

## **NADP<sup>+</sup> Supply Adjusts the Synthesis of Photosystem I in Arabidopsis Chloroplasts**

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**Supplemental Figure S1:** Analysis of the transient increase in chlorophyll fluorescence after termination of AL illumination.

**Supplemental Figure S2:** P700 signals normalized to chlorophyll contents in WT and *nadk2-2* plants.

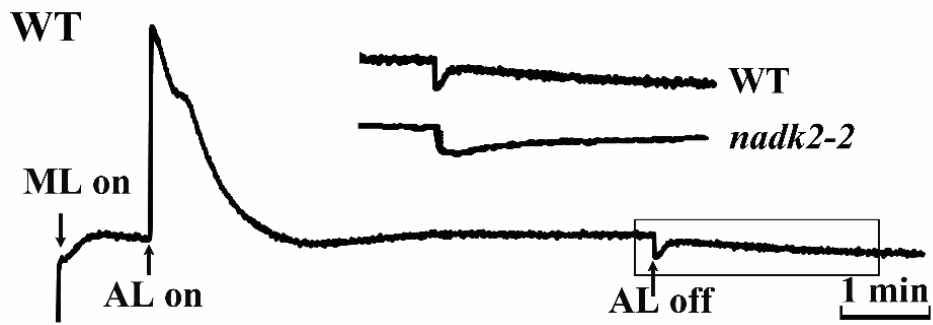
**Supplemental Figure S3:** CET rate in WT and *nadk2-2* plants.

**Supplemental Figure S4:** 2D BN/SDS-PAGE analysis of thylakoid proteins.

**Supplemental Figure S5:** Effect of the *NADK2* mutation on HCF145 activity and accumulation.

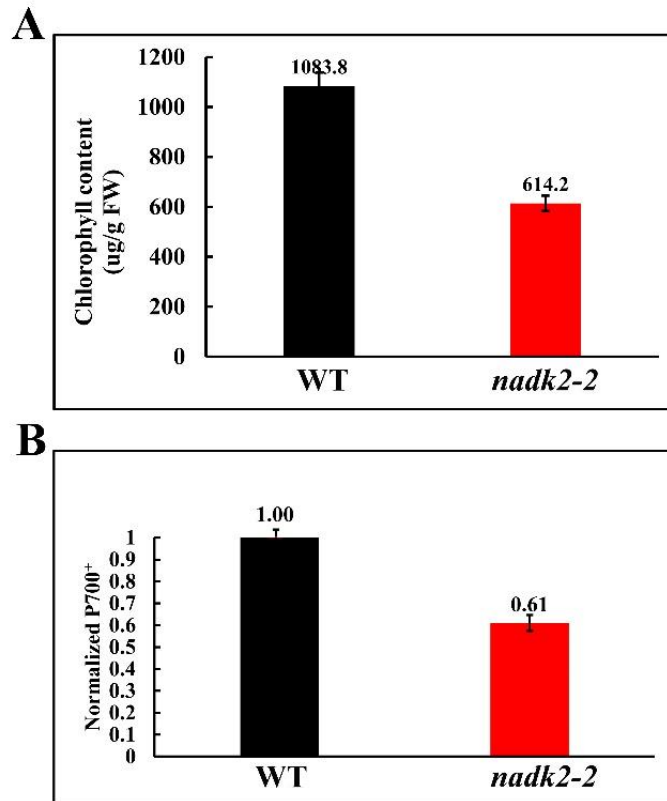
**Supplemental Table S1:** Photosynthetic parameters of WT and *nadk2-2*.

