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GENETIC DIVERGENCE ANALYSIS ON SOME BREAD WHEAT (*Triticum aestivum* L. Em. Thell) GENOTYPES

Tarkeshwar[1], S.C. Gaur[1], S.P. Singh[2]*, Rohit Kumar Sahu[1], Kamlesh Kumar[1], Mohit Yadav[1] and Girijesh Yadav[1]
Department of Genetics and Plant Breeding, Baba Raghav Das Post Graduate College Deoria-274 001 (U.P.)
[2]CSAUAT–Agriculture Research Station, Kalai, Aligarh, U.P.
***Corresponding author Email :** dr.sp.sing24@gmaii.com*

ABSTRACT

In the present investigation, an experiment was conducted to estimate the nature and magnitude of genetic divergence in improved varieties of bread Wheat (*Triticum aestivum* L. em. Thell) during *rabi* 2017-18. A Total number of 84 exotic and indigenous lines of bread wheat including 3 checks were apprised in normal soil, timely sown and irrigated conditions. The experiment was conducted in Augmented Block Design (ABD) at Agriculture Research farm of B.R.D.P.G. College (Campus), Deoria (U.P.). All the wheat germplasm were grouped into 10 different non-overlapping clusters by estimating genetic divergence of 14 quantitative characters. Cluster IX had highest (13) number of genotypes followed by cluster X with 11 entries. The highest inter-cluster distance was present between clusters VIII and X (3019.404). This indicates the existence of high degree of genetic diversity in the wheat exotic and indigenous lines. The genotypes having high mean performance for grain yield per plant and several other yield traits were concentrated in cluster III and V. In the divergence analysis, the formed 10 clusters contain heterogeneous origin of genotypes; indicating non-parallelism between genetic and geographic diversity. Selection of such types of genotypes parent in hybridizing programmes would play an important role in the improvement of yield attributing traits.

Key words : *Divergence, bread wheat, grain yield, euclidean cluster, Mahalanobis D^2 statistics.*

Wheat (*Triticum aestivum* L. em. Thell), a self-pollinating, C_3, allohexaploid (2n=6x=42) annual crop in the true grass family Graminae (Poaceae), is the world's most important energy rich cereal crop for the majority of world's population. It attains unique position in agriculture and economy of our country because of being second most important food crop after rice. It has good nutrition profile with sufficient amount of protein, lipids, ash, carbohydrates, reducing sugars, gluten content and provides @ 314 kcal/ 100 g of food. It is also a good source of minerals and vitamins *viz.*, calcium, iron, thiamine, riboflavin and nicotinic acid (1). It is grown from temperate, irrigated to dry, high rainfall areas, and from warm, humid to dry, cold environments. Undoubtedly, this wide adaptation has been possible due to the complex nature of the plants genome which provides great plasticity to the crop. Wheat has been bred for a wide array of specific end-use quality traits and various adaptive characteristics, resulting in the development of distinct cultivar tailored to specialized production environments. The availability of genetic variability is the basic pre-requisite for genetic improvement through systematic breeding programmes for developing wheat genotypes. 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 (2). Keeping this in view, the present investigation of genetic diversity and identification between selected genotypes and local cultivar of wheat for normal soil and irrigation condition was done by cluster distance analysis.

MATERIALS AND METHODS

In the present investigation, experimental material consisted of 81 exotic and indigenous wheat germplasm lines and three check varieties *viz.*, K-65, NW-2036 and PBW-343; collected from genetic stock available in Wheat Section, Department of Genetics and Plant Breeding, NDUAT Kumarganj, Ayodhya, CSAUAT, Kanpur and B.H.U., Varanasi (U.P.). The experiment was carried out in Augmented Block Design in semi-arid with hot summer and cold winter region of Deoria during *Rabi* 2017-18. The entire experimental field was divided into 9 plots of equal size. Two rows of each test genotype was present only once in each plot with 3 checks in randomized manner along with the distance of 23 cm between the rows and 5 cm between the plants.

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 14 quantitative characters *viz.,* days to 50% flowering, days to maturity, plant height (cm), number of productive tillers/plant, spike length (cm), number of spikelet/spike, grains/spike, 1000-grain weight (g), grain yield/plant (g), flag leaf area (cm^2), peduncle length (cm), grain yield/spike (g), biological yield/plant (g), harvest index (%).

The genetic divergence among the wheat varieties were calculated by canonical (Vector) and non-hierarchical Euclidean methods of divergence estimation. The D^2 values were calculated by using the method

Table-1 : Clustering pattern of 84 genotypes (including 3 Checks) on the basis of Mahalanobis D^2 statistics of wheat germplasm.

Cluster Number	No. of Genotypes	Name of Genotypes
I	9	K9006, K9465, K1317, KD1218, K1213, SONALIKA, K1412, K1502, PBW243
II	5	K1314, K508, K9357, S152, K65
III	9	K68, K1501, KD1418, KD1418, K1304, DBW 14, K1214, K1504, HD2888, K1416
IV	9	K7903, K0402, 1604, DH3171, K402, HD3171, K8434, NW5054, PUSA2733
V	6	PBW74, K1535, K1415, SR99, INQLAB, SR86
VI	10	K1217, K9162, 3LN, SR93, AMSEL, CR100, AKURI, QUATU#2, SR166, PASTOR
VII	3	RAJ4037, SR89, TUKURU
VIII	9	K1006, K1301, RAJ3404, HD74, K1516, HD2967, MURGA, NW2036, PBW343
IX	13	K807, K1310, K818, K307, SR87, DABU, SR169, SR91, SR177, AMSEL87, PBW550, MEGHDUT, NRI88
X	11	K1603, PBW502, RAJ 4120, CRDC 4, SITE, CHAP10, KURUKU, KINGBIRD#1, PRINIA, KACHU, PGQ

Table-2 : Estimate of average Inter and Intra-cluster distances for 10 clusters in wheat germplasm.

