Supplementary material

Figure legends

Table S1 up/down-regulated genes in superior spikelets compared with inferior ones at 3 DPA. Superior spikelets are those flowered on the first 2-d within a panicle and inferior spikelets are those flowered on the last 2-d within a panicle.

Table S2 up/down-regulated genes in superior spikelets compared with inferior ones at 9 DPA. Superior spikelets are those flowered on the first 2-d within a panicle and inferior spikelets are those flowered on the last 2-d within a panicle.

Table S3 Expression of genes related to starch metabolism in developing caryopses by microarray analysis. RNA was extracted from superior and inferior spikelets at 3 and 9 DPA, respectively.

Table S4 Expression of genes related to hormones metabolism in developing caryopses by microarray analysis. RNA was extracted from superior and inferior spikelets at 3 and 9 DPA, respectively.

Table S5 Primers used in the present study.

Table S3

Acc. No.	Gene name	Enzyme	3 DPA			9 DPA		
			Ratio	Inferior	Superior	Ratio	Inferior	Superior
AK073146	*AGPS1*	ADP-glucose pyrophosphorylase small subunit 1	0.66	13479	8896	1.07	22595	24112
AK071826	*AGPS2*	ADP-glucose pyrophosphorylase small subunit 2	1.00	17896	17910	1.25	37124	46459
AK100910	*AGPL1*	ADP-glucose pyrophosphorylase large subunit1	0.82	9786	7994	0.64	6253	4026
AK071497	*AGPL2*	ADP-glucose pyrophosphorylase large subunit 2	1.00	20030	20106	1.22	42281	51738
AK069296	*AGPL3*	ADP-glucose pyrophosphorylase large subunit 3	0.72	5429	3932	1.18	13360	15816
AK121036	*AGPL4*	ADP-glucose pyrophosphorylase large subunit 4	0.63	245	156	0.61	245	151
AK109458	*SSⅠ*	Starch synthase Ⅰ	0.97	6203	6027	1.88	9110	17127
AK101978	*SSⅡa*	Starch synthase Ⅱa	0.82	13436	11022	1.34	22613	30335
AK066446	*SSⅡb*	Starch synthase Ⅱb	1.04	610	633	0.43	134	58
AK072339	*SSⅡc*	Starch synthase Ⅱc	1.11	830	923	1.25	644	804
AK061604	*SSⅢa*	Starch synthase Ⅲa	1.14	2141	2437	1.56	2774	4327
AK059368	*SSⅢb*	Starch synthase Ⅲb	1.08	4743	5139	0.48	2187	1041
AK100976	*SSⅣ-1*	Starch synthase Ⅳa	0.86	480	410	0.82	201	166
AK067577	*SSⅣ-2*	Starch synthase Ⅳb	0.80	1483	1187	1.22	2267	2765
AK070431	*GBSSI*	Granule-bound starch synthase I	0.99	15928	15789	1.29	39345	50615
AK102058	*GBSSⅡ*	Granule-bound starch synthase Ⅱ	0.76	3114	2353	0.49	1196	581
AK065121	*BEI*	Starch branching enzyme I	0.95	11252	10669	1.17	39365	46251
AB023498	*BEⅡa*	Starch branching enzyme Ⅱa	0.81	14602	11761	1.08	8527	9198
D16201	*BEⅡb*	Starch branching enzyme Ⅱb	0.93	26197	24294	1.30	39850	51660
AY578159	*CIN2*	Cell-wall invertase 2	0.66	6571	4364	1.65	2281	3755
AY578164	*CIN7*	Cell-wall invertase 7	0.90	337	304	1.26	195	246

AK100334	*SuS1*	Sucrose synthase 1	0.98	6576	6431	1.21	2290	2763
AK072074	*SuS2*	Sucrose synthase 2	0.93	15724	14612	1.58	21749	34356
AK100306	*SuS3*	Sucrose synthase 3	1.02	26173	26647	1.64	26257	42939
AK102158	*SuS4*	Sucrose synthase 4	1.04	1607	1677	1.24	30011	37084
AK063304	*SuS5*	Sucrose synthase 5	0.67	124	83	1.20	153	184
AK071732	*SPS3*	Sucrose phosphate synthase 3	1.40	1577	2206	0.87	997	867
AK101676	*SPS4*	Sucrose phosphate synthase 4	0.95	1689	1607	0.93	995	928
AK071525	*SPP1*	Sucrose phosphatase 1	0.98	688	675	0.82	652	533
AK063330	*SPP2*	Sucrose phosphatase 2	0.64	1771	1131	0.74	1248	926
AK065780	*UGP1*	UDP-glucose pyrophosphorylase 1	0.93	19072	17664	1.29	32078	41528
AK071248	*UGP2*	UDP-glucose pyrophosphorylase 2	1.16	279	322	1.01	769	777
AK068061	*PGIa*	Phosphate glucose isomerase 1	0.80	3432	2736	1.28	4047	5200
AK068236	*PGIb*	Phosphate glucose isomerase 2	1.31	3284	4287	1.19	2743	3266
AK100027	*SUT1*	Sucrose transporter 1	1.19	1574	1868	1.25	3968	4945
AK109461	*SUT2*	Sucrose transporter 2	0.55	1390	769	0.97	934	910
AK065430	*SUT4*	Sucrose transporter 4	0.98	860	843	1.44	810	1163
AK073105	*SUT5*	Sucrose transporter 5	1.79	579	1036	0.88	120	105
AK060577	*GPT1*	Glc-6-P/phosphate-tranlocator 1	0.85	7187	6144	1.18	28358	33595
AK070124	*GPT2*	Glc-6-P/phosphate-tranlocator 2	0.60	8900	5353	0.19	787	148
AK065618	*GPT3*	Putative Glc-6-P/ phosphate-tranlocator	1.37	2793	3815	1.05	1665	1747
AK062253	*GPT4*	Putative Glc-6-P/ phosphate-tranlocator	1.10	2522	2776	1.08	1841	1981
AK103471	*BT1-1*	Brittle 1-1 protein	1.40	311	434	1.23	232	286
AK107368	*BT1-2*	Brittle 1-2 protein	0.99	20143	19903	1.25	35880	44867
AK059671	*Amy2A*	a-amylase 2A	1.13	115	130	0.50	178	89
AK064300	*Amy3E*	a-amylase 3E				0.39	5118	1980

