Electronic Journal of Plant Breeding

Research Note

Genetic divergence for grain yield and its components in bread wheat (*Triticum aestivum* L.)

J. Pranay Reddy[1], Mandeep Kumar[2], Nidhi Dubey[2*], Harshal Avinashe[2], Kachakayala Rohith[2] and Swapnil Kalubarme[2]

[1]Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Tamil Nadu, India. 608002
[2]Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Phagwara (Punjab), India. 144411
*E-Mail: drnidhi355@gmail.com

Abstract
An investigation about the genetic diversity among 68 wheat genotypes using yield and yield attributing traits was studied at the Agriculture Research Farm, Lovely Professional University, Phagwara (Punjab). Based on Mahalanobis D^2 statistic, the 68 genotypes were grouped in to five clusters. Maximum intra-cluster distance was observed in cluster III (150.64). The highest inter-cluster distance which was observed between clusters II and III (488.73). For yield improvement, hybridization between genotypes in cluster II characterised by highest mean value for 1000 grains weight and cluster III containing genotypes exhibiting highest mean value for harvest index would be promising. High mean grain yield was observed in cluster X (37.62). Protein content (50.13) and days to 50% heading (31.43) contributed maximum towards total divergence.

Keywords: Genetic diversity, Mahalanobis D^2, Clusters, Wheat

Wheat (*Triticum aestivum* L.) is the most important cereal in the world and is one of the crops to be domesticated some 10000 years ago. It is a self pollinated cereal crop of the *Poaceae* family and genus *Triticum*. Wheat is a segmental allohexaploid (2n = 6x = 42, AABBDD) having originated in the fertile crescent area of South-Western Asia. Global wheat production during 2016-17 was 760.1 million metric tons (Food and Agriculture statistics, 2017) while in India it was 99.7 million tones with an area coverage of 29.58 million hectares and an average productivity of 33.71 q/ ha (ICAR-IIWBR, 2018). Developing high yielding wheat cultivars is an important objective of wheat breeding programs (Sabaghnia and Janmohammadi, 2014). 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 D^2 statistic is a form of generalized distance which was first used by Mahalanobis (1936) to evaluate the genetic diversity between genotypes. Rao (1952) suggested the use of this analysis to estimate genetic diversity in crop improvement programs.

The experiment was carried out in Agriculture Research Farm, Department of Plant Breeding and Genetics, Lovely Professional University, Phagwara (Punjab). The experiment comprised of 68 different genotypes of wheat in which 12 genotypes were collected from JNKVV, Jabalpur and rest 56 were collected from BISA (Borlaug Institute for South Asia) Punjab. The experiment was laid out in a Randomized Complete Block Design with three replications and five rows per entry per replication, with a spacing of 22.5 cm x 5 cm and row length of 3m during *Rabi* 2018-19. Data was recorded on total plot basis

for days to 50% heading, days to maturity and canopy temperature whereas plant height (cm), peduncle length (cm), number of productive tillers per plant, number of spikelets per ear , ear length (cm), ear weight (g), number of ears per plant , number of grains per ear, 1000-grain weight (g), biological yield per plant(g), grain yield per plant (g), harvest index (%) and chlorophyll content from individual tagged plant. Mahalanobis D^2 (1936) cluster distance statistical analysis was used to assess the genetic diversity between the genotypes.

A method based on Mahalanobis's D^2 suggested by Tocher (Rao, 1952) was used to group the genotypes into different clusters based on the D^2 values. The 68 genotypes were grouped into five clusters. Among the five clusters, cluster I was the largest with 49 genotypes followed by cluster III (11 genotypes), cluster II (5 genotypes), cluster IV (2 genotypes) and cluster V (1 genotype) **Table 1.** The differentiation of genotypes into distinct clusters indicated existence of genetic diversity among them suggesting that the materials may serve as good source for selecting diverse parents for hybridization program. Similar findings were reported by Degewione and Alamerew (2013) and Dutamo *et al.* (2015).

The mean intra and inter cluster distances are presented in **Table 2**. Maximum intra-cluster distance was exhibited in cluster III (150.64) followed by cluster II (109.73), cluster I (92.40) and cluster IV (34.19) while, cluster V

showed zero intra-cluster distance. The inter-cluster distances varied from 136.43 to 488.73. Clusters II and III exhibited maximum inter cluster distance (488.73) followed by cluster II and IV (451.38) and minimum inter cluster distance was observed between clusters I and V (136.43). 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 choose 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 Ullah *et al. (*2011), Mecha *et al.* (2017), Mishra and Chand (2018), Shimelis *et al.* (2018) and Elahi *et al.* (2021).

