

Evaluation of Genetic Divergence Analysis in Wheat for Yield and its Component Characters

Chitralekha Shyam*, P.K. Chandrakar, N.K. Rastogi and Umakant Banjare

Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

*Corresponding author: shyamchitralekha@gmail.com (ORCID ID: 0000-0001-7311-2255)

Paper No. 748

Received: 16-07-2018

Accepted: 24-11-2018

ABSTRACT

Genetic diversity plays an important role because hybrids between lines of diverse origin generally, display a greater heterosis than those between closely related parents. Genetic diversity arises due to geographical separation or due to genetic barriers to crossability. In this study, genetic diversity of twenty two genotypes of wheat was evaluated for fourteen characters using Mahalanobis D^2 statistics. The wheat genotypes were grouped into three clusters. The cluster III was the largest group which consist of 9 genotypes followed by cluster II (7 genotypes) and cluster I (6 genotypes). From the clustering pattern, it was found that the wheat genotypes were genetically diverse to each other. Hence, the genotypes studied are reliable enough for selection of parents making crosses. The maximum intra cluster distances were observed in cluster III (2.945) followed by cluster I (2.463) and cluster II (2.324). The selection of divergent genotype from above clusters would produce a broad spectrum of variability for quantitative traits studied, which enable further for selection and improvement. The maximum inter cluster distance was observed in between cluster I and cluster III (4.987) followed by between clusters II and cluster III (4.355) and cluster I and cluster II (3.717). This suggested that the hybridization programme involving parents from these clusters is expected to give higher frequency of better segregantes or desirable combination for development of useful genetic stocks or varieties.

Highlights

- ① The maximum intra cluster distances were observed in cluster III (2.945) followed by cluster I (2.463) and cluster II (2.324).
- ② The maximum inter cluster distance was observed in between cluster I and cluster III (4.987) followed by between clusters II and cluster III (4.355) and cluster I and cluster II (3.717).

Keywords: D^2 statistics, genetic divergence, traits, wheat

Wheat has been the prime and staple food crop of many human civilizations in the world. It is the second staple food in India after rice. It is cultivated for dual purpose grain and straw in India, Pakistan, Burma and Thailand. In India also the larger area is under wheat cultivation. About 90 percent of total wheat production is contributed by five states viz., Uttar Pradesh, Punjab, Haryana, Madhya Pradesh and Rajasthan. The other wheat producing states are Bihar, Gujarat, Jammu and Kashmir, Maharashtra, West Bengal and Chhattisgarh. The area, under wheat in India during 2000 to 2014 is increased from 25.73 to 30.00 million hectare where,

production from 69.68 to 93.51 million tonnes and productivity from 27.08 to 31.71 quintals per hectares (Anonymous, 2014 b). In India, wheat is considered as king of cereals and contributing 30% of food basket of the country. 86% of the cultivated area under wheat, in India represents hexaploid spring type belonging to *Triticum aestivum* L. em. Thell., (Singh *et al.* 2008) more commonly called bread wheat. Wheat is widely grown the world-over and stands first among the cereals both in area and production. The annual growth rate for area, production and yield per hectare shows that the rate of increase in area under wheat was highest



during 2011-12 that is 1.31 percent and least during 2002-03 that is 1.30 percent. The average increase in the growth rate of area under wheat during 2000 to 2014 is 1.30 percent in India (Anonymous 2014 a). The average growth rate in the production and yield per hectare during 2000-2014 is 3.7 and 3.9 percent respectively. Uttar Pradesh ranks first in production of wheat with record of 30.30 metric tonnes among the wheat growing states of the country followed by Punjab (16.11) and Madhya Pradesh (13.13) metric tonnes (Anonymous, 2013). Botanically, wheat is a diverse family of related species. Over two dozen individual species have been characterized as members of the genus *Triticum*. Of these, only four (*Triticum monococcum* L., *Triticum turgidum* L., *Triticum timopheevii* Zhuk. and L. em thell.) are widely cultivated. Globally *Triticum aestivum* wheat is most important species which covers 90 percent of the area under cultivation. Total number of species in wheat is 16, out of which 4 species viz., *Triticum aestivum* L., *T. durum* L., *T. dicocum* L., and *T. sphaerococcum* L. are under cultivation. In India *T. sphaerococcum* L., has now practically gone out of cultivation because of its low productivity and high susceptibility to disease rust. The common bread wheat (*T. aestivum* L.) is the most important species, occupying more than 90 percent of the total wheat area in the country. The macaroni wheat (*Triticum durum* L.) is the second most important species, occupy nearly 10 percent of the total wheat area in India. Earlier, its cultivation was primarily confined to the central and southern India, with very small area in Punjab and West Bengal. It is used in the form of chapatti, bread, naan, tandoori, rumali, roti, puri, pudding, bhatore, bran and fodder etc. (Singh *et al.* 2013). Most of the agronomic characters in crop plants are quantitative in nature. Yield is one such character that results due to the actions and interactions of various component characters (Graficus 1960). In this study, genetic divergence analysis of twenty two genotypes of wheat was evaluated for fourteen characters using Mahalanobis D^2 statistics.