Table S4

Acc. no.	Gene name	Enzyme	3d			9d		
			Ratio	Inferior	Superior	Ratio	Inferior	Superior
AB050884	*ZEP*	Zeaxanthin epoxidase	0.97	367	380	0.25	73	289
AK064824	*NCED1*	9-cis-epoxycarotenoid dioxygenase 1	0.92	123	135			405
AK107649	*NCED5*	9-cis-epoxycarotenoid dioxygenase 5	0.80	372	467	0.25	201	813
AK120757	*ABA8ox2*	ABA 8’-hydroxylase 2	0.76	751	994	1.28	3578	2806
AK061017	*GA20ox1*	GA20-oxidase 1	0.66	559	851	0.69	122	176
AY114310	*GA20ox2*	GA20-oxidase 2	1.90	510	269			100
NM_001062119	*GA20ox4*	GA20-oxidase 4	0.89	1408	1573			252
AK101713	*GA2ox3*	GA2-oxidase 3	2.68	477	178	0.91	547	601
AK064250	*ACS2*	ACC synthase 2	1.15	130	112			
AK065212	*ACS6*	ACC synthase 6	0.97	3052	3161	1.60	1750	1097
AK065039	*ACO1*	ACC oxidase 1	1.24	217	176	0.75	8854	11879
AK058296	*ACO2*	ACC oxidase 2	1.67	893	536	0.48	521	1092
AF049889	*ACO3*	ACC oxidase 3	1.23	7327	5940	0.58	1390	2417
AK102472	*ACO7*	ACC oxidase 7	0.59	176	299	0.31	215	688
AK071981	*ckx1*	cytokinin oxidase 1	0.58	435	749	1.40	230	164
AK103272	*ckx3*	cytokinin oxidase 3	1.33	222	167	0.62	129	207
AK101022	*ckx5*	cytokinin oxidase 5	0.79	131	166	1.77	641	363

Table S5

Genes	**Forward primers**	**Reverse primers**
AGPS1	5’ AGAATGCTCGTATTGGAGAAAATG 3’	5’ GGCAGCATGGAATAAACCAC 3’
AGPS2	5’ TCTTTTGTTGCCCATTCATCTGG 3’	5’ TGATTCCAAGCACACTCTCATCGAC 3’
AGPL2	5’ TAGATAGGCCTTGGAATCGCACC 3’	5’ TAGAGTTCCCATTCCAAAACAAACC 3’
SSI	5’ GGGCCTTCATGGATCAACC 3’	5’ CCGCTTCAAGCATCCTCATC 3’
SSIIa	5’ GGCCAAGTACCAATGGTGAA 3’	5’ GCATGATGCATCTGAAACAAAGC 3’
GBSSI	5’ AACGTGGCTGCTCCTTGAA 3’	5’ TTGGCAATAAGCCACACACA 3’
BEI	5’ TGGCCATGGAAGAGTTGGC 3’	5’ CAGAAGCAACTGCTCCACC 3’
BEIIb	5’ ATGCTAGAGTTTGACCGC 3’	5’ AGTGTGATGGATCCTGCC 3’
SuS2	5’ TTCAGCAGGAGAAGCCGTCAGC 3’	5’ CCGGCGTTTATTTGAGGCAAGC 3’
SuS3	5’ CGGTGAAAAGAATGGGCAATG 3’	5’ CCATGAAAAGGCCAGAGCAT 3’
SuS4	5’ TCCGTGAACTGGCGAAGACT 3’	5’ CCCAAGTTCGTCACTTGCTG 3’
UGP1	5’ TCCTGGCCCGGTTTAAGTCA 3’	5’ TGCCGAATGCACACGACAAT 3’
GPT1	5’ AGAAGGGATCCAGATGAAGAATG 3’	5’ AACAAGAAACGAGCAACATAGACC 3’
BT1-2	5’ TGATTGTGCATGGGTGTGATG 3’	5’ AACAGAGGAAATCGAATCCTACG 3’
NCED1	5’CTCACCATGAAGTCCATGAGGCTT3’	5’GTTCTCGTAGTCTTGGTCTTGGCT 3’
NCED5	5’ ACATCCGAGCTCCTCGTCGTGAA 3’	5’ TTGGAAGGTGTTTTGGAATGAACCA 3’
ACO1	5’GATAGCGTGTGTACCACAGCGAC C3’	5’CACGGTACAGCACGCCGCAC3’
ACO3	5’CGCCGCCGAGGTCGTCCACG3’	5’GCCCGTTACACACACTTGAG3’
ACT2	5’CAATGTGCCAGCTATGTATGTCGCC3’	5’TTCCCGTTCAGCAGTGGTAGTGAAG3’
18S rRNA	5’ TCCATTGAAGGGCAAGTCTGG 3’	5’ CTTGGCAAATGCTTTCGCAG 3’