The per cent contribution of characters towards divergence is presented in **Table 3.** It was observed that protein content (50.13%) was the maximum contributor towards divergence followed by days to 50% heading (31.43%). Therefore, these characters should be given importance for selection of parents for hybridization.

Based on cluster mean **(Table 4),** it could be concluded that for yield improvement genotypes of cluster II characterized by highest mean value for 1000 grains weight and cluster III characterized by genotypes with highest mean value for harvest index could be exploited

Table 1. Distribution of 68 genotypes into different clusters in Wheat

Group	Number of genotypes	Name of genotypes
Cluster I	49	HUW 468, WH 1105, Fasilabad 2008, HD 2985, Raj 4120, JW 3020, MP 3288, HP 1744, PBW 502, HW 2004, VL 804, HP 1761, UP 2565, K 1006, HUW 213, MP 4010, WH 542, SKW 196, Chirya 3, HD 2932, HD 2824, Kachu, UP 262, HS 240, HD 2967, PBW 527, KRL 1-9, HW 2045, HI 1531, UP 2382, PBW 373, GW 322, WH 147, GW 366, PBW 509, HD 3086, K 9644, Lok 1, Agra Local, HI 1500, K 0307, MP 1203, RAJ 4037, C 360, HI 8627, DL 788, K 68, Sujata, LOK 42
Cluster II	5	PBW 590, WL 711, HD 2329, Sonalika, WH 896
Cluster III	11	DBW 16, HD 2643, JW 17, JW 3173, DBW 17, C 306, HI 8713, MACS 6145, Raj 3765, HD 2864, GW 273
Cluster IV	2	HS 375, VL 829
Cluster V	1	DBW 14

Table 2. Average intra and inter-cluster D^2 values among 17 traits of Wheat genotypes

Group	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	**92.40**	198.57	207.04	241.27	136.43
Cluster II		**109.73**	488.73	451.38	234.92
Cluster III			**150.64**	339.57	201.10
Cluster IV				**34.19**	437.56
Cluster V					**0.00**

*Diagonal values: Intra-cluster distance

Table 3. Character contribution towards divergence in 68 Wheat genotypes

S. No.	Characters	Percent contribution	Rank
1	Days to 50% heading	31.43	II
2	Days to maturity	1.14	VIII
3	Plant height	6.76	III
4	Peduncle length	0.13	
5	Number of productive tillers per plant	0.00	
6	Number of spikelets per ear	1.23	VII
7	Ear length	1.49	V
8	Ear weight	0.40	
9	Number of ears per plant	0.04	
10	Number of grains per ear	3.56	IV
11	1000-grain weight	0.61	
12	Biological yield plant	0.75	
13	Harvest index	1.45	VI
14	Chlorophyll content	0.09	
15	Canopy temperature	0.66	
16	Protein content	50.13	I
17	Grain yield per plant	0.13	

Table 4. Mean of 17 characters in five clusters in Wheat genotypes

Characters	Cluster					Mean
	I	II	III	IV	V	
Days to 50% heading	108.42	100.07*	111.03	124.00**	101.33	108.97
Days to maturity	154.61	153.87	156.15	166.00**	153.33*	156.79
Plant height (cm)	108.97	105.43	107.93	113.17**	102.27*	107.55
Peduncle length (cm)	37.31	36.97*	37.27	37.23	41.20**	38.00
Number of productive tillers per plant	17.09	17.29	16.98	14.90*	17.93**	16.84
Number of spikelets per ear	19.78	18.81*	19.08	22.97**	21.13	20.35
Ear length (cm)	11.06	10.89	11.13	10.52*	13.58**	11.44
Ear weight (g)	3.23	2.97*	3.25	3.26	3.72**	3.29
Number of ears per plant	18.15	18.21	18.28	15.70*	19.27**	17.92
Number of grains per ear	65.93	63.11	60.17*	68.30	71.93**	65.89
1000-grain weight (g)	48.16	49.15**	48.97	47.76	45.89*	47.99
Biological yield per plant (g)	113.68	122.84	109.17	102.17*	164.33**	122.44
Harvest index (%)	25.80	26.49	29.07**	25.16	24.90*	26.28
Chlorophyll content	40.21*	43.26	40.60	42.48	45.03**	42.32
Canopy temperature	20.07*	20.12	20.38	20.60	20.63**	20.36
Protein content (%)	13.13	14.84**	10.87*	14.43	11.73	13.00
Grain yield per plant (g)	29.00	31.72	29.45	23.61*	37.62**	30.28

* = Minimum value and ** = Maximum value

in hybridization programme. This result is in conformity to the results of Shashikala (2006), Hailegiorgis *et al.* (2011), Pordel-Maragheh (2013), Bhishamkumar 2016, Santosh *et al.* (2019) and Rajaneesh *et al*. (2019).

