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Genetic variability and Selection Parameters for Yield and its Contributing characters in Bread Wheat (*Triticum aestivum* L.)

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ABSTRACT: Eight parents and their all possible cross combinations excluding their reciprocals were evaluated in a Randomized Block Design (RBD) at C.S.A. University of Agriculture and Technology, Kanpur, U.P., India to find out the extent of variability and related parameters for effective selections for yield and its contributing traits. However, the productivity of wheat has been increasing on a definite rate since recent years. So the material was evaluated to examine the extent of genetic variability which can be used further for the improvement of wheat crop. The results showed higher estimates of Phenotypic Coefficient of Variability (PCV) for all the studied characters as compared with corresponding Genotypic Coefficient of Variability (GCV). Differences between PCV and GCV for grain weight per spike and spike length were higher indicated that these two characters were more influenced by environment, while lower the difference between remaining characters showed stability of the characters. High heritability in narrow sense was observed almost for all the characters except 1000 grain weight and number of grains per spike. Moderate genetic advance was noted for days to heading, biological yield per plant, days to maturity and harvest index per cycle of selection at K=2.06. An advancement of 35.69% in grain yield and 32.26% in harvest index was expected per selection cycle at base population.

Both additive genes and non-additive genes were found effective for all the characters whereas 1000 grain weight and weight of grains per spike were under the control of non-additive genes. Simple selection based on progeny performance may be helpful for improving grain yield per plant.

Keywords: *Triticum aestivum*, bread wheat, selection parameter, coefficient of variability, genetic advance and heritability.

INTRODUCTION

Since the dawn of the civilization, wheat became major field crop to feed the human society in every part of the world. It is the crop cultivated under wide area throughout the globe. Wheat is a major staple food crop of the world after rice in the context to its use as a source of human food and energy. It forms the major share of intake of nutrients for the people. Besides staple food for human beings; its straw is used for large population of cattle in India and some other developing countries. Wheat is being grown in more than 120 countries and takes an area of 215.29 million hectares with the production of nearly 736.04 million tonnes and with the productivity of about 3425 kg per hectare (FAO, 2020). Rank of India is second both in area and production next to China. In India area under wheat is 29.58 million hectare with the production of 107.86 million tonnes, productivity of 3568 kg per hectare (DAC&FW, 2020). The present study is based on twelve quantitative characters measured on eight germplasm lines with one check. Information on the variability was measured by estimating the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance for individual quantitative character and through equilibrium distance over the characters. In addition the present study will also helpful in identification of high yielding genotypes with better quality. In crop improvement only the genetic components of variation is important because this is the only component which transmit to the next generation (Mohammadi and Parasana 2003). Heritability is the ratio of genotypic variance (Vg) to the phenotypic variance (Vp). Heritability is an important parameter in the selection process as it determines the response to selection. Heritability is used by plant breeders to enhance the precision of single field trial and/or of series of trials

(Allard, 1962). Study of the estimates of heritability with genetic advance is more meaningful and reliable than considering the parameters individually.

MATERIAL AND METHODS

For present investigation the field experiments were conducted in two cropping season, first in *Rabi* season 2017-18 and second in *Rabi* season 2018-19 at Crop Research Farm, Nawabganj of C. S. A. University of Agriculture and Technology, Kanpur, U.P. India. The material of experiment comprised of 8 diverse lines of bread wheat namely, K 424, K 7903, WR 544, DBW 14, DBW 71, PBW 343, K 307 and K 9162. The salient features of these parental lines are given in Table-A.

Table A: Details of genotypes/varieties.

