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Genetic Divergence in Wheat (*Triticum aestivum* L.Thell.) Under Saline Sodic Condition

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A B S T R A C T

Recently, abiotic stress like salinity, drought and temperature are the severe problems to worldwide wheat production, mostly in arid and semiarid areas. A feasible solution is breeding for salt-tolerant cultivars of wheat, while the presence of genetic variation is a prerequisite for genetic improvement. In the present investigation, an experiment was conducted to estimate the nature and magnitude of genetic diversity in improved varieties of bread wheat during *Rabi*, 2010-11. Total number of 143 exotic and indigenous lines of bread wheat including three checks was apprised in partially reclaimed salt affected soil under late sown and irrigated conditions. The experiment was conducted in Augmented Block Design having 7 blocks of 23 plots each, at Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Faizabad. All the wheat germplam were grouped into twelve clusters by estimating genetic divergence of eleven quantitative traits using the non-hierarchical Euclidean cluster analysis which showed the highest inter-cluster distance between cluster VI and cluster XII. The genotypes having high mean performance for grain yield per plant and several other yield components were found to be concentrated in cluster IV and VI which merit showed due consideration for selection of parents. Thus, crosses between promising lines belonging to cluster pair having higher inter-cluster distances may be attempted for isolating transgressive segregants as these cluster pair were also separated by high inter-cluster distances. The twelve clusters formed in divergence analysis contained genotypes of heterogeneous origin, thereby indicating non-parallelism between genetic and geographic diversity. Therefore, crosses between the members of clusters separated by high inter-cluster distances are likely to throw desirable segregates. This indicated existence of high degree of genetic diversity in the wheat exotic and indigenous lines. Therefore, these exotic and indigenous lines may serve as valuable source for selecting diverse parents for use in hybridization programme.

Introduction

Wheat (*Triticum aestivum* L. em. Thell.) is a major staple food in the world after rice and primarily grown in tropical-temperate region worldwide due to wide high adaptation and greater role in human nutrition as well as in agricultural economy. Abiotic stress factors such as cold, frost, drought, salinity, severely limit plant growth and development as well as the adaptability and mechanisms of plant growth reducing yield in crops including

cereals from the tribe Triticeae (Wang *et al.*, 2003, Kosová *et al*., 2014).

Salinity is the major threat to global wheat production and effect about 6% of the world's area, particularly in arid and semiarid areas of the world. Even in irrigated areas, salt concentration increases in the subsoil due to evaporation of water with the passage of time. Saline soils have soluble salts responsible for reducing economic importance and yield of crop (Munns and James, 2003). Such a large salt-affected area and economical loss is major problems for farmers facing a decline in their income that poses a threat to national and international food security. Possible solutions include increasing the area under wheat cultivation and developing superior varieties that provide a good yield under saline condition. In arid and semiarid areas, yield can be increased significantly by developing salt-tolerant crop varieties (Clark and Duncan, 1993) by exploiting genetic diversity for salt tolerance in species and developing screening techniques.

New genetic sources require developing tolerance to salinity in crops under various breeding programs. Hence, salt tolerant cultivars/genotypes of wheat should be needed to sustain for high yield production under salinity condition (Munns, 2005). Diversity can ensure sustainability and improvement in the livelihoods of farmers in unfavorable environmental conditions providing high yielding crop varieties with important useful traits.

Selection and hybridizations techniques are frequently used for improving genetic constitution of a genotype. Genetic divergence analysis is important tool to estimate genetic diversity among selected genotypes which determine family relationships and genetic affinity or distance of genotypes from each other studying cluster analysis (Mellingers, 1972).

For obtain transgressive segregants, genetic distance between parents is necessary (Joshi *et al*., 2004) to estimate by Euclidean distance (Hoque and Rahman, 2006). Germplasm improvement and genetic diversity are useful for reliable and sustainable production of the food crops. For effective evaluation and utilization of germplasm, measure of extent of available genetic diversity is of utmost importance (Zubair *et al*., 2007). The use of multivariate statistical algorithms is an important strategy for classification of germplasm and analysis of genetic relationships among breeding material (Mohammadi and Prasanna, 2003). The aims of the present study are investigation of genetic diversity and identification between selected genotypes and local cultivar of wheat for salt tolerance by cluster distance analysis.

