Electronic Journal of Plant Breeding

Research Article

Studies of genetic variability, heritability and genetic advance in yield component traits in bread wheat (*Triticum aestivum* L.)

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Abstract

Thirty advanced lines of wheat obtained from Borlaug Institute for South Asia (BISA), Ludhiana, Punjab were evaluated in a randomized block design (RBD) with three replications for yield and its contributing characters at Agriculture Research Farm, Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Phagwara, Punjab, India during *rabi* 2021-2022. Genetic variability, heritability and genetic advance per cent of the mean, Analysis of variance were carried out for fourteen traits. The mean sum of square (MSS) due to genotypes was highly significant for all the fourteen traits. Analysis revealed that grain yield per plant exhibited the highest phenotypic coefficient of variation (PCV) followed by harvest index, the number of spikes per plant, the number of tillers per plant and biological yield per plant. Genotypic coefficient of variation (GCV) was found highest for grain yield per plant followed by harvest index, the number of spikes per plant, the number of tillers per plant and biological yield per plant. Very high heritability estimates were associated with high estimates of genetic advance for the number of tillers per plant, the number of spikes per plant, biological yield per plant, harvest index, grain yield per plant, chlorophyll content, and flag leaf area which revealed the presence of additive gene effects, showing the efficiency of selection for improving these attributes following breeding program for yield improvement in wheat.

Keywords: Genetic variability, PCV, GCV, bread wheat, heritability, genetic advance

INTRODUCTION

Wheat (*Triticum aestivum* L.) is the world's most important cereal and is one of the oldest crops which is domesticated around the world 10000 years ago. It is a self-pollinated cereal grass of the Poaceae family of the genus "Triticum". It has been dubbed the "King of Cereals" due to its large acreage, excellent production, and significant role in the world food grain trade. In contrast to maize and rice, which prefer tropical environments, it is widely produced in temperate countries. Wheat is the most important food crop for people all over the world, and holds the leading position in Indian agriculture, occupying 28 per cent of acreage under cereal and producing 33 per cent of the total food grain output in the country (Agarwal, 2014).

Wheat also provides vital amino acids, minerals, vitamins, beneficial phytochemicals, and dietary fibre to the human diet, with whole-grain products containing most of these. The nutritional content of 100 g of wheat (germ crude) is as follows: Vitamin E 22 mg, Niacin 45 mg, Thiamine 2.01 mg, Riboflavin 0.72 mg, Protein 26.7 g, Carbohydrate 44.7 g, Starch 28.7 g, Fat 9.2 g, Vitamin E 22 mg, Niacin 45 mg, Thiamine 2.01 mg, Riboflavin 0.72 mg (Yadav *et al.,* 2019). Nearly 60% of total wheat production is accounted by developing countries, leading to 20% of the total food calories intake of around 55% of the world population. Wheat output reached 107,860 thousand tonnes in 2020, making it the second-most-produced

crop behind maize (Anonymous, 2021). In India, primarily three species i.e., T*riticum aestivum*, T. *durum*, and T. *dicoccum* are grown, with respective areas of 95 per cent, 4 per cent, and 1 per cent respectively. Wheat contributes about 34% of the total food grain production of the country (Anonymous, 2021). India occupies the second position in both area and production, next to China in the world. Indian share in the world wheat area and production, is about 11.41% and 12.51%, respectively. Wheat is the only crop wherein, production increased more than sixfold, during the last forty years. Production of Wheat during 2020-21 is estimated at a record 108.75 million tonnes. It is higher by 8.32 million tonnes than the average wheat production of 100.42 million tonnes in India (Press Release). The large populations of human and livestock feeding best emphasize the significance of wheat. Around 2.5 billion of the population in the world "depends on wheat which is a key crop in India and around the world (CIMMYT, 2019). Wheat is cultivated in an area of 200.89 million ha, and more than 769.40 million tonnes of grain are produced yearly. Wheat is grown on 31.36 million acres of land in India alone, producing 107.91 million tonnes a year (USDA, 2021). The development of wheat breeding programmes is geared at identifying the ideal selection criteria. These programmes implement the genetically based selection strategy for grain yield and create cultivars that would yield more. Understanding the nature and extent of phenotypic and genotypic diversity in crop species is critical for developing an effective breeding program to generate improved cultivars. According to (Vavilov, 1951), the more diversity, the better the odds of getting good genotypes, which eventually proved to be the cornerstone for agricultural plant development through selection. The capacity to enhance any crop is mostly determined by the kind and extent of variability. A good breeding programme must thus have genetic variability in the germplasm. As a result, it is worthwhile to research estimates of germplasm variability. The evaluation of gene action might benefit from genetic advance and heritability assessment. The genetic advance that can be achieved by selection is indicated by the estimations of heritability, GCV, and genetic advance, and they also provide the knowledge that a breeder would require (Sharma *et al.,* 2021). The goal of the current study was to identify potential genotypes and the best traits of wheat germplasm to strengthen the ongoing breeding programmes by estimating the genetic variability, heritability, and genetic advance for different traits.

