Full Length Research Paper

Genetic variability and divergence analysis of yield and its contributing traits under sodic soil condition in wheat (*T. aestivum* L.)

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This study was carried out during *Rabi* 2010-11 at N.D. University of Agriculture and Technology, Kumarganj, Faizabad (UP), India with 108 bread wheat genotypes to assess the genetic variability and diversity for yield and yield related traits under sodic soils. The genotypes were evaluated for eleven quantitative traits and showed wide variability for the studied components. Maximum variations were observed among the entries for plant height with coefficient of variation 10.68% while minimum variability was found for productive tillers plant[-1]. The entries NW-1014 and NW(S)-6-5 provided maximum number of grain spike[-1] while entry KHARCHIA-65 was mainly characterized by having maximum grain yield plant[-1]. The cluster analysis grouped the 108 bread wheat genotypes into 11 different clusters. The clustering pattern of genotypes showed no definite relationship between genetic divergence and geographical distribution of genotypes. Genotypes grouped into cluster XI showed maximum intra cluster diversity while cluster I and X, exhibited highest inter cluster diversity followed by clusters VIII and XI. From cluster mean value, genotypes in cluster X, VIII and VI deserve consideration for their direct use as parents in hybridization programs to develop high yielding wheat varieties. Thus, hybridization among these cluster pairs is recommended for getting high transgressive segregants in F_2 generation.

Keywords: Wheat, Sodic soils, Variability, Diversity, Cluster.

INTRODUCTION

Wheat (*T. aestivum* L.) is the second major food crop of the world in importance next to rice. In India the crop ranks second in terms of total production next to rice. It is largely grown in Indian states like Uttar Pradesh, Punjab, Haryana, Madhya Pradesh, Rajasthan, Maharashtra, Gujrat, Karnatka, Bihar, West Bengal, Uttrakhand, and Himanchal Pradesh. These states contribute about 99.5 % of total wheat production in the country and play an appreciable role of supplying carbohydrates, proteins and minerals. The genetic diversity between plant species is huge as observed by the large differences in many traits. However also within species substantial genetic variation

is present in nature or has been generated by breeders and researchers. For a successful breeding program, the presence of genetic diversity and variability plays a vital role. It is true that the more diverse plants, the greater chance of obtaining high heterotic crosses and broad variability in segregating generations during genetic improvement. The importance of genetic diversity for selecting plants for recombination breeding in an autogamous crop such as wheat to recover transgressive segregants has also been repeatedly emphasized (Murthy and Anand, 1966; Jatasara and Paroda, 1983). Since published works of bread wheat on genetic diversity are scanty under adverse condition, the aim of this study was to identify genetically divergent bread wheat parents with desirable traits for hybridization particularly for yield under salt affected soils.

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Table 1 Descriptive statistics of the 11 quantitative traits of 108 wheat lines under sodic soil condition.

Characters	Minimum	Maximum	Mean	CV	h^2	GA % mean	SE	SD
Days to 50% flowering	73	94	80	4.00	82.98	6.41	0.31	3.23
Days to maturity	114	126	120	1.96	78.08	3.01	0.22	2.37
Plant height (cm)	61	100	77	10.68	84.66	17.76	0.79	8.26
Productive tillers plant^{-1}	2	7	4	22.54	16.64	7.69	0.10	1.11
Spike length (cm)	6	13	9	11.16	57.31	10.73	0.10	1.10
Spike weight plant^{-1} (g)	3	12	7	27.55	92.15	48.31	0.20	2.15
Grains spike^{-1}	26	49	39	13.52	85.28	22.67	0.51	5.30
1000-grain weight (g)	24	45	36	12.51	79.35	19.44	0.43	4.50
Biological yield plant^{-1} (g)	9	24	16	25.00	92.28	44.73	0.40	4.18
Harvest index (%)	26	44	36	10.98	45.57	10.08	0.38	4.00
Grain yield plant^{-1} (g)	3	10	6	30.19	90.69	52.92	0.17	1.85