Materials and Methods

In the present investigation experiment material consisted of 140 exotic and indigenous wheat germplasm lines and three check varieties *viz*., KRL-210, NW-2036, and NW-1067 with pedigree (Table 1) collected from genetic stock available in Wheat Section, Department of Genetics and Plant Breeding, Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad. The experiment was carried out in Augmented Block Design in semi-arid region of Faizabad during *Rabi* 2010-11. The entire experimental field was divided into 7 blocks of equal size and each block having 23 plots. Out of 23 plots in a block, 20 plots were used for accommodating the test genotypes which were not replicated while remaining 3 checks i.e. KRL-210, NW-2036, NW-1067 which were replicated in three rows plot of 3 m long with inter and intra-row spacing of 25 cm and 5 cm, respectively. Experimental site was reclaimed salt affected soil having EC 0.39, pH >8.5, ESP <15 and rich in potash and low in organic carbon, nitrogen and phosphorus.

Recommended dose of fertilizers N:P:K @ 150:60:60 and cultural packages were applied to raise a good and healthy crop. The observation were recorded from five randomly selected plants for all the quantitative characters *viz.,* plant height (cm), number of productive tillers plant^{-1}, spike length (cm), peduncle length (cm), grains spike^{-1}, 1000-grain weight (g), biological yield plant^{-1} (g), grain yield plant^{-1} (g), harvest index (%), flag leaf area (cm^2) except days to maturity, which was recorded on the plot basis. Cluster analysis was done by using Tocher's method (Rao, 1952) and genetic divergence of the pooled data of all the genotypes analyzed by Mahalanobis (1936) D^2 statistics. The genetic divergence among the wheat varieties were calculated by canonical (Vector) and non-hierarchical Euclidean methods of divergence estimation. The D2 values were calculated by using the method described by Mahalanobis (1936). Genetic divergence analysis using canonical (vector) method is a sort of multivariate analysis where canonical vector and roots representing different axes of differentiation and the amount of variation accounted for by each of such axes, respectively, were derived (Rao,1952). Non- hierarchical Euclidean cluster analysis (Beale, 1969; Katyal *et al*., 1985) was conducted using computer package (Windostat version 8.5).

Results and Discussions

The non-hierarchical Euclidean cluster analysis was studied to survey the genetic divergence among 143 wheat germplasm on the basis of 11 quantitative characters. The pseudo F-test revealed that 12 non-overlapping cluster arrangements were the most appropriate for grouping all the genotypes (Table 1). Among the evaluated genotypes in saline sodic condition, the maximum numbers of genotype were grouped in cluster II (21 genotypes) followed by cluster VII (18 genotypes), while minimum numbers of genotype grouped in cluster VI (only 4 genotypes) (Table 2). The highest intra-cluster distance was observed in cluster V (D^2 = 81.46), followed by cluster VI (D^2 = 78.77) (Table 2). The lowest intra-cluster value was recorded for cluster X (D^2 = 43.93), followed by cluster VII (D^2 = 44.38). Zaman *et al.,* (2005) observed diversity with high range of values of inter and intra cluster distance among wheat genotypes under Inter cluster distance is important to screen genotypes using D^2 analysis Singh *et al*., (2013). Genotypes belonging to those clusters showing higher inter cluster distance considered genetically more divergent and hybridization between these genotypes of dissimilar clusters is likely to generate broad variability with desirable sergeants Gartnar *et al*., (1989) and Singh *et al*., (2006). The analysis of variance exhibited significant variation among the genotypes for all the quantitative characters.

The maximum generalized inter cluster distance (D^2) was recorded between cluster VI and XII (D^2 = 1495.20), followed by cluster VI and VII (D^2 = 1017.754). Thus, hybridization between genotypes from these clusters may result in maximum hybrid vigour and highest number of useful segregates Shwi *et al.,* (1972).The minimum inter-cluster distance was found between cluster VII and VIII (D^2 = 74.95) followed by cluster VII and IX (D^2 = 76.50) indicating that the genotypes in these two clusters were relatively close to each other.

