Original Research Article

Investigations on genetic variability and character associationin*Triticum dicoccum* under salinity stress

Abstract

Salinity is one of the most important abiotic stresses affecting crop yield and quality. Wheat is regarded as a moderately salt tolerant crop; wheat species exhibit high variability that can be conveniently explored to improve wheat species for salt tolerance. Hence, the magnitude of variability for salt tolerance was studied in dicoccum wheat germplasm accessions. High phenotypic and genotypic coefficients of variance were observed for grain yield and yield attributes like tillers per meter, biomass, spikelets per spike and harvest index. The heritability and genetic advance over mean were moderate to high for grain yield, thousand grain weight, tillers per meter, biomass, spikelets per spike, harvest index, plant height, days to 50 per cent flowering and days to maturity. Character association studies revealed that harvest index and SPAD at anthesis stage exhibiteda positive significant correlation under both saline and control condition. Path coefficient analysis revealed that traits like harvest index, biomass, tillers per meter and days to 50 per cent flowering were showing a high direct effect on grain yield under both saline and control condition. Thus, the present study provides valuable genetic resources for grain yield and yield parameters improvement which are associated with the salt tolerance in wheat species.

Keywords: Dicoccum wheat, saline, variability and correlation

1. Introduction

A total of around 7% of the world's land area is salt affected (Flowers *et al*., 1997). Salt affects a higher percentage of cultivated land, with 23 percent of cultivated land being saline and 20 percent of irrigated land suffering from secondary salinization. Furthermore, there is a perilous tendency of a 10 per cent annual rise in the saline area all over the world (Ponnamieruma, 1984). In India, around 6.73 million hectares of land are affected by salt, with 3.77 million hectares affected by sodicity and 2.96 million hectares affected by salinity, respectively (Mondal *et al*., 2010). Saline soils are characterized by pH < 8.5, exchangeable sodium percentage <15 and high soluble salts indicated by high electrical conductivity of the saturation extract >4 dS/m (Qadir *et al.,* 2000).

Wheat is moderately salt tolerant with a threshold without yield loss at 6 dS/m and with 50 per cent yield loss at 13 dS/m (Mass and Hoffman, 1977). Maas and Grieve (1990) found differences in yield between bread and durum wheat in saline soil. They found that at a salt level comparable to around

100 mM NaCl, bread wheat yields were reduced by 7 per cent, while durum wheat yields were reduced by 38 per cent. There was less difference between genotypes at a greater salinity, equal to roughly 150 mM NaCl, with the bread wheat genotype reduced by 43 per cent and the durum wheat genotype reduced by 54 per cent. Salinity tolerance was highly variable among Dicoccom genotypes. Dicoccum wheat is more salt resistant than durum wheat but more susceptible than bread wheat (Abdehpour and Ehsanzadeh, 2019). As a consequence of these characteristics, the work was initiated to identify new genetic sources in the local collection of dicoccum germplasm for salt tolerance that are being unexplored. Further, such information may be great information to set the future path for the salt tolerance breeding program of cultivated tetraploid species of wheat.

Salinity is one of the most important abiotic stresses affecting crop yield and quality. Wheat is regarded as a moderately salt tolerant crop, among wheat species bread wheat is the most salt tolerant species followed by dicoccum wheat and durum wheat is classified as the most salt sensitive species for salinity. *T. dicoccum* exhibits high variability and diversity for salt tolerance that can be conveniently explored to improve cultivated dicoccum species. Hence, the magnitude of variability for salt tolerance was studied in dicoccum wheat germplasm accessions of the local collection in Peninsular India.

2. Materials and methods

The present study included pre-tested 60 dicoccum wheat germplasm accessions under both saline (natural saline soils) and control plot, out of which, 46 local germplasm accessions, 4 advanced breeding lines, and ten checks (Table1) were evaluated in alpha lattice design with four blocks and two replications. Each block consisted of 15 genotypes with two rows per genotype and 3- meter length with a spacing of 20 cm between rows. The present investigation was carried out during *rabi* 2020-21 at Ugar Sugars Pvt. Ltd, Ugar Khurd, Tq- Chikkodi, Dt-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 (AMSL). Two independent experiments were carried out in both salt stress and controlled condition. Under saline condition, pH of less than 8 and EC of more than 4 dS/m and under control condition pH of 6-8 and EC of less than 4 dS/m was maintained. Table 3 represents the pH and EC dS/m (1 soil:2.5 water) of the top layer (0-20 cm) and bottom layer (20-40 cm) of the control and saline field (Table 2).

