

Supplementary Figures

>gb|DQ192187.1|:357-1673 *Daucus carota* subsp. *sativus* putative phytoene synthase (PSY2) mRNA, complete cds

ATGTCAGTTGCTATGTCCTGGATTGTTACTCCCAGTCTTGAGGTTTCCAATTGCTTCGGGTACTTGGAGA
CTGCCCCGAGAGGGAACCCGAGTATTAGATCCATCTAGGTTGGGTTCCCGGGATAAGAATATGAGGTGTGG
AGGCAGACTTGAGAAGGGTAAGCTGCGGAAGTGGAGTTCTAAATCTTCAATGCTGAATATAGCTATTCG
TGTTTGGGTGGTTCTGAATTAGAGAATGGAAGTATATTTCTGTGCATTCAAGTATGGTAGTTAGTGCAG
ATGGAGATATGGCAGTGTCTCAGAGAAAAAGGTATATGACGTGGTTCTTAAACAAGCAGCGTTGGTCAA
AAGACAGTTCAGATCTGATGAGGAATTAGAGGTTAAGCCAGAAATGATTCTCCGGGGACTCTGAGCTTG
TTAAGTGAAGCTTATGATCGATGCGGTGAAGTATGTGCTGAGTATGCCAAAACATTTTACTTGGGAACAC
TACTGATGACCCAGAGAGGCGGAGGGCTATCTGGGCAATATATGTGTGGTGCAGAAGAACTGATGAATT
GGTAGATGGACCTAATGCGTCACATATAACTCCTTCAGCTTTGGATAGGTGGGAGTTGAGATTAGAAGAT
CTTTTCAAGGGGCGTCCATTTGATATGCTTGATGCTGCTTTATCAGATACAGTAATGAAGTTTCTGTG
ACATCCAACCATTCAAAGATATGATTGAAGGGATGAGGATGGACCTTAAGAAGTCGAGATACAAAACTT
CGACGAGCTATATCTTTATTGCTATTATGTTGCTGGTACTGTTGGATTGATGAGCGTTCCAATTATGGGC
ATTGCACCTAATTCACAGGCAACAACGGAGAGTGTTTATAATGCTGCTTTGGCTTTAGGGCTTGCTAATC
AATTGACTAACATACTCAGGGATGTTGGAGAAGATGCCAGAAGAGGAAGGGTTTATCTACCACAAGATGA
ACTGGCTCAAGCAGGGCTTTCTGATGAAGATATATTTGCGGGGAAGGTTACCGATAAATGGAGGAATTC
ATGAAGAAGCAAATTAAGAGGGCAAGGATGTTTTTCGATGAAGCACAAATAGGAGTAAGAGAACTCAGCC
CAGCTAGTAGATGGCCGGTATGGGCATCACTGCTGTTGTACCGTCAAATACTAGATGAAATTGAAGCCAA
CGATTACAATAATTTTACGAAGAGGGCTTATGTCAGCAAACCAAGAAAATACTTGCTTTGCCAGTTGCA
TATGCAAAAGCTTTTGCTCCAACAGCAAGAACAAGTTCAACGTTTCTGAAAACAT**G**A

Supplementary Figure 1. *DcPSY2* cloned sequence. The coding sequence of *DcPSY2* (1276 bp) was amplified and cloned into pCR8® entry vector. Start and stop codons are highlighted in bold.

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Query 184 TCTTTCAATGCTGAATATAGCTATTCGTGTTGGGTGGTTC-TGAATTAGAGAATGGAAG 242
      |||||
Sbjct 190 TCTTTAATGCTGATCCAAGATATTCATGCTTGGGTGGATCAAGAACT-GAAAAGGGAAG 248

Query 243 TATATTTT-CTGTGCATTCAAGTATGGTAGTTAGTGCAGATGGAGATATGGCAGTGTCTAT 301
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Sbjct 249 CA-GTTCTCTGTACAGTCCAGTTTGGTGGCTAGCCAGCTGGAGAAATGACAGTGTCTAT 307

