SUPPORTING INFORMATION

Artemisia argyi allelopathy: a generalist compromises hormone balance, element absorption and photosynthesis of receptor plants

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Figure S1

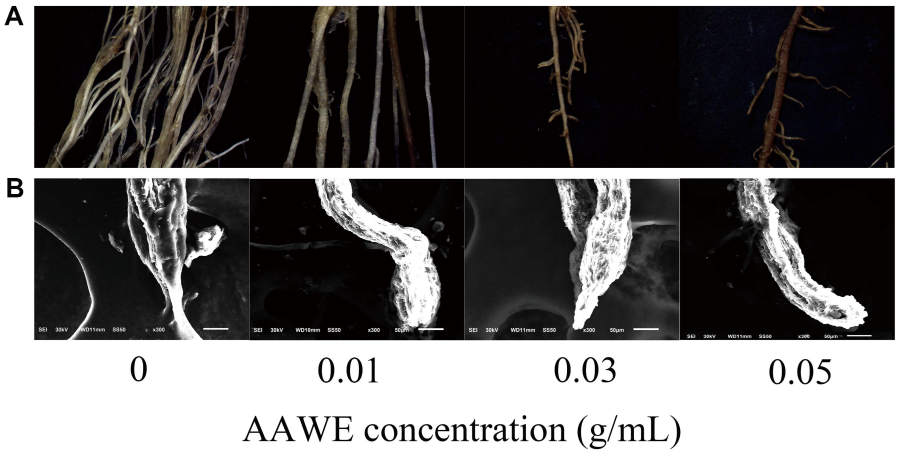

Figure S1. Roots were destructed in AAWE-treated rice.

(A) Root development and branching under different treatment conditions.

(B) Scanning electron microscopy of wild-type and AAWE-treated root tips. Scale bars, 50 μm.

Figure S2

Figure S2. The AAWE-treated rice leaves were abnormal.

Leaf rolling, yellowing and withering occurred in AAWE-treated rice leaves. The leaves from left to right showed control, 0.01 g/mL, 0.02 g/mL, 0.03 g/mL, 0.04 g/mL, 0.05 g/mL AAWE treatment. Scale bar, 1 cm.

Figure S3

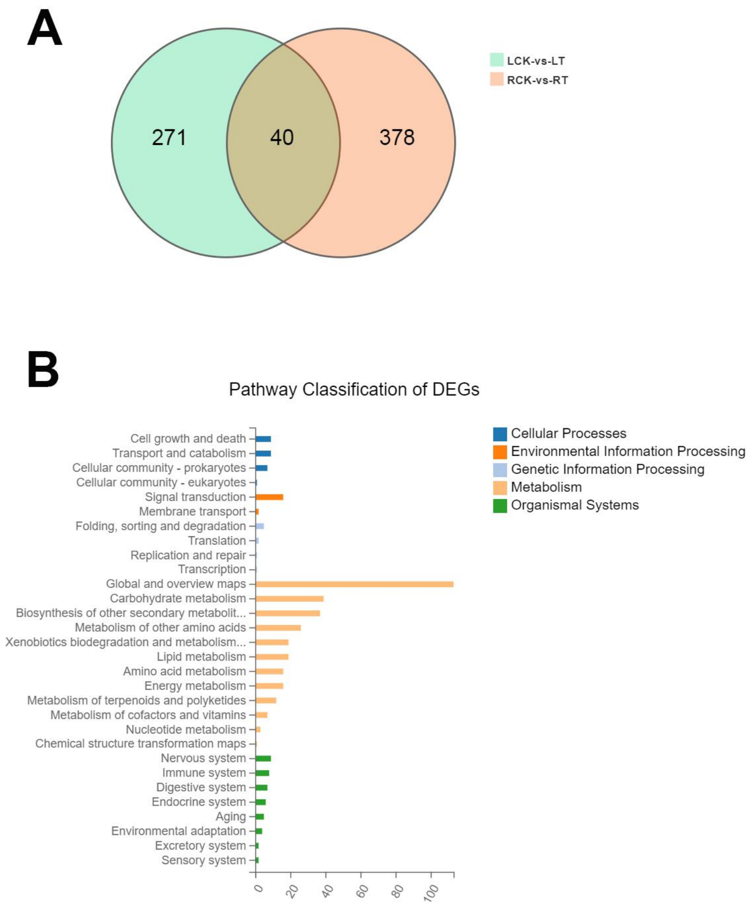

Figure S3. Preliminary analysis of DEGs between control and AAWE-treated rice.