Based on the present study, it could be concluded that sufficient diversity existed among the 68 wheat genotypes. The characters protein content and days to 50% heading were observed to contribute to diversity among the genotypes. Hybridization between the genotypes in cluster II and cluster III, which recorded wide diversity between them and characterized by high 1000

grain weight and harvest index, respectively could result in recombinants with better yielding ability.

REFERENCES

Bhishamkumar. 2016. Studies on variability, correlation and genetic divergence for grain yield and its components in F3 population of wheat (*Triticum aestivum* L.). M. Sc. (Agri.) Thesis, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur.

Degewione, A. and Alamerew, S. 2013. Genetic diversity in Bread wheat (*Triticum aestivum* L.) genotypes. *Pak. J. Biol. Sci*., **16(21)**: 1330-1335. [Cross Ref]

Dutamo, D., Alamerew, S., Eticha, F. and Assefa, E. 2015. Genetic variability in bread wheat (*Triticum aestivum*L.) germplasm for yield and yield component traits. *Journal of Biology, Agriculture and Healthcare*, **5(13)**: 39-46.

Elahi, T., Pandey, S. and Shukla, R.S. 2021. Agro-morphological diversity in promising wheat genotypes grown under restricted irrigated condition. *Electronic Journal of Plant Breeding,* **12(3):**643 – 651. [Cross Ref]

Food and Agriculture statistics. 2017.

Hailegiorgis, D., Mesfin, M. and Genet, T. 2011. Genetic divergence analysis on some bread wheat genotypes grown in Ethiopia. *Journal of Central European Agriculture,* **12(2):** 344-352. [Cross Ref]

ICAR-IIWBR. 2018. Annual Report 2017-18. Karnal, India.

Mahalanobis, P.C. 1936. On the generalized distance in statistics, proceeding of the national institute of sciences of India, **2 (1):** 49-55.

Mecha, B., Alamerew, S., Assefa, A., Assefa, E. and Dutamo, D. 2017. Genetic diversity based on multivariate analysis for yield and it's contributing characters in bread wheat (*Triticum aestivum* L.). genotypes. *Agricultural Research & Technology*, **8(5):** 1-10. [Cross Ref]

Mishra, V. and Chand, P. 2018. Assessing genetic diversity for yield and quality traits in germplasm lines of bread wheat (*Triticum aestivum* L.). *Int. J. Curr. Microbiol. App. Sci*, **7(2):** 2281-2285. [Cross Ref]

Pordel-Maragheh, F. 2013. Assess the genetic diversity in some wheat genotypes through agronomic traits. *Euro. J. Zool. Res,* **2 (4):** 71-75.

Rajaneesh, K., Madakemohekar, A.H., Sravani, M., Swetha, M., Kamboj, A., Thakur, G., Kumar, B. and Talekar, N. 2019. Genetic evaluation of different genotypes of wheat (*Triticum aestivum* L.) in normal sowing condition in Punjab. *Electronic Journal of Plant Breeding,* **10 (3):** 970 – 979. [Cross Ref]

Rao, C.R. 1952. Advanced Statistical Methods in Biometrical Research, *Wiley and Sons,* New York.

Sabaghnia, N. and Janmohammadi, M. 2014. Interrelationships among some morphological traits of wheat (*Triticum aestivum* L.) cultivars using Biplot. *Botanica lithuanica,* **20(1):** 19–26. [Cross Ref]

Santosh, Jaiswal, J.P., Singh, A. and Gahatyari, N. C. 2019. Genetic diversity analysis in bread wheat (*Triticum aestivum* L . em . Thell.) for yield and physiological traits. *Int. J. Curr. Microbiol. App. Sci.,* **8(2):** 3059-3068. [Cross Ref]

Shashikala, S.K. 2006. Analysis of genetic diversity in wheat. M. Sc. (Agri.) Thesis, University of Agricultural Sciences, Dharwad, India.

Shimelis, Y., Mohammed, W. and Letta, T. 2018. Genetic variability and diversity studies in Durum wheat (*Triticum turgidum* L. var. durum) genotypes based on cluster analysis using agronomic and quality traits in Southern Ethiopia. *Journal of Plant Breeding and Crop Science*, **10(5):** 99-104. [Cross Ref]

Ullah, K., Khan, S.J., Muhammad, S., Irfaq, M. and Muhammad, T. 2011. Genotypic and phenotypic variability, heritability and genetic diversity for yield components in bread wheat (*Triticum aestivum* L.) germplasm. *African Journal of Agricultural Research*, **6(23):** 5204-5207.