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Genetic Diversity Analysis in Bread Wheat (*Triticum aestivum* L.)

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ABSTRACT: Genetic divergence study on Bread wheat *Triticum aestivum* L. consisted 50 genotypes of various sources. The experiment was conducted at Zonal Agriculture Research Station, Powarkheda, Narmadapuram, Madhya Pradesh during Rabi season of 2019-20 & 2020-21 in Randomized Block design replicated twice. Standard package and practices were given to raise healthy crop. Results of analysis revealed their association into eight clusters. Approximate configurations of the clusters based on the D^2 values. According to Mahalanobis' D^2 statistic it can be concluded that days to maturity, biological yield, test weight and grain yield/plot contributed the most towards genetic diversity. The clustering pattern indicated no parallelism between the geographical distribution and genetic diversity. Genotypes selected from the two major divergent groups *i.e.* MP-120, MP-0422, MP-1116, MP-1370, NIAW-231 (from group-I) and C-591, CPAN-1532, C-306, PKD-1018, PKD-1112, SONALIKA, PKD-1203 (from group –II), may be used as parents for hybridization after determining their combining abilities, so as to obtained considerably batter and promising segregates and recombinants.

Keywords: *Triticum aestivum*, genetic divergence, multivariate analysis, D^2-statistic.

INTRODUCTION

Wheat is one of the major staple food crops, which provides 20% of the total food calories of human requirement (Bhawsar, 1993). Both in terms of area and production, India is the second largest wheat growing country in the world. A self-pollinating crop, wheat, has been bred for a wide range of specific end-use qualities, as well as an array of adaptive qualities, which result in distinct cultivars tailored to specific production environments. In order to improve a crop species, it is essential to know its genetic diversity. For the development of pureline cultivars, genetic diversity levels among elite germplasm can provide predictive estimates of genetic variation among segregating progeny. According to Franco *et al.* (2001) to conserve, evaluate and utilize genetic resources, it is important to study phenotypic and genotypic diversity to identify groups that have similar genotypes; to study the diversity of pre-breeding and breeding germplasm; and to protect breeders' intellectual property rights by determining the uniqueness and distinctness of genotype phenotypic and genetic constitutions. In India, during season 2021-2022, Rabi season, wheat has been cultivated in 30.54 million hectares and the production of wheat is estimated at a record 106.84 million tons with national average productivity of 3484 kg/ha (Anonymous, 2022).

To identify genetically diverse genotypes for plant breeding programs, genetic divergence analysis plays an essential role in assessing the nature of diversity.

A multivariate analysis using Mahalanobis D^2 statistics is found to be useful for identifying the degree of divergence at genotypic level between biological populations, as well as determining the relative contributions of different components to the total divergence at both the inter and intra cluster levels. In the developing world, wheat is becoming increasingly important as it is the most widely grown cereal in the world, the staple food for 35% of the population. Due to climate change, maintaining grain quality of wheat has become crucial to human nutrition, end-use properties, and commodity value. Physical properties of wheat whole grain, such as size and shape, affect milling yield and screening losses, which determine the efficiency of processing (Elangbam *et al.,* 2022).

It has evolved over the centuries to adapt to a greater range of environmental niches. Wheat exhibits a wide range of adaptability. Conscious or unconscious selection pressures have resulted in specific genotypes adapted to different local environments over time. The cultivation of wheat in Central India is unique, with the species cultivated there being *Triticum aestivum*, which is grown in a hot tropical climate characteristic of high temperatures at the time of maturity. Many crop improvement programs also aimed at improving other characteristics along with yield, which are interconnected with yield (Soni *et al.,* 2023).

MATERIAL AND METHODS

The present investigation was carried out in the experimental fields of the Zonal Agriculture Research Station, Powarkheda, Narmadapuram, Madhya Pradesh during Rabi season of 2019-20 & 2020-21 with 50 wheat accessions of indigenous and exotic origin (*Triticum aestivum* L. em. Thell) representing a countrywide collection from several parts of India. The farm is situated at a latitude of 21°50' N′ longitude of 76°43′ E and altitude of 229 m MSL (Mean Sea level). The experiment was laid in completely randomized block design replicated twice. Each genotype was accommodated in a double row plot of 2-meter length with row to row and plant to plant spacing of 23 and 5 cm, respectively. The sowing was done on 24th December 2019, 26th November 2020 and 24th December 2020 by dibbling the seeds in rows. The experiment was conducted under irrigated and high fertility conditions. The experimental materials consist of fifteen wheat genotypes grown in several parts of India. The observations were recorded on five randomly selected plants of each genotype under each replication and per plant data were obtained by averaging the values.

