

# GENETIC VARIABILITY, ASSOCIATION AND DIVERSITY STUDIES IN BREAD WHEAT (*TRITICUM AESTIVUM* L.)

**BINOD KUMAR\***, CHANDRA MOHAN SINGH<sup>1</sup> AND KUNDAN KUMAR JAISWAL<sup>2</sup>

<sup>1</sup>Department of Plant Breeding and Genetics, Rajendra Agricultural University, Pusa (Bihar) INDIA

<sup>2</sup>IARI, Regional Station, Pusa (Bihar), INDIA

e-mail: binod\_gpb022@rediffmail.com

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\*Corresponding author

## ABSTRACT

Thirty wheat genotypes significant genotypic differences were observed for all the traits studied indicated the considerable amount of variation among genotypes for each character. The estimates of GCV and PCV were moderate for biological yield per plant, number of effective tillers per plant. High heritability estimates were recorded for all the traits and also indicated high genetic advance (except days to 50% flowering and days to maturity). Grain yield per plant showed highly significant positive correlation with 1000 seed weight, plant height and number of effective tillers per plant, spike length and 1000 seed weight highly significant positive correlation with grains per spike. Path coefficient analysis revealed that 1000 seed weight and plant height had the highest direct effect on grain yield per plant and each must be given preference in selection along superior wheat genotypes. On the basis of maximum divergence, inter-mating of K816 and HUW-533 mono-cluster genotypes from cluster VI and VII showing maximum inter-cluster distance between them followed by mono-cluster genotype K816 from cluster VI with 3 genotypes from cluster II exhibiting high degree of genetic diversity may be utilized through inter-varietal hybridization programme. Noteworthy is that cluster II and VI exhibited high cluster means for seed yield per plant, grains per spike and spike length; cluster VI and VII for tillers per plant, seed yield per plant and test weight and it also exhibited high heritability coupled with high genetic advance as percent of mean, might be utilized in hybridization- selection breeding for wheat genotypes.

## INTRODUCTION

Wheat (*Triticum aestivum* L.) is considered as king of cereals and it provides foods to 36% of the global population, contributing 20% of the food calories. It is an important staple food of many countries in the world and occupies a unique position as used for the preparation of a wide range of food stuffs. Over the past century selection of desirable parents for hybridization programme has been found as an effective operating implement in developing high yielding crop varieties upon which, the modern agriculture can rely. Efficient and economic crop improvement scheme refers to the collection of superior alleles into a single population. Genetic variability in a population can be partitioned into heritable and non heritable variation with the aid of genetic parameters such as variance, genotypic coefficient of variation, heritability and genetic advance, which serve as a basis for selection of some outstanding genotypes from existing ones. Choice of parents is not only based on desirable agronomic traits, components of yield and extent of variability but also on heritability of yield contributing traits. The environment, in which selection is made, is also important because heritability and genetic advance vary with change in environment. The study of genetic variability reveals about the presence of variation in their genetic constitution and it is outmost important as it provide the basis of effective selection.

Grain yield is a complex trait and highly influenced by many genetic factors and environmental fluctuations. In plant breeding programme, direct selection for yield as such could

be misleading. A successful selection depends upon the information on the genetic variability and association of morpho-agronomic traits with grain yield. Kumar *et al.* (2003) reported high heritability coupled with high genetic advance for plant height, number of spikelets per panicle and 1000-grain weight. Correlation studies along with path analysis provide a better understanding of the association of different characters with grain yield. The grain yield was significantly and positively correlated with 1000 seed weight and the number of grains per spike (Korkut *et al.*, 2001). Path coefficient analysis separates the direct effects from the indirect effects through other related characters by partitioning the correlation coefficient (Dixet and Dubey, 1984).

In views of these facts, thirty wheat genotypes were evaluated in this study to determine the magnitude of variability among the germplasm and grouping pattern of genotypes in different cluster. To identify genetically diverse and agronomically desirable genotypes for exploitation in a breeding programme aimed at improving grain yield potential of wheat.

