



Studies of genetic variability, character association and diversity analysis for yield and its components in wheat (*Triticum aestivum* L.)

Himani Verma¹, S. K. Dhama^{1*}, D. K. Bahuuguna², Saloni¹ and Nitin Kumar³

¹Department of Genetics and Plant Breeding, R. M. P. (PG) College, Gurukul Narsan, Haridwar, Uttarakhand, India

²Department of Agriculture, Chaman Lal Mahavidhyalya, Landhaura, Haridwar, Uttarakhand, India

³Department of Agriculture, Ch. Shivnath Singh Shandilaya PG college, Machhara, Meerut, Uttar Pradesh, India

*Corresponding author: S. K. Dhama

Received 10 March 2023; Accepted 24 Apr 2023; Published 12 May 2023

Abstract

The experiment was conducted in randomized complete block design in three replications. The data were recorded on days to 50% flowering, plant height, peduncle length, number of tillers per plant, days to maturity, spike length, number of spikelets per spike, number of grains per spike, 1000-grain weight, biological yield per plant, grain yield per plant and harvest index. Analysis of variance revealed significant differences among fifty eight genotypes for all the characters under study. The highest estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for grain yield per plant. High heritability coupled with high genetic advance was observed for grain yield per plant. Grain yield per plant showed positive and significant correlation with Number of tillers per plant, Days to maturity, Spike length, Number of spikelets per spike, Number of grain per spike, 1000 grain weight, biological yield per plant and Harvest index. Based on D² –statistics, 58 genotypes were grouped into eight clusters. The highest inter-cluster distance was found between cluster VII and VIII. This indicates that genotypes included in these clusters possess wide genetic diversity. On the basis of divergence and cluster mean it may be suggested that maximum heterosis and good recombinants could be obtained in crosses between genotypes of cluster VIII, VII, V and IV in varietal improvement programme. Thus, crosses between the genetically diverse genotypes of cluster VII with genotypes PBW-726, K-55, K-23 and PBW-703 and cluster V with genotypes like DBW-6602, WH-1105, K-27, K-54, PBW-292 and Tall-2 expected to exhibit high heterosis and are also likely to produce new recombinants with desired traits. Cluster VII which exhibited excellence for mean for Plant height, peduncle length and grain yield per plant for developing superior variety of wheat.

Keywords: Wheat, Variability, Correlation, Path analysis, Diversity

Introduction

Wheat (*Triticum aestivum* L.) is one of the most widely grown cereal crops, contributing to the global food supply and economic security. This crop provides more nutrition to the human being in comparison to other food crops; hence, it is considered staple food for about 40% of the world's population. In India, wheat is the second most important food crop after rice. It is a challenging task before the breeders to enhance the present level of production as the growing population of the country will require much more food as compared to the present day requirement. It is not possible to increase the area under production. Hence, only alternative is left to increase the productivity by evolving superior varieties and better management of crop production to cope up with increasing demands of food. In this regards, information on nature and magnitude of genetic variability is of immense value for starting any systematic breeding programme in crops. The presence of considerable genetic variability in the base material ensures better chances of evolving desired plant types (Sabharwal and Lodhi, 1995) [12]. The knowledge of genetic parameters such as heritability and genetic advance among characters under selection is very useful for predicting genetic progress in breeding programme and developing efficient breeding strategies (Falconer and Mackay, 1996). Genetic diversity available in the existing germplasm determines the

success of any crop improvement programme (Harlan, 1976; Moose and Mumm, 2008) [3, 10]. Therefore, quantitative assessment of genetic diversity present among population usually helps a plant breeder in choosing desirable parents for breeding programme. The higher genetic distance between parents, the higher heterosis in progeny can be achieved (Joshi and Dhawan, 1966) [5].

Keeping in view, an effort has been made in the present study to evaluate a set of 58 wheat genotypes with an aim, to analyze the variability, heritability, genetic advance, character association and diversity for yield and its component traits among fifty eight genotypes.

