Biological Forum – An International Journal **14(3): 573-576(2022)**

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Analysis of Genetic Divergence in some Elite Cultivars of Bread Wheat (*Triticum aestivum* L. em. Thell)

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(Received 24 May 2022, Accepted 16 July, 2022)
(Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT: Determination of genetic diversity is useful for plant breeding for the production of more efficient plant species under different conditions. Accordingly, twenty genotypes of the most common wheat (*Triticum aestivum* L.) cultivated in different regions of U.P. were selected, grown, and analyzed for genetic diversity. The experiment was conducted at the Agricultural Research Farm of B.R.D. P.G. College, Deoria (U.P.) in a randomized complete block design with three replications. The observations were taken for fourteen metric traits. Cluster analysis based on Mahalanobis'(1936), described by Rao (1952) and Tocher's method, categorized the cultivars into five groups. Cluster I had the highest number of genotypes having nine entries followed by cluster II with six entries, cluster III, cluster IV, and V representing one entry each. The intra-cluster distance varied from 0.00 to 25.60. The inter-cluster distance ranged from 32.81 to 109.26. Cluster III was responsible for the highest group means for the biological yield per plant (28.31 g) and grain yield per plant (16.30 g) whereas, it possessed the lowest cluster group mean for days to 50% flowering (74.00 days). Such differences in the genetic component of traits studied in this manuscript can be applied as a new source of variation in other breeding programs and crossing nurseries for wheat improvement.

Keywords: Genetic divergence, cluster analysis, *Triticum aestivum*, genetic diversity, Mahalanobis' D^2.

INTRODUCTION

Wheat has a long history of serving as an important food crop to mankind. It has been appropriated as a major source of energy through its carbohydrates and in more recent times for its supply of valuables proteins give wheat its unique properties for making food of different kinds of tastes.

Wheat is a self-pollinated C_3 plant with the cleistogamous condition. The wheat is most successfully grown between the latitude of 30 to 60°N and 27 to 40°N (Nuttonson, 1955) but beyond these limits, it also be grown from arctic to high elevated equators. The optimum temperature for best growth and yield is 25°C with a minimum of 20°C and a maximum of 35°C growth temperature.

Wheat is a highly consumed cereal crop by the majority of the people at the global level and holds an important part of food security by providing over 50% calories to the consumers whose staple food is wheat (Gupta *et al.*, 2005). According to Food and Agriculture Organization (FAO), wheat provides 20% of food resources globally and is an essential part of human food (Farzi and Bigloo 2010). Too many food items like bread, chapattis, and many more items are being made of wheat. To meet the demands of wheat for food security for the ever-increasing population it is an urgent need to increase per unit yield by introducing new high-yielding wheat varieties having suitable qualities like baking quality, digestibility, mineral contents etc. as per society's needs (Ali *et al.*, 2020).

The genetic diversity of plants affects their capacity for increased productivity and, thus, their usage in breeding, which may ultimately lead to an increased food supply. The need for breeding experiments is thus shown by the increased focus on developing resistant plant species for prolonged food production under various situations. In this regard analysis of genetic divergence present in cultivars become very important as it serves as a storehouse of valuable genes of desired traits for crop improvement.

MATERIALS AND METHODS

Experimental Site. The experiment was carried out at the Agricultural Research Farm, Baba Raghav Das Post Graduate College, Deoria (U.P.). Geographically, this College is located in the east part of Uttar Pradesh, India at 26.5°N latitude, 83.79°E longitude, and 68 meters (223 feet) above the mean sea level.

Experimental Details. Twenty elite cultivars of bread wheat were sown during *Rabi* 2020-21 in Randomized Block Design with three replications. The row-to-row distance was maintained at 22.5 cm, and the plant-to-plant distance was maintained at 5 cm by hand thinning. All the other recommended agronomic activities were practiced to raise a healthy crop at the experiment station.

Observations Recorded. The observations were recorded for 14 quantitative traits *viz*., days to 50% flowering, days to maturity, flag leaf area (cm^2), plant height (cm), peduncle length (cm), number of productive tillers per plant, spike length (cm), number of spikelets per spike, number of grains per spike, grain yield per spike (g), 1000-grains weight (g), biological yield/plant (g), grain yield per plant (g) and harvest index (%). The data on days to 50% flowering and days to maturity were recorded on plot basis while the rest were measured from five competitive and randomly selected plants from each replication and their mean values were subjected to statistical analysis.

