Multivariate Analysis in Bread Wheat (*Triticum aestivum* L.) for Yield and Yield Contributing Traits

ABSTRACT

The present investigation was conducted to examine the 20 Bread Wheat genotypes to study the genetic parameters, correlation and genetic diversity. The experiment was carried out in main experimental station of Agricultural Research Farm, Rama University (U.P), Mandhana, Kanpur during Rabi Season, 2020-21 in Randomized Block Design (RBD) with three replications. Analysis of variance showed highly significant differences among 20 Bread Wheat for 11 characters studied. Genetic divergence was estimated among 20 genotypes by using Mahalanobis's D^2 statistic. The genotypes were grouped into 5 clusters. Cluster 1 comprises maximum genotypes which is 15 in numbers namely (HPST-16-17-07, BHU 25, BHU 31, ZINCO1, ANKUR, PBW Zn 1, WB 02, HPAN 101, HPAN 147, HPAN 164, HPAN 57, HPAN 65, HPAN 111, HPAN 127, HD 2967) followed by cluster 2 comprises 1genotypes ((HPAN 42), cluster 3 comprises 1 genotype (HPST 16 -17-15), cluster 4 comprises 2 genotype (HPST 16-17-16, CRD GHEHU 1), cluster 5 comprises 1 genotype (PBW 677). The maximum Intra-cluster (D^2) was registered for cluster 1 (7.93). Inter-cluster distance (D^2) was found maximum between cluster 4 and cluster 5.Cluster 4 showed maximum cluster mean value for grain yield per plant. Cluster means indicated that none of the clusters was superior for all the characters studied. Therefore, hybridization between genotypes belonging to different clusters is suggested for development of superior genotypes. Thousand seed weight was the main factor contributing towards genetic diversity accounting for (26.32%) followed by grain per spikelets (25.79%).

Comment [A1]: The results of analysis of variance are not presented

Key words: Bread wheat, genetic parameters, correlation, genetic diversity and cluster.

[1] Introduction

Wheat (*Triticum aestivum*. L.) is considered as king of cereals and contributing more than 30% of food basket of the country. Wheat is one of the most important and widely cultivated crops in the world, used mainly for human consumption and support nearly 40% of the world population (Mohammadi-joo*et al*., 2015) and providing 20 per cent of the total food calories. Wheat is the major staple food crop, providing almost half of all calories in the region of North Africa and West and Central Asia. Bread wheat, (*Triticumaestivum*L.), is allohexaploid annual grass with chromosome number 2n=6X=42 and possess three genomes A, B, and D. Genome 'A' is derived from oinkorn wheat (*Triticumurartu*), 'B' from *A. Speltoides* and genome 'D' belong to a weedy grass *A. tauschii*(*Rajput*., 2018). It is predominantly a self-pollinated crop but cross pollination up to 1 % is also possible. Globally, bread wheat covers 90 per cent of the area followed macaroni wheat with 9 per cent and emmer wheat and einkorn wheat with one per cent of the total area.In world, wheat occupies an area of 216 M ha with total production of 730.65 MT and productivity of 3390 kg ha (Anon, 2019).

The genetic divergence analysis using techniques hierarchical euclidean clusteranalysis, classify the genotypes into homogenous groups/clusters with similarity of genotypes for different characters within clusters while genotypes between two clusters are more divergent than the genotypes of the same clusters. Thus, suitable genotypes from diverse cluster can be used for further planning of a successful breeding programme.

Comment [A2]: The introduction is very short. Explain more about the experimental factor and other researchers' results. New references added (2015-2022)

Comment [A3]: At the end of the introduction, the objectives of the research should be clearly stated

[2]Materials and Methods

The present investigation entitled “Study of screening for tolerance to terminal heat stress in bread wheat (*Triticum aestivum* L. em. Thell)” was carried out during Rabi 2020-21 at Agricultural Research Farm, Rama University, Kanpur (U.P.).

