

Original Research Article

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Assessment of Genetic Diversity in Promising Bread Wheat (*Triticum aestivum* L.) Genotypes

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ABSTRACT

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An experiment with thirty three genotypes of bread wheat carried out to study the nature and magnitude of divergence using Mahalanobis D^2 statistics, in randomized block design with three replications. The data for thirteen important quantitative traits were recorded from the genotypes raised. The variability study indicated high to moderate phenotypic and genotypic coefficient of variation accompanied by high heritability and genetic advance as per cent of mean for traits, plant height, number of tillers per plant, flag leaf area, chlorophyll content, canopy temperature, spike length, grains per spike, grain yield per plot and harvest index indicating their importance in selection for yield improvement. The thirty three genotypes of bread wheat were grouped into six clusters using Tocher's method. The genotypes in cluster III and cluster VI, exhibited high degree of genetic diversity. Cluster I was suitable for spike length, flag leaf area, grains per spike, thousand grain weight, and grain yield per plot. Days to fifty per cent flowering and harvest index contributed maximum towards genetic divergence.

Introduction

Wheat (*Triticum aestivum* L.) is considered as king of cereals and it provides foods to 36% of the global population, contributing 20% of the food calories. It is an important staple food of many countries in the world and occupies a unique position as used for the preparation of a wide range of food stuffs. 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. Efficient and economic crop improvement scheme refers to

the collection of superior alleles into a single population. Genetic variability in a population can be partitioned into heritable and non-heritable variation with the aid of genetic parameters such as variance, genotypic coefficient of variation, heritability and genetic advance, which serve as a basis for selection of some outstanding genotypes from existing ones (Tsegaye *et al.*, 2012). Choice of parents is not only based on desirable agronomic traits, components of yield and extent of variability but also on heritability of yield contributing traits. The environment, in which selection is made, is also important because heritability and genetic advance vary

with change in environment (Korkut *et al.*, 2001). The study of genetic variability reveals about the presence of variation in their genetic constitution and it is outmost important as it provide the basis of effective selection. Grain yield is a complex trait and highly influenced by many genetic factors and environmental fluctuations. In plant breeding programme, direct selection for yield as such could be misleading. A successful selection depends upon the information on the genetic variability and association of morpho-agronomic traits with grain yield. In views of these facts, thirty three wheat genotypes were evaluated in this study to determine the magnitude of variability among the germplasm and grouping pattern of genotypes in different cluster. To identify genetically diverse and agronomically desirable genotypes for exploitation in a breeding programme aimed at improving grain yield potential of wheat.

Materials and Methods

The experiment was conducted in a randomized block design with three replications. The experimental materials were sown during *Rabi*, 2015 keeping plot size 3.0 m × 2.5 m. In each replication each genotype was grown in a plot of 5 rows of 3 meter length each with a spacing of 22.5 cm between rows. In order to compare the genotype unbiasedly, uniform plant population was kept in each row. Five random plants per genotype per replication were tagged to record observations on yield and yield attributing traits *viz.*, days to fifty per cent flowering, days to maturity, plant height, number of tillers per plant, spike length, flag leaf area, chlorophyll content, canopy temperature, relative water content, number of grains per spike, grain yield per plot, harvest index, 1000-grain weight. Flag leaf length and width of five randomly selected plants were taken by measuring scale and flag leaf area was calculated by following formula:

Flag leaf area (cm²) = flag leaf length (cm) x flag leaf width (cm) (Mokhtarpour *et al.*, 2010).

Harvest index was calculated as per the formula (Huhn 2008).

$$\text{H.I.} = \frac{\text{Economic yield}}{\text{Biological yield}} \times 100$$

Where,

Economic yield = Grain yield (g)

Biological yield = Total plant yield (g)

The data were analyzed using WINDOSTAT version 9.1 software for computation of analysis of variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (h²b) and clustering by Tocher's method.

Results and Discussion

In the present investigation, Thirty three diverse genotypes of bread wheat were studied to assess their yield and yield related attributing characters. The analysis of variance clearly indicated that there was highly significant variation among the genotypes for all the traits studied. This in turn indicated that there was sufficient variability in the material studied, which could be utilized in further breeding programme. Similarly, many earlier workers, Bhushan *et al.*, (2013), Degewione *et al.*, (2013), Fellahi *et al.*, (2013), Kumar *et al.*, (2014) and Yadav *et al.*, (2014) reported high variability for different traits in bread wheat which provides ample scope for selecting superior and desire genotypes by the plant breeder for further improvement.