Statistical Analyses

Genetic diversity analysis. The genetic divergence amongst different genotypes is assessed based on the estimated *inter-se* genetic distances amongst the genotypes. One of the potent techniques for assessing genetic divergence is the D^2 statistics proposed by Mahalanobis (1936). D^2 statistics technique measures the forces of differentiation at two levels, namely, intra-cluster and inter-cluster levels, and thus helps in the selection of genetically divergent parents for exploitation in hybridization programs.

Clustering of genotypes using D^2 values. Tocher's method was used for clustering the genotypes into different groups described by Rao (1952). The basis of clustering by this method was that any two varieties belonging to the same cluster would show smaller D^2 values as compared to those belonging to two different clusters. This method started with two closely associated populations to find a third population that had the smallest average of D^2 values. In the same manner, the fourth one was chosen to have the smallest average of D^2 values among the first three and so on. This process was repeated until the D^2 values of all the genotypes were exhausted, except those that were included in the former cluster.

RESULTS AND DISCUSSION

Since the crosses made between the donors having maximum genetic divergence would be more rewarding towards desirable recombinants in the progenies, the diversity of parents is of prime importance for a successful breeding program. However, it is desirable to select suitably genetically divergent parents, based on information about the genetic variability and genetic diversity present in the available germplasm.

Clustering pattern of genotypes. The Clustering pattern of the twenty genotypes was grouped into five different non-overlapping Clusters Table 1. Cluster I had the highest number of genotypes having nineentries followed by cluster II with six entries, cluster III, cluster IV, and V representing one entry each. A similar grouping was also done by Ali and Bharadwaj (2015); Tarkeshwar *et al.* (2019) also recorded ten cluster groups of 84 wheat genotypes.

Inter and intra-cluster distances. The magnitude of inter-cluster distance measures the genetic distance between two clusters while intra-cluster distance measures the extent of genetic diversity between the genotypes of the same cluster. The values of intra-cluster distance values were lower than that of inter-cluster distances, indicating wide genetic diversity among the genotypes.

The averages of average inter and intra-cluster distances represented by the D² value have been given in Table 2. The intra-cluster distance varied from 0.00 to 25.60. The highest intra-cluster distance was observed in the case of cluster II (25.60) followed by cluster I (22.07) while the lowest intra-cluster values were in cases of clusters III, IV, and V (0.00). Earlier studies have also reported substantial genetic divergence in wheat (Kumar *et al*., 2018; Kumar *et al*., 2015).

Table 1: Clustering pattern of 20 genotypes based onMahalanobis' D^2 statistics of wheat genotypes.

Clusters	Number of genotypes	List of genotypes
Cluster I	11	K-1317, PBW-303, Jamuni, K-9107, HD-2967, HD-2858, PBW-19,HD-3086, HD-2693, Black, Shreeram-303
Cluster II	6	PBW-550, PBW-502, K-1006, HD-3171, Raj-4120, PBW-159
Cluster III	1	NW-2036
Cluster IV	1	HD-3003
Cluster V	1	PBW-107

Table 2: Estimate of average inter and intra-cluster distances for 5clusters of wheat genotypes.

	Cluster distances				
	Cluster I	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**
Cluster I	**22.07**	35.89	49.34	32.81	87.50
Cluster II		**25.60**	55.14	40.63	85.35
Cluster III			**0**	33.74	75.89
Cluster IV				**0**	109.26
Cluster V					**0**

The inter-cluster distance ranged from 32.81 to 109.26. The maximum inter-cluster distance observed between clusters IV and V (109.26) followed by clusters I and V (87.50) which suggested that members of these two clusters groups are genetically very diverse from each other showing that the genotypes concerned with these clusters have wide genetic diversity and thus genotypes of these clusters can be used in wheat hybridization program for trait improvement. The results found in the present investigation agreed with the results of Preeti *et al*. (2018).

The minimum inter-cluster distance was observed between clusters I and IV (32.81) followed by clusters III and IV (33.74) suggesting that the genotypes of these groups are genetically closer to each other. The relatively higher inter-cluster distances were also noted between clusters II and V (85.35) and III and V (75.89). The genotypes of these clusters are also diverse from each other. Tarkeshwar *et al*. (2019) also noticed these types of results in their investigation.