Morphological traits like germination per cent, days to fifty per cent flowering, days to maturity and plant height, physiological traits (SPAD and NDVI), yield and yield attributes *viz.,* number of productive tillers per meter row, spike length (cm), number of grains per spike, number of spikelets per spike, harvest index, biomass and thousand-grain weight (g) were measured under the study. The data obtained from two locations were subjected to the biometrical analysis that included heritability and genetic advance in percent mean. Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability (h^2bs) and genetic advance over a mean (GAM) were estimated by the formula suggested by Burton and De Vane (1953), Johnson et al. (1955) and Hanson et al. (1956).

Table 1: List of genotypes used

Germplasm lines			Advanced breeding lines
DIC-1	DIC-39	DIC-74	DDK 50033
DIC-4	DIC-43	DIC-76	DDK 50505
DIC-9	DIC-44	DIC-77	DDK 50444
DIC-12	DIC-45	DIC-83	DDK 50507
DIC-13	DIC-46	DIC-88	**Checks**
DIC-14	DIC-47	DIC-91	Kharchia 65 (Bread wheat, only salt tolerant donor)
DIC-15	DIC-48	DIC-92	KRL 99 (Bread wheat, Salt tolerant released variety,
DIC-17	DIC-49	DIC-93	CCSRI, Karnal)
DIC-18	DIC-50	DIC-101	KRL 3-4 (Bread wheat, Salt tolerant released variety,
DIC-19	DIC-68	DIC-102	CCSRI, Karnal)
DIC-21	DIC-70	DIC-103	IC 0408331 (Bread wheat, salt tolerant genetic stock,
DIC-22	DIC-71	DIC-104	NBPGR)
DIC-23	DIC-72	DIC-105	DDK 1029 (Dicoccum wheat, high yielding variety)
DIC-26	DIC-73	DIC-106	
DIC-107	DIC-94	DIC-95	UAS 334 (Bread wheat, high yielding variety)
DIC-99			

Table 2: Soil pH and Electrical conductivity of saline and control plot at different stages of crop

Crop stage	Soil layer	Saline		Control	
		pH	EC	pH	EC
Sowing	Top layer (0-20 cm)	8.01	6.56	8.02	2.89
	Bottom layer (20-40 cm)	7.98	6.51	8.01	3.01
Booting	Top layer (0-20 cm)	7.8	6.11	7.7	2.21
	Bottom layer (20-40 cm)	7.89	5.89	7.86	2.31
Grain filling	Top layer (0-20 cm)	8.02	6.02	7.95	3.32
	Bottom layer (20-40 cm)	7.77	6.11	7.99	3.11
Harvesting	Top layer (0-20 cm)	7.81	6.31	8.03	3.1
	Bottom layer (20-40 cm)	7.62	6.29	7.56	2.98

3. Results and Discussion

Salinity has affected all the traits under study, grain yield has reduced significantly. Traits like spikelets per spike, days to maturity, and days to fifty per cent flowering are least affected by salt stress (Table 3). All the traits showed a significant difference for all the traits under observation under both saline and control condition. It is interesting to note that germplasm exhibited wide variation for all the traits indicating the existence of useful genetic variability among the entries studied (Table 4). Grain yield and yield attributes like tillers per meter, biomass, spikelets per spike and harvest index were showing high PCV, and high GCV, coupled with high heritability and GAM, under both saline and control condition. Physiological traits like SPAD and NDVI showed low to moderate PCV, GCV, heritability and GAM values, morphological traits like germination per cent, days to 50 per cent flowering and days to maturity showed low PCV, GCV values with high heritability and moderate GAM values for traits days to 50 per cent flowering and days to maturity under both saline and control conditions (Fig1).