On the basis of average cluster mean values (Table 3) for 11 characters, the genotype of cluster IV showed maximum divergence for peduncle length (31.293), spike length (10.948), grains per spike (41.489), biological yield per plant (23.214) and grain yield per plant (8.736).

Table.1 Clustering pattern of 140 wheat genotypes on the basis of non-hierarchical Euclidean cluster analysis of 11 characters

Cluster No.	No. of genotypes	Name of genotypes
I	15	42nd IBWSN-1023, KRL-210, 42nd IBWSN-1119, 27th SAWSN-3052, 30th ESWYT-131, 42nd IBWSN-1175-II, 29th ESWYT-136, EC-663946, 27th SAWSN-3082, EC-664193, 42nd IBWSN-1107, 19th HRWSN-2026, 27th SAWSN-3107, 1st CSISADRYT-5217, 29th ESWYT-130.
II	21	42nd IBWSN-1121, 42nd IBWSN-1166, 4th SAMNYT-411, KRL-302, 27th SAWSN-3097, 1st CSISADRYT-6764, 42nd IBWSN-1152, 1st CSISADRYT-5218, 30th ESWYT-118, 1st CSISADRYT-5212, 27th SAWSN-3011, EC-663954, EC-664196, EC-664244, IC-524282, IC-524284, EC-664236, 27th SAWSN-3027, 27th SAWSN-3069, ESRN-51, 42nd IBWSN-1158.
III	14	42nd IBWSN- 1113, EC-634300-88, KRL-301, KRL-312, 10th EGPYT-7, KRL-315, 1st CSISADRYT-6767, EC-664009, 1st SATYN-60, IC-553917, 1st SATYN-26, EC-663961, KRL-306, 10th DSBWYT-407.
IV	12	42nd IBWSN- 1151, EC-634300-106, EC-634300-103, EC-634300-81, 1st SATYN-45, 42nd IBWSN -1150, 42nd IBWSN-1038-II, 42nd IBWSN-1057, 1st SATYN-37, 1st SATYN-35, 1st SATYN-38, IC-546933.
V	6	42nd IBWSN- 1173, 10th EGPYT-11, 1st SATYN-46, 1st SATYN-53, 10th DSBWYT-420, 42nd IBWSN 1175-I.
VI	4	EC-634300-69, EC-634300-99, EC-634300-64, EC-634300-110.
VII	18	42nd IBWSN -1034,16th HRWYT-206, EC-664229, 4th EBWYT-511, EC-664208, EC-664200, 42nd IBWSN-1112, 27th SAWSN-3004, 42nd IBWSN-1038-I, 42nd IBWSN-1170, ESRN-11, NW-1067, 42nd IBWSN-1039, EC-634300-76,GW-2008-156,GW-2007-87,GW-2007-92, EC-664189.
VIII	8	29th ESWYT-110, EC-634300-95, RAJ-4211, NW-5029, GW-2008-157, NW-2036, 42nd IBWSN-1087, EC-664215.
IX	10	IC-524288, WH-1083, ESRN-15, KRL-307, KRL-322, ESRN-3, 10th DSBWYT-422, KRL-305, KRL-299, GW-2008-153.
X	9	42nd IBWSN-1164, KRL-309, EC-634300-82, KRL-323, 42nd IBWSN -1146, 42nd IBWSN-1167, 42nd IBWSN-1169, 12th EGPSN-51, 42nd IBWSN-1065.
XI	11	30th ESWYT-119, 42nd IBWSN-1021, 1st SATYN-23, WH-1097, 4th EBWYT-509, KRL-300, IC-549914, EC-414149, KRL-303, KRL-304, 42nd IBWSN-1137.
XII	15	42nd IBWSN-1063, KRL-324, EC-664199, 42nd IBWSN -1103, EC-634300-133, EC-664227, LBP-2009-24, KRL-316, GW-2008-159, GW-2006-17, GW-2007-96, EC-634300-94, EC-634300-63, RWP-2009-12, GW-2007-80.

