

# EVALUATION OF GENETIC DIVERGENCE IN WHEAT (*TRITICUM AESTIVUM* L.) GERMPLASMS

**BRIJENDRA KUMAR\*, DHANANJAY AND BHUPENDRA NARAYAN SINGH**

Department of Genetics and Plant Breeding,

Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad - 224 229 (U.P.) INDIA

e-mail: brijendra.nduat@gmail.com

## KEYWORDS

Wheat  
Cluster  
D<sup>2</sup>  
Genetic divergence

## Received on :

17.12.2013

## Accepted on :

26.05.2014

\*Corresponding  
author

## ABSTRACT

In the present study, sixty-four genotypes of wheat germplasm were evaluated for assessing genetic divergence for 11 different characters across six environments for exploitation in a breeding programme aimed at improving yield potential of wheat by using Mahalanobis D<sup>2</sup> statistics. The germplasm were grouped into nine clusters suggesting considerable amount of genetic diversity in the material. The cluster II had maximum 14 genotypes followed by VIII and III having 12 and 11 genotypes, respectively. These clusters having maximum number of genotypes, reflecting narrow genetic diversity. The intra-cluster D<sup>2</sup> value ranged from 7.36 to 22.63 while, inter-cluster D<sup>2</sup> value ranged from 13.69 to 93.06. The maximum intra cluster distance was exhibited by cluster V followed by cluster VI and cluster IX. The maximum inter-cluster D<sup>2</sup> value was observed between V and IX followed by cluster V and VI and cluster I and V. Cluster V had least number of two genotypes and emerged with contained highest cluster mean value for plant height, total number of tillers/plant and good value for test weight, ear length and biological yield/plant. Cluster VII has highest mean value for grains/spike and good value for ear length and test weight and cluster VIII had highest mean value for biological yield/plant, grain yield/plant and good value for ear length, total number of tillers/plant and test weight. Cluster IX showed high mean value for grain yield/plant, total number of tillers/plant and test weight. Maximum contribution toward the total divergence was exhibited by days to heading followed by plant height and number of grains/spike and minimum by total number of tillers/plant. Cluster V and IX showing maximum inter cluster distance and crossing of genotypes DBW-11 and HP1633 from cluster V with five genotypes from cluster IX suggested for improving effective tillers/plant, total number of tillers/plant, test weight and ear length enhancing the yield and chances of getting better recombinants in segregating generations. Noteworthy is that cluster IV, VII and VIII reflected high cluster means for seed yield per plant, effective tillers/plant, total number of tillers/plant and test weight and these clusters can be successfully utilized in hybridization programmes to get desirable transgressive segregants.

## INTRODUCTION

Wheat (*Triticum aestivum* L.) is considered as king of cereals and contributing 30% of food basket of the country. It is an important staple food of many countries in the world and occupies a unique position as used for the preparation of a wide range of food stuffs. It is agronomically and nutritionally most important cereal essential for food security, poverty alleviation and improved livelihoods. To feed the growing population, the country wheat requirement by 2030 has been estimated at 100 million metric tons. To achieve this target, the wheat production has to be increased at the rate of < 1 m.mt per annum (Sharma *et al.*, 2011) and this can be achieved by enhancing the production of wheat by developing improved varieties through heterosis breeding among parents having high genetic divergent. Over the past century selection of desirable parents for hybridization programme has been found as an effective operating implement in developing high yielding crop varieties upon which, the modern agriculture can rely. The presence of genetic diversity and genetic relationships among genotypes is a prerequisite and paramount important for successful wheat breeding programme. Developing hybrid wheat varieties with desirable traits require a thorough knowledge about the existing genetic

variability (Kahrizi *et al.*, 2010). The more genetic diverse parents, the greater chances of obtaining higher heterotic expression in F<sub>1</sub>s and broad spectrum of variability in segregating population as already reported by earlier workers (Shekhawat *et al.*, 2001). Precise information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization (Samsuddin, 1985). Several genetic diversity studies have been conducted on different crop species based on quantitative and qualitative traits in order to select genetically distant parents for hybridization (Shekhawat *et al.*, 2001; Arega *et al.*, 2007; Daniel *et al.*, 2011). Jagadev *et al.* (1991) reported that the character contributing maximum to the divergence should be given greater emphasis for deciding the type of cluster for purpose of further selection and the choice of parents for hybridization.