MATERIALS AND METHODS

Twenty two wheat genotypes including seven check varieties were used in this study. All the twenty two genotypes were grown in Randomized Block Design with three replications during *Rabi* 2013-

14 at the Instructional cum Research Farm, Indira Gandhi Krishi Vishwavidyalaya, Raipur. In each replication twenty two genotypes were grown in 10 rows, 5 m long and 20 cm apart. Chhattisgarh is located in the east - central part of the country between 17°14'N and 24°45' N latitudes and 73°30' E and 84°15' E longitudes. The crop was provided with protective irrigations and recommended doses of fertilizers. Five randomly selected plants from each treatment were chosen for recording the observations on quantitative characters, viz., Days to 50% flowering, Days to maturity, Plant height, Number of tillers per plant, Spike length, Number of spikelets per spike, Number of seeds per spikelet, Number of seeds per spike, Number of seeds per plant, 1000-seed weight, Seed yield per plant, Biological yield per plot, Seed yield per plot and Harvest Index. Genetic divergence analysis measures by two method as metroglyph and D^2 statistics method. D^2 statistics was developed by P.C. Mahalanobis in 1928. This is one of the potential techniques of measuring genetic divergence. Rao, (1952) suggested the application of this technique for the assessment of genetic divergence in plant breeding. Thus, genetic divergence was computed by D^2 statistics and varieties were grouped into a number of clusters. The varieties were grouped into a number of clusters as per the standard procedure described by Spark (1973).

RESULTS AND DISCUSSION

In plant breeding, genetic diversity plays an important role because hybrids belonging to genetically diverse parents generally, display a greater heterosis than those between closely related parents. Genetic diversity may arise due to geographical separation or due to different genetic constitution of accessions. The choice of genetically diverse parents for hybridization is an important feature of any crop improvement programme for getting desirable segregants. The multivariate analysis based on Mahalanobis D^2 or non-hierarchical Euclidean cluster analysis is used for divergence analysis. Multivariate analysis by means of Mahalanobis D^2 statistic is a powerful tool in quantifying the degree of divergence between biological populations at genotypic level to assess the relative contribution of different components to the total divergence. The D^2 analysis classifies the

Table 1: Grouping of twenty two wheat genotypes in different clusters

Cluster	No. of genotypes	Name of genotypes
I	6	HD2932 (IARI, New Delhi), HD4728 (IARI, New Delhi), MACS6604 (ARI, Pune, MH), MP3382 (JNKVV, Jabalpur, MP), HI8750 (IARI, Indore, MP), GW451 (Kusinagar, Gujrat)
II	7	HD4730 (IARI, New Delhi), HI8736 (IARI, Indore), MPO1215 (Powarkheda, MP), HI8498 (IARI, Indore), HI8737 (IARI, Indore), CG1304 (Bilaspur, IGKV), GW322 (Kusinagar Gujarat)
III	9	CG1013 (Bilaspur, IGKV), CG1014 (Bilaspur, IGKV), CG1012 (Bilaspur, IGKV), CG1301 (Bilaspur, IGKV), CG1311 (Bilaspur, IGKV), CG1314 (Bilaspur, IGKV), CG1315 (Bilaspur, IGKV), CG273 (Kusinagar, Gujarat), HI1544 (IARI, Indore)

genotypes into relatively homogeneous groups in such a way that within cluster diversity is minimized and between clusters diversity is maximized. The respective genotypes from diverse clusters can be utilized in breeding programme depending upon the breeding objectives.

