

Table 1S. List of oligonucleotides used for PCR analyses.

Oligo code	Gene(s) amplified	Kazusa code(3.0)	Gene product	Sequence
Control DNA contamination				
LjHar1_F	<i>LjHar1</i>	Lj5g3v1806980.1	receptor-like kinase HAR1	TCATTTTCCATATTGGTCCTTCG
LjHar1_R	<i>LjHar1</i>	Lj5g3v1806980.1	receptor-like kinase HAR1	GAATTGTTCTGTAATGGGTTTGG
Control integrity				
LjGAPDH5'_F	<i>LjGAPDH</i>	Lj4g3v1388980.1	glyceraldehyde-3-P-dehydrogenase	AAGGATCGGGCGTTTGG
LjGAPDH5'_R	<i>LjGAPDH</i>	Lj4g3v1388980.1	glyceraldehyde-3-P-dehydrogenase	AGCAACAAGTCAACATCGTCTCT
LjGAPDH3'_F	<i>LjGAPDH</i>	Lj4g3v1388980.1	glyceraldehyde-3-P-dehydrogenase	CGGTTACACTGAAGATGATGTGG
LjGAPDH3'_R	<i>LjGAPDH</i>	Lj4g3v1388980.1	glyceraldehyde-3-P-dehydrogenase	GATACTTGACCTGTTGTGCCA
Housekeeping				
LjUBQ4_F	<i>LjUbq</i>	Lj5g3v2060710.1	polyubiquitin 4	TTCACCTTGTGCTCCGTCTTC
LjUBQ4_R	<i>LjUbq</i>	Lj5g3v2060710.1	polyubiquitin 4	AACAACAGCACACACAGACAATCC
LjPP2A_F	<i>LjPp2A</i>	Lj2g3v0742070.1	protein phosphatase 2A reg. subunit	TGAGCTATGTGAAGCTGTTGGT
LjPP2A-R	<i>LjPp2A</i>	Lj2g3v0742070.1	protein phosphatase 2A reg. subunit	CAGCCTCATTATCACGCAGTAG
Biosynthetic enzymes				
LjPAL1_F	LjPAL1	Lj1g3v4590760.1	phenylalanine ammonia lyase	GATTGTAGGCGGTCAAAGGAC
LjPAL1_R	LjPAL1	Lj1g3v4590760.1	phenylalanine ammonia lyase	GAATTGCACTGACAGCGATTC
LjPAL2_F	LjPAL2	Lj1g3v4590760.2	phenylalanine ammonia lyase	CCTTATTGTCCATCTGCTTATCGAAG
LjPAL2_R	LjPAL2	Lj1g3v4590760.2	phenylalanine ammonia lyase	GAACAAATTGACTTACCTGCTGG
LjPAL3_F	LjPAL3	Lj1g3v4590840.1	phenylalanine ammonia lyase	GAAGCCTAGCAATTAATGTCAGTAG
LjPAL3_R	LjPAL3	Lj1g3v4590840.1	phenylalanine ammonia lyase	CTTTCTGATAGTCTGCTTAACTGG
LjPAL4_F	LjPAL4	Lj1g3v4590850.1	phenylalanine ammonia lyase	CCACCAAAGCCAAACCGA
LjPAL4_R	LjPAL4	Lj1g3v4590850.1	phenylalanine ammonia lyase	GCTTGACCTCGTCTAGATGG
LjPAL5_F	LjPAL5	Lj1g3v4590850.2	phenylalanine ammonia lyase	ATGGAATGCCTTGAGAGT
LjPAL5_R	LjPAL5	Lj1g3v4590850.2	phenylalanine ammonia lyase	CACGCAGTGGTTACAAGAATTG
LjPAL6_F	LjPAL6	Lj2g3v3339740.1	phenylalanine ammonia lyase	GGAAGAATTAGGGACAGGGTTG
LjPAL6_R	LjPAL6	Lj2g3v3339740.1	phenylalanine ammonia lyase	AGAAGTGGGTCAACAATCCTTG
LjPAL7_F	LjPAL7	Lj3g3v0602630.1	phenylalanine ammonia lyase	CTGTGCTGTCAGAAGTCTTATCAG
LjPAL7_R	LjPAL7	Lj3g3v0602630.1	phenylalanine ammonia lyase	CTTAAGCCTATGCGTCAAATGG
LjPAL8_F	LjPAL8	Lj5g3v0659760.1	phenylalanine ammonia lyase	GAAGAACGTGAACACATCCATC

