



Genetic Variability and Selection Parameters for Yield and Its Contributing Traits in Bread Wheat (*Triticum aestivum* L. em. Thell)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/IJPSS/2024/v36i54522

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://www.sdiarticle5.com/review-history/114694>

Original Research Article

Received: 11/01/2024

Accepted: 15/03/2024

Published: 26/03/2024

ABSTRACT

Ten bread wheat genotype and their all possible cross combinations excluding their reciprocals (10 parents+45 F₁s+45 F₂s) were evaluated in a randomized block design with three replications during Rabi 2022-2023 at Student's Instructional Farm, C. S. Azad University of Agriculture and Technology-208002, Kanpur, U.P to get the extent of variability and related parameters to select effectively for grain yield and quality character. It is the big challenge for researchers to get high grain yield with high protein. The data was recorded on fourteen characters viz., days to heading (50%), days to maturity, plant height (cm), number of productive tillers per plant, chlorophyll content, spike length (cm), number of spikelets per spike, number of grains per spike, weight of

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grain per spike (g), 1000 grain weight (g), biological yield (g), harvest index (%), protein content (%) and grain yield per plant (g). The variability among parents was highest for days to maturity it ranged from 117.33 to 137.67 with the mean value 126.60. The variation in F₁ progenies was highest for plant height ranged from 85.97 to 120.53 with the mean value of 96.71. The variation in F₂ progenies was highest for plant height ranged from 83.70 to 120.20 with the mean value of 94.99. The result showed higher estimated values for phenotypic coefficient of variability (PCV) of all the fourteen characters as compared to their corresponding genotypic coefficient of variability (GCV). Highest value of PCV and GCV were noted for grain yield per plant in both generation F₁s and F₂s except GCV were observed for none of the character F₁s. High heritability estimates were recorded for all characters in both generation F₁s and F₂s. High genetic gain was observed for grain yield per plant followed by biological yield per plant in both generation F₁s and F₂s.

Keywords: Variability; heritability; genetic advance mean and range; grain yield; plant height; genetic gain; genotypic; biological yield; genetic evaluation; morphological diverse.

1. INTRODUCTION

“Wheat (*Triticum aestivum* L.) is one of the most important cereal crop grown in different environments due to its versatile nature over the world. At global level, it's cultivated over 219.15 million ha and production of 808.44 million tons with an average productivity of 36.88 quintals per hectare. In India, it is grown in area of 30.45 million hectares with a production of 107.74 million tons and productivity of 35.37 quintals per hectare” [1]. “Wheat is grown under diverse agro-climatic conditions leading to wide fluctuation in productivity from region to region. Wheat is used for both human and animal nutrition and plays an important role in the nutrition of rapidly growing populations both in our country and the world. A number of biometrical techniques are extensively used for genetic evaluation of plants. Out of them, diallel, partial diallel and line X tester analyses have been frequently used by breeders for genetic study because they provide more genetic information about the material studied. Wheat has been playing an important role in the economy of several countries. The present study was based on fourteen quantitative characters measured on ten genotypes 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 help in identification of high yielding genotypes with better quality. In crop improvement only the genetic components of variation are important because this is the only component which transmits to the next generation. Heritability is an important parameter in the selection process as it determines the response to selection. Estimates of heritability

(narrow sense) and genetic advance for 14 characters in both generations F₁s and F₂s. Heritability is used by plant breeders to enhance the precision of single field trial and /or of series of trials” [2]. Estimates of genetic advance in per cent over mean various range in both generations F₁s and F₂s. Study of the estimates of heritability with genetic advance is more meaningful and reliable than considering the parameters individually [3,4].

2. MATERIALS AND METHODS

Ten genetically diverse genotypes were crossed in all possible combinations excluding reciprocal during Rabi 2022-23 at Student's Instructional Farm, C. S. Azad University of Agriculture & Technology, Kanpur-208002 U.P. Basic material consisting of ten morphological diverse genotypes viz., HD 2733, DBW 187, DBW 222, HD 3086, HUW 666, K 1317, KRL 19, HI 1563, DBW 14 and K 9423. The salient features of these parental genotypes are given in Table-1.

