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Genetic diversity analysis in bread wheat (*Triticum aestivum* L. em Thell.) For quantitative and physiological traits under normal sown condition

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Abstract

The present investigation was carried out with 65 genotypes of bread wheat in complete randomized block design with 3 replications at the Seed Breeding Farm, Department of Plant breeding and Genetics, College of Agriculture, JNKVV, Jabalpur for the screening of genetic diversity for yield and physiological traits under normal sown condition. The observations were recorded on fifteen morphological and two physiological traits. Based on D² Statistics, these 65 genotypes were grouped into five clusters. The highest intra-cluster distance was exhibited by cluster II (24.06) revealing maximum genetic divergence among its constituents. The highest inter-cluster distance was found between clusters II and III (76.64) and the lowest was between cluster I and IV (33.89). Cluster III exhibited highest cluster means for most of the agro-morphological traits like grain yield, 1000 grains weight and number of spikelets per spike while clusters V exhibited highest mean value for harvest index, spike weight and spike density. Maximum mean value for physiological traits like canopy temperature was observed in Clusters V while cluster II for chlorophyll content. On the basis of genetic diversity analysis, it was found that the maximum percent contribution towards genetic divergence in 65 wheat genotypes was from 1000 grain weight, grain yield per plant and biological yield and minimum by number of effective tillers per plant, spikelet number per spike and spike density.

Keywords: Genetic diversity, Mahalanobis D², clusters, physiological traits, wheat

Introduction

Wheat (Triticum aestivum L.) is a highly self-pollinated cereal crop belongs to "Poaceae" family and genus Triticum. It is very popular within farmers due to its easy cultivation, ecologically suitable and wider adaptation in agro-climatic conditions. It is most popular cereal crop between the farmers because it is easy to cultivate, ecologically suitable and wider adaptable in agro-climatic conditions. Bread wheat (Triticum aestivum) accounts for 95% of all the consumed wheat throughout the world and remaining 5% is made up of durum or hard wheat (T. Turgidum sp.) which is mainly used in food production industries. Bread wheat is holding about 17% of crop acreage and feeding about 40% of the world population. It is grown in many areas and environments viz., temperate, irrigated, dry and high rainfall areas and in warm, cold and humid to dry. Wheat is consumed in a variety of ways such as bread, chapatti, porridge, flour, Suji etc. It has high content of niacin and thiamine which are basically concerned in providing the special protein "Gluten". This protein provides the framework of spongy cellular texture of bread and baked products (Bhushan et al., 2013)^[1]. The area, production and productivity of wheat in India was 29.58 million ha, 99.7 million ton and 33.71 qtls/ha, respectively in 2017-18 (ICAR, IIWBR, 2018). It is grown in all the regions of the country and the states, namely, Uttar Pradesh, Punjab, Haryana, Madhya Pradesh, Rajasthan, Bihar, Maharashtra, Gujarat, West Bengal, Uttarakhand and Himachal Pradesh together contribute about 98% to the total wheat production of the country and play an important role of supplying carbohydrate and protein (Jaiswal et al., 2019)^[7]. Breeding of wheat through crossing, followed by the desired choice of individuals in segregation generations, depends on the presence of genetic diversity among the parents. Therefore, the first step in wheat crossbreeding program is the choice of the parents and the analysis of the genetic diversity of genotypes is a prerequisite for their efficient exploitation in the plant breeding program. The accurate determination of the genotype is very important during all steps of the breeding program, start from the choice of parents for breeding to obtain new varieties for use in the production of the crop. Estimation of genetic diversity on the basis of genetic distance is useful for wheat breeding as a tool of the parental selection for promoting new genetic recombination

to increase the grain yield (Poudel *et al.*, 2017) ^[11]. The existence of genetic diversity plays a crucial role in formulating a tangible and successful breeding programme.

