Original Research Article

Studies on Genetic Diversity and Stress Indices for Salinity Tolerance in *Triticum dicoccum*

Abstract

Salinity stands out as a crucial abiotic stress factor that significantly impacts both crop yield and quality. Wheat, considered a moderately salt-tolerant crop, offers a wealth of variability and diversity within its species, presenting an accessible avenue for enhancing wheat's salt tolerance. Consequently, this study investigated the extent of genetic diversity for salt tolerance among sixty *Triticum dicoccum* germplasm accessions. In both saline and control condition, the genotypes were divided into three and nine separate clusters respectively, showing that there was a significant level of genetic variability among the genotypes by multivariate analysis. It was observed that biomass was the largest contributor (85.19 %) to the divergence in the saline situation. Among the yield parameters under saline condition, tillers per meter followed by thousand-grain weight and spike length were observed to be important. Thirteen genotypes were salt-tolerant, according to the Stress susceptibility index (SSI). The stress tolerance index (STI) was defined as a useful tool for determining the high yield and potential stress tolerance of genotypes. Based on the stress tolerance index, only eight genotypes were said to be tolerant.

Keywords: Dicoccum wheat, saline, diversity, clusters and stress index

Introduction

The nutrient-rich cereal wheat is farmed in a wide range of conditions; it covers over 217 million hectares globally, ranking first among all crops in terms of acreage, and produces around 731 million tonnes per year (USDA, 2018). Wheat (*Triticum aestivum* L.) is one of the world's most frequently farmed cereal crops and one of the world's most important staple foods for about 2.5 billion people. Cereals are essential in satisfying the expanding global food demand, especially in underdeveloped nations where cereal-based farming is the only source of nutrients and calories (Alexandratos and Bruinsma, 2012, Shiferaw *et al*., 2013). Wheat is the most significant food crop in North Africa, West Asia, and Central Asia, accounting for more than half of the calories consumed. In terms of calories and dietary consumption, wheat, along with rice, is one of the most important sources of protein in the least-developed and middle-income nations.

Triticum dicoccum, commonly known as emmer wheat, holds significant importance due to its historical, nutritional, and genetic contributions. Emmer wheat is one of the oldest cultivated grains, dating back thousands of years, and played a crucial role in the development of early human civilizations. Its nutritional value, including dietary fiber, protein, and essential nutrients, makes it a valuable dietary component (D'Antuono et al, 2002). Moreover, emmer wheat's genetic diversity is a vital resource for wheat breeding programs, enhancing the resilience of modern wheat varieties. Its adaptability and resistance to pests and diseases promote sustainable agriculture. Emmer wheat remains a source of dietary variety and cultural heritage in regions where it is cultivated, contributing to local food security and traditions. Furthermore, the grain's lower gluten content makes it suitable for individuals with mild gluten sensitivities, though it's not recommended for those with celiac disease Lupo L. (2017).

Biological and abiotic stress, often known as environmental stresses, have a significant impact on wheat grain yield (Shamsi *et al*., 2011; Khavarinejad and Karimov, 2012). Salinity is one of the most important abiotic stresses affecting crop yield and quality (Greenway and Munns, 1980), affecting around 7 percent of the world's total land area (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 percent 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).

Wheat morphophysiological and agronomic traits play a key role in assessing the value of each trait in enhancing yield, therefore these qualities were employed in breeding projects that resulted in higher yields and the introduction of commercial varieties that can survive salt stress. The selection of genotypes with all conceivable yield contributing traits is the most critical requirement in any crop improvement program. The main factor to consider when making a selection is genotype variability for grain yield and yield component characteristics. Further, such information may be great to set the future path for the salt tolerance breeding program in wheat.

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 (Table-1) 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 2 represents the 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.