The genotype parents were sown in a randomized complete block design (RCBD) with three replication where each replication, there were 145 rows in three tiers. Parents and F₁s were sown of single row while F₂s were sown in two row plots. The length of each line was 3 meter with row to row spacing of 22.5 cm and plant to plant spacing of 10 cm. All the recommended agronomical practices were adopted to raise the crop. For fourteen characters viz., days to heading (50%), days to maturity, plant height (cm), number of productive tillers per plant, chlorophyll content, spike length (cm), number of spikelets per spike, number of grains per spike, weight of grain per spike (g), 1000 grain weight (g), biological yield (g), harvest index (%), protein content (%) and grain

Table 1. Salient features of parental genotypes

Sr. No.	Name of Parents	Pedigree	Salient feature	Origin place
1.	HD 2733	ATTILA/3/TUI/CARC//CHEN/CHTO/4/ATTILA	Resistance to brown rust and tolerant to leaf blight.	IARI, N. Delhi
2.	DBW 187	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/KACHU/6/KACHU	Good biscuit spread factor (8.6cm), High Fe content (43.1 ppm), resistance to yellow and brown rust	IIWBR, Karnal
3.	DBW 222	KACHU/SAUAL/8/ATTILA*2/PBW65/6/PVN//CAR422/ANA/5/BOW/CROW//BUC/PVN/3/YR/4/TRAP#1/7/ATTILA/2*PASTOR	Resistant for stripe and leaf rust; Highly resistant to Karnal bunt (9.1%) and loose smut (4.9%).Chapatti quality score (7.5/10).	IIWBR, Karnal
4.	HD 3086	DBW 14/ HD 2733/HUW 468	Resistance to yellow and brown rust	IARI, N. Delhi
5.	HUW 666	-	Drought tolerance	BHU, Varanasi
6.	K1317	K 0307/K9162	Resistant to brown rust and leaf blight. Good Chapatti quality	CSAUA&T, Kanpur
7.	KRL 19	PBW 255/KRL 1-4	Salt affected Wheat Varieties Also suitable for water logging area and tolerant to yellow and brown rust	CSSRI, Karnal
8.	HI 1563	MACS 9496*2/MC10	Resistance to all the pathotypes of the three rusts at seedling stage	IARI, RS, Indore
9.	DBW 14	RAJ 3765/PBW 343	Tolerant to leaf blight	IIWBR, Karnal
10.	K 9423	HP1633/KAL/UP262	Tolerance to heat at grain development stage	CSAUA&T, Kanpur

yield per plant (g) observation were recorded from the five randomly selected plants from each genotype HD 3086 bread wheat variety of this region were used as 'check varieties' in this experiment.

2.1 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 [5].

$$GCV = \frac{\sqrt{V_g}}{\bar{X}} \times 100$$

Where,

V_g = Genotypic variance, and
 \bar{X} = Germplasm mean

$$PCV = \frac{\sqrt{V_p}}{\bar{X}} \times 100$$

Where,

V_p = phenotypic variance, and
 \bar{X} = Germplasm mean

2.2 Heritability (in narrow sense)

in F_1 generation was calculated by the formula proposed by Crumpacker and Allard [6], which is as follows:

$$\hat{h}^2 = \frac{\left(\frac{1}{4}\right)_D^{\wedge}}{\left(\frac{1}{4}\right)_D^{\wedge} + \left(\frac{1}{4}\right)_{H_1}^{\wedge} - \left(\frac{1}{4}\right)_F^{\wedge} + \left(\frac{1}{4}\right)_E^{\wedge}}$$

2.3 Heritability

in F_2 generation was calculated according to the methodology proposed by Verhalen and Murray [7].

$$\hat{h}^2 = \frac{\left(\frac{1}{4}\right)_D^{\wedge}}{\left(\frac{1}{4}\right)_D^{\wedge} + \left(\frac{1}{16}\right)_{H_1}^{\wedge} - \left(\frac{1}{8}\right)_F^{\wedge} + \left(\frac{1}{8}\right)_E^{\wedge}}$$