Cluster analysis is an appropriate method for determining family relationship and genetic affinity i.e., to determine the extent of genetic distance of genotypes from each other. Mahalanobis D² statistic is a form of generalized distance which was first used by Mahalanobis (1936)^[8] to evaluate the genetic diversity between genotypes. Rao (1952) ^[13] suggested the use of this analysis to estimate genetic diversity in crop improvement programs. Genetic diversity available in the existing germplasm determines the success of any crop improvement programme (Harlan, 1976; Moose and Mumm, 2008) ^[6, 10]. Therefore, quantitative assessment of genetic diversity present among population usually helps a plant breeder in choosing desirable parents for breeding programme. The higher genetic distance between parents, the higher heterosis in progeny can be achieved. Therefore, keeping in mind the above facts, we investigated the extent of genetic diversity present in a set of 65 bread wheat genotypes for various traits.

Materials and Methods

The material for the present investigation comprised of total 65 genotypes of bread wheat (50 crosses, 10 female lines i.e., GW 366, HD 2864, MP 1201, GW 273, GW 322, MP 3288, HI 1544, HD 2932, JW-3211 and JW 3173 and 5 testers, PBW 343, DBW 110, PBW 17, MP 3336 and Lok 1). The pure seeds of these 15 selected genotypes were grown in crossing blocks to obtain 50 cross combinations during Rabi, 2016–17. During Rabi 2017-18 these 10 lines and 5 testers along with obtained 50 crosses were grown in randomized complete block design with three replications at Seed Breeding Farm, Department of Plant breeding and Genetics, College of Agriculture, JNKVV, Jabalpur (M.P.) Each plot consists of two rows of 2.5 m length with 20 cm spacing between the rows. The row to row and plant to plant distance was maintained by 20 cm and 10 cm, respectively.

The observations were recorded on seventeen diverse morpho-physiological and yield attributing traits. Data was recorded on whole plot basis for 50% flowering and days to maturity whereas plant height (cm), number of effective tillers per plant, number of spikes per plant, spike length (cm), number of spikelets per spike, peduncle length (cm), spike weight (g), number of grains per spike, 1000-grain weight (g), biological yield per plant (g), grain yield per plant (g), harvest index (%), spike density (%), canopy temperature and chlorophyll content on the basis of five randomly selected plants from each genotype in each replication.

Mahalanobis (1936) $[^{g]}$ D² statistical analysis was used for estimation of genetic divergence among 65 genotypes. The multivariate analysis by means of D² statistics is found to be useful in identifying degree of divergence between biological population at genotypic level and also to assess the relative contribution of different components to the total divergence both at inter and intra cluster level.

Result and Discussion

 D^2 statistical analysis was used for estimation of genetic divergence among 65 genotypes (Mahalanobis, 1936)^[8]. The clustering of D^2 values was formed by using the Tocher's

method as described by (Rao, 1952)^[13]. The 65 genotypes were grouped into five clusters.

Intra and inter-cluster distances

The inter-cluster distance was observed higher than intracluster, suggesting wide genetic diversity among genotypes (Table 1). The intra cluster distances varied from 0.00 to 24.06. Maximum intra-cluster distance was exhibited in cluster II (24.06) followed by cluster I (20.19) and cluster III (15.78). It was noticed that genotypes within cluster with high degree of divergence would produce more desirable breeding materials for attaining the maximum genetic advance (Dobariya et al., 2006)^[3]. While, cluster IV and cluster V showed zero intra-cluster distance indicating homogeneous nature of the genotypes with less deviation between the genotypes, hence selection will be ineffective. The intercluster distance varied from 33.89 to 76.64. Clusters II and III exhibited maximum inter cluster distance (76.64) followed by cluster III and V (69.70), cluster IV and V (53.23), cluster III and IV (49.38) Clusters I and II (48.00) and minimum inter cluster distance was observed between Clusters I and III (37.88) and cluster III and IV (33.89) indicating close relationship between these clusters and would not provide good results. The maximum distance between clusters, indicating that the genotypes included in these clusters show broad spectrum of genetic diversity and may be used in hybridization programme for wheat improvement (Chapla et al. 2008)^[2]. In order to increase the probability of isolating good recombinants in the segregating generations it would be useful to do crossing between the diverse genotypes belonging to clusters separated by large inter cluster distances. So, diversified wheat genotypes may be chosen from cluster II and cluster III which could result in beneficial segregants as a result of genetic recombination. This result is in conformity with the findings of (Elahi et al., 2021) [4], (Mishra et al., 2018)^[9]

