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## Genetic diversity analysis in wheat (*Triticum aestivum* L.)

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**Abstract**

The present investigation was carried out during Rabi 2019-20 in a randomized block design (RBD) with 18 wheat genotypes to assess the genetic diversity for various morphological and quality traits. The data were recorded on days to 50% flowering, plant height, flag leaf length, number of productive tillers per square meter, peduncle length, spike length, spike weight, number of spikelets per spike, number of grain per spike, 1000 grain weight, days to maturity, biological yield, harvest index and grain yield. Based on D<sup>2</sup>-Statistics, 18 genotypes were grouped into five clusters. The highest inter-cluster distance was found between cluster II and V followed by II and III. This indicates that genotypes included in these clusters possess wide genetic diversity. On the basis of divergence and cluster mean it may be suggested that good recombinants could be obtained in crosses between genotypes of cluster V, II and III in varietal improvement programme. Thus, crosses between the genetically diverse genotypes of cluster II with genotype CG-1707, CG-611, CG-1907, CG-1909, CG-1043 and cluster V with genotypes like are CG-1906, CG-1926 and Cluster III CG-1931 are expected to exhibit high heterosis and are also likely to produce new recombinants with desired traits.

**Keywords:** Bread wheat, genetic diversity, cluster analysis, D<sup>2</sup>, *Triticum aestivum* L

**Introduction**

Wheat (*Triticum aestivum* L.) is the most important crop for whole world and second important crop of India. It is belong to the family poaceae and most commonly cultivated cereals. About nearly 55 percent of the world population depends on wheat for about 20 percent of calories intake (Anonymous 2016) <sup>[1]</sup>. This crop provides more nutrition to the human being in comparison to other food crops; hence, it is considered staple food for about 40% of the world's population. It is a challenging task before the breeders to enhance the present level of production as the growing population of the country will require much more food as compared to the present day requirement. It is not possible to increase the area under production. Hence, only alternative is left to increase the productivity by evolving superior varieties and better management of crop production to cope up with increasing demands of food.

A major cause of concern to a plant breeder is the constant improvement of the best available genotypes for further enhancement in their yield potential either directly or through improvement of various factors which contribute indirectly to high yield. The breeding methodology, therefore, should be such, which in essence could incorporate the favorable changes either through selection or through hybridization of superior genotypes. Genetic diversity available in the existing germplasm determines the success of any crop improvement programme (Harlan, 1976; Moose and Mumm, 2008) <sup>[5, 10]</sup>. Therefore, quantitative assessment of genetic diversity present among population usually helps a plant breeder in choosing desirable parents for breeding programme. The higher genetic distance between parents, the higher heterosis in progeny can be achieved (Joshi and Dhawan, 1966) <sup>[6]</sup>. Keeping in view, an effort has been made in the present study to evaluate a set of 18 wheat genotypes with an aim, to analyze the genetic diversity among biological population by D<sup>2</sup> statistics.

**Material and Methods**

The present investigation was conducted during *Rabi* season of 2019-2020 at the IGKV RMD CARS research and instructional farm, ambikapur, Department of genetics and plant breeding, Raj Mohini Devi College of Agriculture and Research Station, research and instructional farm, ambikapur Chhattisgarh. The farm is situated at a latitude of 20°8'N, longitude of 83°15'E and altitude of 592.62m MSL (Mean sea level). The experimental materials consist of Eighteen wheat genotypes *viz.*, CG-611, CG-1034, CG-1906, CG-1907, CG-1908, CG-1909, CG-1910,

CG-1707, CG-1926, CG-1927, CG-1928, CG-1929, CG-1930, CG-1931, GW-322(check), HI-1544(check), GW-273 (check) and CG-Genhu-3 (check) from Arid – legume center BTC CARS Bilaspur, Chhattisgarh. The genotypes were sown in Randomization Block Design with three replications. Each genotype was sown as row to row 20cm and plant to plant distance of 10cm. Crops was provided with protective irrigation and recommended doses of fertilizers. Five competitive plants of each genotypes were randomly selected from each replication during appropriate physiological growth stage and data were recorded on 14 quantitative characters namely, days to 50 percent flowering, plant height (cm), flag leaf length (cm), number of productive tillers per square meter, peduncle length (cm), spike length (cm), spike weight (g), number of spikelets per spike, number of grain per spike, 1000 grain weight (g), days to maturity, biological yield (g), harvest index (%) and grain yield (q/ha). The clustering of D<sup>2</sup> values was formed by using the Tocher's method as described by Rao (1952) [12].

