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## Genetic variability, character association and path coefficient analysis in bread wheat (*Triticum aestivum* Desf.)

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**Abstract**

Genetic variability, correlation and path coefficient analysis was studied for grain yield and its components in 30 diverse genotypes of bread wheat. The analysis of variance revealed the significant differences among the genotypes for all the characters indicating presence of sufficient variability among the genotypes. Highest values for genotypic coefficient of variation was observed for grain yield (14.11) followed by grains per spike (12.05), number of spikelets (8.59) and 1000 grain weight (7.75) indicated wider genetic variation for these traits. Highest estimate of heritability was recorded for number of grains per spike (96.70) followed by days to 50% flowering (95.8), Days to maturity (93.10) and grain weight (91.40). Highest estimate of genetic advance was recorded for grain yield (15.66) followed by plant height (11.37), number of grains per spike (10.73) and Days to maturity (10.03). Genetic advance as a per cent of mean was observed highest for grain yield (27.78%) followed by number of grains (24.42%) and test weight (15.26%). The high heritability combined with high genetic advance as per cent of mean was observed for grain yield per plant indicated that selection may be effective for this character.

The correlation studies indicated that the grain yield showed strong significant and positive phenotypic correlation with test weight (0.9186), number of grains per spike (0.8678), ear head length (0.7805) and number of spikelets per ear head (0.6576), While 50% flowering (0.0366) showing non-significant positive correlation with grain yield. The grain yield showed significant and positive genotypic correlation with test weight (0.9249), number of grains per spike (0.8740), earhead length (0.7807) and number of spikelets per earhead (0.6612), while 50% flowering (0.0494) showing nonsignificant positive correlation with grain yield. The results of path analysis depicting that thousand grains weight, grains per spike, number of spikelets had higher magnitude of positive and direct effects on grain yield, should be important for yield improvement in bread wheat.

**Keywords:** Bread wheat, genetic variation, correlation, path analysis

**Introduction**

Okra [*Abelmoschus esculentus* (L.) Moench] is an annual herbaceous plant, native of tropical Africa commonly known as bhendi or lady's finger in India. It belongs to the family *Malvaceae* under the order *Malvales*, having a somatic chromosome number of cultivated species  $2n=82-130$  and is considered to be an amphidiploid. The recent trend in okra breeding has been towards development of hybrids to meet the specific uses coupled with high yield as it may be difficult to develop a hybrid having all the characters. The line x tester analysis developed by Kempthorne (1957) has been used in the present study to assess the genetic potentialities of the parents in hybrid combination (Griffing, 1956). Combining ability studies are more reliable as they provide useful information for the selection of parents in terms of performance of the hybrids and elucidate the nature and magnitude of various types of gene actions involved in the expression of quantitative traits. Therefore the present investigation was undertaken to study the association among different components and their direct and indirect contribution for productivity and quality in okra.

**Methods and Material**

Present investigation on Studies on performance of newly developed okra hybrids and its parents (*Abelmoschus esculentus* L.) for Productivity & Quality Traits for yield and yield attributing traits in okra was undertaken at Division at Biotechnology and crop improvement, COH, Bagalkot during 2016-17. Thirty Three hybrids were developed by crossing seven lines and three testers in Line x Tester fashion. All the crosses were evaluated along with the parents in randomized block design with two replications with the objective of assessing the performance of newly developed okra hybrids for productivity and quality traits. Statistical analysis were done using Window Stat software version 9.32.

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Wheat is the world's largest cereal crop of the Graminae (Poaceae) family. 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. The majority of the cultivated wheat varieties belong to three main species of the genus *Triticum*. These are the hexaploid, *T. aestivum* L. (bread wheat), the tetraploid, *T. durum* and the diploid, *T. dicoccum*. Globally, *T. aestivum* wheat is the most important species which covers 90 per cent of the area.

