Figure 1. Mean performance of chlorophyll content (ChL) and membrane stability index (MSI) for eighteen wheat genotypes grown under control and salinity conditions.

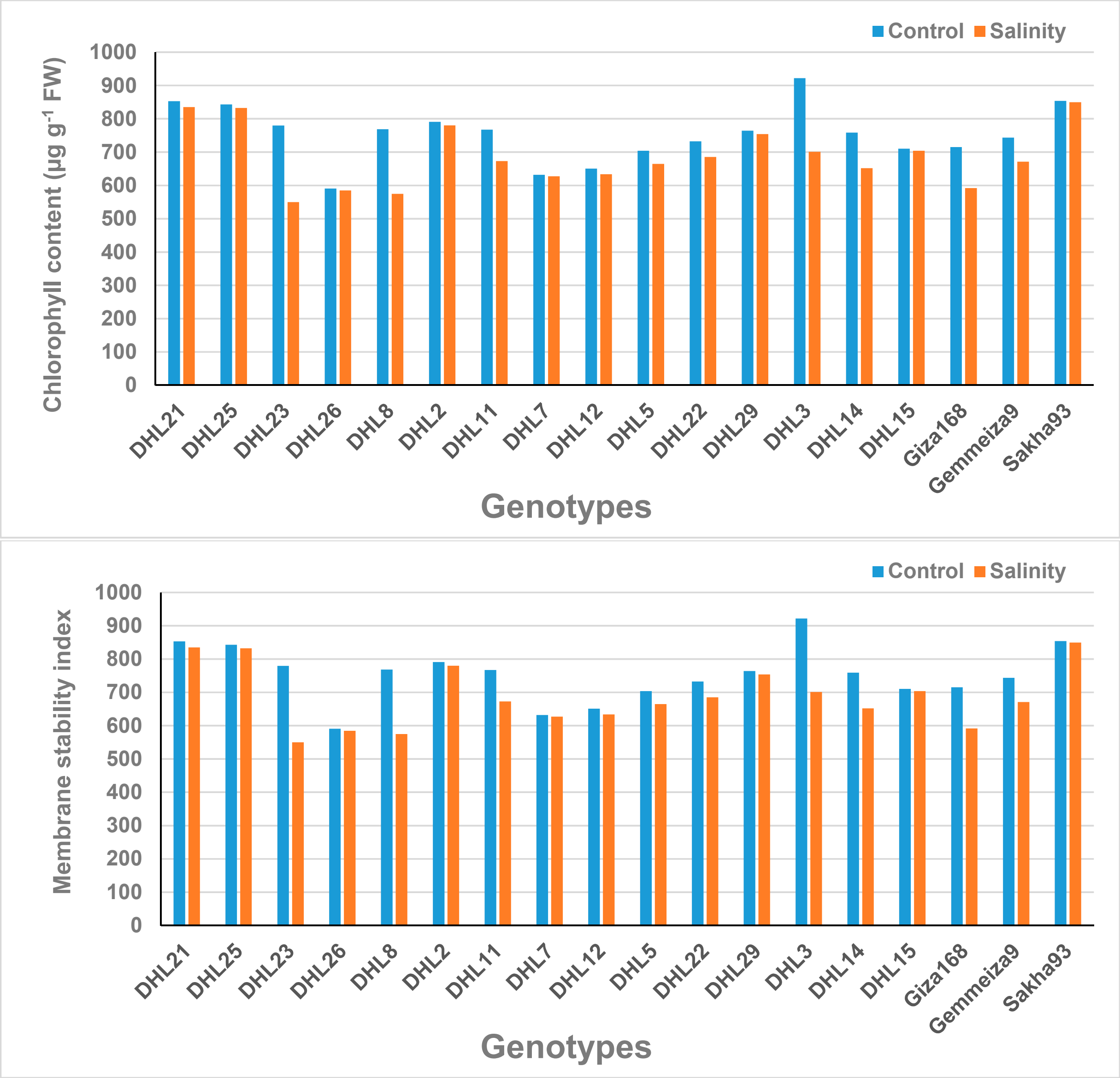

Table S1. The pedigree and salt tolerance of the three check bread wheat cultivars used in this study.