Salt-tolerant wheat varieties are considered to be a viable and effective strategy for reducing the harmful effects of salt stress (Ashraf and O'Leary, 1996; Flowers and Yeo, 1995; Singh and Rana, 1985). Many efforts have been made in the past to develop salinity-tolerant wheat. Using traditional breeding procedures, successful results have been reached in the form of varieties such as KRL 19, KRL 1-4, KRL 210, and others (Shahbaz and Ashraf, 2013), no such efforts are made to breed for a salt-tolerant dicoccum wheat genotype or to identify a salt tolerant dicoccum wheat genotype. However, a significant increase in wheat grain production under salinity stress has yet to be achieved. Low genetic variability for this characteristic in the genetic pool and less targeted studies for salinity tolerance in wheat may be the cause of low improvement in salinity tolerance in wheat (Jones and Gorham, 2002), especially dicoccum wheat. With these considerations in mind, the current study was carried out to investigate the advantages of the existing variation available in dicoccum wheat or gene pools and to identify the most diverse genotypes to be used in a hybridization program to produce the most potential salt-tolerant recombinants for various morpho-physiological, yield, yield attributes, and quality traits.

Morpho-physiological characters like days to maturity, days to flowering, plant height, SPAD and NDVI were showing low to moderate PCV and GCV coupled with low to moderate heritability and genetic advance mean under both saline and control conditions, which indicated that the influence of the environment for expression of these characters was more and selection would be ineffective. The majority of yield and yield attributes were showing moderate to high PCV and GCV indicates the little influence of the environment on the expression of the character. High heritability and GAM under both stress and non-stress condition was recorded as high, which indicates that most likely the heritability was due to additive gene effects and the effectiveness of these traits when considered for selection. Similar findings were reported by earlier workers like Dharmendraand Singh (2010), Dhonde *et al*. (2000), Sharma and Garg (2002), Ehdaie and Waines (1989), Badole *et al*. (2010), Mohammed *et al*. (2011),Fellahi *et al*. (2013)and Srivijay *et al*. (2022).

Correlation analysis is a useful method for determining the extent of the seed yield's association with other yield-influencing traits. The correlation studies indicate the traits indirectly contribute to yield. The findings of the association studies for saline condition are summarized in Table 5. Under the saline condition, only the harvest index showed a positive significant association with grain yield and traits like tillers per meter, biomass, spikelets per spike, spike length, plant height, germination per cent, days to 50 per cent flowering and days to maturity were showing a non-significant positive correlation with grain yield. Under control condition, biomass, harvest index, plant height, days to 50 per cent flowering and days to maturity were showing a positive significant association with grain yield and traits like spikelets per spike and SPAD (booting stage) were associated negatively and significantly with grain yield.

Table 3: ANOVA for alpha lattice design for different traits under saline and control condition

Sl.no	Trait	Saline					Control				
		Mean	**CV**	**SE**	**SS**	**MSS**	**Mean**	**CV**	**SE**	**SS**	**MSS**
1	GY	19.88	7.57	10.65	300780.77	5013.01	36.23	0.54	13.78	909783.54	15163.05
2	TPM	93.81	2.21	1.47	126717.16	2111.95	122.02	2.00	1.72	78828.97	1313.82
3	BM	84.01	0.25	14.56	8196229.52	136603.82	114.24	13.17	10.64	11144858.62	185747.64
4	SPS	19.43	4.81	0.66	6589.48	109.82	20.27	5.48	0.79	10811.57	180.19
5	SL	6.63	1.42	0.07	144.67	2.41	8.58	4.77	0.29	195.92	3.27
6	GPS	29.28	6.20	1.28	3666.52	61.11	34.23	5.71	1.38	5732.57	95.54
7	PH	81.35	1.79	1.03	15328.41	255.47	94.79	3.47	2.32	8652.79	144.21
8	GP	92.89	4.21	2.76	1307.11	21.79	94.44	4.02	2.68	826.10	13.77
9	TGW	29.92	1.52	0.32	2456.77	40.95	35.42	1.58	0.40	724.39	12.07
10	DFF	60.01	0.81	0.35	3500.49	58.34	62.15	0.63	0.28	3426.25	57.10
11	DM	107.37	0.37	0.28	4329.60	72.16	109.52	0.37	0.28	4360.24	72.67
12	HI	25.25	7.97	1.42	10426.69	173.78	33.38	15.95	3.76	9622.01	160.37
13	NDVI	0.53	3.10	0.01	1.23	0.02	0.65	13.92	0.06	0.84	0.01
14	SPAD	43.50	13.15	4.04	1818.11	30.30	43.88	11.61	3.60	2203.52	36.73

