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Genetic Variability, Heritability, Genetic Advance and Divergence Analysis in Wheat (*Triticum aestivum* L.)

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ABSTRACT

Background: Wheat is a cereal crop that is widely farmed across the world and ranks first in global crop production. Wheat cultivation is the world's most important food crop.The assessment of genetic divergence existing in the germplasm collections is very important to select genetically divergent parents for hybridization in a transgressive breeding programme for development of high yielding wheat varieties coupled with quality, multiple resistance and wider adaptability.

Methods: The experiment on 21genotypes including two checks *viz.,* HD 2967 and PBW 824 was conducted to work out the genetic variability, heritability, genetic advance and divergence analysis for yield and yield contributing traits in wheat (*Triticum aestivum* L.). The experiment was laid out in randomised block design (RBD) during *Rabi*, 2021-2022 at Lovely Professional University, Phagwara, Punjab.

Result: The analysis of variance revealed mean sum of square due to genotypes were significant for all the characters indicating sufficient genetic variability among the genotypes. The magnitude of PCV and GCV were moderate for grain yield per plant and harvesting index, which suggests greater phenotypic and genotypic variance among the genotypes and responsiveness of the attributes for making further improvement by selection and indicating limited scope for improvement. High heritability coupled with high genetic advance observed for harvest-index thus these characters show additive gene action in their expression. In divergence analysis, maximum intra-cluster distance exhibited by cluster 2 followed by cluster 1among the different genotypes. The maximum inter-cluster distance between cluster 2 and 3 followed by cluster 2 and 7 and the minimum inter cluster distance was recorded between cluster 5 and 6 followed by cluster 1 and 3. It indicated that for crop improvement in wheat diversified genotypes may be selected from cluster 2 and cluster 3 to received maximum transgressive recombinants from segregating generations.

Key words: Divergence, Genetic advance, Genetic variability, Heritability, Wheat.

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INTRODUCTION

Wheat is a self-pollinated crop belonging to the Gramineae family. *Triticum aestivum* is hexaploidy wheat (2n=6x=42). Wheat is a widely grown cereal crop across the world. It offers 20% of the world's resources. The nutritional content of 100 g of bread wheat revealed that it contains 71 g of carbohydrate, 14 g of protein, 2.5 g of fat, 2 g of minerals and significant amounts of vitamins (thiamine and vitamin B) and minerals (zinc and iron) (Kumar and Nagarajan , 1998; Iquebal and Mishra, 2021). Wheat has a global area of 224.98 million hectares, a production of 735.50 million metric tonnes and a productivity of 3.27 metric tonnes per hectare, with 30.78 million hectares, a production of 98.51 million metric tonnes and a productivity of 3.20 metric tonnes per hectare in 2018-19 (Department of Agricultural Cooperation). During 2020-2021, India has produced 108.75 million tonnes of wheat with covering area about 29.64 million hectares and yielding 3.58 tonnes per hectare. (DAC and FW, 2021).

Analysis of variability among the traits and the association of a particular character with other traits contributing to yield of a crop would be of a great importance in planning a successful breeding programme (Mary and Gopalan, 2006). It is essential for a breeder to measure the variability with the help of parameters like phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance. Hence, these above said parameters give the information regarding the availability of genetic variability for different characters in germplasm (Yagdi, 2009). 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 augmentation of yield and other agronomic characters.

The selection of genetically divergent parents for hybridization in a transgressive breeding programme is also influenced by the classification of breeding materials using appropriate criteria. One of the most effective tools for determining genetic divergence is the Mahalanobis D^2

approach. Genetic diversity is crucial in plant breeding because hybrids between lines of different origins have more heterosis than hybrids between closely related parents and can provide a wide range of genetic variability in segregating populations (Arunachalam, 1981).

MATERIALS AND METHODS

The study was designed to work out the genetic variability, divergence and cluster analysis for various attributes on grain yield per plant among 21 genotypes of wheat including two checks at field experiment under present investigation was conducted during *Rabi*, 2021-2022 at the experimental farm of department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Phagwara, Punjab.

The experimental materials of studies comprised of 21 genotypes including two checks varieties *viz.,* HD 2967 and PBW 824*.* The experiment was laid out in randomised block design (RBD). The observation was recorded on thirteen

Table 1: Analysis of variance for ten characters in wheat.