LjPAL8_R	LjPAL8	Lj5g3v0659760.1	phenylalanine ammonia lyase	TCATATGCAACCCTGGCAC
LjPAL9_F	LjPAL9	Lj5g3v1811400.1	phenylalanine ammonia lyase	GTTTGCTCAGTTCACCGAG
LjPAL9_R	LjPAL9	Lj5g3v1811400.1	phenylalanine ammonia lyase	CAGCACTCTGGACATGGTTG
LjPAL10_F	LjPAL10	Lj0g3v0350889.1	phenylalanine ammonia lyase	GTACCGAGTCAAGCCACAC
LjPAL10_R	LjPAL10	Lj0g3v0350889.1	phenylalanine ammonia lyase	CGAAGCGGTAAACATGGTG
LjPAL11_F	LjPAL11	Lj1g3v4590760.3	phenylalanine ammonia lyase	GTCGCTCAAGTTTTGGATCTAG
LjPAL11_R	LjPAL11	Lj1g3v4590760.3	phenylalanine ammonia lyase	CATAACAATTAGGCTCCTCAGGTC
LjPAL12_F	LjPAL12	Lj0g3v0121549.1	phenylalanine ammonia lyase	CACTCACTTAATTCCAGCTCGATG
LjPAL12_R	LjPAL12	Lj0g3v0121549.1	phenylalanine ammonia lyase	GGAGTAATGATTGTGTCATGTGAG
LjPTR1_F	LjPTR1	Lj3g3v3360890.1	pterocarpan reductase	TGCCACGCTGCATATTTGTG
LjPTR1_R	LjPTR1	Lj3g3v3360890.1	pterocarpan reductase	GCGTGCGAGCCTTATTTTCC
LjPTR2_F	LjPTR2	Lj3g3v3360920.2	pterocarpan reductase	TTTTGTGCCCATACCACCCA
LjPTR2_R	LjPTR2	Lj3g3v3360920.2	pterocarpan reductase	GTTCGCCTGGGGTCTAATGT
LjPTR3_F	LjPTR3	Lj3g3v3360930.1	pterocarpan reductase	GGAATGATGTGGACCGGACT
LjPTR3_R	LjPTR3	Lj3g3v3360930.1	pterocarpan reductase	TTGTGACTCCAGGCTGTGAC
LjPTR4_F	LjPTR4	Lj1g3v2124770.1	pterocarpan reductase	CCACATTAGCACAGCCAGGA
LjPTR4_R	LjPTR4	Lj1g3v2124770.1	pterocarpan reductase	GAGTGTCTGGGGTCTTCCG
LjIFS1_F	LjIFS1	Lj4g3v0485090.1	isoflavone synthase	AGGAGAAAAGAGAGAAACGGAG
LjIFS1_R	LjIFS1	Lj4g3v0485090.1	isoflavone synthase	GTTGTTGATTAGCTCTGCCAAA
LjIFS2_F	LjIFS2	Lj4g3v0486150.1	isoflavone synthase	GAGGTTTTTAAGTCTGAAGGG
LjIFS2_R	LjIFS2	Lj4g3v0486150.1	isoflavone synthase	ATAATTTGCCCTTTGACCCA
LjIFS3_F	LjIFS3	Lj4g3v0485970.1	isoflavone synthase	CTCGTGAGGTGCTTGAG
LjIFS3_R	LjIFS3	Lj4g3v0485970.1	isoflavone synthase	TACACTTTGCTCGCCCTC