Genotypes	Pedigree	Salt tolerance
Check cultivars		
Sakha-93	Sakha 92/TR810328 S8871-IS-2S-IS-0S	Tolerant
Giza-168	MRL/BUC//SERICM 93046-8 M-OY-OM-2Y-OB-OGZ.	Moderate
Gemmeiza-9	Ald"s"/Huac//CMH74 .630/SxCGM 4583 -5GM- 1GM- OGM	Sensitive
Doubled haploid line (DHLs)		
15 DHLs	The DHLs were obtained from the Agronomy Department, Faculty of Agriculture, Al-Azhar University, Nasr City, Cairo, Egypt, and published by El-Hennawy et al. (2011), and selected based on their good grain yield performance as follows: DHLs (21,22,23,25), derived from the cross (Line-115 × Gemmeiza-7) DHLs (5,7,8,11), derived from the cross (Line-115 × Giza-164)	

Table S2. List of SSR markers used in the study across 18 wheat genotypes.

Oligo Name	Chromosome	Sequence 5 to 3		Annealing temp.	Repeat
		F	R		
cslinkkna2	5A	TCTCCATCATTCAACATCAATCG	TGTAGCTCGTCGGGGTGTGTTGC	58	-
Xbarc182	7B	CCATGGCCAACAGCTCAAGGTCTC	CGCAAAACCGCATCAGGGAAGCACCAAT	58	(CT)15
Xcfd1	6B,6D,6A	ACCAAAGAACTTGCCTGGTG	AAGCCTGACCTAGCCCAAAT	60	(GCC)6
Xcfd13	6B,6D	CCACTAACCAAGCTGCCATT	TTTTTGGCATTGATCTGCTG	60	(CT)20(TGTA)3
Xcfd18	5D	CATCCAACAGCACCAAGAGA	GCTACTACTATTTCATTGCGACCA	60	(GA)25
Xcfd183	5D	ACTTGCACTTGCTATACTTACGAA	GTGTGTCGGTGTGTGGAAAG	60	(CA)22
Xcfd19	1,5,6D	TACGCAGGTTTGCTGCTTCT	GGAGTTCACAAGCATGGGTT	60	(GA)18
Xcfd46	7D	TGGTGGTATAGTCGTTGGAGC	CCACACACACACACCATCAA	60	(GT)29
Xcfd49	6D	TGAGTTCTTCTGGTGAGGCA	GAATCGGTTCACAAGGGAAA	60	(GA)33
Xcfd60	6D,5B	TGACCGGCATTCAGTATCAA	TGGTCACTTTGATGAGCAGG	60	(CA)25
Xcfd66	7D	AGGTCTTGGTGGTTTTGGTG	TTTTCACATGCCCACAGTTG	60	(GC)9(AG)60
Xcfd9	3D	TTGCACGCACCTAAACTCTG	CAAGTGTGAGCGTCGG	60	(TC)29
Xgwm133	3A,6,7B,6D	ATCTAAACAAGACGGCGGTG	ATCTGTGACAACCGGTGAGA	60	(CT)39imp
Xgwm148	2B	GTGAGGCAGCAAGAGAGAAA	CAAAGCTTGACTCAGACCAAA	60	(CA)22
Xgwm174	5D	GGGTTCCTATCTGGTAAATCCC	GACACACATGTTCCTGCCAC	55	(CT)22
Xgwm181	3B	TCA TTG GTA ATG AGG AGA GA	GAA CCA TTC ATG TGC ATG TC	51	(GA)28
Xgwm205	5D,5A	CGACCCGGTTCACTTCAG	AGTCGCCGTTGTATAGTGCC	60	(CT)21
Xgwm210	2A	TGCATCAAGAATAGTGTGGAAG	TGAGAGGAAGGCTCACACCT	55	(GA)20
Xgwm247	3A,3B	GCAATCTTTTTTCTGACCACG	ATG TGC ATG TCG GAC GC	55	(GA)24
Xgwm249	2D	CAAATGGATCGAGAAAGGGA	CTGCCATTTTTCTGGATCTACC	55	(GA)11(GGA)8
Xgwm296	2D,7D	AATTCAACCTACCAATCTCTG	GCCTAATAAACTGAAAACGAG	55	(CT)28
Xgwm299	3B,2B	ACTACTTAGGCCTCCCGCC	TGACCCACTTGCAATTCATC	55	(GA)31(TAG)4
Xgwm312	2A	ATCGCATGATGCACGTAGAG	ACATGCATGCCTACCTAATGG	60	(GA)37
Xgwm314	3D,4B	AGGAGCTCCTCTGTGCCAC	TTCGGGACTCTCTTCCCTG	55	(CT)25imp
Xgwm335	5B	CGTACTCCACTCCACACGG	CGGTCCAAGTGCTACCTTTC	55	(GA)14(GCGT)3
Xgwm340	3B	GCAATCTTTTTTCTGACCACG	ACGAGGCAAGAACACACATG	60	(GA)26
Xgwm350	7D	ACCTCATCCACATGTTCTACG	GCATGGATAGGACGCCC	55	(GT)14
Xgwm413	1B,1A	TGCTTGTCTAGATTGCTTGGG	GATCGTCTCGTCCTTGGCA	60	(GA)18
Xgwm455	2D,6B	ATTCGGTTCGCTAGCTACCA	ACGGAGAGCAACCTGCC	55	(GT)19imp

