Electronic Journal of Plant Breeding, 9(1) : 361- 367 (Mar 2018) DOI:10.5958/0975-928X.2018.00040.6
ISSN 0975-928X

**Research Note**

# Evaluation of genetic divergence in wheat (*Triticum aestivum* L.) germplasm

**Deshraj Gurjar and Shailesh Marker**
Department of Genetics and Plant Breeding, Sam Higginbottom Institute of Agriculture, Technology and Sciences, Allahabad - 211 007.
**E-mail:** deshraj.agri@gmail.com

(Received: 8 Jun 2017; Revised: 9 Mar 2018; Accepted: 15 Mar 2018)

## Abstract

In the present study, twenty seven genotypes of wheat genotypes were evaluated for assessing genetic divergence for 14 different characters. The genetic diversity analysis revealed the formation of five clusters suggested the presence of wide genetic diversity among the 27 genotypes studied. The clustering pattern indicated that geographic diversity was not associated with genetic diversity. The maximum inter-cluster distance (D) was observed between clusters II and IV (D=43.62) followed by clusters IV and V (D=35.49) and II and III (D=34.68). The minimum inter-cluster distance (D=23.10) was found between clusters III and IV. Grains per spike, plant height, biological yield per plant, harvest index, days to heading and test weight contributed maximum towards total genetic divergence. Based on the maximum genetic distance, it is advisable to attempt crossing of the genotypes from cluster II with the genotypes of cluster IV, which may lead to the generation of broad spectrum of favorable genetic variability for yield improvement in bread wheat. Noteworthy is that cluster IV and V reflected high cluster means for days to heading, days to 50 % flowering, days to maturity, grains per spike, grain yield per plant, biological yield per plant, grain filling period, tiller per plant and plant height these clusters can be successfully utilized in hybridization programmes to get desirable transgressive segregants.

**Keywords**
Wheat**,** Genetic divergence, Inter-cluster and Intra-cluster distance

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 <1m.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. It is important that variability for economic traits must exist in the working germplasm for profitable exploitation following recombination breeding and selection. The presence of genetic diversity and genetic relationship among genotypes is a prerequisite and paramount important for successful wheat breeding programme. 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). 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. Hence, characterization of genotypes should be based on statistical procedure such as $D^2$ statistics and on hierarchical ecludean cluster analysis.

In view of these facts, twenty-seven wheat genotypes were evaluated in this study: - i) To determine the grouping pattern of genotypes in different cluster. ii) To identify genetically diverse and agronomically desirable genotypes for exploitation in a breeding programme aimed at improving grain yield potential of wheat.

The experimental material comprised of twenty five lines of wheat genotypes along with two checks *viz.*, K 9162 and Raj 4037. The test genotypes obtained from Rajasthan Agriculture Research Institute, Durgapura, exhibited wide spectrum of variation for various agronomic and morphological characters. These were selected on the basis of their diverse geographical origin, wide variation and genotype adaptability for different agro-climatic zones of India. The 27 entries (25 test genotype + 2 checks) were evaluated in Randomized Block Design with 3 replications under normal soil during *rabi* season of 2012-2013 at Field experimental centre of Department of genetics and plant breeding, SHIATS, Allahabad. Each genotype was sown in a two row plots of 2 meter length following inter-row and intra-row spacing of 23 cm and 5 cm, respectively. Thinning was done to maintain a plant to plant spacing. The recommended doses of N: P: K was applied. All the recommended agronomic practices were followed to raise a healthy crop.

Five competitive plants were randomly selected from each genotype in each replication for data collection. However, traits like days to 50% flowering and days to maturity were recorded on whole plot basis. Observations on fourteen quantitative and morphological traits *viz*., days to heading, days to 50 % flowering, tillers per plant, plant height, flag leaf length, flag leaf width, spike length, grains per spike, grain filling period, days to maturity, biological yield, harvest index, test weight and grain yield were recorded from each replication. The data were subjected to statistical analysis of genetic divergence using Mahalanobis's $D^2$ (1936) statistics as described by Rao (1952).