MATERIALS AND METHODS
The experimental design comprised of Thirty Advanced Lines (GS: Genomic Selection; ESWYT: Elite Spring Wheat Yield Trials and released varieties) of Wheat given in **Table 1**. These lines were obtained from CIMMYT/ Borlaug Institute for South Asia (BISA), Ludhiana, Punjab. All these lines were grown in three replications by using Randomized Block Design during *rabi* 2021-2022 at Agriculture Research Farm, Department of Genetics and

Plant Breeding, School of Agriculture, Lovely Professional University, Phagwara, Punjab. Each plot consisted of four rows of 2 m in length and 40 cm apart. The recommended packages of practices were adopted for optimum crop growth. The experimental area was quite uniform in respect of topography and fertility. Observations on yield and yield attributing characters were recorded, leaving border plants in each replication. In each plot, five randomly selected competitive plants were tagged to record observations except for days to 50% heading and days to maturity which were recorded on a plot basis. By taking the average, the mean value for the treatment was computed. Observations were recorded on days to 50% heading, days to maturity, plant height, the No. of tillers per plant, the No. of spikes per plant, Spike Length, the No. of spikelets per spike, the No. of grains per spike, 1000-grain weight, chlorophyll content, Flag leaf area, biological yield per plant, harvest index, grain yield per plant. The data acquired was subjected for Analysis of variance (Panse and Sukhatme, 1961), Heritability (Hanson *et. al.,* 1956), Genetic advance (Johnson *et. al.,* 1955) were estimated.

RESULTS AND DISCUSSION
The mean sum of square due to treatment was highly significant for all fourteen characters (**Table 2**). The mean sum of squares (MSS) due to genotypes were highly significant for all the characteristics at the 1% and 5% level of significance, indicating the presence of a large degree of genetic variability for all the features. The presence of genetic variability in the species gives chance for selection. As a result, the genotype pool was evaluated for variability analysis. Various statistical measures revealed the existence of great variability among the constituent genotypes in terms of the characters under consideration. Similar kind of results was also found by Shankarrao *et al.* (2010); Kumar *et al.*(2013); Gurjar *et al.*(2015); Mohanty *et al.* (2016); Sabit *et al.* (2017).

The highest estimates of PCV and GCV show that these traits have quantitative inheritance and are significantly affected by environmental influences. While low PCV and GCV estimations imply that they are less affected by environmental influences. In order to make inferences concerning these parameters, PCV and GCV estimations were classed as low (less than 10%), medium (10-20%), and high (more than 20%).

