

Supplementary Materials

Table S1. *F*-value/*P*-value for the effect of K nutrition on growth parameters of three barley genotypes in response to drought stress.

Source	<i>F</i> -value/ <i>P</i> -value			
	Shoot DW ($\mu\text{g plant}^{-1}$)	Root DW ($\mu\text{g plant}^{-1}$)	Shoot height (cm)	Root length (cm)
Genotype	3.59/0.036*	3.54/0.0376*	10.74/0.01**	9.65/0.0003**
Treatment	23.37/0**	3.85/0.0157*	7.85/0.0169*	3.61/0.0205*
G×T	2.72/0.025*	5.41/0.0003**	4.2053/0.002**	1.4/0.2464

G×T, Interaction between genotype and treatment; * and **, significant at 0.05 and 0.01 probability level, respectively.

Table S2. *F*-value/*P*-value for the effect of K nutrition on photosynthetic parameters of three barley genotypes in response to drought stress.

Source	<i>F</i> -value/ <i>P</i> -value					
	SPAD	<i>Fv/Fm</i>	<i>Pn</i> ($\mu\text{mol CO}_2$ $\text{m}^{-2} \text{s}^{-1}$)	<i>Gs</i> ($\text{mol H}_2\text{O m}^{-2} \text{s}^{-1}$)	<i>Ci</i> ($\mu\text{mol CO}_2$ mol^{-1})	<i>Tr</i> ($\text{mmol H}_2\text{O}$ $\text{m}^{-2} \text{s}^{-1}$)
Genotype	19.85/0.002**	4.813/0.0185*	17.14/0.0033**	3.414/0.1023	0.342/0.7232	4.02/0.078
Treatment	18.6/0.0019**	32.11/0**	27.736/0.0006**	8.561/0.0138*	13.55/0.0044**	11.91/0.006**
G×T	7.03/0**	1.4/0.26	4.27/0.0008**	12.786/0**	8.757/0**	12.5/0**

G×T, Interaction between genotype and treatment; * and **, significant at 0.05 and 0.01 probability level, respectively.

Table S3. *F*-value/*P*-value for the effect of K nutrition on shoot Ca, Na, K, Mg concentrations and Na⁺/K⁺ ratio of three barley genotypes in response to drought stress.

Source	<i>F</i> -value/ <i>P</i> -value									
	Shoot mineral concentrations (mg g ⁻¹ DW)					Root mineral concentrations (mg g ⁻¹ DW)				
	Ca	K	Mg	Na	Na ⁺ /K ⁺ ratio	Ca	K	Mg	Na	Na ⁺ /K ⁺ ratio
Genotype	1.65/0.215	121.52/0**	7.82/0.0027**	26.23/0**	42.15/0**	3.644/0.043*	123.20/0* *	0.253/0.78	4.994/0.016*	4.2/0.028*
Treatment	13.77/0**	37.3/0.0003**	37.44/0**	10.44/0.0002**	30.1/0**	9.64/0.0003**	37.79/0**	11.4/0.0001**	49.61/0**	17.76/0**
G×T	1.933/0.1202	1.0138/0.44	4.8/0.0029**	6.00/0.0008**	7.6/0.0002**	0.206/0.97	1.13/0.4	0.441/0.843	1.15/0.367	0.33/0.914

G×T, Interaction between genotype and treatment; * and **, significant at 0.05 and 0.01 probability level, respectively.

Table S4. *F*-value/*P*-value for the effect of K nutrition on shoot and root antioxidant enzyme activities and MDA contents of three barley genotypes in response to drought stress.