Xgwm539	2D	CTGCTCTAAGATTCATGCAACC	GAGGCTTGTGCCCTCTGTAG	60	(GA)27
Xgwm614	2B,2A,2D	GATCACATGCATGCGTCATG	TTTTACCGTTCCGGCCTT	60	(GA)23imp
Xgwm674	3A	TCGAGCGATTTTTCCTGC	TGACCGAGTTGACCAAAACA	60	(CT)16CCC(GT)4
Xwmc11	3A, 3D	TTGTGATCCTGGTTGTGTTGTGA	CACCCAGCCGTTATATATGTTGA	61	-
Xwmc169	3, 5A	TACCCGAATCTGGAAAATCAAT	TGGAAGCTTGCTAACTTTGGAG	61	(CA)25 65 to 114
Xwmc17	7A, 7B	ACCTGCAAGAAATTAGGAACTC	CTAGTGTTTCAAATATGTCGGA	51	-
Xwmc170	2A,2D	ACATCCACGTTTATGTTGTTGC	TTGGTTGCTCAACGTTTACTTC	61	(CA)19 378 to 415
Xwmc18	2D	CTGGGGCTTGGATCACGTCATT	AGCCATGGACATGGTGTCCTTC	61	(CA)(CT) CM*
Xwmc367	1B	CTGACGTTGATGGGCCACTATT	GTGGTGGAAGAGGAAGGAGAGG	61	(GCC)5 125 to 139
Xwmc419	4B	GTTTCGGATAAAACCGGAGTGC	ACTACTTGTGGGTTATCACCAGCC	61	(GA)16 111 to 142
Xwmc432	1D	ATGACACCAGATCTAGCAC	AATATTGGCATGATTACACA	51	(GT)14 238 to 265
Xwmc44	1B	GGTCTTCTGGGCTTTGATCCTG	TGTTGCTAGGGACCCGTAGTGG	61	(GT)35 341 to 410
Xwmc503	2D	GCAATAGTTCCCGCAAGAAAAG	ATCAACTACCTCCAGATCCCGT	61	(GT)11 112 to 133
Xwmc661	2B	CCACCATGGTGCTAATAGTGTC	AGCTCGTAACGTAATGCAACTG	61	-

*Compound microsatellite

Table S3. Analysis of the differences between the groups of relative turgidity (RT) and shoot dry matter (SDM) traits.

Groups	RT		SDM	
I	0.030 b		0.334 a	
S	0.057 b		0.142 b	
T	0.166 a		0.027 c	
Pr > F	0.000		0.000	
Significant	Yes		Yes	
Summary (LS means) of all pairwise comparisons for groups (Fisher, LSD)				
Contrast	RT		SDM	
	P value	Significant	P value	Significant
T vs I	< 0.0001	Yes	< 0.0001	Yes
T vs S	< 0.0001	Yes	< 0.0001	Yes
S vs I	0.0954	No	< 0.0001	Yes

Tolerant (T), intermediate (I) and sensitive.

Table S4. Morphological distance estimation between 18 wheat genotypes using relative change of relative turgidity and shoot dry matter traits.

