

Supplementary Information

Involvement of Pyridoxine/Pyridoxamine 5'-Phosphate Oxidase (PDX3) in Ethylene-Induced Auxin Biosynthesis in the Arabidopsis Root

Gyuree Kim^{1,5}, Sejeong Jang^{1,5}, Eun Kyung Yoon^{1,3}, Shin Ae Lee^{1,4}, Souvik Dhar¹, Jinkwon Kim¹, Myeong Min Lee² and Jun Lim^{1,*}

¹Department of Systems Biotechnology, Konkuk University, Seoul 05029, Korea, ²Department of Systems Biology, Yonsei University, Seoul 03722, Korea, ³Present address: Temasek Life Sciences Laboratory, 1 Research Link, National University of Singapore, Singapore 117604, Singapore, ⁴Present address: Department of Agricultural Biology, National Institute of Agricultural Sciences, Wanju, 55365, Korea, ⁵These authors contributed equally to this work.

*Correspondence:

Jun Lim

Email) jlim@konkuk.ac.kr

Tel) +82-2-457-1341

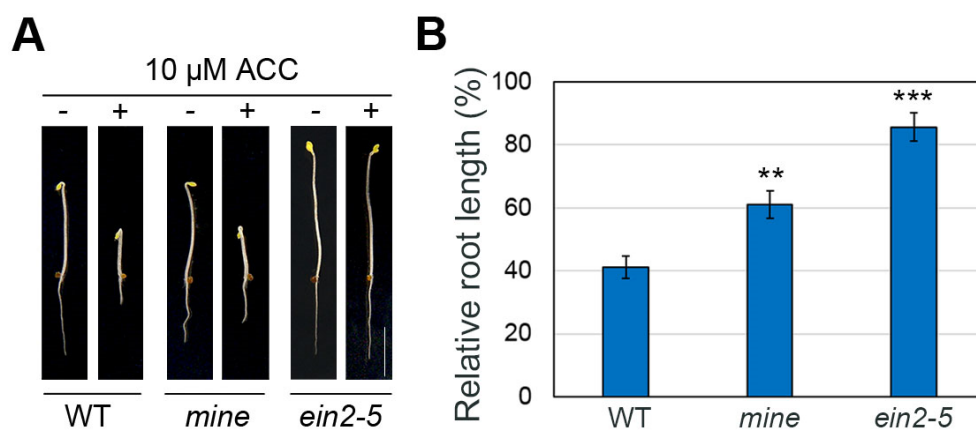


Fig. S1. Isolation of the *mine* mutant that displays an insensitive phenotype to ACC.

(A) Growth phenotypes of 4-d-old etiolated WT, *mine*, and *ein2-5* seedlings grown in MS plates supplemented with 10 μ M ACC. Scale bar= 0.5 cm. (B) Relative growth inhibition of WT, *mine*, and *ein2-5* roots in the presence of 10 μ M ACC. Error bars indicate \pm SD from three biological replicates. Asterisks indicate statistically significant differences compared to WT, as determined by the Student's *t*-test (** $P < 0.01$, and *** $P < 0.001$).

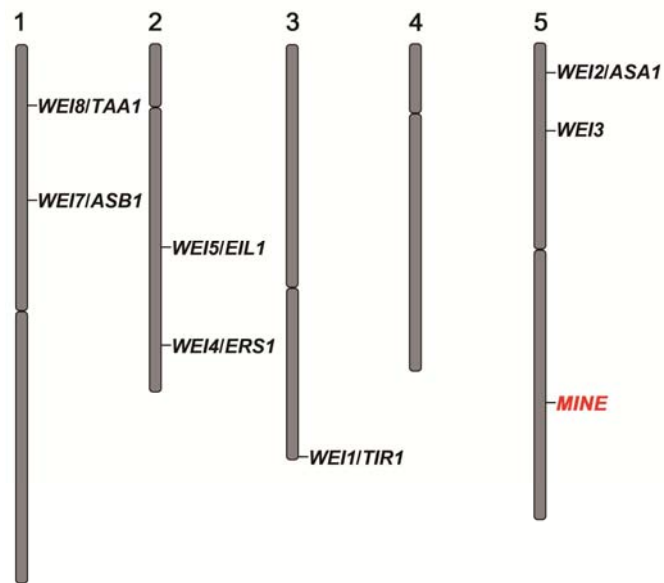


Fig. S2. Chromosomal location of the *MINE* locus.

