ESTIMATION OF GENETIC VARIABILITY AND DIVERSITY IN BREAD WHEAT (*Triticum aestivum* L.) FOR YIELD AND YIELD CONTRIBUTING TRAITS

Abstract

An experiment was carried out to study genetic variability and genetic divergence for 8 traits in 52 diverse genotypes of bread wheat under normal sown condition. The analysis of variance revealed highly significant differences among the mean square due to genotypes for all the characters studied. High genotypic and phenotypic coefficient of variation was observed for traits like grain yield per plot and tillers per meter. High heritability coupled with high genetic advance as per cent of mean was observed for grain yield per plot and tillers per meter and plant height. Genetic divergence was assessed by Mahalanobis D^2 statistic, which grouped 52 genotypes into seven clusters. Maximum genetic divergence was observed between cluster V and VI followed by that between VI and VII (D=34.61). Cluster IV had desirable rating for spike length, spikelets per spike, thousand grain weight and yield per plot. Cluster VII had desirable rating for tillers per meter and had highest contribution towards total genetic divergence.

Keywords: Genetic variability, genetic divergence, heritability, genetic advance and D^2 *statistic.*

1. INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the major staple food grains of India and globally as well with a good source of energy and nutrition. It is grown under diverse agro-ecological conditions of India where growth conditions differ and so is the yield harvest (Mohan *et al*., 2022). Wheat is the second most important food crop after rice in terms of both area and production. In India, during 2020-21, the annual production of wheat was 108.75 million tons with an average national productivity of 3424 kg/ha (IIWBR, 2021). Major wheat producing states are Punjab, Haryana, Uttar Pradesh, Bihar and Rajasthan which are located in the Indo-Gangetic Plains and accounts for 85 per cent of total wheat production in the India.

Crop improvement programmes require an ample amount of genetic variation to be available. For a successful breeding programme, it is critical to understand the variation in traits and the association between a particular trait and other traits that affect crop yield (Mary and Gopalan, 2006). The breeding program's most important consideration is the selection of parents. Effective selection necessitates knowledge of the nature and magnitude of population diversity, the relationships between traits and yield, and the extent to which the environment influences the expression of these traits (Yagdi, 2009). Therefore, a breeder must use measures such as the phenotypic coefficient of variation, genotypic coefficient of variation, heritability, and genetic advance to get a comprehensive picture of the population's variability (Kurmanchali *et al*., 2019). Thus, the abovementioned parameters offer information regarding the availability of genetic variability for different characters in germplasm. Therefore, study of genetic variability of grain yield and its component characters among different varieties provides a strong basis for selection of desirable genotypes for expansion of yield and other agronomic characteristics (Mangroliya *et al*., 2020). In a transgressive breeding programme, the selection of genetically diverse parents for hybridization is also dependent on the categorization of breeding materials. The Mahalanobis D^2 is a powerful genetic divergence measurement technique. Diverse parentage is important in plant breeding because it allows for higher heterosis in hybrids than is possible in crosses between closely related parents, which in turn can lead to a wider range of genetic variety in genetically segregating populations (Arunachalam, 1981).

2. MATERIALS AND METHODS

Fifty-two wheat genotypes were evaluated in a completely randomised block design (RBD) with three replications during *Rabi,* 2020-21 at the N.E. Borlaug Crop Research Centre (NEBCRC), G.B. Pant University of Agriculture and Technology, Pantnagar, District U.S. Nagar, Uttarakhand. Each entry was planted in a 2 m long, two-row plot. The rows were spaced 20 cm apart. All the recommended package of practices for wheat was followed to raise a healthy crop. The observations for eight quantitative traits, *viz*., plant height, spike length, spikelets per spike, tillers per meter, 1000 grain weight and yield per plot were recorded from five randomly selected plants in each entry while the observations for days to heading and days to maturity were recorded on plot basis. Analysis of variance was estimated as suggested by Panse and Sukhatme (1985), coefficient of variation was calculated as suggested by Sivasubramanian and Menon (1973) to estimate the Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV), heritability in broad sense was estimated according to the formulae proposed by Burton and De Vane (1952), genetic advance (GA) was calculated according to the formulae given by Johnson *et al.* (1955). The D^2 statistic (Mahalanobis, 1956) as a measure of genetic divergence was calculated using the procedure as described by Rao (Rao, 1952). Clustering of the genotypes was done according to Tocher's method (Rao, 1952).