## MATERIALS AND METHODS

The experimental material comprised of 30 wheat genotypes grown in randomized block design with two replications at the Field Experimentation Center, Department of Genetics and Plant Breeding, Allahabad Agricultural institute-Deemed University, Allahabad during Rabi-2007-08. The experimental site is situated at 25.87°N L and 81.5°E L and 98 meter above the sea level. It has a sub-tropical climate with extremes of

summer and winter. Each plot consisted of five rows of 2.5m length spaced at 25cm plant and within a row at 5cm. All the recommended package of practices for wheat was followed to raise a healthy crop. Data were recorded on five randomly and competitive plants of each genotype from each replication for eight quantitative characters viz. plant height (cm), number of effective tillers per plant, spike length (cm), number of seeds per spike, test weight (g), biological yield per plant (g), harvest index (%) and seed yield per plant (g). The rest two characters viz., days to 50% flowering and days to maturity were recorded on plot basis. Mean values were subjected to analysis of variance to test the significance for each character as per methodology advocated by Panse and Sukhatme (1967). GCV and PCV were calculated by the formula given by Burton (1952), heritability in broad sense ( $h^2$ ) by Burton and De Vane (1953) and genetic advance i.e. the expected genetic gain were calculated by using the procedure given by Johnson *et al.* (1955). Correlation coefficients were computed according to the method suggested by Singh and Chaudhary (1985). Dewey and Lu (1959) was used to perform the path analysis for grain yield and its components keeping grain yield as resultant variable and its components as causal variables. The genetic divergence was estimated by Mahalanobis (1936)  $D^2$  statistics and the grouping of the genotypes into clusters were done using Tochers method (c. f. Rao, 1952).

## RESULTS AND DISCUSSION

The mean sum of squares due to genotypes showed significant differences for all ten characters under study, suggested that the genotypes were genetically divergent (Table 1). This indicates that there is ample scope for selection of promising lines from the present gene pool for yield and its components. Thus, it indicates ample scope for selection for different quantitative characters for wheat improvement. Asif *et al.* (2004) and Kumar *et al.* (2009) also reported considerable genetic variability for grain yield and its component characters in wheat. Genotypic variance, phenotypic variance, genotypic coefficient of variation, phenotypic coefficient of variation, heritability (broad sense), genetic advance and genetic advance expressed as percent of mean for ten characters are presented in Table 2. The PCV values were higher than GCV values for all the traits which reflect the influence of environment on the expression of traits. The estimates of GCV and PCV were moderate for all the characters studied except days to 50% flowering and days to maturity which showed the low GCV and PCV. High heritability estimates was recorded for all the traits. Sachan and Singh (2003) and Chandra *et al.* (2010) also reported high heritability estimates for grain yield per plant, number of seeds per spike, plant height, 1000 seed weight and number of tillers per plant, which support the present findings. Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone (Johnson *et al.*, 1955). High heritability accompanied with high genetic advance as percent of mean for all the traits except days to 50% flowering and days to maturity. It indicates that most likely the heritability is due to additive gene effect and selection may be effective in early segregating generation for these traits.

Similar findings have been reported by Sharma and Garg (2002). High heritability for days to 50% flowering and days to maturity coupled with low genetic advance indicates non-additive gene effects. Therefore, there seems a limited scope for improvement in these traits.

The phenotypic and genotypic correlations for morpho-agronomic traits are presented in Table 3. Grain yield per plant showed highly significant and positive genotypic and phenotypic correlation with 1000 seed weight whereas effective tillers per plant and plant height had significant only at genotypic level. Some authors are also reported significant positive correlation between yield and plant height (Chaturvedi and Gupta., 1995 and Khan *et al.*, 1999). Days to 50% flowering showed highly significant and positive association with days to maturity. Effective tillers per plant negative significant to highly significant correlation with spike length and grains per spike respectively at genotypic and phenotypic level and positively associated with 1000 seed weight. A positive highly significant correlation of spike length with grains per spike but negative highly significant correlation with harvest index and positive non significant correlation with grain yield per plant, it indicates that the selection for grains per spike not to other characters. Spike length was strongly and positively correlated phenotypically and genotypically with grains per spike and negative and highly significant with harvest index. Number of grains per spike had negative association with biological yield per plant, effective tillers per plant and spike length. 1000 seed weight showed highly significant positive genotypic and phenotypic correlation with grains per spike. Biological yield per plant showed highly significant and positive correlation with plant height whereas spike length significantly positive correlation; this indicated that taller genotypes not only to have taller and heavier spikes.