## Results and Discussion

Genetic diversity in 18 genotypes was measured by following Mahalanobis (1936) D<sup>2</sup> Statistic. The D<sup>2</sup> value estimated by Mahalanobis D<sup>2</sup> statistics, between all possible pairs of 18 genotypes range between 13.00 to 80.51. The percentage contribution of various characters to genetic divergence is presented in table 1. Out of 14 characters studied, the character grain yield per plant (41.83%) had highest contribution for genetic diversity followed by harvest index (20.26%), spike length (13.07%), days to maturity(5.88%), 1000 grain weight (8.5%), biological yield (1.96%), number of grain per spike (1.96%), plant height (1.31%), flag leaf length (1.31%), number of productive tiller per squares meter (1.31%), peduncle length (1.31%) and number of spikelets per spike (1.31%). Lal *et al.*, (2009) [9] also reported that grain yield, tillers per plant, plant height, spike length contributed maximum to genetic diversity. Eighteen genotypes of wheat were grouped into five clusters based on D<sup>2</sup> statistics (Fig 1). The composition of clusters has been depicted in Table 2. The distribution pattern of genotypes showed that cluster I had maximum number of genotypes (9) followed by cluster II (5), V (2), III (1) and IV (1) genotypes. The grouping of genotypes based on multivariate analysis has also been reported earlier by Singh *et al.*, (2014) [13], Varma *et al.*, (2014) [18], Tewari *et al.*, (2015), Kumar *et al.*, (2016) [8] and Vora *et al.*, (2017) [19]. The inter cluster distance varied from 14.85 (cluster III & IV) to 80.51 (cluster II & V) (Table 3). The other notable inter cluster distance were recorded between cluster II and III (52.4), II and IV (49.22), I and V (40.37), IV and V (32.04) which indicates that the genotypes involved in these clusters have wide genetic diversity and thus can be used in hybridization programme for improving grain yield. Similar findings were also reported by Singh *et al.* (2014) [13] and Verma *et al.* (2014) [18]. The maximum intra cluster distance was observed in cluster V (21.17) followed by cluster II (20.65) and cluster I (13.00). The maximum intra cluster distance was mainly due to wide genetic diversity among the genotypes of these clusters. The maximum intra cluster distance was reported 13.96 by Verma *et al.*, (2014) [18], 391 by Kumar *et al.*, (2016) [8], and 26.40 by Vora *et al.*, (2017) [19] in wheat crop. The cluster means analyzed for 14 characters under study are presented in table 4 revealed that the cluster V exhibited highest mean value for 1000 grain weight (43.800) and harvest index (47.55). Cluster IV showed the highest mean value for flag leaf length (29.90) and

peduncle length (49.51). cluster II showed the highest mean value for days to 50 percent flowering (74.53), plant height (103.12), spike length (11.15), spike weight (2.60), spikelets per spike (16.20), number of grain per spike (38.25) and biological yield (32.68). Cluster I showed the highest mean value number of productive tillers per square meter (444.56), days to maturity (122.44), harvest index (46.60) and grain yield (46.85). The results from the present study suggest that crossing among genotypes from different clusters exhibiting good mean performance may help in achieving high yield. Incorporation of more divergent parents in hybridization can enhance the chances of attaining potential varieties and provide broad spectrum of genetic variability in segregating generation. Similar result reported by Deshmukh *et al.* (1999) [3], Singh *et al.* (2005) [16], Peshattiwar *et al.* (2009) [11], Kandel *et al.* (2018) [7] and Singh *et al.*, (2018) [14]. On the basis of divergence and cluster mean it may be suggested that maximum heterosis and good recombinants could be obtained in crosses between genotypes of cluster II, V and III in varietal improvement.