The experimental material comprised of 20 bread wheat genotypes were evaluated in Randomized Block Design (RBD), with 3 Replications. The observations were recorded on 5 randomly selective competitive plants for each genotype for plant height, effective tiller per plant, spikelet’s per spike, spike length, grain per spike, 1000 seed weight, days to maturity, days to 50% flowering, biological yield per plant, harvest index, grain yield per plant observations were recorded on whole plot basis. The data so, obtained were subjected to analysis of variance, estimate the magnitude of genetic variability, heritability and genetic advance, correlation coefficient and genetic divergence.

Comment [A4]: Introduce the origin of genotypes.
Present the results of soil analysis.
How to measure attributes by inserting a reference
Introduce the software used

[3] Resultsand Discussion

Comment [A5]: Present the results of analysis of variance of traits.
Provide mean comparison results.

Comment [A6]: No discussion provided. Provide scientific reasons for each result .Consistent with other researchers' results. Report other tests. Use new references

[3.1] Genetic divergence analysis

The mean, range and mean sum of squares due to genotypes for all the traits studied were highly significant. Thereby, revealing sufficient amount of genetic variation among the genotype for all the characters studied but the extent of genetic diversity present among the genotypes taken for the investigation could not be explained. To overcome this problem and to quantify genetic divergence between any two genotype or group of genotype, Euclidean clustering analysis was employed and the constellation of genotype into cluster was done.D2 statistics measures the

Comment [A7]: genotypes

degree of divergence and determines the relative proportion of each component traits to the total divergence. It measures the forces of differentiation at two levels that is Intra cluster and Inter cluster levels.

Comment [A8]: It is better to use stepwise regression of traits instead of this part

[3.2] Clustering procedure

In the present study, 20 genotypes were grouped into 5 clusters by TOCHER METHOD. Cluster 1 comprises maximum genotypes which is 15 in numbers namely (HPST-16-17-07, BHU 25, BHU 31, ZINCO1, ANKUR, PBW Zn 1, WB 02, HPAN 101, HPAN 147, HPAN 164, HPAN 57, HPAN 65, HPAN 111, HPAN 127, HD 2967) followed by cluster 2(HPAN 42), cluster 3 (HPST 16-17-15), cluster 4 (HPST 16-17-16, CRD GHEHU 1) and cluster 5 (PBW 677).

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Table 1. Cluster distance

Cluster	I	II	III	IV	V
I	**7.93**	9.43	10.28	13.38	14.08
II		**0.00**	9.39	15.46	12.89
III			**0.00**	12.02	19.02
IV				**7.17**	23.25
V					**0.00**

[3.3] Intraand inter cluster average distance

The maximum Intra-cluster (D^2) was registered for cluster 1 (**7.93**) followed by cluster 4 (**7.17**). Cluster 3,4,5,6 does not possess any intra cluster relationship.

Inter-cluster distance (D^2) was found maximum between cluster 4 and cluster 5 (23.25) followed by cluster 3 and cluster 5 (19.02), cluster 2 and cluster 4 (15.46), cluster 1 and cluster 5 (14.08), cluster 1 and cluster 4 (13.38), cluster 3 and cluster 4 (12.02), cluster 1 and cluster 3 (10.28). The minimum Inter-cluster distance was found between cluster 1 and cluster 2 (9.43) followed by cluster 2 and cluster 3 (9.39).

Comment [A10]: Explain more. The meaning of the results should be clear

[3.1] CLUSTER MEAN VALUE

A comparison of the mean values of 11 characters of 5 different clusters was presented in **(Table 1)** and considerable difference in cluster mean was evident for all characters.

Comment [A11]: This explanation is not enough. Explain and discuss each adjective separately

Table 2. Cluster mean value of wheat genotypes

Cluster/Traits	DFF	DM	PH	ETP	SL	SPS	GPS	HI	TSW	BYP	GYP

I	78.13	117.63	92.83	5.17	12.80	19.87	48.73	22.52	40.90	1402.33	309.00
II	76.00	122.50	87.50	6.00	11.50	18.00	49.50	26.94	38.29	1400.00	345.00
III	76.50	116.50	100.00	5.00	12.50	21.00	42.00	25.30	38.05	1700.00	390.00
IV	76.25	111.50	88.75	5.50	14.00	23.00	39.25	31.13	40.31	1675.00	485.00
V	81.00	120.00	100.00	5.50	11.50	18.00	45.00	28.42	37.14	1375.00	400.00