Sr. No.	Genotype	Pedigree	Place of origin
1.	K 424	K 8020/K 9162	CSAU, Kanpur
2.	K 7903	HD 1982/K 816	CSAU, Kanpur
3.	WR 544	KALYANSONA/HD1999//HD2204/DW38	IARI, New Delhi
4.	DBW 14	RAJ 3765/PBW 343	IIWBR, Karnal
5.	DBW 71	PRINIA/UP2425	IIWBR, Karnal
6.	PBW 343	ND/VG1944//KAL//BB/3/YACO'S'/4/VEE#5'S	PAU, Punjab
7.	K 307	K 9321/UP 2003	CSAU, Kanpur
8.	K 9162	K 7827/HD 2204	CSAU, Kanpur

The lines were sown following a randomized complete block design (RCBD) with three replications where each entry sown in one row of 3 meter length per replication. The entries were sown with inter and intra-row spacing of 25 cm and 10 cm, respectively. All the recommended agronomical practices were adopted to raise the crop. For twelve characters *viz.* (1) Days to 50% heading, (2) Number of tillers per plant, (3) Plant height(cm), (4) Days to maturity, (5) Number of spikelets/ spike, (6) Spike length (cm), (7) Number of grains/spike, (8) Grain weight/spike (g), (9) Biological yield per plant (g), (10) Grain yield per plant (g), (11) One thousand grain weight (g) and (12) Harvest index (%) observations were recorded from the five randomly selected plants from each genotype.

"K-7903"a popular wheat variety of this region was also used as 'check variety' in this experiment.

Estimation of coefficient of variability: The computation of genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) was done by the formula given by Burton and de Vane (1953).

$$\text{GCV} = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \text{x} 100$$

$$\text{Or} \quad \frac{\sigma_g}{\bar{\bar{X}}} \text{x} 100$$

$$\text{PCV} = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \text{x} 100$$

$$\text{Or} \quad \frac{\sigma_p}{\bar{\bar{X}}} \text{x} 100$$

Heritability: Heritability (h^2) in broad sense was computed following the formula given by Johnson *et al.* (1955).

h^2_{bs} (%) = Vg/Vp ×100

Where,

h^2 = Heritability in broad sense

Vg = Genotypic variance

Vp = Phenotypic variance

Genetic advance: The calculation of the estimates of genetic advance was done according to the formula given by Robinson *et al.* (1949).

Genetic Advance = $(\sigma_{ph}) \times (K) \times (h^2_{bs})$

Genetic advance in per cent of mean of the character G.A.

$$(\%) = \frac{\sigma_{ph} \text{ x } K \text{ x } h^2}{\bar{X}} \text{x} 100$$

Where,

G.A. = Genetic advance estimate

K = Selection differential at 5% selection intensity (K = 2.06)

h^2 = Coefficient of heritability in broad sense.

σ_{Ph} = Phenotypic standard deviation.

$\bar{X}$ = Mean value of the concerned character

RESULT AND DISCUSSION

Analysis of Variance (ANOVA). The analysis of variance (ANOVA) for all the twelve characters was given in Table 1. Treatments and parents showed highly significant differences for all the characters. The comparison of parent's *vs* F_l generation indicated highly significant differences for number of tillers per plant, number of spikelets per spike, spike length, number of grains per spike, biological yield per plant, grain yield per plant and 1000 grain weight while significant differences for plant height and harvest index. These results indicated the plenty of variability among the genotypes studied and this would respond positively to selection.

Several researchers like Kalimullah *et al.* (2012) reported that the characters *viz.* number of grains per/spike, number of tillers/plant, 1000 grain weight and grain yield per plant showed highly significant differences among 41 bread wheat genotypes. Similarly work of Mecha *et al*. (2016) showed the significant differences among 64 genotypes of bread wheat for thirteen characters and Kumar *et al.* (2020) showed the significant differences among 81 genotypes of bread wheat for 14 quantitative characters.

Range and Mean Values. In Table 2 range and mean values for the 12 characters is presented. Mean value for days to heading reported 74.12 ranged from 65.33 (K-7903) to 82.67(DBW-71). Number of productive tillers per plant is an important character in wheat that ultimately affects the overall grain yield. It showed a wide variation which ranged from 6.70 (K-7903) to 18.17 (K-307) with the mean value of 11.87. Plant height ranged from 82.60 (K-424) to 92.70 (K-307) with the mean value of 87.77. The average of days to maturity was 121 days and it ranged from 111 days (K-424) to 129.67 days (PBW-343). The character number of spikelets per spike ranged from 16.83 (K-7903) to 20.43 (DBW-14) with the mean value of 18.60.