Characters	Source of variation		
Degree of freedom	Replication	Treatment	Error
	2	20	40
Days to 50% flowering	0.492	6.382**	2.175
Days to maturity	1.444	5.196**	1.277
Plant height (cm)	3.336*	83.121**	1.047
No. of tillers/plant	0.237	0.075	0.042
No. of spike/plant	0.023	0.055	0.055
Chlorophyll content	0.298	14.344**	3.213
Spike length (cm)	0.026	0.777	0.050
No. of spiklets/spike	0.374	2.554	0.755
No. of grains/spike	7.706**	20.654**	0.896
1000 grain weight (gm)	74.081**	80.040**	63.403
Biological yield/plant (gm)	1.942	26.329**	1.403
Grain yield/plant (gm)	0.503	3.222*	0.988
Harvesting index (%)	4.294*	53.766**	3.246

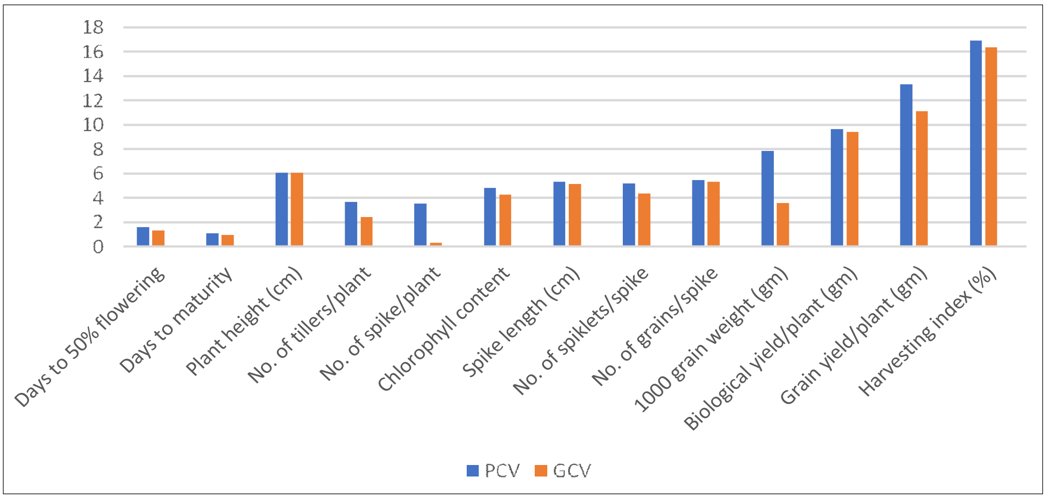

Fig 1: Graphical representation of estimation of coefficient of variation in wheat.

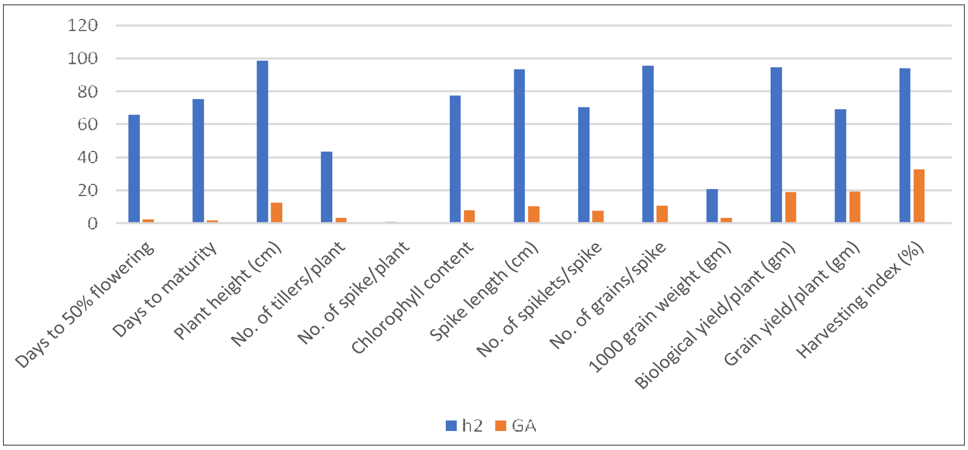

Fig 2: Graphical representation of h^2 (broad sense) and genetic advance in per cent of mean in wheat.

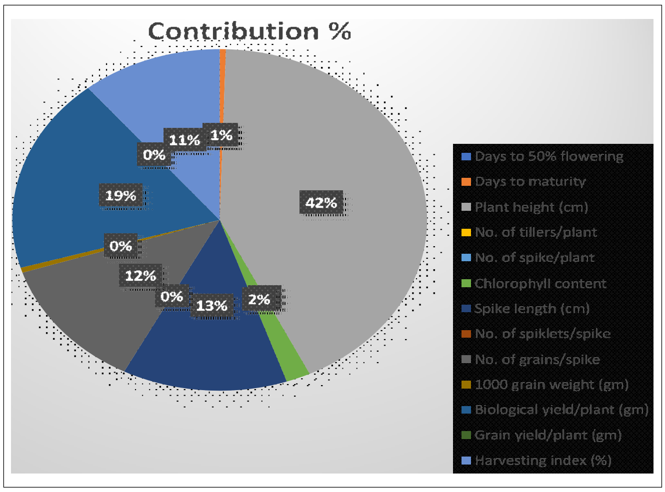

Fig 3: Graphical representation of contribution of thirteen traits of wheat towards divergence.