High Values of PCV were observed in grain yield per plant (30.77), Harvest Index (23.07), No. of Tillers per Plant (21.45), Number of Spikes per Plant (22.43). Moderate values of PCV were recorded in Spike Length (10.67), Flag Leaf Area (13.98), Biological Yield per Plant (16.5). Low Values of PCV were observed in Days to 50% Heading (2.93), Days to Maturity (3.63), Plant Height (4.23), the Number of Spikelets per Spike (6.28), the Number of Grains per Spike (6.65), 1000-Grain Weight (9.97), Chlorophyll Content (9.92). (**Table 3**)

Table 1. List of genotypes used in the study

S. No.	Name of Genotype	Pedigree
1	GS/2020-21/1009	BAJ#1×2/HUIRIVIS#1//KFA/2×KACHU
2	GS/2020-21/1016	KENYA SUNBIRD/KACHU//BORL14
3	GS/2020-21/1027	SHORTENEDSR26TRANSLOCATION//2×WBLL1×2/KKTS/3/BECARD/4/BORL14
4	GS/2020-21/1033	NELOKI//SOKOLL/EXCALIBUR
5	GS/2020-21/1045	PAURAQ/NELOKI/3/WBLL1×2/BRAMBLING×2//BAVIS
6	GS/2020-21/2007	BORL14×2/3/WBLL1×2/BRAMBLING×2//BAVIS
7	GS/2020-21/2008	BORL14×2/3/WBLL1×2/BRAMBLING×2//BAVIS
8	GS/2020-21/2012	BECARD#1/5/KIRITATI/4/2×SERI.1B×2/3/KAUZ×2/BOW//KAUZ×2/6/KACHU/KIRITATI
9	GS/2020-21/2015	BECARD#1/5/KIRITATI/4/2×SERI.1B×2/3/KAUZ×2/BOW//KAUZ×2/6/ND643/2×WBLL1/4/WHEAR/KUKUNA/3/C80.1/3×BATAVIA//2×WBLL1
10	GS/2020-21/2020	KACHU/DANPHE×2//MUNAL #1
11	GS/2020-21/2027	KACHU/DANPHE×2//KFA/2×KACHU
12	GS/2020-21/2031	KACHU/DANPHE×2/4/FRET2/TUKURU//FRET2/3/MUNAL #1
13	GS/2020-21/2056	KACHU/DANPHE×2//KENYA SUNBIRD/KACHU
14	GS/2020-21/3004	MUCUY×2//SUP152/BAJ #1
15	GS/2020-21/3009	SUP152/4/WHEAR/KIRITATI/3/C80.1/3×BATAVIA//2×WBLL1×2/6/PRL/2×PASTOR/4/CHIX/STAR/3/HE1/3×CNO79//2×SERI×2/5/CHONTE
16	GS/2020-21/3012	TUKURU//BAV92/RAYON/4/WHEAR/KUKUNA/3/C80.1/3×BATAVIA//2×WBLL1/5/MUTUS×2/HARIL#1/6/TUKURU//BAV92/RAYON/3/MUNAL #1
17	GS/2020-21/3016	WHEAR/KUKUNA/3/C80.1/3×BATAVIA//2×WBLL1/5/PRL/2×PASTOR/4/CHOIX/STAR/3/HE13×CNO79//2×SERI/6/FRNCLN/3/ND643//2×PRL/2×PASTOR/4/FRANCOLIN#1/7/WHEAR/KIRITATI/3/C80.1/3×BATAVIA//2×WBLL1/4/2×KACHU
18	GS/2020-21/3024	MUU/FRNCLN//FRANCOLIN #1×2/3/BORL14
19	GS/2020-21/3045	FRNCLN/3/KIRITATI//HUW234+LR34/PRINIA/4/FRANCOLIN#1×2/5/FRNCLN/3/ND643//2×PRL/2×PASTOR/4/FRANCOLIN #1
20	GS/2020-21/3046	WBLL1×2/BRAMBLING//NIINI#1/3/VILLAJUAREZF2009×2/4/KFA/2×KACHU
21	GS/2020-21/3049	WBLL1×2/BRAMBLING×2//BAVIS×2/3/BORL14
22	GS/2020-21/3050	WBLL1×2/BRAMBLING×2//BAVIS×2/3/KACHU #1/KIRITATI//KACHU
23	GS/2020-21/4001	SWSR22T.B./2×BLOUK#1//WBLL1×2/KURUKU/3/KACHU#1/KIRITATI//KACHU/4/SWSR22T.B./2×BLOUK #1//WBLL1×2/KURUKU
24	GS/2020-21/4004	TRCH×2/3/C80.1/3×QT4118//3×PASTOR/4/DANPHE×2/8/TOB/ERA//TOB/CNO67/3/PLO/4/VEE#5/5/KAUZ/6/FRET2/7/2×VORB
25	GS/2020-21/4009	YAR/AE.SQUARROSA(783)/4/GOV/AZ//MUS/3/SARA/5/MYNA/VUL//JUN/6/BECARD/7/BECARD/8/2×KUTZ
26	ESWYT/2020-21/110	ND643/2×WBLL1/4/WHEAR/KUKUNA/3/C80.1/3×BATAVIA//2×WBLL1/5/BORL14
27	ESWYT/2020-21/111	WBLL1×2/BRAMBLING×2//BAVIS/3/BORL14
28	HD - 2967	ALONDRA/CUCKOO//URES-81/HD-2160-M/HD-2278
29	HD - 3086	DBW14/HD2733//HUW 468
30	PBW - 343	NORD-DESPREZ/VG 1944//KALYANSONA//BLUEBIRD/3/YACO(SIB)/4/VEERY-5

