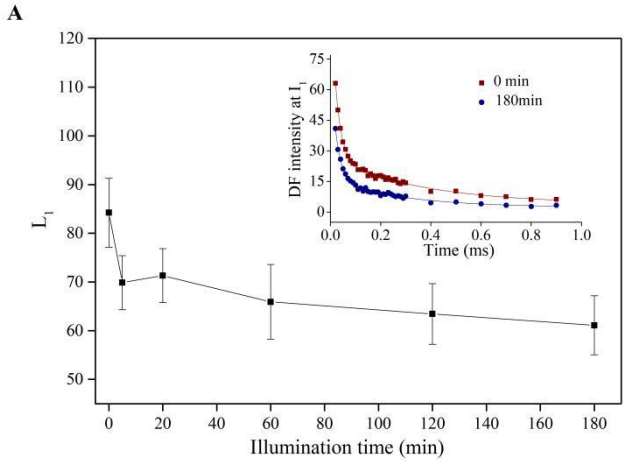
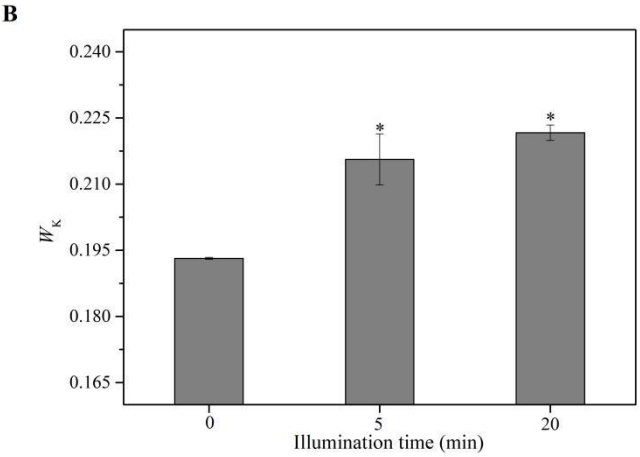
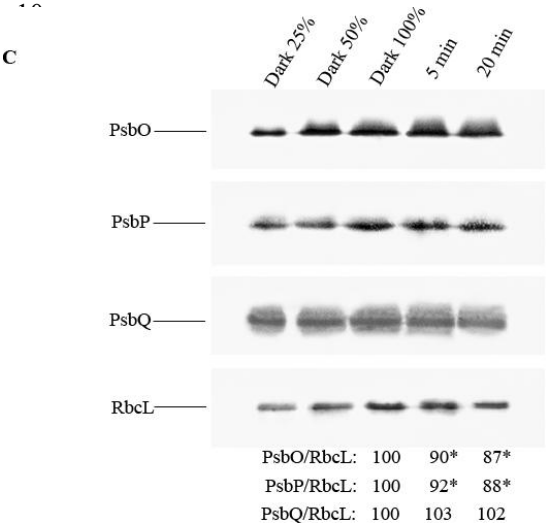
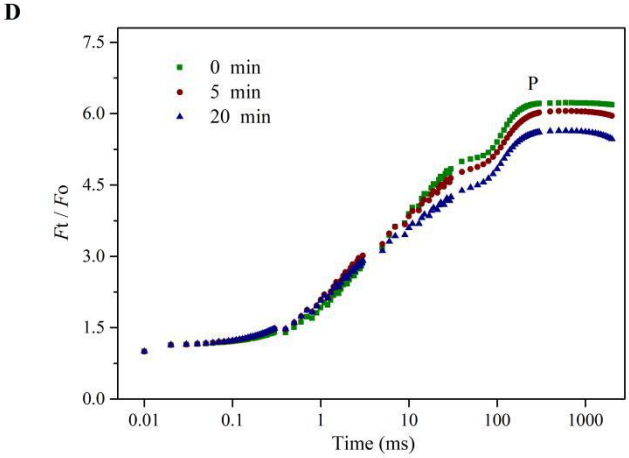
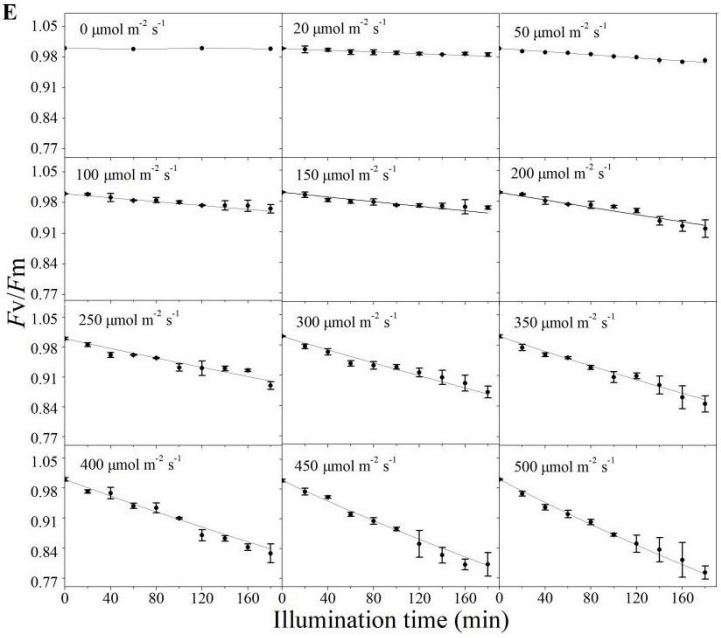
1 Figures