Table 2: Estimate of coefficient of variation, h^2 (broad sense) and genetic advance in per cent of mean in wheat.

Characters	Range	Mean	Coefficient of variation		Heritability in broad sense %	Genetic advance in per cent of mean
			PCV	GCV		
Days to 50% flowering	89.33-94.33	91.460	1.594	1.295	65.9	2.166
Days to maturity	121-125	122.25	1.077	0.935	75.4	1.672
Plant height (cm)	75.643-94.126	86.630	6.076	6.038	98.7	12.359
No. of tillers/plant	3.966-4.666	4.323	3.658	2.411	43.4	3.273
No. of spike/plant	3.60-4.20	3.873	3.524	0.291	0.7	0.049
Chlorophyll content	41.523-48.230	45.261	4.831	4.256	77.6	7.723
Spike length (cm)	8.506-10.536	9.567	5.320	5.143	93.4	10.242
No. of spiklets/spike	16.300-19.433	17.774	5.192	4.358	70.4	7.534
No. of grains/spike	43.600-52.400	48.171	5.447	5.328	95.7	10.734
1000 grain weight (gm)	49.566-72.500	65.922	7.835	3.572	20.8	3.355
Biological yield/plant (gm)	26.643-35.496	30.638	9.669	9.408	94.7	18.857
Grain yield/plant (gm)	5.972-9.542	7.774	13.332	11.101	69.3	19.042
Harvesting index (%)	18.793-33.460	25.057	16.895	16.377	94.0	32.702

Table 3: Clustering pattern of 21 Wheat genotypes and on the basis of Mahalanobis's D^2 statistic.

Cluster No.	No. of genotypes	Genotypes
Cluster 1	11	HPAN-163, 10th HPYT-409, 10th HPYT-414, 10th HPYT-418, 10th HPYT-435, DBW-173, HD-3226, PBW-677, PBW Zn-1, HD-3117, HD-2967.
Cluster 2	05	8th HPYT-480, 10th HPYT-415, 10th HPYT-450, PBW-771, PBW-824.
Cluster 3	01	PBW-752.
Cluster 4	01	10th HPYT-426.
Cluster 5	01	HD-3271.
Cluster 6	01	10th HPYT-463.
Cluster 7	01	HD-3086.

Table 4: Average intra and inter-cluster D2 values of wheat genotypes.

Clusters	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7
Cluster 1	**8.58**	14.63	11.06	11.46	11.17	12.41	11.45
Cluster 2		**9.35**	20.22	13.08	13.76	12.11	19.37
Cluster 3			**0.00**	16.89	15.12	17.91	12.52
Cluster 4				**0.00**	14.99	11.94	15.31
Cluster 5					**0.00**	8.45	14.47
Cluster 6						**0.00**	13.52
Cluster 7							**0.00**

different grain yield traits *viz*., days to 50% flowering, days to maturity, plant height, number of tillers per plant, number of spikes per plant, chlorophyll content, spike length, number of spikelet's per spike, number of grains per spike, 1000 grain weight, biological yield per plant, grain weight per plant, harvest-index.

The study of genetic divergence among 21 genotypes, including checks, was done through Mahalanobis's D^2 statistic (1936). Tocher´s method, as described by Rao (1952), was followed for cluster formation. The analysis of variance was worked out individually for each attribute as per the method suggested by Fisher (1954) and using the standard procedure given by Panse and Sukhatme (1954). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated as per the standard formula suggested by Burton (1952).

RESULTS AND DISSCUSION

Analysis of variance indicated that the mean sum of squares due to genotypes were significant for all the characters revealed that there was considerable genetic variability amongst the material under study for all the characters (Table 1). Moderate value of PCV and GCV were recorded in grain yield per plant was 13.33 and 11.10 and harvesting index was 16.89 and 16.37. The values indicates that there was considerable variability present for these characters under study. Similar kind of results were also substantiated by Kumar et al., (2022), Chaitali and Bini (2007), Shankarrao *et al.,* (2010) and Ranjan and Yadav (2019) on yield and its component traits in wheat. The graphical representation of estimation of coefficient of variation in wheat is given in Fig 1.

Heritability in the broad sense was estimated for all the characters under study and is presented in Table 2; it ranged from 0.7 to 98.7%. High heritability (above 60%) was observed for days to 50% flowering (65.9%), days to maturity (75.4%), plant height (98.7%), chlorophyll content (77.6%), spike length (93.4%), number of spikelet's per spike (70.4%), number of grains per spike (95.7%), biological yield per plant (94.4%), grain yield per plant (69.3%) and harvesting index (94.0%). Similar findings were reported by Kisana *et al.* (1982), Rehman *et al.* (2015), Prasad *et al.* (2007), Bhushan *et al.* (2013), Noorka *et al.* (2009), Nagireddy and Jyothula (2009).

