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Cessation of photosynthesis in *Lotus japonicus* leaves leads to reprogramming of nodule metabolism

Daniela Tsikou, Chrysanthi Kalloniati, Mariangela N. Fotelli, Dimosthenis Nikolopoulos, Panagiotis Katinakis, Michael K. Udvardi, Heinz Rennenberg, Emmanouil Flemetakis

Table S1. Primer pairs used in quantitative real-time PCR reactions

GENE	Lotus gene ID	Forward Primer	Reverse Primer
soluble starch synthase SSIII,	TC16679	CCCCTTTGTACAGCATTAGTGG	CACCTTGCACTTATTTACCGCT
Granule-bound glycogen (Starch)	TC15808	ATGGCCCAAGACTTTTCATGG	AACCTCTAGGCTCAATAGCGCC
soluble starch synthase	TC15963	GGACTGATGAAAAGAGGCATGA	CGTACTGAGTGGCTGCCTTTAC
glycogen(starch) synthase isoform II	TC16015	GCTGAGTGAACGTGAATGCAAA	AGTTCCTTTCCCTAGCACAGGC
Putative starch synthase	TC11131	ACCCATCACAGTGGAGACGAAG	CATTCACCATCCCACGTCAAG
Starch branching enzyme (EC 2.4.1.18)	MWM181h06_r	TTTGATCGAGCTATGCAGCATC	GGTTGCCCCTTTCGAAGACTAT
Starch branching enzyme I precursor	TC14733	GCTTCAATAGGCTCAATCACGC	TCGAGGTCGGTCATCATACCA
Beta-amylase	TC14465	ATCAACCGGAACTGCACTCAG	GCAGATTCAGTGCCTTCTTCCT
Alpha-amylase	TC15116	CCCAGGTTGGTGATGCACTAGT	AGCTCCCTTCCAACTGGTTCTC
Beta-amylase	TC11242	ATTTCAAAGCGGCAGCGAG	CCTGCATCATCTGGTAGTTCCC
starch phosphorylase isoform L	TC14890	CATTGAGCCAGTAAAATTGCCG	CCACATGGCACCAATTCTCTG
Alpha-glucan phosphorylase, H isozyme	TC19579	TCAGCAGTGACCGCACAATT	CACGGCACTCTTCTATGTTCCA
ADP-glucose pyrophosphorylase	TC8396	ACCTGCTGCGCGAAAAGTT	CAATGGAAGTTGCACCAGGAA
ADP-glucose pyrophosphorylase	TC8756	TTGGTATTGGCAGGAACTCCC	CCCCAATTCGAGCATTCTTGT
Cellulose synthase	TC14362	GCTTGCATCCATCTTGACCCT	GGCCATCTCTTGACACAAAAGG
Cellulose synthase	TC9552	GGTCTGGTCCATTCTTCTTGCA	TGTGGTGAACGGATCAACTCG
Phosphoglucomutase, cytoplasmic	TC14676	CCCCACTGGTTGGAAGTTCTTT	TCCCAAAACTTTCTTCACCGC
Phosphoglucomutase, cytoplasmic	TC14675	TTCTTGCCTTCCCTCTGCTATG	TCCCTGGCTCTCCAATCTCAT
Phosphoglucomutase, Chloroplastic	TC10716	AAAACCACTTCCCACAATCAGC	AACCGAACTCGAGCTCTTAGGC
Glucose-6-phosphate isomerase	TC17137	GCCACGCTCCAGAAGATATTGA	TAGTGCTCTATCGTTGGCAGCC
Cytosolic phosphoglucose isomerase	TC10203	AAGATTAACCGCATGTTCAGCG	TACGTGAAGCACCGACCTATCC
Cytosolic phosphoglucose isomerase	TC14615	CAGCTCGTTTCTCGGTTTTTC	CGGTATTCATTCTCAGCAGGAG
Glucose-6-phosphate isomerase	TC17714	CAGAGGCATTGGCTCCTGATAA	CCAGCAGGATCTGTGTTGTCAA
Hexokinase-related protein 1	TC16473	AAGCCTAGCTGGTGCAGGAATT	CTTCCCACAAATGAGGCCTTTT
Hexokinase	BP029610	GGCTGTGATTTTAGGCACTGGA	TGGTATTGCCTGAGCACGTTC
Fructokinase	TC14218	TTGTCACTCTCGGTGAACATGG	CGCCTGTTGTATCAACCGTGT
Fructokinase	TC15313	TGAGAAACGACTTCGAAAGGC	CAGTTACAGTGATGGCACCACA
Vacuolar acid invertase	TC15378	TTGAGAGCTTTGCTCAGGAAGG	GCTGCCCCATATATTGCTTCTG
Vacuolar acid invertase	TC12904	AATTTGAAGGCAGCGCCAG	GCAACAATGTCCAACTGTGTGG
Beta-fructofuranosidase	TC16805	CAGAGTTTATCCCACATTGGCC	CGCGATCTTGACATCAGCAGT
Beta-fructofuranosidase	TC16741	TGAAGGAAGCAGAGGTTGGCT	GCTGTCCTTATCCCGCTTAGCT
Cell wall invertase	AV407850	TCGTGAACTGGACCCCACTAGA	GCCGTTAATATCGGACGGTTG
Fructan 1-exohydrolase	BP071102	TTTCAGCCCCAGCAAAACTG	CACCTTTGTGGTACATAGGCCC
Neutral invertase	TC16464	AGAAAGTGCTCCCGTGTTGCT	GCTTCCAGATAAGGCAGAGCCT
Neutral invertase	AV420108	CTGGCAGTTCACTTTAGCCTGC	AACCGCCTTCTGTGCCAAA
Sucrose synthase LjSUS2	TC10121	TGGTGATTTTCGGTGGATTGTC	TAGCGATACAGCTCCCCGTTAC