A
L_I
Illumination time (min)
DF intensity at I_1
0 min
180min
Time (ms)


B
W_K
Illumination time (min)


C
Dark 25%
Dark 50%
Dark 100%
5 min
20 min
PsbO
PsbP
PsbQ
RbcL
PsbO/RbcL: 100 90* 87*
PsbP/RbcL: 100 92* 88*
PsbQ/RbcL: 100 103 102


D
0 min
5 min
20 min
P
Ft / Fo
Time (ms)


E
0 μmol m-2 s-1
20 μmol m-2 s-1
50 μmol m-2 s-1
100 μmol m-2 s-1
150 μmol m-2 s-1
200 μmol m-2 s-1
250 μmol m-2 s-1
300 μmol m-2 s-1
350 μmol m-2 s-1
400 μmol m-2 s-1
450 μmol m-2 s-1
500 μmol m-2 s-1
Fv/Fm
Illumination time (min)

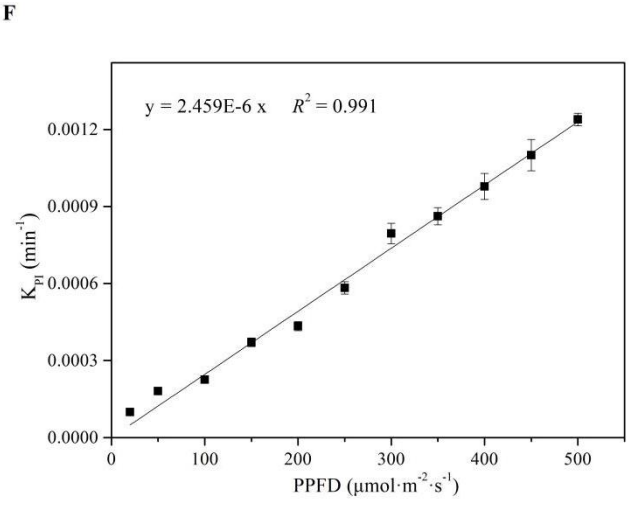
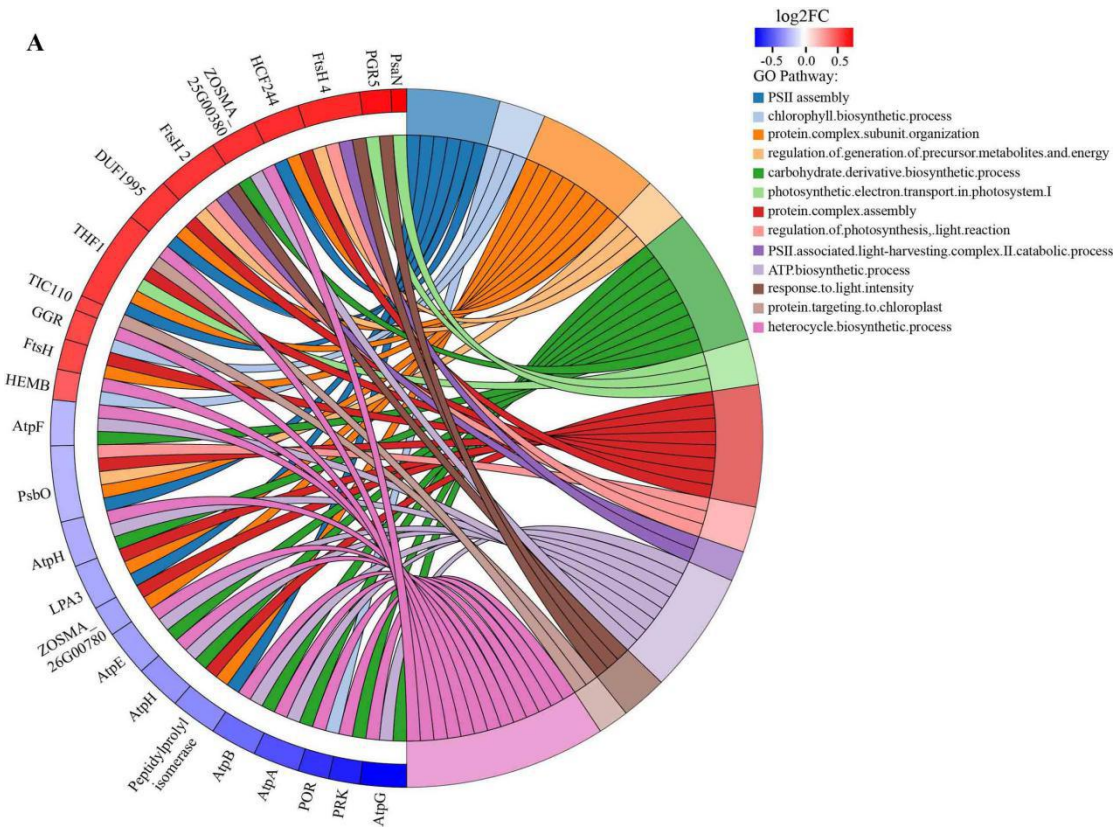