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3. RESULTS AND DISCUSSION

3.1 Genetic Variability

Analysis of variance revealed that the mean square due to genotypes was highly significant for all the traits as shown in Table 1, indicating the presence of a sufficient amount of genetic variability among the genotypes for all the eight characters studied. The various components taken under study are presented in Table 2. A close relationship between genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for all the characters. The magnitude of PCV was slightly greater than GCV, revealing very little influence of environmental variation on their expression. This indicated that phenotypic variability may be considered a reliable measure of genotypic variability.

Similar results have also been reported by Anzer *et al*. (2017); Kumar *et al*. (2018); Rathwa *et al*. (2018) and Gaur (2019).

Table 1: Analysis of variance for various characters in 52 bread wheat genotypes

Source of Var.	**df**	**DH**	**DM**	**PH**	**SL**	**SPS**	**TPM**	**TGW**	**Y/ P**
Replications	2	0.10	0.81	0.49	0.22	0.87	1.03	1.20	1.01
Treatments	51	23.79**	29.20**	301.09**	3.44*	6.96**	2010.43**	37.08**	18721.93**
Error	102	0.65	0.99	0.98	0.04	0.50	50.27	1.82	952.90

*, ** Significant at 5% and 1% levels, respectively.

Where, DH- days to heading, DM- days to maturity, PH- plant height, SL- spike length, SPS- spikelets per spike, TPM- tillers per meter, TGW- thousand grain weight, Y/P- yield per plot

Deshmukh *et al.* (1986) classified PCV and GCV values as low (0-10%), moderate (10-20%) and high (20% and above). The high genotypic coefficient of variation and phenotypic coefficient of variation was observed for yield per plot and tillers per meter. The high genotypic coefficient of variation indicated the presence of wide variation for the characters under study to allow selection for individual traits. High value of genotypic and phenotypic coefficient of variation for traits like grain yield per plot and tillers per meter were reported by Sidharthan and Malik, 2007; Zarkti *et al.* 2012; Yadav *et al*. 2014; Nusrat *et al.* 2015; Anzer *et al.* 2017; Kumar *et al.* 2018; Gaur, 2019, Santosh and Jaiswal, 2019 and Ibrahim, 2019.

Robinson *et al.* (1949) classified heritability values as high (>60%), moderate (30-60%) and values less than 30% low. Heritability estimates reported here was based on broad sense only and hence the total genetic variance may include dominance and epistatic components which are not available for selection. In present study, high heritability in broad sense estimates were observed for plant height (99.02%), spike length (95.98%), days to heading (92.21%), tillers per meter (92.00%), days to maturity (90.47%), 1000-grain weight (86.55%), yield per plot (86.00%) and spikelets per spikes (82.00%). Similar results were reported by Sidharthan and Malik, 2007; Majumder *et al.* 2008; Kamboj, 2010; Alam *et al.* 2013; Kumar *et al.* 2014; Wolde *et al.* 2016 and Bhanu *et al.* 2018. Santosh and Jaiswal, 2019.

Falconer and Mackay (1996) classified genetic advance as percent of mean as low (0-10%), moderate (10-20%) and high (20% and above). The genetic advance expressed as per cent of mean was highest for tillers per meter (50.35%) and yield per plot (48.14%). Similar findings were reported by Yadav *et al.* 2014, Rathwa *et al.* 2018, Guar, 2019 and Mangroliya *et al*., 2020.

Table 2: Phenotypic range, coefficient of range, phenotypic (PCV %) and genotypic (GCV %) coefficients of variation, heritability, genetic advance and genetic advance expressed as a percent of mean for various characters in bread wheat.

Sr.	**Characters**	**Range**	**C. V.**	**Mean**	**PCV**	**GCV**	**h^2**	**G.A.**	**G. A. (%)**

No.			(%)		(%)	(%)	(bs) (%)		
1	Days to heading	73.66-89	1.01	79.26	3.64	3.50	92.21	7.04	8.88
2	Days to maturity	115- 126	0.81	121.98	2.64	2.51	90.47	7.70	6.31
3	Plant height	74.44- 113.22	1.08	91.84	10.94	10.88	99.02	26.27	28.60
4	Spike length	7.60- 13.49	2.04	10.65	10.20	9.99	95.98	2.75	25.84
5	Spikelets per spikes	15.11- 21.55	3.72	19.17	8.50	7.65	80.00	3.48	18.16
6	Tillers per meter	80- 178.66	5.49	129.14	20.53	19.79	92.00	65.02	50.35
7	Thousand grain weight	31.83- 46.46	3.29	40.99	8.98	8.36	86.55	8.41	20.53
8	Yield per plot	204- 508.33	7.88	391.69	21.17	19.64	86.00	188.57	48.14

3.2 Genetic Diversity

In the present investigation, seven different clusters are made from 52 genotypes which are shown in Table 3. Dendrogram showing distribution of 52 genotypes among 7 clusters by using Tocher's method. On the basis of D^2-values, seven clusters were formed from 52 genotypes. The cluster II having largest number of genotypes (18) followed by cluster I (15), cluster VI (7), cluster V (6), cluster IV (3) and cluster III (2). On the other hand, cluster VII was the solitary cluster.