In views of these facts, the present study was undertaken with the aim of examining the magnitude of genetic diversity and characters contributing to genetic diversity among bread wheat genotypes for utilization in wheat breeding programme.

## MATERIALS AND METHODS

The experimental materials consisting of 64 genotypes of

**Table 1: Clustering pattern of 64 wheat genotypes into 9 clusters on the basis of D<sup>2</sup> analysis**

Cluster Number	Number of genotypes	Name of genotypes
I	6	NW-1012, PBW-443, J-501, NW-1067, DL-784-3, PBW-502
II	14	PBW-154, UP-2338, UP-262, RAJ-4077, HD 2329, PBW 343, HD-2733, HD-2824, HS-240, UP-2700, DBW-31, HDR-77, UP-2699, WH- 1021
III	11	RAJ-3733, WH-1022, UP-2003, HI-1539, UP-2697, UAS-281, VW-486, HP-1731, HP-1761, HUW-468, FLW-1
IV	4	NW-1014, WR-1743, HD 2643, HUW-234
V	2	DBW-11, HP-1633
VI	6	NW-2036, HD-2285, NIAW-1417, HP-1744, GW-9712, HALNA
VII	4	HD-2204, HD-2307, NW-1076, NIAW-1342
VIII	12	PBW-373, AKW0770, RAJ-3077, KC-975, RAJ-3765, UP2425, GW-9715WH-2045, AKW-381, WR-783-4, WR-881, RWP-2004-2
IX	5	WR-1695, WH-1031, DBW-14, DBW-22, HI-8498

**Table 2: Estimates of average intra-cluster (bold diagonal) and inter-cluster D<sup>2</sup> value for nine clusters in wheat**

Cluster number	I	II	III	IV	V	VI	VII	VIII	IX
Cluster I	<b>11.76</b>	16.72	19.46	37.23	62.34	48.76	43.56	24.42	26.47
Cluster II		<b>10.02</b>	13.69	39.89	47.65	56.89	37.27	19.66	37.23
Cluster III			<b>10.24</b>	36.96	47.03	42.50	23.83	17.93	33.98
Cluster IV				<b>9.22</b>	25.98	31.94	32.16	23.27	46.52
Cluster V					<b>22.63</b>	69.67	51.15	43.01	93.06
Cluster VI						<b>17.46</b>	18.64	29.17	33.74
Cluster VII							<b>7.36</b>	17.41	35.49
Cluster VIII								<b>9.21</b>	25.01
Cluster IX									<b>17.12</b>

wheat germplasms collected from different coordinating units of All India Coordinated Wheat Improvement Project. Germplasm were grown in randomized block design with three replications at Main Experiment Station Farm of Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad (U.P.), India, under three agronomical different condition i.e. early sown normal soil, timely sown salt affected soil (pH 8.8, ECe (ds/m) 2.0) and late sown reclaimed soil during Rabi seasons of 20007-08 and 2008-09. Thus, a total of six environments were covered by laying six separate trials. Each treatment was planted in two row plot of 3 meter long with inter-row and inter-plant distance of 25 and 5 cm, respectively. Fertilizers and manures were applied as per recommended dose. Recommended cultural practices were followed to raise a healthy crop. Necessary weeding was done to keep the crops free from weeds. Flood irrigation was given to the plants at particular growth stages. Observations were recorded on ten randomly selected competitive plants for eleven quantitative characters viz., Days to heading, plant height, effective tillers/plant, total number of tillers/plant, days to maturity, ear length, number of grains/spike, test weight, harvest index, biological yield and grain yield/plant in each entry of each replication for all the characters except days to heading and days to maturity which were recorded on plot basis. Genetic divergence was estimated by using D<sup>2</sup> statistics of Mahalanobis (1936) and clustering of genotypes was done according to Tocher's method as described by Rao (1952). The per cent contribution of characters towards genetic divergence was calculated according to Singh and Chaudhary (1985).