Where, CV= Coefficient of variation in %, h^2 =heritability (broad sense), GA= genetic advance in %, SE= Standard error, SD= Standard deviation

MATERIALS AND METHOD

A field experiment was conducted during *Rabi* 2010-11 at the Main Experimental Station (MES) of N.D. University of Agriculture and Technology, Kumarganj, Faizabad (UP), India. Kumarganj is situated between 26^0 47 N latitude, 82^0 12 E longitude and at an altitude of 113 m above the mean sea level. The experimental material consisted of 108 diverse genotypes including 4- checks (DBW-14, DBW-17, HD2009 and KRL3-4) of wheat collected from Australia and India. These genotypes were grown under sodic soil condition (pH> 8.8 and redox potential 415.8 mV) in an Augmented Block Design comprising of 4 blocks, where each block contains 26 test entries and 4 checks (randomly allocated). Each genotype was grown in 4 rows of 2.5 m long plot with 23 cm distance between rows. The recommended cultural practices were adopted to raise good crop. Data were recorded on five randomly selected competitive plants from each plot on eleven quantitative characters namely, days to 50% flowering, days to maturity, plant height (cm), productive tillers plant^{-1}, spike length (cm), spike weight plant^{-1} (g), Grains spike^{-1}, 1000-grain weight (g), biological yield plant^{-1} (g), harvest index (%) and grain

yield plant^{-1} (g). Data recorded on the above characters were subjected to Non-hierarchical Euclidean cluster analysis (Beal, 1969; Spark, 1973).

RESULTS AND DISCUSSIONS

The results of the present study showed moderate to high variability for all the eleven quantitative traits under study. This suggested that adequate scope is available for use in a program aimed at enhancing genetic yield potential of wheat under sodic soil condition. The data presented in (Table 1) showed wide range of genetic variability for all the eleven traits. Genetic variability has been also calculated for different yield attributing characters in wheat by several workers (Sachan and Singh, 2003; Kumar *et al.*, 2003; Paul *et al.*, 2006; Chaitali and Bini, 2007) which revealed that selection was effective for a population with broad genetic variability. The magnitude of genetic variability for days to heading was ranged from 73- 94 days with the mean value of 80 days and coefficient of variation 4.00 %.

Two entries HD-3027 and NWL-9-25 have minimum number of days to 50% flowering and only one entry

Table 2. Distributing pattern of 108 genotypes of bread wheat into eleven clusters based on Non-hierarchical Euclidean Cluster analysis.

Cluster No.	No. of genotypes	Name of genotypes
I	10	CHARA, NWL-9-22, WESTONIA, PBW-642, NW-3087, KRL-238, NW-1067, KRL-266, WH-1094, CAMM
II	7	KRL-268, HD-3024, PBW-636, NW-4099, DBW-52, KRL-240, SCHOMBURGK
III	12	PBW-550, KRL-283, NW-4082, KRL-259, HUW-636, KRL-227, KRL-236, PBW-343, PBW-590, KALANNIE, NW-1076, KRL-261
IV	8	RW-3684, DBW-59, SPEAR, UP-2003, DUCULA-4, DBW-50, AMERY, PBW-621
V	16	PBW-635, HI-1563, HD 2009©, PBW-631, GUTHA, UP-262, HUW-635, DBW-58, DBW-39, DBW-60, PBW-634, RSP-561, NW-4092, KRL-249, HD-3028, CUNDERDIN
VI	16	NW-2036, TINCURRAN, NW-4083, KRL-99, RAJ-3765, DBW 14©, PBW-639, KRL-210, NW-3069, HD-2997, KRL-1-4, GAMENYA, BT-SCHOMBURGK, BROOKTON, KRL-229, HD-3027
VII	13	NW-4035, NWL-7-4, NWL-9-23, NW-4081, DBW-51, DBW 17©, HD-2967, CHIRYA-7, HD-2733, NW-1012, KRL-19, RAJ-4201, KRL-233
VIII	5	DBW-55, KRL-213, HD-2985, NW(S)-6-5, NW-4091
IX	12	RAJ-4205, HUW-638, K-0808, CBW-38, KRL-104, KRL-35, KRL-105, NW-4018, PERENJORI, NWL-9-25, KRICHAUFF, NW-4098
X	5	K-0807, K-9107, NWL-9-24, NW-1014, DBW-46
XI	4	BH-1146, KRL 3-4©, NW(S)-2-4, KHARCHIYA-65