Average spike length was 8.69cm with the minimum and maximum values of 7.80cm (PBW-343) and 10cm (K-307) respectively. Number of grains per spike ranged from 43.70 (K-7903) to 49.57 (PBW-343) with the mean value of 46.98. The character weight of grain per spike with mean value of 1.61g ranged from 1.40g (K-424) to 2g (K-7903). The biological yield per plant varied from 39.13g for PBW-343 to 48.10g for K-307 with the average of 42.62g. Grain yield per plant ranged from 12.47g (K-7903) to 18.70g (K-307) with the mean value of 14.31g. The mean value for 1000 grain weight was 47.46g and ranged from 41.07g (DBW-71) to 54.60g (WR-544).

The range observed for harvest index was wide with the minimum value of 29.27% and the highest 41.83% in respect of parents WR-544 and PBW-343, respectively. The observed mean harvest index was 33.71%. Similarly, Maqbool *et al*. (2010) also reported a wide range of variation for the characters namely plant height, number of spikelets/ spike, biological yield per plant, grain yield per plant and 1000-grain weight.

Coefficients of variation. In Table 3 the estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) is presented**.** It is apparent from the table that phenotypic coefficient of variation was invariably greater than the corresponding genotypic coefficient of variation revealed the influence of environment on the expression of all the traits.

Classification of PCV and GCV values as low (0-10%), moderate (10-20%) and high (20% and above) values by Deshmukh *et al.* (1986). Considering this delineation, GCV found high for number of tillers per plant (21.03), medium GCV was observed for grain yield per plant (17.93), harvest index (15.83), grain weight per spike (15.65) biological yield per plant (12.31), spike length (9.45), and low GCV was observed for 1000 grain weight (9.06), days to heading (7.42), plant height (6.04), number of spikelets per spike (5.67), number of grain per spike (5.06) and days to maturity (3.88) (Table 3).

The PCV found high for the character number of tiller per plant(21.68) and medium PCV was observed for grain yield per plant (18.56), grain weight per spike(18.05), harvest index (16.00), biological yield per plant (12.98), spike length (11.10) and low PCV was observed for 1000 grain weight (9.17), days to heading (7.51), plant height (6.41), number of spikelets per spike (6.39) number of grain per spike (5.55) and days to maturity (3.94) (Table 3).

The result observed were in accordance with the findings of Kumar *et al.* (2020) reported for 1000 grain weight and grain yield per plant, Wani *et al.* (2011); Kalimmulah *et al*. (2012) for grain yield per plant, 1000 grains weight, number of grains/spike in wheat. Saini *et al*. (2019) reported low GCV and PCV values for days to heading and plant height.

Heritability and genetic advance. Heritability (h^2bs), genetic advance (GA) and genetic advance as percent of mean (GAM) estimates for characters under study are indicated in Table 4. The genotypic coefficient of variation (GCV) along with estimates of heritability provides reliable estimates of genetic advance to be expected through phenotypic selection (Burton, 1952). Classification of heritability values as high (>60%), moderate (30-60%) and values less than 30% low was done by Robinson *et al.* (1949).

From the present investigation results indicated that high heritability values were observed for all the studied characters. Estimates of heritability high for these characters indicated that the variation observed was under genetic control and have less effects of the environment and this gives possibility of progress from selection. Prasad *et al*. (2020) observed higher heritability value for the characters namely plant height, days to flowering, number of tillers per plant, grain yield/plant and number of grains/spike. Further, Kumar *et al.* (2013); Kumar *et al*. (2020) observed high estimates of heritability for grain yield per plant, number of spikelets/spike, plant height and 1000 grain weight and number of tillers/plant.

