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Multivariate analysis in bread wheat genotypes grown under late sown condition

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Abstract
Bread wheat (*Triticum aestivum* L.) is considered as one of the most important cereal crops and fundamental of human cultivation over the globe. The crop contributes about 20% of the world dietary calories and proteins worldwide. The crop has versatility to grow in diverse range of environments from temperate, sub-tropical to humid regions to the warmer areas of India. In West Bengal, wheat is mainly cultivated as late sown crop due to prolong rainy season, excess soil moisture and delayed paddy harvesting. Study of genetic diversity is one of the potent techniques to identify diverse genotype for future breeding programme. The present investigation aimed at evaluating 24 wheat genotypes to determine the genetic diversity through multivariate analysis. D^2 analysis revealed all 24 genotypes were grouped into seven different clusters. Cluster I had maximum (9 genotypes) whereas Cluster VII was monotypic. Highest inter-cluster distance was observed between Cluster II and Cluster V (57.62) followed by Cluster I and Cluster V (56.38) Cluster IV and Cluster V (54.84). The grouping pattern suggested that selection of the genotypes between Cluster V & any other genotypes selected from Cluster I, II, III and & IV might be intercrossed to recover desirable segregants. The investigation also suggested seven characters namely plant height, tillers per sq.mt, grains per spike, Chl b, biomass, harvest index and economic yield contributed maximum towards total divergence. The principal component analysis revealed that the first principal component explained variation of 34.93% followed by PC II (23.52%), PC III (15.08%) and PC IV (13.51%). When all the four components were altogether considered, sum total of 87.04% variation was explained. The principal component analysis also revealed wide diversity present among the experimental materials.

Keywords: Wheat, genetic diversity, multivariate analysis

Introduction
Bread wheat (*Triticum aestivum* L) is considered as one of the most important cereal crops and its cultivation has been linked to the development of major civilizations all over the world. 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 overall production of wheat in the country has gone up tremendously from 12.26 million tonnes in 1964-65 to 93.5 million tonnes in 2015-16. Recently, an estimate of wheat production by Ministry of Agriculture, Govt. of India states that India is expected to touch the new level of wheat production is about 100 million tonnes in 2018-19. However, raising temperature, unexpected hailstorms, erratic and unusual precipitation during February-March is hampering wheat production almost every year. West Bengal is not categorized as traditional wheat-growing state of the country because of its mild and short winter, humid climate and late sowing due to delay in harvesting of kharif rice and sometimes excessive soil moisture after rice harvest. However, at present, wheat has become a staple food crop next to rice and its consumption is gradually increasing because of change in food habit. It occupies about 0.335 million hectares areas and contributes about 0.950 million tonnes wheat grain productions in the state. The average yield of wheat is about 2.836 t/ha which is less than the national average of 2.989 t/ha suggesting ample scope for improving yield of wheat in West Bengal condition. Short span of winter leading to incidence of high temperature during flowering and grain filling, lack of available short duration and terminal thermal stress in genotypes are the major bottlenecks to enhance area and productivity of wheat in West Bengal. Identification of diverse breeding materials and use these materials in the hybridization programme is the prerequisite to initiate any breeding programme. In southern Bengal, wheat

varietal improvement development is mainly associated with identification of late heat tolerant, short duration and high yielding lines. Therefore, the present study was undertaken to identify potent genotypes through multivariate analysis and used these genotypes in crossing programme to retrieve potential lines from desirable segregants.