Table 3. Average intra and inter cluster distance values among 11 clusters for 108 bread wheat genotypes.

Cluster no.	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	**166.20**	201.74	231.63	399.46	296.19	366.31	535.91	443.96	656.07	1284.96	1178.76
II		**88.00**	227.36	177.14	183.57	266.36	368.98	411.55	368.29	824.10	690.58
III			**117.82**	298.27	228.87	222.68	268.23	260.15	458.06	943.79	1020.48
IV				**93.30**	170.49	320.92	314.39	552.88	233.13	519.17	398.77
V					**110.25**	241.65	289.84	461.68	280.54	652.67	622.85
VI						**130.07**	211.71	251.75	301.24	693.92	808.65
VII							**127.87**	237.89	252.24	472.89	742.91
VIII								**130.39**	526.29	923.38	1258.06
IX									**178.37**	310.76	382.10
X										**207.98**	399.53
XI											**213.94**

CAMM had longest days to 50% flowering while for days to maturity it ranged from 114-126 days with the mean value of 120 days and coefficient of variation 1.96%. Two entries PBW-621 and NW-1014 had minimum days to maturity while other two entries CAMM and KRL-213 took maximum days of maturity. A significant variability was depicted for plant height parameter, which ranged from 61-100 cm with the mean value of 77 cm and coefficient of correlation 10.68%. Minimum plant height was observed in entries NW-4082 and NWL-9-22 while

KHARCHIYA-65 exhibited maximum plant height. A frequent variability was noted for productive tillers plant[-1] which ranged from 2-7 with the mean value of 4 and coefficient of variation was 22.54%.

Two entries KRL-229 and GAMENYA exhibited maximum number of productive tillers plant[-1] while entries AMERY and NW-4081 showed minimum productive tillers plant[-1]. The magnitude of genetic variability for spike length ranged from 6-13 cm with the mean value of 9 cm and coefficient of variation 11.16%. Two entries AMERY and

Table 4. Mean value of 11 clusters and contribution of different characters toward genetic divergence in 108 bread wheat genotypes.

Cluster number	Days to 50% flowering	Days to maturity	Plant height	Productive tillers plant^{-1}	Spike length	Spike weight plant^{-1}	Grains spike^{-1}	1000-grain weight	Biological yield plant^{-1}	Harvest index	Grain yield plant^{-1}
I	83.19	121.64	67.90	4.43	9.22	5.44	33.81	31.19	13.06	32.25	4.14
II	81.08	120.47	76.64	4.30	9.36	5.67	35.81	30.08	14.25	31.81	4.40
III	80.46	120.04	69.67	4.29	10.20	6.77	39.17	34.29	13.22	39.14	5.23
IV	81.84	119.72	83.25	3.94	10.27	6.33	35.53	34.47	12.95	37.40	4.73
V	80.47	121.40	77.17	4.16	9.74	6.60	35.59	39.36	13.97	34.09	4.78
VI	78.54	118.91	73.34	6.04	9.73	9.35	39.50	36.04	21.18	36.60	7.77
VII	80.17	121.40	77.21	5.17	10.30	9.47	46.02	37.81	18.12	39.99	7.30
VIII	81.89	121.74	68.40	5.73	10.18	9.47	48.21	32.09	19.86	37.74	7.55
IX	80.75	120.63	85.21	5.60	10.57	9.11	40.19	38.58	19.91	37.10	7.39
X	82.19	119.69	94.30	5.38	9.94	9.81	46.56	42.49	20.73	38.63	8.01
XI	80.08	121.27	98.13	5.97	9.29	8.27	33.61	36.58	18.38	37.27	6.86

Table 5. Diverse and superior genotypes with desirable traits selected from different clusters.

