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RESEARCH ARTICLE

Assessment of variation among cultivated wheat species for plant nutrient strata under salinity conditions

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Abstract

Six wheat genotypes, two each of bread wheat (UAS BW-13897 and LBPY 2014-5), *Triticum durum* (GW 2010-679 and UAS DW-31403) and T. *dicoccum* (DIC 99 and DIC 26) were grown under natural saline and control conditions to observe the existence of ion discrimination, ion selectivity amenable to ion regulation and ion interactions among them. Bread wheat genotype, UAS BW-13897 showed a high K^+ and K^+/Na^+ ratio at the harvesting stage under saline condition indicating its high salt tolerance. Contrary to it, *T. durum* genotype, UAS DW-31403 was found to be highly salt-sensitive due to its low K^+/Na^+ ratio and high Na^+ absorption. Bread wheat genotypes were found most salt-tolerant due to better exclusion of Na^+ salt, with negligible reduction in grain yield, spike length, SPAD and number of grains per spike. The salt exclusion was found less apparent in *T. durum* and *T. dicoccum* wheat likely due to the absence of the D genome and *Kna1* gene, which is present in bread wheat and not in the two tetraploid species. Durum wheat was observed to be most sensitive with low salt exclusion capacity, whereas *T. dicoccum* wheat was found intermediate between bread and durum wheat with medium salt exclusion capacity. The study revealed a difference in type and level of salt tolerance in different species and genotypes that established high Na^+ salt exclusion capacity as one of the important selection criteria for salt tolerance.

Keywords: Bread wheat, durum wheat, dicoccum wheat, salinity tolerance, sodium exclusion

Introduction

Among abiotic stresses, salinity is one of the major factors reducing plant growth and productivity worldwide and affects about 7% of the world's total land area (Flowers et al. 1997). Salinity stress adversely impacts more than 800 mha of the world's soils (Munns and Tester 2008; Osman et al. 2021). Additionally, about 45 mha of irrigated fields worldwide are adversely affected by salt stress-related issues and it was predicted that 50% of global farmland may be salt-affected by 2050 (Wang et al. 2003; Shrivastava and Kumar 2015). The percentage of cultivated land affected by salt is even greater, with 23% of the cultivated land being saline and 20% of the irrigated land suffering from secondary salinization (Oproi and Madosa 2014). Furthermore, the increasing trend of the saline area at 10% per annum worldwide is a matter of great concern for future food production strategies (Ponnamieruma 1984). In India, salt impacts around 6.73 million hectares of land, of which sodicity impacts 3.77 mha and salinity affects 2.96 mha (Mondal et al. 2010).

Saline soils are characterized by pH < 8.5, exchangeable sodium percentage <15 and high soluble salts indicated by the high electrical conductivity of the saturation extract >4 dS/m. Plants are affected by soil salinity in three ways namely, osmotic stress, toxicity, and mineral shortage, which alters cellular ionic equilibrium (Kirst 1990). When salt is continuously transported into transpiring leaves over an extended period of time, it eventually leads to extremely

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high Na+ and Cl- concentrations, which causes leaves to die (Masarmi et al. 2023). As a result, salt is compartmentalized and accumulates in the older leaves. The *Kna1* was the first relevant gene identified in wheat which controls the discrimination for uptake between K^+ and Na^+. This gene was identified and mapped to the 4DL chromosome of bread wheat (*Triticum aestivum* L.) (Dvorak et al. 1994). Two genes for Na^+ exclusion were identified in *T. durum* line 149: *Nax1* was localized on chromosome 2AL (Lindsay et al. 2004) and has been recently found to control the activity of a Na^+ transporter HKT1-4 (Huang et al. 2006). The contribution of a second gene *Nax2*, which was mapped onto chromosome 5AL (James et al. 2011) which has been well recognized. Salt exclusion is absent or less prominent in *T. durum* and *T. dicoccum* wheats because of absence of D genome and the *Kna1* gene. Many earlier reports also indicated the role of D genome in salt tolerance as many of the QTLs were mapped to D genome only (Mujeeb-Kazi et al. 2019). Taking these factors into account, the current investigation was initiated with the goal of determining the various wheat species respond to nutrient stratification in saline conditions.