Materials and Methods

The present investigation was carried out at AB Block Farm, Bidhan Chandra Krishi Viswavidalaya, Kalyani, situated at 21.5^{O}N latitude and 85^{O}E longitude and 11.7m above the Mean Sea Level. The research farm is located at the Gangetic New Alluvial plain of India. The experimental site belongs to typical sub-tropical climate with regular South-Western monsoon generally between June to October. Twenty four genotypes viz., K1614, UBW14, JKW234, HD3267, HUW820, HD3265, PBW771, DBW240, PBW772, DBW90, DBW237, UP2987, WH1227, NW7010, WH1227, KI612, RAJ4503, K1613, WH1228, DBW239, NW7007, HD3059, UP2984 and HUW819 collected from All India Co-ordinated Wheat and Barley Improvement Project, Bidhan Chandra Krishi Viswavidyalaya constituted the plant material for the present study. These genotypes were evaluated during Rabi season of 2016-17 and 2017-18 under late sown condition (sowing on 25th December) following Randomized Block Design (RBD) with three replications in 2.5m x 0.36 m plot, maintaining a spacing of 18 cm since the crop was planted under late sown condition. Ten random plants per replication were sampled to record the characters viz., plant height (cm), days to heading, spike length (cm), days to maturity, number of grains per spike, grain weight per spike (g), test weight (g), total biomass, harvest index and grain yield per plant (g). Number of tillers was recorded per square metre basis. Chlorophyll a, b and total content of the flag leaf chlorophyll content were estimated as per Sadasivam and Manickam (1996) [13]. Genetic divergence of the 24 genotypes was determined as per generalized distance of Mahalanobis (1936) [6]. The genotypes were clustered following the method suggested by Tocher (Rao, 1952) [12]. Statistical analysis for PCA was carried in STAR software version 2.0.1 freely available in IRRI website.

Result and Discussion

Prof. P.C. Mahalonobis (1936) [6] developed the D^2 statistic model to determine the divergence among population in terms of generalized group distance. It has been widely used in psychometry and anthropometry for classification. Later, Rao (1952) [12] used Tocher's technique for classification or grouping of genotypes on the basis of D^2 statistics. In the present investigation, the clustering pattern based on multivariate analysis revealed that Cluster I had maximum of 9 genotypes followed by Cluster II (4 genotypes), Cluster III and Cluster IV (3 genotypes) whereas only one genotype came in Cluster VII. The intra and inter cluster distances are not very wide depicting low level of biological distance among the genotypes. Highest intercluster distance was recorded between Cluster II and Cluster V (57.62) followed by Cluster I and Cluster V (56.38), Cluster IV and Cluster V (54.84) and Cluster III and Cluster V (43.92) whereas minimum intercluster distance (22.65) was recorded between Cluster I and Cluster IV. It was noted that the characters namely, grains per spike, tillers per square metre, plant height and chlorophyll b contributed very little towards divergence. The grouping pattern of the genotypes due to geographical diversity and genetic divergence were unrelated. Mahalonobis D^2 statistic were utilized earlier to determine the genetic divergence of wheat (Sharma *et al.*, 2007; Kumar *et al.*, 2009; Ferdous *et al.*, 2011; Tahmasebi *et al.*, 2011; Kumar *et al.*, 2013; Amin *et al.*, 2014; Arya *et al.*, 2014; Sanghera *et al.*, 2014; Yadav *et al.*, 2014; Rahman *et al.*, 2015; Pasandi *et al*, 2015) [15, 4, 3, 16, 5, 1, 2, 14, 18, 10, 9]. Grouping pattern suggested that selection of the genotypes from Cluster V and any other genotypes selected from Cluster I Cluster II Cluster III and Cluster IV may be utilized in a crossing programme so that divergent and desirable segregates may be isolated. Similar to the findings of Sanghera *et al.* (2014) [14], Mehari *et al* (2015) [8], Rahman *et al.* (2015) [10] and Tilahun *et al.* (2016) [17] results of this study showed that intercluster distances were more than the intra-cluster distances indicating presence of high genetic divergence among wheat genotypes studied. Cluster number V showed highest values in respect to yield/ ha and grain/spike.