Sucrose synthase LjSUS2	TC17628	TTTGTTAGGACCTGCGATCCAG	TAGGCCCAGCTGATCCATGTAG
Sucrose synthase LjSUS2	TC18457	TCTTCATGCTCCTGATCCGTCT	GAACACCATAGGCACTCTCCCA
Enolase	TC14118	CTGATCTTGCCGTTGGTTTGTC	TTTAGCGAGACGCTCAGACCTG

Enolase	TC17682	TGCTGAAAAGTGCCATTGACG	GCGGAATGCATAAGGTGCAA
Enolase	TC16760	TTCAGGCTGCACTTGACTCAAA	AGTCTCGCCACTCCGATGACTA
Triosephosphate isomerase, chloroplast	TC8011	CCGAGCGAAGACATATCATTGG	CGGTCAAAGCATAGGCAGCTT
Triosephosphate isomerase, cytosolic	TC14860	TGTTGCTGCTCAAAACTGTTGG	TCAGCACTAACCTCCCCGGTAT
Pyruvate kinase	TC14988	CACCAGCAAGGCACAGCTTAA	AGCTTTAGCAGATCCCTCAGCC
Pyrophosphate-dependent phosphofruct	TC15070	ATCCCAAGAGTGCCCATGAAG	CATCCAGAAACTGGTGGTCCA
Pyrophosphate-dependent phosphofuct	TC10213	TTTGCCTCCTTGCGAGATGA	TTGGATCGGACCTGGACTGAT
Glucose-6-phosphate 1-dehydrogenase	TC8851	GCAGTTTGTTGTTGGAGTGCTG	GATTTCACGTATGCCAACCATG
Glucose-6-phosphate 1-dehydrogenase,	TC16472	TGAGCTTGTTATCCGCCTACAA	AGTCCAGGTTGCTTCACCGTA
Putative 6-phosphogluconolactonase	LjNEST74h5r	CCTCACTTCCAAACCCAGCAT	CCGCCATTGAAGCTTTCTGA
6-phosphogluconate dehydrogenase,	TC8770	TGGACAAAACTGGCATGAAGG	GCAGGAACTGATAATTCGGCAG
Cytosolic 6-phosphogluconate dehydro	TC15545	TGGCTACCATGACCCTGAATCT	CAAGCATTATGACGACCCTGG
Ribose-5-phosphate isomerase precursor	TC7994	TCCTATCATCCCCTTTGAGCG	ATTCTGAGGAACCAAGCAAGCA
Probable ribose 5-phosphate isomerase	TC14838	AACCCTTTGTCACTGACCATGG	GGCAGCCTTCAAATCACCAA
Ribulose-phosphate 3-epimerase, chlor	TC7925	TTGGCACCACCAGCAATTG	AACACACATCACTGCGGAAGC
D-ribulose-5-phosphate 3-epimerase	TC15403	CAACTATAGACATGGCCGCGT	CCAAACACTGAACTTCCAGCAA
transketolase precursor - potato	TC9340	TCCTGGTCTGCTTGGTGGTAGT	CCCAAACATTTTCAGCAAGGTC
Transaldolase	TC14521	TTAATCTACGTGGCAAGGCAGC	CCCACCTTGGACCAGAAAATTT
Transaldolase	TC11589	CCTGTTTCTGATTTGCTGCCAT	CGCTGGATTGGTAGTGACACCT
Transaldolase ToTAL2	TC10369	GCTGCAAAATCCTGAGGCAA	TTCGCCAAGTCAGTACCGACA
Trehalase 1	TC18454	CAGACTGGTTTTGGCTGGTCA	GCCATCCAAACTCCTCCAAGA
Trehalose-6-phosphate synthase	TC8431	GAAGTGTTCCCTTGTGCCGTT	GCCTTGCAGCATTCTCAGAATC
Trehalose-6-phosphate synthase	TC9466	TGCCAGGTTTAGCCTGTGTTT	CAACCATTATCTTTTCCAGGCC
Trehalose-6-phosphate synthase	TC14996	GCCAGGCCAAGTATTACTTGGA	GCAAGGCCATGCAACATTCT
Trehalose-6-phosphate synthase	TC19005	AAGTGTGATGCCCAGACATGC	GCAACCACAACAACCCTAGCA
Trehalose-6-phosphate phosphatase	TC16872	CAAGGAAAGCCACGCATTTT	CCGCGAGTGATTTGAGGAAT
Trehalose-6-phosphate phosphatase	LjU20	TCATGGAGCAGATTTACGCACA	CCCGGAATTTACACTTGCCAC
Aconitase (Aconitate hydratase)	TC14176	AGCACCCACTGGCTCTGATTT	CATTGAACTGACCTTTGCTCCC
Cytosolic aconitase	TC15109	TCACCAAAGGAAATCCCATGTG	CCCAGGCATAAAGATTGCCAG
Aconitate hydratase, cytoplasmic	TC14371	CCCATTGAAAATGAGGCCAA	ATAATGCCCGCCCACAATC
Isocitrate dehydrogenase (NAD+)	TC14549	GCTCCTGATATTGCCGGAAAG	CGTAACACCACTCAGCAGCAAG
NADPH-specific isocitrate dehydrog	TC7991	CCCTGATGGAAAGACCATTGAA	TTCCCCACCCTTCTGATGAAC
Cytosolic malate dehydrogenase	TC7834	CTTACCGAGGAAAAGGCTTTGG	GGAACCAGCAAATGGCAGTAGA
NADP-dependent malic enzyme	TC17304	TGGCTTCTCATCTACCTCGACC	GGCTGTACATGCAACTTTCTGC
NADP-dependent malic enzyme	TC8784	TCCACCATTCACCAACATCAGA	AGCCTTAGCAGCAACTTTGGC
NAD-dependent malic enzyme 1.1.1.39	TC16102	CGGCCGTGAATTATGCGTAT	CATCAACGCTGCCTCCAATAG
Malate dehydrogenase mitochondrial	TC7960	GTTCCAGTTGCCGAGGTCAAT	GGCTTGTGGTGTTGCTTGAGA