Table 3: Grouping of 52 genotypes of bread wheat in various clusters on the basis of D^2 statistic

Cluster	No. of genotypes	Name of genotypes
I	15	IPS-2020-8, IPS-2020-9, IPS-2020-10, IPS-2020-13, IPS-2020-15, IPS-2020-25, IPS-2020-26, IPS-2020-27, IPS-2020-28, IPS-2020-38, IPS-2020-39, IPS-2020-40, IPS-2020-43, IPS-2020-44, IPS-2020-49
II	18	IPS-2020-1, IPS-2020-4, IPS-2020-14, IPS-2020-18, IPS-2020-19, IPS-2020-24, IPS-2020-29, IPS-2020-30, IPS-2020-32, IPS-2020-33, IPS-2020-34, IPS-2020-35, IPS-2020-36, IPS-2020-41, IPS-2020-42, IPS-2020-47, IPS-2020-48, IPS-2020-50
III	2	IPS-2020-51, IPS-2020-52
IV	3	IPS-2020-2, IPS-2020-5, IPS-2020-7
V	6	IPS-2020-3, IPS-2020-17, IPS-2020-20, IPS-2020-22, IPS-2020-23, IPS-2020-31
VI	7	IPS-2020-6, IPS-2020-11, IPS-2020-12, IPS-2020-16, IPS-2020-45, IPS-2020-46, IPS-2020-47
VII	1	IPS-2020-21

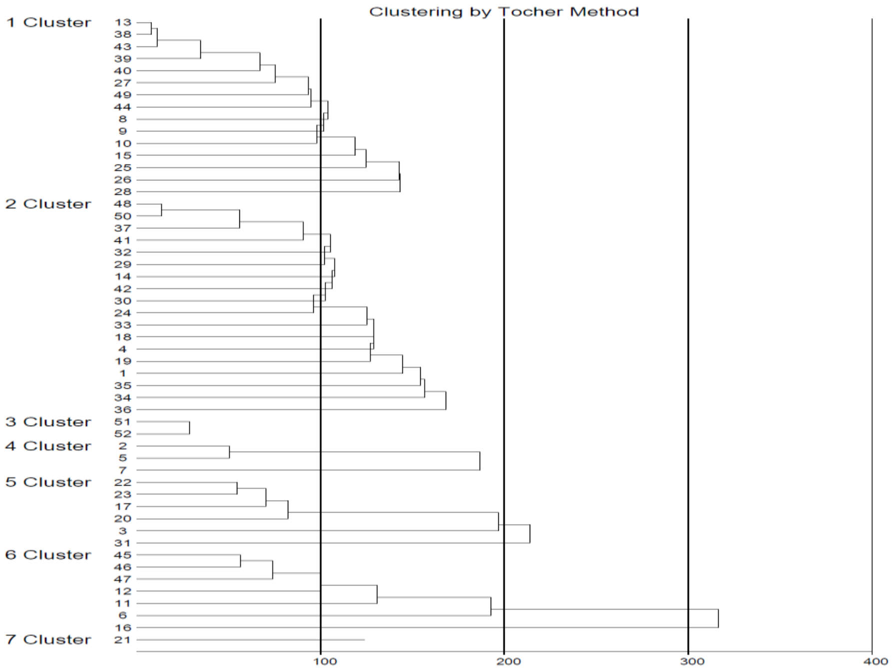

Fig 1: Dendrogram showing distribution of 52 bread wheat genotypes into 7 different clusters

In general, intra cluster distances were lower than the inter-cluster distances and this was in accordance with Alam *et al.* (2013), Santosh *et al.* (2019) and Mangroliya *et al*., (2020). Thus, the genotypes included within a cluster tended to less diverse from one another. The intra-cluster distance (D) ranged from 5.36 (cluster-III) to 14.96 (cluster-VI). High intra-cluster distance indicated about the wider genetic diversity among the genotypes which could be used in yield improvement of bread wheat. The intra and inter-cluster distances are shown in Table 4. The maximum inter-cluster distance was found between cluster V and VI (D=35.34) followed by that between VI and VII (D=34.61). The minimum inter-cluster distance was observed between cluster I and IV (D=16.17). D^2 analysis indicated wider genetic diversity among 52 genotypes of bread wheat which were grouped into seven clusters. Maximum genetic divergence was observed between cluster V and VI followed by between cluster VI and VII.

