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Genetic diversity analysis in bread wheat (*Triticum aestivum* L.) for grain yield and its attributing traits

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Abstract
The present investigation was carried out during *Rabi* 2020-21 in a randomized block design (RBD) with 23 wheat genotypes to assess the genetic diversity for various morphological and quality traits. The experiment is performed at Indira Gandhi Krishi Vishwavidyalaya, Raj Mohini Devi College of Agriculture & Research Station, Research cum Instructional Farm, Ambikapur (Chhattisgarh). The statistical analysis for genetic divergence was done using Mahalanobis-D^2 statistics and clustering of genotypes was done using Tocher method, 23 genotypes grouped into five clusters. Clustering of genotypes revealed that cluster-II has maximum number of genotypes (13) and clusters IV and V each has two genotypes only. The highest intra-cluster distance was exhibited by cluster-IV (60.64) revealing maximum genetic divergence among its constituents. The highest inter-cluster distance was found between clusters I and V (656.39) and the lowest was between cluster-II and III (410.95). Cluster-I exhibited highest cluster means for most of the agronomic traits like days to 50 percent flowering, days to maturity, flag leaf length, number of productive tillers per square meter, number of spikelets per spike, biological yield per plot and grain yield per plot while clusters-IV revealed highest cluster means for plant height, spike length, spike weight, number of grains per spike and test weight. The genotypes bearing the desired values from different clusters can be exploited in future breeding programme for the improving the wheat genotypes for yield and physiological traits.

Keywords: Bread wheat, genetic diversity, cluster analysis, D^2, *Triticum aestivum* L.

Introduction
After rice, wheat (*Triticum aestivum* L., 2n=42) is the world's second most important staple food crop dominate all other cereal crops in area and production and providing around 20% of total food calories to the world's population. It is a self-pollinated crop that belongs to the Poaceae family and is one of the most widely grown cereals in many countries, including India. Wheat is known as the "king of cereals" due to its large acreage, high production, and well-known positions in the global food grain market. Hexaploid wheat resulting from the combination of three genomes A, B, and D, accounts for over 95% of all wheat farmed today, and it is used to make bread and other baked goods (Debasis and Khurana, 2001) [1]. The majority of cultivated wheat types are members of one of three *Triticum* species. Hexaploid (2n=6x=42) *T. aestivum* (90% area), the tetraploid (2n=4x=28) *T. durum* (9% area) and the diploid (2n=2x=14) *T. dicoccum* (less than 1%) are the three types of wheat.

In India, wheat covers an area of 31.36 million ha, with total production of 107.80 million tonnes per ha and productivity 3084 kg per ha (USDA 2020/21). Wheat is a major *Rabi* crop in Chattisgarh, and it is primarily farmed under irrigated conditions. Wheat is grown on 138.30 ('000 ha) in Chhattisgarh, with a production of 214.36 ('000 tonnes) and a productivity of 1550 kg/ha (anonymous, 2017-18). Uttar Pradesh, Punjab, Haryana, Madhya Pradesh, Rajasthan, Bihar, Maharashtra, Gujarat, Karnataka, West Bengal, Uttarakhand, and Jammu & Kashmir are the key wheat-producing states. These states account for around 99.5 percent of total wheat output in the country, whereas the remaining states, notably Jharkhand, Assam, Chhattisgarh, Delhi, and other North Eastern states, account for only about 0.5 percent.

Any successful breeding programme requires genetic diversity and relationships between genotypes. Plant genetic diversity impacts their ability to improve efficiency and, as a result, their usage for breeding, which could lead to increased food supply. For pure-line cultivar development, genetic diversity levels among acclimated, elite germplasm can provide predicted estimates of genetic variation among segregating progeny. Geographic diversity, release place, ploidy level, and other factors do not always influence genotype genetic diversity.

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As a result, statistical approaches should be used to define genotypes. D^2 statistics and hierarchical ecludean cluster analysis are two statistical methods that have been developed to analyse genetic diversity. These methods calculate genetic divergence by calculating similarity or dissimilarity based on the aggregate influence of many economically significant traits.