Inter and intra-cluster group means for six clusters. To validate the clusters responsible for a trait or a group of traits under investigation, the intra and inter clusters group means were estimated for various traits and clusters presented in Table 3.

The clusters I had the highest group mean for plant height (85.6 cm) and lowest mean for number of productive tillers per plant (4.32), biological yield per plant (22.49 g), and grain yield per plant (12.30 g).Cluster II had maximum means for days to maturity (118.92), number of spikelets per spike (19.72),and test weight (47.17 g) while minimum cluster means for peduncle length (42.81 cm).Cluster III was responsible for the highest group means for biological yield per plant (28.31 g) and grain yield per plant (16.30 g) whereas, it possessed the lowest cluster group mean for days to 50% flowering (74.00 days) and grain yield per spike (1.60 g). Cluster IV exhibited the highest means for the characters peduncle length (45.69 cm), number of productive tillers per plant (5.20), and harvest index (63.46%) while the lowest means for flag leaf area (28.88 cm^2), days to maturity (81.33 days), number of spikelets per spike (17.23) and number of grains per spike (35.90).Clusters V showed the highest mean for days to 50% flowering (79.00 days), flag leaf area (64.26 cm^2), and grain yield per spike (3.30 g) and it also recorded the lowest mean for length of spike (11.27 cm), plant height (78.12) and harvest index (55.21%). The genotypes from the clusters having the lowest values for days to 50% flowering, plant height, and maturity can be incorporated in our breeding program for earlier flowering, short stature, and early maturity and hence can be avoided the stress that develops during late rabi season. On the other hand, genotypes from the clusters having the highest cluster group mean can be used as donor parents for higher values of that trait. The earlier workers also noted similar results for most of the clusters formed in this investigation *viz*., Kumar *et al*. (2018) for plant height, biological yield per plant and days to maturity, Gurjar and Marker (2018) for days to maturity, plant height.

Table 3: Intra and inter-cluster group means for14 characters of wheat genotypes.

	Day to 50% flowering	Flag leaf area (cm^2)	Length of spike (cm)	Peduncle length (cm)	No. of productive tillers/ plant	Plant height (cm)	Days to maturity	Biological yield/ plant (g)	No. of spikelets/ spike	No. of grains per spike	Grain yield/ spike (g)	1000-grains weight	Harvest index (%)	Grain yield/ plant
Cluster I	75.39	33.05	11.90	45.44	4.32	85.6	115.24	22.49	19.09	37.77	2.36	43.51	55.45	12.30
Cluster II	78.00	32.29	12.00	42.81	4.94	84.39	118.92	26.83	19.72	37.77	3.09	47.17	58.93	14.35
Cluster III	74.00	38.05	12.50	43.93	4.73	82.47	113.0	28.31	19.40	39.40	1.60	37.66	59.14	16.30
Cluster IV	75.00	28.88	13.47	45.69	5.20	84.30	81.33	23.14	17.23	35.90	2.27	44.00	63.46	13.67
Cluster V	79.00	64.26	11.27	43.32	4.36	78.12	118.00	24.20	18.55	38.26	3.30	40.66	55.21	13.27

CONCLUSION

The characters contributing maximum to the diversity would give supreme opportunity to decide the cluster type for further selection and the choice of parents for a hybrid breeding program. The results revealed that the genotypes from cluster III can be selected for early flowering and higher grain yield per plant and from cluster IV for early maturity so that the direct selection for these traits would helpful as evident from several times these traits appeared or were ranked first during contribution to diversity.

Acknowledgment. The authors thank the Principal and Dr. S. C. Gaur, Associate Professor, B.R.D.P.G. College, Deoria (U.P.) for providing the necessary facilities and mentorship during this research work.

Conflict of Interest. None.

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How to cite this article: Shivani Chaudhary, Atul Gautam, Avanish Pandey, Tarkeshwar and S.C. Gaur (2022). Analysis of Genetic Divergence in Some Elite Cultivars of Bread Wheat (*Triticum aestivum* L. em. Thell). *Biological Forum – An International Journal*, *14*(3): 573-576.