



Genetic Divergence in Bread Wheat (*Triticum aestivum* L.) Germplasm under Alkali Soil

Dharmendra Singh*, S.K. Singh and K.N. Singh

Division of Crop Improvement
Central Soil Salinity Research Institute, Karnal, Haryana

The nature and magnitude of genetic divergence was assessed using non-hierarchical Euclidean cluster analysis in 305 genotypes (including checks) of bread wheat for grain yield and its associated characters. All the genotypes grouped in 7 different clusters. The clustering pattern of genotype belonging to the same country revealed their distribution in more than one cluster showing non-parallelism between geographic and genetic diversity. Members of cluster III and VII are highly diverse from each other. Cluster VII had higher mean values for grain yield per plant and tillers per plant. A number of genotypes were also identified which may serve as potent genetic donors for some metric characters.

Key words: Wheat, morpho-physiological traits, clusters analysis, genetic divergence, alkali soil

Reduction in genetic variability makes the crops increasingly vulnerable to salt stress in alkali soil and adverse climatic changes (Munns and James, 2003). Improving the salt tolerance of crop to new genetic diversity and efficient technique for identifying salt tolerance. There is probably a wide range of genetic diversity in salinity tolerance in National and International collections in bread wheat genotypes. Among the high yielding varieties of bread wheat, most of the present day varieties are derived from six broad groups (Rao, 1988). This situation of narrowing down of genetic base point towards the preservation, management, enhancement and evaluation of wide genetic variability. Mahalanbis' D^2 described by Rao (1952) has been utilized by a number of workers for estimating genetic divergence. Although D^2 statistic is a quantitative measure of genetic divergence, yet the clustering pattern of the genotypes is arbitrary (Upreti *et al.*, 2003). The main objective of the present study was to identify and classify the available wheat materials into genetically different, distinctive group so as to enable the breeders to efficiently plan the hybridization programme. The present investigation was, thus aimed at assessing the genetic divergence among three hundred and five bread wheat lines under alkali soil condition.

Materials and Methods

Three hundred and five genotypes (300 test genotypes + 5 checks namely, KRL 19, HD 2009, PBW 343, HD 4530 and *Kharchia* 65) maintained at the Division of Crop Improvement, Central Soil Salinity Research Institute, Karnal (Haryana), constituted the material for the present study. The material was evaluated at CSSRI experimental Farm,

Kaithal under alkali soil condition ($pH_2 \sim 9.2$). The experimental materials were evaluated in augmented design with twelve blocks with each block containing 25 test genotype plus five checks. Recommended agronomic practices were followed to rise a good crop. In the blocks each genotype was evaluated in a single row of 1 meter with plant distance 5 cm and row to row distance of 23 cm, respectively. The data on nine quantitative characters were recorded. Five competitive plants were randomly selected from the middle row of each experimental plot to record observation on quantitative character on plant basis, while days to 50 per cent heading and days to maturity were recorded on plot basis. Adjusted mean values for all the characters of 300 test genotypes and estimates of error mean squares were obtained following Federer (1956) and used for subsequent statistical analysis.

The mean, range, variance and coefficient of variation were calculated as per the standard statistical procedures. The non-hierarchical Euclidean cluster analysis (Beale, 1969 and Spark, 1973) was conducted to estimate the intra and inter cluster distances and to group the genotypes into different clusters. The appropriate number of clusters to group 300 genotypes was determined following the sequential pseudo F-ratio tests (Beale, 1969 and Spark, 1973).

Results and Discussion

The analysis of variance showed that the blocks were homogenous and genetic difference existed for most of traits among the varieties. Maximum value of coefficient of variability (Table 1) was observed for grain yield per plant, grains per spike, tillers per

*Corresponding author email: dsingh4678@rediffmail.com

plant and 1000- grain weight. Therefore, these traits have higher contribution towards the total genetic divergence. The variability was observed to be moderate for plant height; spike lets per spike and spike length.

The clustering pattern of the genotypes revealed that there were 7 clusters and the distribution of genotypes from different ecogeographical regions into these clusters was apparently random (Table

Table 1. Mean variance and coefficient of variation for nine characters under alkali soil

Character	Days to 50% heading	Days to maturity	Plant height (cm)	Spike Length (cm)	Spikelets/ spike	Tillers/ plant	Grains/ spike	1000- grain weight (g)	Grain yield / plant (g)
Mean	96.52	140.15	81.26	10.07	18.36	3.93	51.23	35.47	6.55
Range	83.47-141.87	133.83-146.43	61.75-114.15	5.79-14.25	12.63-25.51	2.34-6.54	20.88-72.43	22.15-46.06	1.33-10.69
Variance	39.06	5.80	59.14	1.54	3.45	0.42	80.46	25.70	2.59
Coefficient of variation (%)	6.43	1.72	9.46	12.31	10.13	16.54	17.50	14.29	25.80

2). This tendency of genotypes to occur in cluster cutting across geographical boundaries demonstrates that geographical isolation is not the only factor causing genetic diversity. Similar finding has also been made by earlier workers Singh and Chatrath (1993).