The world acreage under wheat crop is 221.12 million ha with production of 736.1 million tons with an average yield of 3160 kg ha<sup>-1</sup> (Anonymous, 2018) [2]. India contributes 12 per cent of the world wheat production. In India, wheat is the second most important crop after rice. Uttar Pradesh, Madhya Pradesh and Punjab are important states for both the area and production.

Wheat cultivation in Maharashtra is unique wherein all three cultivated species viz., *Triticum durum*, *Triticum aestivum*, and *Triticum dicoccum* are grown in typical hot tropical climate, characterized by the prevalence of high temperature during the crop growth. The area under wheat is about 1.07 million ha with annual production of 1.60 million tons (2017-18). The productivity is very low (1558 kg ha<sup>-1</sup>) as compared to national average of 3072 kg ha<sup>-1</sup>. Collection and evaluation of genotypes of wheat is a pre-requisite for any breeding programme, therefore, variability existing within each component trait must be exploited by selection to realize maximum gain in grain yield. Yield being a complex character is a function of several component characters and their interaction with environment. Information of genetic variability in the genetic system of a particular crop is sought as prerequisite with any crop improvement programme. Although increased grain yield is the ultimate goal of the plant breeders, grain yield itself is a product of interaction of many component traits which influence it directly or indirectly. The genotypic and phenotypic correlation reveals the degree of association between different characters and thus aid in selection to improve the yield and yield attributing characters simultaneously. A quantitative assessment of the genetic divergence among the collection of germplasm and their relative contribution of different traits towards the genetic divergence provide essential and effective information to breeder in hybridization programme for genetic improvement of yield. Genetic diversity plays an important role in plant breeding either to exploit heterosis or to generate productive recombinants. The choice of parents is importance in breeding programme. Correlation and path coefficient

analyses together give a clear cut picture of interrelationships and relative contribution of independent characters on dependent characters, which enables to a plant breeder to apply suitable selection procedures for crop improvement. The present investigation was, therefore, conducted to find out the major yield contributing traits in bread wheat.

### Materials and Methods

The present investigation consisted of 30 genotypes of bread wheat (*Triticum aestivum* L.) was conducted at Post graduate institute Farm, Mahatma Phule Krishi Vidyapeeth, Rahuri, Tal. Rahuri, Dist. Ahmednagar during Rabi, 2017-18. The details of origin/source of selected genotypes are given in Table 1. The experiment was conducted in Randomized Block Design (RBD) with two replications. The seeds were sown by dibbling. Each entry was represented by two rows of 2.5 meter length with spacing of 20 cm between the rows for timely sown irrigated conditions. The recommended dose of chemical fertilizers 120:60:40 NPK (kg/ha) was applied with all other recommended package of practices were carried out to raise a good crop.

Five plants were selected randomly from each treatment. The average from these five plants was worked out for the statistical computation on Days to 50 per cent flowering, Days to maturity, Plant height (cm), Earhead length (cm), Number of spikelets per earhead, Number of grains per earhead, Thousand grains weight (g), Grain yield (q/ha). The mean data were subjected to analysis of variance to test the level of significance among the genotypes for different characters according to Panse and Sukhatme (1995) [13]. Genotypic and phenotypic variances, genotypic and phenotypic coefficient of variability, broad sense heritability and correlation coefficients were computed according to the method suggested by (Johnson *et al.* 1955a) [8]. The genotypic and phenotypic coefficients of variation were calculated by the formulae as suggested by Burton and Devane (1953) Heritability percentage in broad sense was estimated as per the formula given by Burton (1952) [4]. Genetic advance was calculated by the formula given by Johnson *et al.* (1955a) [8]. The methodology proposed by Dewey & Lu (1959) [7] was used to perform the path analysis for grain yield and its components keeping grain yield as resultant variable and its components as causal variables. Cluster analysis was performed by using the STATISTICA software. The analysis of divergence was carried out by D<sup>2</sup> statistic of Mahalanobis (1936) as described by Rao (1952) [14]. The analysis of covariance for characters pairs, based on plot averages was carried out (Cochran and Cox, 1957) [5].

