

Table S1 The primers for qRT-PCR analysis.

Genes	Forward primers (5'-3')	Reverse primers (5'-3')
Ion transports		
<i>PpHKT1;5</i>	GCGATGCTCCTTTCTTCTTG	GCTCCTTACCCTCCTTATGCT
<i>PpNHX1</i>	GCTAGGATTGGTTCTGGTTGG	CTTATTTTCTCGGCGGGC
<i>PpSOS1</i>	TCTCGTCTCCTTTTCCACC	CTGACAATAACCTCTTCTCCC
<i>PpHKT2;1</i>	AGAAGTTGAGTGGATCGTTTCT	GGCCTTTTCACCGCTATG
<i>PpAKT1</i>	CCAAACCCAAAGCAAACG	GATAATCCCCATAACCCACAG
<i>PpHAK5</i>	GCTGGGTCACGACACTACA	AGACATCACACCAAGGAGG
<i>PpHKT2;4</i>	ATCACTCTCCAGCGACCCT	CCCCACATTCCCATATGC
<i>PpKOR</i>	GTGGGCGAGTCAAACAAC	CCATAAAAAGCGGCGGTAT
Photosynthesis-related genes		
<i>PpHEMA1</i>	TGGGCTTGACTCTTTGGTTC	GCTGTGATTGCATCCTTGAAC
<i>Pppsba</i>	GAAAATGAATCCGCTAACGAG	CAGCCAAGAAGAAGTGTAAGA
<i>Pppsbd</i>	ACCGGAAGCCCAAGGAGAT	ATTGAACAGACCGAGCAAG
<i>PprbcL</i>	GAGGGTATTCGTGCGTGGA	GCTTTAGTTTCTGTTTGTGGTGA
<i>PprbcS</i>	GGCTTGAAGGCGATGAAG	TGGAGGAGGTGAAGAAGGAGTA
<i>PpPRK</i>	CTTGACCCCCCAGAACTCAT	GCTCTCTCACACGCTCATCG
<i>PpPGK</i>	GTCATCCTCGCCAGCCATCT	TCATTGCGCCATCACAACTC
<i>PpFBPase</i>	GTACTTGACATCATGCCACA	CCACCTTCTCCACTTCCTCC
<i>PpSBPase</i>	GGTGTGTGGCCTGGAGATAAG	GGAGGAGGAATTCGTGGGT
Genes related to ROS-scavenging system		
<i>PpSOD</i>	CAGGAAATGCTGGTGGGAG	GGGACAATAGAACTGAAGGC
<i>PpCAT</i>	CCTCTTATCGGCAAGGGTT	CGACAGTGCGTGGAATGA
<i>PpAPX</i>	CCATTTCCCCAAACACGC	AGAGACCCCAGATATCCCGC
<i>PpMDAR</i>	CATCCAGGAAAGCAAGAAAGA	GATACAGCCGCAAAAACCC
<i>PpDHAR</i>	CCAAGCCAACCAGGGAGAA	GAAAGGGACTGATAAGACACGA
<i>PpGR</i>	CCAGACATCCCAGGAATAGAGC	GAAAATGCCAGCAAACCTCCA
<i>PpGST</i>	CAATGGCGTCGGAGAAGA	CGTAGGTGTAGGGCAGGTTC
<i>PpGPX</i>	AAGTGCTGGAGGATTTTGGG	TGGAATGGTGAAGTCGTTGGT
<i>PpPOD</i>	CACGCTAATCTCCAAGTTCG	TGTCGTTGTAGATGTGGTCG
<i>PpGLP</i>	CCTTCTCAGCTGAAACCAGAGG	ACATGACATGCACACGCGC
<i>PpTrx</i>	CCAGAGAAAGATCGAGGAGCA	TCACAGCCAAGCGGACAAC
<i>PpPrdx</i>	GCTGATGGATCGGGAACAT	AACCGCCTCGAACGAAGAC
Reference gene (glyceraldehyde-3-phosphate dehydrogenase)		
<i>PpGAPDH</i>	TGGTATTGTTGAGGGTCTGATG	CAGTGCTGCTTGGAATGATG

Table S2 The relative expression level of genes related to photosynthesis in Kentucky bluegrass cultivars “Explorer” and “Blue Best” under 400 mM NaCl for 0 h (Control), 6 h or 48 h. Data are means (\pm SE), $n = 3$. Different letters indicate significant differences at $P < 0.05$ (Tukey’s HSD test).