Phosphoenolpyruvate carboxylase	TC14124	ATAATGTGAAGCTACGCCCCC	TCATCCGCAGGTTTACTCACG
Phosphoenolpyruvate carboxylase	TC7830	GCGTGTGACAGTTCAAGGTGA	ACGCTGCAGTGTTCTAAAGCAC
Phosphoenolpyruvate carboxylase kinas	TC14602	GAAGGTGGATGTGTGGAGCTGT	GCCGCAGAATCACCGTAAAA
RuBisCO subunit binding-protein alpha	TC8373	GGAGCTGACATTGTGCAAAAGG	AACTTCCCCCTCTACTCCAGCA
Ribulose bisphosphate carboxylase	TC19857	GAACGAGATCCAGGAATGCAAA	TGTCAAATGCAATGCAGCGT
Ribulose bisphosphate carboxylase	TC14081	ATTGTTGACACCTTCCCTGGTC	ACACTCTAGCCCTCAATGCACC
Carbonic anhydrase LjCA1	TC14306	CACTGAACCCCATGAGTTGACA	CATGCTTCAGAGCCTCCCTACT
3-deoxy-D-arabino-heptulosonate	TC8510	GTCACCTTCGATGACCTGAGCT	ATTGAGAAGCATTGAGCCTTGG
chorismate mutase	TC14425	GTTTTTGTGGCTCATTGGTCG	AGCCATAGCTTGAATGGCCTC
Phenylalanine ammonia-lyase 1	TC9381	TGGAAGCCATAACCAAGCTCA	ACAAGATCACCGGAAGCTGTG
Phenylalanine ammonia-lyase 2	TC18515	CACCAACAGCCAAAACAGTTCC	GCCACACCCCAATTTAATGGA
Chalcone reductase	TC8351	CCACAGCGCAGGCAATACTTA	CCAAAGTTCTTCCACGGTCTTG
Chalcone synthase 4	TC7870	CAAACTCTTAGGTCTTCGCCCG	ACCTGCAAAGCACCCTTGTTG
mRNA for chalcone isomerase	NP645869	AACAAGGCACTCTCAGAGGCAG	GCCAAAGGAACAACGCTTCA
4-hydroxyphenylpyruvate dioxygenase	TC8682	ATCCGAAACCCAACACTCACTC	ACCCGGTTTGGACTTCTTCAG
Putative flavanone 3-hydroxylase	TC7931	CGTTGCCTATTTCATTCGCC	TTACCAATGCCTTTGCAGGTTC
Cytochrome P450, Isoflavone synthase	TC14262	TGGAGGAAAGAGCTGGTCTCAC	TGCAACCTTGGATCTTGCAAG
Probable ribose 5-phosphate isomerase	TC14838	TCAGGACCGGAAAAATGAAGC	TTGGCTGTATCGAGTTGCGTG
Sucrose synthase LjSUS3	TC7847	GCCAACATTTGCTACCTGCAA	TAAATCGGCAGCAGCGTCA
Sucrose Synthase LjSUS1	TC7848	CCAATTCAGGTGGATTTCCTCA	CATAGATTGCAGGCTGCACAAA
Alkaline/neutral Invertase 1	CAG30577	TCCTGCCCGAATGGATTTTC	TCATCCCAGCGAGCTTCAATAA
Ornithine decarboxylase	CAC02644	TGCAAATCCGAGTCCGACA	TCATAGGTTGCGAGGTTGACG
Arginine decarboxylase 1	CAE02645	GGTGTTTCCCATTATCCCCATT	GAGAGGATGCCTTTCACAGTGG
Arginine decarboxylase 2	TC5158	AGAACATGTCTTCTGCAACCATTC	CTTGAACTGCTCGGCGTAGC

Spermine synthase	Ljnest12b2r	AGATGCACACAGCTGCTTTCG	TAAGCGGAAGGATCACGGATC
Spermidine synthase	TC10068	GACATTGTGGCAAACTGTCGC	CGGTGGTCCAAGCATAGTTGAC
Pyruvate decarboxylase I	Ljnest11h9r	GCCTGCGAATTGTGGTTATGA	TAGCGCCTACTGACCAACCAA
Pyruvate decarboxylase II	TC7922	GTTGGTGCAACCCTTGGCTAT	CCATCACCAATGCAAGCAATC
Alcohol dehydrogenase	Ljnest14brc	AGCATCCAGGCCATGATCTCT	AGTACAGCAACACCCCAACCAT
putative NADP-GDH	Ljnest22b7r	TTGCCCAACTCATGCTTGCT	TGCGATCTTTCCAGAACCACTC
NADPH-dependent mannose 6-phosph	TC15046	GGAAACTACCTGGCATGCGAT	ATCCCTATGCTGCGAACCAAG
CA a-type 1	Ljnest13e5	TGAGATCAATGCAAGGCCAAC	CCCTTCACACCACATTTGGAGT
CA a-type 2	Ljnest20a7rc	ATGCCCAAATTCCTATCGGC	CCTGCTGTGTGTCCTTGCATT
proline oxidase	TC7864	CGTTGAAGACGCCAATGACA	TCTGCTGACATCAACGGTGTG
sucrose-UDP glucosyltransferase	TC7848	CGGCCTCATCGAGACATACAA	GGTCCATCTGTGAGGAAATCCA
14-3-3 protein GF14omega (grf2)	TC7839	TTCATGGAGAAAGTCTCCGCC	GGTTCCTTTCTTCCACCGTGA
monodehydroascorbate reductase	TC15657	ACATGTTGACCATGCTCGCA	ACTGTTTTCCCATCCTCAGCTG
acidic endochitinase	TC14167	CATCGAAGGCGGTACAAACCT	TTGTGTCTCAAAGCGTCGAGG
Nitrilase 4 (sp P46011)	TC14107	GCCTCCACCATCTTCTACGACA	AGCAGCTTCAGCCAGCAATCT
thiazole biosynthetic enzyme precursor	TC14068	CTTCACCACCTCCACCCTATGA	ACAATGGACTCCTTGATCGGC
chalcone isomerase	NP591666	TCAATTTCCGGCGTCGATTA	TGCGCCACCAAGGAAATAAG