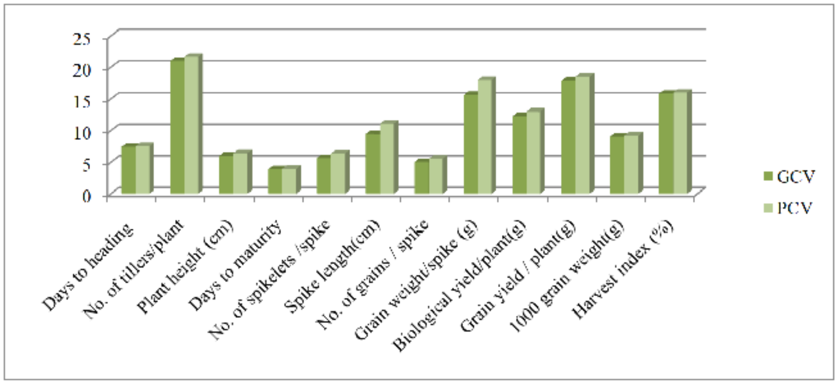
The expression of expected genetic advance as a percentage of the mean by selecting the top 5% of the bread wheat advanced genotypes ranged from 7.89% for days to maturity to 42.04% for number of tillers per plant (Table 4). It indicated that selecting the top 5% of the base population could have the advancement of 7.89 to 42.04 percent over the respective population mean. Genetic advance as percentage of mean was maximum for number of tillers per plant (42.04%) followed by grain yield per plant (35.69%) and harvest index (32.26%).

High heritability associated with high genetic advance were observed for number of tillers per plant (94.10%, 42.04%), grain yield per plant (93.30%, 35.69%), harvest index (97.90%, 32.26%) and biological yield per plant (90.0%, 24.07%), respectively. The results were reported in the earlier work done by Kalimullah *et al.* (2012); Kumar *et al*. (2020).

Table 1: ANOVA for grain yield and its components in bread wheat.

Source of variance	d.f.	Days to heading	No. of tillers/ plant	Plant height (cm)	Days to maturity	No. of spikelets /spike	Spike length (cm)	No. of grains /spike	Grain weight /spike (g)	Biological yield /plant(g)	Grain yield/ plant (g)	1000 grain weight (g)	Harvest index %
Replications	2	1.083	0.659	17.84**	2.120*	0.041	0.670	4.039*	0.006	0.232	0.210	2.15*	0.68
Treatments	35	92.14**	27.59**	89.34**	67.02**	3.75**	2.70**	19.30**	0.22**	98.46**	23.71**	56.84**	87.95**
Parents	7	121.99**	40.97**	39.29**	96.00**	5.35**	1.56**	16.09**	0.13**	30.10**	14.05**	58.62**	62.70**
F_1s	27	87.74**	18.60**	104.98**	61.96**	3.37**	2.42**	18.18**	0.25**	109.16**	25.50**	58.30**	97.60**
P *vs.* F_1s	1	2.149	176.71**	17.55*	0.765	2.93**	18.40**	71.89**	0.07	288.18**	43.04**	5.04**	4.30*
Error	70	0.75	0.56	3.61	0.64	0.31	0.30	1.23	0.02	3.51	0.55	0.46	0.62

*Significant at 5% level; **Significant at 1% level



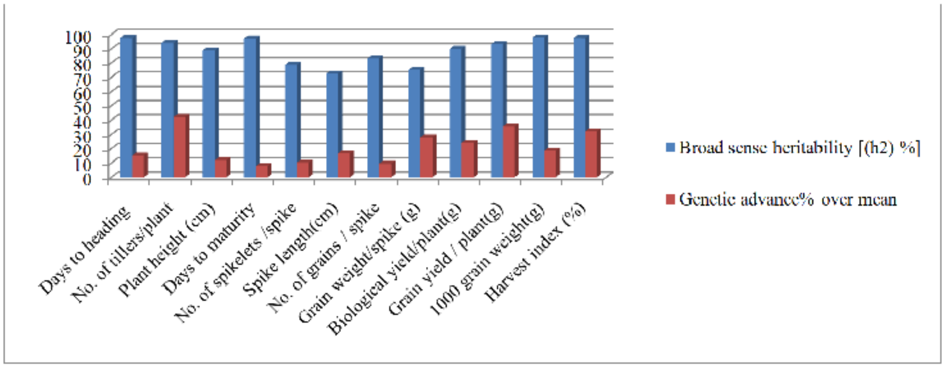
Graph 1: Graphical representation of Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV).