GY- Grain yield (q/ha), TPM-Tillers per meter, BM- Biomass (q/ha), SPS- Spikelets per spike, SL-Spike length (cm), GPS-Grains per spike, PH-Plant height (cm), GP-Germination percentage (per cent), TGW-Thousand grain weight (g), DFF- Days to 50 per cent flowering, DM-Days to maturity, HI-Harvest index, NDVI- anthesis stage, SPAD-Chlorophyll content before anthesis.

Table 4: Genetic variability parameters for morpho-physiological traits in wheat genotypes grown under saline and control conditions

Sl.no	Trait	Saline					Control				
		Range	PCV	GCV	h^2	GAM	Range	PCV	GCV	h^2	GAM
1	**GY**	9.44-26.32	19.34	24.60	95.50	49.52	20.21-54.28	24.03	24.03	99.65	49.49
2	**TPM**	74-156	34.64	34.60	99.80	71.21	64-175	21.01	20.96	99.50	43.08
3	**BM**	27.32-189.77	31.11	31.11	99.59	64.08	65.99-220.36	26.67	25.00	87.80	48.25
4	**SPS**	9.50-36.50	38.13	37.98	99.20	77.92	11.00-54.00	46.83	46.67	99.30	95.80
5	**SL**	4.44-11.41	16.57	16.54	99.60	34.00	6.21-11.79	14.89	14.50	94.90	29.10
6	**GPS**	15-40.50	18.88	18.36	94.60	36.80	23.00-52.00	20.19	19.78	96.00	39.93
7	**PH**	59.08-104.73	13.89	13.84	99.20	28.38	73.96-107.84	8.96	8.62	92.50	17.07
8	**GP**	85.00-96.50	3.55	1.94	29.90	2.19	90.00-99.00	2.78	0.59	24.60	-0.26
9	**TGW**	20.15-39.89	15.12	15.08	99.50	30.99	28.60-43.03	6.94	6.85	97.40	13.92
10	**DFF**	48.73-67.59	9.00	8.98	99.60	18.47	50.65-70.23	8.60	8.59	99.70	17.67
11	**DM**	95.20-119.12	5.59	5.59	99.80	11.50	95.20-119.12	5.50	5.50	99.80	11.31
12	**HI**	10.52-46.05	36.91	36.48	97.70	74.27	17.62-49.94	26.83	24.34	82.30	45.50
13	**NDVI**	0.32-0.75	19.04	18.92	98.70	38.71	0.44-0.78	12.92	8.37	42.00	11.18
14	**SPAD**	35.01-54.29	8.95	2.52	7.90	1.46	35.63-53.08	9.77	5.29	29.30	5.89

GY- Grain yield (q/ha), TPM-Tillers per meter, BM- Biomass (q/ha), SPS- Spikelets per spike, SL-Spike length (cm), GPS-Grains per spike, PH-Plant height (cm), GP-Germination percentage (per cent), TGW-Thousand grain weight (g), DFF- Days to 50 per cent flowering, DM-Days to maturity, HI-Harvest index, NDVI- anthesis stage, SPAD-Chlorophyll content before anthesis.

Fig. 1: Variability, Genetic advance as percent of mean and heritability (broad sense) in wheat genotypes for the different traits under saline (A) and control condition (B)

Table 5: Phenotypic correlation among morpho-physiological and yield traits in wheat genotypes under the saline and control condition