**Table 1:** List of Bread Wheat Genotypes with Pedigree

S. N.	Genotype	Pedigree	SN	Genotype	Pedigree
1	NIAW-3170	SKOLL/ROLF07	16	NIAW-3553	AKAW 4210-6 X NIAW 1594
2	NIAW-3354	FRET2*/BRAMBLING//MESIA/3/BECARD	17	NIAW-3562	MACS 6348 X LOK 62
3	NIAW-3390	BECARD/CHYAK	18	NIAW-3584	RAJ 4083 X NIAW 1594
4	NIAW-3386	BECARD/QUAIU#1	19	NIAW-3592	(LOK 62 X RAJ 4083)X(HD 2987)X(LOK 1)
5	NIAW-3523	WBLLI*2/KURUKU//HEIIO	20	NIAW-3636	AKAW 4210-6 X RAJ 4083
6	NIAW-3525	CS/TH.SC//3*PVN/3/MIRIO/BUC/4/URES/JUN//KAUZI//5/HUIT/7/CS/TH.C	21	NIAW-3559	NIAW 1621 X NIAW 1594
7	NIAW-3270	NIAW 917 X NIAW 1415	22	NIAW-3575	LOK 62 X VW 514
8	MACS-6478	CS/TH.SC//3*VN/3/MIRLO/BUC/4/MILAN/5/TILHI	23	NIAW-3578	LOK 62 X NIAW 1621
9	MACS-6222	HD 2189*2/MACS 2496	24	NIAW-3583	RAJ 4083 X LOK 63
10	HD-2932	KAUZ/STAR//HD2643	25	NIAW-3633	AKAW 4210-6 X MACS 3040
11	AKAW-4627	WH-147/SUNSTAR*6/C-80-1	26	NIAW-34	CNO 79 / PRL "S"
12	NI-345	MONDHYA 417-5/HOFED I	27	Phule Samadhan	NIAW 34/PBW435
13	NIAW-3581	LOK 54 X KING BIRD	28	TRIMBAK	SERI 82/3/MRS/JUP/HORK 'S'
14	NIAW-3624	DL 1022 X NIAW 1415	29	TAPOVAN	GW 244 / BOB WHITE
15	NIAW-3643	RAJ 4083 X NIAW 1275	30	NETRAVATI	GW 9506/PRL/PRL

## Results and Discussion

### Genetic variability

Mean squares for Days to 50 per cent flowering, Days to maturity, Plant height (cm), Earhead length (cm), Number of spikelets per earhead, Number of grains per earhead,

Thousand grains weight (g) and Grain yield (q/ha) showed highly significant differences between genotypes (Table 2). Such considerable range of variations provided a good opportunity for yield improvement.

**Table 2:** Range, mean, mean squares and standard error of means for eight quantitative characters of thirty wheat genotypes

S. N.	Character	Range	Mean	Mean square	Standard error of means
1	Days to 50% flowering	56.50-69.50	60.66	22.873**	0.4965
2	Days to maturity	97.50-115.50	105.40	52.772**	1.8735
3	Plant height (cm)	72.25-96.50	82.34	78.569**	6.5383
4	Earhead length (cm)	9.26-12.70	10.67	1.316**	0.1134
5	No.of spikelets	10.50-17.50	14.03	3.756**	0.8482
6	Grains/ spike	35.50-52.50	43.95	57.150**	0.9706
7	Thousand grains weight(g)	39.60-51.50	45.92	26.560**	1.1984
8	Yield q/ha	41.33-68.31	56.47	133.246**	6.2329

\*, \*\* Significant at 5% and 1% probability respectively

The analysis of variance revealed significant differences among the genotypes for all the eight characters studied (Table 3). The magnitude, phenotypic coefficients of variation were greater than genotypic coefficients of variation. Highest phenotypic coefficient of variation was exhibited by grain yield (14.78) followed by grains per spike (12.26), number of spikelets (10.81) and 1000 grain weight (8.11). Highest values for genotypic coefficient of variation were observed for grain yield (14.11) followed by grains per spike (12.05), number of spikelets (8.59) and 1000 grain weight (7.75). Comparatively lower phenotypic and genotypic coefficient of variation was observed for days to 50% flowering and Days to maturity.