Source	<i>F</i> -value/ <i>P</i> -value				
	SOD (Unit mg ⁻¹ protein)	POD (Unit mg ⁻¹ protein)	APX (Unit mg ⁻¹ protein)	CAT (Unit mg ⁻¹ protein)	MDA (nmol g ⁻¹ FW)
Shoot					
Genotype	9.55/0.001**	2.23/0.131	10.20/0.0007**	2.69/0.09	14.54/0.005**
Treatment	15.62/0**	5.53/0.005**	29.33/0**	14.86/0**	39.07/0.0002**
G×T	4.24/0.0055**	1.095/0.396	5.38/0.001**	4.92/0.002**	4.126/0.0063**
Root					
Genotype	1.71/0.26	2.697/0.146	16.21/0**	2.2/0.14	12.55/0.0072**
Treatment	3.66/0.083	1.2662/0.37	21.43/0**	6.15/0.003**	8.91/0.0125*
G×T	16.15/0**	24.471/0**	7.04/0.0003**	0.976/0.47	7.82/0.0001**

G×T, Interaction between genotype and treatment; * and **, significant at 0.05 and 0.01 probability level, respectively.

Table S5. *F*-value/*P*-value for the effect of K nutrition on shoot and root H⁺/K⁺ ATPase and Ca²⁺/Mg²⁺ ATPase activities of three barley genotypes in response to drought stress.

Source	<i>F</i> -value/ <i>P</i> -value			
	Shoot H ⁺ /K ⁺ ATPase (μmol Pi mg ⁻¹ protein h ⁻¹)	Root H ⁺ /K ⁺ ATPase (μmol Pi mg ⁻¹ protein h ⁻¹)	Shoot Ca ²⁺ /Mg ²⁺ ATPase (μmol Pi mg ⁻¹ protein h ⁻¹)	Root Ca ²⁺ /Mg ²⁺ ATPase (μmol Pi mg ⁻¹ protein h ⁻¹)
Genotype	50.1455/0**	74.6149/0**	3.7012/0.0412*	2.1047/0.1458
Treatment	27.3965/0**	91.6315/0**	7.0094/0.0018**	4.4523/0.0137*
G×T	11.1092/0**	43.2296/0**	3.1811/0.0211*	1.2271/0.3303

G×T, Interaction between genotype and treatment; * and **, significant at 0.05 and 0.01 probability level, respectively.

Table S6. *F*-value/*P*-value for the effect of K nutrition on shoot and root proline, glycine betaine, soluble sugar and soluble protein contents of three barley genotypes in response to drought stress.

Source	<i>F</i> -value/ <i>P</i> -value							
	Shoot				Root			
	Proline ($\mu\text{g g}^{-1}$ FW)	Glycine betaine ($\mu\text{g g}^{-1}$ DW)	Soluble sugars (mg g^{-1} DW)	Soluble proteins ($\mu\text{g g}^{-1}$ FW)	Proline ($\mu\text{g g}^{-1}$ FW)	Glycine betaine ($\mu\text{g g}^{-1}$ DW)	Soluble sugars (mg g^{-1} DW)	Soluble proteins (mg g^{-1} DW)
Genotype	91.31/0**	57.52/0**	6.144/0.0076**	1610.10/0**	0.81/0.4575	13.42/0.0002**	271.503/0**	808.56/0* *
Treatment	546.43/0* *	186.84/0* *	133.898/0**	694.5/0**	2.87/0.0596	42.97/0**	140.34/0**	16.44/0**
G×T	22.88/0**	24.91/0**	128.969/0**	534.87/0**	6.91/0.0003**	1.77/0.151	109.66/0**	39.32/0**

G×T, Interaction between genotype and treatment; * and **, significant at 0.05 and 0.01 probability level, respectively.

Table S7. *F*-value/*P*-value for the effect of K nutrition on secondary metabolism related enzymes of three barley genotypes in response to drought stress.