putative chalcone isomerase	NP591668	CAGCCACCGCCAAGTCTTATT	CCCTCAATCGTCAACCCTCTCT
Isoflavone reductase	TC7899	ACATTGAACAAGGCTGTCCACA	CCCACAATGCCATGATCTCA
Cytochrome P450	TC15466	CATCTACCATCATGACCCTCGC	TGAGCTGTGCCAAAGCAAGAG
cytochrome P450	TC8343	CTTTCGTTGTCCACACCATCG	GGTCTTGGTCCAAGCCACATAA
Trans-cinnamate 4-monooxygenase	TC14933	AACCTCGTCGTTGTCTCATCCC	ATTCGACACCCTGTGTGTGGAG
Prolyl 4-hydroxylase	TC15896	CAAGATCGCGTTCCCTTCTGT	CGAAGAATCCAGCGAGGAAGA
Prolyl 4-hydroxylase, alpha subunit-like	TC11925	TTCCCCAATGCATCCTCTGA	TTGCGAGCGATGGAGTTGA
Putative oxidoreductase	TC14685	CCCCCTATAGTTGTCGTTGCAT	TGGTGATTCGTTTGGAGTTGG
N-hydroxycinnamoyl/benzoyltransferas	TC8570	GGTTGCTCAGGTGACCAAGTTC	CCAATGCCATCAAACATGCA
Isoliquiritigenin 2'-O-methyltransferase	TC14525	CAGCCTCTGAAATCGCTTCTGA	CGAGCCTGTTTGGCAAATCA
4-coumarate:CoA ligase 2	TC7977	GCATTGTTGATTGCTCACCCA	CCTGCAGCTTCATCTTTCAAGG
Laccase	TC17617	ACGCAACACAATTGCTGTGC	CCCTGGATTGTTTGCTTGGA
Putative diphenol oxidase	TC20034	TCCAGGTGTATGGTTCATGCAT	TCATAGCCATTCCCCAACGT
Putative diphenol oxidase	GENf079a06	GGCATCACAAGTTCGAGGTGA	AAGAGTTGGCCCAGGAAACTG
Copper amine oxidase	LjNEST6a8r	CAGCCCACTTCTCAGACCTGTT	TAGAGCCCAGCAGCAACTTCA
Amine oxidase	TC11726	CTGGCATGATGGTTACGGAAGT	CCACTGCTACTGCAATCCGAA
Similarity to ornithine cyclodeaminase	TC11292	ACCCCAATTCGCCAAAGCTA	ACCAAGAAGGCATGAGGAGGAG
Proline dehydrogenase	TC7860	GGAGTTTGGCTTCGTCTTTGG	TGTGCGTGTCCTGGATGGTAT
Proline dehydrogenase	TC7863	ACCACACACCGAAAAGACCTGA	TGGCAAGTTGAAGGTCGCTCT
Pyrroline-5-carboxylate reductase	TC15604	AACGTCGTCATTTTCTCCGTGA	AGCGGCTTCAACTTCAACACC
Ornithine aminotransferase	TC8388	TCCTTGCCAAGCCAACACAT	GCTTCCAGAATCTCATCCCGA
Delta-1-pyrroline-5-carboxylate dehydr	TC8648	TGGAGATCAGGTTCGGTTCCT	GGCTTTGTTGCCCAAGATGA
Choline monooxygenase	TC17741	CAGAAAGGTCTCCAATCCCCA	GCCTGCTCCACTGTAGGAACAT
Betaine aldehyde dehydrogenase	TC16536	ATTCCGATCATCAACCCCTCC	CCTTAGTAGCCGCCGGAATATC
NAD-dependent sorbitol dehydrogenase	TC17752	GAAATGACTGTCCCACTCACCC	GCGGAAAATGCCAATCACA
NAD-dependent mannitol dehydrogena	TC10721	TGGCGATGATGATGTTGCTATC	TGTGCAGATCAGAATGGCAAAC
Putative cinnamyl alcohol dehydrogen	TC8891	TGAGTTTGCTTGGTGCAGACC	CGATTTAGCCAATGCCCTCAT
Aspartate aminotransferase	TC14495	ATACCGATGGCTCCACCTGAT	TGAGATCGCATTTGTCCGC
Glutamine synthetase chloroplastic	TC14146	GCTGGAATCAACATCAGTGGC	CCAACTTGATACTCCCACTGCC
Glutamine synthetase, cytosolic isozyme	TC8035	TTTGGCCGTGATATTGTGGAC	CTGATGTTCACACCGGCATAAA
Glutamate dehydrogenase	TC10844	CCGGAACATAAAGGCAATGTGT	TCCAAGAGTGAAGGCTCCCAT
NADH glutamate dehydrogenase	TC10856	CCGTGAGCTGCAGAAGTACATG	GTGAGTTTTGCACATTGCCTTG
Asparagine synthase	TC14104	TCCACCAAGAAACATGCAGC	GTTGGCACGCAAACAATCAT
Asparagine synthase	TC8451	GCAACCACAAAAGCTGCTGAA	TGAACCCTCAAGGCCTACACAG
Uricase	TC14572	TGGATGGTCAACCTCATGAACA	AGCCTCTGCTGTATGCTTCTCG
Probable 2-isopropylmalate synthase	TC14289	GCCAGGAGTTTAGGTTGCACTG	TGTCCGATCTTGCAGCATCTT
Branched-chain amino acid aminotransf	TC16062	ATGAGATTGTGCCACGCGA	TGAGTCACCTCCTTGGACAACC
Alanine:glyoxylate aminotransferase 2	TC9107	CATCTCATTCGCAACCTCCAA	GGAAAAGCTGCTGCATGCA
L-asparaginase	TC8339	TTCAACTCTGGTCGTGGATCTG	TGCTAGCCTCCATTTCCACAG
Alanine aminotransferase	TC14752	GCGTGCAAAGATTCTGGAAGAT	TGCTTTGTTGCATGTTACACCC
Histidinol dehydrogenase	TC10151	TGAAGCCCACAAGAGAGCTGTT	CTGAACCTGCCTGGCTTCTATG
Glycine dehydrogenase	TC14097	TTGGCATTGACTGCGTTGAA	AGCCGAGCCAACGACAATATC