The maximum number of genotypes (63) was presented in cluster I and the minimum (5) in cluster VI. Cluster means showed appreciable differences for all the traits particularly for tillers per plant, grains per spike, 1000-grain weight and grain yield per plant. The lower mean for grain yield per plant, 1000-

Table 2. Cluster mean, standard deviation and coefficient of variance for nine characters under alkali soil

Cluster No.	No. of genotype	Character	Days to 50% heading	Days to maturity	Plant height (cm)	Spike length (cm)	Spikelets/ spike	Tillers/ plant	Grains / spike	1000-grain weight (g)	Grain yield/ plant (g)
I	63	Mean	92.26	139.04	77.58	9.67	16.50	4.07	49.92	38.72	7.16
		S.D.	3.73	1.88	6.32	0.97	1.35	0.57	6.53	3.38	1.11
		C.V. (%)	4.04	1.35	8.14	10.03	8.18	14.00	13.08	8.72	15.50
II	55	Mean	101.22	142.33	82.14	10.91	20.20	3.65	58.00	32.76	6.66
		S.D.	4.37	1.53	6.80	1.04	1.25	0.54	7.40	4.79	1.15
		C.V. (%)	4.31	1.07	8.27	9.53	6.18	14.79	12.75	14.62	17.26
III	44	Mean	94.87	137.80	80.18	10.56	19.60	3.84	54.84	32.33	6.23
		S.D.	4.31	1.80	4.97	1.07	1.02	0.49	7.74	4.28	1.08
		C.V. (%)	4.54	1.30	6.19	10.13	5.20	12.76	14.11	13.23	17.33
IV	56	Mean	98.65	141.08	76.28	8.85	17.79	3.75	50.15	33.65	5.50
		S.D.	3.91	1.57	5.60	1.01	1.18	0.57	8.23	5.01	1.29
		C.V. (%)	3.96	1.11	7.34	11.41	6.65	15.2	16.41	14.88	23.45
V	33	Mean	92.68	138.46	87.57	9.93	17.17	3.70	39.45	38.64	5.26
		S.D.	3.27	1.68	6.65	0.83	1.53	0.44	6.18	3.00	1.07
		C.V. (%)	3.52	1.21	7.59	8.35	8.91	11.89	15.66	7.76	20.34
VI	5	Mean	120.71	141.51	80.82	10.57	18.43	3.24	45.87	29.20	2.82
		S.D.	12.12	1.61	3.26	1.12	1.91	0.60	13.69	5.60	1.44
		C.V. (%)	10.04	1.13	4.03	10.59	10.36	18.51	29.84	19.17	51.06
VII	44	Mean	95.83	141.27	88.18	10.72	19.17	4.66	51.87	37.98	8.55
		S.D.	4.56	2.18	7.92	1.05	1.13	0.65	7.10	3.93	1.10
		C.V. (%)	4.75	1.54	8.98	9.79	5.89	13.94	13.68	10.34	12.86

grain weight, tillers per plant in cluster VI. Cluster VI had the highest coefficient of variability and were high for grain yield per plant, grain per spike, 1000-grain weight and tillers per plant. These results are reflected in intra -cluster distances as cluster VII and III had more intra- cluster distances (3.011, 2.245, respectively).

The intra and inter cluster distances are given in Table 3. The magnitude of inter cluster distances

measures the extent of diversity between the genotype of the same cluster. Intra cluster distances ranged from 1.931-3.011. Relatively lower values of intra- cluster distance suggested the presence of narrower genetic variation within a cluster. Inter cluster distances is a measure of genetic distances between two clusters. The maximum (7.302) inter cluster distance was observed between cluster I and VII while the minimum (2.236) between cluster II and V. Cluster III contained 44 genotypes viz., VL

Table 3. Estimates of average intra and inter cluster distances for seven clusters under alkali soil condition.

