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## Estimation of variability, heritability and genetic advance of yield contributing traits in bread wheat (*Triticum aestivum* L.)

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### Abstract

An experiment was conducted to study genetic variability, heritability and genetic advance in wheat population including 40 F<sub>1</sub>'s + 14 parents in RBD during Rabi 2020-22. ANOVA was performed with ten characteristics to test the significance of the differences between different treatments *viz.*, ten lines, four testers and forty F<sub>1</sub>s evaluated under two environments *i.e.* timely sown (E1), late sown (E2) and their pooled analysis. The result revealed that treatment mean sum of squares for all the ten characters was found highly significant in both the environments *i.e.*, E1 and E2 and in pooled analysis except number of effective tillers per plant in pooled estimate. On the other hand variances due to replications have been found insignificant for all the traits. The high estimates of PCV and GCV (>20%) were recorded for seed yield per plant in E2, whereas high PCV in pooled analysis. Whereas, moderate estimates (10-20%) of PCV and GCV observed in biological yield per plant in both E1, E2 and pooled, whereas number of effective tillers per plant, number of spikelets per spike and number of grains per spike in E2. The high estimates of heritability in broad sense (>75%) were found for days to 50 per cent flowering, days to maturity, plant height (cm), test weight (%) in both the environment, whereas biological yield per plant (g) and seed yield per plant (g) in E1 only. High genetic advance in per cent of mean (>20%) were recorded for seed yield per plant (g) in E1, E2 and Pooled estimates. High heritability coupled with high genetic advance in per cent of mean was found for seed yield per plant and biological yield per plant in both E1 and E2 environments, which in fact demonstrated the presence of additive gene effects indicating effectiveness of selection for improvement of these traits.

**Keywords:** Genetic variability, PCV, GCV, heritability and genetic advance

### Introduction

Wheat (*Triticum aestivum* L.; 2n=42) is a self-pollinated crop belong to *Poaceae* family and one of the most leading cereal of the world including India. It is the most important food crop of India and is a main source of protein and energy. In India, wheat is the second most important food crop after rice both in terms of area and production. Although wheat production in India during 2019-20 has made a landmark achievement but the data displayed the yield stability, which may become a major constraint in upcoming years for food security. The world population increasing day by day and climatic conditions are going to be adverse for crop production; this will present an alarming situation of food security in upcoming years. Thus researchers must have to set a goal to boost up the crop productivity as well as production of wheat by employing recent technologies and to breed high yielding varieties to feed the burgeoning population effectively. Thus, keeping in the view of future goal researchers must have to develop high yielding wheat varieties which confer resistance to various biotic and abiotic stresses. Timely sown wheat matures in the march, its reproductive growth phase met with the temperature as required for proper growth and development. Whereas, late sowing of wheat is done in mid to last week of October, due to that there is sufficient reduction in time for reproductive growth and development has been noticed. Late sown wheat faces high temperature stress during its reproductive growth phase. Heat stress affects wheat at various stages at flowering, grain filling and maturation of grains are drastically affected that cause significant reduction seed weight with shriveled seed shape and yield. The wheat breeders are concentrating to improve and maintain the yield potential of wheat by developing new varieties with desirable genetic makeup in order to overcome the biotic and abiotic stress. This can be achieved by using genetic potential and genetic variability present for traits in the available germplasm. High heritability associated with high genetic advance for quantitative traits in wheat offer better chance to select the genotypes in early

segregating generations. Hence in present investigation an attempt was made to assess the variability on grain yield and biological yield contributing traits which indicating genetic variability *i.e.* genotypic coefficient variation (GCA), phenotypic coefficient variation (PCV), environment coefficient variation (ECV), heritability in broad sense ( $h^2_{bs}$ ), genetic advance (GA) in percent of mean.

### Method and Materials

The experimental material consisted of 54 treatments including 40  $F_1$ 's + 14 parents and conducted at Student's Instructional Farm of School of Agriculture, Career Point University Kota Rajasthan during Rabi, 2020-22 in RBD with three replications. Each line was grown in one row of 4 meter length. Row to row and plant-to-plant spacing was 30cm and 10cm, respectively. Data were recorded on five randomly selected plants for plant height (cm), number of effective tillers per plant, number of spikelet's per spike, number of grains per spike, 1000-grain weight (g), biological yield per plant (g), seed yield per plant (g), harvest index (%) except days to 50% flowering and days to maturity which were recorded on plot basis. Data recorded on above quantitative traits were subjected to statistical analysis following analysis of variances, Sukhatme (1967), heritability in broad sense ( $H_{bs}$ ) and genetic advance (GA) (Robinson *et al.*, 1949) [12].