Serine hydroxymethyltransferase)	TC9418	TGGCAGCAATGGCTTTATACCT	TGATGCTTTGCATGGCTTGA
Methionine synthase protein	TC8911	CCGCTGTGTCAAACCACCTATC	AAGACGGTCATCGGCTTAGGAC

S-adenosylmethionine synthetase	TC14111	TGAGGCAAGCTGCTAAGAGCA	CCAATGGCATAGGAAACCTGG
S-adenosylmethionine synthetase	TC14110	TGAGATCACAACCAAGGCCAA	CGATGTTCCTGCAAGTGGTTCT
Methionine synthase	TC14073	AGAACGACCGCAGAAAACTGG	TGCGACGCCATTTCTCTGA
Cystathionine-gamma-synthase precurs	TC19008	ATGAAAACGCTGCATCTCCG	GCCTCTAAAAGTTTGGCCATCC
Adenosylhomocysteinase	TC7865	TGACCCTGGAGGATGTTGTCTC	TGATGTCCTTGTTACCGGTGG
serine O-acetyltransferase	TC11304	CACTCTGAGTGATGCTGGATGC	CCACGGTGTTTAGCAGCTCTTC
Serine acetyltransferase	TC17048	CGCCGTCTCTCTAAACCACACT	TTCGCCGGTTGGCATTAGT
Serine acetyltransferase 1	TC18157	CCCAGTTTCTCCGATCGTGTT	GCGAGGTTTTGTCACGGTTCT
Cysteine synthase	TC8523	TAGCCTTCATGGCAGCAGCTA	CTCATTGAAGCAGGCATCGTAA
Cysteine synthase	TC14692	ACCATTCTTCGAGCTTTCGGA	AGCCTTCTGAACAGCTCCCTTC
Cysteine synthase, chloroplast precursor	TC10541	CGGTTTTGTGCTGTGAATTGTG	TGGAACACGATGATGATGGAGA
O-acetylserine (Thiol)lyase	TC8232	CCCAGCTTTGGAGAGCGTTAT	AGACCATGCTCTCTGCTTCTCG
Adenosine 5' phosphosulfate reductase	TC14588	GCATTCACAAACGCCATCAAG	AGGCCCATCAAGTATCCCTCAG
Plastidic cysteine synthase 1	TC17110	ATTTCTTCAGGAGCTGCTGCC	TCCCGCATTCTCAGGTCTCTT
Aminodeoxychorismate synthase	TC15188	TGCACCGAAGTTGAGATCCA	TGCAGCCTGAGTAGATACCTCG
Anthranilate synthase alpha subunit	TC10990	TTCCCTGGCTGAAACTTTGATG	GCAAGCAGAAGCTGCAGAACA
tryptophan synthase beta-2 chain precur	TC20070	CACATCTTCACCGGCAATTGA	TGAGTTGAGGCTTGCACTGGA
threonine dehydratase/deaminase	TC18952	TCGCCATTGAGTCCCCTTT	TGAGCCAGATGTTAACGCCA
Precursor monofunctional aspartokinase	TC14781	AGCAGAACCTGTCCCTCATTTG	GATGCAGAACCTGAGCACCAA
Aspartokinase-homoserine dehydrogen	TC9572	TTCGACCAGATGTTTGCCAAG	ATCTCAACACTTCCCCAGCGT
threonine synthase	TC9527	TTCAGATTGGTGACCCGGTTT	CCACCATAACTCTTCAGCGCAT
dihydrodipicolinate synthase	TC18091	TGAGCCAACCCCAATTGCT	AACTGGCTTGACAACCCCAAG
amino acid acetyltransferase (N-acetylgl	TC18260	ATTGCTTGCGCTTCCCTTATTC	CAATGGCAGCAATCTCACCAC
amino acid acetyltransferase (N-acetylgl	TC18465	CAAACCTGATTCCCAGGTGATG	GGTCCCTTTCTGGATCCCATT
N-acetylornithine deacetylase	Ljnest56a2r	CTGGACAGAGATTCCTTCGTGC	GGAGGTGTAAGAATTCGCCGAT
Beta-cyanoalanine synthase	TC14185	CTGGAATCCACACCAAATGCTT	AATGCACCTGAGTGTTGGCAG
pantoate--beta-alanine ligase	TC12836	AAGCTGGAGAAACCCCTTTGTG	ACAATGGTGGCAACCCCTCTA
1-aminocyclopropane-1-carboxylate	TC14222	TGATTGCTCAAACAGATGGTGC	GCATCATCCCCTGGATTGTAGA

Table S2. Gene expression in nodules after prolonged darkness: Gene expression in *L. japonicus* nodules harvested from plants grown under normal photoperiod (N. Ph.), or subjected to 24 and 72 h continuous dark, respectively. Transcript levels of these genes decreased significantly (<2-fold, P<0.05) or increased significantly (>2-fold, P<0.05) under extended dark conditions and are indicated in bold. Genes with decreased expression are marked by an asterisk. Genes with increased expression are marked in italics. The numbers indicate ratios of gene expression after 24 and 72 h continuous dark versus expression in normal photoperiod (control). P value represents the level of significance between the relative gene expression levels (ANOVA).