F
y = 2.459E-6 x R^2 = 0.991
K_{PI} (min-1)
PPFD (μmol·m-2·s-1)

Fig. 1 Preferential impairment of OEC induced by light. (A) Variations in the amplitude L_1 of the kinetics component calculated by fitting the DF decay kinetics to the time function $DF(t) = L_1 \times \exp(-t/\tau_1) + L_2 \times \exp(-t/\tau_2) + L_3$. The inset shows DF decay kinetics at I_1 in response to light exposure. (B) Changes in the relative variable fluorescence at the K-step (Wk) in response to light exposure. (C) Variations in OEC peripheral proteins PsbO, PsbP and PsbQ during light exposure. Values were % of dark 100% and normalized to RbcL amount. The significantly different value (Tukey's tests, $P < 0.05$) from 0 min or dark is marked with an asterisk (*). (D) Changes in the normalized chlorophyll fluorescence intensity of OJIP transients (F_t/F_O) in response to light exposure and plotted on a logarithmic time scale. (E and F) Photoinhibition measured by the decrease in F_v/F_m in the presence of lincomycin. (E) The decreases of F_v/F_m standardized based on 0 min fitted well with the function $F_v/F_m = \exp(-K_{PI} \times t)$ (all R^2 values > 0.9). (F) Dependence of the K_{PI} on photon flux density ($P < 0.05$). The means ± s.d. were calculated from three independent samples. The means ± s.d. were calculated from three independent samples. Each curve represents the average of three replicates.


A
log2FC
-0.5 0.0 0.5
GO Pathway:
PSII assembly
chlorophyll.biosynthetic.process
protein.complex.subunit.organization
regulation.of.generation.of.precursor.metabolites.and.energy
carbohydrate.derivative.biosynthetic.process
photosynthetic.electron.transport.in.photosystem.I
protein.complex.assembly
regulation.of.photosynthesis,.light.reaction
PSII.associated.light-harvesting.complex.II.catabolic.process
ATP.biosynthetic.process
response.to.light.intensity
protein.targeting.to.chloroplast
heterocycle.biosynthetic.process
PsaN
PGR5
FtsH 4
HCF244
ZOSMA_25G00380
FtsH 2
DUF1995
THF1
TIC110
GGR
FtsH
HEMB
AtpF
PsbO
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AtpB
AtpA
POR
PRK
AtpG