Genetic divergence ($D^2$) is the basis of variability and helps to craft the designed genotypes as per the requirement. The significant mean squares due to genotypes suggested the preface of ample variability. The $D^2$-values between all possible pairs, which indicated the presence of greater diversity among the genotypes for all the traits. Grouping of the genotype was carried-out by following Tocher's Method (Rao, 1952) with the assumption that the genotypes within the cluster have smaller $D^2$-values among themselves than those from groups belonging to different clusters.

Based on Mahalanobis' $D^2$ analysis, twenty-seven genotypes were grouped into five clusters with variable number of genotypes (Table 2) suggesting considerable amount of genetic diversity is present in the material. The cluster I had maximum of 15 genotypes followed by II and V having 8 and 2 genotypes, respectively. The clusters having maximum number of genotypes, reflecting narrow genetic diversity. Two clusters (III & V) possessed 1 genotype each. Only two genotypes (GW 2010-288 and K 9162) formed a separate cluster. Similarly twenty seven germplasms were dispersed in five clusters. The possible reason for grouping of genotypes of different places into one cluster could be free exchange of genotypes 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 $D^2$ value ranged from 12.92 to 21.08 while, inter-cluster $D^2$ value ranged from 23.10 to 43.61 (Table 3). The maximum intra cluster distance was exhibited by the genotype of cluster II (21.08) followed by cluster I (19.02) and cluster IV (12.92). The maximum inter-cluster $D^2$ value was observed between II and IV ($D^2$ = 43.16) followed by cluster IV and V ($D^2$ = 35.49) and cluster II and III ($D^2$ = 34.68) suggesting wide diversity between them and genotypes 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 (Zaman *et al.,* 2005, Saxena *et al.,* 2013).

The comparison of cluster means revealed considerable differences among the clusters of different quantitative characters (Table 4). Cluster V had highest cluster mean for plant height (103.87) and second highest cluster for tillers per plant (13.87) grain filling period (35.00), biological yield per plant (44.13) and test weight (15.63). Cluster III had high mean value for flag leaf length (31.20), flag leaf width (2.47), spike length (14.37), grain yield per plant (39.04) and harvest index (45.27). Cluster IV had highest values for days to heading (83.17), days to 50 % flowering (88.17), days to maturity (120.67), grains per spike (80.53).

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. Grains per spike, plant height, biological yield per plant, harvest index, days to heading and test weight were important components and these should be taken into account while breeding in wheat.

Genetic improvement mainly depends upon the amount of genetic variability present in the population. The use of Mahalanobis's $D^2$ statistics for estimating genetic divergence have been emphasized by many workers (Murthy and Arunachalam, 1966) because it permits precise comparison among all the population given in any group before effecting actual crosses. So, for improving the grain yield, selection of parents based on number of characters having quantitative divergence is required which can be assessed by $D^2$ statistic developed by Mahalanobis (1936). The clustering pattern could be utilized in selecting the parents and deciding the cross combinations which may generate the highest possible variability for various traits. The genotypes with high values of any cluster can be used in hybridization programme for further selection and improvement.

It has been well-established fact that more the genetically diverse parents used in hybridization programme, greater will be the chances of obtaining high heterotic hybrids and broad spectrum variability in segregating generations (Arunachalm, 1981). Therefore, based on the maximum genetic distance, it is advisable to attempt crossing of the genotypes from cluster II with the genotypes of cluster IV, which may lead to the generation of broad spectrum of favourable genetic variability for yield improvement in bread wheat.

## Reference

Allard, R. W. 1960. Principles of Plant Breeding. John Willey and Sons, New York.

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. 1981. Genetic distance in plant breeding. *Indian J. Genet.* **41**: 226-236.

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.

Dobariya, K. L., Ribadia, K. H., Padhar, P. R. and Ponkia, H. P. 2006. Analysis of genetic divergence in some synthetic lines of bread wheat (*Triticum aestivum* L.). *Adv. Pl. Sci.* **19**: 221-225.

Gartan, S. L. and Mittal, R. K. 2003. Genetic divergence in bread wheat. *Crop Improv.* **30**: 185-188.