Path coefficient analysis provides an effective way of finding out of direct and indirect sources of correlations. The results are given in Table 4, which reveals that the 1000 seed weight exhibited the highest positive direct effect followed by plant height. Direct effects of biological yield per plant and days to maturity were negative and moderate. Test weight and plant height exhibited high positive direct effect and highly significant correlation coefficient with yield indicated the true relationship therefore direct selection through this trait will be effective for yield improvement. The indirect effect of these traits were contributed *via* grains per spike, biological yield per plant for plant height, respectively. The direct effect of biological yield per plant with grain yield was negative however the correlation coefficient was positive due to the indirect effects *via* effective tillers per plant and harvest index. Since the direct effect was negative, so the direct selection for this trait to improve yield will be undesirable. However, improvement in 1000 seed weight and plant height may help to compensate the positive effect of biological yield per plant. The highest positive direct effects and highly significant positive correlation coefficient was recorded between 1000 seed weight and grain yield per plant. The direct selection for this trait will be effective.

Based on Mahalanobis'  $D^2$  analysis, thirty genotypes were grouped into seven clusters with variables number of genotypes (Table 5) suggesting considerable amount of genetic diversity in the material. The cluster III was the largest having

**Table 1: Analysis of variance for 10 quantitative characters of 30 wheat genotypes**

S.N.	Characters	Mean sum of squares replications(df = 01)	Treatments(df = 29)	Error(df = 29)
1.	Days to 50% flowering	2.016	61.540**	0.602
2.	Days to maturity	0.066	20.730**	1.308
3.	Plant height	1.872	449.212**	1.790
4.	Effective tillers per plant	0.113	5.262**	0.425
5.	Spike length	0.386	2.939**	0.295
6.	Number of seeds per spike	2.948	39.836**	1.063
7.	1000 seed weight	0.475	34.333**	0.677
8.	Biological Yield/ Plant	7.350	94.956**	13.108
9.	Harvest Index	8.740	110.342**	24.827
10.	Seed yield per plant	0.143	7.780**	1.112

**Table 2: Estimates of genetic parameters for 10 quantitative characters of 30 wheat genotypes**

S. No	Characters	VG	VP	GCV	PCV	h <sup>2</sup> (bs)	GA	GG
1	Days to 50% flowering	30.46	31.07	7.38	7.45	98.1	11.26	15.05
2	Days to maturity	9.53	10.83	2.69	2.87	87.9	5.96	5.21
3	Plant height	223.71	225.50	14.78	14.84	99.2	30.68	30.33
4	Effective tillers per plant	2.41	2.84	19.03	20.64	85.0	2.95	36.15
5	Spike length	1.32	1.61	11.93	13.20	81.7	2.14	22.22
6	Number of seeds per spike	19.38	20.45	10.45	10.73	94.8	8.83	20.97
7	1000 seed weight	16.61	17.72	10.39	10.73	93.7	8.12	20.72
8	Biological Yield/ Plant	40.92	54.03	19.53	22.44	76.0	11.47	35.02
9	Harvest Index	42.76	67.58	15.21	19.12	63.3	10.71	24.92
10	Seed yield per plant	3.55	4.22	16.75	18.28	84.0	3.55	31.62

VG = Genotypic variance, VP = Phenotypic variance GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, h<sup>2</sup> = heritability, GA = Genetic Advance and GG = Genetic gain

**Table 3: Genotypic and phenotypic correlation coefficient between yield and its component characters in 30 wheat genotypes**