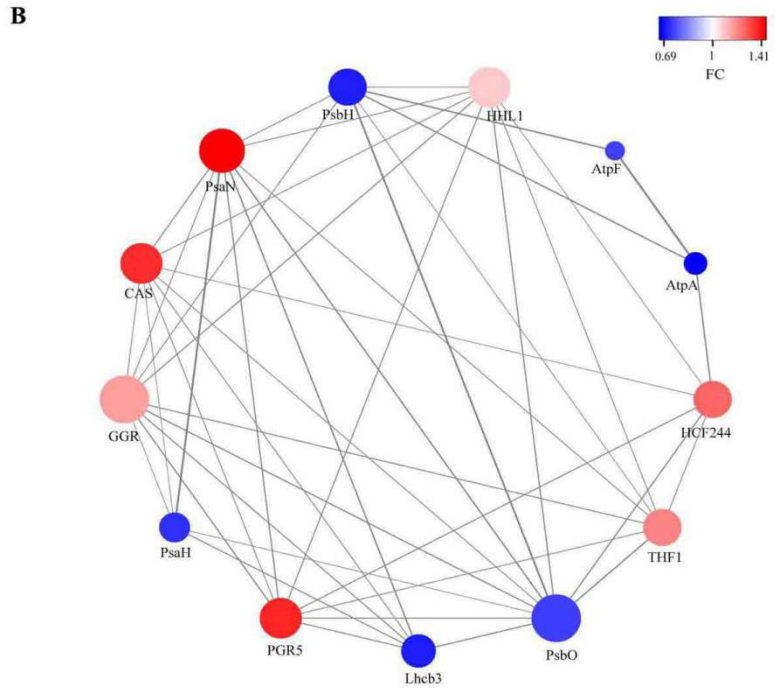
B
0.69 1 1.41
FC
PsbH
HHL1
PsaN
AtpF
CAS
AtpA
GGR
HCF244
PsaH
THF1
PGR5
PsbO
Lhcb3

Fig. 2 GO enrichment analysis and PPI network of DEPs. (A) The biological processes in GO enrichment analysis of DEPs. The DEPs are on the left and the GO pathway names are on the right ($P < 0.05$). (B) PPI network of DEPs. Red nodes indicate upregulated proteins and blue nodes indicate downregulated proteins. The larger size of the node represented the higher connectivity of the protein, which indicated more interactions with other proteins. The width of the line represents the capacity of the interaction between proteins.

