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Comprehensive Assessment of Variability, Heritability and Genetic Advance for Quantitative Characters in Bread Wheat (*Triticum aestivum* L.)

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ABSTRACT: Assessment of the variability, heritability and genetic advance in the wheat genotypes (*Triticum aestivum* L.) is most significant role in the plant breeding because, analysis of these parameters in selected genotypes has not been made earlier so to use these genotypes for breeding programme it require a proper study about these characters. So all these requirement intrigued me to study about these parameters in respected genotypes. The present field experiment was conducted at the CRC of SVP University of Agriculture and Technology, Meerut (Uttar Pradesh) India during *Rabi* 2019-20 and 2020-21 for attempting of crossing programme in a line × tester (10 lines × 4 tester). The experimentation covering 54 genotype was arranged in Randomized Block Design with three replications. The assessment of mean sum square, mean and range performance value of parent and f_1, coefficient of variation (PCV and GCV), heritability and genetic advance. Analysis of variance the 'F' test indicated that mean squares for all the characters were highly significant for all traits under study. The mean and range performance of wheat genotype for twelve characters present very wide range of variation was observed. The percentage PCV was greater than the percentage of GCV for all of the characteristics studied in this study. In context high heritability coupled with high genetic advance (GA) as per cent of mean was apparent for the characters like grain yield per plant and number of productive tiller per plant, while high heritability is associated with moderate genetic advance for biological yield per plant. Moderate heritability is associated with moderate genetic advance (GA) for harvest index and moderate heritability is associated with low genetic advance for 1000 grain weight, length of peduncle, grain per spike, plant height and days to 50% flowering. In the present study, outcomes based on high variability and high heritability coupled with high genetic advance for quantitative traits can be used for further improvements of yields and its related traits, through ideal breeding scheme.

Keywords: Variability, Heritability, Genetic Advance and Wheat.

INTRODUCTION

Wheat (*Triticum aestivum* L) refers to the genus *Triticum* of the Poaceae (Gramineae) family coining from the Levant region of the Near East and Ethiopian Highlands, but now cultivated worldwide. The three species of wheat explicit *Triticum aestivum* L2n = 42(bread wheat), *Triticum durum* 2n=28 (pasta wheat or macaroni wheat) and *Triticum dicoccum 2n=28* (Emmer or Khapli wheat) grown on economic basis in the Indian landmass from primitive times with allocation of production in percent 95%, 4% and 1% respectively, are being cultivated in the country. It is a autogamous crop and grown yearly plant having height about 60 to 150 cm long. Inflorescence of wheat is erect terminal spike of spikelet's called as ear or head of grains, flower clustered into 15-20 spikelet's organised alternatively on rachis, each spikelet's with 2-6 flowers out of which only 2-3 flowers are fertile and yield grains. Wheat grain be made up of 3 % germ, 17 % bran (outer layers of wheat grain) and 85 % mealy endosperm on dry matter basis (Prasad *et al.*, 2000).

MATERIALS AND METHODS

The present field experiment was conducted at the CRC of Sardar Vallabhbhi Patel University of Agriculture and Technology, Meerut (Uttar Pradesh) India during *Rabi* 2019-20 and 2020-21 for attempting of crossing programme in a line × tester (10 lines × 4 tester). The testing comprising 54 genotype was laid out in Randomized Block Design with three replications. Experimental material constituted of 54 wheat genotypes (Table 1). The spacing between rows was 22.5 cm, respectively maintained by thinning. Five economical plants from each plot were randomly selected for recording observations for all the quantitative characters excluding days to flowering and days to maturity which were recorded on the experimental site basis. The Data were recorded for twelve characters namely, days to 50% flowering (DF), days to maturity (DM), plant height per plant cm (PH), number of productive tillers per plant (PT), length of peduncle per plant cm (LP), spike length cm (SL), spikelets per spike (SS), number of grains per spike (GS), 1000 grain weight g (GW), biological yield per plant g (BY), harvest index % (HI) and grain yield per plant g (GY). The current studies that have discussed to work out analysis of variance Panse and Sukhatme (1967), estimate of genetic variability, heritability Kempthorne and Curnow (1961) and genetic advance Johnson *et al*. (1955).