Cluster	I	II	III	IV	V	VI	VII
I	(2.242)	3.362	3.679	3.140	2.380	5.182	4.939
II		(2.036)	2.238	2.507	2.236	2.686	4.939
III			(2.245)	2.603	2.611	2.637	4.540
IV				(2.202)	3.374	2.563	5.850
V					(1.931)	4.325	6.333
VI						(2.126)	4.98
VII							(3.011)

858, VL 802, HD 2687, HD 2733, UP 2596, UP 2620, UP 2623, UP 2624, Raj 3077, Raj 1482, MP 1165, K 2008, K 8034, NW 2095, NW 2036, NW 1067, NW

1076, HS 440, HS 449, HI 1536, HI 1532, HI 1533, HUW-468, HD 2855, HD 2886, HP 1878, HP 1876, HP 1880, Bwir 7, Raj 4085, 96W639-D5-15, 96W639 D5-20, 96W639-D6-2, KRL 99, KRL 107, KRL 113, KRL 123, HUWI 2, NW(S) 02-8, KYZ 162, KYZ 165, AKJ 03-1, AKJ-03-7 and Westonia, whereas cluster VII had 44 genotypes namely, Gamenya, VL 830, VL 738, UP 2594, UP 2519, MP 1150, WH 736, WH 773, K 2021, HS 295, HS 451, HS 457, HI 1530, KRL 35, HUW-524, PS 711, HP-1731, PBW 396, PBW 502, PBW 509, KLP-317, KO 111, WH 1009, WH 1011, NW(S) 3-5, NW(S) 3-6, Raj 4077, 96W639-D3-9, 96W639-D5-5, KRL 105, KRL3-4, HUWJ 13, NW(S) 02-6, NW(S) 02-15, KLPO 268, KYZO 294, KYZO 295, K 142, KYZ 176, AKJ-03-2, AKZ-03-6, Cunderdin, Carnamah, and Ducula 4 (Table 4).

Table 4. Genetic donors of bread wheat from cluster III and VII for different characters under alkali soil

Characters	Genotypes
High grain yield:	KRL 35, KRL 105, KRL3-4, HUWJ 13, KRL 99, KRL 113, KRL 123, HUWJ 2, Westonia, NW 1067, NW 1076, BWIR 7, Raj 4085, 96W639-D5-15, 96W639 D5-20, 96W639-D6-2, NW(S) 02-8, KYZ 162, KYZ 165, HI 1536, HI 1533, HUW-468.
1000-grain weight:	KRL 35, KRL 105, KRL3-4, HUWJ 13, KRL 99, Cunderdin, Carnamah, Ducula 4, AKJ 03-1.
High tillering:	KRL 105, KRL3-4, HUWJ 13, PBW 396, PBW 502, PBW 509, KLP-317, KO 111, WH 1009, WH 1011, NW(S) 3-5, NW(S) 3-6, KRL 99, KRL 107, KRL 113, KRL 123, HUWI 2, NW(S) 02-8, KYZ 162, KYZ 165.
Grains per spike:	KRL 35, KRL 105, HUWJ 13, HUWI 2, PBW 509, KLP-317, KO 111, WH 1009, WH 1011.

The parents for hybridization could be selected on the basis of their large intra-cluster distances for isolating useful combination in segregating generations. A hybridization programme involving genotypes, viz. KRL 99, KRL 113, KRL 123, HUWJ 2, Westonia, HI 1536, HI 1532, HI 1533, HUW-468, KYZ 165 in cluster III and KRL 35, KRL 105, KRL3-4, HUWJ 13, PBW 502, Ducula 4, KLP-317, KO 111, WH 1009, NW(S) 3-5 in cluster VII could be under taken to isolate high yielding segregants since these genotypes had high grain yield per plant, 1000-grain weight, high tillering capacity and grains per spike with large genetic distance. The genotypes could also be utilized for introgressing their useful traits in the comerial bread wheat cultivars.

References

Beale, E.M.L. 1969. Euclidean cluster analysis. A paper contributed to 37th session of the International Statistical Institute.

Federer, W.T. 1956. Augmented designs. *Hawaiian Planters' Record*. **55**: 191-208.

Munns, R. and James, R.A. 2003. Screening method for salinity tolerance: a case study with tetraploid wheat. *Plant and Soil*, **253**: 201-208.

Rao, C.R. 1952. *Advanced Statistical Methods in Biometrical Research* John Wiley and Sons, Inc., New York.

Rao, M.V. 1988. Thrust areas for sustaining the Indian wheat evaluation. All India Wheat Research Workers Workshop, Haryana Agricultural University, Hissar.

Singh, K.N. and Chatrath, R. 1993. Genetic divergence in bread wheat (*Triticum aestivum* L. em. Thell.) under sodic soil condition. *Wheat Information Service*. **76**: 35-38.

Spark, D.N. 1973. Euclidean cluster analysis. *Algorithm As*. **58**. *Applied Statistics*. **22**: 126-130.

Upreti, M.C., Jeena, A.S., Malik, S.K. and Singh, T.B. (2003). Genetic diversity pattern in wheat (*Triticum aestivum* L.). *Indian J. Genet.* **63**: 335-336.