Genotypes	DHL2	DHL3	DHL5	DHL7	DHL8	DHL11	DHL12	DHL14	DHL15	DHL21	DHL22	DHL23	DHL25	DHL26	DHL29	Sakha93	Giza168
DHL3	0.352																
DHL5	0.006	0.350															
DHL7	0.298	0.055	0.296														
DHL8	0.203	0.157	0.203	0.102													
DHL11	0.115	0.237	0.114	0.183	0.089												
DHL12	0.131	0.227	0.131	0.172	0.073	0.024											
DHL14	0.353	0.023	0.352	0.056	0.153	0.238	0.225										
DHL15	0.332	0.025	0.331	0.034	0.134	0.217	0.205	0.022									
DHL21	0.072	0.383	0.067	0.332	0.248	0.160	0.182	0.388	0.366								
DHL22	0.311	0.043	0.310	0.014	0.114	0.196	0.185	0.042	0.021	0.345							
DHL23	0.190	0.205	0.192	0.153	0.061	0.095	0.071	0.196	0.181	0.249	0.163						
DHL25	0.043	0.325	0.037	0.272	0.185	0.097	0.118	0.328	0.307	0.064	0.286	0.185					
DHL26	0.072	0.282	0.073	0.228	0.131	0.045	0.059	0.282	0.262	0.128	0.241	0.121	0.066				
DHL29	0.315	0.043	0.314	0.020	0.116	0.200	0.188	0.037	0.018	0.351	0.008	0.163	0.291	0.245			
Sakha93	0.042	0.378	0.039	0.325	0.236	0.147	0.166	0.381	0.360	0.033	0.339	0.229	0.053	0.109	0.344		
Giza168	0.161	0.216	0.162	0.161	0.060	0.064	0.040	0.210	0.192	0.218	0.173	0.032	0.154	0.090	0.174	0.199	
Gemmeiza9	0.342	0.012	0.341	0.045	0.146	0.228	0.217	0.019	0.013	0.375	0.032	0.194	0.316	0.273	0.031	0.369	0.205

Doubled haploid line (DHL)

Table S5. Genetic distance estimation between 18 wheat genotypes using SSR molecular markers.

Genotypes	DHL2	DHL3	DHL5	DHL7	DHL8	DHL11	DHL12	DHL14	DHL15	DHL21	DHL22	DHL23	DHL25	DHL26	DHL29	Sakha93	Giza168
DHL3	0.731																
DHL5	0.423	0.667															
DHL7	0.846	0.611	0.821														
DHL8	0.781	0.741	0.645	0.708													
DHL11	0.774	0.731	0.633	0.846	0.607												
DHL12	0.773	0.625	0.696	1.000	0.833	0.826											
DHL14	0.654	0.125	0.593	0.650	0.714	0.750	0.500										
DHL15	0.958	0.667	0.833	0.867	0.870	0.913	0.727	0.706									
DHL21	0.700	0.867	0.645	0.852	0.750	0.655	0.783	0.800	0.960								
DHL22	0.920	0.625	0.846	0.417	0.783	0.826	0.933	0.667	0.727	0.880							
DHL23	0.767	0.815	0.667	0.840	0.417	0.630	0.870	0.786	0.909	0.774	0.818						
DHL25	0.813	0.731	0.677	0.800	0.742	0.480	0.875	0.750	0.958	0.500	0.773	0.630					
DHL26	0.654	0.750	0.593	0.826	0.714	0.409	0.857	0.769	0.900	0.667	0.909	0.786	0.704				
DHL29	0.714	0.591	0.655	0.727	0.577	0.714	0.750	0.500	0.789	0.724	0.684	0.704	0.714	0.821			
Sakha93	0.647	0.829	0.639	0.882	0.730	0.563	0.793	0.806	0.900	0.484	0.939	0.750	0.563	0.613	0.743		
Giza168	0.692	0.682	0.679	0.870	0.793	0.786	0.647	0.591	0.765	0.750	0.789	0.821	0.867	0.760	0.667	0.688	
Gemmeiza9	0.846	0.438	0.821	0.533	0.708	0.800	0.813	0.500	0.583	0.893	0.273	0.739	0.800	0.875	0.667	0.882	0.700

Doubled haploid line (DHL)