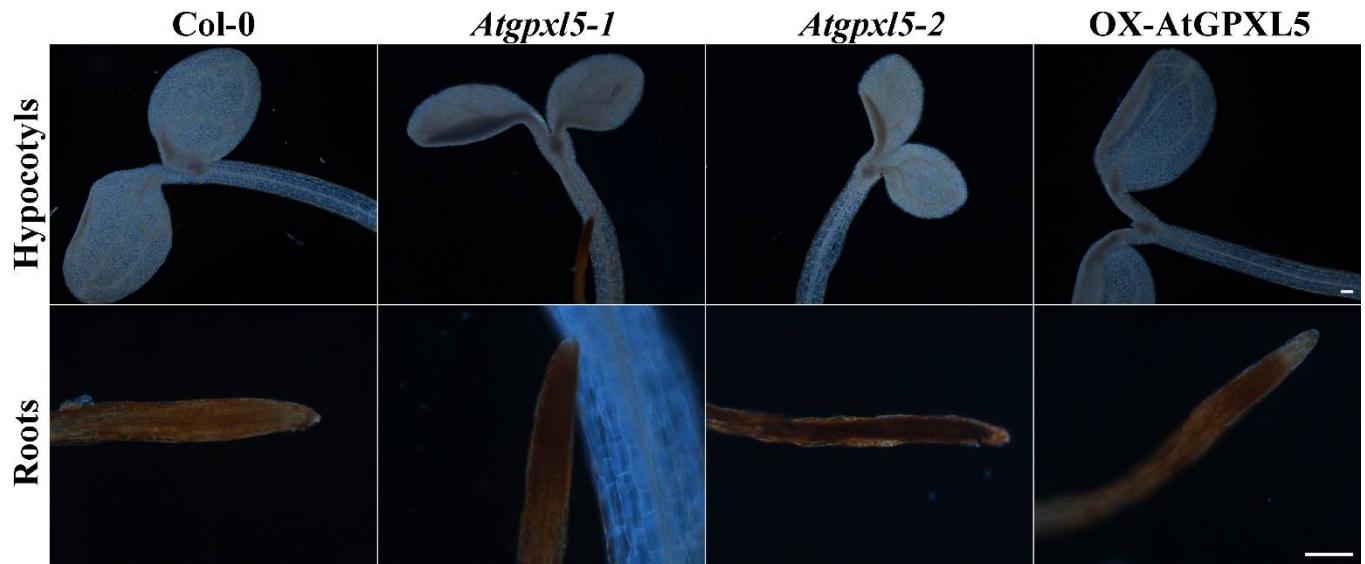


*Supplementary Material*

## Crosstalk between the *Arabidopsis* Glutathione Peroxidase-Like 5 Isoenzyme (AtGPXL5) and Ethylene



**Figure S1.** Histochemical assay of 4-day-old light-grown seedlings using DAB (3,3'-diaminobenzidine) staining to visualize the H<sub>2</sub>O<sub>2</sub> content in the investigated genotypes (scalebar = 100 µm).

**Table S1.** The mean 2<sup>(-ΔΔCt)</sup> data of RT-qPCR analysis.

Genes	Shoot						Root					
	Control			1 µM ACC			Control			1 µM ACC		
	Col-0	Atgpxl5	OX-AtGPXL5	Col-0	Atgpxl5	OX-AtGPXL5	Col-0	Atgpxl5	OX-AtGPXL5	Col-0	Atgpxl5	OX-AtGPXL5
<i>ACS2</i>	1	2.5 × 10 <sup>-8</sup>	6.7 × 10 <sup>-10</sup>	7.1 × 10 <sup>-8</sup>	1.8 × 10 <sup>-8</sup>	1.1 × 10 <sup>-8</sup>	1	332.57	69.31	2.61	4.26	2.17
<i>ACS6</i>	1	3.57	2.13	2.69	1.42	1.66	1	54.66	25.28	44.63	21.30	36.32
<i>ACO1</i>	1	0.70	0.58	1.53	0.84	0.18	1	1.17	1.67	5.54	6.83	2.16
<i>ACO2</i>	1	0.14	0.59	0.76	1.53	1.19	1	0.31	0.33	2.35	2.29	2.77
<i>ACO3</i>	1	0.90	0.34	0.97	0.69	1.40	1	0.12	0.08	0.19	0.20	0.36
<i>ACO4</i>	1	1.81	0.63	1.44	3.38	1.91	1	2.86	1.95	5.17	4.26	5.44
<i>ACO5</i>	1	1.22	0.40	1.06	0.68	0.44	1	2.54	2.68	0.24	0.27	1.75
<i>ETR1</i>	1	3.05	1.17	2.54	2.51	2.36	1	1.64	1.83	2.18	2.26	1.26
<i>ETR2</i>	1	0.55	0.89	0.24	0.93	0.49	1	0.36	2.81	1.20	1.99	2.34
<i>ERS1</i>	1	2.19	0.43	0.82	3.19	2.25	1	2.22	1.84	1.72	2.02	3.12
<i>ERS2</i>	1	0.96	0.26	0.11	1.49	2.70	1	1.94	1.40	2.85	3.45	8.53
<i>EIN4</i>	1	4.80	0.85	3.64	8.31	3.84	1	1.46	1.25	1.24	1.10	1.19
<i>CTR1</i>	1	1.05	0.24	0.87	0.80	5.5 × 10 <sup>-4</sup>	1	1.73	1.57	1.38	1.33	1.90
<i>ERF1</i>	1	17.60	4.05	5.47	24.34	20.04	1	37.60	43.56	32.22	54.10	78.11