		GY	**TPM**	**BM**	**SPS**	**SL**	**GPS**	**PH**	**GP**	**TGW**	**DFF**	**DM**	**HI**	**NDVI**	**SPAD**
GY	**S**	1													
	C	1													
TPM	**S**	0.250^{NS}	1												
	C	0.125^{NS}	1												
BM	**S**	0.042^{NS}	0.320^{*}	1											
	C	0.382^{**}	0.165^{NS}	1											
SPS	**S**	0.071^{NS}	-0.049^{NS}	-0.244^{NS}	1										
	C	-0.400^{**}	-0.128^{NS}	-0.054^{NS}	1										
SL	**S**	0.208^{NS}	0.036^{NS}	0.168^{NS}	0.198^{NS}	1									
	C	-0.145^{NS}	-0.106^{NS}	0.143^{NS}	0.682^{**}	1									
GPS	**S**	0.001^{NS}	-0.036^{NS}	0.011^{NS}	0.052^{NS}	0.508^{**}	1								
	C	0.075^{NS}	0.132^{NS}	0.223^{NS}	0.549^{**}	0.722^{**}	1								
PH	**S**	0.064^{NS}	0.170^{NS}	0.246^{NS}	-0.262^{*}	0.239^{NS}	0.454^{**}	1							
	C	0.471^{**}	0.379^{**}	0.434^{**}	-0.389^{**}	-0.005^{NS}	0.110^{NS}	1							
GP	**S**	0.039^{NS}	0.011^{NS}	0.195^{NS}	-0.364^{**}	0.052^{NS}	0.055^{NS}	0.263^{*}	1						
	C	0.137^{NS}	-0.139^{NS}	0.023^{NS}	-0.143^{NS}	-0.019^{NS}	-0.203^{NS}	-0.014^{NS}	1						
TGW	**S**	-0.065^{NS}	-0.024^{NS}	0.070^{NS}	0.189^{NS}	0.112^{NS}	0.166^{NS}	0.216^{NS}	-0.033^{NS}	1					
	C	0.221^{NS}	0.111^{NS}	0.121^{NS}	-0.121^{NS}	-0.153^{NS}	-0.137^{NS}	0.201^{NS}	0.029^{NS}	1					
DFF	**S**	0.009^{NS}	0.297^{*}	0.041^{NS}	-0.461^{**}	-0.272^{*}	-0.053^{NS}	0.170^{NS}	0.066^{NS}	-0.337^{**}	1				
	C	0.527^{**}	0.078^{NS}	0.163^{NS}	-0.693^{**}	-0.419^{**}	-0.143^{NS}	0.395^{**}	0.096^{NS}	0.064^{NS}	1				
DM	**S**	0.073^{NS}	0.361^{**}	0.117^{NS}	-0.461^{**}	-0.276^{*}	-0.031^{NS}	0.180^{NS}	0.072^{NS}	-0.327^{**}	0.941^{**}	1			
	C	0.486^{**}	0.163^{NS}	0.159^{NS}	-0.735^{**}	-0.458^{**}	-0.204^{NS}	0.419^{**}	0.086^{NS}	0.097^{NS}	0.958^{**}	1			
HI	**S**	0.494^{**}	-0.019^{NS}	-0.640^{**}	0.309^{*}	0.006^{NS}	0.006^{NS}	-0.041^{NS}	-0.020^{NS}	-0.002^{NS}	-0.135^{NS}	-0.127^{NS}	1		
	C	0.504^{**}	-0.044^{NS}	-0.565^{**}	-0.307^{*}	-0.268^{*}	-0.152^{NS}	0.047^{NS}	0.070^{NS}	0.104^{NS}	0.293^{*}	0.271^{*}	1		
NDVI	**S**	-0.079^{NS}	-0.080^{NS}	-0.307^{*}	-0.172^{NS}	-0.152^{NS}	-0.130^{NS}	-0.381^{**}	-0.065^{NS}	-0.318^{*}	0.084^{NS}	0.134^{NS}	0.130^{NS}	1	
	C	0.121^{NS}	-0.050^{NS}	-0.025^{NS}	-0.118^{NS}	-0.319^{*}	-0.131^{NS}	0.058^{NS}	0.007^{NS}	0.051^{NS}	0.143^{NS}	0.135^{NS}	0.161^{NS}	1	
SPAD	**S**	-0.257^{*}	-0.291^{*}	0.001^{NS}	0.131^{NS}	0.075^{NS}	-0.161^{NS}	-0.216^{NS}	-0.083^{NS}	0.013^{NS}	-0.338^{**}	-0.319^{*}	-0.145^{NS}	-0.009^{NS}	1
	C	-0.261^{*}	-0.323^{*}	-0.093^{NS}	0.195^{NS}	0.013^{NS}	-0.119^{NS}	-0.274^{*}	0.003^{NS}	-0.119^{NS}	-0.298^{*}	-0.265^{*}	-0.231^{NS}	-0.043^{NS}	1

