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Research Article

Genetic diversity analysis in bread weat (*Triticum aestivum* L.) under Gangetic Alluvium Zone of West Bengal

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Abstract
Forty-nine genotypes of bread wheat (*Triticum aestivum* L.) were screened at District farm, AB Block, B.C.K.V., Kalyani, Nadia, West Bengal during *Rabi* season for two years, i.e. 2015-2016 and 2018-2019 following Randomized Block Design with two replications to study genetic diversity following the Mahalanobis D^2 statistics and principal component analysis. The highest contribution towards total divergence was yield plant^{-1} followed by the number of grains spike^{-1}, plant height, weight of grains spike^{-1} and the test weight. The maximum inter-cluster distance was observed between cluster IX and I (86.392), followed by clusters VIII and IX (82.829) indicating that the genotypes being represented in these clusters were distantly related. Therefore, any two genotypes selected from these two clusters may be utilized in crossing programs to synthesis potential high yielding genotypes. Principal component analysis (PCA) extracted 5 principal components explaining 80% to genetic variation. The PCA suggested that the genotypes are highly diverse.

Key words
Bread wheat, Cluster analysis, Genetic diversity analysis, Principle component analysis, Yield.

INTRODUCTION

Central Asia, the Near East, the Mediterranean, and the Ethiopian region are the most important centers of diversity for wheat and its associated species (Kundu and Nagarajan, 1996). Most varieties of cultivated wheat belongs to the three main species of the genus *Triticum*. These are hexaploids (n = 21), *T. aestivum* L. (bread wheat), tetraploid (n = 14), *T. Durum*, and diploid (n = 7), *T. Dicoccum* and *T. monococcum*. Globally, *T. aestivum* is the most important species covering 90 per cent of the area. A wide array of materials including wheat landraces, local varieties, advance lines, and crosses with ancestral species are being used by different wheat breeding programs in the country to generate the necessary genetic diversity. Genetic diversity information among elite germplasm or cultivars is useful to (i) classify lines for desirable traits (Mahmood *et al*., 2004), (ii) determine the genetic diversity reduction due to long term plant breeding programs (Fu and Somers, 2009), and (iii) evaluate genetic differentiation by different breeding programs (Ali *et al*., 2008). With the improvement in yield, the emphasis is on better quality products such as bread, biscuits, and chapati to improve the quality of bread wheat. Therefore, an accurate knowledge of the nature and degree of genetic diversity present in the wheat collection from its main areas will help to select parents for evolving the superior varieties. D^2 statistics is a concept developed by Mahalanobis (1936) an important tool and technique to assess the genetic diversity. The principal component

analysis (PCA) is performed as a multivariate analysis tool which helps investigators to distinguish significant relationships between the characters.

MATERIALS AND METHODS

In the present experiment, forty-nine genotypes of bread wheat (**Table 1**) were sown during the *Rabi* season for two years i.e. *Rabi* 2015-2016 and *Rabi* 2018-2019 in a Randomized Block Design, with two replications at District Farm, AB Block, B.C.K.V. Kalyani, West Bengal, which is situated at the Latitude of 23.5^{0}N and Longitude of 89.0^{0}E and at an altitude of 9.75 m above the mean sea level. The experimental soil was Gangetic alluvial sandy loam in texture having soil pH 6.9 to 7.0 with good drainage facility. It had a medium fertility level. The gross plot was separated by two blocks and the size of each plot was 6 m x 1.2 m. In each plot, there were 6 rows of one genotype. The blocks were taken as the replication and each block, in turn, was divided between 49 equal plots. Five randomly selected plants were taken per replication for individual genotype to record data for the characters *viz.* Days to heading (the time when 50% of the spikes have emerged from the flag leaf sheath), Days to flowering (the time when 50% of plants in each genotype flower from the sowing date), Days to maturity, plant height (cm), the number of tillers plant^{-1}, Spike length (cm), the number of spikelets spike^{-1}, the number of grains spike^{-1}, Grain weights spike^{-1} (g), Test weight (g), Yield plant^{-1}(g) and Grain protein percent (%). The Multivariate analysis of D^2 statistics was done according to Mahalanobis (1936). Correlated variables for significance have been tested according to Rao (1952) using 'V' statistics which in turn uses Wilk's criterion. After Tocher's method (Rao, 1952), the cultivars were divided into different groups called clusters. The principal component analysis was done as per Harman (1976).