**Table S2.** Responsiveness of the growth *Arabidopsis thaliana* wild type (Col-0) and glutathione peroxidase-like 5 mutants (*Atgpxl5-1* and *Atgpxl5-2*) and overexpressing line (OX-AtGPXL5) seedlings to 1 µM ACC (1-aminocyclopropane-1-carboxylic acid) treatment. The dark-gown seedlings were germinated and kept for 4 days in the presence of 1 µM ACC. The decrease of the hypocotyl and primary root length compared to untreated controls are calculated from data presented in Figure 3a.

	Control	1 µM ACC Treatment	Changes in Hypocotyl Length due to ACC Treatment (% of Control)	Changes in Primary Root Length due to ACC Treatment (% of Control)
	Ratio of Hypocotyl and Root Length	Ratio of Hypocotyl and Root Length		
Col-0	1.48 ± 0.20 ns	1.04 ± 0.13 b	32.46 ± 5.70 b	46.22 ± 5.77 b
<i>Atgpxl5-1</i>	1.78 ± 0.71 ns	1.62 ± 0.24 a	41.50 ± 7.38 a	45.71 ± 6.31 b
<i>Atgpxl5-2</i>	1.76 ± 0.67 ns	1.64 ± 0.30 a	39.57 ± 8.94 a	42.51 ± 7.01 b
OX-AtGPXL5	1.51 ± 0.15 ns	1.01 ± 0.06 b	40.20 ± 4.73 a	59.87 ± 3.37 a

**Table S3.** Primers pairs used for the quantitative real time PCR (RT-qPCR) analysis and the size of PCR products.

Genes	Forward Primers	Reverse Primers	Product Sizes	References
ACS2 (AT1G01480)	GGTGGTTATGAGCGGAGGA	TACGGGGAGGAAATGAGGA	93 bp	[1]
ACS6 (AT4G11280)	AGGCACGCTGAGATAACCAC	AATCCCATCCACAAGAACAAACC	85 bp	[1]
ACO1 (AT2G19590)	TCAGATGCAGATTGGGAAAGC	TCTCACACATGAGCTTGGAGACTC	160 bp	[2]
ACO2 (AT1G62380)	TCACCTCCCTCAATCCAATC	ATCCAACAAATCCTCAGCAAGA	112 bp	[1]
ACO3 (AT1G12010))	GACCCAGAAAGAAGGAAACAGG	AATGTCTCAACCACAGCCACC	240 bp	[3]
ACO4 (AT1G05010)	CTTGTGAAAATGGGGCTTC	TGTTCCCTGGTCATCTCTCC	88 bp	[1]
ACO5 (AT1G77330)	TGGATCGATGTTCAGCCTTACCC	TGCCACGCACTCTTGACCTTC	95 bp	[4]
ETR1 (AT1G66340)	GTGTGTGTATGTGAGAGAGG	GCAATGAAGAAATGGAGATG	131 bp	[1]
ETR2 (AT3G23150)	TCGTCCTCGCCTTCTACTTC	TCCCACATTCTTCATCCAAG	149 bp	[1]
ERS1 (AT2G40940)	AACCACGAGATGAGGACACC	GCCACAAGATTGCTGCTTT	125 bp	[1]
ERS2 (AT1G04310)	GTTCTGTGCTTGCCTCAGTG	ATGTGAATGCCCTCTGGTGT	115 bp	[1]
EIN4 (AT3G04580)	TGACTTTGATTCCGTTGCTG	TCATTTCCCTGCCTCTTC	111 bp	[1]
CTR1 (AT5G03730)	CAGAAAATGGTGGTGGGTCT	TGTTTGGAACTGGCTGACTG	126 bp	[1]
ERF1 (AT3G23240.1)	TCCCTCAACGAGAACGACTC	ACGGATTGATCGGAAGGTC	111 bp	[2]
Actin2 (At3g18780)	GGTAACATTGTGCTCAGTGGTGG	AACGACCTTAATCTTCATGCTGC	108 bp	[5]
AtGPXL5 (At3G63080)	TCATCATCATCATCTGTGTCGGA	GGACTCCGTGAATCCGCATT	144 bp	[6]
GAPDH (At1G16300)	GAATCAACGGTTTCGGAAGA	CTCGGTGGTGTGAAAGGA	104 bp	[6]

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