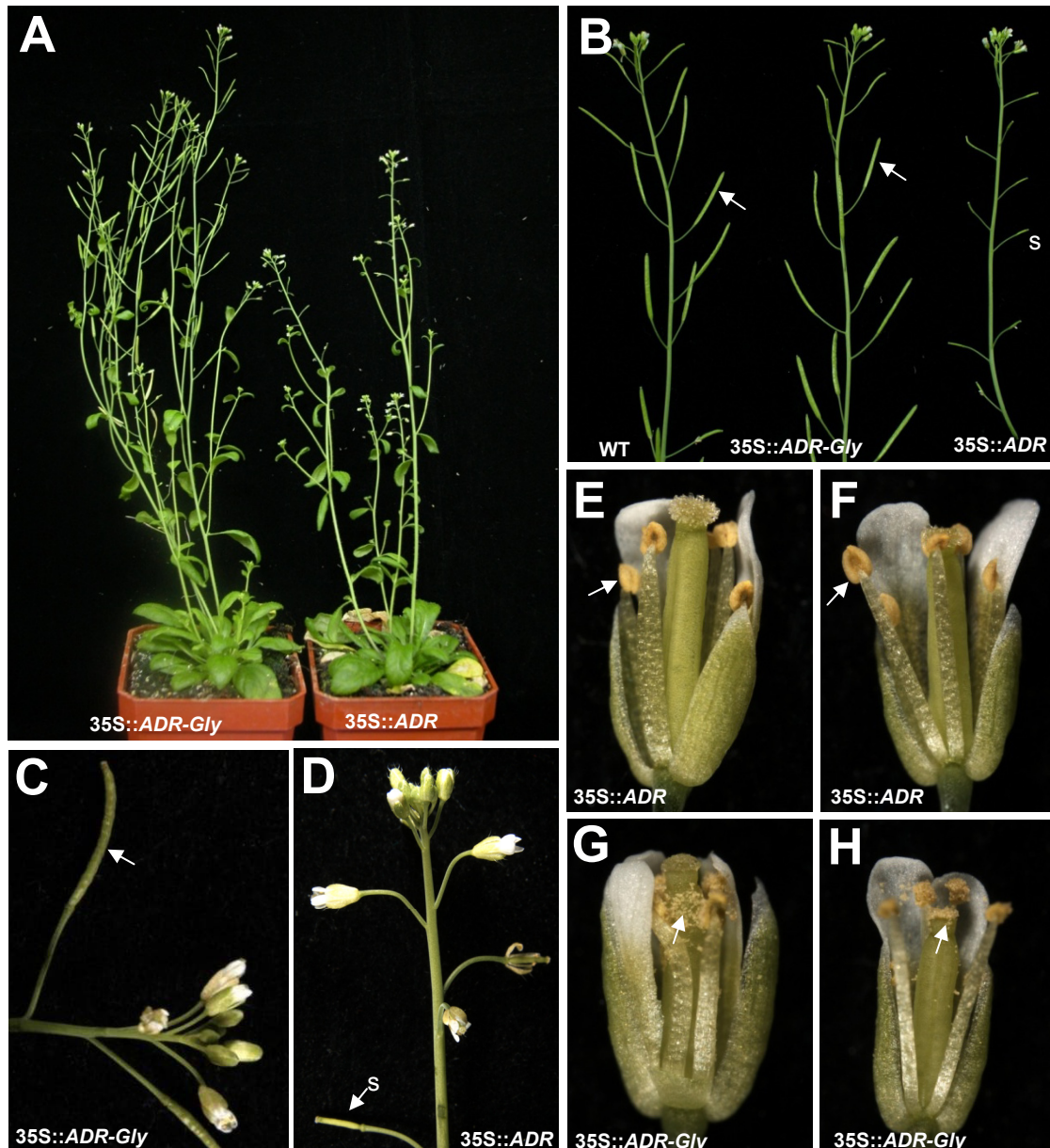
(A) Genomic region of *ADR*. Green boxes and blue boxes represent UTR and exons for *ADR* cDNA, respectively. Triangle indicates the location of T-DNA insertion in promoter region in SALK_072305 mutants.

(B) A 40-day-old SALK_072305 plant was phenotypically indistinguishable from wild-type plants and produced long, well-developed siliques (arrowed).

(C) Dehiscent anthers (arrowed) were observed in SALK_072305 flowers.

