



Genetic Diversity Analysis among Genotypes of Bread Wheat (*Triticum aestivum* L.) for Yield and Its component Traits under Timely Sown Conditions

Neeru¹, Vikram Singh¹, Anu², Satender Yadav¹, D. K. Janghel¹ and Kiran^{1*}

¹Department Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar-125 004, Haryana, India.

²Shri Vaishnav Vidyapeeth Vishwavidyalaya Indore, (MP) (453111), India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Genetic diversity analysis for yield and its component traits among 60 genotypes of bread wheat (*Triticum aestivum* L.) under timely sown conditions distributed into seven clusters via D² statistics using Euclidean distance method which revealed that the cluster IV had maximum number of genotypes followed by cluster II, Cluster VI, cluster I, cluster V and, cluster III and VII. The highest inter-cluster genetic distance existed between cluster IV and VII and the average intra cluster distance between the genotypes of cluster V was maximum. Therefore, genotypes in these clusters may be used to produce the superior hybrids and transgressive segregants. For grain yield and effective tillers had highest mean value in cluster V and cluster VI. Cluster V and VII had highest mean value for 1000-grain weight and plant height respectively. Traits such as by plant height followed by canopy temperature, days to maturity, days to anthesis and grain filling duration contributing total of 50 per cent to the total divergence.

Keywords: *Wheat; genetic diversity; cluster analysis; morphological traits.*

1. INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is an annual *Kharif* season cereal crop belongs to the family Poaceae (grasses). It is a self-pollinating, hexaploid (AABBDD) plant with chromosome number of 42 ($2n = 6x = 42$) and estimated genome size of 16 GB [1]. The global production of wheat during 2020-2021 has been recorded 765 million metric tonne [2]. As per 4th Advance estimates production for major crops during 2020-2021, wheat cultivation acreage were 34.6 million hectares and giving total production of 109.52 million tonne [3]. During the course of evolution, wheat gained sufficient genetic diversity along the road from einkorn to bread wheat. Today, however, its diversity is weakening due to repeated cultivation of landraces for specific characters, narrow adaptation, farmers' varietal selection and the requirement of uniform varieties in industrial seed grain processing [4,5]. This depletion has now encouraged the use of genetic resources in wheat breeding programmes. At the same time, high temperature is one of the major abiotic stresses in tropical countries like India that has adverse impact on development, growth and overall yield of wheat. At some particular stage of life cycle of wheat, even a little increase or rise in temperature can lead to a complete loss of crop yield. Genetic diversity is crucial for adaptability and survival of wheat species against the threat of disease attack [6]. Hence, it is beneficial to assess the genetic diversity at a particular level that may facilitate the efficient exploitation of the germplasm. Such assessment programmes are imperative for man advanced breeding lines by identifying genotypes for hybridization programme. Thus, the present investigation focuses on the analysis of genetic diversity using cluster distance method.

2. MATERIALS AND METHODS

The experimental material for the present investigation comprised 60 accessions drawn from wheat gene pool maintained at National Bureau of Plant Genetic Resources (NBPGR), New Delhi and procured by the Indian Institute of Wheat and Barley Research (IIWBR) Karnal. The accessions were raised and followed recommended packages and practices at IIWBR research farm Karnal during *Rabi* season. The sixty accessions/ genotypes were raised under timely sown conditions in Randomized Block Design (RBD) with three replications. Each plot

comprises two rows of 3 mts length spaced at 0.20 mts.

Observations were recorded for traits namely days to heading, days to anthesis, days to physiological maturity, grain filling duration, plant height, number of effective tillers, thousand grain weight, grain yield, chlorophyll fluorescence and canopy temperature. Genetic divergence was computed through multivariate analysis using D^2 Statistic as described by Singh & Pawar [7].