In the present investigation, medium estimates of genotypic and phenotypic coefficients of variation were observed for the characters viz., grain yield followed by grains per spike, number of spikelets, 1000 grains weight, plant height and earhead length. Similar results were obtained for grain yield per plant, number of tillers per plant and number of grains per ear head by Kumar *et al.* (2009)<sup>[9]</sup> and Devi *et al.* (2014)<sup>[6]</sup>. Whereas, low estimates of genotypic and phenotypic coefficients of variation were observed for the characters days to 50% flowering and Days to maturity. Low estimates of GCV and PCV were reported by Kumar *et al.* (2009)<sup>[9]</sup> for days to 50% flowering and Asaye *et al.* (2013)<sup>[3]</sup> for days to maturity. Highest heritability in broad sense was recorded for number of grains per spike (96.70) followed by days to 50% flowering (95.8), Days to maturity (93.10), grain weight (91.40) and grain yield (91.70). An estimate of genetic advance was recorded for grain yield (15.66) followed by plant height (11.37), number of grains per spike (10.73) and Days to maturity (10.03). Genetic advance as a per cent of mean was observed highest for grain yield (27.78%) followed

by number of grains (24.42%) and test weight (15.26%). The differences between GCV and PCV were very low for all the characters indicating less role of environment in the expression of these characters. The presence of high genetic variability is an indication of good scope for their improvement through hybridization followed by selection. These results are in conformity with results of Majumder *et al.* (2008)<sup>[12]</sup>. High heritability coupled with moderate genetic advance was reported earlier by Subhashchandra (2009)<sup>[15]</sup> for plant height. Whereas, high heritability with low genetic advance was also reported by Kumar *et al.* (2013)<sup>[10]</sup> for days to maturity. Heritability and genetic advance are important selection parameters. The correlation coefficients estimated between grain yields with all other characters are presented in Table 4. The grain yield showed strong significant and positive phenotypic correlation with test weight (0.9186), number of grains per spike (0.8678), earhead length (0.7805), number of spikelets per earhead (0.6576), While 50% flowering (0.0366) showing non significant positive correlation with grain yield. Grain yield showed significant negative correlation with days to maturity (-0.1326). The grain yield showed strong significant and positive genotypic correlation with test weight (0.9249), number of grains per spike (0.8740), earhead length (0.7807), number of spikelets per earhead (0.6612), While 50% flowering (0.0494) showing non significant positive correlation with grain yield. Grain yield showed significant negative correlation with days to maturity (-0.1276). It was observed that, seed yield per plot had significant positive correlation with thousand grains weight, grains per spike, earhead length, number of spikelets, 50 per cent flowering at both genotypic and phenotypic levels while character like days to maturity and plant height negatively correlated at both the levels.

**Table 3:** Estimation of variability parameters for different characters of bread wheat

S. N.	Characters	Genotypic Variance	Phenotypic Variance	Genotypic coefficient of variability%	Phenotypic coefficient of variability%	Heritability % (bs)	Genetic advance	Genetic Advance as% mean
1	Days to per cent flowering	11.189	11.685	5.51	5.63	95.80	6.74	11.114
2	Days to maturity	25.449	27.323	4.786	4.959	93.10	10.03	9.516
3	Plant height (cm)	36.016	42.554	7.288	7.922	84.60	11.37	13.811
4	Earhead length (cm)	0.602	0.715	7.26	7.92	84.10	1.466	13.72
5	Yield (q/ha)	63.507	69.74	14.11	14.78	91.10	15.66	27.73
6	Number of grains per spike	28.09	29.06	12.05	12.26	96.70	10.73	24.42
7	Thousand grains weight (g)	12.68	13.87	7.75	8.11	91.40	7.01	15.26
8	Number of spikelets/earhead	1.45	2.302	8.59	10.81	63.20	1.97	14.06