(D) Close-up of the SALK_072305 dehiscent anthers (arrowed) with released pollen (po) from (C).

(E) Detection of *ADR* expression in SALK_072305 mutant and wild-type (WT) Arabidopsis. mRNA accumulation for *ADR* was determined by real-time quantitative PCR. Gene expression level in SALK_072305 plant is presented relative to that of the wild-type plant, which was set at 1.



Supplementary Figure S3. Phenotypic analysis of *Arabidopsis* plants ectopically expressing *ADR-Gly* or *ADR*.

(A) A 46-day-old *35S::ADR-Gly* plant (left) produced long, well-developed siliques similar to those of wild-type plants, whereas *35S::ADR* plants produced short, undeveloped siliques (right).

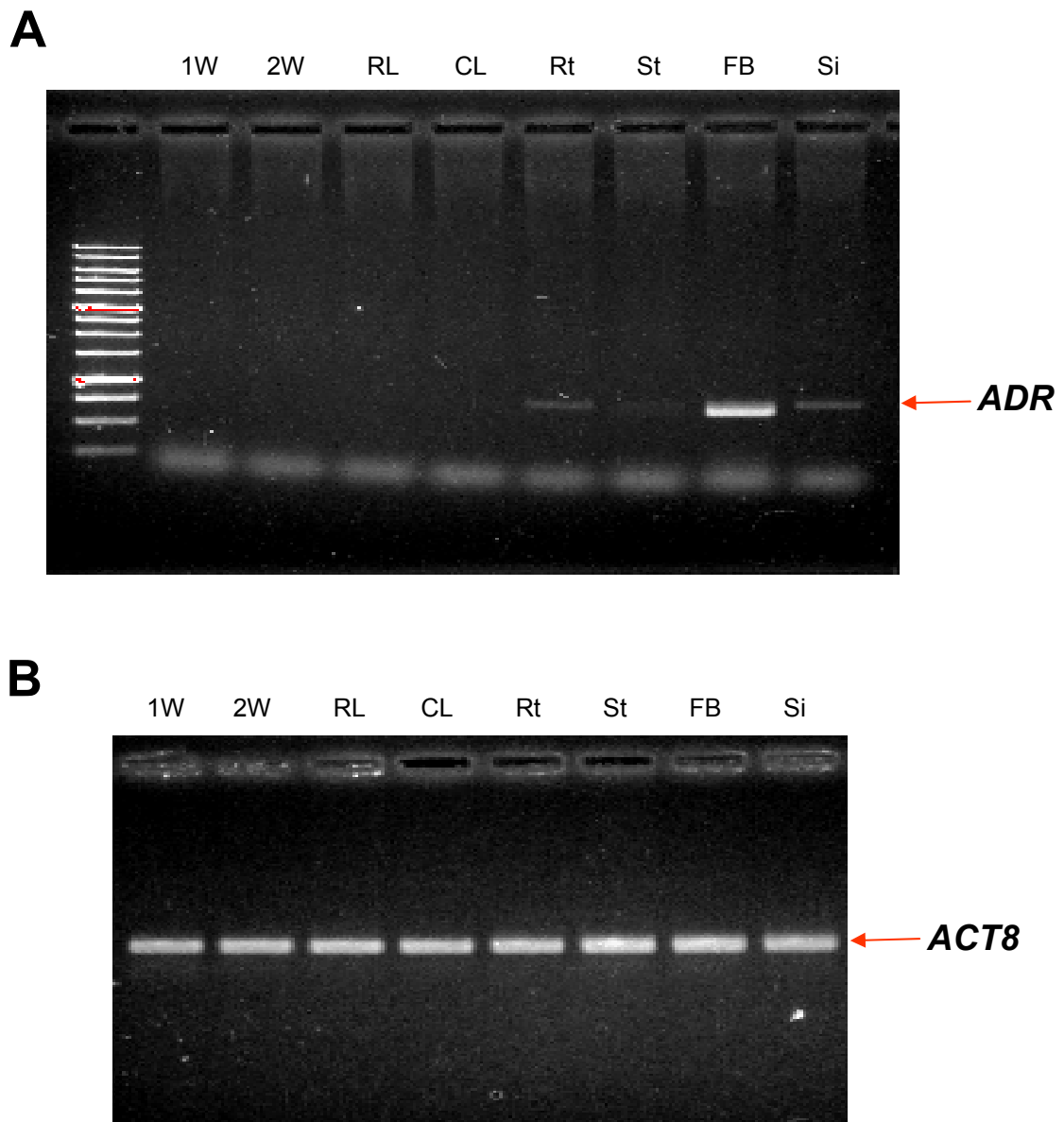
(B) Inflorescences with elongated siliques (arrowed) from a wild-type plant (WT, left) and a *35S::ADR-Gly* plant (middle), with short and undeveloped siliques (s) from a *35S::ADR* plant (right).