Clustering pattern in genotypes

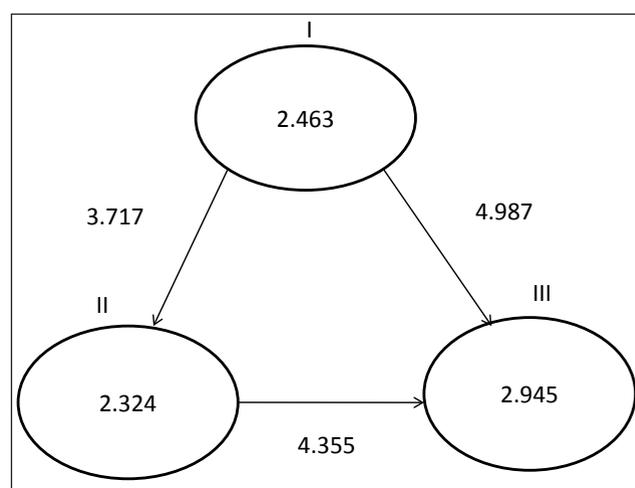
A set of 22 genotypes of wheat were subjected to D² analysis for fourteen characters. Based on D² values three clusters were formed (Table 1). This indicated that substantial diversity exists in the available genotypes of wheat. Results of cluster analysis revealed that the cluster III was the largest group consisting of 9 genotypes followed by cluster II (7 genotypes) and cluster I (6 genotypes). From the clustering pattern, it was found that the wheat genotypes were genetically diverse to each other. Hence, the genotypes studied are reliable enough for hybridization and selection. HD varieties are distributed over I and II clusters, HI varieties are distributed over I, II and III clusters, GW varieties are distributed over I and II clusters and CG varieties are also distributed over II and III clusters indicating there is little role of geographical origin in genetic diversity.

Table 2: Inter and Intra cluster distance of genotypes in wheat

Cluster	I	II	III
I	2.463		
II	3.717	2.324	
III	4.987	4.355	2.945

On the other hand, the MACS varieties, MP varieties and MPO varieties were grouped exclusively in Cluster I, I and II respectively, indicating some role of geographical origin in the composition of

clusters. So, the role of geographical origin cannot be overruled as a whole in cluster composition. Present results confirms the finding of previous workers Kumar *et al.* (2009), Ferdous *et al.* (2011), Ajmal *et al.* (2013), Kumar *et al.* (2013), Verma *et al.* (2013), Verma *et al.* (2014) and Yadav *et al.* (2014).

**Fig. 1:** Digrammatic representation of different inter and intra cluster distance in wheat

Intra and inter cluster distance

The maximum inter cluster distance was observed in between cluster I and cluster III (4.987) followed by between cluster II and cluster III (4.355) and cluster I and cluster II (3.717). This suggested that the hybridization programme involving parents from the diverse clusters is expected to produce better desirable segregants for development of useful genetic stocks or varieties. The minimum inter cluster distance was observed in between cluster I and cluster II (3.717). The maximum intra cluster distances were observed in cluster III (2.945) followed by cluster I (2.463) and cluster II (2.324). The selection of divergent genotype from above clusters would produce a broad spectrum

Table 3: Mean performance of genotypes in individual cluster for seed yield and its components in wheat

Clusters	Entries	Characters													
		Days to 50% flowering	Days to maturity	Plant height (cm)	No. of tillers per plant	Spike length (cm)	No. of spikelets per spike	No. of seeds per spikelet	No. of seeds per spike	No. of seeds per plant	1000 seed weight (g)	Seed yield per plant(g)	Biological yield per plot (g)	Seed yield per plot (g)	Harvest index (%)
I	6	52.94	97.22	71.08	4.07	8.31	15.50	2.78	44.61	215.33	43.05	8.58	7.78	6180.56	43.11
II	7	60.00	99.38	70.19	3.55	6.88	15.19	2.53	38.10	158.90	47.81	7.62	5.72	5373.09	42.69
III	9	59.96	103.67	89.61	4.65	9.09	16.59	2.61	41.48	148.26	39.70	7.20	2.96	3798.15	36.62