GY- Grain yield (q/ha), TPM-Tillers per meter, BM- Biomass (q/ha), SPS- Spikelets per spike, SL-Spike length (cm), GPS-Grains per spike, PH-Plant height (cm), GP-Germination percentage (per cent), TGW-Thousand grain weight (g), DFF- Days to 50 per cent flowering, DM-Days to maturity, HI-Harvest index, NDVI- anthesis stage, SPAD-Chlorophyll content before anthesis.

		TPM	**BM**	**SPS**	**SL**	**GPS**	**PH**	**GP**	**TGW**	**DFF**	**DM**	**HI**	**NDVI**	**SPAD**

TPM	**S**	**0.017**	0.003	-0.001	0.005	0.007	0.008	0.003	0.003	0.000	-0.001	0.003	-0.003	-0.003
	C	**0.048**	0.008	-0.006	-0.005	0.006	0.018	-0.007	0.005	0.004	0.008	-0.002	-0.002	-0.016
BM	**S**	0.171	**0.834**	-0.203	0.140	0.009	0.205	0.163	0.058	0.039	0.087	-0.534	-0.256	0.001
	C	0.159	**0.967**	-0.053	0.138	0.216	0.420	0.023	0.117	0.157	0.159	-0.547	-0.024	-0.090
SPS	**S**	-0.002	-0.006	**0.024**	0.005	0.001	-0.006	-0.009	0.004	-0.011	-0.011	0.007	-0.004	0.003
	C	0.006	0.003	**-0.045**	-0.031	-0.025	0.018	0.007	0.006	0.032	0.033	0.014	0.005	-0.009
SL	**S**	0.005	0.003	0.003	**0.017**	0.009	0.004	0.001	0.002	-0.005	-0.005	0.000	-0.003	0.001
	C	0.001	-0.001	-0.003	**-0.004**	-0.003	0.000	0.000	0.001	0.002	0.002	0.001	0.001	0.000
GPS	**S**	0.008	0.000	0.001	0.011	**0.021**	0.009	0.001	0.004	-0.001	-0.001	0.000	-0.003	-0.003
	C	0.013	0.022	0.053	0.070	**0.096**	0.011	-0.020	-0.013	-0.014	-0.020	-0.015	-0.013	-0.012
PH	**S**	-0.019	-0.009	0.010	-0.009	-0.017	**-0.038**	-0.010	-0.008	-0.007	-0.006	0.002	0.015	0.008
	C	-0.011	-0.012	0.011	0.000	-0.003	**-0.028**	0.000	-0.006	-0.011	-0.012	-0.001	-0.002	0.008
GP	**S**	0.005	0.005	-0.009	0.001	0.001	0.007	**0.026**	-0.001	0.002	0.002	-0.001	-0.002	-0.002
	C	-0.008	0.001	-0.008	-0.001	-0.012	-0.001	**0.057**	0.002	0.005	0.004	0.004	0.000	0.000
TGW	**S**	0.005	0.002	0.006	0.003	0.005	0.007	-0.001	**0.030**	-0.010	-0.010	0.000	-0.010	0.000
	C	0.006	0.006	-0.006	-0.008	-0.007	0.011	0.002	**0.053**	0.003	0.005	0.006	0.003	-0.006
DFF	**S**	0.000	0.001	-0.013	-0.008	-0.001	0.005	0.002	-0.010	**0.029**	0.027	-0.004	0.002	-0.010
	C	0.021	0.042	-0.182	-0.110	-0.039	0.102	0.024	0.016	**0.261**	0.249	0.075	0.041	-0.075
DM	**S**	0.000	-0.001	0.003	0.002	0.000	-0.001	0.000	0.003	-0.007	**-0.008**	0.001	-0.001	0.003
	C	-0.040	-0.039	0.173	0.108	0.048	-0.099	-0.018	-0.020	-0.225	**-0.235**	-0.061	-0.033	0.059
HI	**S**	0.190	-0.790	0.382	0.008	0.008	-0.051	-0.025	-0.002	-0.168	-0.146	**1.234**	0.160	-0.179
	C	-0.045	-0.579	-0.314	-0.274	-0.156	0.048	0.072	0.106	0.295	0.264	**1.025**	0.165	-0.236
NDVI	**S**	-0.013	-0.024	-0.013	-0.012	-0.010	-0.030	-0.005	-0.025	0.006	0.010	0.010	**0.078**	-0.001
	C	-0.003	-0.001	-0.007	-0.018	-0.008	0.003	0.000	0.003	0.009	0.008	0.009	**0.058**	-0.003
SPAD	**S**	0.001	0.000	0.000	0.000	0.001	0.001	0.000	0.000	0.001	0.001	0.001	0.000	**-0.003**
	C	-0.034	-0.010	0.021	0.001	-0.013	-0.029	0.000	-0.013	-0.031	-0.027	-0.025	-0.005	**0.106**
GY	**S**	0.125	0.382	-0.400	-0.145	0.075	0.471	0.137	0.221	0.519	0.478	0.504	0.121	-0.261
	C	0.389	0.038	0.142	0.172	0.036	0.149	0.158	0.065	0.111	0.046	0.708	0.040	0.211

