

Supplementary information

Table S1. List of primers used in this study.

Gene name	Forward primer (5-3')	Reverse primer (5-3')
<i>PaIPT1</i>	GGTAGTGAACGCCGACAAGA	CAGCGAGAGATCGAAACCCC
<i>PaIPT2</i>	CTCGAGGACTGAAGCAAGCA	TTCCGTTCAAGGCAGAAGCA
<i>PaIPT3</i>	CTTTATCCTCGGCTCCACCG	TCGGAGTTGATGACTTCGCC
<i>PaIPT4</i>	AGGTACTGTGGCTGCTTACG	CTACTACAGGCGATGCGTCC
<i>PaIPT5</i>	TCAGATCCTCGGGGTTTCCT	CCTCGCACCGCAGATCAATA
<i>PaIPT6</i>	TGAGACGGTGAGGAGGTTTC	GTTCTCTTCGCTGATCTCCAC
<i>PaLOG1</i>	GTGCCCATGAGTTGCTGTCT	GCTGCTCCATCTCCCAACTC
<i>PaLOG2</i>	TCCTGGTGGGTATGGGACAA	TGCCTTGCTGAGCTCTCTATG
<i>PaLOG3</i>	TGGGCTCAATTAGGCATCCA	GATATGCCGAGCACTTGGACT
<i>PaLOG4</i>	GGTGGCGAGGAACATTGACT	CCGCCATTAAAGACTGCCTG
<i>PaLOG5</i>	GTTGGGGAAGTTCTAGCGGT	TTCCATAGCCACCAGGCAAA
<i>PaLOG6</i>	ATTTGGGCCCGAGAACTGGTG	CCAAGAACATCACAACCCCC
<i>PaCKX1</i>	CTGGAGGAAATGGCGATAGG	GGATCAAACCTCCTCTTCAGAT
<i>PaCKX2</i>	CCACGTTCTTCAGGTCAGGA	GGATGGCCAGGGGATCAAAA
<i>PaCKX3</i>	GGCCAACACAACCTATGGGTC	CATCTGGAATTGTTGTTGACATCCT
<i>PaCKX4</i>	CCCCTTCCAATCCCGTGAACA	CCGTTGTGAAGACCGAACCC
<i>PaCKX5</i>	GAGGTGGTGACTGGAAAGGG	TGCTGTGGAGCATCTTGGAG
<i>PaCKX6</i>	AAAGCTAACGAGCGGGCCTA	GGGCCGTAACGAAAGGTCTG
<i>PaUbiquitin</i>	TGAACTCCATCGCCTTCCTCTTC	TGAAGCATGGCATCAATTTTC

Table S2. *IPT* genes identified from *P. aphrodite* genome, along with their molecular details and relevant genomic information.

Gene name ^a	Locus ^b	Chr ^c	Length ^d	IPPT ^e	IPT ^e	Family ^f	E value ^g	Identity (%) ^h	TargetP ⁱ	Glycosylation Site ^j
<i>PalIPT1</i>	PAXXG118600	L10a	335	5.37e-31	1.89e-03	AtIPT1	1.89e-94	48.065	MT	0
<i>PalIPT2</i>	PAXXG226240	L08a	502	2.98e-59	-	AtIPT2	3.17e-156	51.982	Other	1
<i>PalIPT3</i>	PAXXG097640	L04	306	1.51e-34	7.26e-03	AtIPT3	1.52e-89	47.97	Other	1
<i>PalIPT4</i>	PAXXG213053	Sca234	284	2.44e-29	1.61e-03	AtIPT8	3.99e-91	46.181	Other	0
<i>PalIPT5</i>	PAXXG302430	L13	449	3.07e-78	1.13e-06	AtIPT9	2.3e-165	53.125	CH	3
<i>PalIPT6</i>	PAXXG097630-	L04	340	8.93e-35	1.34e-04	AtIPT3	2.95e-90	46.392	Other	2

^aGene Names given to *PalIPTs* in this work.

^bLocus represented by the *P. aphrodite* genome database.

^cChromosomal localization of the *PalIPTs*, Sca represents scaffold.

^dLength the number of amino acids

^ePFAM e-values for having the indicated protein domains. PFAM e-values for having the indicated protein domains. IPT domain means Isopentenyl transferase, and IPPT domain means IPPT transferases in PFAM database.

^fClosest homologs from *Arabidopsis thaliana*.

^gBlastp e-values for having the indicated protein domains.

^hPercentage of identical amino acids with the closest *Arabidopsis thaliana* homologs

ⁱLocalization predicted with TargetP-2.0. "SP" for signal peptide, "MT" for mitochondrial transit peptide (mTP), "CH" for chloroplast transit peptide (cTP), "TH" for thylakoidal lumen composite transit peptide (ITP), "Other" for no targeting peptide (in this case, the length is given as 0).