Genes	Explorer			Blue Best		
	0 h	6 h	48 h	0 h	6 h	48 h
<i>PpHEMA1</i>	1.13 \pm 0.07b	4.34 \pm 0.42a	1.51 \pm 0.11b	1.08 \pm 0.02a	0.28 \pm 0.01b	0.91 \pm 0.03a
<i>Pppsba</i>	1.01 \pm 0.10b	1.42 \pm 0.05a	1.47 \pm 0.05a	1.05 \pm 0.04a	0.28 \pm 0.04b	0.47 \pm 0.01ab
<i>Pppsbd</i>	1.03 \pm 0.15b	1.58 \pm 0.03a	1.30 \pm 0.13ab	1.01 \pm 0.06a	0.14 \pm 0.01b	0.20 \pm 0.00b
<i>PprbcL</i>	1.00 \pm 0.06c	2.85 \pm 0.19a	1.57 \pm 0.36b	1.00 \pm 0.10a	0.45 \pm 0.03b	1.28 \pm 0.25a
<i>PprbcS</i>	1.00 \pm 0.05b	3.09 \pm 0.34a	0.96 \pm 0.12b	1.00 \pm 0.02b	0.09 \pm 0.00c	2.55 \pm 0.25a
<i>PpPRK</i>	1.02 \pm 0.06b	15.22 \pm 1.16a	11.58 \pm 0.16a	1.02 \pm 0.04b	0.78 \pm 0.01b	5.47 \pm 0.19a
<i>PpPGK</i>	1.01 \pm 0.10b	5.74 \pm 0.72a	1.88 \pm 0.02b	1.01 \pm 0.02b	0.43 \pm 0.03c	9.03 \pm 0.40a
<i>PpFBPase</i>	1.03 \pm 0.16c	4.57 \pm 0.45a	1.93 \pm 0.15b	1.02 \pm 0.01b	0.05 \pm 0.00c	1.87 \pm 0.04a
<i>PpSBPase</i>	1.13 \pm 0.04a	0.20 \pm 0.03b	0.21 \pm 0.03b	1.04 \pm 0.08a	0.12 \pm 0.02b	0.12 \pm 0.00b

Table S3 The relative expression level of genes related to Na⁺ and K⁺ transport in roots of Kentucky bluegrass cultivars “Explorer” and “Blue Best” under 400 mM NaCl for 0 h (Control), 6 h or 48 h. Data are means (\pm SE), $n = 3$. Different letters indicate significant differences at $P < 0.05$ (Tukey’s HSD test).

Genes	Explorer			Blue Best		
	0 h	6 h	48 h	0 h	6 h	48 h
<i>PpHKT1;5</i>	1.00 \pm 0.08b	1.69 \pm 0.08a	1.10 \pm 0.08b	1.00 \pm 0.07a	0.88 \pm 0.00ab	0.57 \pm 0.09b
<i>PpNHX1</i>	1.01 \pm 0.11c	34.64 \pm 4.65a	14.52 \pm 1.42b	1.00 \pm 0.14c	16.54 \pm 0.56b	63.76 \pm 6.36a
<i>PpSOS1</i>	1.00 \pm 0.22a	0.61 \pm 0.01b	0.24 \pm 0.02c	1.00 \pm 0.28a	0.08 \pm 0.00b	0.13 \pm 0.01b
<i>PpHKT2;1</i>	1.02 \pm 0.14a	0.50 \pm 0.04b	0.69 \pm 0.05b	1.00 \pm 0.17b	0.78 \pm 0.23b	5.84 \pm 0.38a
<i>PpAKT1</i>	1.00 \pm 0.02a	0.61 \pm 0.02b	0.11 \pm 0.01c	1.01 \pm 0.02a	0.45 \pm 0.02b	0.09 \pm 0.00c
<i>PpHAK5</i>	1.02 \pm 0.10b	0.68 \pm 0.17b	2.52 \pm 0.07a	1.10 \pm 0.15a	0.85 \pm 0.10a	0.37 \pm 0.04b
<i>PpHKT2;4</i>	1.00 \pm 0.04b	1.11 \pm 0.08b	3.31 \pm 0.01a	1.01 \pm 0.04b	1.18 \pm 0.12b	6.44 \pm 1.2a
<i>PpKOR</i>	1.02 \pm 0.04b	1.27 \pm 0.15ab	2.04 \pm 0.16a	1.02 \pm 0.05a	1.04 \pm 0.02a	0.59 \pm 0.04b