### Results and Discussion

Analysis of variance for the design of experiments was performed with ten characteristics to test the significance of the differences between different treatments *viz.*, ten lines, four testers and forty  $F_1$ s evaluated under two environments *i.e.* timely sown (E1), late sown (E2) and their pooled analysis (Table 1.) revealed that mean squares due to treatments were highly significant for all the ten characters studied in both the environments *i.e.*, E1 and E2 and in pooled analysis except number of effective tillers per plant in pooled estimate. On the other hand variances due to replications have been found insignificant for all the characters in both the environments and pooled estimates. These findings were in conformity with finding of Govind *et al.* (2015) [4], Singh *et al.* (2020) [11], Prasad *et al.* (2020) [10], and Kumar *et al.* (2022) [16]. The existence of genetic variability in the population provides ample opportunities for selection being effective. The pool of genotypes was therefore, assessed for variability analysis. The existence of wide diversity among the constituent genotypes with regard to characters under study was confirmed through various statistical parameters.

The estimates of mean, range, variability, heritability (Broad sense) and genetic advance in per cent of mean for E1, E2 and pooled analysis is presented in Table2. The seed yield per plant among parents in E1 ranged from 6.47g (KRL 99, LOK 1) to 8.63g (HD 2967); in E2 from 5.12g (UP 2338) to 6.54g (HD 2967) and in pooled analysis from 5.94g (LOK 1) to 8.53g (HD 2967). Among the crosses, the lowest seed yield per plant 8.18g was produced by the cross combination (KRL 99 X Raj 3765) and its highest value 12.63g was exhibited by the cross combination (HD 2824 X PBW 550) in E1 and in E2 the lowest seed yield per plant 6.12g produced by the cross combination LOK 1 X HD 3226 and its highest value 11.53g was found for the cross combination NW 2036 X PBW 550, whereas in pooled analysis it ranged from 7.35g (KRL 99 X HD 3226) to 11.00g (HD 2824 X Raj 3765). These findings were in conformity with finding of Meena *et al.* (2014) [3],

Pavan *et al.* (2018) [8], Varsha *et al.* (2019) [9], Adnan *et al.* (2021) [12]. The grand mean ( $9.37 \pm 0.27$ ) was more than the parents mean (7.36) and less than the cross mean (10.07) in E1; in E2 grand mean ( $7.76 \pm 0.65$ ) was more than the parent mean (5.68) and less than cross mean (8.50). Whereas, the pooled grand mean value ( $8.58 \pm 0.53$ ) was found in between the mean of the parents (6.63) and crosses (9.27). The high estimates of phenotypic and genotypic coefficient of variation ( $>20\%$ ) were recorded for seed yield per plant in E2, whereas high phenotypic coefficient of variation in pooled analysis. The characters which exhibited moderate estimates (10-20%) of PCV and GCV were biological yield per plant in both E1, E2 and pooled, whereas number of effective tillers per plant, number of spikelet's per spike and number of grains per spike in E2. Except aforesaid characters and remaining traits showed low estimates ( $<10\%$ ) of PCV and GCV in both environments. These findings were in conformity with finding of Meecha *et al.* (2016), Jain *et al.* (2017) [7], Kumar *et al.* (2017) [6], Pavan *et al.* (2018) [8], Singh *et al.* (2020) [11], Prasad *et al.* (2020) [10], Asha *et al.* (2022) [15] and Kumar *et al.* (2022) [16].