S.N.	Characters	Desirable genotypes
1.	Days to 50% flowering (early)	HD-3027, NWL-9-25, KRL-229, PBW-590
2.	Days to maturity (early)	NW-1014, PBW-621, PBW-639, NWL-9-25
3.	Plant height (medium dwarf)	NW-4082, NWL-9-22, NW-3087, KRL-283
4.	Productive tillers plant^{-1}	KRL-229, GAMENYA, DBW-51, KHARCHIYA-65
5.	Spike length	AMERY, K-0808, KALANNIE, DBW-52
6.	Spike weight plant^{-1}	KRL-99, NW-4098, NWL-9-25, NW-1014
7.	Grains spike^{-1}	NW-1014, NW(S)-6-5, DBW-46, RAJ-4201
8.	1000-grain weight	K-0808, DBW-46, NW-4092, K-9107
9.	Biological yield plant^{-1}	RAJ-4201, KHARCHIYA-65, NW(S)-6-5, KRL-99
10.	Harvest index	NW-4091, NW-1014, KRL-19, KRL-259
11.	Grain yield plant^{-1}	KHARCHIYA-65, KRL-99, RAJ-4201, KRL-19

K-0808 have maximum spike length and entry NW-3087 had minimum spike length. A significant result was observed for spike weight plant^{-1}. It varied from 3-12 g with the mean value of 7 g and coefficient of variation 27.55%. The entry KRL-99 and NW-4098 had highest spike weight plant^{-1}. The magnitude of genetic variability for grains spike^{-1} was ranged from 26-49 grains with the mean value of 39 grains and coefficient of variation 13.52%. Maximum number of grains spike^{-1} was observed for the entries NW-1014, NW(S)-6-5 and DBW-

46 while UP-262 and GUTHA showed minimum grains spike^{-1}.

Significant variability was observed for 1000-grain weight character, which ranged from 24-45 g with the mean value of 36 g and coefficient of variation 12.51%. The entry K-0808 had maximum 1000-grain weight. Genetic variability ranged from 9-24 g for biological yield plant^{-1} parameter with the mean value of 16 g and coefficient of variation 25.00%. Maximum biological yield plant^{-1} was observed in case of RAJ-4201 and KHARCHIYA-65 while

minimum value showed by WESTONIA. Significant variability was depicted for harvest index, which ranged from 26-44% with mean value of 36 and coefficient of variation 10.98%. The entry NW-4091 had maximum harvest index value. A significant result was observed for grain yield plant^{-1}. It varied from 3-10 g with the mean value of 6 g and coefficient of variation 30.19%. The entry KHARCHIYA-65 had the highest grain yielder followed by KRL-104 and PBW-550. The heritability estimates ranged from 16.64 to 92.28 % for productive tillers plant^{-1} and biological yield plant^{-1} respectively. High estimates of heritability (broad sense) were obtained for all the characters except productive tillers plant^{-1}, harvest index and 1000-grain weight. High heritability coupled with high genetic advance gives the most effective criteria for selection (Johnson *et al.* 1955).