The phenotypic variances (Table 1) for all the traits under studied were higher than the genotypic variances (Yadav *et al.*, 2006). This

may be due to the non-genetic factor which played an important role in the manifestation of these characters. Wide ranges of variance (phenotypic and genotypic) were observed in the experimental material for all the characters under investigation. The maximum phenotypic and genotypic variance exhibited by the traits, grain yield per plot, grains per spike, harvest index, chlorophyll content, plant height, relative water content, days to fifty per cent flowering and days to maturity. These findings were in accordance of Singh *et al.*, (2003), Sen *et al.*, (2007), Majumder *et al.*, (2008) and Kumar *et al.*, (2009). The genotypic and phenotypic coefficients of variation for grains per spike and harvest index were found high indicating the importance of this trait in evaluation and selection of the genotypes. These results are in agreement with Raj Bahadur and Lodhi (1995), Singh *et al.*, (2003), Yadav *et al.*, (2006), Sen *et al.*, (2007), Ali *et al.*, (2008) and Kumar *et al.*, (2014).

High heritability in broad sense were recorded for all the characters namely tillers per plant, flag leaf area, days to fifty per cent flowering, chlorophyll content, canopy temperature, relative water content, spike length, grains per spike, days to maturity, 1000-grain weight and grain yield per plot. High heritability value for these traits indicated that the variation observed was mainly under genetic control and was less influence by environment. So, these traits may be used as selection criteria for yield improvement in confirmation with the result of earlier workers *viz.*, Islam *et al.*, (2012), Kumar *et al.*, (2014) and Fellahi *et al.*, (2013). In the present investigation, the characters, namely tillers per plant, flag leaf area, chlorophyll content, canopy temperature, spike length, grains per spike, grain yield per plot and harvest index have high heritability and genetic advance as per cent of mean. The high heritability associated with high genetic advance indicated, the variation was mostly

due to additive gene effects. Hence, direct selection can be done through these characters for future improvement of genotypes for higher grain yield. Similar results were also reported by earlier workers (Islam *et al.*, 2012; Singh *et al.*, 2014 and Yadav *et al.*, 2014).

Thirty three genotypes (including check) were grouped into six clusters on the basis of D^2 statistics (Table 2). Cluster I and IV had maximum number of genotypes (9) *viz.*, 21st SAWYT307, 21st SAWYT332, 34th ESWYT146, 46th IBWSN1095, AKAW4900, 8th EBWYT507, LBPY-2014-7, 21st SAWYT316 and LBPY 2013-1 in cluster I and HD2643, PBW343, 3043, 46th IBWSN1113, HD2733, HD2967, 34th ESWYT124., PBW373, 46th IBWSN1107 in cluster IV respectively. Cluster II and V had five genotypes each *viz.*, 4051, 7004, 3054, 4043, HUW234 in cluster II and 6041, HD2932, LBPY-2014-2, RAJ4120 and DBW14 in cluster V respectively. Cluster VI had four genotypes *viz.*, 5011, 34th ESWYT121, DBW15, DBW39. Cluster III was solitary, comprising single genotype *viz.*, GW2013-471. The clustering pattern showed that there was no formal relationship between geographical diversity and genetic diversity. Similar studied based on D^2 statistic was also performed by Shoran and Tondon (1995), Ribadia *et al.*, (2007), Roy *et al.*, (2009) and Ferdous *et al.*, (2011). Different clusters comprises unique feature for different characters under investigation. Cluster III had the maximum mean value for thousand grain weight, grain weight per plot, chlorophyll content, relative water content and harvest index. Cluster III had genotype with low mean value for canopy temperature. Cluster I had the genotype with the highest mean value for tillers per plant, spike length, flag leaf area and grains per spike. Cluster V may be selected as a donor for dwarfness as well as for early maturity (Table 3).