Query 302 CAGAGAAAAAGGTATATGACGTGGTCTTAAACAAGCAGCGTTGGTCAAAAGACAGTTCA 361
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Sbjct 308 CAGAGAAAAAGGTCTATGATGTGGTATTGAAGCAAGCAGCTTTAGTGAAGAGGCAGCTGA 367

Query 362 GATCTGATGAGGAATTAGAGGTAAAGCCAGAAATGATTCTCCGGGGACTCTGAGCTTGT 421
      |||||
Sbjct 368 GATCTACCGATGAATTAGAAGTGAAACCTGATATAGTTGTTCCAGGGAATTTGGGCTTGT 427

Query 422 TAAGTGAAGCTTATGATCGATGCGGTGAAGTATGTGCTGAGTATGCCAAAACATTTTACT 481
      |||||
Sbjct 428 TGAGTGAAGCATATGATCGTTGTGGCGAAGTATGTGCAGAGTATGCCAAAGACATTTTACT 487

Query 482 TGGGAACACTACTGATGACCCAGAGAGCGGAGGGCTATCTGGGCAATATATGTGTGGT 541
      |||||
Sbjct 488 TAGGAACAAAGCTAATGACTCCAGAGAGAAGAAGAGCTATCTGGGCAATATATGTGTGGT 547

Query 542 GCAGAGAAGCTGATGAATTGGTAGATGGACCTAATGCGTCACATATAACTCCTTCAGCTT 601
      |||||
Sbjct 548 GCAGGAGAAGCGGATGAGCTAGTCGATGGCCCTAAAGCATCACACATAACTCCACAAGCTT 607

Query 602 TGGATAGGTGGGAGTTGAGATTAGAAGATCTTTTCAAGGGGCGTCCATTGATATGCTTG 661
      |||||
Sbjct 608 TAGACAGGTGGGAGGCCAGGCTGGAAGATATTTTCAAGTGGGCGGCCATTGATATGCTTG 667

Query 662 ATGCTGCTTTATCAGATACAGTAATGAAG-TTTCCTGTTGACATCCAACATTCAAAGAT 720
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Sbjct 668 ATGCTGCTTTATCCGATACTGTC-TCCAGATTCTCTGTTGATATTCAAGCATTCAGAGAT 726

Query 721 ATGATTGAAGGGATGAGGATGGACCTTAAGAAGTCGAGATACAAAACTTCGACGAGCTA 780
      |||||
Sbjct 727 ATGATAGAAGGAATGCGTATGGACTTGTGGAATCCAGATATAACAACCTCGATGAGCTA 786

Query 781 TATCTTTATTGCTATTATGTTGCTGGTACTGTTGGATTGATGAGCGTTCGAATTATGGGC 840
      |||||
Sbjct 787 TATCTCTATTGTTATTATGTTGCTGGTACAGTAGGACTGATGAGTGTCCAGTTATGGGT 846

Query 841 ATTGCACCTAATTCACAGGCAACCAAGAGAGTGTATATAATGCTGCTTTGGCTTTAGGG 900
      |||||
Sbjct 847 ATTGCACCTGAATCAAAGGCAACCAAGAGAGTGTATATAATGCTGCTTTGGCTTTAGGG 906

Query 901 CTGCTAATCAATTGACTAACATACTCAGGAGTGTGGAGAAGATGCCAGAGAGGGAAGG 960
      |||||
Sbjct 907 CTGCAAAATCAACTAACCAATATACTCAGAGATGTAGGAGAAGATGCCAGAGAGGACGA 966

Query 961 GTTATCTACCAAGATGAAGTGGCTCAAGCAGGGCTTCTGATGAAGATATATTGCG 1020
      |||||
Sbjct 967 GTATACCTTACCTCAAGATGAATTAGCACAGGCAGGGCTTCTGATGAAGATATATTGCT 1026

Query 1021 GGAAG-GTTACCGATAAATGGAGGAATTTATGAAGAAGCAAATTAAGAGGGCAAGGAT 1079
      |||||
Sbjct 1027 GG-AAGAGTGACGATAAGTGGAGGAACTTATGAAGAAACAATTCAGAGGGCGAGGAA 1085