Morphological traits like germination percent, days to fifty percent flowering, days to maturity and plant height, physiological traits (SPAD and NDVI) at booting, anthesis and grain filling stages, 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 statistical analysis for genetic divergence was done using Mahalanobis-D^2 statistics (Mahalanobis, 1936) and the clustering of genotypes was done using the Tocher method (Rao, 1952). Character contribution towards genetic divergence was computed using the method given by Singh and Chaudhary (1977). Stress indices *viz.,* Stress Susceptibility Index (Fischer and Maurer, 1978) and Stress Tolerance Index (Fernandez, 1992) were calculated to classify genotypes into salt tolerant and salt susceptible. The genotypes were grouped in three different tolerance categories based on stress susceptibility index as shown under (Khanna-chopra and Viswanathan, 1999). The genotypes were grouped in three different tolerance categories based on stress susceptibility index as shown under (Sang et al., 2014). Following are the formulas to calculate the indices, where Ys is the yield under saline condition and Yp is the control condition, - indicated their respective means.

$$SSI = \frac{1-(Ys/Yp)}{1-(\bar{Ys}/\bar{Yp})} \qquad STI = \frac{(\bar{Ys} \times Yp)}{(Yp)^2}$$

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, CCSRI, Karnal)
DIC-17	DIC-49	DIC-93	
DIC-18	DIC-50	DIC-101	KRL 3-4 (Bread wheat, Salt tolerant released variety, CCSRI, Karnal)
DIC-19	DIC-68	DIC-102	
DIC-21	DIC-70	DIC-103	IC 0408331 (Bread wheat, salt tolerant genetic stock, NBPGR)
DIC-22	DIC-71	DIC-104	
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)

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

Results and Discussion

Salinity affected all the traits under study and grain yield has reduced significantly. Traits like spikelets per spike, days to maturity, and days to fifty percent flowering are least affected by salt stress (Table 3). All the traits showed a significant difference for all the traits under saline and control condition. 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 genotypes. 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.

The sum of squares of the difference between the mean values obtained between any two genotypes for all morpho-physiological, yield, and yield attributing traits in sixty wheat genotypes under two environments *viz.,* saline and control condition were used for the final grouping of the genotypes. The genetic diversity analysis was carried out using Tocher's (Rao, 1952) approach, which was used to arrange 60 wheat genotypes into various clusters by considering the estimated D^2 value as the square of the generalized distance. The pattern of distribution of genotypes into various clusters under saline and control condition was presented in Tables 4 and 5 respectively. Under saline condition, three clusters were created by combining all 60 wheat genotypes in such a way that the genotypes in each cluster had a lower D^2 value than the genotypes in the other clusters. Cluster I had the most genotypes *i.e.*, 58 genotypes, followed by Cluster II and III the ones that were solitary with genotypes DIC 18 and DIC 94 respectively. Nine clusters were formed under control condition, cluster I was the largest with 16 genotypes, followed by cluster III and cluster V with 12 genotypes each, cluster II had 7 genotypes which included the checks. Cluster IV had six genotypes and Cluster VI had four genotypes, cluster VII, VIII, IX were solitary clusters with genotypes KRL 210, UAS 334 and DIC103 respectively.

The divergence analysis showed that all sixty genotypes were grouped into three clusters in saline condition and seven clusters, under control condition. A maximum number of genotypes were grouped into cluster I under both saline and control condition. Genotypes namely DIC 18 of cluster II and DIC 94 of cluster III in saline environment were showing high inter-cluster distance. Hybridization between the genotypes of these clusters might yield desirable segregants (Table 6). These results are supported by those of Mundiyara *et al*. (2013), Vinod *et al*. (2014), Singh *et al*. (2015), Ibrahim and Arafa (2020) and Srivijay *et al*. (2022).

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-I	0.53	3.10	0.01	1.23	0.02	0.65	13.92	0.06	0.84	0.01
14	NDVI-II	0.59	3.19	0.01	1.30	0.02	0.65	14.30	0.07	0.79	0.01
15	NDVI-III	0.62	17.95	0.08	1.04	0.02	0.60	19.03	0.08	0.98	0.02
16	SPAD-I	43.50	13.15	4.04	1818.11	30.30	43.88	11.61	3.60	2203.52	36.73
17	SPAD-II	37.71	12.31	3.28	1646.48	27.44	41.23	10.46	3.05	1905.92	31.77
18	SPAD-III	36.69	19.55	5.07	1823.46	30.39	41.48	12.29	3.60	2128.23	35.47

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 booting and grain filling stages, SPAD- Chlorophyll content before anthesis, booting and grain filling stages.

