

Determination of genetic variability and diversity in bread wheat for yield and yield contributing traits

Abstract

A study was conducted to estimate genetic variability and genetic divergence for 8 traits in 52 diverse genotypes of bread wheat (*Triticum aestivum* L.) under normal sowing condition. For all of the features studied, the analysis of variance revealed extremely significant differences in mean square owing to genotypes. Grain yield per plot and tillers per meter have high genotypic and phenotypic coefficients of variation. High heritability coupled with high genetic advance as percent of mean was observed for grain yield/plot and tillers/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/spike, thousand grain weight and yield/plot. Cluster VII had desirable rating for tillers/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). Punjab, Haryana, Uttar Pradesh, Bihar, and Rajasthan, which are located on the Indo-Gangetic Plains and account for 85 percent of total wheat production in India, are the major wheat producing states. 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 characters 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 aforesaid 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 picking of suitable 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 classification 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 randomized 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/spike, tillers/meter, 1000 grain weight and yield/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. ANOVA was estimated as suggested by Panse and Sukhatme (1985), to estimate the Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV), the coefficient of variation was calculated as suggested by Sivasubramanian and Menon (1973), heritability in the broad sense was estimated using the formulae proposed by Burton and De Vane (1952), and genetic advance (GA) was calculated using the formulae proposed 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). The genotypes were clustered according to Tocher's approach (Rao, 1952).

3. RESULTS AND DISCUSSION

3.1 Genetic Variability

Individual genotypes in a population have a tendency to differ from one another, which is measured by genetic variability. The variability of a trait refers to how much it varies in response to environmental and genetic factors. In this study, ANOVA showed that the mean sum of squares due to genotypes was highly significant for all the traits as shown in Table 1, suggesting the existence of ample quantity of genetic variation among the genotypes for all the eight characters under study. Table 2 lists the various components under investigation. For all of the traits, there was a close relationship between genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). PCV had a slightly higher magnitude than GCV, indicating that environmental variation had minimal effect on their expression. This suggested that phenotypic variability may be used to estimate genotypic variability.

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

Table 1: ANOVA for various characters in 52 bread wheat genotypes

Source of Var.	d.f.	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/spike, TPM- tillers/meter, TGW- thousand grain weight, Y/P- yield/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/plot and tillers/meter. The high genotypic coefficient of variation revealed that the characters under investigation had a wide range of variation, allowing for individual trait selection”. For traits with high genotypic and phenotypic coefficients of variation like grain yield/plot and tillers/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”. The heritability estimates presented here were made in a broad sense only, and hence the overall genetic variance may contain dominance and epistatic components that are not selectable. 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/meter (92.00%), days to maturity (90.47%), 1000-grain weight (86.55%), yield/plot (86.00%) and spikelets/spikes (82.00%). Similar findings were also 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 percent of mean was highest for tillers/meter (50.35%) and yield/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.

S. No.	Characters	Range	C. V. (%)	Mean	P.C.V. (%)	G.C.V. (%)	h^2 (bs) (%)	G. A.	G. A. (%)
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/spikes	15.11- 21.55	3.72	19.17	8.50	7.65	80.00	3.48	18.16
6	Tillers/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/plot	204- 508.33	7.88	391.69	21.17	19.64	86.00	188.57	48.14

3.2 Genetic Diversity

Genetic diversity is different from variability, genetic diversity is the amount of variation seen in a particular population. Genetic divergence analysis plays an important role in assessing the nature of diversity in order to identify the genetically diverse genotypes for their use in plant breeding programmes. In the present study, seven diverse clusters are formed from 52 genotypes which are shown in Table 3. Dendrogram depicting the distribution of 52 genotypes among 7 clusters by employing 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

Clusters	Number of genotypes	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

Cluster VII outperformed the other clusters in terms of days to heading and days to maturity, whereas Cluster IV received favourable ratings for spike length, spikelets/spike, thousand grain weight, and yield/plot in this study. Cluster VII had desirable rating for tillers/meter. Therefore, intercrossing of these genotypes involved in these clusters should thus be beneficial for producing diversity in the corresponding traits and rationally improving 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/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/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/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

S. 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/spike	19.67	19.13	17.83	20.44	16.70	20.16	19.11
6	Tillers/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/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. For tillers/meter and yield/plot, estimations of high heritability along with high GCV and genetic progress expressed as a percentage of mean were observed in this study. The more genetically varied parents employed in a hybridization program, the more likely high heterotic hybrids will result (Arunachalam, 1981). Therefore, in the present investigation, based on high yielding genotypes and large inter-cluster distances, it is recommended that genotypes from cluster IV be crossed with genotypes from cluster VII which may result in a broad spectrum of favourable genetic variability for yield improvement in bread wheat.

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