The high estimates of heritability in broad sense ( $>75\%$ ) were found for days to 50 per cent flowering, days to maturity, plant height (cm), test weight (%) in both the environment, whereas biological yield per plant (g) and seed yield per plant (g) in E1 only. The moderate estimates of heritability (50-75%) were found for number of spikelet's per spike, number of grains per spike in both the environments *viz.*, E1 and E2. Whereas, days to 50 per cent flowering days to maturity, plant height (cm), test weight (%) and seed yield (g) in pooled estimates. The low estimate of broad sense heritability was found for number of effective tillers per plant and harvest index (%) in E1, E2 and pooled estimates. Whereas, number of spikelet's per spike, grains per spike and seed yield per plant (g) in pooled estimate. High genetic advance in per cent of mean ( $>20\%$ ) were recorded for seed yield per plant (g) in E1, E2 and Pooled estimates, biological yield per plant (g) in E1 and E2, whereas number of effective tillers per plant in E2 only. Moderate estimates (10-20%) of genetic advance in per cent of mean were estimated for number of spikelet's per spike, number of grains per spike and plant height in both E1, E2 and pooled estimate, whereas days to 50 per cent flowering in both E1 and E2 and biological yield per plant in pooled estimate only. Low genetic advance in per cent of mean ( $<10\%$ ) were estimated for days to maturity, test weight and harvest index in E1, E2 and pooled estimate; Whereas, days to 50% flowering and number of effective tillers per plant in pooled estimate only. Similar finding were reported by Kumar *et al.* (2017) [6], Pavan *et al.* (2018) [8], Singh *et al.* (2020) [11], Prasad *et al.* (2020) [10], Asha *et al.* (2022) [15] and Kumar *et al.* (2022) [16]. High heritability coupled with high genetic advance in per cent of mean was found for seed yield per plant and biological yield per plant in both E1 and E2 environments. Whereas, high heritability coupled with moderate genetic advance in per cent of mean was recorded for days to 50 per cent flowering and plant height in both the environments. High heritability coupled with low genetic advance in per cent of mean was found for test weight in both the environments. Rest of the traits was found with moderate to low estimates of heritability in broad sense and genetic advance per cent of mean and vice-versa. Similar finding were reported by Meecha *et al.* (2016), Jain *et al.* (2017) [7], Kumar *et al.* (2017) [6], Pavan *et al.* (2018) [8], Singh *et al.*

(2020) [11], Prasad *et al.* (2020) [10], Seyoum and Sisay (2021) [13], Asha *et al.* (2022) [15], Sharma *et al.* (2022) [14] and Kumar *et al.* (2022) [16]. High or low heritability coupled with low genetic advance in per cent of mean, demonstrated the presence of additive gene effects indicating effectiveness of selection for improvement of these traits. High to medium

values of heritability estimates were found associated with moderate expected and actual gain in the most traits. These obtained results indicated that, these traits could be used in the early generation, but would be more effective if postponed to late generation (Kaumber and Gammaal, 2012) [17].

**Table 1:** Analysis of variance for randomized block design for 10 characters in Wheat under timely sown (E1), late sown (E2) and pooled analysis

Characters df	Sources of variation								
	Replications			Treatments			Error		
	2			53			106		
	E1	E2	Pooled	E1	E2	Pooled	E1	E2	Pooled
Days to 50% flowering	12.52*	1.17	10.00	70.55**	61.82**	93.88**	2.16	1.62	9.80
Days to maturity	0.45	0.82	0.05	27.01**	26.25**	38.72**	1.98	0.83	4.82
Plant height (cm)	9.51	2.26	7.63	158.57**	140.19**	196.62**	3.04	82.78	24.16
Number of effective tillers per plant	1.41	0.15	1.12	1.11**	2.18**	1.60	1.09	0.63	1.02
Number of spikelet's per spike	1.93	2.15	3.86	10.14**	8.19**	12.51**	1.58	1.17	2.21
Number of grains per spike	13.36	16.78	28.49	71.64**	73.70**	99.13**	11.75	10.20	17.66
1000-grain weight (Test Weight) (g)	0.02	0.27	0.11	4.83**	4.51**	6.62**	0.34	0.40	0.80
Biological yield per plant (g)	4.18	0.47	3.84	32.83**	35.35**	46.07**	1.78	4.24	6.65
Harvest index (%)	1.34	22.29	6.70	7.61*	25.29**	17.82**	3.81	6.74	6.97
Grain yield per plant (g)	0.71	0.66	0.83	7.21**	11.68**	12.86**	0.22	1.28	1.75

\*,\*\* Significant at 5% and 1% probability levels, respectively

**Table 2:** General Mean, range, coefficient of variation, heritability and genetic advance for 10 characters in wheat in timely, late sown environments and in pooled analysis

