

Table S1. The pedigree, salt tolerance and response of anther culture of the bread wheat genotypes used in this study.

Genotypes	Pedigree	Salt tolerance	Anther culture response
Doubled haploid line (15 lines):			
DHLs (21,22,23,25)	Derived from the cross (Line-115 × Gemmeiza-7)	Unknown	Unknown
DHLs (5,7,8,11)	Derived from the cross (Line-115 × Giza-164)	Unknown	Unknown
DHLs (12,14,15,26,29)	Derived from the cross (Gemmeiza-7 × Giza-164)	Unknown	Unknown
DHLs (2,3)	Derived from the cross (Giza-164 × Giza-168)	Unknown	Unknown
Crosses parents :			
Giza-164	KVZ / Buha "S" // Kal / Bb	Moderate	Low
Giza-168	MRL/BUC//SERICM 93046-8 M-OY-OM-2Y-OB-OGZ.	Sensitive	Moderate
Gemmeiza-7	CMH74A.630/SX//SERI82/AGENTCGM 4611-2GM-3GM-1GM-OGM	Sensitive	High
Gemmeiza-9	Ald"s"/Huac//CMH74 .630/SxCGM 4583 -5GM- 1GM-OGM	Moderate	Low
Line-115	Line-115 was obtained from Prof. Dr. M.A. El-Hennawy, Agronomy Dept., Fac. of Agric., Al-Azhar Univ.	Tolerant	High
Check cultivar Sakha-93	Sakha 92/TR810328 S8871-IS-2S-IS-0S	Tolerant	Unresponsive

Table S2. Partitioning of correlation coefficient between shoot dry weight (SDW) with six related attributes; root dry weight (RDW), shoot length (SL), membrane stability index (MSI), chlorophyll content (CHL), polyphenol oxidase (PPO) and catalase (CAT).

	Direct effect	Indirect effected						Correlation SDW (y)
		RDW(x ₁)	SL(x ₂)	MSI(x ₃)	CHL(x ₄)	PPO(x ₅)	CTA(x ₆)	
RDW(x ₁)	0.119		0.131	-0.008	-0.034	0.000	0.241	0.449
SL(x ₂)	0.497	0.031		-0.035	-0.042	0.026	0.128	0.605
MSI(x ₃)	-0.049	0.020	0.351		-0.031	0.034	0.079	0.404
CHL(x ₄)	-0.109	0.037	0.192	-0.014		0.029	0.198	0.333
PPO(x ₅)	0.160	0.000	0.081	-0.011	-0.020		0.198	0.409
CTA(x ₆)	0.421	0.068	0.151	-0.009	-0.051	0.068		0.648

Table S3. Prior and posterior classification, membership probabilities in salinity groupings by linear discriminant analysis.

Genotype	Prior	posterior	HS	HT	I	S	T
DHL2	T	T	0.000	0.000	0.000	0.000	1.000
DHL3	HS	HS	1.000	0.000	0.000	0.000	0.000
DHL5	T	T	0.000	0.000	0.000	0.000	1.000
DHL7	S	S	0.000	0.000	0.009	0.991	0.000
DHL8	S	S	0.000	0.000	0.090	0.910	0.000
DHL11	T	T	0.000	0.000	0.000	0.000	1.000
DHL12	I	I	0.000	0.000	0.994	0.000	0.006
DHL14	S	S	0.014	0.000	0.000	0.986	0.000
DHL15	S	S	0.002	0.000	0.000	0.998	0.000
DHL21	HT	HT	0.000	1.000	0.000	0.000	0.000
DHL22	HS	HS	0.989	0.000	0.000	0.011	0.000
DHL23	I	I	0.000	0.000	0.564	0.436	0.000
DHL25	T	T	0.000	0.000	0.000	0.000	1.000
DHL26	T	T	0.000	0.000	0.000	0.000	1.000
DHL29	S	S	0.003	0.000	0.000	0.997	0.000
Sakha93	HT	HT	0.000	1.000	0.000	0.000	0.000

Highly tolerant (HT), tolerant (T), intermediate (I), sensitive (S) and highly sensitive (HS).

Table S4. Total canonical structure of eigenvalue, canonical discriminant function and class means of salinity group to canonical discriminant function.

	Can1	Can2
Eigenvalue	39.14	0.60
Discrimination (%)	98.46	1.50
Cumulative %	98.46	99.96
Variable		
SL	0.89	0.41
SDM	0.95	-0.24
CAT	0.87	-0.16
Salinity Group		
HS	-7.76	-0.91
HT	8.49	-1.03
I	-0.65	-0.47
S	-4.08	0.41
T	4.05	0.55

Shoot length (SL), shoot dry weight (SDW) and catalase (CAT), highly tolerant (HT), tolerant (T), intermediate (I), sensitive (S) and highly sensitive (HS).

Table S5. Summary (LS means) of all pairwise comparisons for Class (Fisher (LSD))

Contrast	SL	Significant	SDW	Significant	CAT	Significant
HT vs T	0.564	No	0.004	Yes	0.079	No
HT vs I	0.010	Yes	0.001	Yes	0.036	Yes
HT vs S	0.002	Yes	< 0.0001	Yes	0.001	Yes
HT vs HS	0.000	Yes	< 0.0001	Yes	0.001	Yes
T vs I	0.010	Yes	0.053	No	0.378	No
T vs S	0.001	Yes	< 0.0001	Yes	0.005	Yes
T vs HS	< 0.0001	Yes	0.000	Yes	0.005	Yes
I vs S	0.820	No	0.037	Yes	0.118	No
I vs HS	0.036	Yes	0.016	Yes	0.054	No
S vs HS	0.024	Yes	0.326	No	0.397	No