

ANALYSIS OF GENETIC DIVERGENCE FOR YIELD CONTRIBUTING TRAITS IN BREADWHEAT (*TRITICUM AESTIVUM* L.) GENOTYPES

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ABSTRACT

In the present study, fifty genotypes of wheat germplasms were evaluated for assessing genetic divergence for 14 different characters. The genetic diversity analysis revealed the formation of ten clusters suggested the presence of wide genetic diversity among the 50 genotypes studied. The clustering pattern indicated that geographic diversity was not associated with genetic diversity. The maximum inter-cluster distance (D) was observed between clusters VII and X (D = 81.93) followed by clusters I and X (D = 75.77) and VII and IX (D = 74.84). The minimum inter-cluster distance (D = 19.78) was found between clusters VI and VII. The 1000 grain weight, number of grains per main spike and grain yield per plant, number of spikelet per main spike, grain weight per main spike and length of main spike contributed maximum towards total genetic divergence. Based on the maximum genetic distance, it is advisable to attempt crossing of the genotypes from cluster VII with the genotypes of cluster X, which may lead to the generation of broad spectrum of favorable genetic variability for yield improvement in bread wheat. The genotypes from cluster X (KYP 853) can be crossed with VII, IX, and I in hybridization programme for obtaining a wide range of variation among the segregants.

INTRODUCTION

Wheat (*Triticum aestivum* L. em. Thell.) is a self-pollinated crop of the member of *Poaceae* family and one of the most leading cereal of many countries of the world including India. It is the most important food crop of India and is a main source of protein and energy. In India, wheat is the second most important food crop after rice both in terms of area and production. It has been described as the 'King of cereals' because of the acreage it occupies, high productivity and the prominent position it holds in the international food grain trade. To feed the growing population, the country wheat requirement by 2030 has been estimated at 100 million metric tons. To achieve this target, the wheat production has to be increased at the rate of < 1m.mt per annum (Sharma *et al.*, 2011) and this can be achieved by enhancing the production of wheat by developing improved varieties through heterosis breeding among parents having high genetic divergent. Over the past century selection of desirable parents for hybridization programme has been found as an effective operating implement in developing high yielding crop varieties upon which, the modern agriculture can rely. The presence of genetic diversity and genetic relationships among genotypes is a prerequisite and paramount important for successful wheat breeding programme. Developing hybrid wheat varieties with desirable traits require a thorough knowledge about the existing genetic variability. The more genetic diverse parents, the greater chances of obtaining higher heterotic expression in F₁'s and broad spectrum of variability in segregating population as

already reported by earlier workers (Shekhawat *et al.*, 2001). Precise information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization (Samsuddin, 1985). Several genetic diversity studies have been conducted on different crop species based on quantitative and qualitative traits in order to select genetically distant parents for hybridization (Shekhawat *et al.*, 2001; Arega *et al.*, 2007; Daniel *et al.*, 2011). Jagadev *et al.* (1991) reported that the character contributing maximum to the divergence should be given greater emphasis for deciding the type of cluster for purpose of further selection and the choice of parents for hybridization. Genetic improvement mainly depends upon the amount of genetic variability present in the population. The use of Mahalanobis's D² statistics for estimating genetic divergence have been emphasized by many workers (Murthy and Arunachalam, 1966) because it permits precise comparison among all the population in given any group before effecting actual crosses. In view of these facts, the present study was undertaken with the aim of examining the magnitude of genetic diversity and characters contributing to genetic diversity among bread wheat genotypes for utilization in wheat breeding programme.