RESULTS AND DISCUSSION

For testing the significance, the Chi-square test was carried out which indicated the population was divergent. So D^2 analysis was carried out. The highest contribution towards total divergence was yield plant^{-1} followed by the number of grains spike^{-1}, plant height, weight of grains spike^{-1}and test weight (**Table 2**). Bergale *et al.* (2001) had reported that plant height had the greatest contribution to genetic divergence. Singh *et al.* (2006) also reported similar findings.

Table 1. List of Bread Wheat genotypes used in the experiment.

Sl. No.	Genotypes	Sl. No.	Genotypes	Sl. No.	Genotypes
1	UP 2936	17	DBW 88	33	HD 1962
2	HD 3218	18	BRW 3785	34	UP 2937
3	DBW 189	19	WH 1202	35	DBW 191
4	HUW 801	20	UP 2939	36	DBW 192
5	JKW 230	21	RAJ 4464	37	K 1502
6	WH 1200	22	BRW 3786	38	PBW 761
7	DBW 190	23	HD 2967	39	PBW 744
8	NW 6078	24	PBW 747	40	DBW 187
9	HD 3221	25	HD 3219	41	PBW 746
10	WH 1204	26	HUW 802	42	K 0307
11	PBW 745	27	DBW 194	43	DBW 188
12	WH 1105	28	WH 1203	44	HD 3223
13	NW 6094	29	RAJ 4465	45	UP 2938
14	RAJ 4463	30	UP 2940	46	WH 1201
15	K 1501	31	RAJ 4462	47	HD 3217
16	DBW 193	32	HD 222	48	K 1503
				49	HD 3200

Cluster analysis:Forty-nine genotypes were grouped into 9 clusters. Cluster IV has the highest number of genotypes i.e. 20 and it was followed by clusters III with 14 genotypes. Cluster I, II, V, VI, VII, and VIII were with 2 genotypes, cluster IX with 3 genotypes (**Table 3**). Genotypes within the same cluster were highly closely related as compared to genotypes in other clusters. The intra-cluster values indicated the distance of genotypes falling in the same cluster; therefore, the high intra-cluster D values mean more heterogeneity within the same cluster. The average values of intra-cluster distances varied from 10.214 to 60.86, the maximum intra-cluster distance was observed in cluster number IX (60.86) followed by cluster number IV (52.414). The above result indicated a high degree of heterogeneity in cluster IX followed by cluster IV (**Table 4**). The maximum inter-cluster distances between clusters IX and I (86.392) were observed, followed by cluster VIII and IX (82.829), indicating that the genotypes were most closely related. The minimum inter-cluster distances (29.429) between cluster numbers II and V were observed, indicating that genotypes maintained a low divergence between these clusters. From the divergence

analysis, it will be concluded that the genotypes belonging to different clusters can be used to obtain variation between different spectrums in the hybridization program by high predictive statistical distances. Similar findings were also reported by Bergale *et al*. (2001), Verma *et al*. (2006) and Kumar *et al*. (2014).

Table 2. Contribution of individual characters towards divergence

Sl. No.	Characters	Contribution (%)
1	Days to heading	0.850
2	Days to flowering	0.000
3	Days to maturity	0.255
4	Plant height(cm)	17.602
5	No. of tillers Plant-1	1.020
6	Spike length(cm)	0.340
7	No. of spikelets spike-1	5.187
8	No. of grains spike-1	17.857
9	Wt. of grains spike-1(g)	11.479
10	Test wt.(g)	10.799
11	Grain protein (%)	8.588
12	Yield plant-1(g)	26.020
	Total	100.000

Table 3. Grouping of 49 genotypes of Bread wheat (*Triticum aestivum* L.) into 9 clusters.