S.N.	Character	Days to 50% flowering	Days to maturity	Plant height	Tillrers/ plant	Spike length	Grains/ spike	Test weight	Biological yield/Plant	Harvest index	Grain yield/ plant
1.	Days to 50% Flowering (rg)	1.000	0.823**	0.196	-0.040	0.050	0.028	0.159	0.186	-0.136	-0.077
	(rp)	1.000	0.769**	0.192	-0.024	0.048	0.019	0.152	0.159	-0.114	-0.072
2.	Days to Maturity (rg)		1.000	-0.046	-0.167	-0.037	0.026	0.274	0.080	0.004	-0.133
	(rp)		1.000	-0.034	-0.142	-0.009	0.010	0.231	0.060	0.056	-0.136
3.	Plant Height (rg)			1.000	0.152	0.274*	-0.209	0.049	0.384**	-0.318*	0.337**
	(rp)			1.000	0.136	0.258*	-0.201	0.045	0.347**	-0.261*	0.308*
4.	Tillrers/ Plant (rg)				1.000	-0.294*	-0.402**	0.210	-0.111	0.177	0.268*
	(rp)				1.000	-0.197	-0.349**	0.222	-0.151	0.078	0.331**
5.	Spike Length (rg)					1.000	0.394**	0.086	0.223	-0.631**	0.127
	(rp)					1.000	0.404**	0.107	0.246	-0.486**	0.195
6.	Grains/ Spike (rg)						1.000	0.354**	-0.015	-0.165	0.225
	(rp)						1.000	0.358**	0.014	-0.135	0.232
7.	Test Weight (rg)							1.000	0.269	0.015	0.561**
	(rp)							1.000	0.203	0.011	0.543**
8.	Biological /Yield/ Plant (rg)								1.000	-0.403**	0.041
	(rp)								1.000	-0.315*	0.005
9.	Harvest Index (rg)									1.000	-0.088
	(rp)									1.000	-0.101

17 genotypes indicating overall genetic similarity among them, followed by cluster I and III having 6 and 3 genotypes respectively. Whereas, cluster IV, V, VI and VII having mono-genotype cluster. The pattern of distribution of genotypes in different clusters exhibited that geographical diversity was not related to genetic diversity as genotypes of same geographical region were grouped into different cluster and vice-versa. The data of intra and inter - cluster distances (Table 6) and the mean performance of the clusters (Table 7) were used to select genetically diverse genotypes. The highest intra - cluster distance was shown by cluster I whereas zero for mono-

genotype clusters which indicated presence of moderate to high diversity within clusters. Hence, there is a scope for exchange of genes among genotypes within these clusters. Maximum divergence was observed between Cluster VI and VII followed by between cluster II and VI and cluster V and VII. High cluster means, for spike length, grains per spike, 1000 seed weight and seed yield per plant (cluster V), for seed yield per plant, spike length and biological yield per plant (cluster II), cluster VII for number of tillers per plant, 1000 seed weight and biological yield per plant and Cluster VI had the lowest cluster mean value for number of tillers per plant, thousand

**Table 4: Genotypic and Phenotypic path analysis (direct effects on seed yield given in bold) of wheat**

No	Character	Days to 50% flowering	Days to maturity	Plant height	Tillrers/ plant	Spike length	Grains/ spike	Test weight	Biological yield/ plant	Harvest index	Grain yield/ plant
1.	Days to 50% Flowering (G)	0.012	0.010	0.002	-0.000	0.001	0.000	0.002	0.002	-0.002	-0.077
	(P)	-0.092	-0.071	-0.017	0.002	-0.004	-0.002	-0.014	-0.014	0.011	-0.072
2.	Days to Maturity (G)	-0.237	-0.288	0.013	0.048	0.011	-0.007	-0.079	-0.023	-0.001	-0.133
	(P)	-0.098	-0.127	0.004	0.018	0.001	-0.001	-0.029	-0.007	-0.007	-0.136
3.	Plant Height (G)	0.080	-0.019	0.410	0.062	0.112	-0.085	0.020	0.157	-0.130	0.337**
	(P)	0.067	-0.012	0.349	0.047	0.090	-0.071	0.015	0.121	-0.091	0.308*
4.	Tillrers/ Plant (G)	-0.000	-0.002	0.002	0.014	-0.004	-0.005	0.003	-0.001	0.003	0.268*
	(P)	-0.004	-0.027	0.026	0.194	-0.038	-0.067	0.043	-0.029	0.015	0.331**
5.	Spike Length (G)	-0.005	0.004	-0.031	0.034	-0.115	-0.045	-0.010	-0.025	0.073	0.127
	(P)	0.002	-0.001	0.012	-0.009	0.048	0.019	0.005	0.012	-0.023	0.195
6.	Grains/ Spike (G)	0.002	0.002	-0.021	-0.040	0.040	0.101	0.036	-0.001	-0.016	0.225
	(P)	0.003	0.002	-0.034	-0.059	0.068	0.170	0.061	0.002	-0.023	0.232
7.	Test Weight (G)	0.107	0.184	0.033	0.141	0.058	0.239	0.674	0.181	0.011	0.561**
	(P)	0.076	0.115	0.022	0.111	0.053	0.179	0.501	0.102	0.005	0.543**
8.	Biological Yield/ Plant (G)	-0.057	-0.024	-0.118	0.034	-0.068	0.004	-0.083	-0.308	0.124	0.041
	(P)	-0.031	-0.011	-0.068	0.029	-0.048	-0.003	-0.039	-0.196	0.062	0.005
9.	Harvest Index (G)	0.020	-0.000	0.047	-0.026	0.093	0.024	-0.002	0.059	-0.148	-0.088
	(P)	0.005	-0.003	0.012	-0.004	0.023	0.007	-0.001	0.015	-0.049	-0.101