Table 2S. Effect of methyl jasmonate (MeJA) and salicylic acid on isoflavane accumulation in leaves of *Lotus japonicus*. The compounds were applied in solution with 0.05 % *Tween 20*. Control plants were sprayed or submersed to 0.05 % *Tween 20* in distilled water for 24 h. Results are the means of 4 biological replicates \pm SEs, different letters indicate the significant differences using ANOVA with Tukey's post-hoc test. n.d. - not detectable

Treatments	Vestitol	Vestitol derivative	Sativan
Control sprayed 15 d	0.147 \pm 0.023 ^a	0.049 \pm 0.006 ^a	n.d.
MeJA 0.5 mM sprayed 5 d	0.216 \pm 0.012 ^b	0.092 \pm 0.017 ^b	n.d.
MeJA 0.5 mM spray 15 d	0.173 \pm 0.011 ^{ab}	0.058 \pm 0.003 ^{ab}	n.d.
Control submersed 24 h	0.138 \pm 0.019 ^a	0.050 \pm 0.005 ^a	n.d.
MeJA 7.5 mM submersed 24 h	0.209 \pm 0.013 ^{ab}	0.042 \pm 0.004 ^a	n.d.
Control sprayed 15d	0.175 \pm 0.031 ^a	0.063 \pm 0.008 ^a	0.090 \pm 0.005 ^a
Salicylic acid 0.5 mM sprayed 5 d	0.117 \pm 0.010 ^a	0.052 \pm 0.003 ^a	0.103 \pm 0.005 ^a
Salicylic acid 0.5 mM sprayed 15 d	0.143 \pm 0.027 ^a	0.052 \pm 0.004 ^a	0.123 \pm 0.006 ^a
Control submersed 24 h	0.191 \pm 0.030 ^a	0.046 \pm 0.009 ^a	0.112 \pm 0.008 ^a
Salicylic acid 7.5 mM submersed 24 h	0.338 \pm 0.032 ^b	0.175 \pm 0.028 ^b	0.129 \pm 0.016 ^a

Table 3S. List of protein-coding sequences of Phenylalanine ammonia-lyase (PAL) used to build the phylogenetic tree (Fig. 1S). Orys - *Oryza sativa*, Nict - *Nicotiana tabacum*, At - *Arabidopsis thaliana*, Mt - *Medicago truncatula*, Gm - *Glycine max*, Lj - *Lotus japonicus*.

Gene	Sequence Id. code
	National Center for Biotechnology Information (GenBank, https://www.ncbi.nlm.nih.gov/genbank/)
OrysPAL	KF556681.1
NictPAL	M84466.1
	The Arabidopsis Information Resource (TAIR) (https://www.arabidopsis.org/index.jsp)
AtPAL1	AT2G37040.1
AtPAL2	AT3G53260.1
AtPAL3	AT5G04230.1
AtPAL4	AT3G10340.1
	Medicago truncatula A17 r5.0 genome portal (https://medicago.toulouse.inra.fr/MtrunA17r5.0-ANR/)
	LeGOO: (https://lipm-browsers.toulouse.inra.fr/k/legoo/)
MtPAL1	MtrunA17_Chr1g0181091
MtPAL2	MtrunA17_Chr1g0199551
MtPAL3	MtrunA17_Chr2g0326921
MtPAL4	MtrunA17_Chr5g0448361
MtPAL5	MtrunA17_Chr7g0264311
MtPAL6	MtrunA17_Chr7g0264351
	SoyBase (https://www.soybase.org)
GmPAL1.3	Glyma.03g181600.1
GmPAL1.2	Glyma.03G181700.1
GmPAL1.1	Glyma.19G182300.1
GmPAL2.1	Glyma.10G058200.1
GmPAL2.2	Glyma.20G180800.1
GmPAL2.3	Glyma.13G145000.1
GmPAL2.4	Glyma.10G209800.1
GmPAL3.1	Glyma.02G309300.1
	LotusBase (https://lotus.au.dk/)
LjPAL1	Lj1g3v4590760.1
LjPAL2	Lj1g3v4590760.2
LjPAL3	Lj1g3v4590840.1
LjPAL4	Lj1g3v4590850.1
LjPAL5	Lj1g3v4590850.2
LjPAL6	Lj2g3v3339740.1
LjPAL7	Lj3g3v0602630.1
LjPAL8	Lj5g3v0659760.1
LjPAL9	Lj5g3v1811400.1
LjPAL10	Lj0g3v0350889.1
LjPAL11	Lj1g3v4590760.3
LjPAL12	Lj0g3v0121549.1

