

Table 1 Suppl. Changes in phosphoenolpyruvate carboxylase (PEPC) activity, relative water content, soluble sugar content, ATP content, anthocyanin content, glucose content, and fructose content of *C₄*-phosphoenolpyruvate carboxylase gene transgenic rice type (PC) and wild type (WT) leaves under PEG 6000 simulated drought treatment after spraying with 1 % (m/v) exogenous sucrose and 1 % (m/v) sucrose non-metabolic analog turanose. CK - control with distilled water; PEG - 4h-PEG 6000 treatment alone; PEG+Suc - pre-spraying with 1 % (m/v) exogenous sucrose (Suc) and then PEG 6000 treatment for 2h; PEG+Tur - pre-spraying with 1 % (m/v) exogenous turanose (Tur, a Suc non-metabolic analog) and then PEG 6000 treatment for 2h. Data are means $\pm$ SEs from measurements of at least three independent experiments with different letters indicating significant differences at $P < 0.05$.

Parameters	Rice lines	CK	PEG	PEG+Suc	PEG+Tur
PEPC activity [$\mu\text{mol mg}^{-1}(\text{protein}) \text{min}^{-1}$]	WT	0.34 $\pm$ 0.011b	0.34 $\pm$ 0.010b	0.44 $\pm$ 0.009a	0.43 $\pm$ 0.008a
	PC	2.55 $\pm$ 0.101c	3.29 $\pm$ 0.112b	3.77 $\pm$ 0.103a	3.76 $\pm$ 0.104a
Relative water content [%]	WT	96.10 $\pm$ 3.71a	57.60 $\pm$ 2.30c	64.60 $\pm$ 2.21b	63.40 $\pm$ 2.10b
	PC	95.40 $\pm$ 3.51a	70.20 $\pm$ 2.21c	74.90 $\pm$ 2.11b	70.20 $\pm$ 2.04c
Soluble sugar content [$\text{mg g}^{-1}(\text{protein})$]	WT	203.20 $\pm$ 8.7c	267.40 $\pm$ 4.9a	225.20 $\pm$ 5.9b	228.10 $\pm$ 4.9b
	PC	263.20 $\pm$ 6.4c	316.20 $\pm$ 6.9a	280.10 $\pm$ 6.1b	274.20 $\pm$ 6.1b
Sucrose content [$\text{mg g}^{-1}(\text{protein})$]	WT	81.60 $\pm$ 3.1b	119.20 $\pm$ 4.1a	129.20 $\pm$ 5.2a	121.20 $\pm$ 4.9a
	PC	135.20 $\pm$ 5.8d	192.50 $\pm$ 7.9b	224.20 $\pm$ 8.7a	176.90 $\pm$ 6.2c
Glucose content [$\text{mg g}^{-1}(\text{protein})$]	WT	25.10 $\pm$ 0.9c	37.90 $\pm$ 1.1b	39.90 $\pm$ 1.2a	36.42 $\pm$ 1.0b
	PC	57.20 $\pm$ 1.2a	45.40 $\pm$ 1.3c	48.60 $\pm$ 1.1b	45.10 $\pm$ 1.2c
Fructose content [$\text{mg g}^{-1}(\text{protein})$]	WT	6.80 $\pm$ 0.2b	9.30 $\pm$ 0.3a	9.70 $\pm$ 0.4a	9.70 $\pm$ 0.3a
	PC	13.80 $\pm$ 0.4b	11.60 $\pm$ 0.3a	12.70 $\pm$ 0.4a	12.20 $\pm$ 0.2a
Anthocyanin content [$\mu\text{g g}^{-1}(\text{protein})$]	WT	2.02 $\pm$ 0.07d	3.73 $\pm$ 0.05c	4.18 $\pm$ 0.06a	3.93 $\pm$ 0.04b
	PC	2.02 $\pm$ 0.05d	5.42 $\pm$ 0.04c	6.65 $\pm$ 0.06a	5.73 $\pm$ 0.03b
ATP content [$\mu\text{mol g}^{-1}(\text{protein})$]	WT	5.76 $\pm$ 0.19a	4.82 $\pm$ 0.18b	4.93 $\pm$ 0.17b	4.88 $\pm$ 0.16b
	PC	6.35 $\pm$ 0.17a	5.27 $\pm$ 0.16b	5.22 $\pm$ 0.13b	5.23 $\pm$ 0.12b