RESIDUALEFFECT = 0.6917

**Table 5: Distributing pattern of thirty genotypes of wheat into six clusters based on D<sup>2</sup> statistic**

Cluster group	No. of genotypes	Name of genotypes
Cluster-1	6	HD 2009, PBW 373, PBW 524, HUW 468, HUW 510, K 9351
Cluster-2	3	K 9465, K 68, K 65
Cluster-3	17	Kalyansona, Sonalika, RAJ 1972, RAJ 6560, RAJ 1555, HD 2891, HD 2643, HD 2824, HD 2733, HD 1981, PBW 343, HUW 55, K 9162, K 9106, K 9006, K 9533, UP 2594
Cluster-4	1	K 9107
Cluster-5	1	HD 2687
Cluster-6	1	K 816
Cluster-7	1	HUW 533

**Table 6: Average intra and inter cluster D<sup>2</sup> values among 6 clusters for 30 genotypes of wheat**

Column1	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster	7 Cluster
Cluster 1	78.235	752.142	265.955	524.721	614.001	229.436	824.007
Cluster 2		102.153	554.735	238.527	1062.339	1427.017	193.174
Cluster 3			162.580	282.748	292.019	492.823	673.918
Cluster 4				0.000	597.690	943.229	413.818
Cluster 5					0.000	606.819	1270.675
Cluster 6						0.000	1627.880
Cluster 7							0.000

**Table 7: Mean values of clusters and contribution of different characters towards genetic divergence in 30 wheat genotypes**

Column1	Days to 50% flowering	Days to maturity	Plant height	Tillrers/ plant	Spike length	Grains/ spike	Test weight	Biological yield/ plant	Harvest index	GrainYield/ plant
Cluster 1	69.000	111.083	90.747	8.550	9.264	38.817	36.943	31.750	45.983	10.667
Cluster 2	73.667	113.667	132.567	7.867	10.547	40.767	41.257	38.500	40.858	13.683
Cluster 3	76.794	115.471	98.825	7.971	9.506	42.868	39.355	32.412	43.011	11.212
Cluster 4	78.500	114.000	117.750	7.300	10.910	45.800	34.480	27.000	40.170	10.200
Cluster 5	81.500	119.500	88.850	7.300	10.570	51.700	48.175	29.500	39.715	12.200
Cluster 6	63.500	113.500	76.750	7.100	10.520	48.600	37.840	27.500	39.600	9.100
Cluster 7	79.500	115.500	129.340	13.000	8.190	33.400	41.450	41.500	40.890	10.315

grain weight, biological yield, harvest index and grain yield, Similar findings have been reported by ( Tsegaye *et al.*, 2012) reflected probability of getting better segregants and primary recombinants expected to more, in case if the genotypes of these clusters will be used in hybridization programme. Inter-mating of K-816 and HUW-533 from the mono-genotype

clusters, cluster VI and VII showing maximum inter-cluster distance followed by crossing between mono-genotype cluster (cluster VI) K-816 with three genotypes from cluster II suggested for improving spike length, biological yield per plant and 1000 seed weight enhancing the yield and chances of getting better recombinants in segregating generations. Noteworthy is that

cluster II and VI reflected high cluster means for seed yield per plant, grains per spike and spike length; cluster VI and VII for tillers per plant, seed yield per plant and test weight, and it also exhibited high heritability coupled with high genetic advance as percent of mean, might be utilized in hybridization-selection breeding programme for wheat genotypes.