MATERIALS AND METHODS

Fifty genotypes of bread wheat were sown in a Randomized Block Design (RBD) with three replications during *rabi* 2013. Each genotype was accommodated in a single row of 2.5 m

length with a spacing of 22.5 cm between rows. The experiment was surrounded by two guard rows to avoid damage and border effects. Other recommended agronomical practices in vogue were followed for reaping good crop. The observations were recorded on various quantitative characters *viz.*, days to 50% flowering, grain filling period, days to maturity, plant height, number of effective tillers per plant, length of main spike, peduncle length of main spike, number of spikelet per main spike, number of grains per main spike, grain weight per main spike, 1000 grain weight, grain yield per plant, biological yield per plant, harvest index. Five randomly selected competitive plants in each row of each replication for all the characters were recorded for all the traits under study except of days to 50 per cent flowering, grain filling period and days to maturity which were recorded on plot basis. The data subjected to different statistical analysis *viz.*, Analysis of genetic divergence using Mahalanobis's D^2 (1936) statistics was carried out as described by Rao (1952).

RESULTS

Genetic divergence (D^2) is the basis of variability and helps to craft the designed genotypes as per the requirement. The significant mean squares due to genotypes suggested the presence of ample variability. The D^2 -values between all possible pairs, which indicated the presence of greater diversity among the genotypes for all the traits. Grouping of the genotype was carried out by following Tocher's Method (Rao, 1952) with the assumption that the genotypes within the cluster have smaller D^2 -values among themselves than those from groups belonging to different clusters. In all, 10 clusters were formed from 50 genotypes. The composition of each cluster is given in Table 1 while clustering pattern is shown in Table 2.

The cluster I was having 8 genotypes from different geographical regions comprising 4 from Rajasthan, 3 from Gujarat and 1 from Haryana (Table 1). The cluster II was the largest one containing 20 genotypes of which, 7 from Gujarat, 5 from Uttaranchal, 3 from Haryana, 2 each from Maharashtra and Uttar Pradesh and 1 from Himachal Pradesh. The cluster III contained 7 genotypes of which 4 from Haryana and 3 from Gujarat. The cluster IV contained 9 genotypes of which 5 from Gujarat, 1 each from Uttaranchal, New Delhi, Uttar Pradesh and Himachal Pradesh. The cluster V, VII and VIII contained single genotype from Haryana. The cluster VI and IX contained single genotype from Uttaranchal. The cluster X contained single genotypes from Uttar Pradesh. Thus, the observed clustering pattern of genotypes was independent of their geographical origin (Table 2).

The inter and intra cluster distance values are given in Table 3. The maximum inter-cluster distance ($D=81.93$) was found between clusters VII and X carrying each one genotype followed by between clusters I and X ($D=75.77$) and VII and IX ($D=74.84$). The minimum inter-cluster distance ($D=19.78$) was found between clusters VI and VII. The Intra cluster distance ranged from 17.42 (cluster III) to 25.02 (cluster IV). The clusters V, VI, VII, VIII, IX and X each contained single genotype and therefore, their intra cluster distance was zero.

The cluster means for 14 characters are presented in Table 4. The coefficient of variation (CV %) was calculated for all the attributes. The maximum coefficient of variation was recorded for grain yield per plant (20.52%) followed by biological yield per plant (18.96%) and number of effective tillers per plant (17.42%). The lowest coefficient of variation was noted for grain filling period (1.63%) followed by days to 50% flowering (2.48%), 1000 grain weight (2.77%), number of spikelet per

Table 1 : Grouping of 50 genotypes of bread wheat in various clusters on the basis of D^2 – statistic

Cluster	No. of Genotypes	Name of the genotypes	Source
I	8	Raj-4216, Raj-4264, Raj-4266, Raj-4265 NWL-9-8, GW 2010-299, GW-366 LBPY-08-25	Rajasthan Gujarat Haryana
II	20	VW-20102, VW-20106, VW-0915, VW-20104, VW-867 GW 2010-276, GW-273, GW 2010-218, GW 2010-287, GW 2010-291, GW-322, J-07-40 LBPY-08-6, LPBY-08-2, LBPY-08-3 AKDW-4537, AKAW 4731 KLY-1082, KLY-1085 HPW-324	Uttaranchal Gujarat Haryana Maharashtra Uttar Pradesh Himachal Pradesh
III	7	LBPY-08-12, LBPY-08-5, LBPY-08-11, LBPY-08-13 GW-173, GW-496, GW 2010-285	Haryana Gujarat
IV	9	GW 09-201, NIAW-2075, LOK-65, GW 2010-297, GW 2010-296 VW-0916 KLY-1035 DL 1038 HPW-327	Uttaranchal Uttar Pradesh New Delhi Himachal Pradesh
V	1	DBPY-08-6	Haryana
VI	1	VW-0912	Uttaranchal
VII	1	DBPY-08-9	Haryana
VIII	1	LBPY-08-7	Haryana
IX	1	VW-0913	Uttaranchal
X	1	KYP-853	Uttar Pradesh