Table S4 The relative expression level of genes related to the ROS-scavenging system in leaves Kentucky bluegrass cultivars “Explorer” and “Blue Best” under 400 mM NaCl for 0 h (Control), 6 h or 48 h. Data are means (\pm SE), $n = 3$. Different letters indicate significant differences at $P < 0.05$ (Tukey’s HSD test).

Genes	Explorer			Blue Best		
	0 h	6 h	48 h	0 h	6 h	48 h
<i>PpSOD</i>	1.00 \pm 0.02b	2.15 \pm 0.04a	1.31 \pm 0.01b	1.03 \pm 0.04b	0.94 \pm 0.05b	1.89 \pm 0.03a
<i>PpCAT</i>	1.02 \pm 0.01c	4.92 \pm 0.60a	2.70 \pm 0.16b	1.03 \pm 0.02b	0.85 \pm 0.04b	1.81 \pm 0.08a
<i>PpAPX</i>	1.02 \pm 0.10b	4.14 \pm 0.24a	0.83 \pm 0.05b	1.08 \pm 0.14b	0.84 \pm 0.06b	6.18 \pm 0.67a
<i>PpMDAR</i>	1.00 \pm 0.00ab	1.26 \pm 0.05a	0.78 \pm 0.01b	1.03 \pm 0.02a	0.28 \pm 0.00b	1.07 \pm 0.01a
<i>PpDHAR</i>	1.01 \pm 0.03b	1.93 \pm 0.16a	0.85 \pm 0.02b	1.00 \pm 0.00a	0.61 \pm 0.01b	0.94 \pm 0.05a
<i>PpGR</i>	1.00 \pm 0.02b	3.10 \pm 0.05a	3.33 \pm 0.07a	1.00 \pm 0.03b	0.49 \pm 0.00c	2.15 \pm 0.25a
<i>PpGST</i>	1.01 \pm 0.02a	1.31 \pm 0.03a	0.50 \pm 0.00b	1.01 \pm 0.03a	0.48 \pm 0.00b	1.28 \pm 0.10a
<i>PpGPX</i>	1.02 \pm 0.11b	3.07 \pm 0.12a	0.29 \pm 0.01c	1.05 \pm 0.01a	1.42 \pm 0.29a	0.14 \pm 0.02b
<i>PpPOD</i>	1.05 \pm 0.02b	4.81 \pm 0.59a	3.18 \pm 0.07a	1.03 \pm 0.05b	0.85 \pm 0.04b	3.23 \pm 0.14a
<i>PpGLP</i>	1.00 \pm 0.04a	0.31 \pm 0.00b	0.04 \pm 0.00c	1.02 \pm 0.01a	0.04 \pm 0.00b	0.05 \pm 0.00b
<i>PpTrx</i>	1.00 \pm 0.01a	0.43 \pm 0.00b	0.47 \pm 0.02b	1.00 \pm 0.02a	0.21 \pm 0.00b	0.44 \pm 0.00b
<i>PpPrdx</i>	1.00 \pm 0.01a	0.77 \pm 0.01ab	0.57 \pm 0.01b	1.00 \pm 0.02a	0.19 \pm 0.00c	0.41 \pm 0.01b