		Expression Ratio vs Control		
GENE	Lotus gene ID	24 h / N. Ph.	72 h / N. Ph.	*P*
Starch metabolism				
soluble starch synthase SSIII, precursor - potato	TC16679	0.31	0.18	*0.106*
Granule-bound glycogen (Starch) synthase	TC15808	0.22	0.16	*0.046*
*soluble starch synthase {Arabidopsis thaliana;}	TC15963	**0.34**	**0.17**	*0.024*
glycogen(starch) synthase isoform II precursor -	TC16015	0.38	0.30	*0.13*
Putative starch synthase	TC11131	0.27	0.04	*0.072*
Starch branching enzyme (EC 2.4.1.18)	MWM181h06_r	0.46	0.41	*0.309*
Starch branching enzyme I precursor	TC14733	0.47	0.34	*0.052*
*ADP-glucose pyrophosphorylase small subunit	TC8396 5-end	0.08	**0.02**	*0.004*
*ADP-glucose pyrophosphorylase small subunit	TC8756 3-end	0.06	**0.03**	*0.011*
Beta-amylase	TC14465	1.57	2.35	*0.194*
Alpha-amylase	TC15116	0.22	0.24	*0.099*
starch phosphorylase isoform L precursor,	TC14890	0.08	0.25	*0.068*
Alpha-glucan phosphorylase, H isozyme (Starch	TC19579	0.48	0.10	*0.053*
Other Carbohydrate metabolism				
Cellulose synthase	TC14362	0.36	0.30	*0.053*
Cellulose synthase	TC9552	0.98	0.70	*0.557*
Trehalase 1	TC18454	1.88	**2.97**	*0.007*
Trehalose-6-phosphate synthase homolog	TC8431	0.96	0.34	*0.181*
Trehalose-6-phosphate synthase homolog	TC9466	1.92	2.96	*0.134*
*Trehalose-6-phosphate synthase homolog	TC14996	0.12	**0.03**	*0.004*
*Trehalose-6-phosphate phosphatase	LjU20	**0.29**	0.75	*0.012*
*Phosphoglucomutase, cytoplasmic	TC14676	0.14	**0.09**	*0.025*
*Phosphoglucomutase, cytoplasmic	TC14675	0.40	**0.07**	*0.036*
Phosphoglucomutase, Chloroplastic	TC10716	0.49	0.28	*0.086*
*Glucose-6-phosphate isomerase	TC17137	**0.28**	**0.20**	*0.033*
*Glucose-6-phosphate isomerase	TC17714	**0.38**	**0.40**	*0.031*
*Cytosolic phosphoglucose isomerase	TC10203	**0.45**	**0.28**	*0.025*
Cytosolic phosphoglucose isomerase	TC14615	0.60	0.32	*0.097*
*Fructokinase	TC14218	**0.65**	**0.30**	*0.004*
*Fructokinase	TC15313	0.52	**0.33**	*0.046*
Beta-fructofuranosidase	TC16805	1.76	**3.56**	*0.039*
Beta-fructofuranosidase	TC16741	1.57	1.10	*0.21*
Fructan 1-exohydrolase	BP071102	1.48	1.25	*0.465*
Sucrose synthase LjSUS2	TC17628	1.05	0.60	*0.487*
*Sucrose Synthase LjSUS3	TC7847	0.16	**0.08**	*0.004*
*Sucrose Synthase LjSUS1	TC7848	**0.21**	**0.30**	*0.003*
Cell wall invertase	AV407850	1.61	2.37	*0.432*
Neutral invertase	TC16464	1.97	2.70	*0.067*
Neutral invertase	AV420108	1.70	2.53	*0.118*
Alkaline/neutral Invertase LjINV1	CAG30577	1.05	0.76	*0.56*
*sucrose-UDP glucosyltransferase	TC7848	**0.26**	**0.29**	*0.001*
Glycolysis				
Hexokinase-related protein 1	TC16473	0.29	0.59	*0.075*
Hexokinase	BP029610	0.26	0.23	*0.05*
*Enolase	TC14118	**0.36**	**0.13**	*0.004*

Enolase	TC17682	0.83	0.61	*0.326*
*Enolase	TC16760	0.73	**0.17**	*0.004*
*Triosephosphate isomerase, chloroplast precursor	TC8011	0.79	**0.23**	*0.04*
*Triosephosphate isomerase, cytosolic	TC14860	**0.32**	**0.19**	*< 0.001*
Pyruvate kinase	TC14988	0.91	0.54	*0.104*
Pyrophosphate-dependent phosphofructo-1-kinase-	TC15070	0.85	0.31	*0.05*
Pyrophosphate-dependent phosphofuctokinase beta	TC10213	0.78	0.75	*0.63*
*Pyruvate decarboxylase I	Ljnest11h9r	**0.49**	**0.27**	*0.004*
*Pyruvate decarboxylase II	TC7922	**0.27**	**0.17**	*< 0.001*
*Alcohol dehydrogenase	Ljnest14brc	**0.59**	**0.21**	*< 0.001*
Pentose phosphate pathway				
*Glucose-6-phosphate 1-dehydrogenase	TC8851	0.29	**0.06**	*0.004*
Glucose-6-phosphate 1-dehydrogenase, cytoplasmic	TC16472	0.53	0.71	*0.052*
*6-phosphogluconate dehydrogenase,	TC8770	**0.45**	**0.22**	*< 0.001*
*Cytosolic 6-phosphogluconate dehydrogenase	TC15545	**0.53**	**0.29**	*0.012*
*transketolase precursor - potato	TC9340	**0.35**	**0.23**	*0.031*
Transaldolase	TC14521	0.79	0.56	*0.221*
*Transaldolase	TC11589	0.02	**0.01**	*0.011*
*Transaldolase ToTAL2	TC10369	0.18	**0.08**	*0.011*
Ribulose-phosphate 3-epimerase, chloroplast	TC7925	**3.27**	**2.09**	*0.004*
D-ribulose-5-phosphate 3-epimerase	TC15403	0.90	0.70	*0.476*