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster	7 Cluster	8 Cluster	9 Cluster	10 Cluster
1 Cluster	492.325	869.738	802.732	858.090	816.163	993.188	1377.010	1052.881	1774.823	2527.195
2 Cluster		0.000	1627.999	468.902	1523.965	1505.851	303.859	1000.532	1045.138	941.375
3 Cluster			0.000	1324.980	360.327	1161.824	2093.776	1302.125	1973.431	2905.332
4 Cluster				0.000	1094.675	1275.258	1240.587	2046.452	1898.356	1307.672
5 Cluster					0.000	1007.495	2136.760	1772.745	1537.388	2400.788
6 Cluster						962.423	2102.238	1922.233	2350.600	2808.591
7 Cluster							0.000	997.821	954.125	919.344
8 Cluster								0.000	1445.921	3019.404
9 Cluster									0.000	1497.548
10 Cluster										0.000

described by (3). Genetic divergence of the pooled data of all the genotypes analyzed by Mahalanobis (1936) D^2 statistics and Cluster analysis was done by using Tocher's method (4).

RESULTS AND DISCUSSION

The non-hierarchical Euclidean cluster analysis was studied to survey the genetic divergence among 84 wheat germplasm on the basis of 14 quantitative characters. Among the evaluated genotypes, the maximum numbers of genotype were grouped in cluster IX (13 genotypes) followed by cluster X (11 genotypes), while minimum numbers of genotype grouped in cluster VII (only 3 genotypes) (Table-1). The highest intra-cluster distance was observed in cluster VI (D^2 = 962.423), followed by cluster I (D^2 = 492.325) (Table-2). The lowest intra-cluster value (0.00) was recorded for clusters II, III, IV, V, VII, VIII, IX and X. 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 (5). The maximum generalized inter cluster distance (D^2) was observed between the clusters VIII and X (D^2 = 3019.404), followed by clusters III and X (D^2 = 2905.332). 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 D^2 value (303.859) was found between clusters II and VII, followed by clusters IV and V (D^2 = 360.327) 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 14 characters, the genotypes of cluster I and II showed maximum divergence for days to maturity (125.423) and Harvest index (58.850) respectively. These clusters did not showed minimum or maximum values for rest of the characters. Cluster III showed the minimum inter-cluster group means for the traits days to maturity (122), number of spiklets per spike (13.259), plant height (cm) (74.588), grains per spike (27.881) and grain yield per pant (g) (5.430); none of the traits showed maximum mean values for this cluster. Cluster IV had maximum mean values for number of spiklets per spike (20.459), yield per spike (g) (2.963), grains per spike (40.081) and grain yield per plant (g) (13.830) and no traits had minimum mean value. Cluster V has minimum values for days to 50% flowering (76.667), length of spike (cm) (8.513), peduncle length (cm) (38.852) and yield per spike (g) (1.296). Others traits *viz.,* days to 50% flowering (85.333), effective tillers per plant (5.430), length of spike (cm) (12.398), peduncle length (cm) (59.652), plant height (cm) (118.155), biological yield per plant (g) (30.933) and weight of 1000 grains (g) (56.704) exhibited maximum cluster mean in the cluster VII, X, IX, X, X, IX and VIII respectively. The identified genotypes superior in the

Table-3 : Cluster group means for 14 characters among wheat genotypes.

	Days to 50% Flowering	Flag Leaf Area (cm²)	Days to Maturity	Tillering	No.of Spikelets	Length of Spike (cm)	Peduncle Length (cm)	Plant Height (cm)	Biological Yield/ Plant (g)	Yield/ Spike (g)	Grains/ Spike	Grain Yield/ Plant (g)	Weight 0f1000 Grains (g)	Harvest Index
1 Cluster	82.796	24.184	125.423	4.795	17.074	10.326	40.134	83.224	17.201	2.025	34.706	9.536	34.525	55.419
2 Cluster	80.333	20.356	125.333	5.363	18.459	12.167	52.299	102.761	20.704	2.496	39.881	11.896	30.704	58.850
3 Cluster	79.000	33.670	122.000	4.363	13.259	8.600	48.199	74.588	13.170	1.363	27.881	5.430	36.037	41.123
4 Cluster	78.000	24.240	125.000	5.363	20.459	10.020	52.639	87.348	23.970	2.963	40.081	13.830	17.037	58.125
5 Cluster	76.667	26.616	127.000	4.430	14.059	8.513	38.852	78.855	20.437	1.296	30.281	6.763	27.037	35.416
6 Cluster	83.630	20.999	125.123	4.356	16.039	9.348	39.506	80.841	17.574	1.751	29.950	8.208	28.189	51.324
7 Cluster	85.333	27.236	123.333	4.963	17.259	9.667	49.979	114.562	13.904	2.496	38.881	7.896	33.704	57.173
8 Cluster	77.333	23.753	123.000	4.496	16.593	10.980	44.699	96.595	9.304	1.963	37.081	6.163	56.704	53.735
9 Cluster	83.667	27.104	121.889	5.022	19.311	12.398	44.156	111.269	30.933	2.200	37.000	10.356	40.000	33.647
10 Cluster	78.667	22.676	124.000	5.430	16.459	9.673	59.652	118.155	21.037	1.896	30.681	9.163	11.037	46.569

above cluster may be involved in a multiple crossing programmes to recover transgressive segregants with high genetic yield potential. Earlier studied have also reported substantial genetic divergence in wheat (6, 7, 8). 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 (8, 9). In conclusion the existence of considerable significant genetic variations was acquired among the genotypes for all the 14 selected quantitative characters under normal 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.

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