^jGlycosylation sites are predicted with NetNGlyc - 1.0

Table S3. *LOG* genes identified from *P. aphrodite* genome, along with their molecular details and relevant genomic information.

Gene name ^a	Locus ^b	Chr ^c	Length ^d	Lysine_decarbox ^e	Family ^f	E value ^g	Identity (%) ^h	TargetP ⁱ	Glycosylation Site ^j
<i>PaLOG1</i>	PAXXG136830	L03	221	9.17e-60	AtLOG1	3.81e-122	76.555	Other	1
<i>PaLOG2</i>	PAXXG166050	L05a	244	2.58e-56	AtLOG1	5.12e-110	67.805	Other	0
<i>PaLOG3</i>	PAXXG233850	Sca192	215	1.19e-65	AtLOG1	1.19e-138	85.849	Other	0
<i>PaLOG4</i>	PAXXG280860	Sca468	192	1.20e-58	AtLOG1	4.41e-114	83.240	Other	0
<i>PaLOG5</i>	PAXXG038340	L15	229	3.81e-61	AtLOG7	1.46e-117	80.612	Other	0
<i>PaLOG6</i>	PAXXG106310	L06	225	4.65e-57	AtLOG8	8.9e-110	71.981	Other	0

^aGene Names given to *PaLOGs* in this work.

^bLocus represented by the *P. aphrodite* genome database.

^cChromosomal localization of the *PaLOGs*, Sca represents scaffold.

^dLength the number of amino acids

^ePFAM e-values for having the indicated protein domains.

^fClosest homologs from *Arabidopsis thaliana*.

^gBlastp e-values for having the indicated protein domains.

^hPercentage of identical amino acids with the closest *Arabidopsis thaliana* homologs

ⁱLocalization predicted with TargetP-2.0. "SP" for signal peptide,"MT" for mitochondrial transit peptide (mTP),"CH" for chloroplast transit peptide (cTP),"TH" for thylakoidal lumen composite transit peptide (ITP),"Other" for no targeting peptide (in this case, the length is given as 0).

^jGlycosylation sites are predicted with NetNGlyc - 1.0

Table S4. CKX genes identified from *P. aphrodite* genome, along with their molecular details and relevant genomic information.

Gene name ^a	Locus ^b	Chr ^c	Length ^d	FAD_ binding_4 ^e	CK-bind ing ^e	Family ^f	E value ^g	Identity (%) ^h	TargetP ⁱ	Glycosylation Site ^j
<i>PaCKX1</i>	PAXXG012950	L15	496	5.11e-23	4.64e-102	AtCKX1	4.14e-134	41.955	SP	2
<i>PaCKX2</i>	PAXXG031040	L10a	520	5.47e-19	8.73e-172	AtCKX1	0	64.155	SP	4
<i>PaCKX3</i>	PAXXG242550	Sca318	529	4.64e-23	6.56e-163	AtCKX3	1.58e-176	52.119	SP	0
<i>PaCKX4</i>	PAXXG031510	L10a	527	2.01e-17	0e+00	AtCKX5	0	69.535	SP	3
<i>PaCKX5</i>	PAXXG232040	Sca286	544	3.99e-19	5.85e-143	AtCKX6	6.51e-152	46.951	SP	0
<i>PaCKX6</i>	PAXXG098230	L01	509	1.47e-31	2.62e-145	AtCKX7	0	55.907	Other	2

^aGene Names given to *PaCKXs* in this work.

^bLocus represented by the *P. aphrodite* genome database.

^cChromosomal localization of the *PaCKXs*, Sca represents scaffold.

^dLength the number of amino acids.

^ePFAM e-values for having the indicated protein domains.

^fClosest homologs from *Arabidopsis thaliana*.

^gBlastp e-values for having the indicated protein domains.

^hPercentage of identical amino acids with the closest *Arabidopsis thaliana* homologs

ⁱLocalization predicted with TargetP-2.0. "SP" for signal peptide,"MT" for mitochondrial transit peptide (mTP),"CH" for chloroplast transit peptide (cTP),"TH" for thylakoidal lumen composite transit peptide (ITP),"Other" for no targeting peptide (in this case, the length is given as 0).

^jGlycosylation sites are predicted with NetNGlyc - 1.0

Figure S1. Western blot assay showing the production of PaCKX4, PaLOG2, PaIPT1, and green fluorescent protein (GFP, the control) in the agroinfiltrated *N. benthamiana* leaves.

