

Supplementary Materials for

**Expression of *OsTPX* Gene Improves Cellular Redox Homeostasis and Photosynthesis Efficiency  
in *Synechococcus elongatus* PCC 7942**

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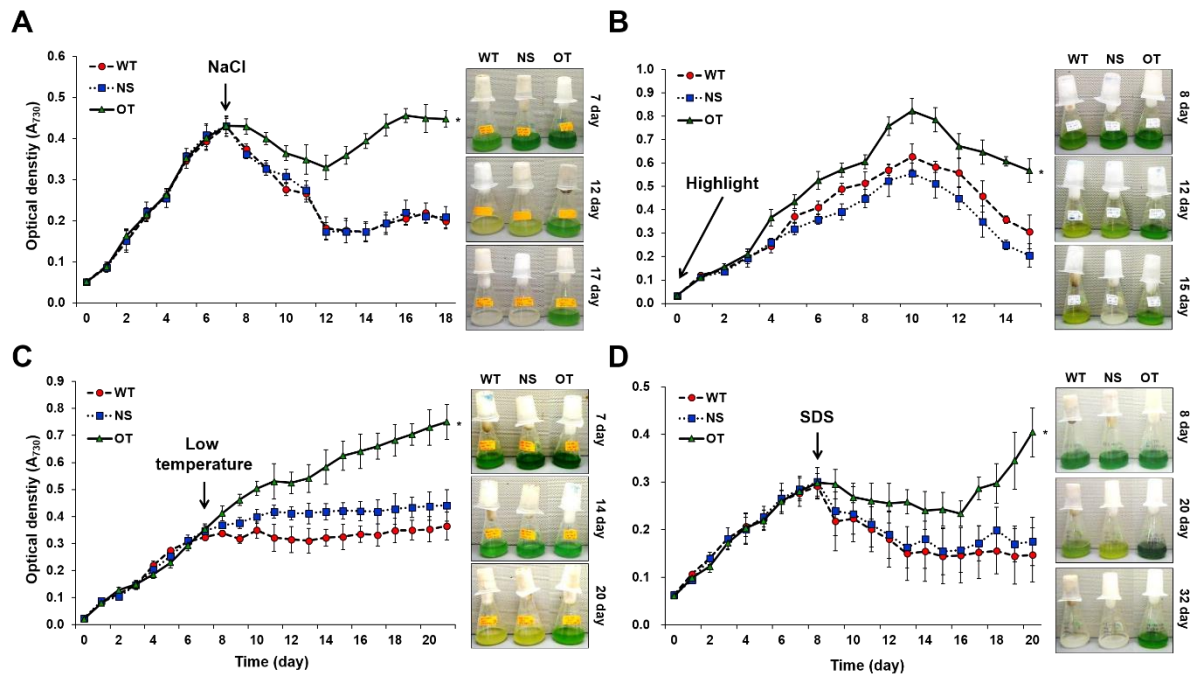
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**Supplementary Figure S1**

**Supplementary Tables S1 to S4**



**Supplementary Figure S1.** Growth curve measurement of WT, NS, and OT strains under various abiotic stresses. The OT strain grows better than other strains under various stress conditions. **(A–D)** Strains were grown in only BG11 medium, and the initial optical density at 730 nm was adjusted to 3.0. Next, each sample was exposed to the following stress treatments: **(A)** 200 mM NaCl after 7 days, **(B)** 250  $\mu$ E high light intensity during the first day, **(C)** 10  $^{\circ}$ C low temperature after 7 days, and **(D)** 20% SDS after 8 days. After culturing at 30  $^{\circ}$ C with shaking, aliquots of each sample were collected daily and absorbance was measured at 730 nm. Error bars indicate  $\pm$  SD of three independent experiments. Asterisks indicate significant differences between treatments as estimated by Student's *t*-test ( $P < 0.05$ ).

**Supplementary Table S1.** Cyanobacterial strains and plasmids used in this study

Strain or Plasmid	Characteristic(s)	Antibiotic resistance	Source or reference
<b>Strains</b>			
AMC06	Wild type <i>Synechococcus elongatus</i> PCC 7942	none	Lab collection
DH5 $\alpha$	<i>Escherichia coli</i> cloning host	none	Lab collection
<b>Plasmids</b>			
Relevant characteristics*			
<i>pGA2897::OsTPX</i>	The <i>pGA2897</i> binary vector plasmids that contained the maize ubiquitin promoter ( <i>Ubi</i> ) and <i>OsTPX</i> into the <i>A. tumefaciens</i> strain <i>LBA4404</i> via electroporation; Hpt <sup>r</sup>	Hpt	This work
<i>pCV0069</i>	<i>S. elongatus</i> carrying <i>pCV0069</i> as a single recombinant; Nat <sup>r</sup>	Nat	Lab collection
<i>pCV0069::OsTPX</i>	S7942NS2-Nat1-Ptrc/Swal-TPX-RBS_OsTPX, 5815 bp, Nat <sup>r</sup> , for IPTG-inducible <i>OsTPX</i> gene expression	Nat	This work

\* Abbreviations for antibiotics: nourseothricin (Nat) and hygromycin B phosphotransferase (Hpt).