Table.1 Estimates of variability parameter of yield and yield attributing traits

Sl. No	Characters	σ_g^2	σ_p^2	GCV	PCV	h^2 (Broad sense)%	GA as % of Mean
1	Plant height (cm)	37.91	96.20	7.04	11.21	39.41	9.10
2	Days to 50 per cent flowering	26.48	27.12	7.08	7.16	97.65	14.41
3	Flag Leaf Area(cm ²)	11.12	14.81	16.62	19.18	75.11	29.67
4	Numbers of Tillers per Plant	1.24	1.87	19.57	24.06	66.17	32.79
5	Chlorophyll content	42.17	46.31	16.13	16.90	91.07	31.72
6	Canopy temperature	10.48	14.88	15.68	18.69	70.43	27.12
7	Relative water content	35.17	55.63	6.59	8.29	63.23	10.79
8	Spike length	1.44	1.61	11.14	11.80	89.09	21.66
9	Number of grains per spike	115.14	126.54	22.72	23.82	90.99	44.65
10	Days to maturity	24.70	31.52	4.35	4.91	78.36	7.94
11	1000 grain weight	12.39	14.73	8.68	9.46	84.16	16.41
12	Grain yield per plot	3589.82	4304.15	14.96	16.39	83.40	28.16
13	Harvest Index (%)	103.85	114.81	22.14	23.27	90.46	43.36

Where, σ_g^2 = Genotypic variance, σ_p^2 = Phenotypic variance, GCV= Genotypic coefficient of variation, PCV=Phenotypic coefficient of variation h^2 =heritability, GA= Genetic Advance

Table.2 Clustering pattern of 33 genotypes of bread wheat on the basis of D^2 statistic

Cluster No.	No. of Genotypes within cluster	Genotypes in cluster
I	9	21 st SAWYT307, 21 st SAWYT332, 34 th ESWYT146, 46 th IBWSN1095, AKAW4900, 8 th EBWYT507, LBPY-2014-7, 21 st SAWYT316, LBPY 2013-1
II	5	4051, 7004, 3054, 4043, HUW234
III	1	GW2013-471
IV	9	HD2643, PBW343, 3043, 46 th IBWSN1113, HD2733, HD2967, 34 th ESWYT124., PBW373, 46 th IBWSN1107
V	5	6041, HD2932, LBPY-2014-2, RAJ4120,DBW14
VI	4	5011, 34 th ESWYT121, DBW15, DBW39

Table.3 Cluster mean for thirteen characters in bread wheat

Cluster No.	PH	TPP	SL	FLA	DFP	G/S	TGW	GWP	CC	RWC	CT	DTM	HI
I	95.45	6.01	12.23	21.42	74.41	59.11	42.85	435.56	44.04	92.07	19.48	113.85	51.79
II	85.28	5.90	10.31	17.92	65.27	48.69	37.33	349.33	32.80	81.87	25.47	110.40	35.94
III	86.73	5.90	12.20	20.80	69.00	51.50	44.00	515.00	47.33	96.67	16.33	115.00	62.48
IV	84.27	5.86	10.32	21.17	77.30	41.37	40.00	420.19	43.81	94.11	18.85	116.96	49.06
V	81.94	4.87	9.73	17.55	67.07	40.89	40.73	403.33	42.33	93.67	18.33	108.53	48.09
VI	86.75	5.22	9.91	20.17	75.75	38.62	39.50	307.25	28.67	79.67	25.17	120.17	32.26

Abbreviations- Plant Height (PH), Tillers per plant (TPP), Spike length (SL),Flag Leaf Area (FLA), Days to 50 per cent flowering (DFP), Grains per spike (GPS),1000-Grain weight (TGW), Grain yield per plot (GWP), Chlorophyll content (CC), Relative water content (RWC), Canopy temperature (CT), Days to Maturity (DTM), Harvest Index (HI)

Table.4 Mean intra and inter cluster distance (D^2) among six cluster in bread wheat

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	34.12	138.36	59.05	69.86	115.56	124.98
Cluster II		22.67	145.25	187.99	93.52	118.96
Cluster III			0.00	89.73	51.46	208.33
Cluster IV				49.36	125.17	119.81
Cluster V					32.27	196.07
Cluster VI						50.05

Table.5 Diverse bread wheat genotypes based on cluster mean and superior per se performance for the traits under investigation