3. RESULTS AND DISCUSSION

The cluster IV in Table 1 had maximum 19 (HD2967, DBW88, IBWSN1109, WH1124, IBWSN1156, WH711, IBWSN1155, P13648, KRL210, IBWSN1182, IBWSN1138, WH542, IBWSN1205, WH1202, P13644, IBWSN1151, PBW723, WH1227, WH1226) genotypes followed by cluster II with 17 genotypes (KRL19, WH1123, WH283, WH157, WH1228, WH147, WH1232, WH416, HD3086, WH1164, P13643, P13647, WL711, P13649, IBWSN1118, DPW621-50, IBWSN1142), Cluster VI with 14 genotypes (PBW343, IBWSN1145, IBWSN1162, IBWSN1155, IBWSN1152, WH1179, IBWSN1170, IBWSN1213, WH1184, WH1025, IBWSN1207, PBW725, IBWSN1159, IBWSN1171), cluster I with 5 genotypes (WH1021, HD3059, DBW90, Raj3765, WH730), cluster V with 3 genotypes (WH1080, WH1142, WH1105), and cluster III (ATLAS 66) and VII (C306) each having one genotype. The D^2 values amongst various genotypes within a cluster ranged from 0.000 to 3.228. Under both divergence analysis, genotypes related by their place of origin have shown tendency to group in the same cluster to some extent which may be due to dependence upon the directional selection pressure. Similar results were obtained by Dutamo et al. [8] (clustered 60 genotypes of bread wheat into six clusters), Kumar et al. [9] (grouped the 50 genotypes into 10 diverse clusters under both normal and heat stress environment), Kumar et al. [10] distributed the 30 genotypes into 8 clusters and observed that the distribution pattern of genotype in different clusters was random and Jaiswal et al. [11] (grouped the genotypes into twenty three different clusters, each cluster bearing different number of genotypes). To get more heterotic and large number of desirable transgressive segregates, selection of parents for hybridization should be properly based on genetic diversity rather than geographic diversity.

3.1 Intra and Inter Cluster Distances

The intra and inter cluster distance values between seven clusters under timely sown conditions are presented in Table 2. The genotypes of cluster IV and VII exhibited maximum divergence (8.905) followed in descending order by the genotypes of II and VII (8.845), V and VII (8.581), III and VII (8.381), I and VII (8.344), III and V (7.653), III and VI (7.255), VI and VII (7.094), I and III (7.077), III and IV (6.706), II and III (6.384), V and VI (6.303), I and V (6.215), II and V (5.834), I and VI (5.752), IV and V (5.591), I and IV (4.891), II and VI (4.623), I and II (4.270), IV and VI (3.915), II and IV (3.466). The higher inter cluster distance indicated the presence of more diversity among the genotypes included among these clusters. The average intra cluster distance between the genotypes of cluster V was maximum followed in descending order by clusters VI (3.228), II (3.119), I (3.066), IV (2.570), III (0.000) and VII (0.000). With the help of D² values a cluster diagram between and within clusters is drawn showing the relationship between different genotypes (Fig. 1). Therefore, the genotypes of cluster IV and VII exhibited maximum cluster divergence indicated that these genotypes may be used to produce a greater number of the superior heterotic F₁s and large number of desirable transgressive segregants. The genetic divergence is an outcome of several factors such as exchange of breeding material, genetic drift, natural variation and artificial selection in addition to geographical diversity. Similar finding was also reported by Sharma and Panwar [12], Mohanty et al. [13], Arya et al. [14], Naik et al. [15], Gupta et al. [16], Singh et al. [17], Yashpal et al. [18], Verma et al. [19], Ribadia et al. [20] and Marker and Tripathi [21]. Dutamo et al. [8] recorded the

lowest intra cluster distance in cluster V (0.00), which shows the absence of genetic variability within this cluster. The inter cluster distance was range from 44.83 to 179.72 and cluster IV and VI showed maximum inter cluster distance of 179.72. This indicates that the crossing between superior germplasm of above diverse cluster pair's might provide desirable recombinants for developing high yielding bread wheat varieties.