**Supplementary Table S2.** Primer sequences for PCR amplification

	<b>Name</b>	<b>Sequence</b>
<i>O. sativa</i>	OsTPX-F	CACCAATCCCCTCCTCATCCACT
	OsTPX-R	AAAAACTCCCTACATCCATCACC
	Tubulin-F	GAGTACCCTGACCGCATGAT
	Tubulin-R	GTGGTCAGCTTGAGAGTCCT
	OsTPX-RT-F	GCCGCTCCCACCGCAGCAGC
	OsTPX-RT-R	GGGCTTGTCGGAGAGGTCCATC
<i>S. elongatus</i>	rpoA-F	GCCGCCTGCTGCTCCTCCCT
	rpoA-R	AGCAAGTCAGCAACGGAGTTC
	NS2-F	GTC AACGTAAATGCATGCCGC
	NS2-R	GGTCACTACTTGGTAGCAACTC
	OsTPX-RT-PCR-F	ATGGCCGCCTGCTGCTCCTCCCT
	OsTPX-RT-PCR-R	CTGTCGAAGTGCAACTACTTGAGGACCAGC
	OsTPX-F-Swal	TGCGGATCCTAAGGAGGAAAATTTATGGCCGCCTGCTGCTCCTCCCTCGCCACCGCCG
	OsTPX-R-Swal	GCCGGGGAGCTCCTTCATTTATTTTATAGATGGCCGCGAAGTACTCCTTGCTTCCCTGGG

**Supplementary Table S3. Upregulated genes expression levels under H<sub>2</sub>O<sub>2</sub> stress screened using RNA seq**

Gene symbol	Fold change	Protein ID	Product
<b>Redox balance</b>			
SYNPCC7942_RS13385	<b>5.193</b>	WP_040113194.1	ferredoxin
SYNPCC7942_RS05790	<b>2.605</b>	WP_011377875.1	ferredoxin-thioredoxin reductase
SYNPCC7942_RS08440	<b>2.457</b>	WP_011244741.1	catalase peroxidase
SYNPCC7942_RS07035	<b>2.051</b>	WP_011378008.1	flavodoxin2
SYNPCC7942_RS02235	<b>1.825</b>	WP_011377579.1	glutathione peroxidase
SYNPCC7942_RS13770	<b>1.745</b>	WP_011242314.1	flavodoxin
<b>Photosynthesis</b>			
SYNPCC7942_RS10560	<b>2.359</b>	WP_011378308.1	chlorophyll synthase ChlG
SYNPCC7942_RS02240	<b>1.866</b>	WP_011243390.1	magnesium protoporphyrin IX methyltransferase
SYNPCC7942_RS05735	<b>1.741</b>	WP_071818114.1	high light inducible protein
SYNPCC7942_RS09665	<b>1.508</b>	WP_011244498.1	magnesium-protoporphyrin IX monomethyl ester cyclase
<b>Ion homeostasis</b>			
SYNPCC7942_RS08465	<b>2.338</b>	WP_011244737.1	potassium channel protein
SYNPCC7942_RS05795	<b>2.209</b>	WP_011242728.1	ABC transporter ATP-binding protein
SYNPCC7942_RS07205	<b>2.155</b>	WP_011242460.1	Fe <sup>3+</sup> ABC transporter substrate-binding protein
SYNPCC7942_RS05775	<b>2.115</b>	WP_011377873.1	haemolysin-type calcium-binding repeat
SYNPCC7942_RS05545	<b>2.102</b>	WP_011242780.1	K <sup>+</sup> transporter
<b>Molecular chaperone</b>			
SYNPCC7942_RS11715	<b>2.083</b>	WP_011378399.1	molecular chaperone DnaJ
SYNPCC7942_RS12135	<b>1.811</b>	WP_071818122.1	molecular chaperone DnaJ
SYNPCC7942_RS09200	<b>1.686</b>	WP_011244591.1	molecular chaperone HtpG

**Supplementary Table S4. Upregulated genes expression levels under normal and H<sub>2</sub>O<sub>2</sub> stress screened using RNA seq (raw data\_log normalization)**

Protein ID	Product	NORMAL		STRESS	
		WT	OT	WT	OT
WP_011244671.1	thioredoxin family protein	11.673	11.291	11.613	11.276
WP_011244428.1	thioredoxin reductase	13.837	13.388	13.683	13.390
<b>Redox balance</b>					
WP_040113194.1	ferredoxin	6.805	6.712	7.040	9.088
WP_011377875.1	ferredoxin-thioredoxin reductase	10.439	10.241	9.977	11.622
WP_011244741.1	catalase peroxidase	10.599	10.836	9.587	12.133
WP_011378008.1	flavodoxin2	11.828	12.292	11.657	13.329
WP_011377579.1	glutathione peroxidase	8.921	8.426	8.562	9.294
WP_011242314.1	flavodoxin	9.770	10.659	10.967	11.462
<b>Photosynthesis</b>					
WP_011378308.1	chlorophyll synthase ChlG	12.196	12.395	11.568	13.634
WP_011243390.1	magnesium protoporphyrin IX methyltransferase	10.042	10.457	10.071	11.357
WP_071818114.1	high light inducible protein	11.013	11.126	10.907	11.926
WP_011244498.1	magnesium-protoporphyrin IX monomethyl ester cyclase	11.386	11.382	11.203	11.975
<b>Ion homeostasis</b>					
WP_011244737.1	potassium channel protein	11.004	11.177	10.546	12.402
WP_011242728.1	ABC transporter ATP-binding protein	11.432	11.746	11.898	12.889
WP_011242460.1	Fe <sup>3+</sup> ABC transporter substrate-binding protein	10.619	10.737	10.247	11.845
WP_011377873.1	haemolysin-type calcium-binding repeat	11.326	11.097	10.732	12.177
WP_011242780.1	K <sup>+</sup> transporter	12.286	12.425	11.667	13.497
<b>Molecular chaperone</b>					
WP_011378399.1	molecular chaperone DnaJ	10.952	11.021	10.633	12.080
WP_071818122.1	molecular chaperone DnaJ	12.849	12.303	12.558	13.160
WP_011244591.1	molecular chaperone HtpG	13.259	13.155	13.215	13.909