The Non-hierarchical Euclidean cluster analysis grouped 108 exotic and indigenous genotypes into eleven distinct clusters (Table 2). The grouping of genotypes and their possible classification for use in hybridization programme as donors for yield traits are very clear and largely parents selection for stress environment (sodic soil), based on present study might give transgressive segregants for desired traits. Earlier studied have also reported substantial genetic divergence in wheat materials (Deshmukh *et al.*, 1999; Roy *et al.*, 2004; Verma et al. 2006; Singh *et a*l. 2006; Iqubal *et al.* 2007). The average intra cluster distance in cluster XI was maximum suggesting that the genotypes in this cluster were relatively more diverse among themselves. The highest inter-cluster distance was observed between clusters I and X followed by clusters VIII and XI. The estimates of average intra-and inter-cluster distances (Table 3) revealed that the genotypes present in a cluster had little genetic divergence from each other with respect to aggregate effect of 11 characters under study, while much more genetic diversity was observed between the exotic and indigenous genotypes belonging to different clusters.

According to Ghaderi *et al.* (1984), increasing parental distance implies a great number of contrasting alleles at the desired loci, and to the extent that these loci recombine in the F_2 and F_3 generation following a cross of distantly related parents, the greater will be the opportunities for the effective selection for yield factors. Thus, crossing between the genotypes belonging to cluster pairs separated by very high inter-cluster distances as mentioned above may throw desirable transgressive segregants.

The eleven clusters showed considerable differences in mean values for different characters under study (Table-4). Cluster I consisted of 10 genotypes and had characteristic feature of very low yielding, low spike weight, minimum spike length, shortest plant height and maximum number of days to 50% flowering. The genetic distance value of these varieties was 166.20. Cluster II, comprising 7 genotypes, exhibited lowest cluster means

value for harvest index and 1000-grain weight, while it had moderate means for remaining 9 characters. The genetic distance value of these varieties was 88.00.

Cluster III, containing 12 genotypes, exhibited second highest cluster mean for harvest-index. The genetic distance value of these varieties was 117.82. Cluster IV had 8 genotypes having a characteristic feature of lowest biological yield plant^{-1} and minimum number of productive tillers plant^{-1}. The genetic distance value of these varieties was 93.30. Sixteen genotypes which include the standard check HD 2009 constituted cluster V and characterized by moderately high 1000-grain weight and very small number of productive tillers plant^{-1}. The genetic distance value of these varieties was 110.25. Cluster VI which consisted of 16 genotypes including standard check DBW-14 was responsible for highest biological yield plant^{-1} and maximum number of productive tillers plant^{-1} and minimum number of days to 50% flowering. The genetic distance value of these varieties was 130.07.

Cluster VII comprising of 13 genotypes including a standard check DBW-17 is characterized by highest mean performance for harvest index. The genetic distance value of these varieties was 127.87. Five genotypes constitute cluster VIII and this cluster had a characteristics of maximum number of days to maturity and grains spike^{-1}. The genetic distance value of these varieties was 130.39.

Cluster IX had 12 genotypes with a characteristic feature of longest spike. The genetic distance value of these varieties was 178.37. Cluster X had 5 genotypes and the characteristic feature of highest grain yield plant^{-1}, spike weight plant^{-1} and 1000-grain yield. The genetic distance value of these varieties was 207.98. Four genotypes which include the standard check KRL-3-4 constitute cluster XI. This cluster is mainly characterized by highest plant height. The genetic distance value of these varieties was 213.94. Most diverse and superior genotypes with desirable traits selected from different clusters are represented in Table 5.

CONCLUSIONS

Highly significant differences were obtained among the genotypes for all the eleven selected quantitative characters; which indicated adequate variability among the genotypes considered in this study. The entry AMERY had maximum spike length and NW-1014 had maximum number of grains spike^{-1} while KHARCHIYA-65 had maximum grain yield plant^{-1}. Clustering pattern of 108 genotypes provided considerable information useful in genetic improvement of bread wheat. Genotypes grouped into cluster XI showed maximum intra cluster diversity while cluster I and X, followed by clusters I and XI exhibited highest inter cluster diversity. From cluster mean value, genotypes in cluster X, VIII and VI deserve

consideration for their direct use as parents in hybridization programmes to develop high yielding wheat varieties suitable for sodic soils.

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