3.2 Cluster Means of Different Clusters for Various Characters

Mean values of seven clusters of 60 genotypes under timely sown conditions are presented in Table 3. Difference in cluster means existed for all characters. Cluster III had lowest mean values for days to heading and days to anthesis indicating earliness whereas, late genotypes were observed in cluster VII. For days to maturity, lowest mean value was observed in cluster I whereas, cluster VII had higher values. For plant height lowest values were in cluster V indicating these genotypes were shortest while cluster VII had the tallest genotypes. Cluster VI had highest mean values for effective tillers per meter while cluster VII had lowest mean. For chlorophyll fluorescence cluster III, VI and VII had highest mean value while cluster II had lowest mean values. Cluster III had highest mean values for canopy temperature and cluster I had lowest mean values. For grain yield per meter cluster V had highest whereas cluster VII had lowest mean values. Cluster V had highest and cluster VI had lowest mean values for 1000-grain weight. Similar findings were also observed by Gartan et al. [22], Dwivedi et al. [23], Dobariya et al. [24], Jaiswal et al. [11], Kumar et al. [10], Arya et al. [14], Verma et al. [25], Ahmad et al. [26] and Naik et al. [15].

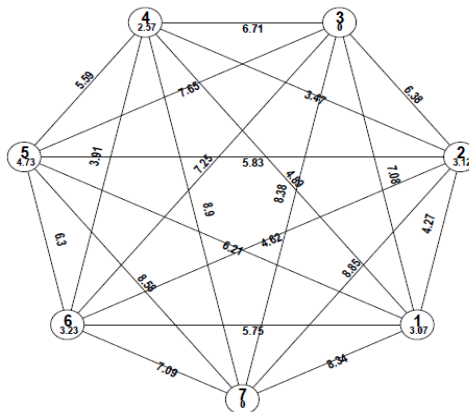


Fig. 1. D² Euclidean distance among different clusters of bread wheat under timely sown conditions

Table 1. Distribution pattern of 60 bread wheat genotypes under timely sown conditions

Clusters	Number of genotypes	Bread wheat genotypes
I.	5	WH1021, HD3059, DBW90, Raj3765, WH730
II.	17	KRL19, WH1123, WH283, WH157, WH1228, WH147, WH1232, WH416, HD3086, WH1164, P13643, P13647, WL711, P13649, IBWSN1118, DPW621-50, IBWSN1142
III.	1	ATLAS 66
IV.	19	HD2967, DBW88, IBWSN1109 WH1124, IBWSN1156, WH711, IBWSN1155, P13648, KRL210, IBWSN1182, IBWSN1138, WH542, IBWSN1205, WH1202, P13644, IBWSN1151, PBW723, WH1227, WH1226
V.	3	WH1080, WH1142, WH1105
VI.	14	PBW343, IBWSN1145, IBWSN1162, IBWSN1155, IBWSN1152, WH1179, IBWSN1170, IBWSN1213, WH1184, WH1025, IBWSN1207, PBW725, IBWSN1159, IBWSN1171
VII.	1	C306

Table 2. Average inter- and intra- (diagonal) cluster D² Euclidean distance among different clusters of bread wheat under timely sown conditions

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	3.066	4.270	7.077	4.891	6.215	5.752	8.344
Cluster II		3.119	6.384	3.466	5.834	4.623	8.845
Cluster III			0.000	6.706	7.653	7.255	8.381
Cluster IV				2.570	5.591	3.915	8.905
Cluster V					4.726	6.303	8.581
Cluster VI						3.228	7.094
Cluster VII							0.000

Table 3. Cluster mean values of different clusters for yield and its component traits under timely sown conditions

Yield and its component traits	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Days to heading	86.80	87.49	85.66	90.36	88.00	95.19	97.33
Days to anthesis	91.73	92.22	90.00	95.19	93.00	100.07	102.00
Days to maturity	137.27	139.41	150.00	138.97	144.11	141.83	150.33
Plant height (cm)	106.03	105.98	110.11	106.71	105.37	110.32	121.44
Effective tillers per meter	96.53	111.49	94.66	128.98	133.44	115.07	72.66
Chlorophyll fluorescence	0.70	0.69	0.72	0.72	0.70	0.72	0.72
Canopy temperature	21.06	27.11	27.70	26.75	22.67	27.25	21.72
Grain yield per meter (g)	95.51	116.15	100.44	134.35	138.89	119.85	74.25
1000-Grain weight (g)	43.64	43.26	41.76	44.24	44.37	40.98	43.20
Grain filling duration	32.00	31.49	32.33	30.93	51.11	33.59	48.33

Table 4. Per cent contribution of yield & its component traits towards total divergence under timely sown conditions