Table 2 : Source and clustering pattern in 50 genotypes of bread wheat

Source	I	II	III	IV	V	VI	VII	VIII	IX	X	Total number of genotypes
Gujarat	3	7	3	5	-	-	-	-	-	-	18
Maharashtra	-	2	-	-	-	-	-	-	-	-	2
Rajasthan	4	-	-	-	-	-	-	-	-	-	4
Uttaranchal	-	5	-	1	-	1	-	-	1	-	8
New Delhi	-	-	-	1	-	-	-	-	-	-	1
Haryana	1	3	4	-	1	-	1	1	-	-	11
Uttar Pradesh	-	2	-	1	-	-	-	-	-	1	4
Himachal Pradesh	-	1	-	1	-	-	-	-	-	-	2
Total	8	20	7	9	1	1	1	1	1	1	50

Table 3 : Average inter and intra-cluster distance (D="D²) values 50 genotypes of bread wheat

	I	II	III	IV	V	VI	VII	VIII	IX	X
I	17.56	46.97	57.66	29..79	44.4	33.1	41.22	54.27	50.23	75.77
II		21.03	31.33	31.08	27.44	43.46	51.41	31.3	36.78	37.69
III			17.42	41.07	38.08	41.97	53.87	36.86	51.54	40.92
IV				25.02	33.42	33.31	43.6	38.58	39.09	56.34
V					0	34.02	32.7	50.4	53.47	53.84
VI						0	19.78	57.37	63.35	72.57
VII							0	71.1	74.84	81.93
VIII								0	20.99	29.47
IX									0	41.47
X										0

Table 4 : Cluster mean for 14 different characters in 50 genotypes of bread wheat

Clusters	Days to 50% flowering	Grain Filling Period	Days to maturity	Plant height (cm)	Number of effective tillers per plant	Length of main spike (cm)	Peduncle length of main spike (cm)	Number of spikelet per main spike (cm)	Number of grains per main spike	Grain weight per main spike	1000 grain weight (g)	Grain yield per plant (g)	Biological yield per plant (g)	Harvest index (%)
I	58.38	37.88	96.25	76.31	3.88	7.81	32.18	16.99	49.18	2.7	57.16	8.73	17.79	49.02
II	56.13	37.93	94.07	76.04	4.13	10.48	31.9	18.76	61	2.77	45.45	9.15	18.24	50.47
III	62.48	35.38	97.86	78.88	4.58	10.88	32.32	17.88	47.1	2.04	41.98	7.29	16.59	45.21
IV	59.26	37.52	96.78	75.56	4.07	8.95	32.45	16.99	53.35	2.72	50.64	8.83	17.76	50.03
V	59.67	33	92.67	78.79	5.6	11.35	27.1	19	61.67	3.27	53.13	12.44	23.7	52.87
VI	52.33	40.67	93	81.37	5.07	10.87	36.61	16.2	42.27	2.45	56.62	9.77	18.84	51.41
VII	56	37.33	93.33	82.19	4.53	12.04	34.47	18.27	48.47	2.71	62.55	13.98	29.53	47.64
VIII	73	40.33	113.33	94.67	4.87	11.29	42.37	22.87	59.33	2.12	38.34	8.23	20.26	40.71
IX	60.67	36	96.67	75.49	3.4	7.1	32.97	16.93	63.8	2.86	40.33	7.75	15.73	49.02
X	73	39	112	99.35	5.07	13.35	33.44	24.8	68.47	2.18	33.51	8.31	24.97	33.35
Mean	58.7	37.46	96.25	77.5	4.21	9.89	32.41	18.14	55.34	2.62	48.01	8.87	18.32	48.86
S.Em. ±	0.84	0.91	0.88	1.93	0.42	0.25	0.89	0.4	1.76	0.14	0.77	1.05	2.01	2.6
C.V.%	2.48	1.63	4.1	4.32	17.42	4.51	4.79	3.81	5.53	9.51	2.77	20.52	18.96	9.23
Percentage contribution of characters towards total divergence														
No. of times appearing first	0	1	1	4	5	6	7	8	9	10	11	12	13	14
% contribution	0	0	0.08	0.08	0.16	1.06	0.24	19.43	22.12	8.57	25.96	22.12	0	0.16