Table.2 Estimates of average intra and inter- cluster distances for 12 clusters in exotic and indigenous lines of wheat

Cluster no.	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	**50.459**	107.919	207.148	184.839	417.185	783.524	143.680	81.681	199.293	99.952	200.399	245.049
II		**64.726**	129.939	127.409	203.186	475.977	221.040	153.341	207.827	136.471	261.090	405.992
III			**61.992**	84.273	193.024	492.581	174.211	180.486	113.419	141.786	166.004	381.173
IV				**51.732**	210.339	440.298	205.062	207.749	176.660	111.925	153.766	442.735
V					**81.46**	188.211	534.267	472.904	405.757	377.517	519.219	858.093
VI						**78.769**	1017.754	921.181	874.149	756.484	944.062	1495.208
VII							**44.381**	74.957	76.500	110.332	82.788	109.961
VIII								**46.170**	110.919	119.362	147.435	136.426
IX									**49.220**	131.383	104.060	173.591
X										**43.928**	97.459	240.134
XI											**53.777**	199.403
XII												**67.654**

Bold figures indicate intra–cluster distances.

Table.3 Cluster means for different characters in exotic and indigenous lines of wheat

Cluster number	Flag leaf area (cm^2)	Days to maturity	Peduncle length (cm)	Plant height (cm)	Spike length (cm)	Grains per spike	Reproductive tillers per plant	1000 grain weight (g)	Biological yield per plant(g)	Grain yield per plant(g)	Harvest index(%)
I	19.723	125.400	29.226	81.493	10.398	40.629	4.879	39.343	20.484	7.823	38.117
II	18.570	124.952	29.548	82.694	9.950	38.673	4.879	39.770	19.982	7.591	37.892
III	19.391	124.357	27.720	79.753	9.883	39.494	5.118	40.336	21.038	8.155	38.779
IV	20.352	123.833	31.293	85.035	10.948	41.489	5.282	39.565	23.214	8.736	37.587
V	18.885	125.500	30.250	80.848	9.418	38.660	4.817	40.107	19.345	7.427	38.590
VI	20.550	125.250	26.425	76.200	9.605	39.323	5.525	40.520	22.860	8.705	38.033
VII	21.525	124.000	30.061	81.853	9.924	39.564	4.568	39.589	18.987	7.161	37.817
VIII	22.334	124.375	30.425	85.563	9.628	38.520	4.940	39.112	19.336	7.454	38.425
IX	18.616	124.900	28.510	80.814	10.201	40.225	5.140	39.453	20.514	8.121	39.568
X	22.662	125.444	30.183	84.429	10.469	40.177	4.827	41.013	21.208	8.150	38.433
XI	19.618	125.455	29.755	81.753	10.422	40.440	4.785	41.079	20.706	7.916	38.299
XII	18.699	123.733	30.127	81.390	9.403	38.449	4.736	39.699	18.912	7.255	38.429

Table.4 Diverse and superior genotypes with desirable traits selected from different clusters

SN	Characters	Genotypes
1.	Flag leaf area (cm^2)	**GW 2007-80, ESWYT-110, KRL-315, GW 2008-153,** 1CSISADRYT-5217, RWP 2009-12, IBWSN-175, 1SATYN-53, IBWSN-34, IC-524284
2.	Days to maturity (Early)type	**IC-546933, GW 2008-157, GW 2008-156, EC-634300-99,** GW 2007-92, KRL-315, EC-634300-64, IC-549914, IC-524288, EC-664236, EC-634300-110
3.	Peduncle length (cm)	**IBWSN-103, IBWSN-63, EC-634300-63, 43IBWSN-1107,** EC-664199, EC-664189, EC-634300-133, EC-634300-95., ESWYT-110, IBWSN-137, IBWSN-112
4.	Plant height (cm) (Dwarf)	**EC-634300-133, EC-634300-94, IBWSN-103, IBWSN-63,** GW 2006-17, RWP 2009-12, KRL-324, GW 2008-159, GW 2007-96., LBP 2009-24, EC-634300-63
5.	Spike length (cm)	**10EGPYT-11, EC-664236, GW 2008-153, 10DSBWYT-420**, 27SAWSN-3027, ESRN-51, 27SAWSN-3069, EC-663954, EC-634300-110, EC-664244, EC-664215
6.	Grains per spike	**27SAWSN-3027, 27SAWSN-3069, ESRN-51, EC-664236, EC-634300-63,** EC-664196, 10DSBWYT-420, GW 2008-153
7.	Reproductive tillers per plant	**IC-524282, GW 2008-157, 29ESWYT-130, IC-524284, 43IBWSN-1107, EC-664236, 29ESWYT-136,** IC-553917, EC-634300-110, EW-EC-664215, NW-5029
8.	1000- grain weight (g)	**45IBWSN-1175, 1CSISADRYT-5218, IBWSN-152, ESRN-51, 27SAWSN-3107**, 30ESWYT-131, KRL-323, 43IBWSN-1107, 29ESWYT-130
9.	Biological yield per plant (g)	**EC-664236, EC-634300-110, 29ESWYT-130, IC-524282**, IBWSN-158, 27SAWSN-3107, 1CSISADRYT-5217, EC-664244, EC-663946, EC-664215
10.	Harvest index (%)	**KRL-306, EC-663961, 1SATYN-46, GW 2007-80, 1SATYN-60,** 29ESWYT-130, 1SATYN-26 EC-634300-94, NW-5029, EC-634300-76
11.	Grain yield $plant^{-1}$ (g)	**29ESWYT-130, IBWSN-158, 27SAWSN-3107, EC-664236, EC-634300-110, IC-524282, 19HRWSN-2026,** 1CSISADRYT-5217, 43 IBWSN-1107, 27 SAWSN-3027

