

Supplementary Table S1. Primer sequences for qPCR

Primer name	sequence(5'→3')
Gln1;1-RF (Ishiyama et al. 2004)	CATCAACCTTAACCTCTCAGACTCCACT
Gln1;1-RR (Ishiyama et al. 2004)	ACTTCAGCTGCAACATCAGGGTTGCTA
Gln1;2-RF (Ishiyama et al. 2004)	TGTTAACCTTGACATCTCAGACAACAGT
Gln1;2-RR (Ishiyama et al. 2004)	ACTTCAGCAATAACATCAGGGTTAGCA
Gln1;3-RF (Ishiyama et al. 2004)	CGTTAACCTCAACCTCACCGATGCCACC
Gln1;3-RR (Ishiyama et al. 2004)	TCCTCCTTGGCAACGTCGGGGTGGCTG
NADH-GOGAT_F	ATCGTCATTTTCCGCTGTTC
NADH-GOGAT_R	TTGCTCTCACAACCACAAGC
GLN2_F	CACCAAACCTTACTCTGACAGG
GLN2_R	CACTATCTTCACCAGGTGCTTG
qGLU1_ forward (Takabayashi et al. 2016)	TTGGGACAGGATGTTGTTGA
qGLU1_reverse (Takabayashi et al. 2016)	GCCTTCACCCAGAAAGACAA
qGLU2_ forward (Takabayashi et al. 2016)	GCTGGGATGACAGGTGGATTG
qGLU2_reverse (Takabayashi et al. 2016)	AAGCTGTGTTTGTCCCACTGG
AT3G55410_F	AGGATGTCTGAACGAGGAACA
AT3G55410_R	TAACCCAATTCGAACCCAAG
UBQ2_F (Ishiyama et al. 2004)	CCAAGATCCAGGACAAAGAAGGA
UBQ2_R (Ishiyama et al. 2004)	TGGAGACGAGCATAACACTTGC

Supplementary Table S4. Significant GO term of the differentially expressed genes in F1 hybrid

Significantly up- or down-regulated genes between F1 hybrid and parents was described in Supplemental table 2.

agriGO (bioinfo.cau.edu.cn/agriGO/) was used for singular enrichment analysis(SEA) of the differentially expressed genes in the F1 hybrid.

Ontology; P = Biological process, F = Molecular function, C = Cellular component.

Significant GO term of the up-regulated genes in F1 Hybrid

GO term	Ontology	Description	Number in input list	Number in BG/Ref	FDR
GO:0010200	P	response to chitin	8	134	1.4E-08
GO:0010243	P	response to organonitrogen compound	8	166	3.7E-08
GO:1901698	P	response to nitrogen compound	8	264	8.3E-07
GO:0009611	P	response to wounding	6	217	0.00009
GO:1901700	P	response to oxygen-containing compound	12	1557	0.00019
GO:0010033	P	response to organic substance	12	2023	0.0021
GO:0009719	P	response to endogenous stimulus	11	1732	0.0022
GO:0042221	P	response to chemical	14	2853	0.0025
GO:0001071	F	nucleic acid binding transcription factor activity	11	1730	0.0003
GO:0003700	F	transcription factor activity, sequence-specific DNA binding	11	1729	0.0003

Significant GO term of the down-regulated genes in F1 Hybrid

GO term	Ontology	Description	Number in input list	Number in BG/Ref	FDR
GO:0006810	P	transport	6	2391	0.0017
GO:0051234	P	establishment of localization	6	2406	0.0017
GO:0051179	P	localization	6	2517	0.0017
GO:0044435	C	plastid part	6	1455	0.00053
GO:0044434	C	chloroplast part	6	1419	0.00053
GO:0009536	C	plastid	8	4213	0.0014
GO:0009507	C	chloroplast	8	4148	0.0014
GO:0032991	C	macromolecular complex	6	2658	0.0062
GO:0043234	C	protein complex	5	1834	0.0083
GO:0044446	C	intracellular organelle part	7	4882	0.016
GO:0044422	C	organelle part	7	4894	0.016