(C) Close-up of a *35S::ADR-Gly* inflorescence with flowers that developed into well-elongated siliques (arrowed).

(D) Close-up of a *35S::ADR* inflorescence with short and undeveloped siliques (s).

(E, F) Anthers (arrowed) of *35S::ADR* flowers remained indehiscent at stage 13 (E) and stage 15 (F).

(G, H) Anthers of *35S::ADR-Gly* flowers were completely dehiscent, and pollen (arrowed) was released at stage 13 (G) and stage 15 (H).



Supplementary Figure S4. Analysis of *ADR* expression in different *Arabidopsis* organs. **(A)** The original gel for the detection of *ADR* expression in different *Arabidopsis* organs. The mRNA levels were determined by RT-PCR. Total RNA was isolated from 1-week-old seedlings (1W), 2-week-old seedlings (2W), rosette leaves (RL), cauline leaves (CL), roots (Rt), stems (St), floral buds (FB) and siliques (Si). **(B)** The original gel for the detection of *Arabidopsis ACTIN8 (ACT8)* gene which was used as internal controls.

Supplemental Table S1. Oligo nucleotide sequence of primers used in gene cloning and PCR analysis.

	Primer name	Primer sequence	Restriction site	Use
ADR-real-time	ADR-real-For	5'-GAGGAAAGAGAGGAAGAGACTGAG-3'		Real-time PCR
	ADR-real-Rev	5'-ACATCTGTTCCACGACCCATTC-3'		
UBQ10-real-time	RT-UBQ10-1	5'-CTCAGGCTCCGTGGTGGTATG-3'		Real-time PCR
	RT-UBQ10-2	5'-GTGATAGTTTTCCAGTCAACGTC-3'		
ADR:GUS	pADR-For	5'-CTGCAGACCATCTGATTCTTGTATTGTC-3'	PstI	ADR Promoter cloning
	pADR-Rev	5'-TCTAGAGAAGAAAAGCTCTCTTTCTCTCTC-3'	XbaI	
35S:ADR+GFP	ADR-dsc-For.	5'-CTGCAGTCTTCATGGGTGGTTCTACAAG-3'	PstI	GFP C-ter fusion
	ADR-dsc-Rev.	5'-GGTACCTTTACACCCGATGAATTTTGT-3'	KpnI	
35S:CAT3+mORG2	CAT3-For	5'-TCAACCTTCTAGAATCACCATGGA-3'	XbaI	mORG2 C-ter fusion
	CAT3-dsc-Rev	5'-GGTACCGATGCTTGGCCTCACGT-3'	KpnI	
NST1	NST1-For	5'-GCTTAACGGACCCACATCATATTC-3'		Real-time PCR
	NST2-Rev	5'-TACGGAGATCGGACGGAAGG-3'		
NST2	NST2-For	5'-CGCCGTCGTTCAATGAGGAG-3'		Real-time PCR
	NST2-Rev	5'-TCGTGATGGTGGTGTGTTATGG-3'		
ACT8	ACT8-For	5'-ATGAAGATTAAGGTCGTGGCACC-3'		RT-PCR
	ACT8-Rev	5'-TTATCCGAGTTTGAAGAGGCTACAA-3'		
35S::ADR	ADR-cDNA-For	5'-TCTAGAGAGAGAAAGAGAGCTTTTCTTC-3'	XbaI	cDNA cloning and RT-PCR
	ADR-cDNA-Rev	5'-GGTACCGAAGCTTACTGAGTCTACTTAT-3'	KpnI	
35S::ADR-Gly	ADR-dsc-dG-For	5'-CTGCAGCTTTTCTTCATGTCTACAAG-3'	PstI	cDNA cloning
	ADR-cDNA-Rev	5'-GGTACCGAAGCTTACTGAGTCTACTTAT-3'	KpnI	