A genetic advance as a percentage of the mean was observed ranging from 0.049% to 32.70%. The highest genetic advance as a percentage of the mean (above 20%) (At 1% selection intensity) was recorded for the harvesting index (32.70%). A similar finding was reported by Singh *et al.* (2013).The harvest index revealed high estimates of heritability combined with genetic progress. High heritability coupled with moderate genetic advance observed in traits *viz.,* plant height, spike length, number of grains per spike, biological yield per plant and grain yield per plant. Thus, these characters showed additive gene action in their expression and can be improved through various breeding techniques. The graphical representation of the estimation of h2 (in the broad sense) and genetic advance in percent of the mean in wheat is given in Fig 2.

Table 5: Cluster means for different characters in wheat.

Cluster no.	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of tillers/plant	No. of spike/plant	Chlorophyll content	Spike length (cm)	No. of spikelets/spike	No. of grains/spike	1000 Grain weight	Biological yield/plant	Grain yield/plant	Harvesting index
Cluster 1	90.91	122.48	89.38	4.29	3.86	45.77	9.62	17.55	47.99	65.15	30.08	7.85	24.43
Cluster 2	91.87	121.60	79.19*	4.41	3.95	42.59*	9.45	17.64	46.95	65.95	33.63	7.34	23.85
Cluster 3	92.00	122.00	94.13**	4.17	3.73	48.23**	9.62	16.57*	44.70*	67.53	27.81	6.43*	33.46**
Cluster 4	94.33**	123.33	86.74	4.10*	3.87	48.17	10.50**	19.43**	51.60	71.53	35.45**	8.32	22.37*
Cluster 5	93.00	121.00*	86.27	4.13	3.73	47.84	8.51*	17.43	48.67	61.63*	27.18	7.96	26.32
Cluster 6	92.33	122.00	82.27	4.20	3.60*	46.75	9.61	19.37	52.40**	71.63**	27.26	8.17	26.85
Cluster 7	89.67*	123.67**	90.67	4.67**	4.20**	43.06	9.64	19.17	51.53	65.70	26.64*	9.32**	29.28

Table 6: Contribution of thirteen traits of Wheat towards divergence.

Source	Times ranked	Contribution %
Days to 50% flowering	0	0.00%
Days to maturity	1	0.48%
Plant height (cm)	89	42.38%
No. of tillers/plant	0	0.00%
No. of spike/plant	0	0.00%
Chlorophyll content	4	1.90%
Spike length (cm)	27	12.86%
No. of spiklets/spike	0	0.00%
No. of grains/spike	26	12.38%
1000 grain weight (gm)	1	0.48%
Biological yield/plant (gm)	39	18.57%
Grain yield/plant (gm)	0	0.00%
Harvesting Index (%)	23	10.95%

The Mahalanobis D^2 analysis was employed to study genetic diversity existing among 21 Wheat genotypes on the basis of thirteen quantitative characters. The pseudo-F-test revealed that seven clusters arranged were the most appropriate for grouping the 21 genotypes. The distribution of 21 wheat genotypes in seven clusters is presented in Table 3

The highest number of genotypes appeared in cluster 1 which contained 11 genotypes followed by cluster 2 having 5 genotypes. Cluster 3, 4, 5, 6 and 7 each contain 1 genotype. The estimates of average intra and inter cluster distance for the seven cluster is presented in Table 4. The highest intra-cluster distance was recorded in cluster 2 (9.35) followed by cluster 1 (8.58). The maximum inter cluster distance was recorded between cluster 2 and cluster 3 (20.22) followed by 2 and cluster 7 (19.37). This observation is presented in Table 5. Similar findings have been reported by Singh and Dwivedi (2002), Hailegiorgis *et al.* (2011).

The contribution of thirteen characters towards divergence in Table 6 showed the highest contribution by plant height (42.38%) followed by biological yield per plant (18.57%). The graphical representation in contribution of thirteen traits of Wheat towards divergence is given in Fig 3.

CONCLUSION

The analysis of variance revealed sufficient genetic variability among the genotypes. High heritability coupled with high genetic advance observed for harvest-index thus these character show additive gene action in their expression. In divergence analysis, maximum intra-cluster distance exhibited by cluster 2 followed by cluster 1, among the different genotypes. The maximum inter-cluster distance between cluster 2 and 3 followed by cluster 2 and 7. It indicated that for crop improvement in wheat diversified genotypes may be selected from cluster 2 and cluster 3 to received maximum transgressive recombinants from segregating generations. The presence of significant genetic diversity in the germplasms examined in this study suggested that this material may be used to select the various parents for a future hybridization programme for further enhancement of yield and yield contributing traits in context of crop improvement.

Conflict of interest: None.

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