SUPPLEMENTARY MATERIAL

Expression of *Castanea crenata* Allene Oxide Synthase in Arabidopsis Improves the Defense to *Phytophthora cinnamomi*

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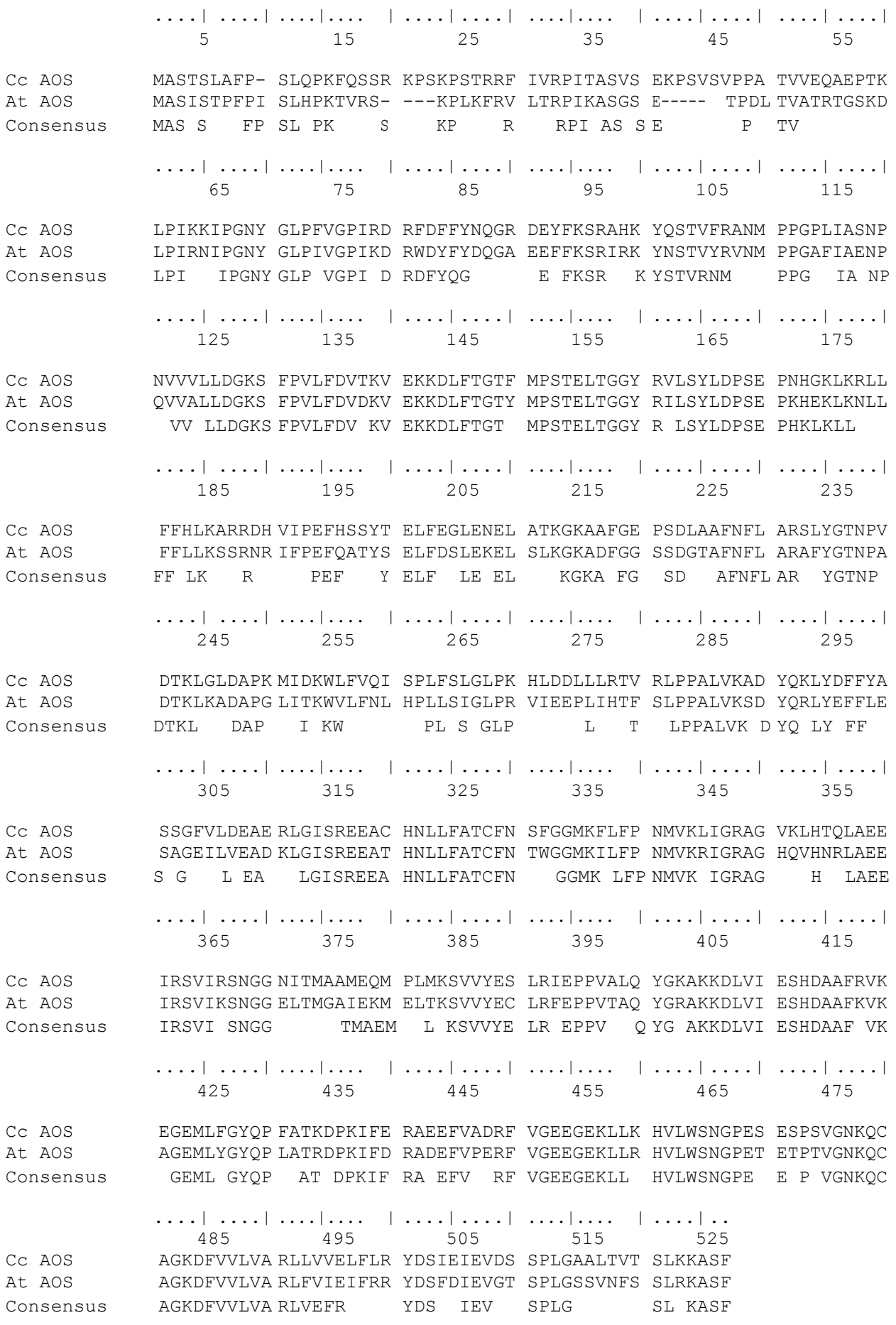
	Wild type	CcAOS1	CcAOS2	CcAOS3
Rosette area (cm^2)	0.61 ± 0.14	0.71 ± 0.19 *	0.79 ± 0.30 *	0.83 ± 0.22 *
Root (dry weight; g)	0.0006±0.0002	0.0009±0.0005	0.0007±0.0005	0.0005±0.0002
Aerial (dry weight; g)	0.0049±0.0009	0.0069±0.0006 *	0.0098±0.0034 *	0.0078±0.0006 *
Time of flowering	73±6.67	81±14.67	94±6.0	100±0.00 *
Primary root length (cm)	2.28±1.22	3.30±1.02 *	2.77±1.14	3.55±1.38 *
Lateral root number	6.4±3.5	11±4.08 *	7.7±6.2	10.8±5.5 *
Root hair number (between 5-10mm)	67.3±33.1	43.6±31.2	37.5±25.2 *	49.3±40.3
Root hair length (µm) (between 5-10mm)	243.24±47.79	209.13±47.7	226.27±38.22	228.46±33.14