Cluster No.	No. of genotypes	Genotypes
I	2	HD 1962, K 1503
II	2	HD 2967©, DBW 194
III	14	UP 2936, HD 3218, DBW 189, HUW 801, JKW 230, WH 1200, DBW 190, NW 6078, HD 3221, WH 1204, PBW 745, WH 1105©, NW 6094, RAJ 4463
IV	20	K 1501, DBW 193, DBW 88©, DRW 3785, WH 1202, UP 2939, RAJ 4464, DRW 3786, PBW 747, HD 3219 HUW 802, WH 1203, RAJ 4465, UP 2940, RAJ 4462 HD 222, UP 2937, DBW 191, DBW 192, K 1502
V	2	K 0307©, HD 3200
VI	2	DBW 187, HD 3223
VII	2	UP 2938, HD 3217
VIII	2	PBW 744, WH 1201
IX	3	PBW 761, PBW 746, DBW 188

The different clusters exhibited marked differences in respect of means for all the characters studied. Cluster I showed high values for days to heading, days to flowering and plant height (**Table 5**). In Cluster II, the average values of all characters were lower than the mean of all genotypes. In cluster III, the average values for weight of grains spike^{-1} were higher than the mean of all genotypes. In cluster IV, V, VI and IX, the average values for all the characters were lesser than the mean of all genotypes. In cluster VII, the average values for days to maturity, protein content and test weight were higher than the mean of all genotypes. In cluster VIII, high values were noted for the number of tillers plant^{-1}, spike length, the number of spikelets spike^{-1}, the number of grains spike and yield plant^{-1}. Since improvement in yield is the basic objective in any breeding program, cluster mean of yield plant^{-1} and their major components should be considered for the selection of genotypes. Cluster VIII consisting of genotypes PBW 744 and WH 1201 showed the highest cluster means for the number of tillers plant^{-1}, spike length, the number of spikelets spike^{-1}, the number of grains spike and yield plant^{-1} followed by cluster I *viz.* genotypes HD 1962 and K 1503 which showed the highest cluster means for days to heading, days to flowering and plant height. Then cluster VII which is consisting of genotypes UP 2938 and HD 3217 showed the highest cluster means for days to maturity, test weight, and protein content. These genotypes can be utilized as parents in the hybridization program. These genotypes could be exploited for their direct release as a variety after testing under a wider range

of environments. In addition, these genotypes can also be used as parents in hybridization programs to develop high-yield wheat varieties under irrigated conditions over time. Similar findings were also reported by Kumar *et al*. (2009) and Bellundagi *et al*. (2013) and Hailegiorgis *et al*. (2011).

Table 4. Average inter and intra-cluster distances (D)

CLUSTERS	I	II	III	IV	V	VI	VII	VIII	IX
I	**10.214**	32.363	50.88	48.892	42.275	40.053	57.193	50.712	86.392
II		**14.601**	38.32	39.239	29.429	32.562	34.751	56.503	67.996
III			**46.08**	50.808	49.647	44.829	55.242	60.877	62.215
IV				**52.414**	45.061	46.355	56.119	61.902	73.958
V					**21.364**	45.288	48.296	67.007	77.923
VI						**35.046**	53.03	46.1	69.978
VII							**39.548**	79.034	77.201
VIII								**51.295**	82.829
IX									**60.86**

(Figures in Bold size indicate average intra-cluster distance which varies from 10.214 to 60.86.)

Table 5. Cluster means of yield and quality traits of Bread Wheat genotypes (*Triticum aestivum* L.).

Clusters	DH	DF	DM	PH (cm)	NTP	SL (cm)	NSS	NGS	GWS (g)	TW (g)	GP (%)	YPP (g)
I	85.25	89.875	114.4	95.44	5.713	10.403	19.645	43.765	1.01	37.47	10.597	9.392
II	76.625	82.75	116.5	92.06	5.823	10.533	18.407	39.26	1.155	38.405	11.575	8.988
III	73.018	78.857	110.6	87.438	6.403	10.725	18.625	39.992	1.273	37.255	11.021	9.577
IV	71.875	76.7	112.8	91.008	6.251	10.313	18.708	40.862	1.246	36.448	12.121	9.426
V	66.875	72.625	115.8	94.395	6.738	10.083	17.743	38.62	1.195	35.635	10.823	9.015
VI	71	76.375	113.3	90.263	6.233	10.718	16.86	45.408	1.26	41.595	11.52	11.725
VII	77.625	82.125	116.6	92.838	5.838	10.165	17.37	33.717	1.17	42.84	12.72	8.775
VIII	72.125	78.5	114.6	90.12	8.48	11.292	21.413	50.95	1.155	37.537	12.215	15.782
IX	63	69.667	110.8	78.155	7.488	9.748	18.787	38.737	1.272	37.445	10.313	11.083