Table 2 Suppl. Transcripts of *sucrose nonfermenting-1-related protein kinases (SnRKs)* *SnRK3.1*, *SnRK3.4*, and *SnRK3.21*, *calcineurin B-likes (CBLs)* *CBL1*, *CBL3*, and *CBL10* in leaves of *C₄*-phosphoenolpyruvate carboxylase gene transgenic rice type (PC) and wild type (WT) plants with Ca^{2+} , Ca^{2+} chelator (EGTA) and Ca^{2+} release antagonist ruthenium red (RR) pretreatment under PEG 6000 simulated drought treatment. CK - control with distilled water; PEG - 4h-PEG 6000 treatment alone; EGTA+PEG - 10 mM EGTA treatment combined with PEG treatment; RR+PEG - 80 μM RR treatment combined with PEG treatment. Data are means $\pm$ SEs from measurements of at least three independent experiments with different letters indicating significant differences at $P < 0.05$.

Genes	Rice lines	CK	PEG	EGTA+PEG	RR+PEG
<i>SnRK3.1</i>	WT	1.01 $\pm$ 0.02c	1.75 $\pm$ 0.03a	1.24 $\pm$ 0.02b	1.22 $\pm$ 0.04b
	PC	1.02 $\pm$ 0.03c	2.51 $\pm$ 0.04a	1.12 $\pm$ 0.03b	1.12 $\pm$ 0.02b
<i>SnRK3.4</i>	WT	1.02 $\pm$ 0.02c	1.15 $\pm$ 0.04b	1.41 $\pm$ 0.03a	1.15 $\pm$ 0.02b
	PC	1.03 $\pm$ 0.03d	2.44 $\pm$ 0.05a	1.48 $\pm$ 0.02b	1.17 $\pm$ 0.03c
<i>SnRK3.21</i>	WT	1.02 $\pm$ 0.03a	1.02 $\pm$ 0.04a	0.85 $\pm$ 0.02b	1.03 $\pm$ 0.04a
	PC	1.04 $\pm$ 0.02c	1.67 $\pm$ 0.04a	1.17 $\pm$ 0.03b	0.68 $\pm$ 0.01d
<i>CBL1</i>	WT	1.02 $\pm$ 0.03c	1.12 $\pm$ 0.04b	1.22 $\pm$ 0.03a	1.04 $\pm$ 0.04c
	PC	1.03 $\pm$ 0.02c	2.21 $\pm$ 0.03a	1.45 $\pm$ 0.04b	1.02 $\pm$ 0.02c
<i>CBL3</i>	WT	1.02 $\pm$ 0.03c	1.21 $\pm$ 0.04a	0.91 $\pm$ 0.02d	1.14 $\pm$ 0.03b
	PC	1.04 $\pm$ 0.02d	1.74 $\pm$ 0.02a	1.15 $\pm$ 0.03c	1.21 $\pm$ 0.03b
<i>CBL10</i>	WT	1.02 $\pm$ 0.03c	1.34 $\pm$ 0.04a	1.12 $\pm$ 0.02b	1.32 $\pm$ 0.04a
	PC	1.05 $\pm$ 0.04d	2.11 $\pm$ 0.03a	1.23 $\pm$ 0.05c	1.54 $\pm$ 0.04b