Materials and methods

Six wheat genotypes, two each belonging to three different wheat species, *Triticum aestivum* L. (bread wheat, UAS BW-13897 and LBPY 2014-5), *T. durum* Desf. (macaroni, GW 2010-679 and UAS DW-31403) and *T. dicoccum* Schrank ex Schubl. (khapli, DIC 99 and DIC 26) were taken for the present study. The investigation was carried out during *rabi* 2020-21 and 2021-22 at the Research Station of the University of Agricultural Sciences, Dharwad at Ugar Sugars Pvt. Ltd, Ugar Khurd, Chikkodi, Belagavi, Karnataka, which is situated in the northern transitional tract of Karnataka with 16°38′ N latitude and 74° 49′ E longitude at an altitude of 537 m above mean sea level. Two separate experiments were conducted using a randomized block design with four replications under controlled and (saline) salt stress conditions. The soil properties of saline condition with pH< 8 and EC> 4 mmhos/cm and the control condition with pH of 6-8 and EC< 4 mmhos/cm were maintained throughout the crop season. Soil analysis was done in both crop seasons at different crop stages, *viz*., sowing, booting, grain filling and harvesting stages to monitor soil salinity by estimation of pH and EC dS/m (1 soil:2.5 water) of top layer (0-20 cm) and bottom layer (20–40 cm) of the control and saline field (Supplementary Table S1). Plant samples were collected from each plot of treatments by uprooting the entire plant carefully for plant nutrient analysis using standard procedure was done. Total Nitrogen content was analyzed using Kjeldhal method (Piper 1966), total phosphorus following Vanadomolybdate yellow color method (Jackson and Harrrington 1973), and total potassium and sodium by flame photometry (Piper 1966). Observations were recorded at different stages of crop growth on morphological, yield and yield parameters namely, germination percent, days to 50% flowering, days to maturity, plant height, spike length, number of grains per spike, number of productive tillers per meter row, thousand-grain weight and grain yield (calculated as q/ha) for all six genotypes. The data on physiological traits, SPAD and NDVI were taken at the booting, anthesis and grain-filling stages. The data for the four environments, i.e., two years, two conditions were pooled and an analysis of variance was done. The descriptive statistics and graphical representations have been carried out through RStudio and MS Office, respectively.

Results and discussion

The data collected for 18 characters from all four replications of each genotype under salinity and control conditions of both seasons were used to estimate pooled ANOVA (Supplementary Table S2). In the results, only the treatments i.e., the genotypes were found significant and the mean sum of squares with estimated F values showed significant differences at a 1% level of significance. A wide range was observed for all the morphological, physiological, yield and yield component traits under both controlled as well as in saline conditions (Table 1; Supplementary Table S3). A two-way T-test was done for the combined mean of all the genotypes for 18 different traits under saline and control conditions and reduction under salinity conditions was estimated among genotypes and species (Fig. 1, Supplementary Table. 4).

Morphological traits

All the morphological traits were drastically affected by salinity and showed a reduction in the mean of all the characters. The mean of germination percent was reduced from 95.65 to 92.2% due to salinity, similarly days to flowering and days to maturity were reduced from 58 to 56 days and 107 to 105 days, respectively due to salinity stress. Plant height was drastically reduced from a mean of 91.08 to 68.47 cm i.e., a 24.8% reduction in plant height. Among the three species of wheat, bread wheat was found to be early maturing (101 days), *T. durum* wheat was found early flowering (50 days) and dicoccum wheat was late flowering and late maturing under both stress and control conditions.

Arid and semi-arid regions of the world experience the severe effects of salinity. Soluble salt concentrations in arid and semi-arid soils harm plant growth and yield (Evelin et al. 2009) as excessive salts in the soil have a negative impact on all key biological processes, including growth, photosynthesis, protein, and lipid metabolism (Bacu et al. 2020; Hasanuzzaman et al. 2023). Wheat growth parameters are key indicators for cultivar potential against stress tolerance and adaptability (Sanghera and Thind 2014). In the present investigation, the high salt level in soil adversely affected vegetative growth as indicated by the mean performance of different traits under salt stress conditions.

Table 1. Pooled range, mean and change (%) for various morpho-physiological and yield traits for two seasons mean

S. No	Traits	Control		Salinity		Reduction (%) under salinity condition
		Range	Mean	Range	Mean	
1	GP	90-99	95.65*	88.23-96.5	92.2*	3.61
2	DFF	51-66	58*	48-66	56*	3.45
3	DM	100-119	107*	96-117	105*	1.87
4	PH	79.60-106.00	91.08*	55-80	68.47*	24.82
5	NDVI-I	0.60-0.71	0.65*	0.30-0.81	0.59*	9.23
6	NDVI-II	0.61-0.90	0.68*	0.30-0.77	0.52*	23.53
7	NDVI-III	0.40-0.85	0.61*	0.35-0.67	0.55*	9.84
8	SPAD-1	33.00-66.00	49.98*	19.10-66.00	49.75*	0.46
9	SPAD-II	32.98-55.51	45.13*	36.75-45.00	40.95*	9.26
10	SPAD-III	35.15-52.25	43.75*	33.00-49.00	41.12*	6.01
11	SL	6.60-12.00	9.13*	4.20-8.10	6.23*	31.76
12	SPS	13-23	17.16*	11-14	12.16*	29.41
13	GPS	27-50	35*	23-31	26*	25.71
14	TPM	84-144	115*	70-114	114*	0.87
15	TGW	29.35-42.00	36.33*	23.11-37.08	30.55*	15.91
16	BM	82.88-158.90	122.73*	42.20-111.12	71.37*	41.85
17	HI	14.00-51.12	29.33*	15.85-42.00	25.72*	12.31
18	GY	19.11-41.54	33.93*	7.54-26.1	17.83*	47.45