Supplementary Table 1. Phenotypical parameters of transgenic *CcAOS* Arabidopsis plants.

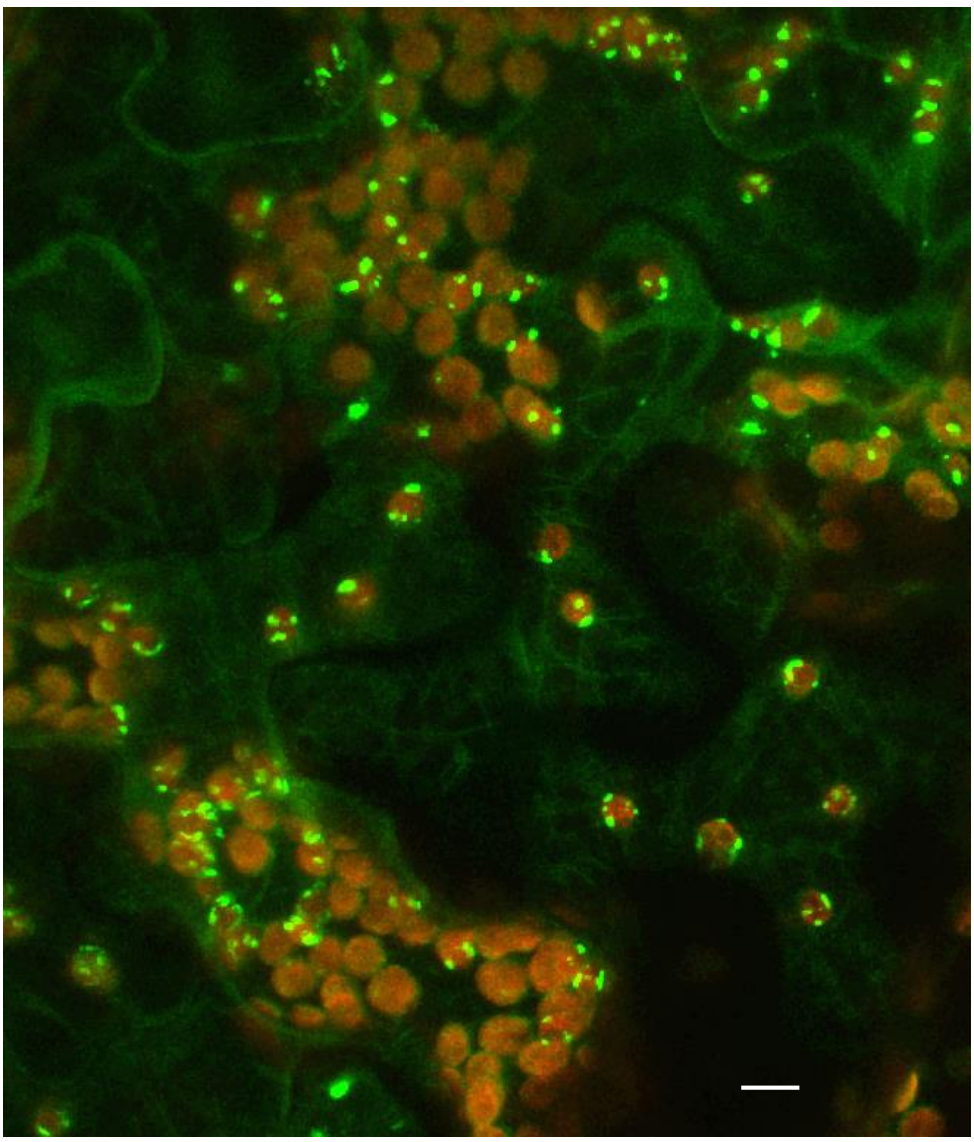
Rosette area and dry weight were measured 1 month after germination. Time of flowering was measured 2 weeks after germination. The remaining root parameters were measured 13 days after germination. Measurements (means ± standard deviation) are from three independent assays, each using 5 plants per genotype. Asterisks refers to significant differences from the L*er*-0 wild type ($P<0.05$, *t*-test).