Source	<i>F</i> -value/ <i>P</i> -value							
	Shoot				Root			
	PAL (Unit mg^{-1} protein)	PPO (Unit mg^{-1} protein)	CAD ($\mu\text{mol mg}^{-1}$ protein)	SKDH ($\mu\text{mol mg}^{-1}$ protein)	PAL (Unit mg^{-1} protein)	PPO (Unit mg^{-1} protein)	CAD ($\mu\text{mol mg}^{-1}$ protein)	SKDH ($\mu\text{mol mg}^{-1}$ protein)
Genotype	0.27/0.77	18.04/0**	0.8303/0.4491	17.04/0**	14.49/0.0001**	19.2/0**	34.8/0**	4.96/0.0167*
Treatment	62.94/0**	4.72/0.011*	33.4/0**	26.9/0**	16.44/0**	6.37/0.0029* *	12.19/0.0001**	0.94/0.4401
G×T	18.72/0**	1.69/0.171	4.71/0.0032**	6.1/0.0007**	11.87/0**	3.0454/0.0253*	59.63/0**	4.16/0.0061**

G×T, Interaction between genotype and treatment; * and **, significant at 0.05 and 0.01 probability level, respectively.

Table S8. *F*-value/*P*-value for the effect of K nutrition on secondary metabolites of three barley genotypes in response to drought stress.

Source	<i>F</i> -value/ <i>P</i> -value							
	Shoot				Root			
	Callose ($\mu\text{g g}^{-1}$ FW)	Phenols (mg g^{-1} FW)	Flavonoids (mg g^{-1} FW)	Chitinase (U mg^{-1} protein)	Callose ($\mu\text{g g}^{-1}$ FW)	Phenols (mg g^{-1} FW)	Flavonoids (mg g^{-1} FW)	Chitinase (U mg^{-1} protein)
Genotype	8.8/0.016 4*	5.09/0.051	1.996/0.217	4.35/0.068	7.04/0.0267	0.81/0.488	1.155/0.37 7	4.27/0.070 1
Treatment	3.7/0.081 2	0.86/0.513	34.7/0.0003 **	4.505/0.05 6	47.9/0.0001 **	19.5/0.0017 **	0.44/0.731	5.17/0.042 *
G×T	50.21/0**	2853.02/0 **	689.12/0**	37.4/0**	28.006/0**	110.09/0**	46.57/0**	165.59/0* *

G×T, Interaction between genotype and treatment; * and **, significant at 0.05 and 0.01 probability level, respectively.

Table S9. *F*-value/*P*-value for the effect of K nutrition on antioxidant enzymes related gene expression of three barley genotypes in response to drought stress.

Source	<i>F</i> -value/ <i>P</i> -value							
	Shoot				Root			
	<i>CAT1</i>	<i>CAT2</i>	<i>CuZn-SOD</i>	<i>APX</i>	<i>CAT1</i>	<i>CAT2</i>	<i>CuZn-SOD</i>	<i>APX</i>
Genotype	0.047/0.9 5	2.73/0.143	11.24/0.0004* *	4.34/0.068	1.16/0.3 7	5.45/0.044 *	4.964/0.05 3	7.93/0.02* *
Treatment	2.22/0.19	1.21/0.38	10.33/0.0002* *	8.30/0.014 *	2.5/0.16	6.32/0.028 *	2.98/0.11	2.78/0.13 3
G×T	55.99/0**	103.77/0* *	9.14/0**	11.52/0**	19.7/0**	68.71/0**	27.71/0**	14.33/0**

G×T, Interaction between genotype and treatment; * and **, significant at 0.05 and 0.01 probability level, respectively.

Table S10. *F*-value/*P*-value for the effect of K nutrition on secondary metabolism related gene expression of three barley genotypes in response to drought stress.

Source	<i>F</i> -value/ <i>P</i> -value							
	Shoot				Root			
	<i>PAL</i>	<i>PPO</i>	<i>CAD</i>	<i>SKDH</i>	<i>PAL</i>	<i>PPO</i>	<i>CAD</i>	<i>SKDH</i>
Genotype	1.017/0.42	0.63/0.565	0.273/0.77	2.6/0.154	4.74/0.058	1.332/0.33	6.12/0.036*	4.1/0.076
Treatment	0.79/0.54	1.41/0.33	0.75/0.562	6.02/0.03*	1.96/0.22	1.89/0.23	1.663/0.273	2.5/0.16
G×T	30.89/0**	448.75/0**	352.3/0**	33.75/0**	30.98/0**	1046.8/0**	102.48/0**	36.13/0**

G×T, Interaction between genotype and treatment; * and **, significant at 0.05 and 0.01 probability level, respectively.