**Supplemental Table S2:** PCR primers used in this study.



**Supplemental Figure S1. Analysis of the transient increase in chlorophyll fluorescence after termination of AL illumination.**

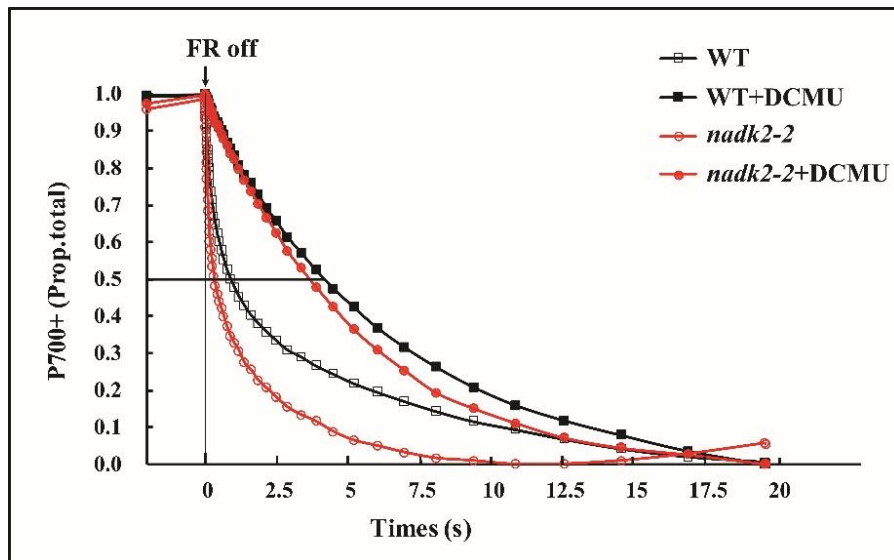
Chlorophyll fluorescence of Arabidopsis leaves was monitored using a pulse-amplitude-modulation chlorophyll fluorometer as described (Shikanai et al. 1998). For WT and *nadk2-2* a bordered area is enlarged.



**Supplemental Figure S2: P700 signals normalized to chlorophyll contents in WT and *nadk2-2* plants.**

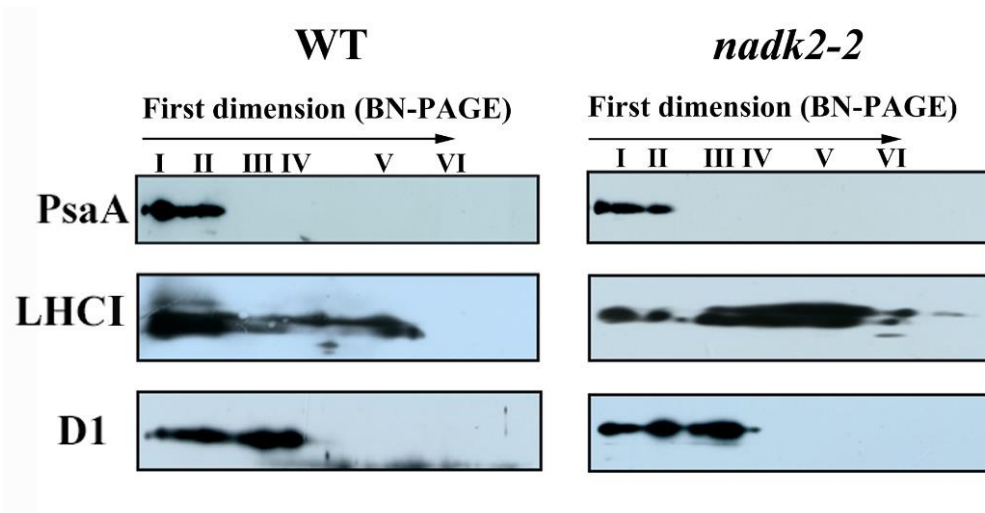
(A) Chlorophyll contents of three-week-old WT and *nadk2-2* plants. Values shown are means  $\pm$  SD of six replicate experiments.

(B) Relative P700 signals normalized to chlorophyll contents in WT and *nadk2-2* plants. The P700 signal of WT was set to 1. Values shown are means  $\pm$  SD of six replicate experiments.