Sr. No.	Yield and its component traits	Contribution (%)
1	Days to heading	8.14
2	Days to anthesis	11.27
3	Days to maturity	11.48
4	Plant height (cm)	15.25
5	Effective tillers per meter	7.89
6	Chlorophyll fluorescence	8.07
7	Canopy temperature	13.19
8	Grain yield per meter (g)	5.68
9	1000-Grain weight (g)	8.74
10	Grain filling duration	10.30

3.3 Per Cent Contribution towards Total Divergence

Per cent contribution towards total divergence was calculated as per Mahalanobis D^2 statistic (Mahalanobis, 1936). The maximum contribution towards the total divergence under timely sown conditions (Table 4) was exhibited by plant height (15.25%) followed by canopy temperature (13.19%), days to maturity (11.48%), days to anthesis (11.28%), grain filling duration (10.30%), 1000-grain weight (8.74%), days to heading (8.14%), chlorophyll fluorescence (8.07%), effective tillers per meter (7.89%) and grain yield per meter (5.68%). The traits viz., plant height followed by canopy temperature, days to maturity, days to anthesis, grain filling duration, contributed more than 60% per cent towards total divergence. Hence, these characters should be given importance during hybridization and selection in the segregating population for improvement of yield and its component traits. Similar results for traits contributing maximum to the total divergence obtained by Singh et al. [27] for days to 50 per cent, flowering, plant height, spikelet's per ear, biological yield per plant, Dobariya et al. [24] for days to flowering, number of tillers per meter, days to maturity and 1000 grain weight, Peshattiwar et al. [28] for days to maturity, days to 50 per cent flowering, plant height and number of spikelet's per ear and Naik et al. [15] for plant height, grain yield and sedimentation value and Singh et al. [17] for days to 50 per cent flowering, plant height, spikelet's per ear, biological yield per plant and 1000 grain weight.

4. CONCLUSION

The sufficient genetic diversity found in present study, showed considerable scope for genetic

improvement through hybridization between the genotypes from divergent clusters. The genotypes of cluster IV and VII followed by cluster II and VII condition exhibited maximum cluster divergence indicated that these genotypes may be used to produce the superior hybrids and transgressive segregants. The traits viz., plant height followed by canopy temperature, days to maturity, days to anthesis, grain filling duration, under timely sown conditions contributed maximum to the total variability, thus, these characters should be given importance during hybridization and selection in the segregating population for improvement of yield and its component traits.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Wicker T, Gundlach H, Spannagl M, Uauy C, Borrill P, Ramírez-González RH, De Oliveira R, Mayer KF, Paux E, Choulet F. Impact of transposable elements on genome structure and evolution in bread wheat. *Genome Biology*. 2018;19(1):1-18.
2. Shajbandeh M. Wheat: production volume worldwide 2011/2012-2021/22; 2022. Available:www.statista.com
3. Anonymous. Fourth Advance Estimates of Production of Food grain, Oil seeds and other commercial crops for 2019-20. Department of Agriculture, Cooperation and Farmer Welfare; 2020. Available:www.agricoop.nic.in