**Table 4:** Estimates of genotypic correlation (below diagonal) and phenotypic correlation (above diagonal) for different quantitative characters of wheat

S. N.	Characters	50% flowering	Days to maturity	Plant height(cm)	Earhead length (cm)	Number of spikelets	Grains / spike	Thousand grain weight (g)	Yield (q/ha)
1.	50% flowering	1.000	0.483**	0.022	0.068	0.074	0.064	-0.109	0.036
2.	Days to maturity	0.524**	1.000	0.068	-0.017	-0.027	0.0004	-0.143	-0.132
3.	Plant height (cm)	0.014	0.052	1.000	-0.519**	-0.529**	-0.590**	-0.439**	-0.489
4.	Earhead length (cm)	0.084	0.0008	-0.470**	1.000	0.626**	0.689**	0.739**	0.780
5.	Number of spikelets	0.106	0.0006	-0.455**	0.583**	1.000	0.518**	0.595**	0.657
6.	Grains / spike	0.071	0.004	-0.594**	0.696**	0.537**	1.000	0.821***	0.867
7.	Thousand grain weight (g)	-0.101	-0.136	-0.401**	0.726**	0.596**	0.826**	1.000	0.918
11.	Yield (q/ha)	0.049	-0.127	-0.447**	0.780**	0.661**	0.874**	0.924**	1.000

Path coefficient analysis provides an effective way of finding out direct and indirect sources of correlations. The results of path analysis are summarized in the Table 5 depicting that thousand grains weight, grains per spike, number of spikelets had higher magnitude of positive and direct effects on grain yield. Days to 50% flowering, earhead length showed low but positive direct effect on grain yield.

Highest positive direct effect was exerted by test weight on grain yield followed by grains per spike, number of spikelets, 50% flowering, earhead length which is in conformity with the reports of Zeeshan *et al.* (2013) [16] wherein they observed appreciable positive direct effect of thousand grains weight. Ajmal *et al.* (2009) [1] reported high direct effect of 1000 seed weight on seed yield.

**Table 5:** Direct and indirect effect of different quantitative and nutritional characters on seed yield of wheat

S. N.	Characters	50% flowering	Days to maturity	Plant height (cm)	Earhead length (cm)	Number of Spikelets	Grains/spike	Thousand grains weight (g)	Yield (q/ha)
1.	50% flowering	0.108	-0.057	-0.0005	0.0074	0.0134	0.0287	-0.0446	0.0494
2.	Days to maturity	0.056	-0.110	-0.002	0.0001	0.0001	0.0017	-0.059	-0.127
3.	Plant height (cm)	0.001	-0.005	-0.037	-0.041	-0.057	-0.238	-0.175	-0.447
4.	Earhead length (cm)	0.009	-0.0001	0.017	0.088	0.073	0.279	0.317	0.780
5.	Number of spikelets	0.011	-0.0001	0.017	0.051	0.125	0.215	0.260	0.661
6.	Grains/spike	0.007	-0.0005	0.022	0.061	0.067	0.401	0.361	0.874
7.	Thousand grain weight (g)	-0.011	0.015	0.150	0.064	0.074	0.331	0.437	0.924

Estimation of genetic divergence by Mahalanobis D<sup>2</sup> statistics for 30 bread wheat genotypes with eight characters were grouped into eight clusters in which cluster II was with thirteen genotypes emerged as the largest cluster.

Cluster I was with nine genotypes, cluster III with three genotypes. The clusters IV, V, VI, VII, VIII contained 1 genotype each (Table 6).

The maximum inter cluster distance was observed between cluster III and VII (944.33) followed by cluster III and V (792.98), cluster VI and VII (685.91) and cluster I and VII (583.22). The maximum Intra cluster divergence among the eight clusters revealed that cluster III had maximum intra cluster distance (135.48) followed by cluster II (134.32) and cluster I (100.60).