RESULTS AND DISCUSSION

The estimate of mean sum square, mean and range performance value of parent and f_1, coefficient of variation (PCV and GCV), heritability and genetic advance. The significance of variance in treatments for different characters was shown by F test at 5% and 1% level of probability. The observed value of 'F' is compared with the table value 'F' for the error and treatment degree of freedom. If the observed value of 'F' is more than the value of table. It is considered to be significant and vice-versa. The mean sum of square value revealed in Table 2 Analysis of variance the 'F' test indicated that mean squares for all the characters were highly significant for all traits under study. These results are in accordance with report of Arya *et al.* (2018); Thapa *et al.* (2019); Prasad *et al.* (2021).

The mean and range performance of wheat genotype for twelve characters is presented in Table 3 Very wide range of variation in mean performance of genotypes was observed for all the 12 characters under study. A thorough study range value is observed days to 50% flowering (86.74-105.17), days to maturity (130.53-141.98), plant height per plant (85.33-104.98), number of productive tillers per plant (3.80-8.60), length of peduncle per plant (30.53-40.60), spike length (8.83-11.50), spikelets per spike (16.50-20.40), number of grains per spike (46.40-62.54), 1000 grain weight (31.37-47.33), biological yield per plant (29.67-40.67), harvest index (26.60-39.76) and grain yield per plant (8.33-15.50).

Table 1: List of parent and their F_1 hybrid.

Sr. No.	Parent	Sr. No.	F1 Hybrid	Sr. No.	F1 Hybrid
	Lines	17.	K9162 × HD3086	36.	UP2628 × PBW226
1.	K9162	18.	K9162 × WH1105	37.	UP2628 × HD3086
2.	HD3237	19.	HD3237 × WR544	38.	UP2628 × WH1105
3.	HD2177	20.	HD3237 × PBW226	39.	PBW373 × WR544
4.	UP1109	21.	HD3237 × HD3086	40.	PBW373 × PBW226
5.	RAJ3777	22.	HD3237 × WH1105	41.	PBW373 × HD3086
6.	UP2628	23.	HD2177 × WR544	42.	PBW373 × WH1105
7.	PBW373	24.	HD2177 × PBW226	43.	DBW187 × WR544
8.	DBW187	25.	HD2177 × HD3086	44.	DBW187 × PBW226
9.	NW5054	26.	HD2177 × WH1105	45.	DBW187 × HD3086
10.	PBW175	27.	UP1109 × WR544	46.	DBW187 × WH1105
	Tester	28.	UP1109 × PBW226	47.	NW5054 × WR544
11.	WR544	29.	UP1109 × HD3086	48.	NW5054 × PBW226
12.	PBW226	30.	UP1109 × WH 1105	49.	NW5054 × HD3086
13.	HD3086	31.	RAJ 3777 × WR544	50.	NW5054 × WH1105
14.	WH1105	32.	RAJ 3777 × PBW226	51.	PBW175 × WR544
	F1 Hybrid	33.	RAJ 3777 × HD3086	52.	PBW175 × PBW226
15.	K9162 × WR544	34.	RAJ 3777 × WH1105	53.	PBW175 × HD3086
16.	K9162 × PBW226	35.	UP2628 × WR544	54.	PBW175 × WH1105

Table 2: Mean sum of square of parent and hybrid for 12 characters in wheat.

