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Genetic diversity study in Novel bread wheat (*Triticum aestivum* L.) genotypes for yield and yield-attributing traits

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Abstract

The present investigation was carried out in Randomized Block Design with three replications during the *Rabi* season of 2020-21 at the Wheat Breeding section fields of Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar, India taking 24 hexaploid bread wheat (*Triticum aestivum* L.) genotypes to identify genetically divergent genotypes of Bread Wheat for donors with desired features in hybridization programme for grain yield and other yield-related attributes. The genotypes were grouped into six different clusters. Cluster I included the highest number of genotypes. Cluster VI had the utmost mean value for the majority of the characters. Genotype RAUW-183 can serve as a donor for dwarfness. Genotypes RAUW-199, DBW-17, RAUW-210, RAUW-205, RAUW-155, and RAUW-159 were recorded genetically diverse, having the highest intra-cluster distance. The finding of the highest inter-cluster distance indicates that we can exploit genotypes RAUW-6, RAUW-4, RAUW-7, PBW-656 and RAUW-199, DBW-17, RAUW-210, RAUW-205, RAUW-155, RAUW-159 under inter-varietal hybridization programmes. Days to 50% flowering was revealed to have the most decisive influence in manifesting genetic divergence, followed by chlorophyll content, 1000- grain weight, number of grains/spike, canopy temperature, and the total number of tillers/plant.

Keywords: Bread wheat; randomized block design; cluster; genetic divergence

Introduction

Wheat (*Triticum* spp.) is considered one key staple food crop in numerous parts of the globe in terms of the area under cultivation and as a source of food. Wheat is a C₃, self-pollinated, long-day, monocot plant belonging to the tribe Triticeae, under the plant kingdom's widely diverse and significant "Poaceae" family. The species of the *Triticum* genus to which the cultivated wheat belongs are partitioned into diploid, tetraploid and hexaploid groups, with somatic chromosome numbers 14, 28 and 42, respectively. Among them, the hexaploid wheat species (*Triticum aestivum* L., 2n=6x=42) is nurtured most extensively. The green revolution resulted in a spectacular boost in wheat production of the country from 12 million tons in 1960-61 to 36.3 million tons in 1980-81. The current prevailing scenario is different where wheat has achieved its position among the 'big three' cereal crops. More than 107 million tons of production in India has been documented in 2019-20. It covers all the continents of the globe, engaging 17% of the world acreage of crops and feeding almost 40% of populations globally. It supplies more nutrition than any other crop, ranking first in area coverage and second in overall production after maize (FAOSTAT, 2019) [1].

Growing cultivars with high yield potential besides satisfactory quality is the principal objective of any plant breeding programme. Genetic distance between individual genotypes can help compare genetic similarity or dissimilarity and help define their genetic divergence. Genetically distant parents yield heterotic F₁ upon crossing and release more significant genetic variability in segregating generations.

Keeping the above considerations insight, the current investigation was executed to identify genetically divergent genotypes of Bread Wheat for donors with desired features in hybridization programme for grain yield and other yield-related attributes.

Materials and Methods

The present study was carried out during the *Rabi* season of 2020-21 at the Wheat Breeding section fields of Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar, India. The investigation counted 24 hexaploid bread wheat (*Triticum aestivum* L.) genotypes

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namely, RAUW-192, RAUW-221, DBW-14, RAUW-218, RAUW-179, RAUW-171, RAUW-209, RAUW-202, RAUW-215, RAUW-206, RAUW-177, RAUW-6, RAUW-4, RAUW-7, PBW-656, RAUW-183, RAUW-201, RAUW-199, DBW-17, RAUW-210, RAUW-205, RAUW-155, RAUW-159 and HD-2733 with variety HD-2733 serving as a check. The experimental design followed in this study was a Randomized Block Design with three replications wherein each replication, all the genotypes were sown in a plot divided into a number of rows (5) of 3 m isolated by a spacing of 20 cm. Irrigation was made available in the field at regular intervals based on rainfall patterns. To produce healthy and enhanced crops, prescribed agronomic and traditional cultural approaches were applied. Observations were documented for 12 quantitative traits *viz.*, plant height, total number of tillers/ plant, flag leaf area, days to 50% flowering, canopy temperature, relative water content, number of grains/ spike, chlorophyll content, days to maturity, spike length, 1000- grain weight, and Grain yield/plant. WINDOSTAT V7.0 was taken in use to perform

statistical analysis of the recorded data. D^2 statistics as proposed by Mahalanobis (1936) [2], was used to analyse genetic divergence among the considered 24 genotypes of bread wheat under study and Tocher's approach, as suggested by Rao (1952) [3] grouped them into distinct clusters.