Characters		General mean ±SE	Range		Coefficient of Variation (%)		Heritability in Broad sense (%)	Genetic advance in per cent of mean
			Parents	Crosses	Phenotypic	Genotypic		
Days to 50% flowering	E1	90.02±0.84	85.00-101.33	81.67-95.33	5.54	5.30	91.30	10.44
	E2	78.87±0.73	77.67-87.00	71.00-85.33	5.90	5.68	92.50	11.25
	Pooled	84.50±1.26	81.00-92.83	77.83-89.83	5.77	4.43	58.80	7.00
Days to maturity	E1	122.31±0.80	121.00-129.00	117.00-127.00	2.63	2.36	80.80	4.37
	E2	112.69±0.52	112.67-118.00	107.33-117.33	2.71	2.58	91.10	5.08
	Pooled	117.57±0.89	117.17-123.17	112.67-124.00	2.75	2.02	53.90	3.06
Plant height (cm)	E1	83.02±1.00	70.60-103.30	69.70-96.97	8.92	8.67	94.50	17.36
	E2	71.34±0.74	59.10-89.93	58.50-85.37	9.70	9.52	96.50	19.27
	Pooled	77.26±1.99	70.62-92.00	67.10-89.00	9.41	6.94	54.30	10.54
Number of effective tillers per plant	E1	4.46±0.60	3.33-5.00	3.67-6.00	23.56	4.39	33.00	2.17
	E2	4.38±0.45	2.67-4.33	3.33-6.00	24.41	16.43	45.30	22.78
	Pooled	4.43±0.41	3.33-4.83	3.67-5.50	23.90	6.98	28.50	6.20
Number of spikelet's per spike	E1	17.03±0.72	14.00-17.00	15.00-20.67	12.36	9.92	64.40	16.39
	E2	14.23±0.62	11.67-13.33	12.33-17.67	13.17	10.45	66.60	18.06
	Pooled	15.66±0.60	12.83-15.83	14.33-18.17	12.67	8.37	43.70	11.93
Number of grains per spike	E1	47.09±1.96	38.00-47.67	41.00-56.33	11.96	9.49	63.00	15.51
	E2	40.12±1.82	32.00-37.67	34.67-50.67	13.96	11.45	67.50	19.40
	Pooled	43.69±1.70	35.00-44.67	39.83-50.00	12.79	8.43	43.50	11.45
1000-grain weight (Test Weight) (g)	E1	40.70±0.33	38.86-41.88	38.78-43.00	3.33	3.00	81.40	5.59
	E2	40.18±0.36	38.13-41.31	38.22-42.41	3.31	2.91	77.40	5.28
	Pooled	40.45±0.36	38.84-40.74	38.78-42.53	3.29	2.43	54.80	3.71
Biological yield per plant (g)	E1	21.23±0.76	15.03-18.74	18.37-26.70	16.41	15.15	85.30	28.83
	E2	17.48±1.18	13.17-15.47	14.50-24.17	21.86	18.42	71.00	31.98
	Pooled	19.38±1.04	14.15-18.49	16.78-23.87	18.76	13.22	49.70	19.20
Harvest index (%)	E1	44.14±1.12	42.33-45.98	39.46-47.79	5.11	2.55	24.80	2.61
	E2	43.88±1.48	37.30-42.53	41.42-48.14	8.19	5.67	47.80	8.08
	Pooled	44.05±1.07	40.56-46.12	40.44-46.82	6.72	3.05	20.60	2.86
Grain yield per plant (g)	E1	9.37±0.27	6.47-8.63	8.18-12.63	17.06	16.29	91.20	32.05
	E2	7.76±0.65	5.12-6.54	6.12-11.53	28.07	23.98	73.00	42.20
	Pooled	8.58±0.53	5.94-8.53	7.35-11.00	22.11	15.86	51.50	23.44

**Conclusion**

It is concluded from the above results that there is sufficient genetic variability in the materials studied. The magnitude of PCV as expected was greater than the corresponding GCV for

all the characters indicating importance of environment in expression of characters. High heritability coupled with high estimate of genetic advance in per cent of mean was observed for seed yield per plant and biological yield per plant in both

E1 and E2 environments indicates that most likely the heritable is due to the primacy of additive gene effects and potential of selection for those characters to improve the seed yield. It is apparent that seed yield and biological yield in wheat can be improved by selection of such genotype having more number of effective tillers per plant, number of spikelet's per spike, number of grains per spike, 1000-grain weight (Test weight) (g) and biological yield per plant (g).

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