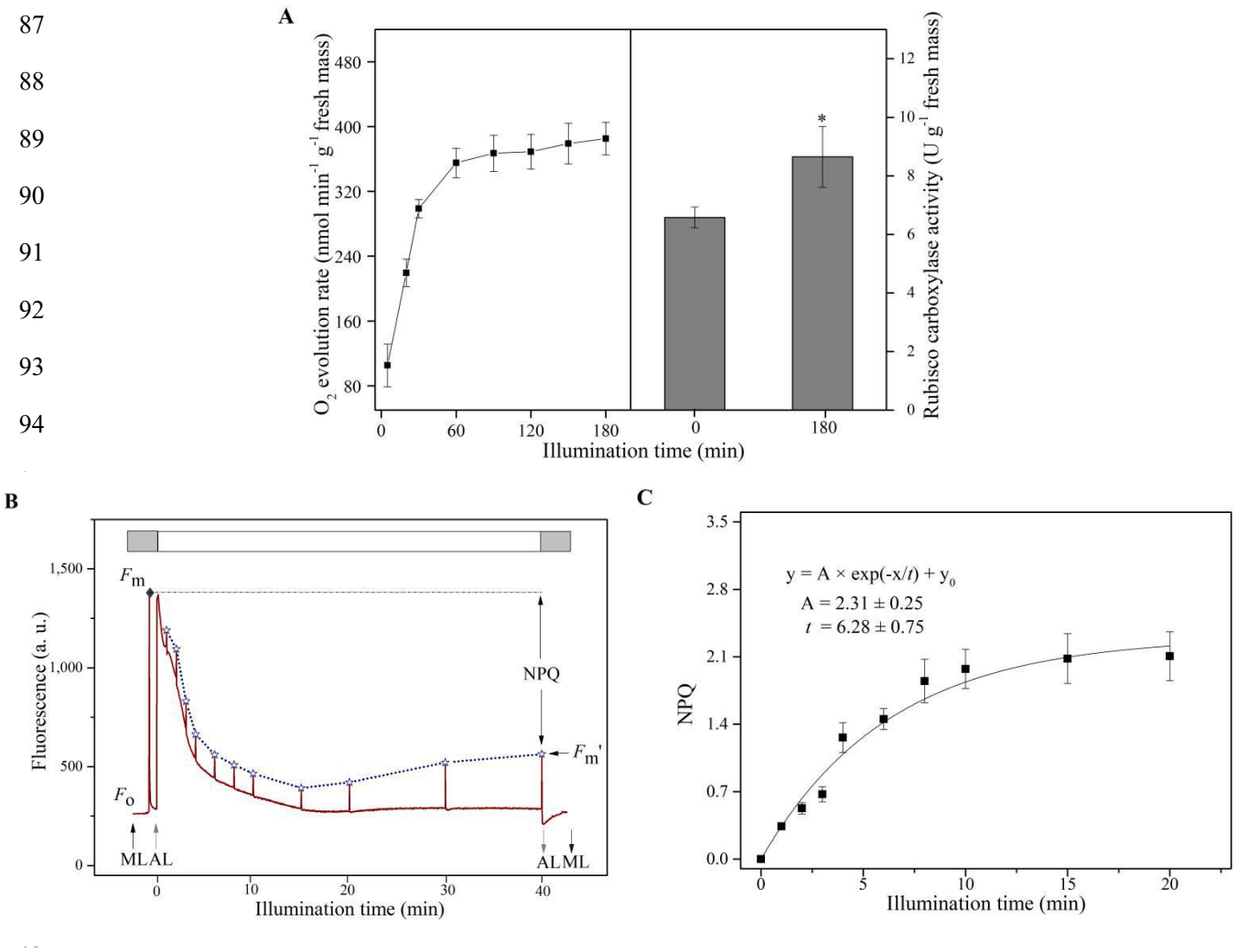

Fig. 3 Photosynthetic activity and NPQ response to light exposure. (A) Changes in O_2 evolution rate and Rubisco carboxylase activity in response to light exposure. The significantly different value (Tukey's tests, $P < 0.05$) from 0 min is marked with an asterisk (*). (B) chlorophyll fluorescence during NPQ formation. (C) The kinetics of NPQ induction fitted with the function NPQ = A × exp (-x/t) + y_0. The means ± s.d. were calculated from three independent samples.