Material and Methods

The experiment is performed during the year *Rabi season* 2020-21 at Indira Gandhi Krishi Vishwavidyalaya, Raj Mohini Devi College of Agriculture and Research Station, Research & Instructional Farm, Ambikapur (Chhattisgarh), which is situated at a latitude of 20^0 8'N, longitude of $83^0 15$'E, and an elevation of 592.62m MSL (Mean sea level). The experimental material included of 23 diverse genotypes of wheat *viz.,* CG-1039, CG-2011, CG-2012, CG-2013, CG-2014, CG-2015, CG-1711, CG-1815, W 16.68, WA 18-93, 21/280, 17th HTWYT 18-05, 18th HTWYT 19-46, OS 301, CG 1029 (Ch), HD 2932 (Ch), MP 4010 (Ch), HD 2864 (Ch), MP 3336 (Ch), CG-1935, HI 1634 (Ch), HD, 3407[M] and CG-1937 received from BTC CARS Bilaspur, Chhattisgarh and AVT, ICAR-IIWBR Karnal Haryana India. 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, days to maturity, 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, test weight (g), biological yield per plot (g), harvest index (%) and grain yield per plot. The clustering of D^2 values was formed by using the Tocher's method as described by Rao (1952) [7].

Results and Discussion

The existence of genetic divergence among the 23 genotypes of wheat was examined by employing Mahalanobis D^2-statistics. The clustering pattern of 23 genotypes on the basis of the D^2-statistics analysis has been presented in Table 4.7. The genotypes were a grouped into five distinct clusters. The grouping of genotypes based on multivariate analysis has also been reported earlier by Singh *et al.,* (2014) [11], Verma *et al.,* (2014) [11], Tewari *et al.,* (2015) [10], Kumar *et al.,* (2016) [4] and Vora *et al.,* (2017) [12]. The highest number of genotypes appeared in cluster III which possessed 12 genotypes namely, CG-2012, CG-1711, W 16.68, WA 18-93, 21/280, 18th HTWYT 19-46, OS 301, CG-1029, HD 2932, MP 3336, CG-1935, HI 1634. The second highest number of genotypes was found in cluster II which was comprised of 4 genotypes namely, CG-1039, CG-2011, 17th HTWYT 18-05 and CG-1937. Cluster I comprised of 3 genotypes *viz*; MP 4010, HD 2864 and HD 3407[M]. The lowest genotypes were found in cluster IV (CG-2013, CG-1815) and V (CG-2014, CG-2015). They all possessed only two genotypes. The estimate of intra

and inter cluster distance represent by D2 values have been given in Table no. 2. The maximum intra-cluster distance was obtained for cluster IV (60.64) followed by cluster V (60.27), cluster I (60.03) and cluster II (48.27). The minimum intra-cluster D^2 values were shown by cluster III (19).

The highest inter cluster D^2 values were observed between cluster I and V (656.39) followed by cluster II and V (508.22), cluster I and IV (474.93), cluster III and V (389.13) and cluster I and III (272.77). The lowest inter-cluster D2 value was found between cluster II and III (166.62) followed by cluster III and IV (211.78). Similar findings were also reported by Singh *et al.* (2014) [11] and Verma *et al.* (2014) [11]. Cluster V (75.34) showed the highest cluster mean for days to 50% flowering followed by cluster IV (71.33) and cluster III (68.17). The lowest cluster mean was showed by cluster I (64.55). Cluster V (111.17) showed the highest cluster mean for days to maturity followed by cluster I (109.55) and cluster III (109.39). The lowest cluster mean was showed by cluster II (107.33). Cluster IV (91.40) showed the highest cluster mean for plant height followed by cluster V (89.50) and cluster III (87.53). The lowest cluster mean was showed by cluster I (78.07). Cluster V (21.60) showed the highest cluster mean for flag leaf length followed by cluster IV (19.60) and cluster II (18.14). The lowest cluster mean was showed by cluster III (17.35). Cluster IV (271.67) showed the highest cluster mean for number of productive tillers per square meter followed by cluster V (353.83) and cluster II (336.25). The lowest cluster mean was showed by cluster I (293.00). Cluster II (34.80) showed the highest cluster mean for peduncle length followed by cluster III (34.99) and cluster I (33.58). The lowest cluster mean was showed by cluster IV (33.44). Cluster IV (9.47) showed the highest cluster mean for spike length followed by cluster III (9.23) and cluster V (9.10). The lowest cluster mean was showed by cluster I (8.29). Cluster IV (2.80) showed the highest cluster mean for spike weight followed by cluster V (2.79) and cluster II (2.76). The lowest cluster mean was showed by cluster I (2.08). Cluster IV (17.24) showed the highest cluster mean for number of spikelets per spike followed by cluster V (15.87) and cluster II (15.83). The lowest cluster mean was showed by cluster I (12.76). Cluster IV (40.24) showed the highest cluster mean for number of grains per spike followed by cluster V (36.83) and cluster II (35.50). The lowest cluster mean was showed by cluster I (29.31). Cluster IV (44.58) showed the highest cluster mean for test weight followed by cluster III (43.46) and cluster V (42.60). The lowest cluster mean was showed by cluster I (37.89). Cluster V (3233.34) showed the highest cluster mean for biological yield per plot followed by cluster IV (2983.33) and cluster III (2873.06). The lowest cluster mean was showed by cluster I (2654.44). Cluster II (50.35) showed the highest cluster mean for harvest index followed by cluster IV (49.20) and cluster III (44.98). The lowest cluster mean was showed by cluster I (42.60). Cluster IV (1463.34) showed the highest cluster mean for grain yield per plot followed by cluster V (1433.33) and cluster II (1372.84). The lowest cluster mean was showed by cluster III (1291.42). These results are in accordance with the findings of Gashaw *et al.* (2007) [2] and Singh *et al*, (2018) [9].