Query 1080 GTTTTTCGATGAAGCACAAATAGGAGTAAGAGAAGTCAAGCCAGCTAGTAGATGGCCGGT 1139
      |||||
Sbjct 1086 ATTCTTTGATGAGTCAGAGAAAGGTGTCACAGAACTGGACTCTGCTAGTAGATGGCCGT 1145

Query 1140 ATGGGCATCACTGCTGTTGTACCGTCAA-ATACTAGATGAAATTGAAGCCAACGATTACA 1198
      |||||
Sbjct 1146 GTTAGCAGCGCTGCTGTTGTATCG-CAAGATATTGGACGAGATTGAAGCCAATGACTACA 1204

Query 1199 ATAATTTTACGAAGAGGGCTTATGTACGAAACCAAGAAAATACTTGTCTTGGCCAGTTG 1258
      |||||
Sbjct 1205 ATAACCTCACAGGAGGGCTTATGTTAGCAAGCCAAGAAAGCTTCTCACCTTGCCCATTTG 1264

Query 1259 CATATGCAAAAGCTTTTG 1276
      |||||
Sbjct 1265 CTTATGCAAAATCTCTTG 1282

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Supplementary Figure 2. *DcPSY2* and *NtPSY2* alignment. The *DcPSY2* coding sequence (subject, 184bp-1276bp) presents 80% identity with *NtPSY2* (query, 190-1282bp; LOC107761716; XM 016579975.1). Score: 817 bits (442)



Supplementary Figure 3. DcPSY1 and DcPSY2 alignment. The predicted proteins DcPSY1 (398 aa) and DcPSY2 (437 aa) share 64% identity and present the same amino acids at the active site (highlighted in dark), Mg²⁺ binding site (highlighted in blue). Two squalene/phytoene synthase signatures are present in both *D. carota* PSY proteins (in red). Identical amino acids are highlighted in green. Similar amino acids are highlighted in light blue. The squalene/phytoene synthase, isoprenoid synthase and the trans-isoprenyl diphosphate synthase domains are depicted in Figure 2A.

PSY-[A.thaliana] MSSSSAVLVWATSSLNPD-----MNNCG-LVRVLESSRLFSPO-----NORLNKGGKKQ-IPTWSSSFVR-NRSRRIG---VSSSLVASPSGEIALSSEKQYVNVVVKQAALVVKQLRSS 108

PSY-[N.pseudonarcissus] --MVVALRVVS-AIEIPIR-----LGFSEAN-WRFSSPKY-----DNLGRKKSRLSVSYSLTYTSKYACVG-FAENNKGFLIRSSLVANPAGEATISSSEKQYVDVVLKQAALVKDQTKSSR 107

PSY-[D.kaki] --MSVALLSVVSPNSEVSN--FGVFESSRREGNRVSDSKFIARYKSLICHVALKSKKSNVYGSFYADSSYPSPDGSGLKKGKFPULLSNVANPAGEMAVSSSEKQYVDVVLKQAALVVKQLRTG 122

PSY-[Z.mays] --MAITLVRAAS-----PGLSADS--TSHQGT-----LQCSLTLLTKRPAARRRMPCSLLGLHPWEAGRSP--AIVSSLPVMPAGEAVVSSSEKQYVDVVLKQAALVVKQLRTG 99

PSY1-[D.carota] --MACNFARVIV-----YPKIEHG--VSVLNT-----NRSRKSRSFCRMVMLS-----TGVSAAVANR-----VRTSEERVYEVVLKQAALVREEKRSSR 77

PSY2-[D.carota] --MSVAMSWIVTPSLEVSN-C-FGYLETAREGTRVLDPSRLGSRDKMRCGRLEKGLRKWSKSFNAEYSYSCLGSELENGSIFPVHSSMVVSADGMVAVSSEKQYVDVVLKQAALVVKQFRSD- 123