Note: The use of the number sign (#) in the pedigree of some CIMMYT germplasm indicates that seed was bulked in that generation of the pedigree.

For all characteristics in each analysis, the phenotypic coefficient of variation was greater in magnitude than the genotypic coefficient of variation. As a result, these parameters were rendered unit free by calculating the phenotypic and genotypic coefficients of variation (GCV). Because GCV captures the heritable genetic component of the otal variation, it is very acceptable to utilize this metric to compare trait variability. This suggests that the observed variance is caused not just by genetics, but is affected by the environment (Singh and Narayan, 2017). Similar Kind of results were Found by Gurjar *et al.* (2015); Mohanty *et al.* (2016); Kumar *et al.* (2019); Barman *et al.* (2020); Devesh *et al.* (2021); Kumar *et al.* (2022).

Table 2. Mean sum of squares

Source of variation	d.f	Days to 50% heading	Days to maturity	Plant height	Number of tillers plant-1	Number of spikes plant-1	Spike length	Number of spikelets per spike
Replication	2	4.67	3.10	41.42	1.92	2.06	0.34	1.02
Genotypes	29	24.63**	80.10**	33.85**	7.49**	7.00**	2.89**	3.45**
Error	58	1.58	2.84	20.66	0.86	0.65	0.11	0.68
CV		1.28	1.18	5.72	12.58	11.83	3.60	4.81

Table 2. Continued.

Source of variation	d.f	Number of grains per spike	1000-grain weight	Chlorophyll content	Flag leaf area	Biological yield per plant	Harvest index	Grain yield per plant
Replication	2	7.44	31.88	10.37	6.71	9.47	7.45	0.25
Genotypes	29	29.62**	49.26**	54.61**	130.61**	68.50**	115.31**	17.36**
Error	58	6.13	12.17	4.53	3.42	7.80	9.37	1.08
CV		5.24	8.58	4.94	3.91	9.65	11.38	13.27

**=significant at 5% and 1% level of probability, NS = non-significant.

Table 3. Genetic parameters of variation for grain yield and its components in wheat

S.No.	Characters	Range		Mean	Co-Variance		Heritability broad sense (%)	Genetic advance	GA% mean
		Minimum	Maximum		GCV	PCV			
1.	Days to 50% heading	92.67	103.33	97.84	2.83	2.93	93.60	5.52	7.24
2.	Days to Maturity	131.00	151.00	142.20	3.57	3.63	96.40	10.27	9.25
3.	Plant Height (cm)	71.73	86.47	79.33	2.64	4.23	39.02	2.70	4.36
4.	Number of Tillers Plant-1	4.61	11.33	7.36	20.18	21.45	88.50	2.88	50.13
5.	Number of Spikes Plant-1	4.17	10.48	6.81	21.36	22.43	90.70	2.86	53.71
6.	Spike Length	7.07	11.20	9.21	10.47	10.67	96.20	1.95	27.11
7.	Number of spikelets per Spike	14.20	19.47	17.11	5.63	6.28	80.40	1.78	13.32
8.	Number of grains per Spike	38.53	53.87	47.22	5.93	6.65	79.30	5.13	13.93
9.	1000-grain weight (g)	32.50	46.80	40.62	8.65	9.97	75.30	6.28	19.82
10.	Chlorophyll Content	35.92	53.20	43.00	9.50	9.92	91.70	8.06	24.02
11.	Flag Leaf Area	37.36	61.99	47.21	13.79	13.98	97.40	13.24	35.93
12.	Biological yield per plant (g)	20.84	36.27	28.90	15.56	16.53	88.60	8.72	38.68
13.	Harvest index	16.28	42.01	26.88	22.11	23.07	91.90	11.73	55.95