Table 1: Genotypes included in different clusters based on D^2 analysis in wheat genotype

Clusters No.	No. of genotypes	Name of the genotypes
I	3	MP 4010, HD 2864, HD 3407^M
II	4	CG-1039, CG-2011, 17th HTWYT 18-05, CG-1937
III	12	CG-2012, CG-1711, W 16.68, WA 18-93, 21/280, 18th HTWYT 19-46, OS 301, CG 1029, HD 2932, MP 3336, CG-1935, HI 1634
IV	2	CG-2013, CG-1815
V	2	CG-2014, CG-2015

Table 2: Average intra and inter cluster distance

Clusters	I	II	III	IV	V
I	60.03				
II	257.651	48.27			
III	272.763	166.616	19		
IV	474.926	272.231	211.779	60.64	
V	656.386	508.217	389.13	252.582	60.27

Table 3: Cluster means for yield and its components in 23 wheat genotypes

Cluster No.	No. of genotypes	DF	DM	PH	FLL	NPTPS	PL	SL	SW	NSPS	NGPS	TW	BYPP	HI	GYPP
I	3	64.55	109.55	78.07	18.02	293.00	33.58	8.29	2.08	12.76	29.31	37.89	2654.44	42.60	1130.56
II	4	67.67	107.33	87.30	18.14	336.25	35.19	8.98	2.76	15.83	35.50	42.33	2729.17	50.35	1372.84
III	12	68.17	109.39	87.53	17.35	316.44	34.99	9.23	2.47	15.09	35.22	43.46	2873.06	44.98	1291.42
IV	2	71.33	107.67	91.40	19.60	371.67	33.44	9.47	2.80	17.24	40.24	44.58	2983.33	49.20	1463.34
V	2	75.34	111.17	89.50	21.60	353.83	33.50	9.10	2.79	15.87	36.83	42.60	3233.34	44.39	1433.33

DF = Days to 50% flowering	PL = Peduncle length	TW = Test weight
DM = Days to maturity	SL = Spike length (cm)	BYPP= Biological yield per plot (g)
PH = Plant height (cm)	SW= Spike weight (g)	HI = Harvest index
FLL = Flag leaf length (cm)	NSPS = No. of Spikelets per spike	GYPP = Grain yield per plot (g)
NPTPS = No. of productive tillers/ m^2	NGPS= No. of grains per spike	

Conclusion

The genetic diversity was observed in grain yield, harvest index, spike length, days to maturity, test 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 IV and V cluster were good because of their desirable yield attributing traits. Thus, crosses between the genetically diverse genotypes of cluster V with genotypes CG-2014, CG-2015 and cluster I with genotypes like MP 4010, HD 2864, HD 3407M and cluster III with genotypes CG-2012, CG-1711, W 16.68, WA 18-93, 21/280, 18th HTWYT 19-46, OS 301, CG 1029are expected to exhibit high heterosis and are also likely to produce new recombinants with desired traits.

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