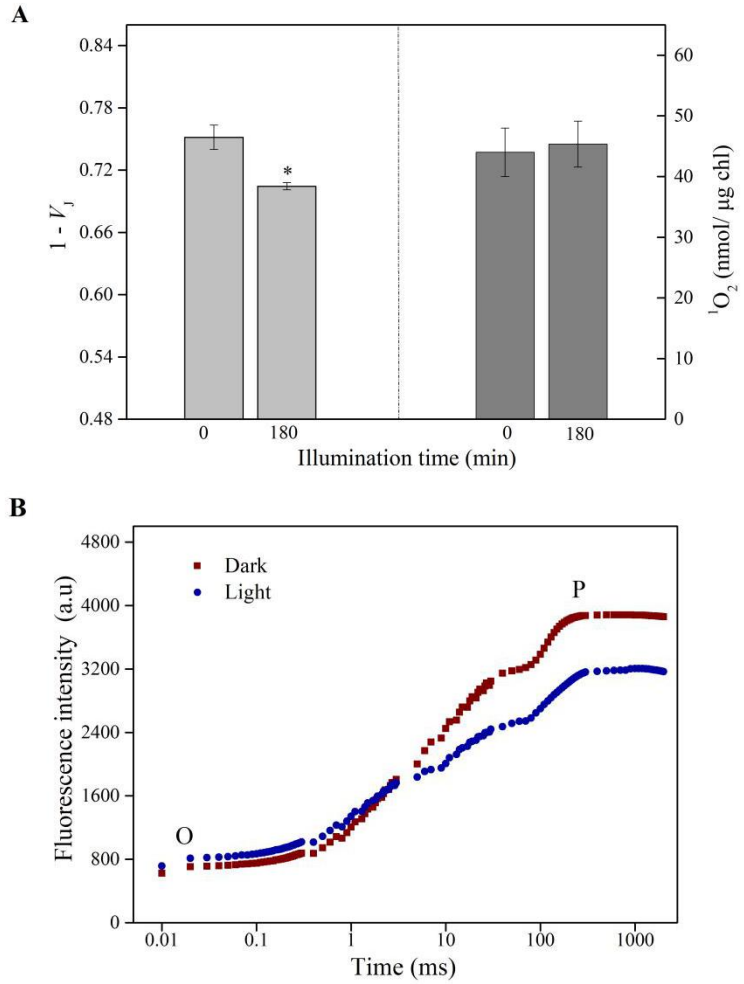

Fig. 4 The relevant parameters of PSII damage response to light exposure. (A) Variations in probabilities for an electron moving further than Q_A (1-V_J) and chloroplast $^1O_2$ contents after light exposure. The significantly different value from Dark (Tukey's tests, $P < 0.05$) is marked with an asterisk (*). (B) Changes in OJIP transients in response to light exposure and plotted on a logarithmic time scale. The means ± s.d. were calculated from three independent samples. Each curve represents the average of three replicates.