(A) The number of DEGs distributed in leaves and roots after screening (|Log2FC|≥1).

(B) KEGG classification results of DEGs.

Figure S4

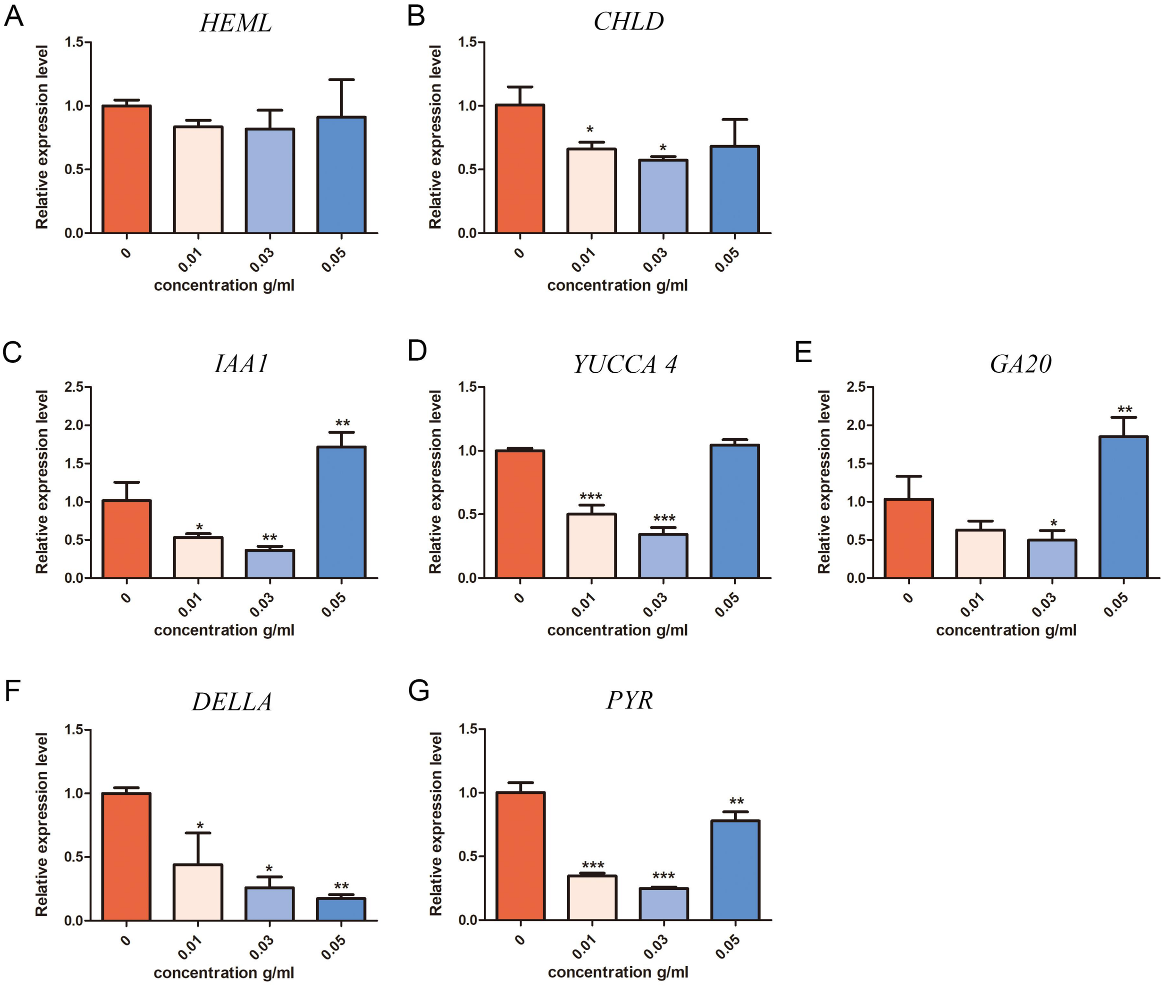

Figure S4. Relative expression levels of genes in rice leaves and roots under AAWE treatment.

(A-B) Genes that are not differentially expressed related to the chlorophyll synthesis pathway in control and AAWE-treated leaves.

(C-G) Expression levels of hormone-related genes in roots. C, *IAA1*, related to auxin synthesis; D, *YUCCA4*, related to auxin signalling pathways; E, *GA20*, related to gibberellin synthesis; F, *DELLA*, related to gibberellin signalling pathways; G, *PYR*, related to abscisic acid signalling pathways.

Table S1. Details of key driver genes.

