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Genetic diversity analysis for various morphological and quality traits in bread wheat (*Triticum aestivum* L.)

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Abstract: The present investigation was carried out during 2011-12 in a randomized block design (RBD) with 35 diverse wheat genotypes to assess the genetic diversity for various morphological and quality traits. The analysis of variance for grain yield and its contributing components namely days to 50% flowering, days to maturity, productive tillers, plant height, spike length, spikelets pet spike, grains per spikelet, biological yield, harvest index, 1000 grain weight, grain yield and gluten content showed highly significant differences (at <1% level of significance) among the genotypes under present study. High heritability along with high genetic advance and high phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for grain yield (g), biological yield (g), harvest index (%), spike length (cm) and 1000 grain weight (g) indicated substantial contribution of additive gene action in the expression and thus selection would be effective for genetic improvement of these traits for improving grain yield in wheat. On the basis of multivariate analysis, 35 genotypes were grouped into '6' clusters based on genetic divergence (D^2) value. The compositions of clusters revealed that the Cluster IV contained the highest number of genotypes (9) followed by Cluster II (8), Cluster VI (8) and Cluster III (7). The highest inter cluster values were recorded between cluster III and V (8357.19) followed by cluster IV and V (7513.88), cluster IV and VI (6009.44) and cluster III and VI (5530.40) exhibiting wide genetic diversity. Among different traits, biological yield (32.12%), productive tillers (28.74%), harvest index (26.71%), plant height (24.20%), grain yield (19.23%) and grains per spikelets (14.89%) had maximum contribution to total genetic divergence, therefore may be used as selection parameters in transgressive segregants. Selection of genotypes from the clusters may be used as potential donors for further hybridization programme to develop genotypes with high yield potential in wheat crop.

Keywords: Bread wheat, Genetic diversity, Genetic parameters, Gluten content, Yield traits

INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is the second most important cereal crop of India and plays a vital role in food and nutritional security. About nearly 55 percent of the world population depends on wheat for about 20 percent of calories intake (Anonymous 2016). India holds second position in both area and production after china and second most important crop planted to an area of 30.23 million hectares with production amounting to 93.50 million tons (Anonymous 2016). To feed the growing population, the country wheat requirement by 2030 has been estimated at 100 million metric tons and hence, there is an immediate need to increase wheat production to achieve this target (Sharma *et al.*, 2011). This can be achieved by enhancing the production of wheat by developing improved varieties through heterosis breeding among parents having high genetic divergence. The main objective of any plant breeding programme is to develop cultivars of high yield potential with acceptable quality. The knowledge of genetic variability for yield and its contributing components helps in the improvement of grain yield and planning of effective breeding programme. The creation and utilization of genetic diversity is essential to overcome the problems of narrow genetic base and also to generating precise information on the nature and degree of genetic diversity in selecting the parents for targeted hybridization. The cluster analysis is an appropriate method for determining family relationship i.e. to determine the extent of genetic distance of genotypes from each other. Therefore, information on the genetic diversity for grain yield is important to meet the diversified goal of plant breeding such as breeding for increasing yield, wide adaptation and desirable quality traits (Lal *et al.*, 2009). A wide range of genetic variability present in the material under study provides chances for selection of desired plant types. Therefore this experiment was conducted to identify genetically divergent wheat genotypes as donors, with desirable traits for hybridization for grain yield and other yield contributing components in wheat crop.