PSY1-[M.Domestica] --VKNFQMCSTIS-----FAGKTY-----IGESNGIRRRIRSMVTAAGA-----QVITAPKQSRPVPFPELSIQGFPLADLVHQEIVQRQSQTR- 77

PSY2-[M.Domestica] --MSGVLLVWVS-----PKNASSLLGLMPR-----ICTPRRSKFCPKLGFSSR-----VLAYSQAVVNP-----ARSSEKQYEVVVLKQAALVKEQSTVKR 80

PSY3-[M.Domestica] --MSVALVWVSPNTEVFK-FYGLDSSR-----FVLGHQSSIR-----AKMGKGDWKSCLCTDVKYSSVGGSGLGSEAKFPVLSLMVANPLGESAVSSEKQYVDVVLKQAALVVKQLRSN- 110

PSY4-[M.Domestica] --MSGVLLVWVS-----PKNASSPLGLLPR-----ICTPRRSKLSKLGFSFG-----VLAYSQAVANR-----ARSSEKQYEVVVLKQAALVREPNTVKR 80

PSY-[A.thaliana] YDLD-VKKPQ-----DVVLPGSLSLLVGEAYDRGCEVCAEAKTFYLGTLMTTPERRRAIWAIV-----VWCRRTDELVDSPINASHITPMALDRWEARLEDFRGRPFMDLDA 211

PSY-[N.pseudonarcissus] --KSTDVKP-----DIVLRGTVYLLK-DAYDRGCEVCAEAKTFYLGTLMTTPERRRAIWAIV-----VWCRRTDELVDSPINASHITPMALDRWEARLEDFRGRPFMDLDA 207

PSY-[D.kaki] --EDYEVKP-----DIVLRGTLSLMT-EAYDRGCEVCAEAKTFYLGTLMTTPERRRAIWAIV-----VWCRRTDELVDSPINASHITPMALDRWEARLEDFRGRPFMDLDA 222

PSY-[Z.mays] --VLDARPO-----DMDMP--RNLGK-EAYDRGCEVCAEAKTFYLGTLMTTPERRRAIWAIV-----VWCRRTDELVDSPINASHITPMALDRWEARLEDFRGRPFMDLDA 197

PSY1-[D.carota] GLCLDTKRTGSKSFDKSEN-DDAGMKSNNLLN-EAYDRGCEVCAEAKTFYLGTLMTTPERRRAIWAIV-----VWCRRTDELVDSPINASHITPMALDRWEARLEDFRGRPFMDLDA 189

PSY2-[D.carota] --EELVEKP-----EMILRGTLSLLS-EAYDRGCEVCAEAKTFYLGTLMTTPERRRAIWAIV-----VWCRRTDELVDSPINASHITPMALDRWEARLEDFRGRPFMDLDA 223

PSY1-[M.Domestica] --SVQEGG-----RRRQPNPSFLE-EAYERCKNLCAEAKTFYLGTLMTTPERRRAIWAIV-----VWCRRTDELVDSPINASHITPMALDRWEARLEDFRGRPFMDLDA 190

PSY2-[M.Domestica] SLXLDERTIVT-----EGLDNMQLLD-KAYDRGCEVCAEAKTFYLGTLMTTPERRRAIWAIV-----VWCRRTDELVDSPINASHITPMALDRWEARLEDFRGRPFMDLDA 181

PSY3-[M.Domestica] --GYLDVKP-----DILLRGNLSLLS-KAYDRGCEVCAEAKTFYLGTLMTTPERRRAIWAIV-----VWCRRTDELVDSPINASHITPMALDRWEARLEDFRGRPFMDLDA 210

PSY4-[M.Domestica] SLDLDERITE-----GLNNMDLLN-KAYDRGCEVCAEAKTFYLGTLMTTPERRRAIWAIV-----VWCRRTDELVDSPINASHITPMALDRWEARLEDFRGRPFMDLDA 180