(A) Pre-harvest observations: days to heading, days to maturity, flag leaf length, flag leaf width, flag leaf area, canopy temperature at vegetative stage, canopy temperature at flowering stage and chlorophyll content (SPAD).

(B) Post-harvest observations: awns length (cm), spike length (cm), peduncle length, biological yield, grain yield/plot (g), harvest index, number of spikelets/spike, number of grains/spike, test weight (cm), tillers/plant, paniculated leaf distance (cm) and plant height (cm).

RESULTS AND DISCUSSION

The present study was undertaken to evaluate the performance of bread wheat genotypes for various yield and its attributes.

Multivariate analysis of divergence. The quantitative assessment of genetic divergence was carried out for all the 20 characters, using Mahalanobis' D^2 statistic. To estimate the D values, correlated means of characters were transformed to standard uncorrelated characters, using pivotal condensation method. The statistical distance between pairs of treatments was obtained as the sum of squares of the differences between the pair of corresponding uncorrelated values of any two treatments considered at a time.

Grouping of lines into various clusters. All the genotypes were grouped into clusters to study the genetic variability existing among the lines. Tocher's procedure (Singh and Chaudhary, 1977) was adopted for grouping. The distribution of line into clusters and their mean values have been presented in Table 1 and 3, respectively.

Intra and Inter cluster divergence D^2 Values. The average D^2 values within (intra) and between (inter) clusters were calculated as per the procedure given by Singh and Chaudhary (1977) and have been presented in Table 2. The average intra-cluster divergence (diagonal D^2 values in the table) varied from 120.7 to 190.0. The maximum intra-cluster divergence was found within the cluster II (190.0) followed by cluster VIII (186.0), cluster I (178.9), cluster IV (173.5), cluster VII (155.5), cluster VI (122.4) and cluster VI (120.7) and the minimum were found within the cluster VI 120.7. These genotypes considerable intra cluster distances which indicate that within the cluster, genetic diversity is present in a little extent. Cluster I contained the maximum number of genotypes (10) followed by cluster VII (9 genotypes), VI (7 genotypes), V (6 genotypes) while clusters IV and VIII contained 5 genotypes and clusters II and III contained 4 genotypes each. Highest inter cluster distance (100832.5) was found between cluster VII and cluster VIII followed by cluster VI and VIII (95734.6) and cluster V and VIII (93689.4). Conversely, lowest inter cluster distance (268.6) was observed between cluster IV and VI. The cluster mean values for various characters ranged from 67.67 to 72.08 for days to heading, 82.57 to 104.63 days for days to maturity, 6.85 to 7.84 cm for awn length, 9.24 to 10.96 cm for spike length,16.55 to 17.76 cm for peduncle length, 21.9 to 24.27 cm for flag leaf length, 1.5 to 2.0 cm for flag leaf width, 23.3 to 29.0 for flag leaf area, 18.5 to 20.1^o for canopy temperature at vegetative stage, 27.7 to 28.3^o for canopy temperature at flowering stage, 25.5 to 31.2^o for chlorophyll content, 712.9 to 960.8 gm for biological yield, 34.1 to 38.3 harvest index, 15.3 to 16.7 for number of spikelets/spike, 38.4 to 41.9 for grains/spike, 36.9 to 41.2 gm for test weight, 3.5 to 4.7 for number of tillers/plant, 22.4 to 25.5 cm for peniculated leaf distance, 94.8 to 106.1 cm for plant height and 257.8 to 368.4 gm for grain yield/plot.

The present investigation on genetic divergence was carried out using Mahalanobis' D^2 statistics. The study revealed a wide diversity among the genotypes studied. As the genotypes were grouped into VIII clusters. Cluster I contained the maximum number of genotypes (10) followed by cluster VII (9 genotypes), VI (7 genotypes), V (6 genotypes) while clusters IV and VIII contained 5 genotypes and clusters II and III contained 4 genotypes each.

The inter-cluster D^2 value was maximum (100832.5) between cluster VII and cluster VIII and thus genotypes included in these clusters were genetically most divergent. Cluster means for various characters in present study indicated that days to maturity, biological yield, test weight and grain yield/plot contributed the most towards divergence among genotypes.

Earliest maturity and canopy temperature at vegetative stage genotypes were observed in cluster IV, whereas, genotypes having higher awns length and test weight in cluster III. In cluster IV, genotypes with high biological yield, harvest index and grain yield/plot were grouped and in cluster X, genotypes grouped with high flag leaf width, flag leaf area and tillers/plant. The present investigation was an attempt to determine various parameters of genetic divergence among 50 genotypes of bread wheat. The method used to assess genetic divergence was Mahalanobis' D^2 statistic.