Table 4: Desirable genotype based on cluster performance in wheat

Characters	Cluster		
	I	II	III
Days to 50% flowering	HD4728	CG1304	CG1301
Days to maturity	HD4728	CG1304	CG1301
Plant height (cm)	MACS6604	GW322	CG1012
No. of tillers per plant	GW451	HI8736	CG1311
Spike length (cm)	HD2932	GW322	CG1012
No. of spikelets per spike	MP3382	HD4750	CG1301
No. of seeds per spikelet	HI8750	GW322	CG1013
No. of seeds per spike	MACS6604	HD4730	GW273
No. of seeds per plant	GW451	HI8737	GW273
1000 seed weight (g)	HI8750	HI8736	CG1315
Seed yield per plant (g)	MACS6604	HD4730	GW273
Biological yield per plot (g)	MACS6604	HI8750	CG1311
Seed yield per plot (g)	MACS6604	HD4730	GW273
Harvest index (%)	MACS6604	MPO1215	GW273

of variability for quantitative traits studied, which enable further for selection and improvement. The minimum intra cluster distance was observed in cluster II (2.324). Present results confirm the finding of previous worker Singh *et al.* (2014). Many researchers 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 as suggested by Moll *et al.* (1965) and Arunachalam and Bandyopadhyay (1984).

Components of cluster mean

The comparison of cluster means revealed

considerable differences among the clusters of different quantitative characters (Table 3). The cluster I had the highest mean value for number of seeds per spikelets (2.78), number of seeds per spike (44.61), number of seeds per plant (215.33), seed yield per plant (8.58), biological yield per plot (7.78), seed yield per plot (6180.56) and harvest index (43.11) similarly, genotypes included in cluster II recorded the highest mean value for days to 50 % flowering (60.00) and 1000 seed weight (47.81) whereas, the cluster III exhibited highest mean value for days to maturity (103.67), plant height (89.61), number of tillers per plant (4.65), spike length (9.09) and number of spikelets per spike (16.59). Present results confirms the finding of previous workers Kumar *et al.* (2009), Kumar *et al.* (2013), Verma *et al.* (2013), Yadav *et al.* (2014) and Singh *et al.* (2014).

Desirable genotypes based on cluster performance

The better genotypes were identified in respect of most of the characters on the basis of mean performance in the cluster (Table 4). The result revealed that the genotype CG1301 of cluster III possessed the highest mean value for days to 50% flowering (70.00) and days to maturity (114.00). The genotype CG1012 (98.53 cm) of cluster III possessed the highest mean value for plant height. The genotype GW451 (5.60) of cluster I and CG1311 (5.60) of cluster III displayed highest mean value for number of tillers per plant. The genotype CG1012 (9.57 cm) of cluster III possessed the highest mean value for spike length. The genotype CG1301 (18.53) of cluster III was characterized by highest mean value for number of spikelets per spike. The genotype HI8750 (3.00) of cluster I possessed the highest mean value for number of seeds per spikelet. The genotype GW273 (208.00) of cluster III possessed the highest mean value for number of seeds per plant. HI8736 (52.11) of cluster II showed the highest mean value for 1000-seed weight. Genotype MACS6604 of cluster I showed the highest mean value for seed yield per plant (48.00), biological yield per plot (15000.00), seed yield per plot (6750.00), seeds per spike (48.00) and harvest index (48.00). The mean value of different characters of three clusters indicated the superior expression of some characters in different clusters. Present results confirm the finding of previous workers like Verma *et al.* (2013) and Singh *et al.* (2014). 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 demonstrated 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 I and III showed maximum inter cluster distance and crossing of genotypes from cluster I with genotypes from cluster III would like to produce desirable recombinants in segregating generations with improvement in traits to enhance the yield. 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.

CONCLUSION

Maximum inter cluster distance was found between the genotypes of cluster I and III. So, if crossing is done between genotypes of cluster I with III. Then crosses between the genotypes of cluster I with III would like to exhibit high heterosis and produce recombination's with desired traits and also generate wide variability in genetic architecture.

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