Source of variation	Replication	Treatment	Error	Total
Degree of freedom	2	53	106	161
DF	5.68	26.08**	4.93	11.9
DM	1.19	16.69**	4.96	8.77
PH (cm)	11.12	60.62**	15.51	30.3
PT	0.03	2.88**	0.19	1.07
LP (cm)	3.15	14.30**	4.14	7.47
SL (cm)	0.14	2.03**	0.35	0.9
SS	0.13	2.96**	1.34	1.86
GS	9.18	25.73**	7.56	13.56
GW (g)	0.04	22.46**	6.29	11.54
BY (g)	5.11	20.14**	3.3	8.87
HI (%)	7.41	27.86**	6.13	13.3
GY (g)	0.55	8.49**	0.4	3.06

*, ** significant at 5% and 1% level, respectively

Table 3: Mean and range performance of wheat genotype for twelve characters.

Character	Mean	Minimum	Maximum
DF	93.26	86.74 (K9162 × HD3086)	105.17 (UP2628)
DM	134.96	130.53 (K9162 × HD3086)	141.95 (UP2628)
PH (cm)	94.38	85.33 (HD3086)	104.64 (PBW175 x WR544)
PT	6.86	3.80 (HD3086)	8.60 (RAJ3777 x WR544)
LP (cm)	36.50	30.53 (PBW175)	40.60 (PBW175 x WR544)
SL (cm)	10.27	8.83 (UP1109, RAJ3777)	11.50 (HD2177 x PBW226)
SS	18.49	16.50 (UP1109)	20.40 (HD3237 x HD3086)
GS	52.68	46.40 (UP1109)	62.54 (DBW187 x HD3086)
GW (g)	39.32	31.37 (WH1105)	47.33 (PBW175 x WH1105)
BY (g)	36.26	29.67 (HD2177)	40.67 (DBW187 x PBW226)
HI (%)	32.65	26.60 (K9162)	39.76 (UP1109 x PBW226)
GY (g)	11.86	8.33 (RAJ3777 × WR544)	15.50 (DBW187 x PBW226)

The percentage of Phenotypic coefficient of variation (PCV) was greater than the percentage of genotypic coefficient of variation (GCV) for all of the characteristics studied in this study. The phenotypic and genotypic coefficients of variation can be used to analyze and relate the kind and amount of variability present in breeding materials for various characteristics. The estimates of coefficient of variation for the twelve characters under study have been presented in Table 4. In the present study moderate phenotypic and genotypic coefficient of variation (PCV and GCV) was found for number of productive tiller per plant, grain yield per plant and moderate PCV found for harvest index. Similar results have also been reported by Bhushan *et al.* (2012); Yadawad *et al.* (2015). Low phenotypic coefficient of variation was found for harvest index while, all the remaining character found low PCV and GCV for spike length, biological yield per plant, 1000 grain weight, length of peduncle, grains per spike, plant height per plant, spikelet's per spike, days to 50 % flowering and days to maturity. The magnitude of phenotypic coefficient of variation was higher than genotypic coefficient of variation for the characters revealed higher degree of interaction of genotypes with the environment. These findings are in close agreement with the findings of earlier workers Kumar *et al.* (2014); Devesh *et al.* (2018); Imran *et al.* (2018); Singh *et al.* (2020).

The estimation of heritability and genetic advance values are presented in Table 4. The values for heritability estimates in broad sense were observed ranging from 28.74 % for the trait spikelet's per spike to 87.21% for grain yield per plant. Broad sense heritability estimates can be categorized as low (<40%), moderate (40-60%) and high (>60%). In present study, highest values for heritability were estimated for grain yield per plant (87.21%) followed by number of productive tiller per plant (82.84%), biological yield per plant (62.95%) and spike length (61.22%). Similar results have also been reported by Yadav *et al.* (2011); Bhushan *et al.* (2012); Kumar *et al.* (2014); Arya *et al.* (2018); Singh *et al.* (2020; Thapa *et al.* (2019); Porte *et al.* (2020); Yadav *et al.* (2021). Moderate value of heritability were observed for days to 50 % flowering (58.84%), harvest index (54.16%), plant height per plant (49.23%), 1000 grain weight (46.14%), length of peduncle (44.97%), grain per spike (44.49%) and days to maturity (44.11%). Similar results were also found by Singh *et al.* (2010) and the remaining traits such as spikelets per spike (28.74%) were observed to possess lower estimates of heritability.