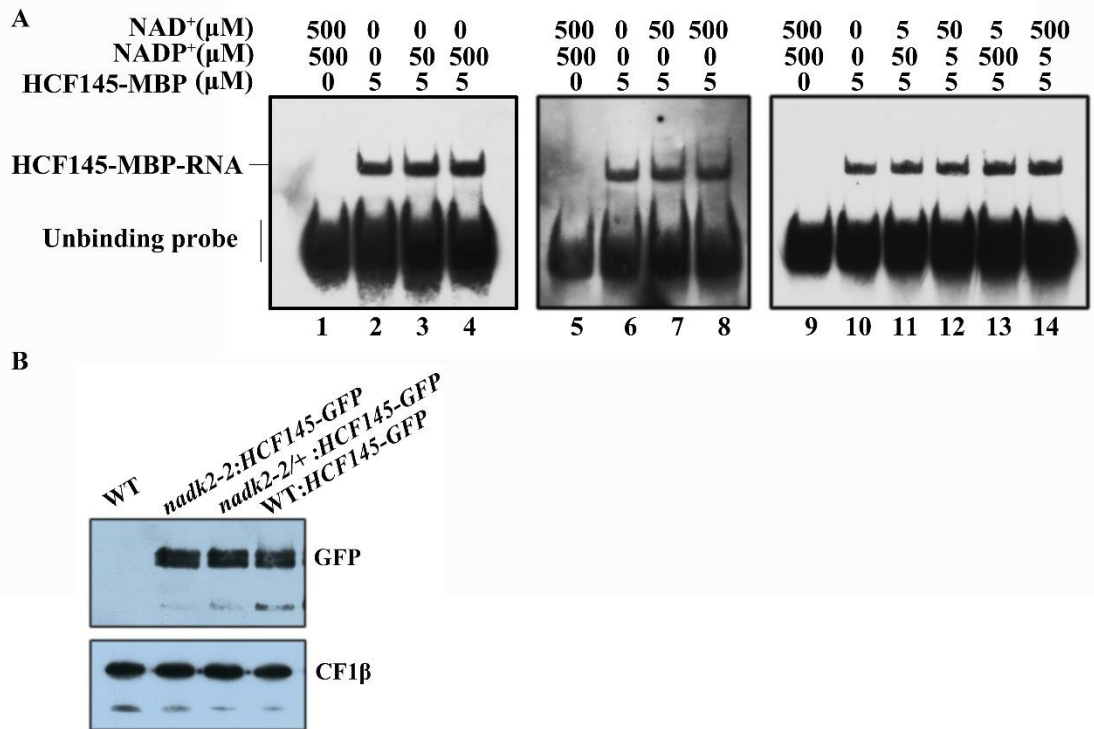
**Supplemental Figure S3: CET rate in WT and *nadk2-2* plants.**

The reduction of P700<sup>+</sup> following a 20 s flash of saturating far red (FR) light ( $\sim 8,000 \mu\text{mol m}^{-2} \text{s}^{-1}$ ) in leaves of WT and *nadk2-2* infiltrated with 20  $\mu\text{M}$  DCMU was measured. To avoid osmotic effects, leaves were infiltrated in the presence of 300 mM sorbitol. The mean value of the half-time of P700 re-reduction ( $t_{1/2}$  P700 red) with or without DCMU treatment in WT and mutant plants were shown in Supplemental Table1.



**Supplemental Figure S4: 2D BN/SDS-PAGE analysis of thylakoid proteins.**

Thylakoid complexes were separated by BN-PAGE as shown in **Figure 4** and further subjected to SDS-PAGE. Gels were probed with antibodies against PsaA, LHCI, and D1.



**Supplemental Figure S5: Effect of the *NADK2* mutation on HCF145 activity and accumulation.**

**(A)** EMSA assay of RNA-binding of HCF145 in the presence of NAD<sup>+</sup> and NADP<sup>+</sup>. The *psaA* 5' UTR probe used was described previously (Manavski et al., 2015). The binding reaction contained the indicated concentrations of recombinant HCF145-MBP, NAD<sup>+</sup>, and NADP<sup>+</sup>.