The locations of *WEI* loci on Arabidopsis chromosomes 1 to 5 are shown. The *MINE* locus is indicated as red.

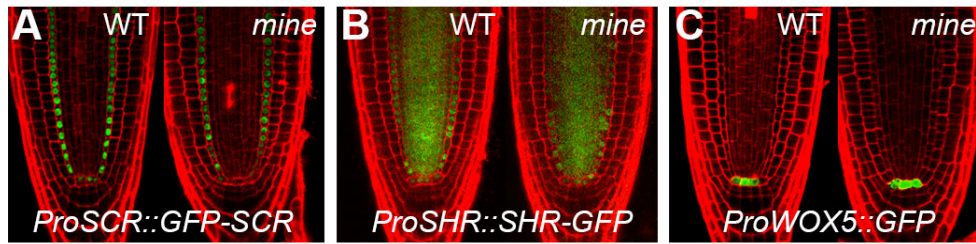


Fig. S3. Analysis of root growth phenotypes in WT and *mine* seedlings using root development markers.

(A) *ProSCR::GFP-SCR*. (B) *ProSHR::SHR-GFP*. (C) *ProWOX5::GFP*.

Table S1. Sequence information of primers used in this study

Purpose	Name	Sequence (5' → 3')	
TAIL-PCR	DEG1	WGCNAGTNAGWANAAG	
	DEG2	AWGCANGNCWGANATA	
	pBIBLB372	GCAGCTGGCACGACAGGTTTC	
	pBIBLB262	GCTCGTATGTTGTGTGGAATTGT	
	pBIBLB172	GTCGACAGATCTCATGCCCTGCA	
Mapping	KLPNHC	FP	CGTTGCTCGTGGATTTTGTA
		RP	CTTGTATAAGTTCTTGCCGTGA
	PDC2	FP	CAGTGGATCACTCCCAAGACGCCTC
		RP	GCACTCAACTTATATATATTTTCAG
	ATTED2	FP	CGTAGACAAGGTACTGTCAACC
		RP	GATAATCTCGTCTCCAAGTGTC
Genotyping	<i>mine</i>	FP	CAGCGAACAAGGACAAAAAACC
		RP	CATGCCGTGCCAGGTACAACAG
		LB	CGACAGATCTCATGCCCTGCAGG
	<i>ein2-5</i>	FP	GCTCTTGTCTTCTCTAGTC
		RP	GAAGCATCATTGCCACCAAG
	<i>wei2</i>	LP	ACTTGGTGGCCAAGTTACATG
		RP	GAAGGAGACTCCACCAAAAC
	<i>wei8</i>	LP	TCTTTTCCATTACAACGTGGG
		RP	CGTCAAGACCATGACATCATG
	<i>sur2</i>	LP	TTTCGTGGTTCTCTCTTTTCG
		RP	GTGGTATGGGCCATGACTTA
	<i>pdx3-3</i>	LP	TTGAGGAGCAGGTTGAAACTG
		RP	ACCTGACGTTCAAAATTTCC
	SALK_LBb1.3		ATTTTGCCGATTTTCGGAAC
	RT-qPCR	<i>MINE/PDX3</i>	FP
RP			TACGAATTTTCCACGCAGGA
<i>UBQ10</i>		FP	TGGTGGTTTGTGTTTGGGGCCTT
		RP	AGAGTCGAGTCACTTTGCAGGCCT