The highest intra-cluster distance was obtained by cluster I (167.61), and between clusters II and III highest inter-cluster distance (863.27) was obtained under saline condition, followed by clusters I and III (589.92), represented in Table 6. Under non-stress condition (Table 7), cluster IV (44.50) showed the highest intra-cluster distance, clusters IX and VII were showing the highest inter-cluster (222.80) distance, followed by cluster IX and cluster II (211.02). The cluster means for all the characters under saline conditions are represented in Table 8. The solitary cluster III had early flowering having the genotype DIC-94 (55 days), high grain yield (2,735 kg/ha) and the highest mean values for biomass (18,977 kg/ha), number of tillers per meter (157.00), spike length (11.41cm), germination percent (96.50 percent), plant height (104.73 cm), NDVI at anthesis stage (0.70), lowest NDVI at booting stage (0.37), chlorophyll content at anthesis stage (34.68), number of spikelets per spike (15.00) and least harvest index of 14.40 percent were recorded by this cluster. Under control condition (Table 9), cluster IX with genotype DIC 103 had the highest grain yield (5428.62 kg/ha), biomass (12965.64 kg/ha), late flowering (69 days), late maturing (118 days), highest harvest index (42.06 %) and highest NDVI at grain filling stage (0.74). Cluster VII with genotype KRL 210 was showing the highest mean values for number of spikelets per spike (51), spike length (11.08 cm) and highest grains per spike (49.50).

The percent contribution of each character towards total genetic divergence under saline and control condition is presented in Table 10. It was observed that under saline condition, biomass (85.19 %) was the largest contributor to the divergence. Days to maturity (6.28 %), tillers per meter row (4.32 %) ranking III and IV contributed the highest to the diversity among various yield attributes. On the contrary, the contribution of other yield attributes such as thousand-grain weight (1.69 %), spikelets per spike (0.33 %), spike length (0.93 %) and grains per spike (0.05 %) was less. Among the morphological traits, days to flowering 0.27 percent to diversity. The NDVI reading at the booting stage (0.16 %) and anthesis (0.11) were observed to be important. Under control condition, it was observed that among various groups of traits in general, the contribution of grain weight (66.12 %) was found highest, followed by NDVI at the anthesis stage (12.24 %), days to maturity (10.49 %), tillers per meter (5.14 %), days to 50 percent flowering (3.39 %) and spikelets per spike (1.97 %) respectively.

Table 4: Clustering of wheat genotypes based on morpho-physiological, yield and yield attributing traits under saline condition

Cluster	Number of genotypes	Genotypes
Cluster I	1	DIC-1, DIC-4, DIC-9, DIC-12, DIC-13, DIC-14, DIC-15, DIC-17, DIC-19, DIC-21, DIC-22, DIC-23, DIC-26, DIC-39, DIC-43, DIC-44, DIC-45, DIC-46, DIC-47, DIC-48, DIC-49, DIC-50, DIC-68, DIC-70, DIC-71, DIC-72, DIC-73, DIC-74, DIC-76, DIC-77, DIC-83, DIC-88, DIC-91, DIC-92, DIC-93, DIC-95, DIC-99, DIC-101, DIC-102, DIC-103, DIC-104, DIC-105, DIC-106, DIC-107, DDK 50033, DDK 50505, DDK 50444, DDK 50507, KRL 210 , KRL 19, UAS 304, UAS 334, UAS 428, DDK 1029, HD 2009, Kharchia 65, KRL 3-4, IC 0408331
Cluster II	1	DIC-18
Cluster III	1	DIC-94

Table 5: Clustering of wheat genotypes based on morpho-physiological, yield and yield attributing traits under control condition

Cluster	Number of genotypes	Genotypes
Cluster I	16	DIC-1, DIC-4, DIC-18, DIC-23, DIC-26, DIC-12, DIC-15, DIC-50, DIC-72, DIC-91, DIC-46, DIC-47, DIC-76, DDK 50033, DIC-83, DIC-93
Cluster II	7	KRL 3-4, IC 0408331, UAS 304, HD 2009, Kharchia 65, KRL 19, UAS 428
Cluster III	12	DIC-13, DIC-19, DIC-22, DIC-44, DIC-68, DIC-70, DIC-74, DIC-95, DIC-99, DIC-102, DDK 50505, DDK 1029
Cluster IV	6	DIC-14, DIC-43, DIC-94, DIC-39, DIC-17, DIC-71
Cluster V	12	DIC-2, DIC-45, DIC-48, DIC-49, DIC-77, DIC-92, DIC-101, DIC-104, DIC-105, DIC-106, DIC-107, DDK 50507
Cluster VI	4	DIC-73, DIC-88, DDK 50444, DIC-9
Cluster VII	1	KRL 210
Cluster VIII	1	UAS 334
Cluster IX	1	DIC-103