GP = Germination percentage (per cent), DFF = Days to 50% flowering, DM = Days to maturity, PH- Plant height (cm), NDVI-I = NDVI before anthesis, NDVI-II = NDVI at anthesis, NDVI-III = NDVI at grain filling, SPAD-I = Chlorophyll content before anthesis, SPAD-II = Chlorophyll content at anthesis, SPAD-III = Chlorophyll content at grain filling stage, SL = Spike length (cm), SPS = Number of spikelets per spike, GPS = Number of grains per spike, TPM = Number of tillers per meter, TGW = Thousand grain weight (g), BM = Biomass (q/ha), HI = Harvest index, GY = Grain yield (q/ha)and **Two tail T-test significance*

In general, there was an overall reduction in crop growth period under the saline condition as indicated by mean values for days to 50% flowering and days to maturity.

Physiological traits

NDVI and SPAD at three stages (booting, anthesis and grain filling) varied from 0.3 to 0.9 and 19.1 to 66, respectively, under both saline and normal conditions. The highest reduction in SPAD (24%) and NDVI (10%) was observed at the anthesis stage. The SPAD and NDVI were recorded higher for bread wheat, lowest for *T. dicoccum* wheat and average for *T. durum* wheat at all three stages of the crop. Among the physiological traits, the higher chlorophyll content under control conditions indicated that salinity stress leads to an energy problem for plants where the photosynthetic capacity of the plant is not able to supply the carbohydrate requirement of young leaves further reducing their growth (Munns and Tester 2008; Shirvani et al. 2021; Uzair et al. 2022). As expected, the NDVI values were high under the controlled condition compared to the saline situation, indicating the reduction in the greenness of the crop under salt stress conditions due to damage to the photosynthetic components and forced maturity (Abdehpour and Ehsanzadeh 2019; Masarmi et al. 2023). When the salt concentration of the soil solution increases, water potential decreases and the turgor potential of plant cells declines and ultimately ceases cells to grow (Ali et al. 2022). Such ion-specific toxicity develops as a result of the uptake of specific ions like sodium, chlorine, and sulphate from the irrigated water and their accumulation in the lower leaves of the plant causing early wilting (Yadav et al. 2011; Zhang et al. 2022).

Yield and yield attributes

There was a wide variation in the yield and yield traits under saline and control conditions. Spike length and number of spikelets per spike reduced drastically due to salinity from 9.13 to 6.23 cm (33.33% reduction) and 17 to 12 (29% reduction), respectively. Thousand grains weight was reduced by 17% from 36.33 to 30.55 g, and harvest index was reduced from 29.33 to 25.72% (14% reduction) due to salinity. Most of the yield and yield attributing traits such as tillers per meter, grains per spike, and grain yield were severely affected under saline conditions and exhibited a drastic reduction in mean performance as compared to non-stress conditions as shown in Table 1. Further, due to reduced crop growth, plant height and tillers a significant reduction was manifested in biomass accumulation. The traits such as spike length, number of spikelets per spike, and thousand-grains weight were least affected probably due to the compensation effect resulting from reduced tillers per meter and grains per spike (Kumar et al. 2014; Dadshani et al. 2019; Khedr et al. 2022).

Due to a reduction in all the above morphological, physiological and yield parameters, grain yield and biomass weight were highly affected due to salinity, grain yield mean reduced from 33.93 to 17.83 q/ha, with 48% reduction and biomass showed 42% reduction from 122.73 to 71.37 q/ha due to salinity. The highest grain yield, number of tillers and biomass weight were recorded by *T. dicoccum* wheat under both stress and non-stress conditions. Bread wheat was average in yield, highest in number of spikelets per spike, and number of grains per spike whereas durum wheat has the lowest yield and highest thousand-grain weight under both stress and non-stress conditions. In general, bread wheat was found early flowering and early maturing, and *T. dicoccum* wheat was late flowering, late maturing and taller than the other two species. Bread wheat was able to maintain a constant greenness, early maturity and early flowering under saline soils. Among physiological traits like NDVI and SPAD, bread and durum wheat species showed more greenness and chlorophyll content when compared to khapli wheat. *Triticum dicoccum* was better than the other two species in yield and majority yield attributing characters under study under both saline and control conditions. Based on the performance of wheat species for all the traits studied together, bread wheat was identified as most tolerant to salt followed by khapli and macaroni wheats is the most sensitive species (Ehsanzadeh et al. 2009; Moghaieb et al. 2011; Abdehpour and Ehsanzadeh 2019; Naeem et al. 2022).