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 R.S. Paroda, 1983. Genetic divergence in wheat. *Ind. J. Genetics,* **43**: 63-67.

Langade, D. M., Ram, C. N., Vishwakarma, D. N and Sharma, A.2013. Evaluation of genetic divergence in berseem (*Trifolium alexandrinium* L.) germplasms. *The Bioscan.* **8**(3): 767-770.

Mahalanobis, P.C. 1936.On the generalized distance in statistics. *Proc. Nat. Inst. Sci.* (India). **2**: 49-55.

Murthy, B. R. and Anand, I. J. 1966. Cobining ability and genetic divergence in some varieties of *Linum usitatissimum*. *Ind. J. Genetics,* **26**:21-26.

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.

Rao, C. R. 1952.Advanced Statistical Methods in Biometric Research. John Wiley and Sons, New York, pp. 357-363.

Samsuddin, A. K. M. 1985. Genetic diversity in relation to heterosis and combining ability analysis in spring wheat. *Theor. Appl. Genet.* **70**: 306-308.

Saxena, 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 50th All India Wheat and Barley Research Workers, Meet, New Delhi. p. 11.

Sharma, S. C. and Suri, V. 2005. Genetic divergence in relation to geographical origin/pedigree in wheat (*Triticum aestivum* L.). *Crop Improv*. **32**: 14-19.

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. Agri. 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.

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.

**Table 1. List of wheat genotypes.**

| S. No. | Genotype name | Pedigree | Origin |
|---|---|---|---|
| 1. | AKAW-4731 | WAWSN 12, KAUZ//STAR | Akola, Maharashtra |
| 2. | AKAW-4739 | II SSN 98.99/DF$_2$98.99 | Akola, Maharashtra |
| 3. | DL 1012 | SFW/VAISHALI//UP2425 | New Delhi |
| 4. | GW 09-211 | J96-1/K9533 | Vijapur, Gujarat |
| 5. | GW-2010-272 | TUSN(NS)NIAW835/CPAN-11931/WH147 | Vijapur Gujarat |
| 6. | GW-2010-275 | SORA/2PLATA12//GW 1102 | Vijapur Gujarat |
| 7. | GW-2010-282 | GW 1193/ SULA | Vijapur Gujarat |
| 8. | GW-2010-287 | GW 336/HW 1042//KAZU | Vijapur Gujarat |
| 9. | GW-2010-288 | WR196/CMH 83-2578 | Vijapur Gujarat |
| 10. | GW-2010-289 | GW 273/GW 353 | Vijapur Gujarat |
| 11. | GW-2010-290 | STAR//KAZU/STAR/3/GW 241 | Vijapur Gujarat |
| 12. | GW-2010-291 | W 462//NEE/KOEL/3/PEG | Vijapur Gujarat |
| 13. | HPW 355 | CMH79;1384/4/AGA/3/SN64/CN067//INIA 66/5 | Palampur, Himachal Pradesh |
| 14. | J 07- 40 | GW 273/MACS 2496 | Junagadh, Gujarat |
| 15. | KLY-1090 | HUW 468/PBW 343 | Kanpur, Uttar Pradesh |
| 16. | LBPY 2010-10 | BAE 923//SOURAY/ K 8801 | Karnal, Haryana |
| 17. | LBPY 2010-24 | NL 887//NL888//BL 2037 | Karnal, Haryana |
| 18. | NWL 9-11 | NW=2036/HD 2733 | Faizabad, UP |
| 19. | VW 921 | VL 830/BUDIFEN//VL829 | Almora, Uttaranchal |
| 20. | VW 20107 | RAJ3765/CHINA 84-4000022 | Almora, Uttaranchal |
| 21. | VW 20143 | VL 832/Druchamp/PHR 1010 | Almora, Uttaranchal |
| 22. | WSM-30 | DWR1331/GREEN 3 | Washim, Maharashtra |
| 23. | WSM-55 | EDULT 51.DWR 192 | Washim, Maharashtra |
| 24. | GW-2011-347 | CMH 84-3379/PBW 475 | Vijapur Gujarat |
| 25. | JS 6-4 | RAJ 4014 X HUW 510 | Madhya Pradesh |
| 26. | RAJ-4037 | CHECK 1 | Durgapura, Rajasthan |
| 27. | K 9162 | CHECK 2 | Kanpur, Uttar Pradesh |