## RESULTS AND DISCUSSION

Based on Mahalanobis' D<sup>2</sup> analysis, sixty four genotypes were grouped into nine clusters with variables number of genotypes

(Table 1) suggesting considerable amount of genetic diversity in the material. The cluster II had maximum 14 genotypes followed by VIII and III having 12 and 11 genotypes, respectively. These clusters having maximum number of genotypes, reflecting narrow genetic diversity. Two clusters (I & VI) possessed 6 genotypes and clusters IV and VII had 4 genotypes and one cluster (IX) had 5 genotypes. It means the overall genetic similarity was found in the germplasms were presented within the cluster and the pattern of distribution of genotypes in different clusters exhibited that geographical diversity was not related to genetic diversity as genotypes of same geographical region were grouped into different cluster and vice-versa, as supported by earlier finding of Langade *et al.*, 2013, Kumar *et al.*, 2013 and Singh *et al.*, 2014. Only two genotypes (DBW11 and HP1633) formed a separate cluster. Similarly sixty four germplasms were dispersed in nine clusters. The possible reason for grouping of genotypes of different places into one cluster could be free exchange of germplasm among the breeder of different region or unidirectional selection practiced by breeder in tailoring the promising cultivar for selection of different region (Verma and Mehta, 1976). The intra-cluster D<sup>2</sup> value ranged from 7.36 to 22.63 while, inter-cluster D<sup>2</sup> value ranged from 13.69 to 93.06 (Table 2). The maximum intra cluster distance was exhibited by the genotype of cluster V (22.63) followed by cluster VI (17.46) and cluster IX (17.12). The maximum inter-cluster D<sup>2</sup> value was observed between V and IX (D<sup>2</sup> = 93.06) followed by cluster V and VI (D<sup>2</sup> = 69.67) and cluster I and V (D<sup>2</sup> = 62.34) suggesting wide diversity between them and germplasm in these clusters could be used as parents in hybridization programme to develop desirable type because crosses between genetically divergent lines will generate heterotic segregants. As heterosis can be best exploited and chances of getting transgressive segregants are maximum when generating diverse lines are crossed

**Table 3: Cluster means for 11 characters in wheat**

Clusters	Days to heading	Plant height (cm)	Effective tillers/plant	Total number of tillers/plant	Days to maturity	Ear length (cm)	Number of grains/spike	Test weight (g)	Harvest index (%)	Biological yield/plant (g)	Grain yield/plant (g)
I	79.16	80.04	4.158	4.703	117.90	7.87	39.78	38.67	53.88	16.79	8.99
II	79.04	83.82	4.027	4.572	118.03	9.16	42.20	39.65	47.92	18.68	8.93
III	77.89	81.90	4.081	4.639	116.30	9.20	45.99	37.99	52.05	17.16	8.84
IV	69.47	87.86	4.292	4.786	118.80	8.10	39.83	40.78	56.21	16.12	8.93
V	70.97	98.61	4.246	4.840	112.30	9.10	44.77	40.49	49.35	18.19	8.73
VI	68.55	74.95	4.277	4.779	111.80	7.78	45.79	39.78	53.51	16.35	8.62
VII	70.46	78.08	4.030	4.611	112.60	9.19	49.15	39.77	49.62	17.78	8.73
VIII	72.87	80.35	4.217	4.736	114.60	9.17	41.73	40.22	49.67	19.00	9.33
IX	75.48	70.42	4.207	4.753	114.90	8.15	38.49	39.60	53.21	17.21	9.09

**Table 4: Per cent contribution of 11 characters towards total genetic divergence**

S. No.	Characters	Contribution (%)
1.	Days to heading	33.33
2.	Plant height (cm)	23.51
3.	Effective tillers/plant	0.25
4.	Total number of tillers/plant	0.00
5.	Days to maturity	7.84
6.	Ear length (cm)	8.63
7.	Number of grains/spike	17.26
8.	Test weight (g)	0.89
9.	Harvest index (%)	1.84
10.	Biological yield/plant (g)	6.35
11.	Grain yield/plant (g)	0.10

(Zaman *et al.*, 2005, Saxesena *et al.*, 2013). Many workers in different crops have also reported that selection of parents for hybridization should be done from two clusters having wider inter-cluster distance to get maximum variability in segregating generations. Heterosis is generally attributed to genetic divergence among the parental lines involved in the cross. Nevertheless, the genetic divergence for the maximum expression of the heterotic effects has a limit (Moll *et al.*, 1965) and Arunachalam and Bandyopadhyay, 1984).