Percent contribution of different characters towards genetic divergence

The percent contribution of characters towards divergence is presented in Table 3. It was observed that biological yield (34.09%) was the maximum contributor towards divergence followed by 1000 grains weight (30.48%), grain yield per plant (20.72), Canopy Temperature (6.15%), Days to maturity (3.61%), No of grains per spike (2.40%) and Chlorophyll Content (1.15%). Therefore, for selection of parents for hybridization, these characters *viz*. biological yield, 1000 grains weight, grain yield per plant and Canopy Temperature should be given importance.

Cluster means

The cluster means analysed for seventeen characters under study are presented (Table 2) revealed that the cluster V characterized by highest mean value for days to maturity (118.67), plant height (93.58), spike weight (3.87), harvest index (46.45), spike density (1.90) and canopy temperature (24.13). However, cluster IV characterized by genotypes with highest mean value for number of effective tillers per plant (15), number of spikes per plant (14.00), spike length (12.67) and peduncle length (17.00).

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	20.19	48.00	37.88	33.89	42.51
Cluster 2		24.06	76.64	41.47	40.43
Cluster 3			15.78	49.38	69.70
Cluster 4				0.00	53.23
Cluster 5					0.00

Table 1: Average intra and inter-cluster D² values among 17 traits of wheat genotypes

*Diagonal values: Intra-cluster distance

Table 2: Cluster mean for yield and i	ts component traits
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Clusters	DF	DM	PH	NTEP	NSP	SL	NSS	PL	SW
Ι	78.97	116.3	90.37	11.76	10.74	11.99	20.66	14.11	3.17
II	79.90	118.4	89.03	11.50	10.47	11.12	19.35	13.93	2.94
III	79.40	116.27	87.31	11.13	10.27	12.18	22.40	12.54	3.50
IV	76.33	113.67	91.55	15.00	14.00	12.67	17.00	17.00	3.60
V	78.33	118.67	93.58	10.67	13.67	11.23	21.33	13.13	3.87

DF-Days to 50% flowering, DM-Days to maturity, PH-Plant height, NTEP-Number of effective tillers per plant, NSP-Number of spikes per plant, SL-Spike length, NSS- Number of spikelets per spike, PL-Peduncle length, SW- Spike weight

Clusters	NGS	TGW	BYP	GYP	HI	SD	СТ	CC
Ι	50.98	48.54	50.32	18.21	36.15	1.74	22.88	48.83
II	46.57	38.03	41.51	15.03	36.37	1.76	23.11	48.90
III	49.87	52.21	58.07	21.19	36.50	1.85	20.51	45.83
IV	36.33	40.93	50.33	15.48	30.77	1.35	19.63	47.30
V	42.33	48.64	40.16	18.66	46.45	1.90	24.13	47.33
	+2.55	+0.04	40.10	10.00	+0.45	1.90	24.13	+7.55

NGS-Number of grains per spike, TGW-1000 grain weight, BYP-Biological yield per plant, GYP-Grain yield per plant, GWS-Grain weight per spike, HI-Harvest index, SD-Spike density, CT-Canopy temperature, CC- chlorophyll content

 Table 3: Characters contribution towards divergence in 65 Wheat genotypes

programmes to develop high-yielding wheat varieties.

Source	Times Ranked	Contribution
	Ist	%0
Days to 50% flowering	7	0.34%
Days to maturity	75	3.61%
Plant Height	1	0.05%
No. of effective tillers per plant	0	0.00%
No. of spike per plant	0	0.00%
Spike Length	1	0.05%
No. of spikelets per spike	0	0.00%
Peduncle Length	1	0.05%
Spike Weight	13	0.63%
No. of grains per spike	50	2.40%
1000 Grain Weight	634	30.48%
Biological yield per plant	709	34.09%
Grain yield per plant	431	20.72%
Harvest Index	5	0.24%
Spike Density	1	0.05%
Canopy Temperature	128	6.15%
Chlorophyll Content	24	1.15%