Plant nutrient analysis

Plant samples from all six genotypes were analyzed to know the concentrations of nutrients namely, nitrogen, phosphorus, potash and sodium along with the potassium: sodium ratio (Table 2) which indicated a wide genotypic variation for nutrient uptake under normal and saline conditions. A reduction in nitrogen (UAS BW 13897, DIC 99), phosphorus (UAS DW 31403, DIC 26) and potash (LBPY 2014-5, UAS DW 31403, DIC 99, DIC 26) contents under salinity conditions was also observed (Fig. 2). Every genotype except UAS BW13897 showed a decrease in sodium levels. Contrary to it, an enhancement was also observed for nitrogen (GW 2010-679), phosphorus (LBPY 2014-5, DIC 99), potash (UAS BW13897, GW 2010-679) and sodium (DIC 26) contents under salinity conditions as compared to non-stress conditions. Similar results from plant nutrient analysis for determining the nutrient absorption and salt exclusion mechanisms underlying salt tolerance were also reported in wheat (Ahmad et al. 2005; Munns 2005; Abdehpour and Ehsanzadeh 2019; Ashraf et al. 2023).

An enhanced K/Na ratio was observed in UASBW13897

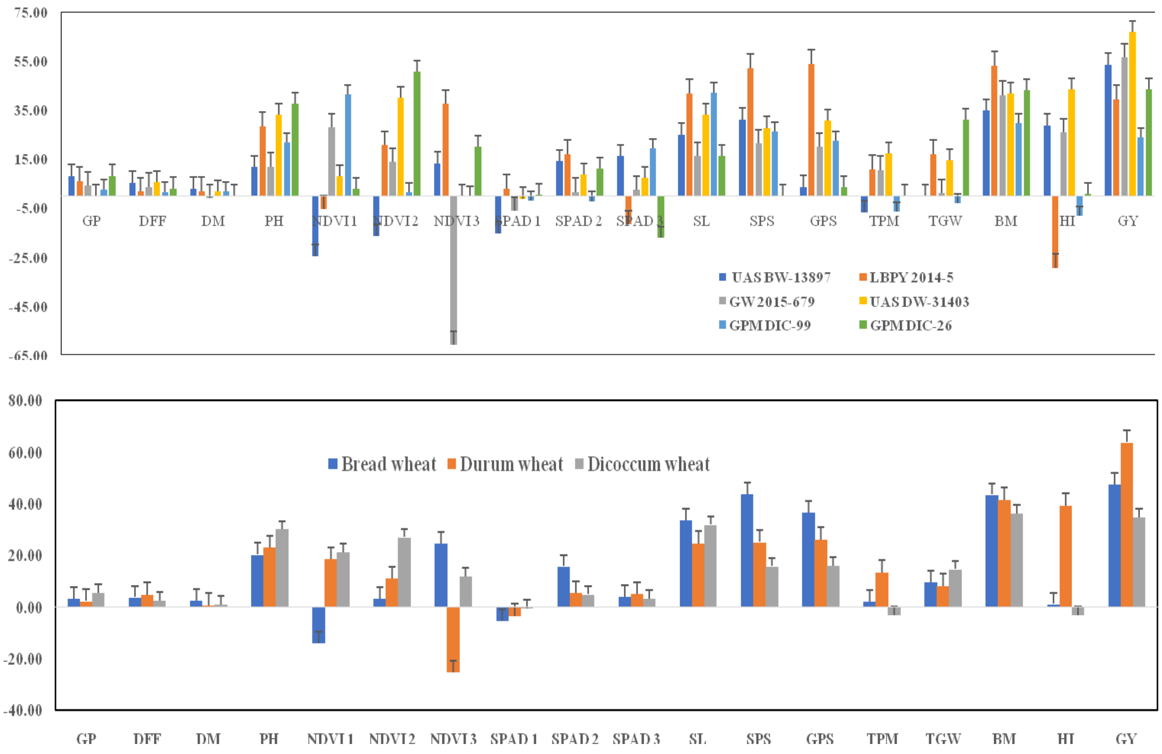

Fig. 1. Change (in %) in various traits in different genotypes and species under salinity conditions

