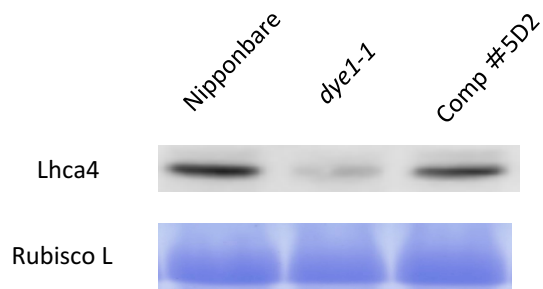


Supplementary Fig. S1. Genotype and phenotype of recombinant individuals in the *DYE1* candidate region. Recombinants obtained from F_2 and its progeny population between *dye1-1* and the CSSL SL224 are shown. The *DYE1* candidate region delimited by these recombinants is shown in gray. SNP positions were referenced by IRGSP Releases Build 5.0.

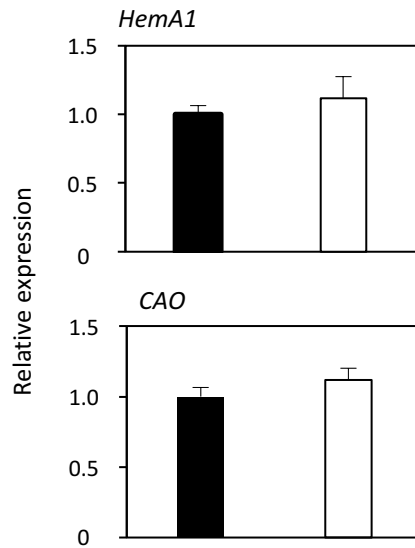
			20			40			80		80											
A.thaliana	MATVTT	HASAS	SIFRP	CTS-K	PRFLT	GSSGR	LNRDLS	SFTSI	GSSAKT	SSFK	VEAKK	GEWLP	GLASPD	YLTG	SLAGDN	GFDP	79					
G.max	MATVTT	QASAS	AIFRP	CTS-K	SRFLT	GSSGK	LNREVT	MRPM	GCPP-	SASF	VEAKK	GEWLP	GLASPT	YLNG	TLPGDN	GFDP	78					
S.lycopersicum	MATVTT	QASAS	AVFPP	SAT-K	TRFLN	GSSGK	LNRFDS	FKS-	-STLS	YNSFK	VEAKK	GEWLP	GLTSPT	YLNG	SLAGDN	GFDP	77					
O.sativa	MASVT	ARTPV	AALRS	SASLK	STFLG	QSSSTR	LAR-	- - - - -	-APT	TRRNVR	AEAK-	GEWLP	GLPSPT	YLNG	SLPGDN	GFDP	71					
			100			120			140		160											
A.thaliana	LGLAED	PENL	KWVFV	QAE	LVN	GRWAML	GVAG	MLLPE	VFTKI	GIIN	VP	EWYD	AGKEQ	YFASS	STLFV	IEFIL	FHYVE	IRRWQ	159			
G.max	LGLAED	PENL	RWYV	QAE	LVN	GRWAML	GVAG	MLLPE	VFTKF	GIIN	AP	QWYD	AGKSE	YFASS	STLFV	IEFIL	FHYVE	IRRWQ	158			
S.lycopersicum	LGLAED	PENL	RWYV	QAE	LVN	GRWAML	GVAG	MLLPE	VFTSI	GLLN	VP	KWYD	AGKSD	YFASS	STLFV	IEFIL	FHYVE	IRRWQ	157			
O.sativa	LGLAED	PENL	RWYV	QAE	LVN	GRWAML	GVAG	MLLPE	VLTKI	GLID	AP	QWYD	AGKAT	YFASS	STLFV	IEFIL	FHYVE	IRRWQ	151			
			180			200			220		240											
A.thaliana	DIKNP	GSV	NQ	DP	IFK	QYSLP	KGEV	GYP	GGI	FNPL	NF	APTQ	EAKE	KE	LANG	RLAML	AFLGF	VVQHN	VTGKG	PFEN	LLQHL	239
G.max	DIKNP	GC	VNQ	DP	IFK	QYSLP	PHEC	GYP	GSV	FNPL	NF	APTL	EAKE	KE	LANG	RLAML	AFLGF	IVQHN	VTGKG	PFEN	LLQHL	238
S.lycopersicum	DIKNP	GSV	NQ	DP	IFK	SYSLP	PNEV	GYP	GGI	FNPL	NF	APTL	EAKE	KE	LANG	RLAML	AFLGF	IVQHN	VTGKG	PFEN	LLQHL	237
O.sativa	DIKNP	GC	VNQ	DP	IFK	SYSLP	PHEC	GYP	GSV	FNPL	NF	EPTL	EAKE	KE	LANG	RLAML	AFLGF	LVQHN	VTQKG	PFEN	LLQHL	231
A.thaliana	DPWHNT	I	VQT	FN	- - -	251																
G.max	DPWHNT	I	INT	IRGY	-	252																
S.lycopersicum	DPWHNT	I	IQT	FSN	- -	250																
O.sativa	DPWHNT	I	IQT	LSG	- -	244																