Table S11. Candidate genes and corresponding primers used for qRT-PCR experiments.

Gene	Forward primer (5'-3')	Reverse primer (5'-3')
<i>HvCZSOD</i>	CACCCAGGAGGGAGATGGTA	GGTTGAAGTGCGGTCCTACA
<i>HvAPX1</i>	CGGAGCTTTTGAGTGGTGACA	CCGCAGCATATTTCTCCACAA
<i>HvCAT1</i>	CCCGTCTGGAACAACAAC	CCCCGTGCATGAACAAC
<i>HvCAT2</i>	CGACGACAAGATGCTGCAGT	TGGTTGTTCTTGAAGCCGC
<i>PAL</i>	CCCAAGTTTGACTATGGCT	ATCTTGTTGTGCTGCTCTG
<i>PPO</i>	TCTACAACGAGAGGCGTGAC	GGTCGATCAGCTGGTCTCTT
<i>CAD</i>	AAGAGACAGGAGGCTTTGGA	GGTAAGGCTCAAGAGGGTGA
<i>SKDH</i>	TCTTGCAAACACAACAGCAA	CACATTCTGCAGCTTCCCTA

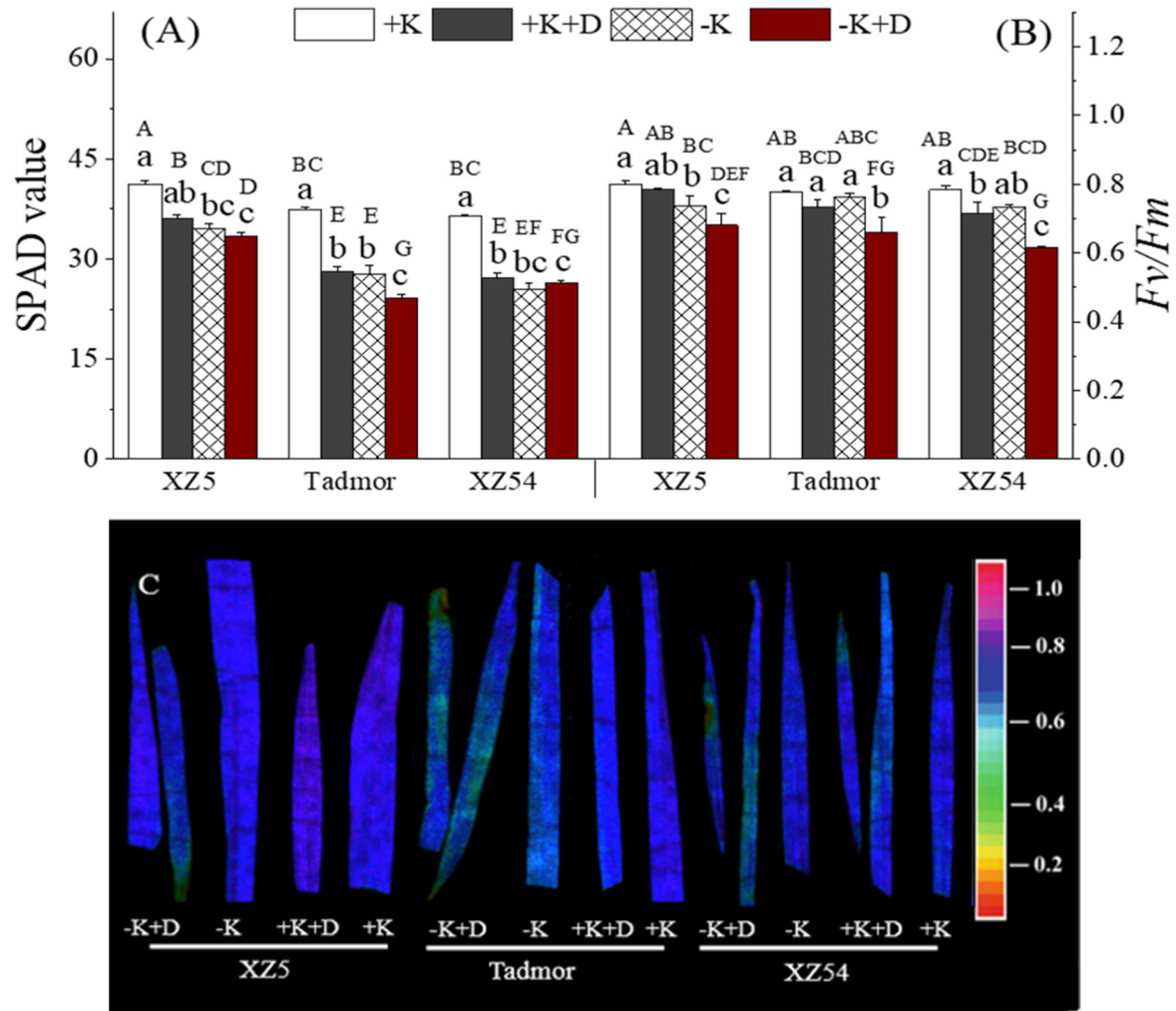


Figure S1. Effect of drought and K deprivation, applied either alone or in combined, on relative chlorophyll contents (SPAD values) (A) and chlorophyll fluorescence yield (F_v/F_m) (B), and false color images of F_v/F_m in response to drought stress (C) of three barley genotypes. Different capital and small letter(s) indicate significant differences ($P < 0.05$) among the genotypes and among the 4 treatments within each genotype, respectively. Error bars represent standard deviations ($n = 4$).