Table 3 Suppl. Transcripts of basic helix-loop-helix (bHLH) proteins *OsB1* and *OsB2*, *R2R3-myeloblastosis transcription factor OsC1*, *purple acid phosphatase 2 OsPAP2*, *chalcone synthase OsCHS*, *dihydroflavonone reductase OsDFR*, and *anthocyanin synthase OsANS* in leaves of C₄-phosphoenolpyruvate carboxylase gene transgenic rice type (PC) and wild type (WT) plants with Ca²⁺, Ca²⁺ chelator (EGTA), and Ca²⁺ release antagonist ruthenium red (RR) pretreatment under PEG 6000 simulated drought treatment. CK - control with distilled water; PEG - 4h-PEG 6000 treatment alone; EGTA+PEG - 10 mM EGTA treatment combined with PEG treatment; RR+PEG - 80 μ M RR treatment combined with PEG treatment. Data are means $\pm$ SEs from measurements of at least three independent experiments with different letters indicating significant differences at $P < 0.05$.

Genes	Rice lines	CK	PEG	EGTA+PEG	RR+PEG
<i>OsB1</i>	WT	1.01 $\pm$ 0.02c	2.63 $\pm$ 0.03a	1.90 $\pm$ 0.02b	1.88 $\pm$ 0.04b
	PC	1.02 $\pm$ 0.03c	9.33 $\pm$ 0.04a	3.35 $\pm$ 0.03b	2.68 $\pm$ 0.02b
<i>OsB2</i>	WT	1.02 $\pm$ 0.02c	2.15 $\pm$ 0.04b	1.31 $\pm$ 0.03a	1.15 $\pm$ 0.02b
	PC	1.03 $\pm$ 0.03d	3.07 $\pm$ 0.05a	1.48 $\pm$ 0.02b	1.29 $\pm$ 0.03c
<i>OsC1</i>	WT	1.02 $\pm$ 0.03a	7.02 $\pm$ 0.04a	1.15 $\pm$ 0.02b	1.03 $\pm$ 0.04a
	PC	1.04 $\pm$ 0.02c	16.27 $\pm$ 0.04a	1.27 $\pm$ 0.03b	1.38 $\pm$ 0.01d
<i>OsPAP2</i>	WT	1.02 $\pm$ 0.03c	1.12 $\pm$ 0.04b	2.55 $\pm$ 0.03a	1.54 $\pm$ 0.04c
	PC	1.03 $\pm$ 0.02c	10.03 $\pm$ 0.03a	3.45 $\pm$ 0.04b	2.63 $\pm$ 0.02c
<i>OsCHS</i>	WT	1.02 $\pm$ 0.03c	1.31 $\pm$ 0.04a	1.21 $\pm$ 0.02d	1.14 $\pm$ 0.03b
	PC	1.04 $\pm$ 0.02d	5.74 $\pm$ 0.02a	1.65 $\pm$ 0.03c	1.25 $\pm$ 0.03b
<i>OsDFR</i>	WT	1.02 $\pm$ 0.03c	1.65 $\pm$ 0.04a	1.03 $\pm$ 0.02b	1.12 $\pm$ 0.04a
	PC	1.02 $\pm$ 0.03c	2.03 $\pm$ 0.04a	1.23 $\pm$ 0.02b	1.33 $\pm$ 0.04a
<i>OsANS</i>	WT	1.02 $\pm$ 0.03c	4.23 $\pm$ 0.04a	1.52 $\pm$ 0.02b	1.32 $\pm$ 0.04a
	PC	1.05 $\pm$ 0.04d	6.79 $\pm$ 0.03a	1.48 $\pm$ 0.05c	1.36 $\pm$ 0.04b

Table 4 Suppl. Gene primers for quantitative reverse transcription PCR.