DH-Days to heading; DF-Days to flowering; DM-Days to maturity; PH-Plant height (cm); NTP-Number of tillers plant^{-1}; SL-Spike length (cm); NSS-Number of spikelets spike^{-1}; NGS-Number of grains spike^{-1}; GWS-Grain weights spike^{-1} (g); TW-Test weight (g); YPP-Yield plant^{-1} (g) and GP- Grain protein percent (%).

Principal component analysis is a mathematical tool that converts many correlated variables into a smaller number of unrelated variables, called principal components. The Eigen values refer to the total variance explained by each factor. The Eigen values are often used to determine how many factors should retain graphically are presented in the scree plot (**Fig. 1)**. Ten principal components were extracted from the original data accounting for 99.56 % of total variation amongst the wheat genotypes assessed for various quantitative traits. The Eigen values, individual and cumulative percentage of variance are presented in **Table 6.** The first principal component (PC1), accounted for about 32.06% of the variation. The second principal component (PC2) accounted for about 19.15 % of the total variation. But it was interesting to note that up to the four components Eigen values were greater than 1, and therefore another component was considered to explain the variation. When all the five components were altogether considered, the sum total of 80.00% variation was explained. The present PCA analysis confirmed the genetic diversity present among the experimental materials and the position of different genotypes has been presented in the biplot diagram (**Fig. 2)**. This variability could be utilized in designing a breeding program for selecting diverse parents which directly shows the way to get maximum heterosis. These findings also support the findings of Baranwal *et al*. (2013).

The highest contribution towards total divergence was yield plant^{-1} followed by the number of grains spike^{-1}, plant height, weight of grains spike^{-1}and test weight. Cluster pattern pointed out that the genotypes were

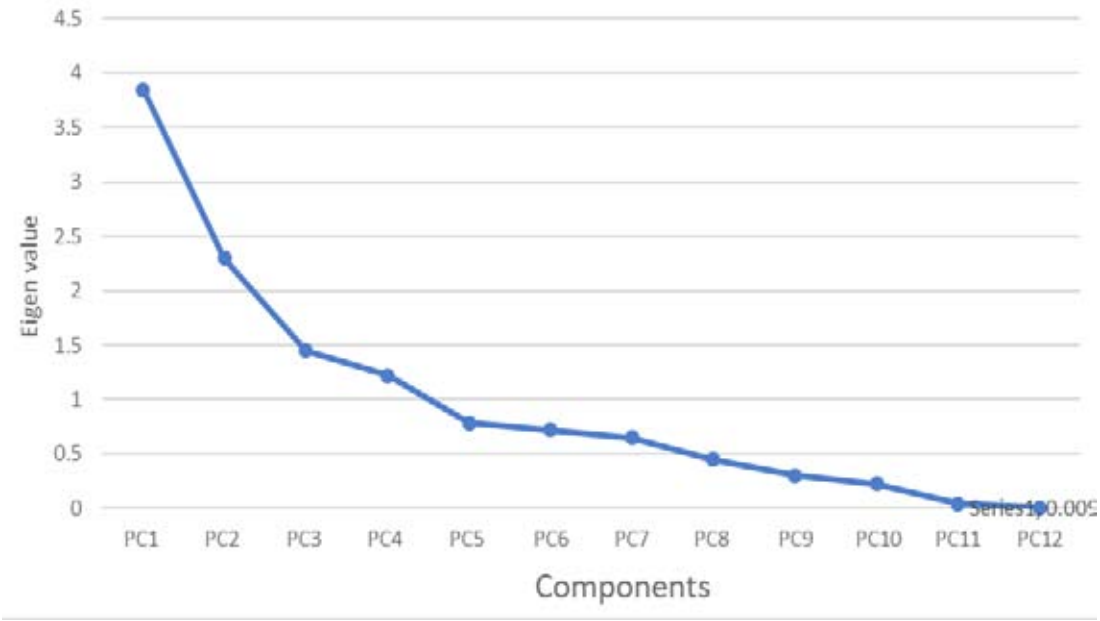

Fig.1. Scree plot showing principal component.