## REFERENCES

- Asif, M., Mujahid, M. Y., Kisana, N. S., Mustafa, S. Z. and Ahmad, I. 2004.** Heritability, genetic variability and path coefficient of some traits in spring wheat. *Sarha. J. Agric.* **20(1)**: 87-91.
- Burton, G. W. 1952.** Quantitative inheritance of grasses. *Proc 6<sup>th</sup> Int. Grassland Congress.* **1**: 277-283.
- Burton, G. W. and De Vane, E. H. 1953.** Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agron. J.* **45**: 478-481.
- Chandra, D., Sharma, R., Rani, S., Singh, D. K., Sharma, R. and Sharma, S. K. 2010.** Genetic variability for quantitative traits in wheat [*Triticum aestivum* L. em. Thell] *Plant Archives.* **10(2)**: 871-874
- Chaturvedi, B. L. and Gupta, R. R. 1995.** Divergence in spring wheat (*Triticum aestivum* L.). *Indian J. Agric. Res.* **29(1/2)**: 36-40.
- Dewey, J. R. and Lu, K. H. 1959.** A correlation and path coefficient analysis components of crested wheat grass seed production. *Agron. J.* **51**: 515-518.
- Dixet, P. and Dubey, D. K. 1984.** Path analysis in lentil (*Lens culinaris* Med.). *Lens Newsletter.* **11**: 15-17.
- Johnson, H. W., Robinson, H. E. and Comstock, R. E. 1955.** Estimates of genetic and environmental variability in soybean. *Agron. J.* **47**: 314-318.
- Korkut, K. Z., Baser, I. and Bilgin, O. 2001.** Genotypic and phenotypic variability, heritability and phenotypic correlation for yield and yield components in bread wheat varieties. *Acta Agronomica Hungarica.* **49(3)**: 237-242.
- Kumar, S., Dwivedi, V. K., Tyagi, N. K. and Kumar, S. 2003.** Genetic variability in some metric traits and its contribution to yield in wheat (*Triticum aestivum* L.). *Progressive Agric.* **3(1-2)**: 152-153.
- Kumar, B., Lal, G. M., Ruchi and Upadhyay, A. 2009.** Genetic variability, diversity and association of quantitative traits with grain Yield in bread wheat (*Triticum Aestivum* L.). *Asian J. Agril. Sci.* **1(1)**: 4-6.
- Mahalanobis, P. C. 1936.** On generalized distance in statistics. *Proceedings of national institute of science.* **2**: 49-55.
- Panase, V. G. and Sukhatme, P. V. 1967.** Statistical Methods of agricultural Workers. 2<sup>nd</sup> edition, pp: 381, *I.C.A.R Publ.* New Delhi.
- Rao, C. R. 1952.** Advanced statistical method in biometrical research. *Ed. 1<sup>st</sup> Wiley and sons Inc.,* New York.
- Sachan, M. S. and Singh, S. P. 2003.** Genetics of yield and its components in durum wheat (*Triticum durum* Desf.). *J. Interacademia.* **7(2)**: 140-143.
- Sharma, A. K. and Garg, D. K. 2002.** Genetic variability in wheat (*Triticum aestivum* L.) crosses under different normal and saline environments. *Annals Agric. Res.* **23(3)**: 497- 499.
- Singh, R. K. and Chaudhary, B. D. 1985.** Biometrical methods in quantitative genetic analysis. *Kalyani Publ.,* New Delhi
- Tsegaye, D., Dessalegn, T., Dessalegn, Y. and Share, G. 2012.** Analysis of genetic diversity in some durum wheat (*Triticum durum* Desf) genotypes grown in Ethiopia. *African J. Biotech.* **11(40)**: 9606-9611.