PSY-[A.thaliana] LADTVARYPVDIOPFRDMIEGMRMDLKRKYQNFDDLYLYCYVYAGTVGLMSVPMVMDIPKSKATTESVYNAALALGIANQLTNILFDVGEDARRGRVYLPQDELAQAGLSDEDFRGRPFMDLDA 338

PSY-[N.pseudonarcissus] LSDTVKRFVVDIOPFRDMIEGMRMDLKRKYQNFDELYLYCYVYAGTVGLMSVPMVMDIPKSKATTESVYNAALALGIANQLTNILFDVGEDARRGRVYLPQDELAQAGLSDEDFRGRPFMDLDA 334

PSY-[D.kaki] LSDTVTKFPVDIOPFRDMIEGMRMDLKRKYQNFDELYLYCYVYAGTVGLMSVPMVMDIPKSKATTESVYNAALALGIANQLTNILFDVGEDARRGRVYLPQDELAQAGLSDEDFRGRPFMDLDA 349

PSY-[Z.mays] LSDTISRFPDIOPFRDMIEGMRMDLKRKYQNFDELYLYCYVYAGTVGLMSVPMVMDIPKSKATTESVYNAALALGIANQLTNILFDVGEDARRGRVYLPQDELAQAGLSDEDFRGRPFMDLDA 324

PSY1-[D.carota] LADTVSTYVVDIOPFRDMIEGMRMDLKRKYQNFDELYLYCYVYAGTVGLMSVPMVMDIPKSKATTESVYNAALALGIANQLTNILFDVGEDARRGRVYLPQDELAQAGLSDEDFRGRPFMDLDA 316

PSY2-[D.carota] LSDTVMKFPVDIOPFRDMIEGMRMDLKRKYQNFDELYLYCYVYAGTVGLMSVPMVMDIPKSKATTESVYNAALALGIANQLTNILFDVGEDARRGRVYLPQDELAQAGLSDEDFRGRPFMDLDA 350

PSY1-[M.Domestica] LTHTVFNPFLDIOPFRDMIEGMRMDLKRKYQNFDELYLYCYVYAGTVGLMSVPMVMDIPKSKATTESVYNAALALGIANQLTNILFDVGEDARRGRVYLPQDELAQAGLSDEDFRGRPFMDLDA 317

PSY2-[M.Domestica] LSDTVTKYVVDIOPFRDMIEGMRMDLKRKYQNFDELYLYCYVYAGTVGLMSVPMVMDIPKSKATTESVYNAALALGIANQLTNILFDVGEDARRGRVYLPQDELAQAGLSDEDFRGRPFMDLDA 308

PSY3-[M.Domestica] LSDTVTKFPVDIOPFRDMIEGMRMDLKRKYQNFDELYLYCYVYAGTVGLMSVPMVMDIPKSKATTESVYNAALALGIANQLTNILFDVGEDARRGRVYLPQDELAQAGLSDEDFRGRPFMDLDA 337

PSY4-[M.Domestica] LSDTVAKYVVDIOPFRDMIEGMRMDLKRKYQNFDELYLYCYVYAGTVGLMSVPMVMDIPKSKATTESVYNAALALGIANQLTNILFDVGEDARRGRVYLPQDELAQAGLSDEDFRGRPFMDLDA 307