4. Bellon MR. The dynamics of crop infraspecific diversity: A conceptual framework at the farmer level. *Economic Botany*. 1996;50:26-39.
5. Smale M. The green revolution and wheat genetic diversity: some unfounded assumptions, world development. 1997; 25:1257-1269.
6. Fu Y, Somers D. Genome wide reduction of Genetic Diversity in Wheat Breeding *Crop Science*. 2009;49:161-168.
7. Singh S, Pawar IS. *Theory and Application of Biometrical Genetics*. CBS Publishers, New Delhi. 2005; 467.
8. Dutamo D, Alamerew S, Eticha F, Assefa E. Genetic Variability in Bread Wheat (*Triticum aestivum* L.) Germplasm for Yield and Yield Component Traits. *Journal of Biology, Agriculture and Healthcare*. 2015;5:140-147.
9. Kumar R, Prasad BK, Singh MK, Singh G, Verma A. Genetic divergence analysis for morpho-physiological traits, under timely and late sown condition in bread wheat (*Triticum aestivum* L.). *Journal of Wheat Research*. 2015;7(1):27-30.
10. Kumar R, Gaurav SS, Bhushan B, Pal R. Study of genetic parameters and genetic divergence for yield and yield components of bread wheat (*Triticum aestivum* L.). *J. of Wheat Res*. 2013; 5(2):39-42.
11. Jaiswal JP, Arya Mamta, Kumar Anil, Swati, Rawat RS. Assessing Genetic Diversity for Yield and Quality Traits in Indigenous Bread Wheat Germplasm. *Electronic Journal of Plant Breeding*. 2010;1:4.
12. Sharma V, Pawar IS. Genetic divergence for yield, its components and quality traits in bread wheat. *Haryan agric. Univ. J. Res*. 2007;37:27-31.
13. Mohanty S, Mukherjee S, Dash AP, Mandal AB. Genetic analysis for identification of terminal heat tolerance genotypes in wheat. *Indian Journal of Genetics and Plant Breeding*. 2017;77(1): 160-162.
14. Arya VK, Singh J, Kumar L, Kumar R, Kumar P, Chand P. Genetic variability and diversity analysis for yield and its components in wheat (*Triticum aestivum* L.). *Indian J. Agric. Res*. 2017;51(2):128-134.
15. Naik VR, Biradar SS, Yadawad A, Desai SA, Veerasha BA. Assessing genetic diversity for yield and quality traits in germplasm lines of bread wheat (*Triticum aestivum*); 2016.
16. Gupta RS, Tiwari DK, Deol SS, Singh RP. Genetic divergence in bread wheat (*Triticum aestivum* L.em. Thell). *New Botanist*. 2002;29(1/4)1-7.
17. Singh SP, Dwivedi VK. Genetic divergence in wheat (*Triticum aestivum* L.). *Agricultural Science Digest*. 2005; 25(3):201-203.
18. Yashpal Porwal, Mridula Billore, Prasad SVS. Morphological variability and genetic in relation to grain yield and its component traits in wheat. *National Journal of Plant Improvement*. 2005;7(2): 69- 72.
19. Verma AK, Singh PK, Vishwakarma SR, Tripathi RM. Genetic divergence in wheat (*Triticum aestivum* L.). *Farm Science Journal*. 2006;15(1):32-34.
20. Ribadia KH, Dobariya KL, Ponika HP, Jivani LL. Genetic diversity in macroni wheat (*Triticum durum* Desf.). *Journal of Maharashtra Agriculture University*. 2007; 32:32-34.
21. Marker S, Tripathi Atul. Estimation of genetic divergence among durum wheat (*Triticum durum* L.) genotypes for yield and yield contributing traits. *Indian Journal of Plant Genetic Resources*. 2008;21(1):99-106.
22. Garten SL, Mittal RK. Genetic divergence in bread wheat. *Crop Improvement*. 2003; 30(2):185-188.
23. Dwivedi AN, Pawar IS. Evaluation of genetic diversity among wheat germplasm lines for yield and quality attributing traits in bread wheat. *Haryana Agriculture University Journal of Research*. 2005; 34(1):35-39.
24. Dobariya KL, Ribadia KH, Padhar PR, Ponkia HP. Analysis of genetic divergence in some synthetic lines of breadwheat (*Triticum aestivum* L.). *Advances in Plant Sciences*. 2006;19(1): 221-225.
25. Verma PN, Singh BN, Yadav RK. Genetic variability and divergence analysis of yield and its contributing traits under sodic soil condition in wheat (*T. aestivum* L.). *International Journal of Agricultural Sciences*. 2013;3(2):395-399.
26. Ahmad HM, Awan SI, Aziz O, Ali MA. Multivariate analysis of some metric traits in bread wheat (*Triticum aestivum* L.). *European Journal of*

- Biotechnology and Bioscience. 2014;1(4): 22-26.
27. Singh SP, Dwivedi VK. Genetic divergence in wheat (*Triticum aestivum* L.). New Agriculturist. 2002; 13(1/2):5-7.
28. Peshattiwar PD, Ghorpadi PB, Dandge MS, Archana Thorat, Gomase DG. Genetic divergence in durum wheat cultivars. International Journal of Agricultural Sciences. 2009;5(1):243-247.

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