Gene	Primers
<i>ACTIN</i>	5'- CCCTCTTTCATCGGTATGGA -3' (forward) 5'- TTGATCTTCATGCTGCTTGG -3' (reverse)
<i>OsCOP1</i>	5'-ATAATCCTGGGTCGAGCCAC-3' (forward) 5'-TATGGTGATCAGCAGAACCCAC-3' (reverse)
<i>OsHY5</i>	5'-GGCGGGTGCCGGAGATGG-3' (forward) 5'-CGCCGTCGTGTTCTTCTTGAGTATCTGG-3' (reverse)
<i>OsB1</i>	5'-GGATGGTCTCCTTGGA CTGA -3' (forward) 5'-GGGTGGCAGATTCATCACTT-3' (reserve)
<i>OsB2</i>	5'-GTGGCAATAACGACGACGACTCC -3' (forward) 5'-CGTACGGTGTTGACGAGGTA -3' (reserve)
<i>OsC1</i>	5'-CGGGTTCTTCTTCCACGAC -3' (forward) 5'-CCCGCAACTGCACTTAAAAAT -3'(reserve)
<i>OsPAL</i>	5'-CAAGCTCATGACCTCCACCTA-3' (forward) 5'-GTTTCATGGTGAGCACCTTCTT-3' (reverse)
<i>OsCHI</i>	5'-CGAGCAGTACTCGGACAAGG-3' (forward) 5'-TGAAGGCCCTCCTTGAAC TTG-3' (reverse)
<i>OsF3H</i>	5'-GAGCAATGGGAGGTTCAAGA-3' (forward) 5'-CTTCGATTTTCGACGGAAGA-3' (reverse)
<i>OsF3'H</i>	5'-CCGCTACAGTACCAGCCTTC-3' (forward) 5'-TGCCACCATTTCTAGAGTTCC-3' (reverse)
<i>OsCHS</i>	5'-TCATGTATGGGTGGTTTGGTT-3' (forward) 5'-GCCAGGCATCTCTTACACAGG-3'(reverse)
<i>OsDFR</i>	5'-CGGATGGATGTACTTCGTGTC -3' (forward) 5'-CATCCCCGTTGCTGATGAAG -3' (reverse)
<i>OsANS</i>	5'-CTCCTCCAGCTCAAGATCAAC -3' (forward) 5'-GTTGTGGAGGATGAAGGAGAG -3' (reverse)
<i>OsPAP2</i>	5'-CCCGGGATGGCCGGGATCGTGGTGGTG-3' (forward) 5'-CCCGGGTCAGTTCTTGATCCGGAGCGT-3' (reverse)
<i>OsSAPK8</i>	5'-ATAGATGATAATGTCCAGCGTGAG-3' (forward) 5'-TTGCCATCGTATTCTTTCT-3' (reserve)
<i>OsSAPK9</i>	5'-CACAGCAACGCCGTCTCC-3' (forward) 5'-CACACTTCCACCGCTACCAA-3' (reserve)
<i>OsSAPK10</i>	5'-TGCTGATGTGTGGTCCGTGTG-3' (forward) 5'-TGCTGGTATGGTCGCCCTCT-3' (reserve)
<i>OsSnRK3.4</i>	5'-ACATGTGGCAGCCCTAACTACA-3' (forward) 5'-TATGTCCGACAAAGAGCCATCA-3' (reserve)
<i>OsSnRK3.16</i>	5'-CATGAAAAATGGCAGGGGTT-3' (forward) 5'-CAGACGGGCAAGAAGAGAGC-3' (reserve)
<i>OsSnRK3.21</i>	5'-GCTTGGCCCTTCTGTAAATG-3' (forward) 5'-CGGTGGCTAGTTTTTGAACC-3' (reserve)
<i>OsCBL1</i>	5'-GCCTTTAGCGTAAGTGAG-3' (forward) 5'-CTGGGAAATGTGGTTGT-3' (reserve)
<i>OsCBL3</i>	5'-GTAGGTGAGTAAGAGAGTAG-3' (forward) 5'-GCAAAGCCTCAAAAGCAACG-3' (reserve)
<i>OsCBL10</i>	5'-ACGAGTCCCGCTGCTT-3' (forward) 5'-CGCCGCTGTAGTGTCTT-3' (reserve)
<i>OsSUT1</i>	5'-AGTCCGGTCCGTCAGCAT-3' (forward) 5'-ACCGAGGTGGCAACAAAG-3' (forward)
<i>OsSUT5</i>	5'-CTAGTGCGAACTCCATCAAA-3' (forward) 5'-AAAATATTTGGGTTTCCTGAGAT-3' (reserve)