Number of spikelets per spike (22.40), 1000 grain weight (52.21) grain yield (21.19) and biological yield (58.07) were maximum in cluster III. Cluster II characterized by genotypes with highest mean value for days to 50% flowering (79.9) and chlorophyll content (48.90) whereas cluster I exhibited only maximum number of grains per spike (50.98). On the basis of cluster mean it may be suggested that maximum heterosis and good recombinants could be obtained in crosses between genotypes of cluster III and V in varietal improvement. They are expected to exhibit high heterosis and also likely to produce new recombinants with desired characters. Similar result was also in conformity to the results of (Santosh et al., 2019), (Rajneesh et al., 2019) ^[12]. Therefore, these genotypes could be exploited for their direct release as a variety after testing under different environments. Moreover, these genotypes can also be used as parents in hybridization

Conclusion

Based on the present investigation, it could be concluded that sufficient diversity existed among the 65 wheat genotypes. The characters grain yield per plant, biological yield and 1000 grain weight were observed to major contributor to diversity among the genotypes. Hybridization between the genotypes in cluster II and III and cluster III and V which recorded wide diversity between them and they could result in recombinants with better yielding ability.

References

- Bhushan B, Bharti S, Ojha A, Pandey M, Singh S, Singh B. Genetic variability, correlation coefficient and path analysis of some quantitative traits in bread wheat. Journal Wheat Research. 2013;5(1):24-29.
- 2. Chapla JN, Dobariya KL, Khanpara MD, Jivani LL, Kachhadia VH. Genetic divergence in bread wheat (*Triticum aestivum* L.). J of Plant Improvement. 2008;10(2):97-102.
- 3. Dobariya KL, Ribadia KH, Padhar PR, Ponkia HP. Analysis of genetic divergence in some synthetic lines of bread wheat (*Triticum aestivum* L.). Advances in Plant Sciences. 2006;19(1):221-225.
- 4. Elahi T, Pandey S, Shukla RS. Agro-morphological diversity in promising wheat genotypes grown under restricted irrigated condition. Electronic Journal of Plant Breeding. 2021;12(3):643-651.
- 5. ICAR-IIWBR. Director's Report of AICRP on Wheat and Barley Improvement Project 2017-18. Ed: G. P. Singh, ICAR-Indian Institute of Wheat and Barley Research, Karnal, India, 2018, 87.
- 6. Harlan. Genetic resources in wild relatives of crop. Crop Sci. 1976;16:329-333
- 7. Jaiswal SP, Singh A, Gahatyari NC. Genetic diversity analysis in bread wheat (*Triticum aestivum* L. EM.

Thell.) For yield and physiological traits. Int. J Curr. Microbiol. App. Sci. 2019;8(2):3059-3068.

- 8. Mahalanobis PC. On the generalized distance in statistics, proceeding of the national institute of sciences of India. 1936;2(1):49-55.
- 9. Mishra V, Chand P. Assessing genetic diversity for yield and quality traits in germplasm lines of bread wheat (*Triticum aestivum* L.). Int. J Curr. Microbiol. App. Sci. 2018;7(2):2281-2285.
- 10. Moose SP, Rita HM. Molecular plant breeding as the foundation for 21st century crop improvement. Plant Physiol. 2008;147:969-977.
- 11. Poudel A, Thapa DB, Sapkota M. Assessment of genetic diversity of bread wheat (*Triticum aestivum* L.) genotypes through cluster and principal component analysis. Int. J. Exp. Res. Rev. 2017;11:1-9.
- 12. Rajneesh K, Madakemohekar AH, Sravani M, Swetha M, Kamboj A, Thakur G, *et al.* Genetic evaluation of different genotypes of wheat (*Triticum aestivum* L.) in normal sowing condition in Punjab. Electronic Journal of Plant Breeding. 2019;10(3):970-979.
- 13. Rao CR. Advanced Statistical Methods in Biometrical Research, Wiley and Sons, New York, 1952.
- 14. Reddy JP, Kumar M, Dubey N, Avinashe H, Rohith K, Kalubarme S.. Genetic divergence for grain yield and its components in bread wheat (*Triticum aestivum* L.). 2022;13(1):258-261.