Material and Methods

Fifty eight wheat genotypes were grown during rabi season 2022-2023 at the research Farm of Department of Genetics and Plant Breeding, R.M. P. (PG) College, Gurukul Narsan, Haridwar, Uttarakhand, India. The 58 genotypes of wheat were sown in a randomized block design (RBD) with three replications at the research farm. Each genotype was grown in two rows per replication of 3 meter length and row to row and plant to plant spacing was kept 30 and 10cm, respectively. The variability, correlation, path coefficient and genetic diversity were calculated as per the standard statistical procedures.

Result and Discussion

Genetic variability

The analysis of variance revealed highly significant differences among the genotypes for all the characters studied (Table 1), thereby suggesting the presence of sufficient variability among

the genotypes and provides ample scope for further improvement. Similar results were also reported by Tanzeen *et al.* (2009) [18]. The presence of large amount of variability might be due to diverse sources of breeding materials collected as well as environmental effects on phenotypes.

Table 1: Analysis of variance (ANOVA) for 12 characters among fifty eight genotypes in bread wheat

Source of variation	D.F.	Mean Sum of Squares											
		Days to 50% flowering	Plant height (cm)	Peduncle length (cm)	Number of Productive tillers per plant	Days to maturity	Spike length (cm)	Number of spikelets per spike	Number of grains per spike	1000-grain weight (g)	Biological yield per plant (g)	Grain yield per plant (g)	Harvest index (%)
Replication	2	1.75	14.50	2.50	4.40	5.30	2.60	1.10	2.28	2.40	5.55	17.80	70.90
Treatment	60	7.80*	114.23**	43.37**	8.85*	6.21*	6.24*	5.54*	34.32**	30.78**	100.88**	20.34**	115.64**
Error	120	0.56	10.32	5.43	2.44	4.21	0.90	2.96	14.76	6.28	60.00	11.32	47.89

*, **Significant at 5% and 1% level of significance respectively

The genetic parameters studied are presented in Table 2. The magnitude of phenotypic coefficient of variation (PCV) was greater than genotypic coefficient of variation (GCV) for all the characters studied indicating vital role of environmental interaction in the expression of all the characters. The findings were in agreement with previous study in wheat (Gollen *et al.* 2011) [2]. A perusal coefficients of variation revealed that the highest GCV and PCV were observed for grain yield per plant (41.70%, 42.51%) followed by plant height (40.12%, 41.75%), 1000-grain weight (39.88%, 41.35%), number of spikelets per spike (38.41%, 38.89%) and number of grains per spike (38.36%, 38.71%). Similar results were also reported by Kaul and Singh, 2011; Kumar *et al.* 2013, Yadav *et al.* 2014) [6, 9, 19]. However, harvest index content revealed high difference between GCV and PCV in comparison to other characters, suggested that environmental effect was prominent for harvest index. The least difference between PCV and GCV was noticed for number of spikelets per spike, number of grains per spike and grain yield/plant indicating these characters are less influenced by environment on the expression of the characters under study. These results match with the findings of Shankarrao *et al.* (2010). Moderate estimate of GCV and PCV were noticed for spike length (31.03%, 31.62%), number of tillers per plant (30.12%, 30.43%) and Harvest index (18.24 %, 21.75%). These results were contrary to the findings of Jagshoran *et al.* (1995). Days to 50% flowering (14.49%, 14.61%), days to maturity (13.47%, 14.42%) and peduncle length (12.99%, 14.15%) showed low values of GCV and PCV. This suggested low variability for such characters among genotypes.

The proportion of variability inherited from parents to off spring is manifested by heritability (Lush, 1949). In this concern, high estimates of heritability were observed for grain yield per plant (96.07) followed by biological yield per plant (94.77), number of grains per spike (89.37), number of spikelets per spike (87.87), days to 50% flowering (86.27), plant height (85.77), peduncle length (81.67), harvest index (81.27) and 1000-grain weight (69.47) whereas moderate for