Table 2. Concentrations (%) of different nutrients in six wheat genotypes

Genotype	Treatment	N%	P%	K%	Na%	K/Na
UAS BW-13897	Control	0.78	0.35	1.37	0.028	48.9
	Saline	0.72	0.36	1.5	0.027	55.6
16-LBPY 2014-5	Control	0.71	0.40	1.64	0.024	68.3
	Saline	0.70	0.45	1.24	0.023	53.9
44GW 2010-679	Control	0.71	0.42	1.45	0.024	60.4
	Saline	0.77	0.38	1.48	0.025	59.2
UAS DW-31403	Control	0.77	0.41	1.78	0.031	57.4
	Saline	0.76	0.32	1.14	0.023	49.6
DIC 99	Control	0.77	0.46	1.32	0.023	57.4
	Saline	0.72	0.48	1.24	0.023	53.9
DIC 26	Control	0.72	0.43	1.33	0.022	60.5
	Saline	0.72	0.39	1.24	0.025	49.6

N = Nitrogen, P = Phosphorous, K = Potassium, Na = Sodium

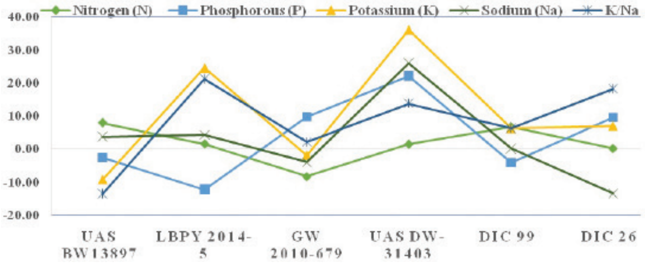

Fig. 2. Reduction (in %) in nutrient content under salinity condition

whereas LBPY2014-5, UASDW31403, DIC 99 and DIC 26 showed a reduction in K/Na ratio under salinity conditions. Maximum adverse effect on nutrient contents was observed in UASDW 31403 whereas GW2010-679 has the least adverse effect due to salinity condition. a decreased K/Na ratio in proportion to the increase in NaCl concentration was also reported and a genotype with low sodium uptake and high K/Na ratio under the saline condition was described as a salt-tolerant genotype (Ehsanzadeh et al. 2009; Ahmad 1 2014; Omrani et al. 2022). The *Kna1* gene mapped to 4DL chromosome of bread wheat has the function of salt exclusion at the roots i.e., selective absorption of K^+ ions over toxic Na^+ ions (Dvorak et al. 1994). Based on the low sodium content and high K/Na ratio under saline conditions, among the three-wheat species, bread wheat was the most tolerant followed by *T. dicoccum* wheat. The *T. durum* wheat was classified as the most sensitive based on the amount of sodium and potassium absorbed (Fig. 3). Durum wheat is not a good excluder of sodium making it a comparatively susceptible genotype as compared to tolerant crops like rice (de Ocampo et al. 2022) and barley (Zhu et al. 2023) which exclude at least 94% of the soil Na^+ from the transpiration stream.

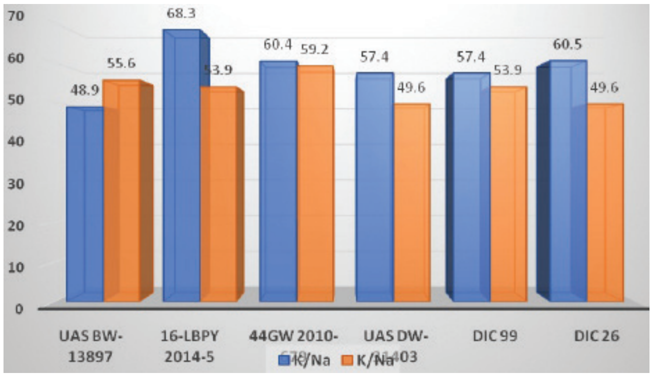

Fig. 3. K/Na ratio of genotypes under saline and control conditions

Salinity is increasingly influencing wheat productivity as an abiotic stress. Among all the three cultivated wheat species grown in India, bread wheat was found more salt tolerant followed by *T. dicoccum* wheat and *T. durum* wheat. When selecting for salt tolerance, it is important to focus more on the least impacted traits by the salt stress namely tiller number, heading and maturity duration, SPAD-I, initial germination etc. Differential behavior of different species for sodium exclusion capacity may be used as one of the key selection criteria for salt tolerance.