PSY-[A.thaliana] MKRQDIKARMFDEAEKGVTELSEASRWPVWASLLLYRQILDTEANDYNNFTKRAYVSKAKKLALPLAYAKSLTKSSRLSI----- 423

PSY-[N.pseudonarcissus] MKRQDIKARTFFQAEKGVTELSEASRWPVWASLLLYRQILDTEANDYNNFTKRAYVSKAKKLALPLAYAKSLTKPLSLRPPSLSKA----- 423

PSY-[D.kaki] MKRQDIKARMKFFNEAEKGVTELSEASRWPVWASLLLYRQILDTEANDYNNFTKRAYVSKAKKLALPLAYAKSLTKPLSLRPPSLSKA----- 435

PSY-[Z.mays] MKRQDIKARMFDEAEKGVTELSEASRWPVWASLLLYRQILDTEANDYNNFTKRAYVSKAKKLALPLAYAKSLTKPLSLRPPSLSKA----- 410

PSY1-[D.carota] MKRQDIKARMFDEAEKGVTELSEASRWPVWASLLLYRQILDTEANDYNNFTKRAYVSKAKKLALPLAYAKSLTKPLSLRPPSLSKA----- 398

PSY2-[D.carota] MKRQDIKARMFDEAEKGVTELSEASRWPVWASLLLYRQILDTEANDYNNFTKRAYVSKAKKLALPLAYAKSLTKPLSLRPPSLSKA----- 438

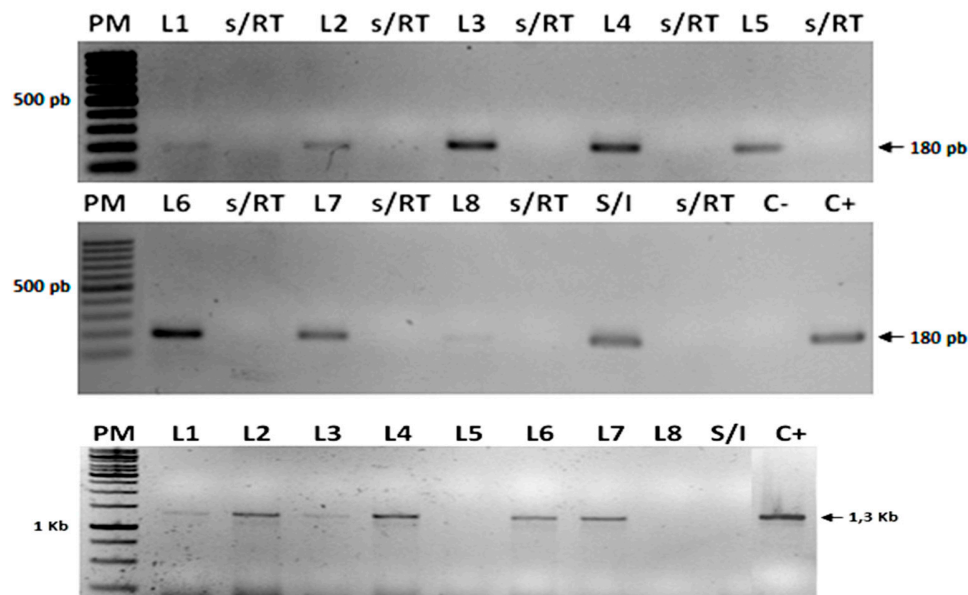
PSY1-[M.Domestica] MKRQDIKARFYFNXAEAGSGLDKASRWPVWASLLLYRQILDTEANDYNNFTKRAYVSKAKKLALPLAYAKSLTKPLSLRPPSLSKA----- 400

PSY2-[M.Domestica] MKRQDIKARMFDEAEKGVTELSEASRWPVWASLLLYRQILDTEANDYNNFTKRAYVSKAKKLALPLAYAKSLTKPLSLRPPSLSKA----- 396

PSY3-[M.Domestica] MKRQDIKARMFDEAEKGVTELSEASRWPVWASLLLYRQILDTEANDYNNFTKRAYVSKAKKLALPLAYAKSLTKPLSLRPPSLSKA----- 427

PSY4-[M.Domestica] MKRQDIKARMFDEAEKGVTELSEASRWPVWASLLLYRQILDTEANDYNNFTKRAYVSKAKKLALPLAYAKSLTKPLSLRPPSLSKA----- 395

Supplementary Figure 4. Multiple alignment of amino acid sequences of different enzymes encoded by PSY genes. The figure shows the alignment of the amino acid sequence of AtPSY (GenBank accession number: AAA32836.1), NpPSY (CAA55391.1), DkPSY (ACM44688.1), ZmPSY (ACY70935.1), DcPSY1 (DQ192186.1), and DcPSY2 (DQ192187.1). In addition, the characteristic functional domain of the PSY enzymes (Trans_IPPS-HH) are indicated; the aspartate-rich regions (red rectangles), the residues that cover the active site (green rectangles) and those residues that comprise both the active site and the substrate-binding pocket (black underlined). Those residues that are most conserved among the analyzed proteins are shown on a gray background, the higher the hue of this color, the higher the degree of conservation.