main spike (3.81%), days to maturity (4.10%), plant height (4.32%), length of main spike (4.51%) and peduncle length of main spike (4.79%) while it was moderate for the number of grains per main spike (5.53%), harvest index (9.23%) and grain weight per main spike (9.51%).

Greater range of mean values among the clusters was recorded for different traits. Cluster X expressed the highest cluster mean values for days to maturity (73.00), plant height (99.35), length of main spike (13.35), number of spikelet per main spike (24.80) and number of grains per main spike (68.47). The cluster VIII had the highest mean values for days to 50% flowering (73.00), days to maturity (113.33) and peduncle length of main spike (42.37). The cluster VII had the highest mean values for grain yield per plant (13.98), 1000 grain weight

(62.55) and biological yield per plant (29.53). The cluster V was good for number of effective tillers per plant (5.60), grain weight per main spike (3.27) and harvest index (52.87). Similar findings have been also reported by Kumar *et al.*, 2013 reflected probability of getting better segregants and primary recombinants expected to more, in case if the genotypes of these clusters will be used in hybridization programme.. The cluster VI was good for grain filling period (40.67). The analysis of per cent contribution of various characters towards the expression of total genetic divergence (Table 4) indicated that 1000 grain weight (25.96%) followed by number of grains per main spike and grain yield per plant (22.12%), number of spikelet per main spike (19.43%), grain weight per main spike (8.57%) and length of main spike

(1.06%) contributed maximum towards total genetic divergence in the present study. These characters accounted for more than 99% of total divergence in the material studied.

DISCUSSION

Success of plant breeding programme depends largely on the choice of appropriate parents. It is expected that the utilization of divergent parents in hybridization results in promising recombinants. Genetic improvement mainly depends upon the amount of genetic variability present in the population. The use of Mahalanobis's D^2 statistics for estimating genetic divergence have been emphasized by many workers (Murthy and Arunachalam, 1966) because it permits precise comparison among all the population given in any group before effecting actual crosses.

Earlier, geographic diversity among the parents was generally taken as an index of genetic diversity. However, Gartan and Mittal (2003), Sharma and Suri (2005) and Dobariya *et al.* (2006) did not agree with this view and pointed out that geographical diversity need not result in genetic diversity. As a plant breeder, single character is not of much importance as the combined merit of number of desirable traits and it becomes more important when he is concerned with a complex trait like yield. So, for improving the grain yield, selection of parents based on number of characters having quantitative divergence is required which can be assessed by D^2 statistic developed by Mahalanobis (1936). In the present study, D^2 statistic estimated on 50 genotypes of bread wheat for 14 characters showed that the generalized distance ($\sqrt{D^2}$) between two populations varied from 17.42 to 25.02, which was an indicator of considerable diversity available in the material evaluated. On the basis of D^2 values, 10 clusters were formed from 50 genotypes. The clustering pattern of genotypes showed that the genotypes of different origins were clubbed into one cluster, whereas the genotypes belonging to same state or origin were grouped into different clusters indicating that the geographic distribution was not the sole criterion of genetic diversity. The results obtained in the present study are in accordance to the findings of Gartan and Mittal (2003), Sharma and Suri (2005) and Dobariya *et al.* (2006) who also reported that there was no parallelism between geographic distribution and genetic diversity.