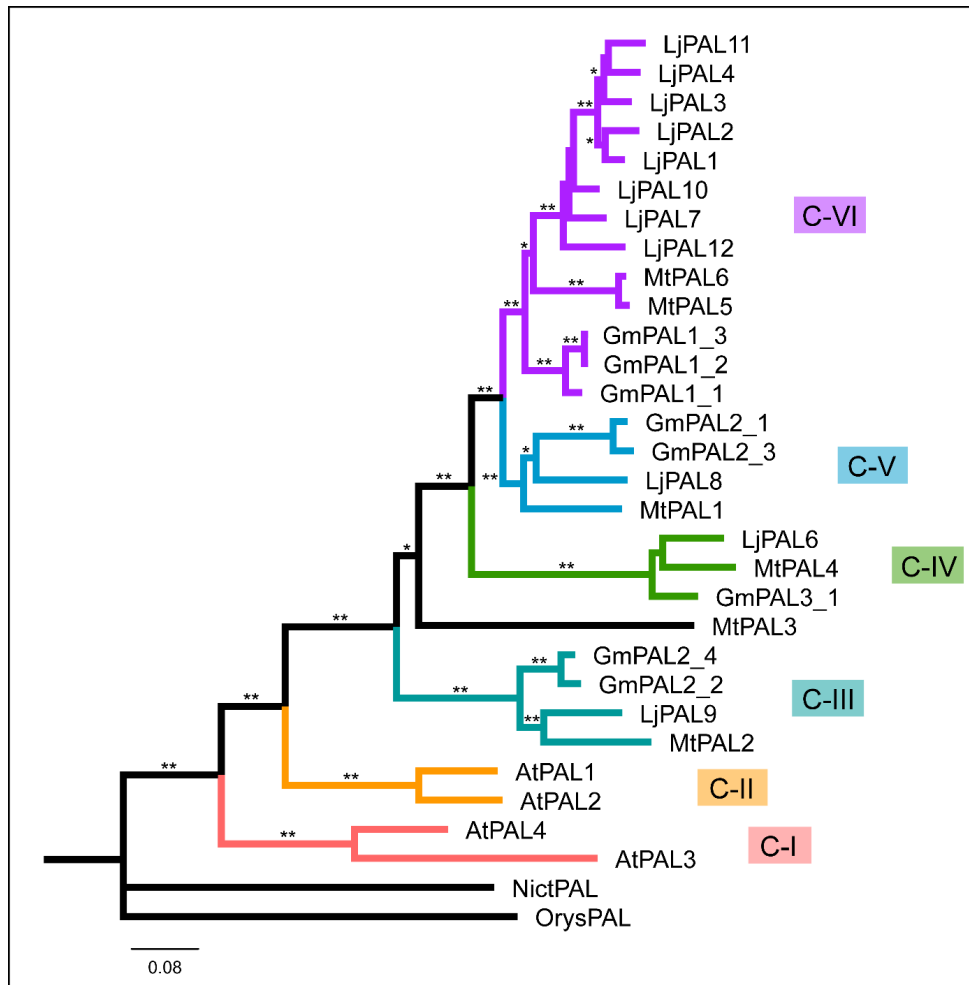


Fig. 1S. Bayesian majority-rule consensus tree of protein coding nucleotide sequences of phenylalanine ammonia lyase (PAL) with a list of all of their id. codes. Bayesian posterior probability values for branch support: * - 80 -<100 %, ** - 100 %; Orys - *Oryza sativa*, Nict - *Nicotiana tabacum*, At - *Arabidopsis thaliana*, Mt - *Medicago truncatula*, Gm - *Glycine max*, Lj - *Lotus japonicus*.