In Principal component analysis the values are first scaled to make their variances equal followed by choosing a new axis in the multivariate space followed by choosing a new set of axis shows that the variances of first and second axis is as large as possible but at right angles to each other. The coefficient of data points on each new axis is a weighted sum of its coefficient on the originally scale axis. In the present study, seven different quantitative character namely, plant height, days to 75% heading, test weight, chlorophyll b content, biomass content, harvest index and grain yield contributed substantial amount of genetic divergence used in principal component analysis. The first principal component (PCI) explained variation up to 34.93% followed by PC II (23.52%) and PC III (15.08%). These three principal components explained variation up to 73.53%. These three principal components showed eigen values greater than 1 however, the fourth principal component having eigen value 0.945 was considered to explain variation up to 87.04 percent. Pasandi *et al.* (2015) [9] observed similar types of results while working with 56 wheat genotypes. The principal component analysis revealed that the seven characters (plant height, tillers per sq.mt, grains /spike, chlorophyll b content of flag leaf, biomass content, harvest index and economic yield contributed maximum to the total divergence of the genotypes. The present PCA analysis confirmed the genetic diversity preset among the experimental materials.

Table 1: Grouping of genotypes into different clusters

Sl. No.	Clusters	Genotypes
1.	Cluster I	K1614, UBW14, JKW234, HUW820, HD3265, PBW771, WH1227, NW7010
2.	Cluster II	DBW240, PBW772, K1613, HD3059
3.	Cluster III	DBW90, UP2987, DBW237
4.	Cluster IV	WH1227, K1612,WH1228
5.	Cluster V	UP2984, HUW819
6.	Cluster VI	RAJ4503, NW7007
7.	Cluster VII	DBW239

Table 2: Contribution of the quantitative characters towards divergence

Sl. No.	Characters	% Contribution
1.	Plant Height	2.5362
2.	Days to Head	0
3.	Tillers per sq metre	3.9855
4.	Days to Maturity	0
5.	Test Weight	0
6.	Spike Length	0
7.	Grains per spike	7.6087
8.	Chlrolophyl a	0
9.	Chlorophyl b	1.087
10.	Total chlorophyl	0
11.	Biomass content	19.9275
12.	Harvest index	16.6667
13.	Economic yield	48.1884
Total		100

Table 3: Intra and Inter cluster distance of different wheat genotypes

Clusters	I	II	III	IV	V	VI	VII
I	24.75	33.25	41.27	22.65	56.38	39.77	38.42
II		19.96	30.94	31.38	57.62	29.68	41.51
III			22.53	40.37	43.92	26.01	40.12
IV				25.56	54.84	37.46	35.62
V					21.82	40.08	30.02
VI						24.85	32.02
VII							0

Table 4: Cluster means of different wheat genotypes

Characters	Plant Height (cm)	Days to heading	Tillers/m2	Days to maturity	Test weight (g)	Spike length (cm)	Grains per spike	Chl a (mg/ml)	Chl b (mg/ml)	Total chl (mg/ml)	Total biomass (g)	Harvest index	Yield (q/ha)
I	93.60	64.70	65.14	99.57	10.35	28.94	38.58	1.07	0.65	1.72	807.09	33.74	30.24
II	94.15	66.5	58.75	98.29	10.25	28.79	39.24	1.14	0.65	1.8	689.04	39.94	30.49
III	84.43	64.22	65.88	98.16	10.33	28.33	38.59	1.24	0.50	1.74	666.77	42.85	31.75
IV	95.20	67	65.66	99.11	10.43	28.55	37.60	1.22	0.67	1.9	805.55	34.06	30.65
V	85.90	66.08	69	98.73	10.25	28.58	39.90	0.96	0.33	1.3	818.83	40.46	36.60
VI	90.87	65	54	98.05	10.00	27.58	34.52	1.13	0.46	1.6	731.66	40.57	32.89
VII	98.53	66.33	72.67	100.33	10.1	30.16	38.96	1.23	0.60	1.83	829.66	38.30	35.22

Table 5: Cumulative and proportion of variance for different principal components