Putative 6-phosphogluconolactonase	LjNEST74h5r	0.94	1.03	*0.97*
Ribose-5-phosphate isomerase precursor	TC7994	1.04	0.21	*0.039*
Probable ribose 5-phosphate isomerase	TC14838	0.96	0.60	*0.387*
TCA Cycle				
Malate dehydrogenase mitochondrial precursor	TC7960	0.22	0.18	*0.054*
*Cytosolic malate dehydrogenase (1.1.1.37)	TC7834	0.28	**0.15**	*0.011*
Aconitase (Aconitate hydratase) (Citrate hydro-	TC14176	**8.80**	3.80	*0.002*
Cytosolic aconitase	TC15109	**3.09**	2.06	*0.011*
*Aconitate hydratase, cytoplasmic	TC14371	0.37	**0.16**	*0.004*
*Isocitrate dehydrogenase (NAD+) precursor	TC14549	**0.54**	**0.28**	*0.011*
NADPH-specific isocitrate dehydrogenase	TC7991	1.03	0.76	*0.384*
CO$_2$ metabolism				
*Carbonic anhydrase LjCA1	TC14306	0.01	**0.00**	*0.004*
*Carbonic anhydrase a-type 1	Ljnest13e5	**0.33**	**0.13**	*< 0.001*
*Carbonic anhydrase a-type 2	Ljnest20a7rc	0.20	**0.08**	*0.004*
Phosphoenolpyruvate carboxylase	TC14124	1.33	1.98	*0.132*
*Phosphoenolpyruvate carboxylase	TC7830	0.60	**0.11**	*0.009*
*Phosphoenolpyruvate carboxylase kinase	TC14602	0.19	**0.07**	*0.004*
NADP-dependent malic enzyme 1.1.1.40	TC17304	0.90	1.96	*0.093*
NADP-dependent malic enzyme 1.1.1.40	TC8784	0.20	0.26	*0.071*
NAD-dependent malic enzyme 1.1.1.39	TC16102	0.25	0.28	*0.086*
RuBisCO subunit binding-protein alpha subunit	TC8373	0.45	0.33	*0.182*
*Ribulose bisphosphate carboxylase small chain	TC19857	1.19	**0.29**	*0.013*
*Ribulose bisphosphate carboxylase/oxygenase	TC14081	**0.17**	**0.03**	*0.012*
Ammonium assimilation				
Aspartate aminotransferase	TC14495	1.33	2.36	*0.244*
Glutamine synthetase chloroplastic precursor	TC14146	0.63	0.25	*0.05*
*Glutamine synthetase, cytosolic isozyme	TC8035	**0.39**	**0.13**	*0.007*
*Glutamate dehydrogenase	TC10844	**0.20**	**0.16**	*0.008*
NADH glutamate dehydrogenase	TC10856	6.97	**40.99**	*0.004*
Asparagine synthase	TC14104	12.16	**19.19**	*0.031*
*Asparagine synthase	TC8451	**0.48**	**0.26**	*0.025*
Other aminoacid metabolism				
*Alanine:glyoxylate aminotransferase 2 homolog	TC9107	0.48	**0.10**	*0.016*
L-asparaginase	TC8339	0.78	0.85	*0.785*
*Histidinol dehydrogenase	TC10151	**0.17**	**0.06**	*0.004*
Glycine dehydrogenase [decarboxylating],	TC14097	1.52	0.76	*0.382*
Serine hydroxymethyltransferase) (Serine methylase)	TC9418	1.07	0.49	*0.114*
Methionine synthase protein	TC8911	1.85	1.50	*0.482*
S-adenosylmethionine synthetase	TC14111	0.84	0.72	*0.667*

S-adenosylmethionine synthetase	TC14110	0.88	0.43	*0.128*
Methionine synthase	TC14073	0.32	0.50	*0.05*
Cystathionine-gamma-synthase precursor	TC19008	0.53	0.72	*0.501*
Adenosylhomocysteinase	TC7865	0.51	0.45	*0.094*
serine O-acetyltransferase	TC11304	0.54	0.58	*0.306*
*Serine acetyltransferase	TC17048	0.19	**0.05**	*0.004*
*Serine acetyltransferase 1	TC18157	**0.48**	**0.50**	*0.023*
Cysteine synthase	TC8523	0.82	1.78	*0.213*
*Cysteine synthase	TC14692	0.15	**0.08**	*0.011*
Cysteine synthase, chloroplast precursor	TC10541	0.38	0.50	*0.094*
*Plastidic cysteine synthase 1	TC17110	**0.03**	**0.07**	*< 0.001*
O-acetylserine (Thiol)lyase	TC8232	0.36	0.30	*0.05*
*threonine dehydratase/deaminase	TC18952	**0.20**	**0.17**	*< 0.001*
*Aspartokinase-homoserine dehydrogenase (HDH)	TC9572	0.07	**0.01**	*0.004*
*threonine synthase	TC9527	0.20	**0.07**	*0.004*
*N-acetylornithine deacetylase	Ljnest562r	**0.38**	**0.43**	*0.011*
*Beta-cyanoalanine synthase	TC14185	**0.39**	0.71	*0.049*
*pantoate--beta-alanine ligase	TC12836	**0.19**	**0.14**	*< 0.001*
Ornithine decarboxylase	CAC02644	0.53	0.47	*0.112*
Ornithine aminotransferase	TC8388	**6.31**	**7.78**	*0.007*
*Similarity to ornithine cyclodeaminase	TC11292	**0.23**	**0.08**	*0.001*
Arginine decarboxylase 1	CAE02645	0.75	1.42	*0.06*
Arginine decarboxylase 2	TC5158	0.45	0.24	*0.168*
proline oxidase	TC7864	0.81	0.54	*0.196*
Proline dehydrogenase	TC7860	1.01	1.01	*1*
Proline dehydrogenase	TC7863	**4.51**	**10.84**	*< 0.001*
*Prolyl 4-hydroxylase	TC15896	**0.29**	**0.11**	*< 0.001*