Supplementary material

Supplementary Tables S1 to S4 are provided online, www.isgpb.org.

Authors' contributions

Conceptualization of research (SSB, SAD, SKS); Designing of the experiments (SSM, SSB, LJ); Contribution of experimental materials (SSB, SKS); Execution of field/lab experiments and data collection (SSM, LJ, SSG, ST); Analysis of data and interpretation (SSM, ST, SKS); Preparation of the manuscript (SSM, SSB, SKS).

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Supplementary Table S1. The soil properties at different crop stages under control and salinity conditions

Crop stage	Soil layer	Soil pH				Electrical Conductivity (mmhos/cm)			
		2020-21		2021-22		2020-21		2021-22	
		Control	Saline	Control	Saline	Control	Saline	Control	Saline
Sowing	TL	7.02	8.01	7.71	7.82	2.89	6.56	2.21	6.67
	BL	7.21	7.98	7.89	7.7	3.01	6.51	3.08	5.96
Booting	TL	7.7	7.8	7.61	7.89	2.21	6.11	2.95	6.37
	BL	7.86	7.89	7.59	7.91	2.31	5.89	2.75	6.11
Grain filling	TL	7.95	8.02	7.92	7.56	3.32	6.02	3.11	6.34
	BL	7.99	7.77	8.1	8.06	3.11	6.11	2.39	5.82
Harvesting	TL	6.03	7.81	7.77	7.69	3.1	6.31	3.26	6.41
	BL	7.56	7.62	7.73	7.56	2.98	6.29	2.64	6.54

TL = Top layer (0-20 cm) and BL = Bottom layer (20-40 cm)

Supplementary Table S2. Pooled ANOVA of two seasons for RCBD design for different traits under saline and control condition

Traits	Source of variation	DF	Control condition			Saline condition		
			SS	MSS	F Value	SS	MSS	F Value
GP	Genotype (G)	5	137.85	27.57**	13.83	158.25	31.65**	4.37
	Replication (R)	3	7.82	2.61	1.36	33.74	11.25	1.55
	Year (Y)	1	6.02	6.02	3.02	0.01	0.01	0.00
	G * Y	5	7.85	1.57	0.79	37.42	7.48	1.03
DFF	Genotype (G)	5	1660.42	332.08**	11.34	608.09	121.62**	19.35
	Replication (R)	3	400.97	133.66	4.73	34.29	11.43	4.09
	Year (Y)	1	4.08	4.08	0.19	0.80	0.80	0.35
	G * Y	5	13.42	2.68	0.92	31.43	6.29*	2.73
DM	Genotype (G)	5	1342.69	268.54**	221.16	1395.85	279.17**	78.01
	Replication (R)	3	33.83	11.27	3.42	206.18	68.73	7.46
	Year (Y)	1	1.11	1.11*	0.92	0.21	0.21	0.60
	G * Y	5	9.02	1.80	1.49	14.67	2.93	0.82
PH	Genotype (G)	5	3026.50	605.30**	187.42	3033.76	606.75**	111.70
	Replication (R)	3	151.64	50.55	14.59	22.33	7.44	1.37
	Year (Y)	1	0.930	0.930	0.288	12.02	12.02	2.21
	G * Y	5	3.94	0.79*	0.244	20.29	4.06	0.75
NDVI-I	Genotype (G)	5	0.073	0.015**	11.25	1.26	0.25**	117.16
	Replication (R)	3	0.008	0.003	2.018	0.004	0.001	0.647
	Year (Y)	1	0.003	0.003	2.198	0.006	0.006	2.604
	G * Y	5	0.007	0.001	1.154	0.005	0.001	0.432
NDVI-II	Genotype (G)	5	0.056	0.011**	2.663	0.833	0.167**	52.39
	Replication (R)	3	0.017	0.006	1.370	0.021	0.007	2.153
	Year (Y)	1	0.001	0.001	0.275	0.002	0.002	0.665
	G * Y	5	0.012	0.002	0.596	0.044	0.009	2.757