Table 2: Mean and range of parents and F_1s for twelve characters based on eight parents diallel in bread wheat.

Characters	General mean		Range			
			Parents		F_1s	
	Parents	F_1^s	Minimum	Maximum	Minimum	Maximum
Days to heading	74.12	74.46	65.33	82.67	67.00	87.67
No. of tillers / plant	11.87	14.95	6.70	18.17	9.43	19.63
Plant height (cm)	87.77	88.74	82.60	92.70	80.90	103.40
Days to maturity	121.00	121.20	111.0	129.67	112.33	130.33
No. of spikelets/spike	18.60	18.99	16.83	20.43	16.87	20.77
Spike length (cm)	8.69	9.68	7.80	10.00	8.30	11.23
No. of grains /spike	46.98	48.95	43.70	49.57	44.57	53.10
Weight of grain/ spike(g)	1.61	1.67	1.40	2.00	1.33	2.60
Biological yield /plant(g)	42.62	46.55	39.13	48.10	36.77	60.17
Grain yield / Plant (g)	14.31	15.83	12.47	18.70	10.93	22.40
1000 Grain weight (g)	47.46	47.98	41.07	54.60	41.07	56.53
Harvest index (%)	33.71	34.19	29.27	41.83	25.09	46.23

Table 3: Estimates of components of genetic variability for yield and its components in bread wheat.

Characters	Grand mean	GCV	PCV	Broad sense heritability [(h^2) %]	Genetics advance	Genetic advance % over mean
Days to heading	74.38	7.42	7.51	97.60	11.23	15.10
No. of tillers/plant	14.27	21.03	21.68	94.10	6.00	42.04
Plant height (cm)	88.25	6.04	6.41	88.80	10.38	11.72
Days to maturity	121.16	3.88	3.94	97.20	9.55	7.89
No. of spikelets /spike	18.91	5.67	6.39	78.60	1.96	10.35
Spike length(cm)	9.46	9.45	11.10	72.50	1.57	16.57
No. of grains / spike	48.51	5.06	5.55	83.10	4.61	9.50
Grain weight/spike (g)	1.66	15.65	18.05	75.10	0.46	27.93
Biological yield/plant(g)	45.68	12.31	12.98	90.00	11.00	24.07
Grain yield / plant(g)	15.49	17.93	18.56	93.30	5.53	35.69
1000 grain weight(g)	47.87	9.06	9.17	97.90	8.82	18.43
Harvest index (%)	34.09	15.83	16.00	97.60	11.00	32.26



Graph 2: Graphical representation of heritability in broad sense (h^2_{bs}) % and Genetic advance % over mean.

CONCLUSION

From this study it can be generally indicated that there was plenty of genetic variability among the genotypes. Thus, there is vast opportunity in the improvement these bread wheat genotypes. Therefore, the results and information generated from current study need to be used by interested plant breeders.

Studies revealed that the grain yield/plant, harvest index and number of tillers/plant with high heritability and high genetic advance followed by days to 50% heading, plant height, number of spikelets per spike, spike length, grain weight/spike and biological yield were the major yield attributing characters coupled with moderate genetic advance, so emphasis should be given for these characters at the time of simple selection.

FUTURE SCOPE

Through the studies of genetic variability, selection parameters the desirable genotypes for the improvement of yield and its contributing traits can be identified. The higher extent of genetic variability has found among the material used and it can be used further for the improvement of wheat crop by making improved varieties for doubling the production of wheat in the upcoming years. . However, the present results are only an indication and by which we cannot reach a definite conclusion. Since the experiment was carried out at one location and in one season, it is advisable to continue over several years and locations with this study.

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