spike length (58.57) (Table 2). Yadav *et al.* (2014) [19] also observed high heritability for days to 50% flowering, days to maturity, tillers per plant, grain per spike, test weight and grain yield per plant. This shows the presence of additive gene effect and selection may be made for the improvement of these characters. Although low heritability exhibited that the characters were highly influenced by environmental effect and genetic improvement through selection will be difficult due to effect of environment. Johanson *et al.* (1955) have reported that a character showing high heritability may not be inevitable impart high genetic advance. High heritability coupled with high genetic advance as percent mean were revealed for 1000 grain weight (35.95), biological yield per plant (35.14), number of grains per spike (34.48), grain yield per plant (32.86), plant height (32.34), spike length (32.24), number of spikelets per spike (32.21), days to 50% flowering (23.62) and number of tillers per plant (21.86) and low genetic advance for harvest index (16.38), peduncle length (17.67) and days to maturity(11.70) and It can be find out with greater degree of accuracy when heritability coupled with genetic advance is studied (Dudley and Moll, 1969). Therefore, estimation of heritability along with high genetic advance is more useful to understand the type of gene action involved in the expression of various polygenic characters. High heritability coupled with high genetic advance as percent mean were revealed for number of grains per spike (35.79), number of spikelets per spike (35.72), plant height (32.48), length (31.51) spike 1000 grain weight (30.71), grain yield per plant (30.89) biological yield per plant (28.09), number of tillers per plant (26.77) and days to 50% flowering (21.86). Similar findings were reported by Nagireddy and Jyothula, (2009) [11] and Khokhar *et al.*, (2010) [7]. This indicates substantial contribution of additive genetic action in the expression of the characters. Hence, direct selection for such characters would be more effective. The characters peduncle length and harvest index exhibited high heritability along with low genetic advance suggested predominance of non-additive gene action hence; direct selection for such characters would mislead the expected result.

Table 2: Estimate of genetic variability, heritability and genetic advance for 12 characters in wheat

Characters	Coefficient of variation (%)		Heritability (%) in broad sense	Genetic advance	GA as percentage of mean
	GCV	PCV			
Days to 50% flowering	14.49	14.61	86.27	23.62	21.86
Plant height (cm)	40.12	41.75	85.77	32.34	32.48
Peduncle length (cm)	12.99	14.15	81.67	17.67	17.46
Number of tillers per plant	30.12	30.43	29.57	21.86	26.77
Days to maturity	13.47	14.22	18.27	11.7	8.35
Spike length (cm)	31.03	31.62	58.57	32.24	31.51
Number of spikelets per spike	38.41	38.89	87.87	32.21	35.72
Number of grains per spike	38.36	38.71	89.37	34.48	35.79
1000-grain weight (g)	39.88	41.35	69.47	35.95	30.71
Biological yield per plant (g)	32.13	32.87	94.77	35.14	28.09
Grain yield per plant (g)	41.7	42.51	96.07	32.86	30.89
Harvest index (%)	18.24	21.75	81.27	16.38	13.52

Correlation analysis

Days to 50% flowering showed positive and significant correlation with days to maturity (0.180*) and harvest index (0.181*) but positive and non significant correlation with grain yield per plant (0.135); Plant height revealed positive and significant correlation with number of tillers per plant (0.210*), days to maturity (0.247*), spike length (0.215*), number of grain per spike (0.229*) and biological yield per plant (0.172*) but positive and non significant correlation with grain yield per plant (0.036); Peduncle length showed positive and significant correlation with number of tillers per plant (0.307**), days to maturity (0.193*), spike length (0.263*), number of spikelets per spike (0.406**), number of grain per spike (0.192*) and biological yield per plant (0.403**) while it had showed positive and non significant correlation with grain yield per plant (0.135); Number of tillers per plant showed positive and significant correlation with spike length (0.259*), number of spikelets per spike (0.886**), number of grain per spike (0.192*) and biological yield per plant (0.804**) and grain yield per plant (0.664**); Days to maturity showed positive and significant correlation with spike length (0.486**), number of grain per spike (0.982*), number of spikelets per spike (0.886**), biological yield per plant (0.184*), harvest index