Gene ID	Gene Symbol	Describe	Function comment information	
			KEGG Pathway	GO Biological Process
LC4342117	LOC_Os06g51084	1,4-alpha-glucan-branching enzyme, chloroplastic/amyloplastic-like	Starch and sucrose metabolism	carbohydrate metabolic process glycogen biosynthetic process
LC4333062	LOC_Os03g28330	sucrose synthase 1-like	Starch and sucrose metabolism	sucrose metabolic process response to carbon dioxide
LC4343045	LOC_Os07g23944	alpha-glucosidase 2	Galactose metabolism Starch and sucrose metabolism	carbohydrate metabolic process
LC4331252	LOC_Os02g58480	sucrose synthase 6-like	Starch and sucrose metabolism	sucrose metabolic process
LC4329561	LOC_Os02g33110	beta-fructofuranosidase, insoluble isoenzyme 1-like	Galactose metabolism Starch and sucrose metabolism	carbohydrate metabolic process
LC4335447	LOC_Os04g24430	sucrose synthase 5-like	Starch and sucrose metabolism	sucrose metabolic process
LC4332788	LOC_Os03g22120	sucrose synthase 4-like	Starch and sucrose metabolism	sucrose metabolic process
LC4348840	LOC_Os10g32810	beta-amylase 1, chloroplastic-like	Starch and sucrose metabolism	polysaccharide catabolic process
LC4331577	LOC_Os03g04770	beta-amylase 2, chloroplastic-like	Starch and sucrose metabolism	polysaccharide catabolic process
LC4335790	LOC_Os04g33740	beta-fructofuranosidase, insoluble isoenzyme 2-like	Galactose metabolism Starch and sucrose metabolism	carbohydrate metabolic process cell proliferation defense response to bacterium leaf development cotyledon development defense response to fungus carbohydrate storage

Table S2. The sequence of gene-specific primers for RT-qPCR analysis.

Primer name	Primer sequence	Description
Actin-F	TGTAAGCAACTGGGATGA	RT-qPCR
Actin-R	CCTTCGTAGATTGGGACT	
HEMA-F	GATGCAATCACTGCTGGAAAGCGT	RT-qPCR
HEMA-R	CCATCTTGCCAGCACCAATCAACA	
HEML-F	AGAACAAAGGGCAGATTGCTGCTG	RT-qPCR
HEML-R	TGTTTCGTCAAGTCACGGAGAGCA	
CHLD-F	TAGCACAGCTGTCAGAGTGGGTTT	RT-qPCR
CHLD-R	TTGCCAGCCACCTCAAGTATCTCA	
CHLH-F	GCACGGGAACTTGGCGTTTCATTA	RT-qPCR
CHLH-R	ACATGTCCTGGAGCTGCTTCTCAT	
CRD-F	TGGATCTAACATGACACGCACCCA	RT-qPCR
CRD-R	ACTGTAACGGCATTCTTCTCCGGT	
CHLG-F	CCAGCCACTGATGAAAGCAGCAAT	RT-qPCR
CHLG-R	AGAGCGCTAATACACTCGCGAACA	
CAO-F	ACACCTTCATCTGGGCTTCAAGGA	RT-qPCR
CAO-R	AGATGCGTCGAACATTGCTTGGTG	
PsbY-F	CGCAGCGACATTGCACTCACC	RT-qPCR
PsbY-R	TGACGCCTTCTTCTTCCTCCTCTT	
Os04g38410-F	TGACGCCTTCTTCTTCCTCCTCTT	RT-qPCR
Os04g38410-R	GCTACTGCTCCTCCGACCTCCAAT	
YUCCA4-F	GGCCGGCCTAATTTTAACTGG	RT-qPCR
YUCCA4-R	TTCTCAAAAAAGACGCGCGAC	
IAA1-F	GCCGCTCAATGAGGCATT	RT-qPCR
IAA1-R	GCTTCCACTTTCTTTCAATCCAA	
GA20-F	GCCACTACAGGGCCGACAT	RT-qPCR
GA20-R	TGGTTGCAGGTGACGATGAT	
DELLA-F	CTACTACTCCACCATGTTCGAT	RT-qPCR
DELLA-R	CTGTTTGTAGGCATTGGAGC	
NCDE4-F	GATTGCACGGCACCTTCATT	RT-qPCR
NCDE4-R	CTCTGTAATTTGATTTTTCACTGGCTAAT	
PYR-F	GTAGTTCCTCCATTGTCTTC	RT-qPCR
PYR-R	GACCTAAGCCCATCACTA	