Table 1: Components of clusters of bread wheat genotypes grown at ZARS Powarkheda under pooled over the environment.

No. of Clusters	No of Genotypes	Name of Genotypes
I	10	CPAN-6220, HI-2240, JW-322, MP-1070, MP-9676, MP-3288, RBW-594, PKD-153, PKD-1024, PKD-1201
II	4	HY-2026, IBWSN-156, HI-1500, SAWYT-328(B)
III	4	HI-1544, HD-2004, HD-2756, PBW-9022
IV	5	MP-120, MP-0422, MP-1116, MP-1370, NIAW-231
V	6	GW-322 , H-62, H-965, GW-253, MPO-1215, PNB-1018
VI	7	C-591, CPAN-1532, C-306, PKD-1018, PKD-1112, SONALIKA, PKD-1203
VII	9	H-951, DBW-504, EIGN-I-41, HPW-157, HD-2864, J-260, PKD-1226, IDSN-7059, IDSN-7211
VIII	5	NGSN-35, UP-2462, HI-1531, VL-908, UP-2572

Table 2: Average intra and inters cluster D^2 value between the clusters grown at ZARS powarkheda under pooled over the environment.

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster	7 Cluster	8 Cluster
1 Cluster	178.9	285.6	355.6	404.7	727.4	727.3	866.5	84907.9
2 Cluster		190.0	364.7	308.0	547.6	446.7	698.7	87425.8
3 Cluster			122.4	489.7	466.4	709.3	1022.8	84574.7
4 Cluster				173.5	423.7	268.6	311.1	93328.7
5 Cluster					0.0	515.4	648.1	93689.4
6 Cluster						120.7	365.2	95734.6
7 Cluster							155.5	100832.5
8 Cluster								186.0

Table 3: Mean values of the clusters for bread wheat genotypes under different pooled over the environment.

	Days to heading (X1)	Days to maturity (X2)	Awns length (cm) (X3)	Spike length (X4)	Peduncle length (cm) (X5)	Flag leaf length (X6)	Flag leaf width (X7)	Flag leaf area (X8)	Canopy temperature at vegetative stage (X9)	Canopy temperature at flowering stage (X10)
Cluster I	69.73	102.40	7.41	9.68	17.55	22.43	1.70	24.92	19.08	**27.79**
Cluster II	69.25	95.00	**6.85**	9.80	17.64	23.50	**1.55**	**23.31**	18.91	28.68
Cluster III	**72.08**	**104.63**	**7.84**	10.55	17.00	**21.90**	1.72	24.69	19.27	28.73
Cluster IV	70.97	**92.57**	7.13	**9.24**	17.69	22.68	1.69	24.53	**18.58**	28.34
Cluster V	**67.67**	99.22	7.61	10.80	**17.76**	22.59	**2.00**	**29.04**	19.42	28.96
Cluster VI	68.50	101.48	7.08	9.77	**16.55**	**24.27**	1.58	25.03	**20.16**	28.26
Cluster VII	67.83	99.50	6.92	9.32	16.96	24.24	1.66	25.97	19.88	**29.25**
Cluster VIII	67.90	101.23	7.01	**10.96**	17.32	22.35	1.97	28.28	19.97	29.03

	Chlorophyll content (SPAD) (X11)	Biological yield (X12)	Harvest index (X13)	Number of spikelets/spike (X14)	Number of grains/spike (X15)	Test weight (X16)	Tillers (X17)	Peniculated leaf distance (X18)	Plant height (X19)	Grain yield/plot (g) (X20)
Cluster I	29.34	904.13	36.20	16.40	**41.92**	40.58	4.05	25.14	**106.13**	326.58
Cluster II	30.39	776.04	35.82	15.38	40.21	37.21	4.50	24.60	100.73	279.63
Cluster III	**25.51**	913.13	37.45	16.38	39.38	**41.21**	4.71	25.38	100.63	340.88
Cluster IV	26.99	**960.83**	**38.36**	**15.37**	**38.43**	39.60	4.40	24.03	99.16	**368.40**
Cluster V	27.42	830.94	**34.16**	16.06	41.75	38.86	**4.81**	25.36	101.08	284.03
Cluster VI	30.73	**712.93**	36.20	**16.74**	41.69	38.02	4.62	**25.55**	101.19	**257.86**
Cluster VII	**31.35**	805.74	35.40	16.00	41.26	**36.96**	4.39	23.91	**94.84**	286.09
Cluster VIII	29.70	746.17	35.56	16.53	38.60	38.23	**3.50**	**22.40**	96.74	266.23