*Prolyl 4-hydroxylase, alpha subunit-like protein	TC11925	**0.32**	**0.20**	*0.005*
*Probable 2-isopropylmalate synthase	TC14289	0.64	**0.22**	*0.037*
*Nitrilase 4 (sp P46011)	TC14107	**0.34**	**0.30**	*0.01*
*amino acid acetyltransferase (N-acetylglutamate	TC18260	**0.58**	**0.47**	*0.019*
amino acid acetyltransferase (N-acetylglutamate	TC18465	1.55	1.74	*0.157*
*Branched-chain amino acid aminotransferase-like	TC16062	0.13	**0.01**	*0.004*
Anthranilate synthase alpha subunit precursor	TC10990	1.13	0.16	*0.049*
3-deoxy-D-arabino-heptulosonate 7-phosphate	TC8510	0.74	0.52	*0.149*
Other metabolism				
Phenylalanine ammonia-lyase 1	TC9381	1.11	0.87	*0.816*
*Chalcone reductase	TC8351	0.01	**0.00**	*0.011*
Chalcone synthase 4 (Naringenin-chalcone synthase	TC7870	2.94	3.53	*0.115*
mRNA for chalcone isomerase (chi gene)	NP645869	0.40	1.46	*0.065*
4-hydroxyphenylpyruvate dioxygenase (4HPPD)	TC8682	3.51	**4.93**	*0.037*
*Putative flavanone 3-hydroxylase	TC7931	0.40	**0.14**	*0.004*
Cytochrome P450, Isoflavone synthase	TC14262	1.76	**3.16**	*0.013*
Probable hydroquinone glucosyltransferase	TC16353	0.31	0.53	*0.096*
*14-3-3 protein GF14omega (grf2)	TC7839	**0.31**	**0.43**	*0.008*
monodehydroascorbate reductase (NADH)	TC15657	0.67	0.77	*0.136*
*acidic endochitinase	TC14167	**0.16**	**0.04**	*< 0.001*
*thiazole biosynthetic enzyme precursor	TC14068	0.06	**0.02**	*0.004*
chalcone isomerase	NP591666	**4.05**	**4.47**	*< 0.001*
putative chalcone isomerase	NP591668	0.91	1.51	*0.209*
Isoflavone reductase	TC7899	1.89	**5.52**	*< 0.001*
*Cytochrome P450	TC15466	**0.33**	**0.04**	*0.004*
*cytochrome P450	TC8343	**0.05**	**0.01**	*< 0.001*
Trans-cinnamate 4-monooxygenase	TC14933	1.57	**2.83**	*0.046*
Putative oxidoreductase	TC14685	0.81	**4.10**	*0.026*
*N-hydroxycinnamoyl/benzoyltransferase-like	TC8570	0.23	**0.08**	*0.004*
*Isoliquiritigenin 2'-O-methyltransferase	TC14525	**0.35**	**0.17**	*< 0.001*
*4-coumarate:CoA ligase 2	TC7977	**0.47**	**0.16**	*0.003*
*Laccase	TC17617	0.04	**0.02**	*0.025*
*Putative diphenol oxidase	GENf079a06	**0.45**	**0.27**	*0.005*
Amine oxidase	TC11726	0.86	0.73	*0.336*

*Pyrroline-5-carboxylate reductase	TC15604	**0.25**	**0.17**	< *0.001*
Delta-1-pyrroline-5-carboxylate dehydrogenase	TC8648	0.65	0.99	*0.364*
Choline monooxygenase	TC17741	2.24	0.69	*0.059*
Betaine aldehyde dehydrogenase	TC16536	1.09	0.86	*0.683*
NAD-dependent sorbitol dehydrogenase	TC17752	**8.46**	3.33	*0.004*
NAD-dependent mannitol dehydrogenase	TC10721	**1.86**	1.51	*0.025*
*Uricase	TC14572	**0.24**	**0.32**	*0.01*
Adenosine 5' phosphosulfate reductase	TC14588	0.88	0.50	*0.068*
*Aminodeoxychorismate synthase/glutamine	TC15188	**0.30**	**0.33**	*0.032*
dihydrodipicolinate synthase	TC18091	0.80	0.69	*0.339*
1-aminocyclopropane-1-carboxylate oxidase	TC14222	0.80	0.35	*0.065*
*Spermine synthase	Ljnest12b2r	0.72	**0.29**	*0.03*
*Spermidine synthase	TC10068	**0.42**	**0.46**	*0.005*
putative NADP-GDH	Ljnest22b7r	0.88	0.99	*0.947*
*NADPH-dependent mannose 6-phosphate reductase	TC15046	**0.17**	**0.23**	< *0.001*

Figure S1. Starch accumulation in leaves and nodules of *L. japonicus* plants grown under normal photoperiod conditions and after being subjected to 72 hours of continuous darkness, respectively. Starch is stained blue/black by iodine. After 72 hours of continuous darkness the starch has been exhausted completely. Bars indicate 100 μm in leaves and 1 μm in nodules.

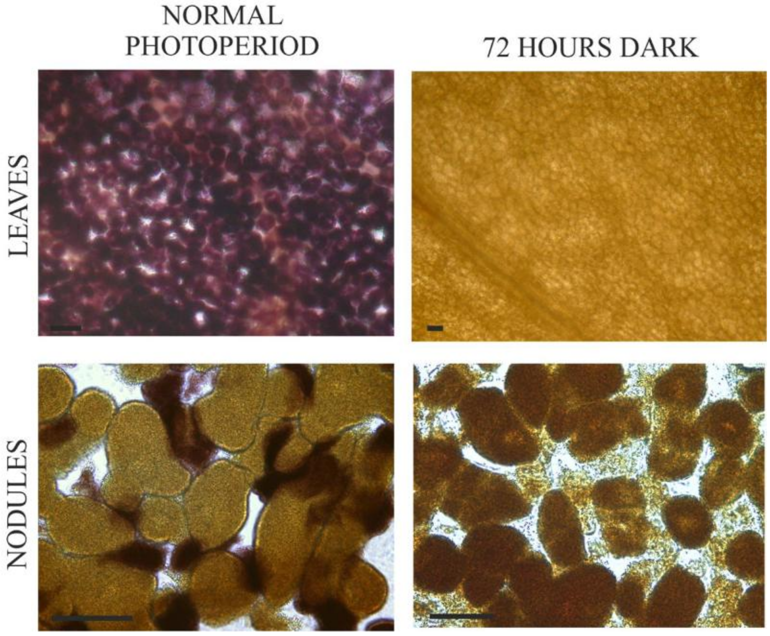

Figure S2. Ethylene (ppm) produced at different time points (after 1-, 2- and 3-h incubation) during the acetylene reduction assay. Measurements were taken from *L. japonicus* plants grown under normal photoperiod (**A**), after the plants had been subjected to extended dark periods for 24 (**B**) and 72 hours (**D**), and after 48 h recovery under normal photoperiod following the 24 h dark (**C**) and the 72 h dark (**E**) periods, respectively. Error bars refer to six biological replications.