The heritability estimates were classified as low (below 30%), medium (30% and 60%), high (60% and 80%), and very high (above 80%).

Very High heritability (above 80%) was observed for Days to 50% Heading (93.60 %), Days to Maturity (96.40 %), the No. of Tillers per Plant (88.50 %), the No. of Spikes per Plant (90.70 %), Spike Length (96.20 %), the No. of Spikelets per Spike (80.40 %), Chlorophyll Content (91.70 %), Flag Leaf Area (97.40 %), Biological Yield per Plant (88.60 %), Harvest Index (91.90 %), Grain Yield per Plant (93.80 %). High Heritability (above 60%) was observed for the No. of Grains per Spike (79.30 %),

1000 - Grain Weight (75.30 %). Low heritability was observed for Plant Height (39.02 %). Similar Kind of results were Found by Kumar *et al.* (2013); Gurjar *et al.* (2015); Rajput, (2018); Singh *et al.* (2021); Prabha *et al.* (2022); Kumar *et al.*(2022). While genetic advance estimates have been broadly characterized as low (below 10%), medium (10-20%), and high (above 20%).

The highest genetic advance as a percentage of mean (above 20%) (at 1% selection intensity) was recorded for the Number of tillers per plant (50.13), the Number of Spike per plant (53.71), Spike Length (27.10), Flag leaf Area (35.93), Biological yield per plant (38.67),

Harvest Index (55.94), Grain Yield per plant (76.19), Chlorophyll content (24.02). The Medium genetic advance as a percentage of mean (above 10%) (at 1% selection intensity) was recorded for the No. of Spikelets per spike (13.31), the No. of Grains per Spike (13.93), 1000 - Grain weight (19.82). Low genetic advance as a percentage of mean (below 10%) was recorded for Days to 50% heading (7.23), Days to Maturity (9.25), Plant Height (4.36). Similar Kind of results were Found by Shankarrao *et al.* (2010); Singh *et al.* (2012); Bhushan *et al.* (2013); Gurjar *et al.* (2015); Rajput*,* (2018); Prabha *et al.* (2022); Kumar *et al.* (2022).

High heritability estimates along with high estimates of genetic advance for the number of tillers per plant, the number of spikes per plant, biological yield per plant, harvest index, grain yield per plant, chlorophyll content, and flag leaf area. High or moderate heritability in combination with high or moderate genetic advance indicates the presence of additive gene effects in the inheritance of responsible traits, and selection may be effective in this case, 50% heading, days to maturity, plant height, Spike Length, the No. of spikelets per spike, the No. of grains per spike, 1000-grain weight. Moderate heritability in combination with low genetic advance indicates the presence of non-additive gene effects, and selection for these traits may be ineffective.

The present study reveals that there is considerable genetic variability among the Thirty advanced lines of wheat. High Values of PCV than GCV were observed in grain yield per plant, Harvest Index, the Number of Tillers per Plant, the Number of Spikes per Plant. High heritability estimates along with high estimates of genetic advance were recorded for the number of tillers per plant, the number of spikes per plant, biological yield per plant, harvest index, grain yield per plant, chlorophyll content, and flag leaf area which suggests the presence of additive gene effects, showing the better response of selection for improving these traits. The advanced lines GS/2020-21/2020, GS/2020-21/1033, GS/2020-21/1027, GS/2020 21/2015 were identified as potential genotypes for advancement and its utilization in the ongoing breeding programme.

ACKNOWLEDGEMENT

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