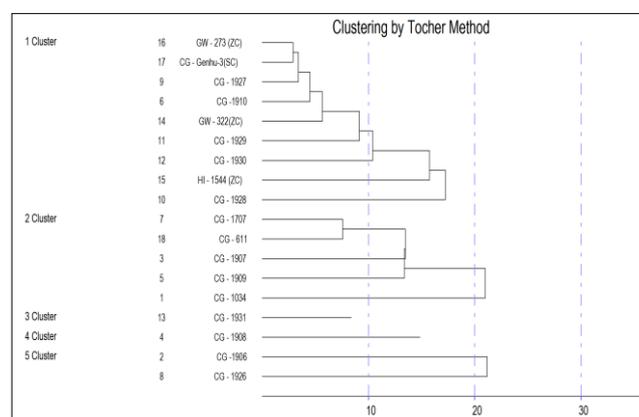


Fig 1: Dendrogram of eighteen genotypes of wheat

Table 1: Percent contribution of various characters to diversity

S. No.	Characters	Percent (%)
1	Days to 50% flowering	0
2	Plant height (cm)	1.31
3	Flag leaf length (cm)	1.31
4	Number of productive tiller per squares meter	1.31
5	Peduncle length (cm)	1.31
6	Spike length (cm)	13.07
7	Spike weight (g)	0
8	Number of spikelets per spike	1.31
9	Number of grain per spike	1.96
10	1000 grain weight (g)	8.5
11	Days to maturity	5.88
12	Biological yield	1.96
13	Harvest index	20.26
14	Grain yield (q/ha)	41.83

Table 2: Distribution of 18 genotypes into different clusters.

Cluster No.	Number of genotype	Name of genotypes
I	9	GW-273(ZC), CG-Genhu-3(SC), CG-1927, CG-1910, GW-322(ZC), CG-1929, CG-1930, HI-1544(ZC), CG-1928
II	5	CG-1707, CG-611, CG-1907, CG-1909, CG-1034
III	1	CG-1931
IV	1	CG-1908
V	2	CG-1906, CG-1926

**Table 3:** Intra and inter cluster D<sup>2</sup> value of 14 character from 18 genotypes of wheat

Cluster Distances					
	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	13.00	28.37	22.85	29.21	40.37
Cluster II		20.65	52.4	49.22	80.51
Cluster III			0	14.85	29.19
Cluster IV				0	32.04
Cluster V					21.17

**Table 4:** Clusters mean performance for characters in wheat

	Days to 50 percent flowering	Plant height	Flag leaf length	Number of productive tillers per square meter	Peduncle length	Spike length	Spike weight	Number of spikelets per spike	Number of grain per spike	1000 grain weight	Days to maturity	Biological yield	Harvest index	Grain yield
Cluster I	69.30	93.60	25.31	444.56	40.86	9.57	2.32	15.87	38.03	39.11	122.44	24.61	46.60	46.85
Cluster II	74.53	103.12	25.24	417.80	41.88	11.15	2.60	16.20	38.25	34.07	122.40	32.68	46.48	44.72
Cluster III	65.00	95.57	27.67	406.00	37.57	9.48	2.39	14.27	37.87	36.93	116.67	24.08	41.91	40.41
Cluster IV	64.67	94.21	29.90	284.33	49.51	10.35	2.15	13.07	30.87	42.93	118.00	19.90	45.85	39.07
Cluster V	60.50	92.62	21.61	433.83	39.77	9.87	2.38	14.17	36.43	43.80	119.67	21.90	47.55	41.42

## Conclusion

The genetic diversity was observed in grain yield, harvest index, spike length, days to maturity, 1000 grain weight (g), number of grain per spike, biological yield, plant height, flag leaf length, number of productive tillers per square meter, peduncle length, number of spikelets per spike, spike weight, days to 50 percent flowering. The genotypes grouped into II and V cluster were good because of their desirable yield attributing traits. Thus, crosses between the genetically diverse genotypes of cluster II with genotypes CG-1707, CG-611, CG-1907, CG-1909, CG-1034 and cluster V with genotypes like CG-1906 and cg-1926 and cluster III with genotypes CG-1931 are expected to exhibit high heterosis and are also likely to produce new recombinants with desired traits.

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