Heritability (in per cent) = Heritability coefficient $\left(\hat{h}^2\right) \times 100$

Where,

\hat{h}^2 = estimate of heritability coefficient
 and \hat{D} , \hat{H}_1 , \hat{F} and \hat{E} are the

2.4 Genetic Advance

The calculation of the estimates of genetic advance was done according to the formula given by Robinson et al. [8].

$$GA = (k) \left(\hat{h}^2\right) (\delta_{ph})$$

and genetic advance over mean of the character

$$GA (\%) = \frac{GA}{\bar{X}} \times 100$$

Where,

GA = estimate of genetic advance
 K = selection differential at 5% selection intensity, i.e., 2.06
 σ_{ph} = phenotypic standard deviation
 \hat{h}^2 = estimate of heritability coefficient (broad sense)
 \bar{X} = mean of the character concerned

3. RESULTS AND DISCUSSION

A. Analysis of Variance (ANOVA)

The analyses of variance (ANOVA) for parents + F_1 s and parents + F_2 s for all the fourteen characters are presented in Table-2 and Table-3.

In case of Table-2, highly significant differences were observed among the parents for all the 14 characters. Similarly, highly significant differences were found among F_1 s for all the 14 traits. It was indicated significant variability in the base material as well as the material generated subsequently, involved all possible combinations except reciprocal cross. Highly significant differences were noted among parents vs. F_1 s for all characters except for days to 50% heading, chlorophyll content and weight of grain per spike which reflected significant amount of heterotic response in these attributes [9,10].

In case of Table-3, highly significant differences were observed among the parents and F_2 s for all the attributes. "Parents vs. F_2 s also exhibited highly significant differences for all the traits except for days to maturity, chlorophyll content and weight of grain per spike" [11,12].

The magnitude of variability in F_1 s was higher for days to heading (50%), days to maturity, plant height, number of productive tillers per plant, spike length, weight of grains per spike, biological yield per plant and protein content in comparison to F_2 s and *vice-versa* for other characters [13,14].

B. Mean and Range

The mean values and range of parents, their F_1 and F_2 progenies for all the fourteen traits are presented in Table-4.

The variability among parents was highest for days to maturity it ranged from 117.33 to 137.67 with the mean value 126.60. Mean value for plant height reported 90.94 with the range from 80.60 to 100.83. The average days to heading (50%) was 81.77 with the minimum 74.33 and maximum values 93.67. Biological yield per plant ranged from 35.53 to 51.27 with the mean value of 41.57. Harvest index ranged from 30.61 to 45.64 with the mean value 38.21 and the average grain yield per plant 15.99 ranged from 12.33 to 23.40 while number of grains/spike ranged from 30.47 to 38.1 with the mean value of 34.28. 1000 grain weight ranged from 38.98 to 44.31 with the average value of 41.72. Chlorophyll content range from 38.47 to 43.39 with the mean value of 40.56 and the average spike length 11.12 ranged from 9.27 to 13.47 while number of productive tillers/plant ranged from 6.33 to 10.00 with the mean value of 7.50. Mean number of spikelets/spike found 17.05 with the range of 15.47 to 18.87 while the average protein content found 10.34 with the minimum and maximum values 9.22 and 11.54 respectively. Weight of grains/spike ranged from 1.53 to 1.87 with the mean value of 1.67 [15,16,17].

The variation in F_1 progenies was highest for plant height ranged from 85.97 to 120.53 with the mean value of 96.71 followed by biological yield per plant ranged from 20.67 to 52.07 with the mean value of 38.77. Days to maturity ranged from 118.00 to 138.67 with the mean value of 125.88 and the average days to heading (50%) 81.20 ranged from 72.00 to 89.67 while grain yield per plant ranged from 8.53 to 22.87 with the mean value of 15.59. chlorophyll content ranged from 34.23 to 48.07 with the mean value of 40.27. number of grains per spike ranged

value 28.53 to 41.60 with the mean value of 36.95 and the average harvest index 40.24 ranged from 36.78 to 44.98 while 1000 grain weight ranged from 39.12 to 46.12 with the mean value of 42.88. Mean number of spikelets per spike found 18.43 with the range of 14.80 to 21.20 while the average number of productive tillers 8.63 with the minimum and maximum values 6.00 and 11.67 respectively. Spike length ranged from 8.30 to 13.47 with the mean value of 10.63 and the average protein content 10.14 ranged from 8.81 to 11.26 while and weight of grain per spike ranged from 1.30 to 2.13 with the mean value of 1.66 [18,19].