Table 4: Average intra and inter-cluster distances between seven clusters in bread wheat.

Clusters	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**
I	10.95	16.76	20.47	16.17	24.47	17.95	23.21
II		11.96	19.14	17.31	16.24	27.07	21.30
III			5.36	22.82	24.53	30.90	26.36
IV				14.27	24.99	24.04	26.14
V					13.81	35.34	19.97
VI						14.96	34.61
VII							0.00

In the present study, the cluster VII differed from other clusters in respect of days to heading and days to maturity while cluster IV had desirable rating for spike length, spikelets per spike, thousand grain weight and yield per plot. Cluster VII had desirable rating for tillers per meter. Therefore, intercrossing of such genotypes involved in these clusters would be useful for inducing variability in the respective characters, and their rational improvement for increasing grain yield in bread wheat.

3.3 Cluster means

Cluster means were calculated for all the characters which exhibited considerable differences among the clusters. The mean performance of the clusters (Table 5) was used to select genetically diverse and agronomically superior genotypes out of 52 genotypes studied.

The highest cluster mean for days to 75% heading was exhibited by cluster III (88.17) followed by cluster I (79.49), cluster II (79.44) and lowest for cluster VII (77.00). The highest cluster mean for days to maturity was exhibited by cluster III (133.50) followed by cluster I (122.20), cluster II (122.15) and lowest for cluster VII (117.00). The highest cluster mean for plant height was exhibited by cluster VI (108.49) followed by cluster I (97.45), cluster IV (91.11) and lowest for cluster V (78.48). The highest cluster mean for spike length was exhibited by cluster IV (12.24) followed by cluster VI (11.04), cluster II (10.82) and lowest for cluster VII (7.61).

The highest cluster mean for spikelets per spike was exhibited by cluster IV (20.44) followed by cluster VI (20.16), cluster I (19.67) and lowest for cluster II (19.13). The highest cluster mean for tillers per meter was exhibited by cluster VII (167.33) followed by cluster IV (159.44), cluster III (157.50) and lowest for cluster V (116.17). The highest cluster mean for thousand grain weight was exhibited by cluster IV (46.20) followed by cluster VII (45.67), cluster III (44.51) and lowest for cluster V (36.51). The highest cluster mean for yield per plot was exhibited by cluster IV (479.67) followed by cluster VII (472.33), cluster III (445.00) and lowest for cluster VI (342.71).

Table 5: Cluster mean values of 8 characters in 7 clusters in 52 bread wheat genotypes

Sr. No.	Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
1	Days to heading	79.49	79.44	88.17	78.11	77.83	77.81	77.00
2	Days to maturity	122.20	122.15	133.50	121.67	119.11	121.14	117.00
3	Plant height	97.45	86.14	88.33	91.11	78.48	108.49	83.55
4	Spike length	10.45	10.82	10.39	12.24	9.98	11.04	7.61
5	Spikelets per spike	19.67	19.13	17.83	20.44	16.70	20.16	19.11
6	Tillers per meter	139.29	119.19	157.50	159.44	116.17	117.62	167.33
7	Thousand grain weight	41.67	40.77	44.51	46.20	36.51	40.08	45.67
8	Yield per plot	419.42	373.52	445.00	479.67	358.83	342.71	472.33

4. Conclusion

Crop improvement relies on a wide range of genetic variation because it provides a greater opportunity for selection. Thus, the effectiveness of selection is dependent upon the nature, extent, and magnitude of genetic diversity present in the material and the extent to which it is heritable. In the present investigation, the estimates of high heritability coupled with high GCV and genetic advance expressed as percentage of mean were observed for tillers per meter and yield per plot. These characters may have contributed to the preponderance of additive gene action, and selection pressure could profitably be applied to these characters for their rationale improvement (Panse, 1957). It has been well documented that the more genetically diverse parents utilised in a hybridization programme, the greater the possibilities of getting high heterotic hybrids and broad spectrum diversity in segregating generations (Arunachalam, 1981). Therefore, in the present study, based upon high yielding genotypes and large inter-cluster distances, it is advisable to attempt crossing of the genotypes from cluster IV with the genotypes of cluster VII which may lead to broad spectrum of favorable genetic variability for yield improvement in bread wheat.

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