**Table 6:** Distribution of 30 genotypes of wheat in to different clusters

Cluster	Number of genotypes included	Genotypes
I	9	NIAW-3386, NIAW-3578, NIAW-3553, NIAW-3575, NIAW-3633, HD-2932, NIAW-3562, NIAW-3636, NIAW- 345
II	13	NIAW-3354, NIAW-3525, AKAW-4627, NIAW-3624, NIAW-3523, NIAW-1994 (Phule Samadhan), NIAW-3583, NIAW-3581, NIAW-301(Trimbak), MACS-6478, NIAW-3270, MACS-6222, NIAW-34
III	3	NIAW-3643, NIAW-3592, NIAW-3584
IV	1	NIAW- 3559
V	1	NIAW- 917 (Tapovan)
VI	1	NIAW- 3390
VII	1	NIAW- 3170
VIII	1	NIAW- 1415 (Netravati)

**Table 7:** Average intra (diagonal) and inter (above diagonal) cluster D and D<sup>2</sup> (in bracket values of 8 clusters formed from 30 genotypes of bread wheat

Cluster	I	II	III	IV	V	VI	VII	VIII
I	10.03 (100.60)	17.69 (312.93)	13.20 (174.24)	16.08 (258.56)	23.13 (534.99)	14.02 (196.56)	24.15 (583.22)	14.02 (196.56)
II		11.59 (134.32)	23.31 (543.34)	14.31 (204.77)	14.70 (216.09)	21.21 (449.86)	13.96 (194.88)	16.42 (269.61)
III			11.64 (135.48)	21.62 (467.42)	28.16 (792.98)	17.10 (292.41)	30.73 (944.33)	17.15 (294.12)
IV				0.00 (0.00)	17.99 (323.64)	19.76 (390.45)	21.65 (468.72)	17.46 (304.85)
V					0.00 (0.00)	20.95 (438.90)	15.10 (228.01)	16.23 (263.41)
VI						0.00 (0.00)	26.19 (685.91)	11.89 (141.37)
VII							0.00 (0.00)	22.32 (498.18)
VIII								0.00 (0.00)



Cluster means for eight characters are presented in Table 8. It revealed a wide range of variability for most of the characters. The summarized information on intra-cluster (diagonal) and

inter cluster distances among eight clusters is presented in the Table 7, which revealed that the intra- cluster distance value ranged from 0.00 to 135.48.

**Table 8:** Mean performance of cluster for 8 characters in 30 wheat genotypes

Characters / Clusters	50% flowering	Days to maturity	Plant height (cm)	Earhead length (cm)	Yield (q/ha)	Grains /spike	Thousand grains weight (g)	Number of spikelets
I	59.61	104.83	78.47	11.36	63.16	48.78	48.65	14.39
II	59.69	105.38	85.02	10.27	50.76	39.73	43.96	13.62
III	61.50	101.50	78.40	10.49	62.55	50.00	48.93	14.50
IV	61.00	110.00	78.95	9.95	41.67	40.50	40.75	11.50
V	68.50	111.50	89.10	9.55	49.17	37.00	39.60	14.00
VI	69.50	109.50	83.20	11.72	65.33	50.00	47.50	14.50
VII	60.50	97.50	91.75	10.55	54.33	36.50	43.40	13.50
VIII	63.50	115.50	80.79	11.35	67.80	49.00	50.50	17.50

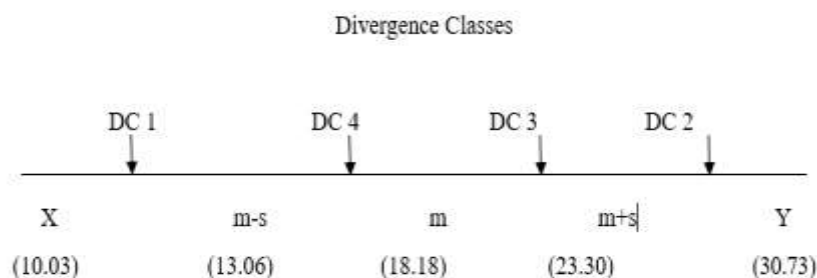
In this context, maximum inter cluster distance was observed between cluster III and VII (944.33). The minimum inter-cluster distance (141.37) was observed between cluster VII and VIII, indicating close genetic association between the genotypes of these two clusters.