**Table 2. Grouping of 27 bread wheat genotypes on the basis of $D^2$ statistic**

| Cluster | No. of Genotypes | Name of the genotypes |
|---|---|---|
| I | 15 | GW-2010-289, J 07- 40, VW 20143, WSM-30, LBPY 2010-10, LBPY 2010-24, VW 20107, GW-2010-275, GW-2010-290, GW 09-211, GW-2010-287, GW-2010-291, VW 921, WSM-55, JS 6-4 |
| II | 8 | AKAW-4731, AKAW-4739, DL 1012, GW-2010-272, GW-2010-282, NWL 9-11, GW-2011-347<br>RAJ-4037 |
| III | 1 | GW-2010-288 |
| IV | 2 | HPW 355, KLY-1090 |
| V | 1 | K 9162 |

**Table 3. Average inter and intra-cluster distance values of bread wheat genotypes**

| | I | II | III | IV | V |
|---|---|---|---|---|---|
| I | 19.020 | 25.906 | 25.940 | 29.416 | 29.321 |
| II | | 21.085 | 34.688 | 43.614 | 31.086 |
| III | | | 0.000 | 23.104 | 27.328 |
| IV | | | | 12.918 | 35.941 |
| V | | | | | 0.000 |

**Table 4. Cluster mean for 14 different characters in 27 genotypes of bread wheat**

| **Clusters** | **Day to heading** | **Days to 50% flowering** | **Plant height (cm)** | **Tillers per plant** | **Flag leaf length (cm)** | **Flag leaf width (cm)** | **Spike length (cm)** | **Days to maturity** | **Grain Filling Period** | **Grains per spike** | **Biological yield per plant (g)** | **Test weight (g)** | **Harvest index (%)** | **Grain yield per plant (g)** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | **(1)** | **(2)** | **(3)** | **(4)** | **(5)** | **(6)** | **(7)** | **(8)** | **(9)** | **(10)** | **(11)** | **(12)** | **(13)** | **(14)** |
| **I** | 80.333 | 85.733 | 96.156 | 8.467 | 26.060 | 2.018 | 12.007 | 116.222 | 30.600 | 56.769 | 24.223 | 35.759 | 32.242 | 8.030 |
| **II** | 75.500 | 81.125 | 88.579 | 7.929 | 24.909 | 1.993 | 11.475 | 113.042 | 31.542 | 44.895 | 27.880 | 36.410 | 37.479 | 10.052 |
| **III** | 80.333 | 84.333 | 98.567 | 4.667 | 31.207 | 2.477 | 14.377 | 117.667 | 33.333 | 71.800 | 27.473 | 39.040 | 45.267 | 10.467 |
| **IV** | 83.167 | 88.167 | 99.950 | 8.483 | 24.183 | 1.947 | 13.010 | 120.667 | 31.667 | 80.533 | 26.362 | 36.753 | 27.767 | 9.668 |
| **V** | 75.333 | 78.000 | 103.407 | 13.867 | 27.630 | 1.783 | 13.460 | 114.000 | 35.000 | 58.533 | 44.133 | 35.487 | 38.167 | 15.633 |
| **Percentage contribution of characters towards total divergence** | | | | | | | | | | | | | | |
| | **1** | **2** | **3** | **4** | **5** | **6** | **7** | **8** | **9** | **10** | **11** | **12** | **13** | **14** |
| **No. of times appearing first** | 11 | 2 | 77 | 0 | 2 | 0 | 0 | 6 | 4 | 161 | 45 | 11 | 32 | 0 |
| **% contribution** | 3.13 | 0.57 | 21.94 | 0.00 | 0.57 | 0.00 | 0.00 | 1.71 | 1.14 | 45.87 | 12.82 | 3.13 | 9.12 | 0.00 |