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MATERIALS AND METHODS

The experimental material comprised 35 diverse genotypes of wheat were evaluated in a randomized block design (RBD) with three replications during 2011-12 at Crop Research Centre, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut (U.P.). Plot size was kept as four rows of 3.0 m length with row to row distance of 23 cm and plant to plant distance of 10 cm. All the recommended agronomical practices (irrigation at all critical stage, dose of fertilizers) were adopted to raise the normal crop. Observation were recorded on five randomly selected plants in each replications for days to 50% flowering, days to maturity, number of productive tillers per plant, plant height (cm), spike length (cm), number of grains per spikelet, number of spikelets per spike, biological yield per plant (g), harvest index (%), grain yield per plant (g), 1000 grain weight (g) and gluten content (%). The mean values from each replication were subjected to statistical analysis using SAS and CROPSTAT (commercial version) computer software. The analysis of variance (ANOVA) was done based on the method suggested by Panse and Sukhatme (1969). The PCV and GCV were calculated by the formula suggested by Burton and De Vane (1953). Heritability and genetic advance as percent of means for each character was calculated following formula as suggested by Johnson *et al.* (1955). Also, data were subjected to non-hierarchal Euclidean cluster statistic (Spark, 1973). The genetic diversity was done through cluster analysis using D^2 statistics suggested by Mahalanobis (1936) and they were grouped into five clusters based on D^2 value using Tochers method suggested by Rao, (1952).

RESULTS AND DISCUSSION

Analysis of variance: The analysis of variance (ANOVA) indicated highly significant differences among the genotypes for days to 50% flowering, days to maturity, productive tillers, plant height, spike length, number of spikelets pet spike, number of grains per spikelet, biological yield, harvest index, 1000 grain weight, grain yield and gluten content (Table 1) revealing the existence of sufficient genetic variability in the present set of breeding materials for all the traits under study. The characters which have sufficient genetic variability suggested that a crossing programme involving diverse genotypes may lead to an overall improvement in wheat crop. Significant differences among the genotypes for different morphological and quality traits were also earlier reported by Singh *et al.* (2013), Singh *et al.* (2014), Tewari *et al.* (2015), and Kumar *et al.* (2016a) in wheat crop.

Genotypic and phenotypic variability: The phenotypic coefficient of variation (PCV) was slightly higher than their corresponding genotypic coefficient of variation (GCV) for all the morphological and quality traits among the genotypes indicated that the characters were less influenced by the environment, therefore selection on the basis of phenotype alone can be effective for the improvement of these traits (Table 2). Higher values of PCV and GCV indicated that there was high variability exiting among the genotypes. The higher values of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded for biological yield (PCV=28.57% and GCV=82.42%) followed by spike length (PCV=27.32% and GCV=26.96%), 1000 grain weight (PCV=26.09% and GCV=26.03%), grain yield (PCV=25.36% and GCV=25.18%), harvest index (PCV=22.35% and GCV=21.14%), number of productive tillers per plant (PCV=18.65% and GCV=16.34%), number of grains per spikelet (PCV=17.09% and GCV=15.67%) and plant height (PCV=10.17% & GCV=10.14%) indicating better opportunity for improvement in these traits through selection. A range of PCV (1.98 to 33.03%) and GCV (1.75% to 32.03%) were reported by Verma *et al.* (2014) whereas a range of PCV (0.81% to 9.07%) and GCV (0.50% to 8.08%) reported by Kumar *et al.* (2017). The other researchers namely Singh *et al.* (2013), Singh *et al.* (2014) and Kumar *et al.* (2016a) also reported high value of PCV and GCV for grain yield and tillers per plant in wheat crop at different location of India. High phenotypic and genotypic coefficient of variation for grain yield, harvest index and tillers per plant were also reported by Kumar *et al.* (2016a) in wheat. A close examination of phenotypic

Table 1. Analysis of variance (ANOVA) for 12 morphological and quality traits in bread wheat.

Character	Replication (d f=2)	Treatments (d f=34)	Error (d f=58)
Days to maturity	11.92	358.66**	7.65
Days to 50 % flowering	0.30	165.01**	7.43
Plant height	0.10	249.08**	0.52
Productive tillers	0.53	2.96**	0.89
Spike length	0.09	1.89**	0.06
Spikelets per spike	0.48	7.48**	0.22
Grains per spikelet	0.01	0.12**	0.02
1000 grain weight	0.04	17.80**	0.13
Harvest index	18.25	72.71**	5.17
Biological yield	10.13	114.28**	15.62
Gluten content	0.01	1.31**	0.02
Grain yield	8.45	27.61**	3.49

Table 2. Estimates of genetic parameters for 12 morphological and quality traits in bread wheat.