Table 6: Intra and inter-cluster D^2 values in wheat genotypes under saline condition

	Cluster I	Cluster II	Cluster III
Cluster I	167.61		
Cluster II	313.33	0.00	
Cluster III	589.92	863.27	0.00

Table 7: Intra and inter-cluster D^2 values in wheat genotypes under control condition

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX
Cluster I	33.46								
Cluster II	121.21	36.88							
Cluster III	62.88	78.11	37.87						
Cluster IV	53.79	106.30	64.74	44.18					
Cluster V	67.63	167.30	113.63	81.41	44.50				
Cluster VI	100.58	62.88	56.75	94.01	153.03	40.96			
Cluster VII	136.01	51.14	90.81	130.53	185.17	75.55	0.00		
Cluster VIII	71.58	79.80	58.08	76.65	111.12	86.55	83.88	0.00	
Cluster IX	99.13	211.02	150.29	125.55	64.01	191.64	222.80	146.63	0.00

Table 8: Cluster means for various quantitative traits in wheat genotypes under saline situation

	GY	**TPM**	**BM**	**SPS**	**SL**	**GPS**	**PH**	**GP**	**TGW**
Cluster I	1969.64	91.88	8318.46	19.54	6.53	29.15	80.78	92.77	29.89
Cluster II	2351.50	144.50	2732.50	17.50	7.88	33.50	91.30	96.50	30.86
Cluster III	2735.00	157.00	18977.00	15.00	11.41	32.50	104.72	96.50	30.94

	DFF	**DM**	**HI**	**NDVI-I**	**NDVI-II**	**NDVI-III**	**SPAD-I**	**SPAD-II**	**SPAD-III**
Cluster I	60.06	107.44	25.17	0.53	0.59	0.62	43.57	37.80	36.61
Cluster II	62.00	106.64	41.03	0.65	0.65	0.70	35.01	35.70	36.92
Cluster III	55.00	104.01	14.41	0.37	0.70	0.61	47.59	34.67	41.15

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 booting and grain filling stages, SPAD- Chlorophyll content before anthesis, booting and grain filling stages.

Table 9: Cluster means for various quantitative traits in wheat genotypes under control situation

	GY	TPM	BM	SPS	SL	GPS	PH	GP	TGW
Cluster I	3940.76	117.06	12199.62	15.91	7.89	31.56	96.47	94.38	36.32
Cluster II	2480.07	112.56	9990.45	35.56	9.74	34.63	86.52	93.94	35.30
Cluster III	3138.67	116.42	11040.57	18.00	8.51	33.46	94.82	94.46	34.79
Cluster IV	3653.37	157.08	12281.30	19.33	9.08	39.75	99.50	94.08	35.89
Cluster V	4786.99	131.04	12743.90	17.50	8.66	36.38	100.49	95.08	35.55
Cluster VI	2383.67	125.63	7994.25	13.63	7.52	27.75	89.38	94.63	34.22
Cluster VII	2429.39	81.00	6599.81	51.00	11.08	49.50	76.33	92.50	31.33
Cluster VIII	3727.00	74.50	11160.66	33.00	7.79	31.50	78.00	94.50	34.54
Cluster IX	5428.62	99.50	12965.64	17.00	9.95	37.50	94.17	95.00	34.52

	DFF	DM	HI	NDVI-I	NDVI-II	NDVI-III	SPAD-I	SPAD-II	SPAD-III
Cluster I	65.62	113.31	35.38	0.67	0.67	0.61	43.79	40.95	40.51
Cluster II	52.06	98.75	25.79	0.59	0.60	0.57	49.02	44.69	45.44
Cluster III	63.13	110.62	30.35	0.68	0.68	0.58	42.90	40.54	41.24
Cluster IV	61.32	108.96	32.01	0.58	0.62	0.56	40.90	38.01	41.18
Cluster V	63.91	111.14	39.18	0.63	0.61	0.62	42.87	40.68	41.38
Cluster VI	64.36	112.94	30.88	0.63	0.63	0.67	42.95	39.93	37.76
Cluster VII	52.84	95.20	37.95	0.72	0.71	0.60	44.46	42.75	42.22
Cluster VIII	52.98	97.62	33.98	0.74	0.74	0.63	46.16	53.00	42.35
Cluster IX	68.92	118.04	42.06	0.70	0.68	0.74	46.99	44.45	44.13

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 booting and grain filling stages, SPAD- Chlorophyll content before anthesis, booting and grain filling stages.