CLUSTER I

Cluster 1 comprises of 15 genotypes (HPST-16-17-07, BHU 25, BHU 31, ZINCO1, ANKUR, PBW Zn 1, WB 02, HPAN 101, HPAN 147, HPAN 164, HPAN 57, HPAN 65, HPAN 111, HPAN 127, HD 2967) and registered maximum mean value for the character Biological yield per plant (1402.33) and minimum for Effective tiller per plant (5.17) and rest of the characters lies between them Grain yield per planthave mean value of (309.00), followed by days to maturity, plant height, days of 50% flowering, grain per spike, thousand seed weight, harvest index, spikelet's per spike, spike length.

CLUSTER II

Cluster 2 comprises of one genotype (HPAN 42) and registered maximum mean value for the character biological yield per plant and minimum for effective tiller per plant and rest of thecharacters lies between them grain yield per plant have mean value of followed by days to maturity, plant height, days of 50% flowering, grain per spike, thousand seed weight, harvest index, spikelet's per spike, spike length.

CLUSTER III

Cluster 3 comprises of only one genotype and registered maximum mean value for the character biological yield per plant and minimum for effective tiller per plant and rest of the characters lies between them grain yield per plant have mean value of followed by days to maturity, plant height, days to 50% flowering, grain per spike, thousand seed weight, harvest index, spikelet's per spike, spike length.

CLUSTER IV

Cluster 4 comprises of only two genotypes (HPST 16-17-16, CRD GHEHU 1) and registered maximum mean value for the character biological yield per plant and minimum for effective tiller per plant and rest of the characters lies between them grain yield per plant have mean value of followed by days to maturity, plant height, days to 50% flowering, grain per spike, thousand seed weight, harvest index, spikelet's per spike, spike length.

Comment [A12]: Scientific reasons should be stated Consistent with the results of other researchers

CLUSTER V

Cluster V comprises of only one genotype (PBW 677) and registered maximum mean value for the character biological yield per plant and minimum for effective tiller per plant and rest of the characters lies between them grain yield per plant have mean value of followed by days to maturity, plant height, days to 50% flowering, grain per spike, thousand seed weight, harvest index, spikelet's per spike, spike length.Hailegiorgis*et al.* (2011), Degewione*et al.* (2013), Ahmad *et al.* (2018)also agreed with the similar findings.

Table 3: PERCENT CONTRIBUTION OF CHARACTER

S.No.	Source	TimesRanked1st	Contribution%
1.	Days to 50% flowering	18	9.47%
2.	Days to maturity	0	0.00%
3.	Plant height	3	1.58%
4.	Effective tillers per plant	4	2.11%
5.	Spike length	1	0.53%
6.	Spikelet's per spike	0	0.00%
7.	Grains per spike	49	25.79%
8.	Harvest index	10	5.26%
9.	Test seed weight	50	26.32%
10.	Biological yield per plant	10	5.26%
11.	Gain yield per plant	45	23.68%

[3.4] Percent contribution

Percent contribution of 11 characters to total genetic diversity is presented in table 3. It was revealed that thousand seed weight was the main factor contributing to divergence accounting for followed by grain per spike, grain yield per plant, days to 50% flowering, biological yield per plant and harvest index, effective tiller per plant, plant height and spike length. Days to maturity and spikelet's per spike had no contribution toward genetic divergence.

Comment [A13]: Discuss further

[4] CONCLUSION

Based on the results, it is concluded that HPST-16-17-16genotype showed high mean performance for grain yield per plant. The characters days to maturity, days to 50% flowering, plant height, grain per spike, spikelets per spike should be given priority during selection.

Hybridization between the genotypes with high mean performance for multiple characters from cluster 5, 4 and 3 is suggested to get heterotic segregates to enhance grain yield.

[5] References

Comment [A14]: New references added in this section
References are in accordance with the journal format.

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