Table 4: Estimate variability, heritability and genetic advance (% mean) for 12 characters in wheat.

Character	Heritability (%)	GA	GA% mean	Coefficient of variation (%)	
				GCV	PCV
DF	58.84	4.20	4.50	2.85	3.71
DM	44.11	2.71	2.01	1.47	2.21
PH (cm)	49.23	5.60	5.94	4.11	5.86
PT	82.84	1.78	25.90	13.81	15.18
LP (cm)	44.97	2.54	6.96	5.04	7.52
SL (cm)	61.22	1.20	11.73	7.27	9.30
SS	28.74	0.81	4.39	3.98	7.42
GS	44.49	3.38	6.42	4.67	7.00
GW (g)	46.14	3.25	8.26	5.90	8.69
BY (g)	62.95	3.87	10.68	6.53	8.24
HI (%)	54.16	4.08	12.50	8.24	11.20
GY (g)	87.21	3.16	26.65	13.85	14.84

The estimates for genetic advance as a percent of means were observed ranging from 2.01 for days to maturity to 26.65 for grain yield per plant. Genetic advance as a percent of mean can be categorized into 3 groups *viz.*, low (<10%), moderate (10-20%) and high (>20%). Accordingly, high estimates of genetic advance as a percent of means were observed for grain yield per plant (26.65%) followed by number of productive tiller per plant (25.90%). Similar results were also found by Arya *et al.* (2018) for grain yield per plant and Thapa *et al.* (2019) for number of productive tiller per plant whereas, moderate estimates of genetic advance as a percent of means were observed for harvest index (12.50%), spike length (11.73%), biological yield per plant (10.68%). Similar results were also found by Kumar *et al.* (2014) for harvest index, while all the remaining traits like 1000 grain weight (8.26%), length of peduncle (6.96%), grain per spike (6.42%), plant height per plant (5.94%), days to 50 % flowering (4.50%), spikelets per spike (4.39%) and days to maturity (2.01%) recorded the low estimates of genetic advance as percent of mean. Similar results were also found by Singh *et al.* (2010) for grain per spike and length of peduncle and Singh *et al.* (2020) for 1000 grain weight, length of peduncle.

In context beyond high heritability coupled with high genetic advance as per cent of mean was observed for the characters like grain yield per plant and number of productive tiller per plant, while high heritability is associated with moderate genetic advance for biological yield per plant. Almost similar findings were also reported by Yadav *et al.* (2011); Kumar *et al.* (2014); Arya *et al.* (2018); Yadav *et al.* (2021). Moderate heritability is associated with moderate genetic advance (GA) for harvest index and Moderate heritability is associated with low genetic advance for 1000 grain weight, length of peduncle, grain per spike, plant height and days to 50% flowering.

CONCLUSION

Analysis of variance the 'F' test indicated that mean squares for all the characters were highly significant witnessed along with very wide range value for all character consequently there is a noble scope for enhancement of the genotypes. The percentage of Phenotypic coefficient of variation (PCV) was greater than the percentage of genotypic coefficient of variation (GCV) for all of the characteristics studied in this study. The degree of percentage phenotypic coefficient of variation was higher than percentage genotypic coefficient of variation for the traits revealed favourable interference of genotypes with the environment.High heritability associated with high genetic advance, revealed that variation was mostly due to additive gene effects and selection may be effective. High heritability linked with high genetic advance was witnessed for grain yield per plant and number of productive tiller per plant. The above result obtain in the study is revealed sufficient amount of variability present among all genotypes and parameter like high heritability coupled with high genetic advance observed in grain yield per plant, number of productive tiller per plant in selected genotypes it could be a better parameters to improve a superior genotypes.

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Conflict of interest. None

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