Gene name, locus and relation to pathway (JA – jasmonate; SA – salicylate)	Forward (5’-3’)	Reverse (5’-3’)	Melting temperature (ºC)
ALLENE OXIDE SYNTHASE AT5G42650.1 (JA)	CGACGGTGGGGAATAAACAA	TCGCCGGAAAATCTCAATCA	60
LIPOXYGENASE 1 AT1G55020.1 (JA)	GATGGGCTTGAGGTTTGGTA	TTCACGGGTTTGCATTTTAGG	62
JASMONATE-ZIM-DOMAIN PROTEIN 10 AT5G13220.1 (JA)	CGATTTCCTCGGACTTGAGA	GGAACCGAACGAGATTTAGC	60
PLANT DEFENSIN 1.2 AT5G44420.1 (JA) (Proietti et al., 2018)	CACCCTTATCTTCGCTGCTCTT	GCCGGTGCGTCGAAAG	58
PATHOGENESIS-RELATED GENE 5 AT1G75040.1 (SA)	ACTCCAGGTGCTTCCCGACA	ACTCCGCCGCCGTTACATCTT	60
NONEXPRESSER OF PR GENES 1 AT1G64280.1 (SA)	TTATCTGGCCGCCGAACAAG	AATCATCCGGCGAGTCAAAG	60

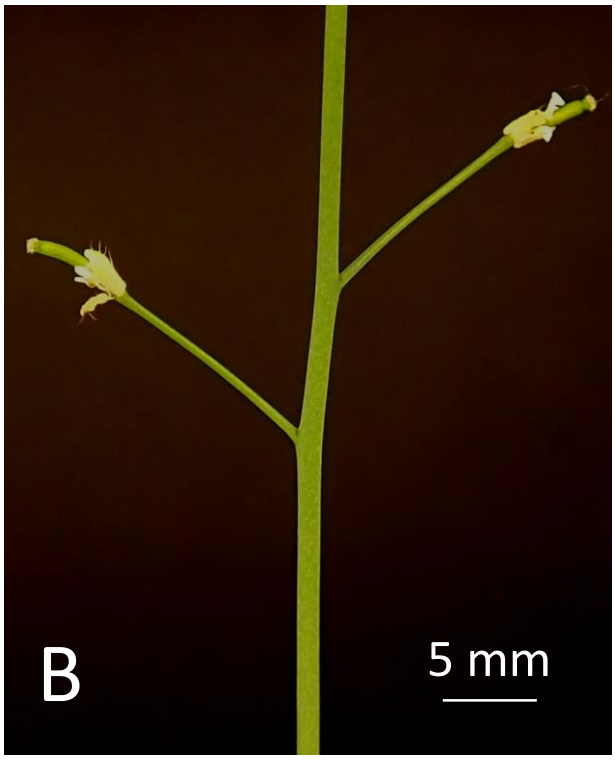
Supplementary Table 2. Primers used in RT-qPCR analysis of jasmonic acid and salycilic acid pathway genes.