The variation in F_2 progenies was highest for plant height ranged from 83.70 to 120.20 with the mean value of 94.99 followed by biological yield/plant ranged from 26.77 to 57.00 with the mean value of 36.70. day to maturity ranged from 117.33 to 141.33 with the mean value of 126.64 and the average days to heading (50%) 80.73 ranged from 73.67 to 90.33 while chlorophyll content ranged from 34.98 to 48.71 with the mean value of 40.36. grain yield/plant ranged from 10.87 to 24.1 with the mean value of 14.84. mean number of grains/spike found 36.35 with the range of 29.13 to 41.93 while the average harvest index 40.44 with the minimum and maximum values 34.96 and 45.78 respectively. 1000 grain weight ranged from 39.65 to 46.61 with the mean value of 43.02. number of productive tiller per plant ranged from 6.00 to 12.67 with the mean value of 8.79 and the average number of spikelets per spike 18.23 ranged from 14.87 to 21.13 while spike length ranged from 8.07 to 13.4 with the mean value of 10.52., protein content ranged from 8.89 to 11.26 with the mean value of 10.02 and weight of grain per spike ranged from 1.33 to 2.27 with the mean value of 1.66 [20,21].

C. Coefficients of variation

In Table-5 the estimates variability parameters i.e., genotypic coefficient of variation and phenotypic coefficient of variation were computed for all the traits having significant difference between the genotypes. GCV and PCV are categories *viz.*, high (above 20%), moderate (above 10 and below 20%) and low (below 10 %).

Table 2. Analysis of variance for fourteen characters of 10 Parents and their 45 F₁s in bread wheat

Source of variation	d.f.	Days to heading (50%)	Days to maturity	Plant height (cm)	Chlorophyll content	No. of productive tillers/plant	Spike length (cm)	No. of spikelets/spike
Replication	2	3.28	7.17	5.05	2.41	0.03	0.34	0.52
Treatment	54	61.51**	109.64**	149.93**	25.90**	6.99**	5.27**	9.27**
Parents	9	111.93**	143.91**	96.82**	8.16**	4.46**	6.69**	5.81**
F ₁	44	52.42**	104.84**	145.68**	30.06**	6.95**	4.96**	9.14**
Parents vs F ₁	1	7.89	12.68**	815.79**	2.07	31.53**	5.93**	46.24**
Error	108	4.64	2.38	3.54	1.37	0.58	0.12	0.27
Source of variation	d.f.	No. of grains/spike)	Weight of grain/spike(g)	1000 grain weight (g)	Biological yield/plant (g)	Harvest index (%)	Protein content (%)	Grain yield /plant (g)
Replication	2	1.98	0.008	0.19	2.30	0.72	0.028	0.17
Treatment	54	31.79**	0.109**	10.05**	145.23**	21.96**	1.178**	27.88**
Parents	9	26.94**	0.051**	11.94**	84.27**	58.18**	1.700**	36.62**
F ₁	44	29.54**	0.124**	9.14**	156.61**	12.77**	1.076**	26.64**
Parents vs F ₁	1	174.44**	0.002	33.08**	193.55**	100.59**	0.979**	4.02*
Error	108	1.23	0.009	0.68	3.31	2.05	0.069	0.80

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

Table 3. Analysis of variance for fourteen characters of 10 Parents and their 45 F₂s in bread wheat