(0.176*) and grain yield per plant (0.238*); Spike length showed positive and significant correlation with number of spikelets per spike (0.190*), number of grain per spike (0.524**) and grain yield per plant (0.198*); Number of spikelets per spike showed positive and significant correlation with biological yield per plant (0.712**) and grain yield per plant (0.685**); Number of grain per spike showed positive and significant correlation with harvest index (0.184*) and grain yield per plant (0.234*); 1000 grain weight showed positive and significant correlation with biological yield per plant (0.243*); Biological yield per plant showed positive and significant correlation with and grain yield per plant (0.577**) but it had negative and significant correlation with harvest index (-0.222*); Harvest index showed positive and significant correlation with and grain yield per plant (0.783**) these data are presented in Table 3. Similar pattern of correlation was also observed by Singh *et al.* (1998) [14], Singh and Singh (1999) [15], Khumkar *et al.* (2001) [8], Sultan *et al.* (2002) [17], and Sharma *et al.* (2004) [13]. The traits exhibiting significant positive association with grain yield suggest that such traits may be important for improving the grain yield, and indirect selection for these traits would be effective for increasing grain yield of the wheat genotypes under study.

Table 3: Estimates of phenotypic correlation coefficients among 12 characters in wheat

Characters	Days to 50% flowering	Plant height	Peduncle length	No. of tillers plant	Days to maturity	Spike length (cm)	No. of spikelets /spike	No. of Grains per spike	1000-grain weight	Biological yield /plant	Harvest index	Grain yield/ plant
Days to 50% flowering		0.140	-0.080	0.158	0.180*	-0.105	0.159	0.169	0.081	0.057	0.181*	0.135
Plant height			0.149	0.210*	0.247*	0.215*	0.138	0.229*	0.048	0.172*	0.021	0.036
Peduncle length				0.307**	0.193*	0.263*	0.406**	0.192*	0.131	0.403**	-0.093	0.135
No. of tillers/plant					-0.123	0.259*	0.886**	0.04	0.065	0.804**	0.075	0.638**
Days to maturity						0.486**	0.029	0.982**	-0.001	0.184*	0.176*	0.238*
spike length (cm)							0.190*	0.524**	0.015	0.22	0.066	0.198*
No. of spikelets/spike								0.015	0.127	0.712**	0.086	0.685**
No. of grains/ spike									0.001	0.162	0.184*	0.234*
1000-grain weight										0.243*	-0.006	0.11
Biological yield/ plant											-0.222*	0.577**
Harvest index												0.783**

Genetic diversity

The fifty eight genotypes of wheat were grouped into eight clusters based on D²-statistics in such a way that genotypes

within a cluster had a low D² values than those of in-between the characters. The composition of clusters has been depicted in Table 4. The distribution pattern of genotypes showed that

cluster VI had maximum number of genotypes (12) followed by cluster I (10), cluster III (9), cluster II (7), cluster V (6) and cluster IV and VIII (5) genotypes each whereas, cluster VII had minimum number of genotypes (4). The inter-cluster distance was observed higher than intra-cluster, suggesting wide genetic diversity among genotypes (Table 5). The inter-cluster distance varied from 51.50 to 8.36. The highest inter-cluster distance was noticed in the cluster VII and VIII (51.50). However, minimum distance was observed in cluster I and V (8.36), indicating close relationship between these clusters would not provide good results. The greater distance between clusters, indicating that the genotypes included in these clusters revealed broad spectrum of genetic diversity and may be used in hybridization programme for wheat improvement. The hybrids developed from the selected genotypes within the limit of

compatibility of these clusters may produce desirable transgressive segregants. This would be useful in wheat breeding programme for developing the high yield potential varieties. Similar findings were registered by (Yadav *et al.* 2006; Chapla *et al.* 2008 and Singh *et al.* 2010). The maximum intra-cluster distance was observed in cluster IV (28.37), followed by cluster VIII (22.14) and cluster VI (21.13). It was noticed that genotypes within cluster with high degree of divergence would produce more desirable breeding materials for attaining the maximum genetic advance (Dobariya *et al.* 2006) [1]. The minimum intra-cluster distance was registered in cluster V (0.06) followed by cluster II (0.10) and cluster VII (0.11) indicating homogeneous nature of the genotypes with less deviation between the genotypes, hence selection will be ineffective.