#### Genetic divergence and selection of potent parent

In the present study, an attempt was made to classify the cluster combination into four divergence classes by following

the above procedure suggested by Arunachalam and Bandyopadhyay (1984).

The statistical distance (D2) given in Table 7, represents the index of genetic diversity among the clusters. The mean of clusters and intra-clusters was 18.18 and standard deviation 5.12. The minimum (X) and maximum (Y) values among these distances were 10.03 and 30.73, respectively. Thus, the divergence classes were as



**Table 9:** Distribution of different clusters combinations into four divergence classes based on D2 values between them (Cluster Combinations).

DC 1 →	Y (30.70) (I, VII), (II, III), (III, V), (III, VII), (VI, VII)
DC 2 →	m + s (23.30) (I, V), (II, VI), (III, IV), (IV, VI), (IV, VII), (V, VI), (VII, VIII)
DC 3 →	m (18.18) (I, II), (I, III), (I, IV), (I, VI), (I, VIII), (II, IV), (II, V), (II, VII), (II, VIII), (III, IV), (III, VIII), (IV, V), (IV, VIII), (V, VIII), (V, VIII)
DC 4 →	m-s (13.06) (VI, VIII)
→	X (8.75)

Keeping in view all the above aspects, the following genotypes in the present studies, deserve to be considered as potent parents for future crossing programme for improvement of seed yield and yield contributing characters.

SN	Genotypes	SN	Genotypes	SN	Genotypes
1	NIAW-3170	6	NIAW-3386	11	NIAW-3592
2	Netravati	7	NIAW-3354	12	MACS-6222
3	HD-2932	8	NIAW-3553	13	NI-345
4	NIAW-3636	9	NIAW-34	14	NIAW-3525
5	NIAW-3390	10	Phule Samadhan		

Considering the inter-cluster distance, cluster means and *per se* performance of genotypes and divergence class, the above

genotypes may be utilized in future breeding programme for creating maximum spectrum of variability for different yield contributing characters which will facilitate to develop superior genotypes with respect to more than one characters and also possible to improve more than one character simultaneously. The per cent contribution of the eight characters studied towards the total divergence was presented in Table 11. It was revealed that grains per spike (28.97%) contributed highest for genetic divergence followed by number of spikelets (25.75%), 50% flowering (10.57), days to maturity (8.51), yield (6.44), thousand grains weight (5.29), earhead length (4.60) However, the characters *viz.*, plant height (0.46) contributed least to genetic divergence.

**Table 10:** Tentative suggested crossing programme

SN	Characters to be improved	Cluster combination with inter cluster distance	Possible crosses
1.	Earliness days to maturity	I x II (17.69)	NIAW-3170 X NIAW-3270
		I x IV (16.08)	HD-2932 x NIAW-3559
2.	Earhead length	I x VI (14.02)	NIAW-3633 X NIAW-3390

		I x VIII (14.02)	NIAW-3553 X Netravati
3.	Number of spikelets	VIII x II (16.42)	Netravati x NIAW-3583
		I x III (13.20)	HD-2932 X NIAW-3592
4.	Number of grains per earhead	III x VIII (17.15)	NIAW-3592 X Netravati
		I x III (13.20)	NIAW-3553 X NIAW-3592
5.	Grain yield per hectare	I x VI (14.02)	HD-2932 X NIAW-3390
		VIII x I (14.02)	Netravati x NIAW-3633
		I x III (13.20)	NI-345 X NIAW-3584
		I x II (17.69)	NIAW-3575 X NIAW-3270