Supplementary Figure 5: Amplification by RT-PCR of the *rRNA18S* and *DcPSY2* from the transgenic *N.tabacum* lines transformed with pGWB2-DcPSY2. RT-PCR was carried out in L1-L8 for the endogenous *rRNA18S* (180bp) and the complete coding sequence of the transgene *DcPSY2* (1300bp). In the s/RT lanes, the respective controls without RT were loaded, in which mRNA from the lines analyzed was used as a template to determine the presence of gDNA in the samples. The positive control (C+) for *rRNA18S* corresponds to gDNA of wild-type *N. tabacum*. The positive control (C+) of *DcPSY2* corresponds to pDNA of the pGWB2/DcPSY2 vector. S/I: amplification using cDNA from *N. tabacum* transformed with the pGWB2 empty vector (negative control). C-: Negative control, without adding DNA. MW: 1 Kb molecular weight standard. EtBr-stained 1% agarose gel electrophoresis.

Supplementary Table S1. List of primers used in this work. *DcPSY1* (DQ192186), *DcPSY2* (DQ192187), *NtPSY1* (JF461341), *NtPSY2* (JX101475), *NtLCYB* (KC484706), *NtNCED3* (JX101472.1), *NtOsmotin* (X61679.1), *RNAr18S* (AJ236016.1) and *Nt EIF1 α* (AF120093.1)

Gene	Primer name	Sequence (5'→3')	Used for
<i>UBI</i>	ubiq-F	GCTCGAGGACGGCAGAAC	qRT-PCR
	ubiq-R	CTTGGGCTTGGTGTAGGTCTTC	
<i>18S</i>	18SF	TTGATTACGTCCCTGCCCTTT	qRT-PCR
	18SR	ACAATGATCCTTCCGCAGGT	
<i>DcPSY1</i>	psy1q-F	AGTCGATGGAGCATTACCATAATTC	qRT-PCR
	psy1q-R	CTAATGGGTTACAGAGGGTTGTGTTA	
<i>DcPSY2</i>	psy2q-F	GCTAATAAACTTCCGTGGGTGTTT	qRT-PCR
	psy2q-R	GCTGGAGTTAGTGCTACCC	
<i>DcPSY2 cds</i>	Psy2F	CGCACGTGTCATGTTTTTCAG	Complete cds amplification, 1276 bp
	Psy2R	AAACG GGACTAGTAATGTCAGTTGC TATGTC	
<i>NtPSY1</i>	qNtPsy1 F	GGAACCAAGCTAATGACCCCAGAGAGA	qRT-PCR
	qNtPsy1 R	TCAGAGATGTTGGAGAAGATGC	
<i>NtPSY2</i>	qNtPsy2 F	TCAGAGATGTTGGAGA AGATGC	qRT-PCR
	qNtPsy2 R	GCTTCAATCTCGTCC AATATCTTG	
<i>NtLCYB</i>	qNtLCYB F	CCGTGTTAAATTCCACCACGCCAA	qRT-PCR
	qNtLCYB R	GAAGCCAGTTGCATCAAGCACCCAC	
<i>NtNCED3</i>	qNtNCED3 F	CTTTACCAAAAACAGCCGACCCACG	qRT-PCR
	qNtNCED3 R	CACCAATGGCTTTAGGAAAAACAGGACG	
<i>NtOsmotin</i>	qNtOsmotin F	CTTCCTCCTTGCCTTGGTGACTTATACT	qRT-PCR
	qNtOsmotin R	CGTGCCATTTTAGTACCTCGTGGTGCAT	
<i>Nt EIF1α</i>	qNt EIF1a F	TGAGATGCACCACGAAGCTC	qRT-PCR
	qNt EIF1a R	CCAACATTGTCACCAGGAAGTG	