Table 4: Clustering pattern of 58 wheat genotypes

No. of clusters	No. of genotypes	Name of Genotypes
I	10	HD-3091, HACS-3949, HD-3194, Tall-3, VL-907, K-34, PBW-166, WP-710/17, WP-712/17, K-35
II	7	HD-2733, HI-1544, Sarwottam, HI-1605, RAJ-4539, HD3195, ARAW-4498
III	9	BW-5572, PBW-725, WP-703/17, DBW-17, PBW-703, Jalwa, Mahycogal, DBW-945, WP-711/17
IV	5	HD-3086, PBW-343, WP-709/17, WP-702/17, HD-3128
V	6	DBW-6602, WH-1105, K-27, K-54, PBW-292, Tall-2
VI	12	K-31, PBW-730, WP-707/17, WP-702/17, HD-2967, HD-8189, HD-3123, DBW-147, PBW-154, DBW-730, SP-goal, WP-708/17,
VII	4	PBW-726, K-55, K-23, PBW-703
VIII	5	WP-705/17, K-26, K-33, Cahu Canada, CPAN-3061

Table 5: Estimates of average inter and intra- cluster distances for 8 clusters in wheat

Clusters	I	II	III	IV	V	VI	VII	VIII
I	7.42	9.54	11.32	14.71	8.36	13.11	26.22	21.41
II		0.10	15.6	30.66	11.83	21.32	25.39	14.87
III			9.51	16.04	18.39	21.81	49.97	20.87
IV				28.37	11.9	19.28	43.23	34.14
V					0.06	14.57	21.25	29.9
VI						21.13	31.18	35.88
VII							0.11	51.5
VIII								22.14

The cluster means analyzed for 12 characters under study are presented (Table 6). Cluster VIII exhibited the highest mean value for days to 50% flowering (85.32) and better spike length (8.76). Cluster VII showed the highest mean for Plant height

(93.29), peduncle length (39.68) and grain yield per plant (18.47). However, maximum number of productive tillers per plant (10.21) was observed in cluster VI. Cluster V had highest for number of spikelets per spike (15.09) and number of grain per spike (50.73). Cluster IV showed the highest mean for days to maturity (135.11). Cluster III had highest 1000-grain weight (42.09). Cluster II showed the highest biological yield (44.86). Cluster I revealed the highest harvest index (48.20). The results were in agreement with the findings of earlier study (Singh and Dwivedi, 2002; Dobariya *et al.* 2006) [16, 1]. The results from the present study suggest that crossing among genotypes from different clusters exhibiting good mean performance may help in achieving high yield. Incorporation of more divergent parents in hybridization can enhance the chances of attaining better heterosis and provide broad spectrum of genetic variability in segregating generation.

Table 6: Cluster mean for 12 characters in wheat

Characters	Days to 50% flowering	Plant height (cm)	Peduncle length (cm)	Number of tillers per plant	Days to maturity	Spike length (cm)	Number of spikelets per spike	Number of grains per spike	1000-grain weight (g)	Biological yield per plant (g)	Grain yield per plant (g)	Harvest index (%)
I	82.05	79.43	33.16	8.63	133.7	8.19	13.11	44.88	40.46	35.83	16.4	48.2
II	82.78	84.49	34.8	9.14	133.56	9.48	14.18	47.85	37.76	44.86	17.14	39.96
III	83.38	83.09	33.59	9.64	135.11	8.43	12.11	41.78	42.09	43.34	17.59	41.87
IV	83.52	76.03	30.7	9.76	133.56	8.16	13.67	46.37	38.24	43.18	18.13	43.52
V	81.26	80.04	29.01	9.03	133.69	7.91	15.09	50.73	36.84	44.11	17.6	39.82
VI	81.78	67.41	25.26	10.21	133.28	6.61	12.68	44.48	35.48	39.54	16.63	43.99
VII	83.16	93.29	39.68	9.18	134.53	8.58	14.06	47.63	40.18	43.18	18.47	44.29
VIII	85.32	78.84	33.96	8.05	133.48	8.76	14.15	47.88	36.56	37.6	14.54	40.42

On the basis of divergence and cluster mean it may be suggested that maximum heterosis and good recombinants could be obtained in crosses between genotypes of cluster VII and V in varietal improvement. Thus, crosses between the genetically diverse genotypes of cluster VII with genotypes PBW-726, K-55, K-23 and PBW-703 and cluster V with genotypes like DBW-6602, WH-1105, K-27, K-54, PBW-292 and Tall-2 are expected to exhibit high heterosis and are also likely to produce new recombinants with desired traits.