The utility of the D^2 statistic is enhanced by its applicability to estimate the relative contribution of various characters to the total genetic divergence. The feature that contributes the most to divergence is utilized to place a higher emphasis on selecting a cluster for further selection and selecting parents for hybridization. It has been noted that under saline condition, biomass (85.19 %) was the largest contributor to the divergence. This suggests that genotype DIC-94 belonging to cluster III exhibiting a high mean for biomass, grain yield, tillers per meter, spike length, thousand-grain weight, plant height, and germination percent can be a potential source for hybridization program to obtain transgressive segregants. These results are in concordance with Sunilyadav *et al*. (2014) wherein they observed a higher contribution of thousand-grain weight, tillers per meter, days to maturity, days to flowering, and grain yield towards diversity.

Table 10: Per cent contribution of morpho-physiological traits, yield and yield attributes to total genetic diversity under control and saline condition

Sl. No.	Source	Per cent contribution	
		Saline condition	Control condition
1	GY		66.12
2	TPM	4.32	5.14
3	BM	85.19	0.05
4	SPS	0.33	1.97
5	SL	0.93	
6	GPS	0.05	0.11
7	PH	0.66	
8	GP		
9	TGW	1.69	0.38
10	DFF	0.27	3.39
11	DM	6.28	10.49
12	HI		
13	NDVI-I	0.16	
14	NDVI-II	0.11	12.24
15	NDVI-III		
16	SPAD-I		
17	SPAD-II		0.11
18	SPAD-III		

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 booting and grain filling stages, SPAD- Chlorophyll content before anthesis, booting and grain filling stages.

The majority of wheat genotypes are vulnerable to salt stress, resulting in low and unpredictable yields. Because current screening approaches for salinity-related traits are time-consuming and impracticable for most researchers, it is critical to estimate genotype yield under saline and control condition, and tolerance indices are currently being used to quantify the effect of salt on yield. These salt tolerance indices indicate whether the genotypes are salt-tolerant or susceptible to the saline condition. To investigate suitable stress resistance indices for screening of genotypes under salt condition, the grain yield of cultivars under both non-stress and stress condition were measured for calculating different sensitivity and tolerance indices. Among them, stress susceptibility (Table 12) and stress tolerance index (Table 12) have been considered for grouping of genotypes. These indices categorized the sixty wheat genotypes into three categories *viz.,* tolerant, moderately tolerant, and susceptible. The tolerant category of SSI included 14 genotypes. Among 13 tolerant genotypes, eight dicoccum wheat genotypes (DIC-9, DIC-13, DIC-68, DIC-73, DIC-88, DIC-94, DIC-95, DDK 50505), along with five checks *viz.,* KRL 210, UAS 334, Kharchia 65, KRL 3-4, and IC 0408331. Based on the stress tolerance index (STI), only 10 genotypes *viz.,* DIC-26, DIC-48, DIC-92, DIC-101, DIC-104, DIC-107, DDK 50507 and UAS 334 were said to be tolerant.

The stress susceptibility index was evaluated based on the yield ratio of each variety in stressed conditions to non-stressed conditions as compared with the proportions in total varieties. Thus, tolerant cultivars identified with high yield or low in both conditions can have the same amount of SSI, so the selection process based on this index led reformers to make a mistake (Naeimi *et al*., 2008). So, according to the stress-sensitive index, it was observed that 13 genotypes *viz*., eight dicoccum wheat (DIC-9, DIC-13, DIC-68, DIC-73, DIC-88, DIC-94, DIC-95, DDK 50505) and five checks (KRL 210, UAS 334, Kharchia 65, KRL 3-4, IC 0408331) as a tolerant. A similar classification of genotypes using SSI was done for 97 bread-wheat genotypes by Sardouie *et al*. (2014). The stress tolerance index (STI) was defined as a useful tool for determining the high yield and stress tolerance potential of genotypes (Farnandez, 1992). Based on the stress tolerance index, only 8 genotypes were identified as salt tolerant *viz.,* seven dicoccum wheat genotypes (DIC-26, DIC-48, DIC-92, DIC-101, DIC-104, DIC-107, DDK 50507) and check UAS 334. Mevlut and Sait (2011) indicated that the genotypes with >0.9 STI value, usually have high-yielding potential under stress condition even greater differences in two different conditions. Hence, there is still scope for both the indices and generating super salt tolerant varieties.