Character	Mean	Range		Heritability (broad sense)	GCV	PCV	Genetic advance as % of mean
		Minimum	Maximum				
Days to 50% flowering	84.50	74.33	97.67	87.60	8.58	9.16	16.54
Days to maturity	125.93	113.00	140.33	93.86	8.59	8.87	17.14
Plant height	89.80	73.87	108.87	99.37	10.14	10.17	20.81
Productive tillers	6.74	4.58	9.03	43.80	16.34	18.65	16.83
Spike length	11.19	9.13	13.13	90.58	26.96	27.32	23.66
Spikelets per spike	17.78	14.53	20.80	91.73	8.76	9.14	17.27
Grains per spikelet	3.30	2.93	3.87	63.96	15.67	17.09	9.34
1000 grain weight	40.27	34.46	45.83	97.77	26.03	26.09	22.27
Harvest index	42.60	30.79	56.66	81.32	21.14	22.35	20.69
Gluten content	8.69	7.04	9.72	99.86	6.93	7.62	15.68
Biological yield	31.44	20.30	46.67	97.80	28.24	28.57	30.94
Grain yield	13.39	9.50	20.66	69.73	25.18	25.36	36.44

Table 3. Distribution pattern of 35 genotypes of wheat into ‘6’ clusters based on non-hierarchal Euclidean cluster analysis.

Clusters	Genotypes	Name of genotypes
I	2	WHEAR//2*PRL/2*PAS-TOR, FRET*2/4/SNI/TRAP#3/KAUZ*2/TR AP///KAUZ/5/.
II	8	MUNAL#1, WHEAR//2*PRL/2*PASTOR, MARCHOUCH*/SAADA/3/2*FRET2/KUKUNA//FRET2, WAXWING/6/PVN// CAR422/AN A/5/BOW/CROW//BUC/, ATTILA*2//CHIL/BUC*2/3/KUKUNA, KAUZ//ALTAR84/AOS/3/MILAN/KAUZ/4/HUITES/7/, ATTI LA/3 / *BCN//BAV92/3/TILHI/5/BAV92/3/PR, ROLF07/YANAC//TAUPETOF2001/BRAMBLI NG.
III	7	PRL/2*PASTOR,INQALAB91*2/TUKURU//WHEAR,WBLL1/KUKUNA//TACUPETOF2001/5/WAXWING/4/, KAUZ//AL TAR 84/ AOS/3/MILAN/KA UZ/7/CAL/NH//, WBLL*2/VIVITSI/4/D67.2/P66.270//,WAXWING/WHEAR//WAXWING/KIRITATI,PBW343*2/KUKUNA*2//YANAC.
IV	9	PBW343, ROELFS F2007, WBLL1//UP2338*2/VINITSI, FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ/5/,CAL/NH/H567.71/3/SERI/4/CAL/NH//H567.71/5/,ROLF07/YANAC/TACUPETO F2001/BRA MB LING, FRET2/KUKU NA//FRET2/3P ARUS/ 5/FRET2*2/4/SNI/, FRET2/KUKUNA//FRET2/3YANAC/4/FRET2*2/4/KIRITATI,WBLL1*2/KUKUNA*2//WHEAE.
V	1	FRET*2/4/SNI/TRAP#/3/KAUZ*2/TRAP///KAU/5/.
VI	8	TACUPETOF2001/BRAMBLING//KIRITATI, OLF07/YANAC//TAUPETOF2001/BRAMBLI NG, ROLF07*2/KIRITAI, FRET*22/4SNI/TRAP#1/3/KAUZ*2/TRAP///KAUZ*2/, FRET2/KUKUNA//FRET2/3PASTOR//HXL7573/2*BAU/, TRCH/SRTU/5/ KAUZ//A LTAR84/AOA/3/MILAN/KAUZ/, PBW343*2/KUKUNA//PARUS/3/PBW343*2/KUKUNA, PBW343*2/KUKUN A//PARUS/3/ PBW3 43*2/KUKUNA

Table 4. Average inter and intra cluster distances among ‘6’ clusters for 35 wheat genotypes.