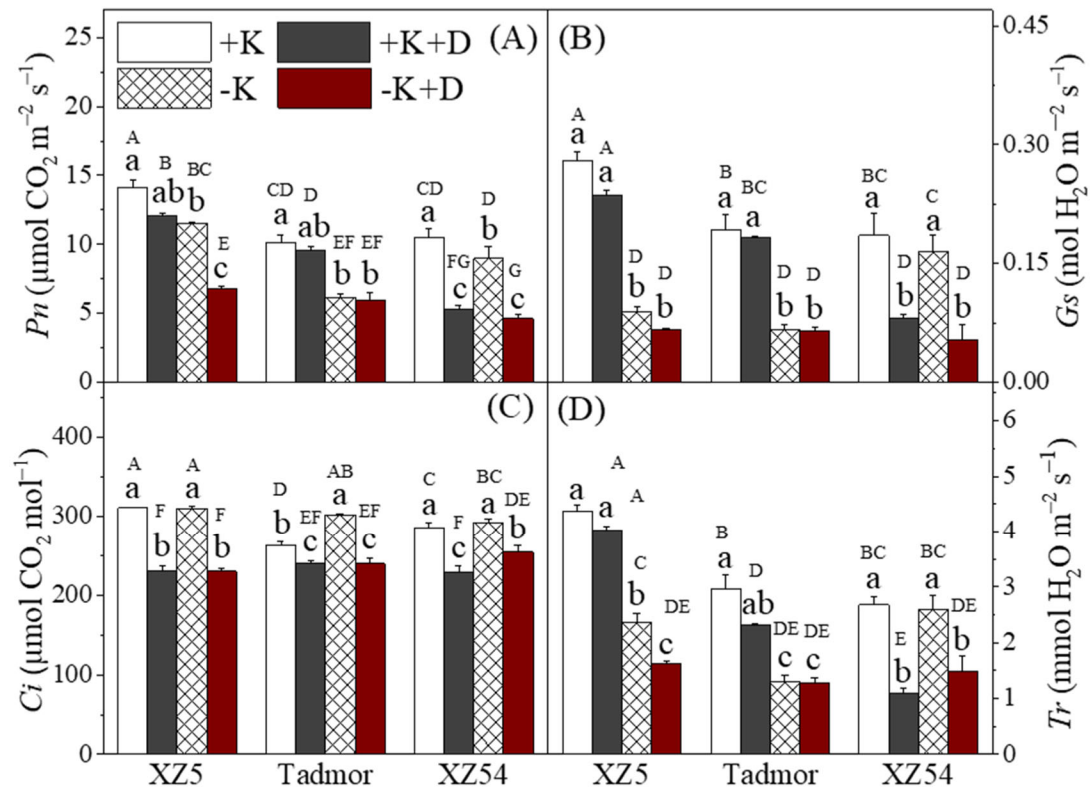


Figure S2. Effect of drought and K deprivation, applied either alone or in combined, on photosynthetic parameters of three barley genotypes. Different capital and small letter(s) indicate significant differences ($P < 0.05$) among the genotypes and among the 4 treatments within each genotype, respectively. Values in parenthesis express the percentage decrease (-) with respect to control. Error bars represent standard deviations ($n = 3$).

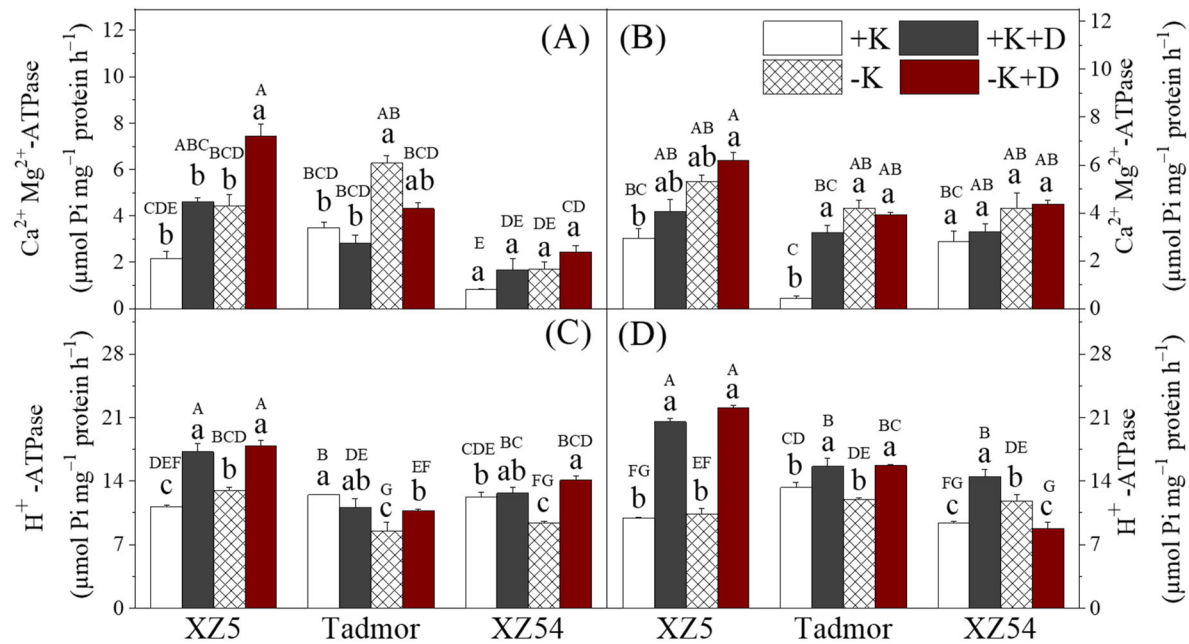


Figure S3. Effect of alone and combined stress of drought and K deprivation on $\text{Ca}^{2+} \text{Mg}^{2+}\text{-ATPase}$ and $\text{H}^{+}\text{-ATPase}$ activities in leaves (A, C) and roots (B, D) of three barley genotypes. Different capital and small letter(s) indicate significant differences ($P < 0.05$) among the geno-types and among the treatments within each genotype, respectively. +K (control), +K+PEG, -K, and -K+PEG, correspond to basic nutrition solution with normal K of 1 mM K (BNS), BNS+20% Polyethylene glycol 6000 (PEG), BNS without K (K deprivation), and BNS without K +20% PEG, respectively. Error bars represent standard deviations ($n = 3$).