**(B)** Accumulation of HCF145 proteins in homozygous *nadk2-2*, heterozygous *nadk2-2*, and WT plants. The full-length HCF145 protein C-terminally fused to GFP was introduced into a heterozygous *nadk2-2* line by the floral dip method. Homozygous and heterozygous *nadk2-2* lines and WT plants were selected by genotyping the resulting T2 population of the same T1 plant and the abundance of the HCF145-GFP protein was assayed via immunoblotting with the GFP antibody. WT plants were used as a negative control. A replicate gel probed with CF1β is shown below as loading control.

**Supplemental Table S1. Photosynthetic parameters of WT and *nadk2-2*.**

<b>Parameter</b>	<b>Wild Type (n≥5<sup>a</sup>)</b>	<b><i>nadk2-2</i> (n≥5)</b>
<b>t<sub>1/2</sub> P700 red (ms)<sup>b</sup></b>	882 ± 42	307 ± 29
<b>t<sub>1/2</sub> P700 red+DCMU(ms)<sup>c</sup></b>	4186 ±147	3612 ±118
<b>NPQ</b>	1.86± 0.04	3.24± 0.07
<b>qE</b>	1.54± 0.04	2.85± 0.07
<b>qI</b>	0.32± 0.04	0.39± 0.07

<sup>a</sup>Number of replicates

<sup>b</sup>Half-time of nonphotochemical P700 re-reduction in the dark (s) without DCMU treatment

<sup>c</sup>Half-time of nonphotochemical P700 re-reduction in the dark (s) with DCMU treatment

**Supplemental Table S2. PCR primers used in this study.**

Names	Primer sequence 5'→3'	Experiment
nadk2-1-LP	TATTGGGAACAGTGCCAACTC	T-DNA insertion
nadk2-1-RP	GAGAAATCCAAGAGACCCAG	
SALKLBb1.3	ATTTTGCCGATTTTCGGAAC	
S1	CGCCGGATGATGAGAGAAGT	Sequencing and RT-PCR
S2	TCTTTCGTGATCGGTCGTGT	
nadk coms	GCGCGGTACCATGTTCTATGCTTTTGCCCTTGCC'	Complementation
nadk coma	GCGCGAGCTCTCATTGTGCATCGTCATCCTTGTAGTCTTTGTGCATCGTC ATCCTTGTAGTCTTTGTGCATCGTCATCCTTGTAGTCTCAGAGAGCCTTTT GATCAAGACGCTCG3'	
Fw-BamHI-HCF145	GCGATATCGTCGACGGATCCAGCGGCGCCGGTGGTA	Recombinant HCF145-MBP
Rev-BamHI-HCF145	CCTGCAGGGAATTCGGATCCATATTGAACCCAATTG	
HCF145-1301-F :	acgggggactctagaATGTCAGTGAGCAAGTTTCCAC	Complementation HCF145-FLAG
HCF145-1301-R :	gtcatccttgtaatcATATTGAACCCAATTGATATCAAG	
<b>Primers used to probe for northern blot and polysome analysis (forward / reverse)</b>		
<i>psbA</i>	ACAACATTGTAGCTGCTCAC / CTAACACTAACGAATTATCC	
<i>psbD</i>	ATGACTATAGCCCTTGGTAA / AGAGCGTTTCCACGTGGTAG	
<i>rps14</i>	ATGGCAAAGAAAAGTTTGAT / TTACCAGCTTGATCTTGTTG	
<i>psaA</i>	CAATTGGCGCATTGGTCTTCGCAG/ GTGCTCGCTGTTTCACCAGGGGCTG	/
<i>ycf3</i>	CGTGGAGAACAGGCCATTCA / TTATTCTGAAGCGCCTCGTGA	
<i>psaC</i>	CGATCCTATGTCACATTAG / TCAATAAGCTAGACCCATAC	
<i>23S rRNA</i>	TTCAAACGAGGAAAGGCTTA / AGGAGAGCACTCATCTTGGG	
<i>psaA</i>	CAUAAUUGCUCUAGUGAAUAACUAAAGAAAAUAGAUGA/ AUAGAUGGAAGAUAGAAGAGA	