The cluster I contained 8 genotypes from different origins. On the other hand, the clusters V, VI, VII, VIII, IX and X possessed only one genotype in each cluster. It means the overall genetic similarity was found in the germplasms were represented within the cluster and the pattern of distribution of genotypes in different clusters exhibited that geographical diversity was not related to genetic diversity as genotypes of same geographical region were grouped into different cluster and vice-versa, as supported by earlier finding of Langade *et al.*, 2013 and Kumar *et al.*, 2013. In general, intra-cluster distance values were lower than the inter-cluster distances. Thus, the genotypes included within a cluster tended to diverse less from each other. The lowest intra-cluster distance was in cluster III ($D=17.42$), whereas the highest intra-cluster distance was in cluster IV ($D=25.02$). The maximum inter-cluster distance (D) was observed between clusters VII and X ($D=81.93$) followed by

clusters I and X ($D=75.77$) and VII and IX ($D=74.84$). The minimum inter-cluster distance ($D=19.78$) was found between clusters VI and VII. The genotypes belonging to different clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. In this context, the genotypes from cluster X (KYP 853) can be crossed with VII, IX, and I in hybridization programme for obtaining a wide range of variation among the segregants. A wide range of variation for several characters among single as well as multi-genotype clusters was observed. However, the differences were clearer for grain yield per plant, biological yield per plant, number of effective tillers per plant, grain weight per main spike and harvest index. The present findings are in conformity with those reported earlier in wheat by Nimbalkar *et al.* (2002) and Singh *et al.* (2010). According to Rahim *et al.* (2010) who showed that the hybrids of genotypes with maximum distance resulted in high yield, the cross between these genotypes can be used in breeding programme to achieve maximum heterosis. The clustering pattern could be utilized in selecting the parents and deciding the cross combinations which may generate the highest possible variability for various traits. The clustering pattern could be utilized in selecting the parents and deciding the cross combinations which may generate the highest possible variability for various traits. The genotypes with high values of any cluster can be used in hybridization programme for further selection and improvement. In the present study, the cluster VII has the highest mean values for grain yield per plant, biological yield per plant and 1000 grain weight and Jagadev *et al.* (1991) reported that the character contributing maximum to the divergence should be given greater emphasis for deciding the type of cluster for purpose of further selection and the choice of parents for hybridization. The cluster V was good for number of effective tillers per plant, grain weight per main spike and harvest index. The cluster X had the highest mean values for length of main spike, number of spikelet per main spike and number of grain per main spike. The cluster VI was good for grain filling period. The cluster VI had the lowest mean values for days to 50% flowering. The cluster V had the lowest mean values for days to maturity and peduncle length of main spike. The cluster IX had the lowest mean values for plant height. Therefore, intercrossing of genotypes involved in these cluster would be useful for inducing variability in respective characters and their rational improvement for increasing the grain yield in wheat.

The analysis of percentage contribution of various characters contributed maximum towards total genetic divergence indicated that 1000 grain weight followed by number of grains per main spike, grain yield per plant, number of spikelet per main spike, grain weight per main spike and length of main spike in the present study. The present finding are supported with earlier reports of Nimbalkar *et al.*, 2002; Dobariya *et al.*, 2006; Chapla *et al.*, 2008 and Kolakar *et al.*, 2014. These characters accounted for more than 99% of total divergence in the material studied.

It has been well-established fact that more the genetically diverse parents used in hybridization programme, greater will be the chances of obtaining high heterotic hybrids and broad-spectrum variability in segregating generations (Arunachalam,

1981). There fore, based on the maximum genetic distance, it is advisable to attempt crossing of the genotypes from cluster VII with the genotypes of cluster X, which may lead to the generation of broad spectrum of favorable genetic variability for yield improvement in bread wheat.

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