Sl. No.	Characters	Cluster	Suitable Parents in Cluster	Per se Performance
1	Plant Height (cm)	V	RAJ4120 DBW14	70.40 75.10
2	Tillers per plant	I	LBPY2014-7	7.13
3	Spike length (cm)	I	8 th EBWYT507* 34 th ESWYT146* AKAW4900* 21 st SAWYT332* LBPY2013-1* 46 th IBWSN1095* 21 st SAWYT307* LBPY-2014-7* 21 st SAWYT316*	13.20 12.73 12.53 12.47 12.43 12.10 11.73 11.46 11.43
4	Flag leaf area (cm ²)	I	AKAW4900	25.45
5	Days to fifty per cent flowering	II	7004* 4043* 4051* 3054* HUW234*	63.00 64.00 64.66 66.33 68.33
6	Grains per spike	I	21 st SAWYT332* 46 th IBWSN1095* 21 st SAWYT307* 21 st SAWYT316* LBPY-2014-7* AKAW4900* LBPY2013-1* 34 th ESWYT146* 8 th EBWYT507*	69.13 65.66 64.20 58.96 57.76 55.93 53.70 53.66 52.96
7	Thousand grain weight	I	LBPY2013-1	46.66
8	Grain yield per plot (g)	I	LBPY-2014-7*	488.33
9	Chlorophyll content	III	GW2013-471*	47.33
10	Relative water content	III	GW2013-471	96.67
11	Canopy temperature (°C)	III	GW2013-471	16.33
12	Days to maturity	V	DBW14* RAJ4120*	104.00 110.00
13	Harvest index	III	GW2013-471*	62.47

Cluster II was suitable for early flowering. Therefore, these clusters may be chosen for transferring the traits having high mean values through hybridization programme. Selection of genotypes based on cluster mean for the better exploitation of genetic potential also reported by Dwivedi and Pawar (2004), Roy *et al.*, (2009), Hailegiorgis *et al.*, (2011) and Desheva and Kyosev (2014). The highest intra cluster distance (Table 4) was observed in cluster VI followed by cluster IV, cluster I, cluster V and cluster II indicating differences in genotypes within cluster. Least intra cluster distance was found in cluster II indicating that close resemblance between the genotypes presented in this cluster.

The genotypes in cluster III and cluster VI due to maximum inter cluster distance between them, exhibited high degree of genetic diversity and thus may be utilized under inter varietal hybridization programme (transgressive breeding) for getting high yielding recombinants. Similar inter varietal crosses may be attempted between genotypes in cluster V and VI and cluster II and IV. The lowest inter cluster distance was observed between cluster III and V followed by cluster I and III and cluster I and IV showing these clusters were relatively less divergent and crossing between them cannot produce vigorous offspring (F_1 progenies). These results of genetic diversity study were in agreement with the finding of Gupta *et al.*, (2002), Ribadia *et al.*, (2007) and Sanghera *et al.*, (2014) suggested that genotypes of most diverse cluster may be used as parents in hybridization programmes to develop high yielding varieties.

In the present study, 33 diverse genotypes were grouped into various cluster and suitable diverse genotypes were selected based on their cluster mean superiority and *per se* performance for different characters. LBPY-2014-7 grouped in cluster I exhibited

superiority for grain yield per plot based on highest cluster mean and significant superior *per se* performance. This genotype also exhibited superiority for tillers per plant based on highest cluster mean and superior *per se* performance. GW2013-471 grouped in cluster III exhibited superiority for chlorophyll content and harvest index based on highest cluster mean and significant superior *per se* performance. GW2013-471 also exhibited superiority for relative water content based on highest cluster mean and superior *per se* performance. This genotype also exhibited superiority for canopy temperature based on lowest cluster mean and superior *per se* performance. RAJ4120 and DBW 14 grouped in cluster V exhibited earliness in days to maturity based on cluster mean (lowest) and significantly superior *per se* performance (Table 5). LBPY-2013-1 grouped in cluster I exhibited superiority for thousand grain weight based on highest cluster mean with superior *per se* performance. RAJ4120 and DBW14 of cluster V also exhibited superiority for plant height based on lowest cluster mean with superior *per se* performance. 4051, 4043, 3054, 7004, HUW234 grouped in cluster II exhibited earliness in days to fifty per cent flowering based on cluster mean (lowest) and significantly superior *per se* performance. 21st SAWYT307, 21st SAWYT332, 34th ESWYT146, 46th IBWSN1095, AKAW4900, 8th EBWYT507, LBPY-2014-7, 21st SAWYT316, LBPY2013-1 grouped in cluster I exhibited superiority for spike length and grains per spike based on highest cluster mean with significantly superior *per se* performance. AKAW 4900 grouped in cluster I also exhibited superiority for flag leaf area based on highest cluster mean with superior *per se* performance.

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