NDVI-III	Genotype (G)	5	0.411	0.082**	42.62	0.411	0.082**	42.62
	Replication (R)	3	0.001	0.000	0.22	0.001	0.000	0.224
	Year (Y)	1	0.028	0.028	14.74	0.028	0.028*	14.74
	G * Y	5	0.033	0.007	3.444	0.033	0.007	3.444
SPAD-1	Genotype (G)	5	3747.80	749.57**	66.52	4701.30	940.27**	25.98
	Replication (R)	3	0.000	0.010	0.001	95.000	31.670	0.875
	Year (Y)	1	0.900	0.890	0.079	3.500	3.480	0.096
	G * Y	5	58.90	11.77	1.04	86.40	17.28	0.48
SPAD-II	Genotype (G)	5	1372.42	274.48**	91.04	170.30	34.06**	4.98
	Replication (R)	3	27.26	9.08	1.17	66.60	22.20	3.25
	Year (Y)	1	19.70	19.70	6.53	26.99	26.99*	3.95
	G * Y	5	4.53	0.91	0.30	34.40	6.88	1.01
SPAD-III	Genotype (G)	5	1390.52	278.10**	36.01	0.23	0.05**	8.71
	Replication (R)	3	27.26	9.09	1.18	28.35	9.45	4.00
	Year (Y)	1	56.10	56.10	7.26	0.002	0.002	0.941
	G * Y	5	7.51	1.50	0.19	0.027	0.005*	2.88
SL	Genotype (G)	5	131.15	26.23**	10.02	40.86	8.17**	32.55
	Replication (R)	3	14.15	4.72	1.80	0.636	0.212	0.472
	Year (Y)	1	1.35	1.35	0.52	1.28	1.28	5.09
	G * Y	5	16.36	3.27	1.25	1.52	0.303	1.21
SPS	Genotype (G)	5	6209.20	1241.84**	180.25	5834.41	1166.88**	1037.23
	Replication (R)	3	6.40	2.13	0.309	160.70	53.58	7.71
	Year (Y)	1	0.200	0.190	0.027	2.08	2.08	1.85
	G * Y	5	50.20	10.04	1.46	14.17	2.83	2.52
GPS	Genotype (G)	5	3531.17	706.13**	167.16	784.66	156.93**	33.08
	Replication (R)	3	46.40	15.47	3.48	96.06	32.02	5.06
	Year (Y)	1	1.00	12.00	12.00	1.33	1.33	0.281
	G * Y	5	11.75	2.35	0.56	26.67	5.33	1.12
TPM	Genotype (G)	5	3531.17	706.23**	167.16	33710.00	6742.00**	462.23
	Replication (R)	3	83.60	27.60	5.92	68.00	22.70	1.56
	Year (Y)	1	12.00	12.00	2.84	21.00	21.30	1.46
	G * Y	5	11.75	2.35	0.556	26.00	5.20	0.355
TGW	Genotype (G)	5	325.80	65.16**	14.10	608.09	5.15**	2.24
	Replication (R)	3	7.09	2.36	0.51	75.24	25.08	3.86
	Year (Y)	1	17.89	17.89	3.87	0.80	0.80	0.35
	G * Y	5	7.02	1.40	0.30	31.43	6.29	2.72
BM	Genotype (G)	5	25775.00	5155.00**	293.70	24336.30	4867.30**	533.11
	Replication (R)	3	35.30	11.80	0.670	34.10	11.40	1.25
	Year (Y)	1	0.90	0.90	0.052	10.90	10.90	1.20
	G * Y	5	100.00	20.00	1.14	113.80	22.80	2.49

HI	Genotype (G)	5	4432.20	886.45**	176.45	3060.48	612.10**	58.09
	Replication (R)	3	9.00	3.00	0.60	37.84	12.61	1.20
	Year (Y)	1	20.00	19.97	3.97	24.09	24.09	2.29
	G * Y	5	14.90	2.98	0.59	70.98	14.20	1.35
GY	Genotype (G)	5	2684.44	536.89**	236.56	1413.77	282.76**	151.43
	Replication (R)	3	7.17	2.39	1.05	15.87	5.29	2.83
	Year (Y)	1	0.350	0.350	0.153	4.81	4.81	2.57
	G * Y	5	21.90	4.38	1.93	17.08	3.42	1.83

GP = Germination percentage (per cent), DFF = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), NDVI-I = NDVI before anthesis, NDVI-II = NDVI at anthesis, NDVI-III = NDVI at grain filling, SPAD-I = Chlorophyll content before anthesis, SPAD-II = Chlorophyll content at anthesis, SPAD-III = Chlorophyll content at grain filling stage, SL = Spike length (cm), SPS = Number of spikelets per spike, GPS = Number of grains per spike, TPM = Number of tillers per meter, TGW = Thousand grain weight (g), BM = Biomass (q/ha), HI = Harvest index, GY = Grain yield (q/ha) and G*Y = Genotype x Year, **Two tail T-test significance*

Supplementary Table S3. Pooled performance of six wheat genotypes under saline and control condition