Supplementary Fig. S2. Alignment of Lhca4 proteins from different species.

Conserved amino acid residues are shaded. The substituted amino acid in *dye1-1* (E146K) and *dye1-2* (V107M) are shown with arrows.



Supplementary Fig. S3. Western blot analysis of Lhca4 in the complementation line. Lhca4 was detected by western blot analysis in *dye1-1* and the complementation transgenic line Comp #5D2. Rubisco L was visualized by Coomassie brilliant blue G-250 staining.



Supplemental Figure S4. Expression of *HemA1* and *CAO* in *dye1-1*. Quantitative RT-PCR analysis of expression of *HemA1* and *CAO* in flag leaves of 1 week before heading. Filled and open bars show Nipponbare and *dye1-1*, respectively. Thin bars indicate standard errors (n = 4).

Supplementary Table S1. Primers used in the quantitative RT-PCR.

Gene	Forward primer	Reverse primer
Lhcb1a	AGTAGCTGAGCTTGAAGCAG	GAACTCGCCGGTCAGGTAG
Lhcb1b	GGAGCTCAAGGTGAAGGAGA	GTCCCCACTTCACTTGCCG
PsaA	ATTAGCCTGGAGTCATGACG	TTCATGAGGAAGTGGTATCTCC
SGR	CGCTACTACATCTTCCGCAA	TGGAGTGGAAAGTAGACCCACA
NYC3	TCTATCTAGGTGCCAAAGGC	ATTCTGGCACCTGCTGTTTC
Os03g0327800	AAGCGCAAGAGATCATCGGA	CTCAGTCCCAGTGACGATCC
HemA1	GTCAAAGAAAAGTGAATCCC	AGGATTTGCCCTTCTCCAAG
CAO	TCACGCAGAGATAGTGATGG	AATCCATGTCGATCGGGTA
actin2	TTCCAACAGATGTGGATCTCA	GGACACCAACAATCCCAAAC

Supplementary Table S2. Information for dCAPS markers used in the positional cloning of *DYE1*

Name	Reverse primer	Reverse primer	Restriction enzyme
P0413H11.2	ATGCCACATGACTGAGTACTGCAGCCAAGA	TTCAGATTACATGGCGCTGC	SacI
Lhca4	ATGTCCTGCCACCGCCGAGCT	CAGGCGATAACGGGTTTCGAC	SacI
dCAPS_5	GCTTGTGTCAGTTGTGT	ATGTATGAAATAATCAAAGATAACATTA	MseI
OSJNBa0016C11.6	TCTCCCTATCGAGATGGCGA	TCGATCTTGACAAGGGGAGCTCCTCCTTC	XbaI

Supplementary Table S3. Analysis of photosynthetic properties of presenescent flag leaves in *dye1-1*.

	Chla mmol /mg FwW	Chlb mmol /mg FwW	Total Chl mmol /mg FW	Chla/b	Fv/Fm	Maximum P700+ 2/3 T sec
Nipponbare	1.85±0.09	0.57±0.02	2.42±0.11	3.21±0.08	0.82±0.001	9.60±2.02
<i>dye1-1</i>	2.66±0.08 **	0.79±0.04 **	3.43±0.12 **	3.38±0.10	0.86±0.063 **	62.69±13.91 **

Flag leaves at heading were used for analysis. Maximum P700+ 2/3 T: Time to reach 2/3 of maximum P700+ (sec). n=4 for Chla, Chlb, Total Chl, Chla/b. n=5 for Maximum P700+ 2/3 T. **, P<0.01 (Student's t-test)