Cluster	I	II	III	IV	V	VI
I	**382.26**	905.86	1841.64	1295.53	3450.59	2668.91
II		**473.58**	1334.14	2087.89	4159.19	2155.33
III			**437.06**	1244.92	8357.19	5530.40
IV				**263.49**	7513.88	6009.44
V					**1047.88**	1625.73
VI						**738.34**

and genotypic coefficient of variation indicating better opportunity for improvement in grain yield based on the selection of above traits in wheat crop.

Estimates of heritability (broad sense) and genetic advance: The estimates of high heritability (>60%) coupled with high genetic advance (>20%) were recorded for plant height (h^2=99.37% and GA=20.81%), spike length (h^2=90.58% and GA=23.66%), 1000 grain weight (h^2=97.77 and GA=22.27%), harvest index (h^2=81.32 and GA=20.69%), biological yield (h^2=97.80% and GA=30.94%) and grain yield (h^2=69.73% and GA=36.44%) whereas high heritability with moderate genetic advance were estimated for days to 50% flowering (h^2=87.60% and GA=16.54%), days to maturity (h^2=93.86% and GA=17.14%), spikelets per spike (h^2=91.73% and GA=17.27%) and gluten content (h^2=99.86% and GA=15.68%) in (Table 2). While, moderate heritability coupled with moderte genetic advance were recorded for productive tillers. Similar findings pertaining to high heritability along with high genetic advance were also earlier reported by Singh *et al.* (2013), Singh *et al.* (2014), Meena *et al.* (2014), and Kumar *et al.* (2016a) in wheat crop. High heritability along with high genetic advance and high coefficient of variability (PCV and GCV) for grain yield, biological yield, harvest index, spike length and

Table 5. Mean values of clusters and contribution of various morphological and quality traits towards total divergence in 35 diverse wheat genotypes.

Character Cluster	**Days to 50% flowering**	**Days to maturity**	**Plant height**	**Productive tillers**	**Spike length**	**Spikelet's/ spike**	**Grains/ spikelet**	**1000 grain weight**	**Harvest index**	**Gluten content**	**Biological yield**	**Grain yield**
I	88.00	132.13	97.29	7.09	11.51	17.87	3.32	40.59	43.47	8.67	32.82	14.34
II	81.37	121.30	83.24	6.68	10.96	17.12	3.19	39.30	40.41	8.70	29.99	12.11
III	80.12	118.67	84.28	6.68	10.99	17.42	3.34	40.30	43.97	9.42	29.70	12.96
IV	97.17	139.00	99.80	6.45	11.73	19.73	3.57	44.35	40.30	9.32	41.67	16.78
V	86.08	127.92	97.48	6.32	11.27	18.87	3.20	39.10	42.31	7.39	30.06	12.75
VI	82.83	127.83	78.60	6.62	10.77	17.57	3.50	41.09	45.49	7.74	30.50	13.91
Contribution to total divergence	2.49	4.35	24.20	28.74	4.67	1.51	14.89	6.22	26.71	5.04	32.12	19.23

1000 grain weight exhibited good scope for improving these traits through selection. However, expression of traits viz; days to maturity and flowering, plant height, grains per spikelet and spikelets per spike that showed high heritability but moderate to low genetic advance and coefficient of variation whereas productive tillers showed moderate heritability, genetic advance and coefficient of variation, may be due to non-additive gene action therefore in such cases simple selection may not be very rewarding and hybridization followed by selecting desirable transgressive segregants would be the better option for improving these traits.

Genetic diversity analysis: The results of genetic diversity among 35 diverse wheat genotypes for various morphological and quality traits are presented in (Table 3). Based on the results of genetic diversity, 35 genotypes were grouped into six clusters by non-hierarchical Euclidean cluster statistics in such a way that the genotypes within a cluster had a small or low D^2 values than those of in between the clusters. The compositions of cluster revealed that Cluster I (2), Cluster V (1), Cluster II (8), Cluster IV (9), Cluster III (7) and Cluster VI (8) had different number of genotypes. These results showed that number of genotype in different cluster as expected varied. The grouping of genotypes based on multivariate analysis has also been reported earlier by Singh *et al.* (2014), Verma *et al.* (2014), Tewari *et al.* (2015), Kumar *et al.* (2016b) and Vora *et al.* (2017).