**Table 11:** Per cent contribution of 8 characters for divergence in wheat

S. N.	Characters	Number of times appeared 1 <sup>st</sup> in ranking
1.	Days to 50 per cent flowering	46
2.	Days to maturity	37
3.	Plant height (cm)	2
4.	Earhead length (cm)	20
5.	Yield (q/ha)	28
6.	Grains per spike	126
7.	Thousand grains weight (g)	23
8.	Number of spikelets	112

### Summary and Conclusions

Considerable amount of variability was observed in the bread wheat genotypes. Phenotypic coefficient of variation (PCV) was found to be marginally higher than the genotypic coefficient of variation (GCV) for all the characters, indicating the dominance of phenotypic coefficient of variation for expression of these traits. Highest phenotypic coefficient of variation was exhibited by grain yield (14.78) followed by grains per spike (12.26). Highest estimate of heritability was recorded for number of grains per spike (96.70) followed by days to 50% flowering (95.8), Days to maturity (93.10). Highest estimate of Genetic advance was recorded for grain yield (15.66) followed by plant height (11.37), number of grains per spike (10.73), Days to maturity (10.03), thousand grain weight (7.01) and Days to 50% flowering (6.74). Genetic advance as a per cent of mean was observed highest for grain yield (27.78%) followed by number of grains (24.42%). High estimates of genotypic coefficient of variation among the genotypes indicates variability for the characters viz., grain yield followed by grains per spike, number of spikelets, thousand grain weight, plant height and earhead length. High heritability coupled with high genetic advance were observed for the traits viz., for grain yield followed by number of grains, thousand grains weight and number of spikelets indicating that the heritability is due to additive gene effect and direct selection in early generations may be effective.

Seed yield per plot recorded significant positive correlation with thousand grains weight, number of grains per spike, earhead length, number of spikelets per earhead at both genotypic and phenotypic levels so these characters could be improved through selection. Whereas, Grain yield showed non significant positive correlation with 50% flowering at genotypic as well as phenotypic level indicating that this variation due to by chance and seed yield is depend on this characters.

Path coefficient analysis revealed that test weight had highest direct effect on seed yield per hectare followed by grains per spike, number of spikelets, 50% flowering and earhead length therefore emphasis should be given on these characters while making selection for desired improvement for seed yield of bread wheat. The genotypes grouped into eight clusters, Cluster II was with 13 genotypes each emerged as the largest cluster. Cluster I was with 9 genotypes, cluster III with 3

genotypes were larger clusters. The clusters IV, V, VI, VII, VIII were mono-genotypic.

The maximum inter cluster distance was observed between cluster III and VII (944.33) followed by cluster III and V (792.98) indicating that genetic constitution of the genotypes in one cluster had close proximity with the genotypes in other clusters of the pair. The maximum Intra cluster divergence among the eight clusters revealed that cluster III had maximum intra cluster distance (135.48) followed by cluster II (134.32) and cluster I (100.60) suggesting that the genotypes present in these cluster might have different genetic architecture and might have originated from different genetic pool, indicating wide divergence among these clusters. On the basis of divergence classes (DC) crosses of genotypes from different clusters can be formulated for next programme and this was grouped on that crosses present between different clusters and separated by moderate genetic distance would give yield with heterotic effect of F<sub>1</sub> and transgressive segregants in advance generation.

On the basis of inter cluster distances, cluster mean and *per se* performance and divergence class observed in the present study, the genotypes viz., NIAW-3170, Netravati, HD-2932, NIAW-3390, NIAW-3386, NIAW-3354, NIAW-3553, Phule Samadhan, NIAW-3592, MACS-6222, NI-345, AKAW-4627, NIAW-3575, NIAW-3270, NIAW-3559 and NIAW-3525 were distinct and diverse and can be classified as promising genotypes. These genotypes could be used in crossing programme to achieve desired segregants in bread wheat.

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