Results and Discussion

All the 24 bread wheat genotypes (including check) in the present study differed significantly for the evaluated characters and exhibited noticeable divergence. D^2 statistics and ward minimum variance grouped them into six different clusters. Cluster I included the highest number of genotypes (11) followed by clusters V and II having 6 and 4 genotypes, respectively. However, clusters III, IV, and VI were monogenotypic, including single genotype. These findings were in line with previous studies reported by Khan *et al.* (2015) [4], Arya *et al.* (2017) [5], Rajshree and Singh (2018) [6], and Barman *et al.* (2021) [7].

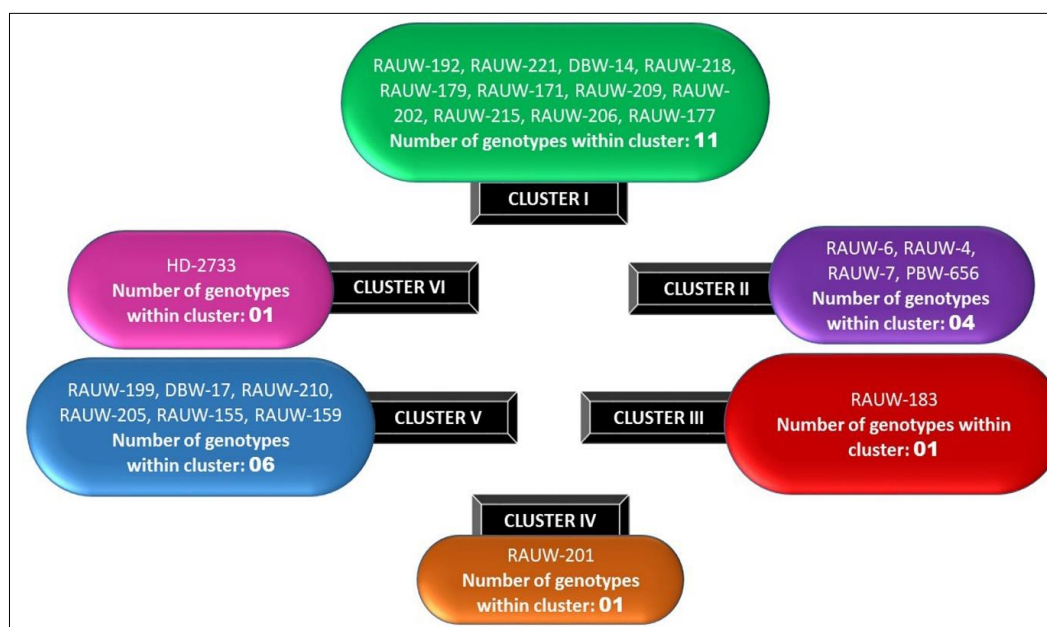


Fig 1: Clustering pattern of 24 genotypes of bread wheat on the basis of D2 statistics

Cluster VI had the utmost mean value for the majority of the characters, including plant height, total number of tillers/ plant, flag leaf area, days to 50% flowering, canopy temperature, relative water content, number of grains/ spike, chlorophyll content, days to maturity, 1000- grain weight, and Grain yield/plant. Cluster I had the highest mean value for spike length. In contrast, it showed the least flag leaf area and days to maturity, indicating the most suited to achieve earliness. Cluster II revealed the minimum days to 50% flowering. Cluster III was recorded with the lowest plant

height, number of grains/ spike, chlorophyll content and 1000- grain weight. The selection of cluster III can be made as a donor for dwarfness. Cluster IV was recorded with the minimum canopy temperature, relative water content and grain yield/plant. Cluster V illustrated the lowest values for total number of tillers/ plant and spike length. Earlier workers namely, Dwivedi and Pawar (2004) [8], Arya *et al.* (2017) [5] and Rajshree and Singh (2018) [6], also reported genotype selection based upon the mean of clusters to attain higher genetic potential exploitation.

Table 1: Cluster means for fifteen characters in bread wheat

	PH	TTP	FLA	DFP	CT	RWC	SL	GPS	CC	DM	TGW	GY
Cluster I	106.61	6.23	34.25	74.15	23.57	81.84	10.86	58.19	39.38	116.09	44.94	19.51
Cluster II	104.84	7.29	43.21	69.67	22.61	86.13	10.45	58.11	43.21	116.58	46.79	22.17
Cluster III	103.10	6.33	37.70	78.00	22.90	82.73	10.95	49.07	37.40	120.67	40.38	18.77
Cluster IV	111.77	8.70	35.53	75.00	21.77	79.31	11.07	56.97	38.91	116.33	42.74	17.94
Cluster V	106.17	6.13	34.54	83.39	23.49	82.54	10.37	57.93	40.50	124.50	43.66	18.78
Cluster VI	113.00	8.90	47.30	84.00	24.03	89.03	10.63	66.77	43.93	125.33	48.23	23.49

Cluster V revealed the highest intra-cluster distance (20.37) followed by cluster I (13.79) and II (13.35), signifying differences among the genotypes within these clusters. Clusters III, IV and VI showed the least intra-cluster distance (0.00), indicating only a single genotype was present within these three clusters. The maximum inter-cluster distance was noted among clusters II and V (89.59), signifying a high degree of genetic diversity. The finding indicates that we can exploit these genotypes under inter-varietal hybridization programmes to achieve recombinants with high-yielding

quality. Similar inter-varietal crosses can be attempted between the genotypes of clusters I and VI, II and III, II and VI, and IV and V. The minimum inter-cluster distance was prominent between the clusters I and III (19.11), displaying relatively less divergence and executing crossing between the genotypes of these clusters would not result in vigorous offsprings. These findings tracked Khan *et al.* (2015)^[4], Arya *et al.* (2017)^[5], Rajshree and Singh (2018)^[6], and Barman *et al.* (2021)^[7].