The inter cluster distance was higher than the intra cluster distance indicating wide genetic diversity among the genotypes (Table 4). The inter cluster distance varied from 905.86 (cluster I & II) to 8357.19 (cluster III & V). The other notable inter cluster distance were recorded between cluster IV and V (7513.88), IV and VI (6009.44), III and VI (5530.40) which indicates that the genotypes involved in these clusters have wide genetic diversity and thus can be used in wheat hybridization programme for improving grain yield. The inter-cluster values that indicated close relationship were to be considered that hybridization among the genotypes of these clusters would not provide good levels of segregation. It is well recognized that greater the distance between clusters, wider the genetic diversity would be between the genotypes. Similar findings were also reported by Singh *et al.* (2014) and Verma *et al.* (2014). Therefore, highly divergent genotypes would produce a broad spectrum of segregation in the subsequent generations enabling further selection and improvement. The hybrids developed from the selected genotypes within the limit of compatibility of these clusters may produce desirable transgressive segregants of high magnitude of heterosis. This information would be very useful in planning wheat breeding programme particularly for improving grain yield in wheat crop. Verma *et al.,* (2014), Tewari *et al.* (2015), Kumar *et al.* (2016b) and Vora *et al.*

(2017) also reported similar findings on genetic diversity for different yield contributing components in wheat.

The maximum intra cluster distance was observed in clusters V (1047.88) followed by cluster VI (738.34), cluster II (473.58), and cluster III (437.06). The maximum intra cluster distance was mainly due to wide genetic diversity among the genotypes of these clusters. The maximum intra cluster distance was (13.96) by Verma *et al.* (2014), (391) by Kumar *et al*. (2016b), and (26.40) by Vora *et al.* (2017) reported in wheat crop. On the other hand, cluster IV (263.49) had minimum intra cluster distance indicating that compactness of clusters changed in different environments. The low genetic diversity and selection of parents within the cluster having higher mean values for a particular character may also be useful for further improving wheat genotypes for grain yield.

'6' clusters showed considerable differences in mean value for different morphological and quality traits under present study (Table 5). Two genotypes of cluster-I were responsible for high cluster mean for productive tillers (7.09) and eight genotypes in cluster-III were responsible for high cluster mean for gluten content (9.42). Nine genotypes in cluster IV were responsible for high cluster mean for days to 50 % flowering (97.17), days to maturity (139.00), plant height (99.80), spike length (11.73), number of spikelets per spike (19.73), number of grains per spikelet (3.57), 1000 grain weight (44.35), biological yield (41.67) and grain yield (16.78) while eight genotypes in cluster VI were responsible for harvest index. These were, thus adjudged to be considered suitable for creating maximum variability by hybridization and selecting the desired genotypes for higher grain yield. The contribution of the characters towards total divergence revealed that maximum percentage of contribution came from biological yield (32.12%) followed by productive tillers (28.74%), harvest index (26.71%), plant height (24.20%), grain yield (19.23%) and number of grains per spikelets (14.89%). The other traits namely days to 50% flowering, days to maturity, spike length, number of spikelets per spike, 1000 grain weight and gluten content had low percentage of contribution to total genetic divergence, therefore these traits may be used as selection parameters in segregating generations. Lal *et al.* (2009) also reported that grain yield, tillers per plant, plant height, spike length contributed maximum to genetic diversity.

Conclusion

Based on the above results may be concluded that analysis of variance (ANOVA) exhibited significant differences among the genotypes for all morphological and quality traits estimated under present study. The traits which have sufficient variability suggested that hybridization programme involving these diverse genotypes may lead to transgressive segregants and thus an overall genetic improvement in wheat crop. Inter and intra cluster distance indicated sufficient genetic diversity between and within clusters. It would be desirable to choose the donor from different clusters. The highest inter cluster distance was observed between cluster (III and V), cluster (IV and V), cluster (IV and VI) and cluster (III and VI) exhibiting wide genetic diversity and therefore could be useful in wheat hybridization programmes aiming high grain yield.

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