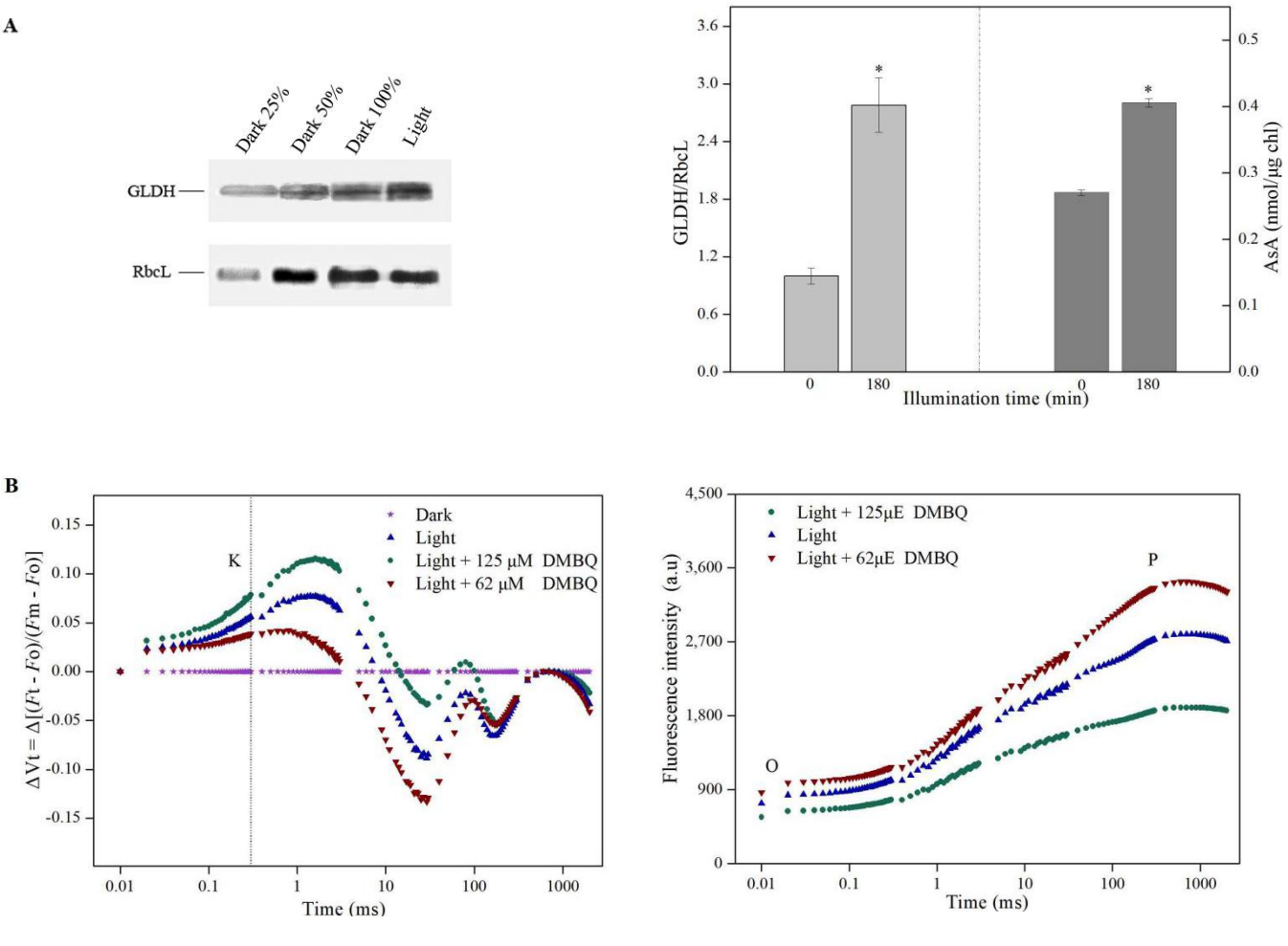

Fig. 5 AsA and PSII-CEF response to light exposure. (A) Variations in GLDH contents determined by densitometry and chloroplast AsA levels in response to light exposure. The significantly different value from 0 min (Tukey's tests, $P < 0.05$) is marked with an asterisk (*). (B) Changes in chlorophyll a fluorescence kinetics as summarized by ΔVt and OJIP curves in response to light exposure and different concentrations of DMBQ. The signals are plotted on a logarithmic time scale. Each curve represents the average of three replicates.