Sl. No.	Statistics	PC1	PC2	PC3	PC4	PC5	PC6	PC7
1.	Standard deviation	1.5637	1.2831	1.0274	0.9726	0.8026	0.5111	0.0409
2.	Proportion of variance	0.3493	0.2352	0.1508	0.1351	0.092	0.0373	0.0002
3.	Cumulative roportion	0.3493	0.5845	0.7353	0.8704	0.9625	0.9998	1
4.	Eigen Values	2.4452	1.6463	1.0555	0.9459	0.6441	0.2612	0.0017

Table 6: Proportion of variance for seven different characters in different principal components

Sl. No.	Characters	PC1	PC2	PC3	PC4	PC5	PC6	PC7
1.	PH	-0.4403	0.0663	-0.0859	0.2361	-0.8324	-0.2135	0.0103
2.	DH	-0.009	0.4637	0.413	-0.6648	-0.0851	-0.4061	0.0157
3.	TW	0.1024	0.0113	-0.8809	-0.3808	-0.0034	-0.2614	-0.005
4.	Cl.b	-0.3787	-0.3652	0.0254	-0.5819	-0.1509	0.6004	-0.0276
5.	BOM	-0.3611	0.5999	-0.1626	0.112	0.2087	0.2778	-0.5916
6.	HI	0.5866	-0.1753	0.0881	-0.0782	-0.3787	0.0573	-0.6816
7.	YLD	0.4215	0.5064	-0.1058	0.0069	-0.3002	0.5294	0.4293

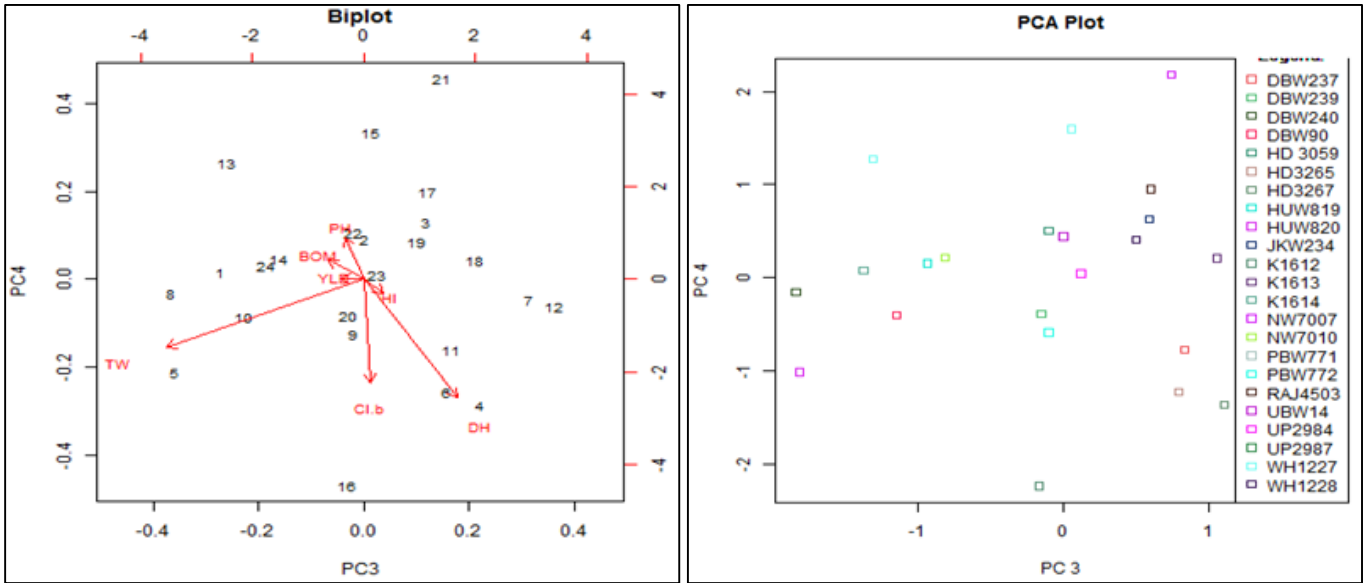

Fig 1: PCA plot and Biplot for wheat genotypes taken under study

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