Others traits *viz.*, flag leaf area (22.662), days to maturity (125.500), plant height (85.563), reproductive tillers per plant (5.525), 1000 grain weight (41.079) and harvest index (39.568) exhibited maximum cluster mean in the cluster X, V, VIII, VI, XI and IX, respectively. Whereas, cluster XII, contained four traits and cluster VI and VII bear two trait, which exhibited minimum cluster mean values and cluster II, IV, VIII, consisted of only one trait which exhibited minimum cluster mean values. These results are in conformity with those obtained by Hailegiorgis *et al*., (2011) for grain yield. Based on cluster means, cluster IV has been identified for selecting parents for incorporating peduncle length, spike length, grains per spike, biological yield per plant and grain yield per plant. Similar grouping of genotypes has also been reported by Bergale *et al.,* (2001). The present study confirms the findings of Verma *et al.,* (2014), who grouped 108 wheat genotypes into eleven clusters based on their various morpho-agronomic traits. The identified genotypes superior in the above cluster may be involved in a multiple crossing programmes to recover transgressive segregants with high genetic yield potential. Evaluation of genetic diversity can be useful for the selection of the most efficient genotypes (Table 4). Accordingly, if such efforts result in the reduction of diversity, production of plants with higher uniformity may guarantee the production of enough food for the world increasing population.

The grouping of genotypes reveled that indentified tolerant genotypes may be used as donor in various hybridization programmes to improve yield under sodic soil created saline stress environment. Earlier studied have also reported substantial genetic divergence in wheat (Deshmukh *et al*., 1999; Roy *et al*., 2004; Verma *et al.,* 2006; Singh *et al.,* 2006; Iqubal *et al.,* 2007). The grouping of genotypes reveled that indentified tolerant genotypes may be used as donor in various hybridization programmes to improve yield under sodic soil created saline stress environment. Earlier studied have also reported substantial genetic divergence in wheat (Deshmukh *et al*., 1999; Roy *et al*., 2004; Verma *et al.,* 2006; Singh *et al.,* 2006; Iqubal *et al.,* 2007). The cluster pattern of the genotypes showed non-parallelism between geographic and genetic diversity (Singh *et al*., 2009). The statistical analysis revealed that the diverse clusters showed high inter cluster distances which might generate a wide range of transgressive segregants for development of high yielding wheat varieties (Kumar *et al.,* 2015). High degree of genetic divergence observed in the present study on the analysis of all the wheat genotypes.

In conclusion the existence of considerable significant genetic variations was acquired among the genotypes for all the eleven selected quantitative characters under sodic soil condition, which may help for further selection and breeding. Identified superior genotypes may be selected from those clusters which had significant genetic distance for crossing in order to obtain genetic recombination and transgressive segregation in the subsequent generations. Results are important to contrast to the sodic soil conditions will assist breeding programs to identify tolerant genotypes under sodic soil conditions.

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