With respect to dicoccum wheat genotype (DIC-88) based on SSI and few genotypes (DIC-101, DIC-92, DIC-48, DIC-26, DDK 50507) based on STI accept the genotype DIC 101 which is the most promising considering both SSI and STI can be involved in biparental mating to complement the mechanisms operating in both categories to improve both salt tolerance and yield simultaneously. It is clear from the present study that there is a lot of scope for improvement of all these genotypes using the potential donors identified. Genome ‘A’ has the next highest genes or QTLs followed by ‘D’ genome of hexaploid wheat. Mechanisms like tissue level compartmentalization *i.e.*, accumulation of toxic ions in the lower leaves of the plant is noted in dicoccum wheat. Cell level compartmentalization in the cell vacuoles was noted by Munns and Tester (2008).

Conclusion

The study's findings indicate that dicoccum wheat germplasms possess significant potential as sources of salt tolerance. Additionally, a handful of promising accessions could be officially recognized as national genetic resources or developed into new wheat varieties. This research underscores the untapped possibilities offered by dicoccum wheat species in addressing global challenges related to hunger and growing populations, particularly in regions characterized by unproductive, saline soils.

Table 11: Grouping of wheat genotypes based on Stress susceptibility index (SSI)

Range of SSI	**Drought tolerance category**	**Number of genotypes**	**Genotypes**
<0.5	Tolerant	13	**Dicoccum wheat (8):** DIC-9, DIC-13, DIC-68, DIC-73, DIC-88, DIC-94, DIC-95, DDK 50505 **Check (5): KRL 210, UAS 334, Kharchia 65, KRL 3-4, IC 0408331**
0.5 to 1.0	Moderate	26	**Dicoccum wheat (24):** DIC-12, DIC-14, DIC-15, DIC-17, DIC-18, DIC-19, DIC-22, DIC-23, DIC-26, DIC-39, DIC-44, DIC-47, DIC-48, DIC-50, DIC-70, DIC-71, DIC-74, DIC-76, DIC-91, DIC-99, DIC-101, DIC-102, DIC-107, DDK 50444 **Check (2): KRL 19, UAS 304**
>1.0	Susceptible	21	**Dicoccum wheat (18):** DIC-1, DIC-4 DIC-21, DIC-43, DIC-45, DIC-46, DIC-49, DIC-72, DIC-77, DIC-83, DIC-92, DIC-93, DIC-103, DIC-104, DIC-105, DIC-106, DDK 50033, DDK 50507 **Check (3): UAS 428, DDK 1029, HD 2009**

Table 12: Grouping of wheat genotypes based on stress tolerance index (STI)

Range of STI	Drought tolerance category	Number of genotypes	**Genotypes**
>0.9%	Tolerant	8	**Dicoccum wheat (7):** DIC-26, DIC-48, DIC-92, DIC-101, DIC-104, DIC-107, DDK 50507 **Check:** UAS 334
0.8-0.9%	Moderate	11	**Dicoccum wheat (10):** DIC-17, DIC-18, DIC-21, DIC-45, DIC-49, DIC-71, DIC-77, DIC-91, DIC-94, DIC-105 **Check:** KRL 210
<0.8%	Susceptible	41	**Dicoccum wheat (33):** DIC-1, DIC-4, DIC-9, DIC-12, DIC-13, DIC-14, DIC-15, DIC-19, DIC-22, DIC-23, DIC-39, DIC-43, DIC-44, DIC-46, DIC-47, DIC-50, DIC-68, DIC-70, DIC-72, DIC-73, DIC-74, DIC-76, DIC-83, DIC-88, DIC-93, DIC-95, DIC-99, DIC-102, DIC-103, DIC-106, DDK 50033, DDK 50505, DDK 50444 **Check (9):** KRL 19, UAS 304, UAS 428, DDK 1029, HD 2009, Kharchia 65, KRL 3-4, IC 0408331

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