The comparison of cluster means revealed considerable differences among the clusters of different quantitative characters (Table 3). Cluster I had highest cluster mean for days to heading (79.16) and second highest cluster for harvest index (53.88) and good value for effective tillers/plant (4.158), total number of tillers/plant (4.703), days to maturity (117.90) and grain yield/plant (8.99) but this cluster also recorded second lowest cluster mean for ear length (7.87), number of grains/spike (39.78) and test weight (38.67). Cluster II had high mean value for days to heading (79.04), days to maturity (118.03), ear length (9.16), test weight (39.65) and grain yield/plant (8.93). Cluster III had highest values for ear length (9.20) and good value for number of grains/spike (45.99), harvest index (52.05) and grain yield/plant (8.84). Cluster IV had highest values for effective tillers/plant (4.292), test weight (40.78), days to maturity (118.80) and harvest index (56.21) and good value for total number of tillers/plant (4.786), ear length (8.10) while, it also showed lowest cluster mean for biological yield/plant (16.12) and second lowest cluster mean for days to heading (69.47). Cluster V had least number of two genotypes and emerged with contained highest value for plant height (98.61), total number of tillers/plant (4.840) and good

value for test weight (40.49), ear length (9.10) and biological yield/plant (18.19) and it also provided second lowest cluster mean for grain yield/plant (8.73). Cluster VI having 6 genotypes exhibited second highest cluster mean for effective tillers/plant (4.277) and lowest cluster mean for days to heading (68.55), days to maturity (111.8), ear length (7.78) and grain yield/plant (8.62). Cluster VII has highest mean value for number of grains/spike (49.15) and good value for ear length (9.19) and test weight (39.77) and second lowest value for days to maturity (112.60 days) and grain yield/plant (8.73) and Cluster VIII had highest value for biological yield/plant (19.00), grain yield/plant (9.33) and good value for ear length (9.17), total number of tillers/plant (4.736) and test weight (40.22). Cluster IX having 5 genotypes showed high cluster mean for grain yield/plant (9.09), total number of tillers/plant (4.753) and test weight (39.60) and lowest value for plant height (70.42) and number of grains/spike (38.49). Similar findings have been also reported by (Tsegaye *et al.*, 2012, Kumar *et al.*, 2013) reflected probability of getting better segregants and primary recombinants expected to more, in case if the genotypes of these clusters will be used in hybridization programme. The importance of genetic diversity in wheat to recover transgressive segregants has also been emphasized by Jatasara and Paroda (1983) and Nimbalkar *et al.* (2002). According to Rahim *et al.* (2010) who showed that the hybrids of genotypes with maximum distance resulted in high yield, the cross between these genotypes can be used in breeding programs to achieve maximum heterosis. Cluster V and IX showed maximum inter cluster distance and crossing of genotypes DBW-11 and HP1633 from cluster V with five genotypes from cluster IX suggested for improving effective tillers/plant, total number of tillers/plant, test weight and ear length to enhance the yield and chances of getting better recombinants in segregating generations. Noteworthy is that cluster IV, VII and VIII reflected high cluster means for seed yield per plant, effective tillers/plant, total number of tillers/plant and test weight and Jagadev *et al.* (1991) reported that the character contributing maximum to the divergence should be given greater emphasis for deciding the type of cluster for purpose of further selection and the choice of parents for hybridization. The maximum contribution towards the total divergence (Table 4) was exhibited by days to heading (33.33%) followed by plant height (23.51%) and number of grains/spike (17.26%). Thus the characters which show more contribution (%) towards the total divergence should be considered during selection.

Thus, it is evident from the present finding that substantial genetic divergence was envisaged in genetic stock of wheat. The varieties of same geographical region clustered with the varieties of other geographical region due to selection pressure and genetic drift. This indicates that there is no parallelism between genetic diversity and geographical region except in some cases. Hybridization between the genotypes of different clusters can give high amount of hybrid vigour and good recombination. Grain yield/plant, days to maturity, number of grains/spike, effective tillers/plant and test weight were important components and these should be taken into account while breeding in wheat.