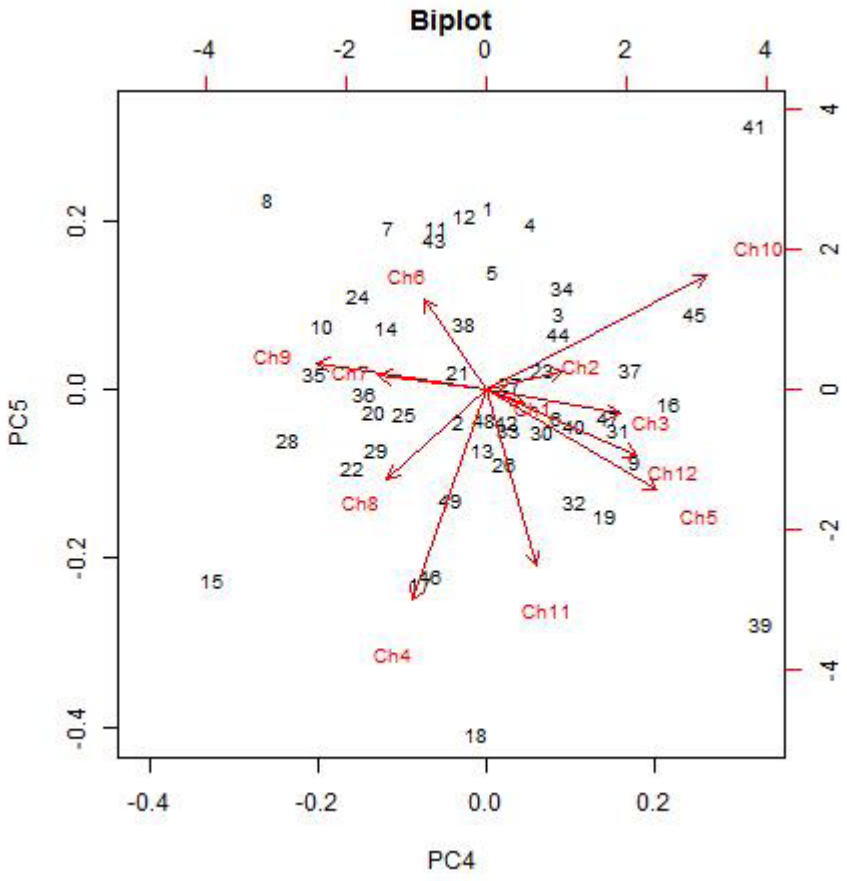

Fig. 2. Biplot of 12 characters of 49 bread wheat genotypes.

Table 6. Eigen values, Individual and Cumulative percentage of variance explained by the Principal components

Statistics	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12
Standard deviation	1.962	1.516	1.204	1.105	0.887	0.850	0.806	0.668	0.551	0.472	0.209	0.095
Proportion of variance	0.321	0.192	0.121	0.102	0.066	0.060	0.054	0.037	0.025	0.019	0.004	0.001
Cumulative proportion	0.321	0.512	0.633	0.735	0.800	0.860	0.915	0.952	0.977	0.996	0.999	1.000
Eigen Values	3.848	2.298	1.450	1.221	0.787	0.722	0.649	0.446	0.304	0.223	0.044	0.009

highly diverse and originated from different geographical regions. The genotypes represented in cluster IX and I were most distantly related followed by Cluster VIII and Cluster IX. Any two genotypes selected from these clusters may be utilized in crossing programs to retrieve potential high yielding genotypes. The PCA suggested that the genotypes are highly diverse, and the diversity of the genotypes obtained considering 80% cumulative proportion of variation. Therefore, D^2 analysis followed by PCA measures the distant relationship among the genotypes was verified in the present investigation.

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