Genotype	Condition	GP	DFF	DM	PH	NDVI 1	NDVI 2	NDVI 3	SPAD 1	SPAD 2	SPAD 3	SL	SPS	GPS	TPM	TGW	BM	HI	GY
UAS BW-13897 (bw)	Salinity	95.0	53	101	70.3	0.76	0.71	0.65	64.40	43.58	43.78	7.34	11	26	112	29.4	78.8	22.2	17.5*
	Control	95.0	56	104	79.7	0.61	0.61	0.75	55.86	50.78	52.25	9.78	16	27	105	29.4	120.7	31.2	37.7*
LBPY 2014-5 (bw)	Salinity	92.5	54	101	58.6	0.76	0.54	0.40	63.50	43.18	46.68	5.80	11	23	90	30.7	49.8	36.9	18.4*
	Control	98.5	55	103	81.8	0.72	0.68	0.64	65.37	52.03	41.78	9.97	23	50	101	37.0	106.5	28.5	30.4*
GW 2015-679 (d)	Salinity	92.5	52	105	78.4	0.49	0.71	0.66	50.23	42.03	43.15	5.93	11	24	110	37.1	69.4	12.0	8.3*
	Control	96.5	54	104	89.0	0.68	0. 72	0.41	47.35	42.68	44.25	7.08	14	30	123	37.5	118.1	16.2	19.1*
UAS DW-31403 (d)	Salinity	90.0	50	104	63.3	0.58	0.36	0.57	49.23	41.78	40.13	4.47	13	27	72	34.9	48.3	27.7	13.4*
	Control	90.0	53	106	94.7	0.63	0.60	0.57	48.67	45.75	43.25	6.68	18	39	87	40.8	82.9	49.0	40.6*
GPM DIC-99 (DIC)	Salinity	92.5	61	109	75.4	0.37	0.64	0.52	37.29	37.88	35.40	6.81	14	31	148	36.5	108.6	23.4	25.4*
	Control	95.0	62	111	96.3	0.63	0.65	0.52	36.53	37.05	43.90		19	40	139	35.4	154.5	21.6	33.3*
GPM DIC-26 (DIC)	Salinity	90.0	65	117	65.6	0.68	0.34	0.60	45.72	36.75	41.13	6.68	13	27	145	25.8	83.7	28.0	23.4*
	Control	98.0	67	117	105.0	0.70	0.69	0.75	45.88	41.35	35.15	7.99	13	28	145	37.5	146.8	28.2	41.4*

**Two tail T-test significance;* bw = *Triticum aestivum*, d = *Triticum durum*, DIC =*T. dicoccum*

Supplementary Table S4. Pooled reduction (%) for two years in various traits under salinity conditions

		GP	DFF	DM	PH	NDVI 1	NDVI 2	NDVI 3	SPAD 1	SPAD 2	SPAD 3	SL	SPS	GPS	TPM	TGW	BM	HI	GY
A	Change (%) at Genotype level																		
1	UAS BW-13897	8.16	5.36	2.88	11.79	-24.59	-16.39	13.33	-15.29	14.18	16.21	24.95	31.25	3.70	-6.67	0.00	34.71	28.85	53.58
2	LBPY 2014-5	6.09	1.82	1.94	28.36	-5.56	20.59	37.50	2.86	17.01	-11.73	41.83	52.17	54.00	10.89	17.03	53.24	-29.47	39.47
3	GW 2015-679	4.15	3.70	-0.96	11.91	27.94	13.88	-60.98	-6.08	1.52	2.49	16.24	21.43	20.00	10.57	1.07	41.24	25.93	56.54
4	UAS DW-31403	0.00	5.66	1.89	33.16	7.94	40.00	0.00	-1.15	8.68	7.21	33.08	27.78	30.77	17.24	14.46	41.74	43.47	67.00
5	GPM DIC-99	2.63	1.61	1.80	21.70	41.27	1.54	0.00	-2.08	-2.24	19.36	42.24	26.32	22.50	-6.47	-3.11	29.71	-8.33	23.72
6	GPM DIC-26	8.16	2.99	0.00	37.52	2.86	50.72	20.00	0.35	11.12	-17.01	16.40	0.00	3.57	0.00	31.20	42.98	0.71	43.48
B	Change (%) at Species level																		
1	Bread wheat	3.10	3.60	2.42	20.19	-14.29	3.10	24.46	-5.50	15.61	3.80	33.47	43.58	36.36	1.94	9.49	43.40	1.01	47.28
2	Durum wheat	2.14	4.67	0.48	22.86	18.32	10.83	-25.51	-3.58	5.22	4.82	24.42	25.00	26.09	13.33	8.05	41.44	39.11	63.65
3	Dicoccum wheat	5.44	2.33	0.88	29.96	21.05	26.87	11.81	-0.73	4.81	3.19	31.80	15.62	15.94	-3.17	14.54	36.18	-3.21	34.67