Table 2: Mean intra and inter-cluster distances (D^2) among nine clusters in bread wheat

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	13.79	27.40	19.11	22.25	42.77	57.02
Cluster II		13.35	51.14	30.28	89.59	85.46
Cluster III			0.00	22.51	20.16	39.89
Cluster IV				0.00	44.08	35.01
Cluster V					20.37	30.67
Cluster VI						0.00

Days to 50% flowering was revealed to have the highest influence in manifesting genetic divergence, followed by chlorophyll content, 1000- grain weight, number of grains/ spike, canopy temperature, and total number of tillers/ plant, indicating worthwhile opportunity to accomplish selection for these attributes. Earlier researchers, namely, Arya *et al.*

(2017)^[5] for grain yield; Rajshree and Singh (2018)^[6] and Barman *et al.* (2021)^[7] for days to 50% flowering, thousand-grain weight reported similar findings. These findings regarding contribution percentages of various characters towards total divergence will benefit in making decisions concerning selection and the choice of parents.

Table 3: Contribution percentages of fifteen characters towards genetic divergence in bread wheat

SI. No.	Source	Time ranked First	Contribution %
1.	Plant height	0	0.00%
2.	Total number of tillers/ plant	19	6.88%
3.	Flag leaf area	5	1.81%
4.	Days to 50% flowering	153	55.43%
5.	Canopy temperature	9	3.26%
6.	Relative water content	1	0.36%
7.	Spike length	4	1.45%
8.	Number of grains/ spike	20	7.25%
9.	Chlorophyll content	34	12.32%
10.	Days to maturity	1	0.36%
11.	1000- grain weight	23	8.33%
12.	Grain yield/plant	7	2.54%

Conclusion

The present investigation can help find appropriate parental genotypes for advancing breeding programs to accomplish superior grain yield. Cluster I included 11 genotypes, the highest number among the entire sets. Cluster VI had the utmost mean value for the majority of the characters. Genotype RAUW-183 can serve as a donor for dwarfness. Genotypes RAUW-199, DBW-17, RAUW-210, RAUW-205, RAUW-155, and RAUW-159 were genetically diverse, with the highest intra-cluster distance. The finding of the highest inter-cluster distance indicates that we can exploit genotypes RAUW-6, RAUW-4, RAUW-7, PBW-656 and RAUW-199, DBW-17, RAUW-210, RAUW-205, RAUW-155, RAUW-159 under inter-varietal hybridization programmes to achieve recombinants with high-yielding quality. Days to 50% flowering was revealed to have the highest influence in manifesting genetic divergence, followed by chlorophyll content, 1000- grain weight, number of grains/ spike, canopy temperature, and the total number of tillers/ plant. These findings indicate that it may be rewarding to execute selection for these traits.

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Reference

1. FAOSTAT. 2019. crop production. Retrieved 31 December 2021 from www.fao.org/faostat/.
2. Mahalanobis PC. On the generalised distance in statistics. Proceedings of National Institution of Science, India. 1936;2:49-55.
3. Rao CR. Advance statistical methods in biometrical research. John Wiley and Sons Inc. New York. 1952, 383.
4. Khan MK, Pandey A, Thomas G, *et al.* Genetic diversity and population structure of wheat in India and Turkey. Oxford Journals Science and Mathematics AOB PLANTS. 2015;10(2):1093.
5. Arya V, Singh J, Kumar L, Kumar R, Kumar P. Genetic variability and diversity analysis for yield and its components in wheat (*Triticum aestivum* L.). Indian

- Journal of Agricultural Research. 2017;51(2):128-134.
6. Rajshree, Singh SK. Assessment of genetic diversity in promising bread wheat (*Triticum aestivum* L.) genotypes. International Journal of Current Microbiology and Applied Sciences 2018;7(3):2319-7706.
 7. Barman M, Choudhary VK, Singh SK, Parveen R, Roy A, Debbarma P. Cluster analysis in bread wheat (*Triticum aestivum* L.) genotypes for morpho-physiological traits and grain micronutrient content. The Pharma Innovation Journal. 2021;10(5):1588-1591.
 8. Dwivedi A N, Pawar I S. Evaluation of genetic diversity among bread wheat Germplasm line for yield and quality attributing traits. Haryana Agriculture University Journal of Research. 2004;32(3):77-80.