Table 6: Direct (diagonal) and indirect effects under saline and control condition of seventeen characters on grain yield per hectare at phenotypic level in wheat genotypes

GY- Grain yield (q/ha), TPM-Tillers per meter, BM- Biomass (q/ha), SPS- Spikelets per spike, SL-Spike length (cm), GPS-Grains per spike, PH-Plant height (cm), GP-Germination percentage (per cent), TGW-Thousand grain weight (g), DFF- Days to 50 per cent flowering, DM-Days to maturity, HI-Harvest index, NDVI- anthesis stage, SPAD-Chlorophyll content before anthesis.

In the present study, path coefficients were computed considering grain yield as a dependent variable under both saline and control conditions. Traits with significant values of correlation coefficients with dependent characters were only considered for path analysis. The results from path analysis are presented in Tables 6. It was evident from the Tables that, residual values for the phenotypic path coefficient with grain yield as a dependent trait was 0.29 under saline condition, while for the control condition, the residue was 0.27. Traits like harvest index, biomass, tillers per meter and days to 50 per cent flowering were showing a high direct effect on grain yield and traits like days to maturity and plant height was showing a negative direct effect on grain yield under both saline and control condition. Spikelets per spike, spike length, SPAD and NDVI were showing a positive direct effect on grain yield under saline condition and a negative direct effect on grain yield under control condition.

The results of the association and path analysis study indicated that wheat genotypes with early flowering and early maturing traits are suitable for saline condition. Similarly, an increased harvest index is suitable for higher grain yield under saline condition. Long spike length, a greater number of tillers, grains per spike, high thousand-grain weight and biomass contribute indirectly towards higher yield under saline environment. Similar findings were reported by earlier workers like Ehsanzadeh *et al.* (2009), Munns *et al.* (2006), Yagmur and Kaydan (2007) and Baky *et al*. (2008).

Conclusion

Under salt stress condition, most of the yield and yield attributing traits were severely affected, the traits such as tillers per meter, grains per spike, biomass, and grain yield which exhibited a drastic reduction in mean performance under the saline condition as compared to control condition. On the contrary, traits like spike length, spikelets per spike, and thousand-grain weight were least affected probably due to the compensation effect resulting from reduced tillers per meter and grains per spike. Under saline condition, traits like harvest index and biomass were showing a high direct effect on grain yield, so the selection for these traits may give better salt tolerant genotypes. It is concluded from the present study that the dicoccum wheat germplasms can serve as the most potential donors for salt tolerance. Further, few promising accessions can be registered as national genetic stocks or identified as varieties. This is a kind of study, which indicates the possibility of exploration of the unrealized potential of wheat species to address the global issue of hunger and increasing population, by wheat production in the unproductive saline soils.

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