

Analysis of Genetic Divergence in Wheat (*Triticum aestivum* L.)

Tabinda Ali, Mithilesh Kumar Singh, D. N. Bharadwaj,
Lokendra Singh

Received 26 September 2016; Accepted 27 October 2016; Published online 15 November 2016

Abstract Thirty genotypes were evaluated for eight quantitative traits to work out genetic divergence in wheat. Analysis of variance indicated significant difference for all the traits indicating diversity among the genotypes. Genetic divergence analysis, using Mahalanobis's D^2 statistic, grouped all the genotypes into 7 clusters. Cluster III had maximum number (11) of genotypes. Maximum inter cluster distance was found between cluster IV and V (2317.25). However, intra cluster distance was maximum in cluster V (233.87). Genotypes from diverse clusters could be utilized in crop improvement program.

Keywords Wheat, *Triticum aestivum* L., Cluster analysis, Genetic divergence.

Introduction

Wheat (*Triticum aestivum* L.) is the most important cereal crop of the world as a source of human food

belonging to grass (*Gramineae*) family and a major commodity in the international grain market. Wheat is the second largest grown cereal in India after rice and globally, it stands second both in acreage (311.88 lakh hectare) and production (95.91 million tonnes) after China [1]. However, in terms of productivity, it is marginally less (3.08 tonnes/hectare) relative to the world productivity of 3.22 tonnes/hectare.

Continuous breeding efforts for high yield have resulted in contraction of genetic variability in natural population of crop species. To optimize and conserve the germplasm for plant breeding and other activities, studies on genetic diversity is important [2]. Genetic diversity of crop plants determines their potential for improved efficiency and hence their use in breeding, which eventually may result in enhanced food production. Genetic divergence analysis provides basis for the selection of diverse parents to yield more heterotic effect and generate wide spectrum of variability during segregation and recombination of genes at heterozygous polygenic blocks [3]. Towards this end, in the present study, Mahalanobis's D^2 statistic was used to quantify the extent of divergence among thirty wheat genotypes with respect to eight quantitative traits. This exercise would help to identify the putative parents and design appropriate crossing plan to obtain high heterotic effect and recovery of transgressive segregants [4].

Materials and Methods

Thirty wheat genotypes collected from Nawabganj farm of CSAUA and T, Kanpur (UP), were evaluated

T. Ali, D. N. Bharadwaj, L. Singh
Department of Genetics and Plant Breeding, CSUA and T,
Kanpur 208002, UP, India

M. K. Singh*
Department of Genetics and Plant Breeding, GBPUA and T,
Pantnagar 263145, UK, India
e-mail: mithileshgpb@gmail.com
*correspondence

Table 3. Cluster means for different traits of wheat genotypes.

Cluster	Days to flowering	Days to maturity	Plant height (cm)	Panicle length (cm)	Panicle/plant	Spikelets/spike	1000-seed weight (g)	Yield /plant (g)
I	51.25	93.00	60.95	8.23	3.35	14.82	35.15	5.70
II	60.50	98.83	64.32	9.48	3.50	13.42	36.60	6.79
III	54.03	95.30	60.88	9.72	3.39	17.62	38.88	6.58
IV	51.00	92.00	53.33	9.93	3.07	12.87	35.27	4.20
V	89.44	129.83	96.04	10.90	3.38	17.68	40.60	7.44
VI	58.67	99.00	79.80	10.27	3.67	15.80	38.53	7.60
VII	66.00	109.00	65.67	5.80	4.00	18.00	38.00	7.60

among genotypes for different traits were significant. The lowest cluster mean for days to flowering was observed in cluster IV (51.00), which indicated the genotypes have early flowering. Days to maturity ranged from 92 days in cluster IV to 129.83 days in cluster V. Therefore, genotypes represented in cluster IV can be used in breeding programs intended to develop short duration varieties. Plant height ranged from 53.33 cm in cluster IV to 96.04 cm in cluster V. Minimum length of panicle was observed in cluster VII (5.80) and maximum in cluster V (10.90). Number of panicles/plant ranged from 3.07 cm (cluster IV) to 4.00 cm (cluster VII). Minimum number of spikelets/spike was observed in cluster IV (12.87) and it was maximum in cluster VII (18). Maximum test weight was observed in cluster V (40.60) and minimum in cluster I (35.15). Range of variation for grain yield was from 4.20 in cluster IV to 7.60 in cluster VI and VII. It was clear from the above results that cluster V is the best cluster as it has high average cluster mean for multiple traits like grain yield/plant (7.44 g), 1000-seed weight (40.60 g), panicle length (10.90 cm), plant height (96.04 cm), days to flowering (89.44) and days to maturity (129.83). Cluster IV was the best cluster regarding traits like early flowering and early maturity. A similar trend was also followed for large collections of wheat by Garg and Gautam [9] for days to flowering and by Suri and Sharma [10] for days to maturity. So, these clusters can be utilized for selecting parents to breed for early flowering and early maturing varieties.

Sharma et al. [11] pointed out that better recombinants can be obtained by selecting genotypes with their phenotypic dissimilarity. Thus, it is quite clear that the genotypes in cluster V are exceptionally di-

vergent from the remaining genotypes of other clusters. Therefore, crossing of the genotypes from this cluster to the remaining genotypes in other clusters may be recommended for the best utilization of heterosis for different economic traits and isolation of transgressive segregants with respect to the same in wheat improvement program.

References

1. Department of agriculture and cooperation (2015) 2014-15 Annual report of Ministry of Agriculture, Government of India, Krishi Bhawan, New Delhi. Available at www.agricoop.nic.in
2. Uddin MS, Boerner A (2008) Genetic diversity in hexaploid and tetraploid wheat genotypes using microsatellite markers. *PI Tiss Cult Biotech* 18 : 65–73.
3. Khan GH, Vaishnavi R, Sanghera GS (2014) Genetic divergence studies in bread wheat (*Triticum aestivum* L.). *Bioinfolet* 11 : 481–485.
4. Bhatt GM (1973) Comparison of various method of selecting parents for hybridization in common wheat. *Australian J Agric Res* 24 : 457–464.
5. Mahalanobis PC (1956) On the generalized distances in statistics. *Proc Natl Sci Ind* 2 : 40–55.
6. Rao CR (1952) Advanced statistical methods in biometric research. John Wiley and sons. New York, pp 590.
7. Hailegiorgis D, Mesfin M, Genet T (2011) Genetic divergence analysis on some bread wheat genotypes grown in Ethiopia. *J Central Eu Agric* 12 : 344–352.
8. Ribadia KH, Ponika HP, Dohariya KL, Jivani LL (2007) Combining ability through line x tester analysis in macaroni wheat (*Triticum durum* Desi). *J Maharashtra Agric Univ* 32 : 34–38.
9. Garg DK, Gautam PL (1997) Genetic divergence studies in wheat germplasm using non hierarchical euclidean cluster analysis. *Ind J Pl Genet Resour* 58 : 271–278.
10. Suri V, Sharma SC (1999) Genetic diversity in relation to number of clusters in wheat (*Triticum aestivum* L.). *Crop Improv* 26 : 208–215.
11. Sharma PK, Gupta PK, Baliyan HS (1998) Genetic diversity in a large collection of wheat (*Triticum aestivum* L.). *Crop Improv* 26 : 208–215.