References

1. Dobariya KL, Ribadia KH, Padhar PR, Ponkia HP. Analysis of genetic divergence in some synthetic lines of bread wheat (*Triticum aestivum* L.). Adv Plant Sci. 2006;19(1):221–225.
2. Gollen B, Yadav RK, Kumar P. Assessment of genetic parameters for spike traits and yield attributes in bread wheat genotypes following Line $\times$ Tester mating system. Environ Ecol. 2011;29(2):752–756.
3. Harlan. Genetic resources in wild relatives of crop. Crop Sci. 1976;16:329–333.
4. Jag Shoran. Estimation of variability parameters and path coefficients for certain metric traits in winter wheat (*Triticum aestivum* L. em. Thell.). Indian J Genet. 1995;55(4):399–405.
5. Joshi AB, Dhawan NL. Genetic improvement of yield with special reference to self fertilizing crops. Indian J Genet. 1966;26A:101–113.
6. Kaul DK, Singh B. Evolution for drought tolerance in elite genotypes of bread wheat (*Triticum aestivum* L.). Adv Plant Sci. 2011;24(1):141–144.
7. Khokhar MI, Hussain M, Zulkiffal M, Sabir W, Mahmood S, Jamil Anwar MW. Studies on genetic variability and inter-relationship among the different traits in wheat (*Triticum aestivum* L.). Krmiva. 2010;52(2):77–84.
8. Khumkar MS, Chaudhary MB, Deshmukh PS. Genetic variability and association of morpho-physiological characters with grain yield in late sown wheat (*Triticum aestivum* L. em. Thell.). Ann Agric Res. 2001;22(2):217–220.
9. Kumar R, Gaurav SS, Bhushan B, Pal R. Study of genetic parameters and genetic divergence for yield and yield components of bread wheat (*Triticum aestivum* L.). J Wheat Res. 2013;5(2):39–42.
10. Moose SP, Rita HM. Molecular plant breeding as the foundation for 21st century crop improvement. Plant Physiol. 2008;147:969–977.
11. Nagireddy AV, Jyothula DPB. Heritability and interrelationship of yield and certain agronomic traits in wheat. Res Crops. 2009;10(1):124–127.
12. Sabhrawal PS, Lodhi GP. Germplasm evaluation for different traits in wheat (*Triticum aestivum* L.). HAU J Agric Res. 1995;25(4):207–210.
13. Sharma PK, Pradeep K, Nitin K. Character association analysis in different height groups of wheat (*Triticum* spp.). Prog Agric. 2004;4(2):167–171.
14. Singh IB, Kumar A, Singh D. Genetics of grain yield and quality of grain yield and quality contribution traits in bread wheat under stress conditions. In: Wheat Research Needs Beyond 2000 AD. Proceedings of the International Conference; DWR; Karnal, India; 1998. p. 58.
15. Singh KH, Singh TB. Character association in segregating generations of bread wheat. Agric Sci Dig. 1999;19(3):207–210.
16. Singh SP, Dwivedi VK. Genetic divergence in bread wheat. New Agric. 2002;13(7):2–7.
17. Sultan S, Islam MA, Islam MR, Morshed MM, Islam MR. Correlation and regression analysis for heading date, yield and yield contributing characters in wheat under water and phosphorus stress. Pak J Biol Sci. 2002;5(2):149–151.
18. Tanzeen M, Naqvi FN. Heritability, phenotypic correlation and path coefficient studies for some agronomic characters in synthetic elite lines of wheat. J Food Agric Environ. 2009;7(3–4):278–282.
19. Yadav SK, Singh AK, Baghel SS, Jarman M, Singh AK. Assessment of genetic variability and diversity for yield and its contributing traits among CIMMYT based wheat germplasm. J Wheat Res. 2014;6(2):154–159.