## REFERENCES

- Arega, G., Hussein, M. and Harjit, S. 2007.** Genetic divergence in selected durum wheat genotypes of Ethiopian plasm. *Afr. Crop Sci. J.* **15(2)**: 67-72.
- Arunachalam, V. and A. Bandyopadhyay. 1984.** Limit to genetic divergence for occurrence of heterosis: Experimental evidence from crop plants. *Indian J. Genet.* **44**: 548-554.
- Daniel, H., Mebrahtom. M. and Tsige, G. 2011.** Genetic divergence analysis on some bread wheat genotypes grown in Ethiopia. *J. Central Eur. Agric.* **12(2)**: 344-352.
- Jagadev, P. N., Shamal, K. M. and Lenka, L. 1991.** Genetic divergence in rape mustard. *Indian J. Genet. Plant Breed.* **51**: 465-466.
- Jatasara, D. S. and Paroda, R. S. 1983.** Genetic divergence in wheat. *Indian J. Genet.* **43**:63-67.
- Kahrizi, D., Maniee, M., Mohammadi, R. and Cheghamirza, K. 2010.** Estimation of genetic parameters related to morpho-agronomic traits of durum wheat (*Triticum turgidum* var. durum). *Biharean Biologist.* **4(2)**: 93-97.
- Kumar, B., Singh, C. M. and Jaiswal, K. K. 2013.** Genetic variability, association and diversity studies in bread wheat (*Triticum aestivum* L.). *The Bioscan.* **8(1)**: 143-147.
- Langade, D. M., Ram, C. N., Vishwakarma, D. N and Sharma, A. 2013.** Evaluation of genetic divergence in berseem (*Trifolium alexandrinum* L.) germplasm. *The Bioscan.* **8(3)**: 767-770.
- Moll, R. H., Lonniquist, J. H. and Johnson E. C. 1965.** The relation of heterosis and genetic divergence in maize. *Genetics.* **52**: 139-144.
- Nimbalkar, C. A., Navale, P. A. and Biradar, A. B. 2002.** Generalized D<sup>2</sup> and genetic diversity in wheat. *J. Maharashtra Agr. Univ.* **27(1)**: 43-45.
- Rahim, M. A., Mia, A. A., Mahmud, F., Zeba, N. and Afrin, K. 2010.** Genetic variability, character association and genetic divergence in mungbean (*Vigna radiate* L. Wilczek). *Plant Omic.* **3**: 1-6.
- Rao, C. R. 1952.** Advanced statistical method in biometri reseach., *John Wiley and Sons, Inc. New York.* **15(10)**: 130-134.
- Samsuddin, A. K. M. 1985.** Genetic diversity in relation to heterosis and combining ability analysis in spring wheat. *Theor. Appl. Genet.* **70**: 306-308.
- Saxesena, R. R., Lal, G. M., Yadav, P. S. and Vishwakarma, M. K. 2013.** Diversity analysis and identification of promising lines for hybridization in field pea (*Pisum sativum* L.). *The Bioscan.* **8(4)**: 1437-1440
- Sharma, I., Shoran, J., Singh, G. and Tyagi, B. S. 2011.** Wheat Improvement in India. *Souvenir of 50<sup>th</sup> All India Wheat and Barley Research Workers Meet, New Delhi.* p. 11.
- Shekhawat, U. S., Vijay, P. and Singhania, D. L. 2001.** Genetic divergence in barley (*Hordeum vulgare* L.). *Indian J. Agric. Res.* **35(2)**: 121-123.
- Singh, P., Singh A. K., Sharma, M. and Salgotra, S. K. 2014.** Genetic divergence study in improved bread wheat varieties (*Triticum aestivum* L.). *African J. Agric. Res.* **9(4)**: 507-512.
- Singh, R. K. and Chaudhary, B. D. 1985.** Biometrical methods in quantitative genetic analysis, Kalyani publishers, New Delhi-Ludhiana,India. p. 318
- Tsegaye, D., Dessalegn, T., Dessalegn, Y. and Share, G. 2012.** Analysis of genetic diversity in some durum wheat (*Triticum durum* Desf) genotypes grown in Ethiopia. *African J. Biotech.* **11(40)**: 9606-9611.
- Verma V. S. and Mehta R. K. 1976.** Genetic divergence in Lucerne. *J. Maharashtra Agr. Univ.* **1**: 23-28.
- Zaman M. R., Paul, D. N. R., Kabir, M. S., Mahbub, M. A. A. and Bhuiya, M. A. A. 2005.** Assessment of character contribution to the divergence for some rice varieties. *Asian J. Plant Sci.* **4(4)**: 388-391.