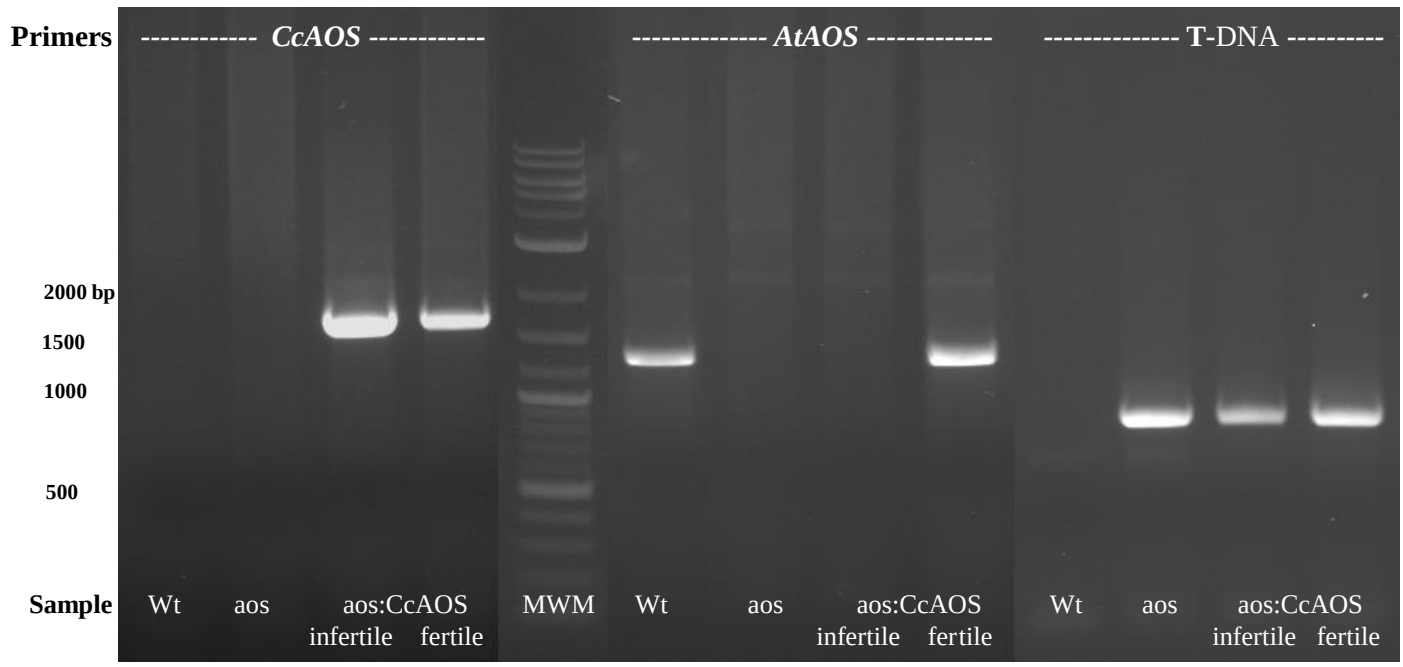
Supplementary Figure 1. Alignment of amino acid sequences of *Castanea crenata* (CcAOS) and *Arabidopsis thaliana* (AtAOS) allene oxide synthase. Clustal W alignment was conducted using the BioEdit Sequence Alignment Editor. Numbers refer to the amino acid position.



Supplementary Figure 2. 2D stack of subcellular imaging upon transient CcAOS-eGFP expression in leaves of *N. benthamiana*. Although CcAOS clearly accumulates at chloroplasts, a reticulate-like signal in the cytosol suggests that trafficking of the protein may involve the endomembrane compartment. Scale Bar = 10 µm.



Supplementary Figure 3. Two-month old *Arabidopsis thaliana aos-GK624b02* mutant plant (A) and detail of siliques (B). The site of the T-DNA insertion in the mutant (5'UTR) is described in https://www.gabi-kat.de/db/visualization.php?lineid=624B02&genecode=At5g42650 and is also reported in https://www.arabidopsis.org/servlets/TairObject?id=503215774&type=polyallele



Supplementary Figure 4. Genotyping of plants after expression of *CcAOS* gene in *aos-GK624b02* mutants. Genomic DNA of F2 *aos:CcAOS*-infertile and *aos:CcAOS*-fertile plants was screened for *CcAOS*, *AtAOS* and T-DNA insertion and further compared with wild-type Col-0 (Wt) and *aos* plants (used as controls). The expected band sizes are 1581 bp for the amplification of *CcAOS* ORF, 1345 bp for the amplification of a fragment of non-disrupted *AtAOS* and 850 bp for the amplification of a fragment of the T-DNA left border fused to *AtAOS* (T-DNA). MWM: molecular weight marker N3200L (New England Biolabs, Ipswich, MA, USA).