These 50 genotypes were chosen from a large stock of wheat genotypes available at the Zonal Agriculture Research Station, Powarkheda, Narmadapuram. The results so obtained in the present investigation have been discussed hereunder:

Divergence of cultivars and derivatives. The importance of genetic diversity within the overall limits of fitness for realizing heterotic response in the F_1 and broad spectrum of variability in segregating generation has been emphasized by Joshi and Dhawan (1996) Murty and Arunachalam (1966) and Bhatt (1970). Generalized distance analysis have been used by many geneticists among cultivars, within a crop under the assumption that cultivar within the group are genetically related where as diverse cultivars are classified in to different clusters. In the present study, dispersion amongst variable for aggregate effect of the 20 characters as tested by Wilk's criterion was however, highly significant indicating the existence of considerable divergence in the material under study. The clustering pattern of genotypes also confirmed the same since all the 50 wheat genotypes were classified into as many as eight clusters on the basis of Mahalanobis D^2 statistic.

At intra cluster level, cluster VIII was highly diverse and comprised 12 entries, of mostly bread wheat varieties. The maximum number of genotypes were included in cluster VIII (23 genotypes) followed by cluster II (16 genotypes) and cluster X (15 genotypes). The diversity in the material was further revealed by existence of appreciable genetic diversity among the genotypes as the statistical D^2 value represents the index of genetic diversity among the clusters. It would be appropriate to make crosses between genotypes belonging to the cluster separated by high estimates of statistical differences. In view of this, the most divergent clusters i.e., cluster VII and cluster VIII followed by cluster VI and VIII (95734.6) have been chosen along with other clusters nearer to these two highly diverse clusters, to group them in two broad categories as below:

Group	Highly diverse cluster	Nearer cluster	Total number of genotypes
Group I	VIII	VI	12
Group II	VII	VIII	14

On the basis of yield performance and some specialized traits, ten genotypes from group IV and five genotypes from group VI have been selected as being the most diverse and high yielding genotypes. The probability of getting better segregants and promising recombinants will be more if crosses are attempted between genotypes belonging to these two groups. These results are in agreement with the findings of Ali *et al.* (2008); Hailegiorgis *et al.* (2011); Desheva and Kyosev (2015).

The compositions of genotypes with good yield of these two groups have been given hereunder:

GROUP-I MP-120, MP-0422, MP-1116, MP-1370, NIAW-231

GROUP-II C-591, CPAN-1532, C-306, PKD-1018, PKD-1112, SONALIKA, PKD-1203

Genetic differences between the clusters were reflected in cluster means also. Days to maturity, biological yield, test weight and grain yield/plot contributed the most towards divergence among genotypes.

Earliest maturity and canopy temperature at vegetative stage genotypes were observed in cluster IV, whereas, genotypes having higher awns length and test weight in cluster III. In cluster IV, genotypes with high biological yield, harvest index and grain yield/plot were grouped and in cluster X, genotypes grouped with high flag leaf width, flag leaf area and tillers/plant. These results were in accordance with the findings of Ahmed *et al*. (1980); Yadav and Murty (1981); Raut *et al.* (1985); Kuruwadi (1988); Sethi *et al.* (1992); Singh (1992); Bhawsar (1993); Mehta and Dhagat (1992); Shoran and Tondan (1995); Jain *et al.* (1979); Mel'nikova *et al.* (2009); Milotova *et al*. (2008); Laidò *et al.* (2013); Terzi *et al*. (2007).

The contributions of the traits such as test weight, biological yield to total genetic divergence may be due to the great influence of selection towards uniformity for early maturity, size and texture of the grain. These findings are in agreement with Somayajulu *et al.* (1970). Thus, these traits offered scope as the selection traits for identifying genetically diverse parents for hybridization programs for breeding high yielding varieties of wheat suited to different conditions based multiple cropping systems.

CONCLUSIONS

The diversity in the material was further disclosed by the existence of appreciable genetic diversity among the genotypes as the statistical D^2 value represents the index of genetic diversity among the clusters. It would be appropriate to make crosses between genotypes belonging to the cluster separated by high estimates of statistical differences. This D^2 statistical analysis to access genetic diversity has been shown to be very useful in selecting parents for hybridization that will meet the objectives of a plant breeder.

FUTURE SCOPE

Following screening for their response to various diseases, genotypes showing a high degree of divergence could be used in different breeding programs aimed at improving wheat crops.

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