

Supplementary material

Table S1. Primers used for Real-Time PCR

Acc#	Putative function	Forward primer	Reverse primer
BX900201	Chitinase	CAGGAGTGAGTGGCAAAGCA	CGGCGGTGCAGTGAACA
CR288152	Vacuolar acid invertase	GAAAGATTTTGGCCGACTCGTA	AAGGAGGGAGGACATGCATTAC
CR286861	LTI6B	TGGGAACAAGCAGAAGAATGG	GCGGCGGCAGGATGA
CR288425	β -expansin EXPB4	CCCGGTTTCTGCAAATCG	AATACTACTACTGCTATGATGTAATTGTGTTACC
BX927912	Protein LEA type 1	CTAGACGCCGTGAATGATTTCC	CGATACAGACTCAAACGACACAAA
BX901668	MADS20	AGACACTTCTCTGAATAACATAAGATCAAGA	TCTCCATCAGCAACTTTTCTTCT
CR293108	Putative zinc finger transcription factor	GGTGTGACCTCGACGTTGA	GCTTCCAATAGCGACTTGGAA
CR290344	NAC6	CGAGGCAGCAGCAGAAAGAT	CGAATCAATCACCATGTACTATGTACA
CR292244	Abscisic acid- and stress-induced protein	CATGCGTGGTGTGCTGTTT	CCCACCTGTCAGCCTCTC
CR291522	CBL-interacting protein kinase 23	CAGACTTCAGTTGCCGTCTT	TGGTGCTAGGATTAGGATCTAGTATTTTC
BX899347	Receptor protein kinase	CGACACCGAAGGCGTACAC	CGTGCCCCAGAGCTAGCA
BX898165	Receptor-like protein kinase	GCTTCGCATATGTTCTTGTCTGT	TGACTTCCCATACCGAGAAGATC
CR287245	Nonspecific lipid-transfer protein	AGGGAGCGTGCAACATAAAGTATA	ACAGCTGCGGCAGACATG
CR282197	OSJNBa0006B20.1	GACCAACAAATTAAGCTAAAATATCACAGA	GCACCATGGGAAAAAAAAATCA
CR288956	Putative GABA-A transaminase subunit precursor isozyme 3	TCAGAGGCCACCAGCCAGATATT	CCCCTTGAACCCATTTTCTTC
CR278485	LIP9	CAAACACTTCCAAATTCACCAT	CCACCGGCGAGCACAA
CR285538	AP2 domain transcription factor EREBP	AGGAGGACGGCCATATAATTACC	CTATGTACTTTGGCGTTAAGCATTG
BX900023	No significant homology	TGAACTCCTTGTCACTCTCAACATG	CACAACGTCTTCTCTGGCAAGTC
CR278984	Abcisic acid-inducible protein kinase	TCCCACACATTTGGCCATAGT	CTAAACCTCCCAGCACTGCAA
CR292239	Longevity factor-related protein	CCAAAAGCAGGCACAGAAAAGTA	GAGTGATGGAGCGATTCTTTGA

CR290553 Neurofilament triplet M protein-like protein	CAAAAACCACAACCTCTGAACATCA	GCAAGAAATGAAAAAGAAGAACTC
CR285756 Floral organ regulator 1	GTAAGGAGAGTCGACCACGC	TGAAGGAGAGTCGACCACGC
CR291219 No significant homology	GGCCAAGAACCATGAGAGA	GCTACATAGAGCACATTACCCG
CR287685 Isoflavone reductase-like protein	GGAGTCCTCGGGCACGTA	TGGTGGCTCTGTGGGAGAA
BX899544 LIP5	ACCATGGCCGGCATCA	TCTCCACCACGCCTTCCTT
BX900828 Putative LHY protein	GCAACCAGGTGAAAGCAA	GGTACCGGCTAGCGATGA
CR287151 Cellulose synthase-like protein OsCslA6	GTGGCGAAACGAATAACG	GGCAATTGAGCAGGAAAGAAA
CR289346 Boron transporter	CAGGCAGTACATCCTCCAAA	TCCTCATACTCTGCTGCATCCA
CR292670 Probable dormancy-associated protein	AGCTGACACGTACCGGTCT	GTCCTTGTGGTTATCTAATA
CR284320 GABA-A receptor epsilon-like subunit	GCCAACAAATTAATGCAAAGATATCA	CATGAGATTGTATATTACCCGTATGGA

Table S2. False positives in a dye-swap experiment

	ck vs.ck	ck vs.dr-2hr	ck vs.dr-6hr*	ck vs.dr-12hr	ck vs. w-2hr	ck vs. w-6hr
Match	10772	9523	6111	11964	7924	11023
Marginal match	11	901	1558	1735	817	831
Not match	1	5	8	15	0	4
Sum	10784	10429	7677	13714	8741	11858
False positive rate	0.01%	0.05%	0.10%	0.10%	0	0.03%

Match: showing a similar expression profile in a dye-swap experiment; Marginal match: showing a significant differently expression profile (≥ 2 -fold changed) in one microarray data set but not (0.5~2 fold changed) in another. Not match: have a contrary expression profile in a dye-swap experiment. The rate of the false positives is being calculated as $\text{Not match}^{\#}/\text{Sum}^{\#} \times 100\%$. * Data derived from the microarray RIFGP12200 and RIFGP12201 (see <http://159.226.24.50> for details).

Table S3. Number of cDNAs showing preferentially expression ratios

Ratio	dr-2hr/ck	dr-6hr/ck	dr-12hr/ck	w-2hr/ck	w-6hr/ck
2	230	961	1097	326	346
1/2	350	1077	1144	220	385
4	5	127	193	40	50
1/4	7	166	298	18	54
8	0	23	54	8	10
1/8	0	8	91	2	14

Supplemental Figure legend

Figure S1. Expression profiles of the pollination/fertilization regulated genes.