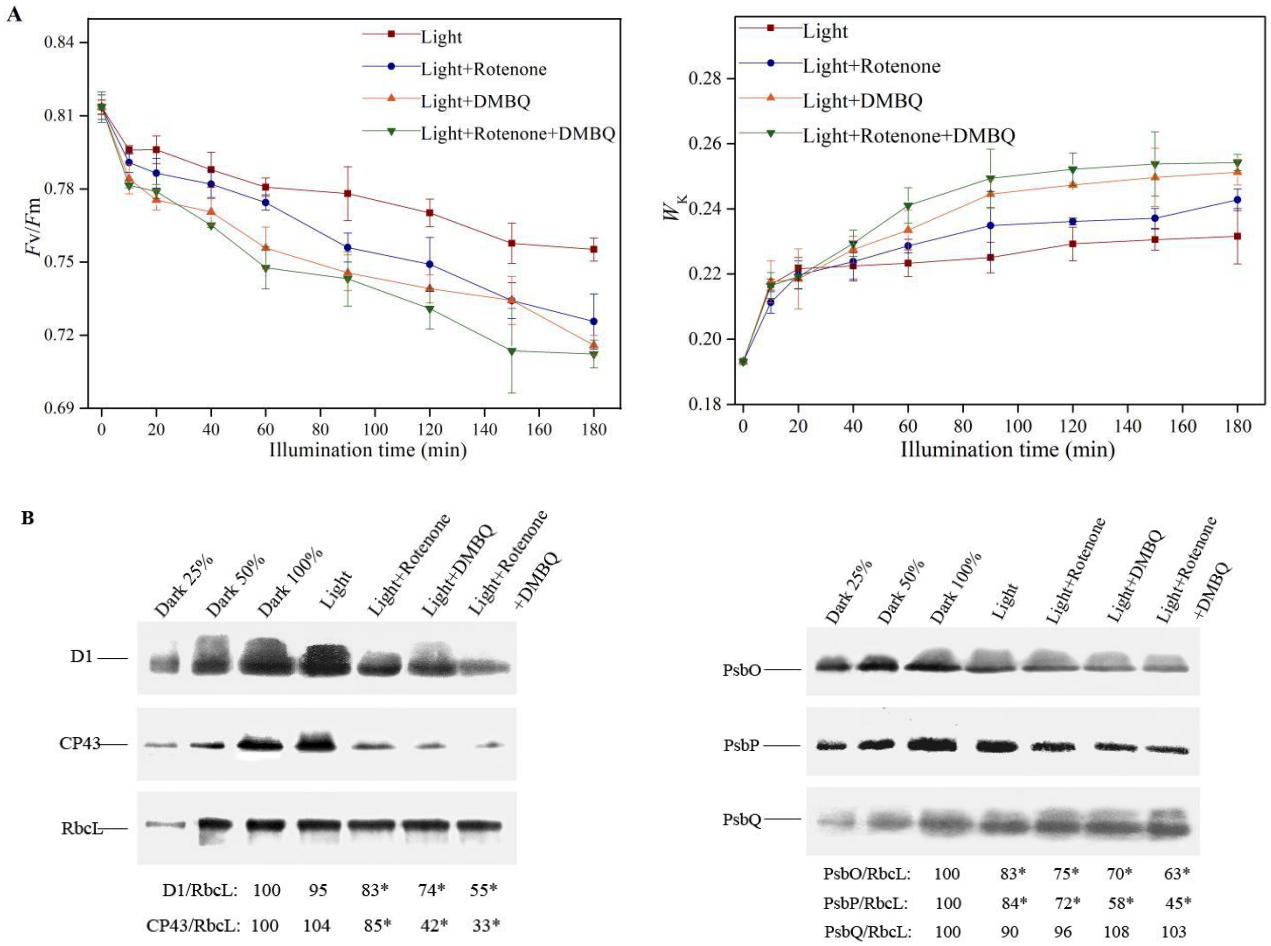

Fig. 6 Photoprotection of AsA and PSII-CEF response to light exposure. (A) Time course of the changes in maximal photochemical yield of the PSII (F_v/F_m) and the relative variable fluorescence at the K-step (Wk) in response to different inhibitors. The significant effects of rotenone and DMBQ on F_v/F_m and W_K during HL exposure were examined with repeated measures ANOVA (all p values < 0.05). (B) The changes in PSII RC proteins D1, CP43 and OEC peripheral proteins PsbO, PsbP, PsbQ after 3 h of treatment. Values were % of dark 100% and normalized to RbcL amount. The significantly different value from 0 min (Tukey's tests, $P < 0.05$) is marked with an asterisk (*). Data are expressed as mean ± s.d. ($n = 3$).

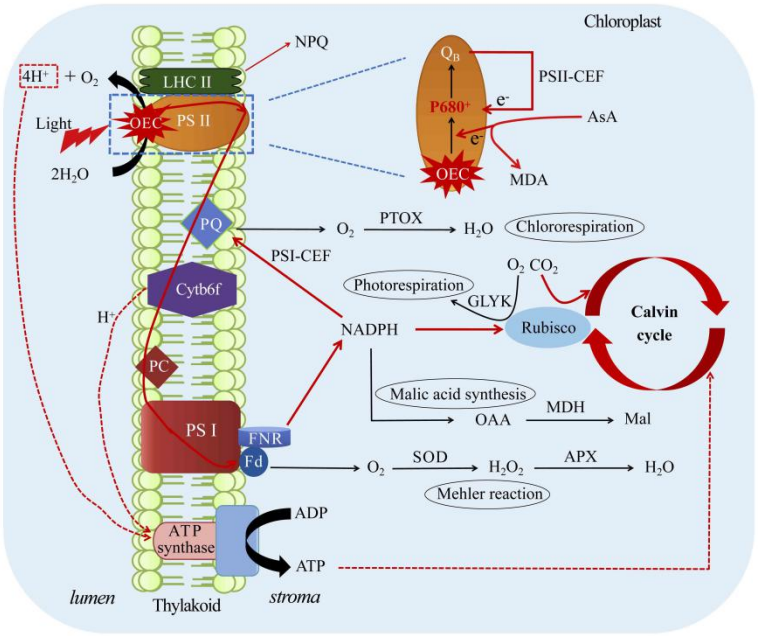

Fig. 7 Schematic model of donor-side photoinhibion derived from the photoinactivated OEC. The red arrows represent the activated pathways in which the degree of activation are represented by the width of line and the dark arrows represent the pathways that were not significantly activated. Positions of photosynthetic complexes in thylakoid membrane are based on published annotations (Gururani et al., 2015), (Eberhard and Finazzi GWollman, 2008), (Li et al., 2018). PQ, plastoquinone; Cytb6f, cytochrome b6f; PC, plastocyanin; Fd, ferredoxin; FNR, ferredoxin NADP$^+$ reductase; MDA, monodehydroascorbate; Mal, malate; PTOX, ubiquinol oxidase; GLYK, D-glycerate 3-kinase; MDH, malate dehydrogenase; OAA, oxaloacetic acid; SOD, superoxide dismutase; APX, ascorbate peroxidase.