Source of variation	d.f.	Days to heading (50%)	Days to maturity	Plant height (cm)	Chlorophyll content	No. of productive tillers/plant	Spike length (cm)	No. of spikelets/spike
Replication	2	0.77	1.82	4.97	0.97	0.48	0.08	0.35
Treatment	54	60.81**	104.45**	132.41**	28.56**	6.14**	4.99**	9.21**
Parents	9	111.93**	143.91**	96.82**	8.16**	4.46**	6.69**	5.81**
F ₂	44	51.13**	98.75**	133.56**	33.35**	5.69**	4.56**	9.34**
Parents vs F ₂	1	26.59**	0.06	402.61**	1.05	41.01**	8.74**	34.10**
Error	108	2.74	2.11	3.54	1.99	0.48	0.12	0.31
Source of variation	d.f.	No. of grains/spike	Weight of grain/ spike(g)	1000 grain weight (g)	Biological yield/plant (g)	Harvest index (%)	Protein content (%)	Grain yield /plant (g)
Replication	2	1.88	0.051	2.12	0.34	0.73	0.045	0.06
Treatment	54	36.60**	0.093**	12.37**	143.78**	22.65**	1.092**	28.67**
Parents	9	26.94**	0.051**	11.94**	84.27**	58.18**	1.700**	36.62**
F ₂	44	37.01**	0.104**	11.79**	145.99**	13.13**	0.933**	26.96**
Parents vs F ₂	1	104.99**	0.003	41.67**	582.59**	121.64**	2.630**	32.34**
Error	108	1.36	0.009	0.42	3.01	2.74	0.090	0.74

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

Table 4. Mean and range of parents and their F₁s and F₂s for fourteen characters in bread wheat

S. No.	Characters	Parent			F ₁		F ₂			
		Mean	Range		Mean	Range	Mean	Range		
1	Days to heading (50%)	81.77	74.33	93.67	81.20	72.00	89.67	80.73	73.67	90.33
2	Days to maturity	126.60	117.33	137.67	125.88	118.00	138.67	126.64	117.33	141.33
3	Plant height (cm)	90.94	80.60	100.83	96.71	85.97	120.53	94.99	83.70	120.20
4	Chlorophyll content	40.56	38.47	43.39	40.27	34.23	48.07	40.36	34.98	48.71
5	No. of productive tillers/plant	7.50	6.33	10.00	8.63	6.00	11.67	8.79	6.00	12.67
6	Spike length (cm)	11.12	9.27	13.47	10.63	8.30	13.47	10.52	8.07	13.40
7	No. of spikelets/spike	17.05	15.47	18.87	18.43	14.80	21.20	18.23	14.87	21.13
8	No. of grains/spike	34.28	30.47	38.10	36.95	28.53	41.60	36.35	29.13	41.93
9	Weight of grain/ spike(g)	1.67	1.53	1.87	1.66	1.30	2.13	1.66	1.33	2.27
10	1000 grain weight (g)	41.72	38.98	44.31	42.88	39.12	46.12	43.02	39.65	46.61
11	Biological yield/plant (g)	41.57	35.53	51.27	38.77	20.67	52.07	36.70	26.77	57.00
12	Harvest index (%)	38.21	30.61	45.64	40.24	36.78	44.98	40.44	34.96	45.78
13	Protein content (%)	10.34	9.22	11.54	10.14	8.81	11.26	10.02	8.89	11.26
14	Grain yield /plant (g)	15.99	12.33	23.40	15.59	8.53	22.87	14.84	10.87	24.10

Table 5. Grand mean, heritability (narrow sense), genetic advance and coefficient of variance for fourteen characters in bread wheat

Chracters		Mean	Min	max	Heritability (%)	GA	GA% mean	GCV (%)	PCV (%)
Days to heading (50%)	F ₁	81.30	72.00	93.67	80.35	8.04	9.89	5.36	5.97
	F ₂	80.92	73.67	93.67	87.60	8.48	10.48	5.44	5.81
Days to Maturity	F ₁	126.01	117.33	138.67	93.76	11.93	9.47	4.75	4.90
	F ₂	126.64	117.33	141.33	94.16	11.67	9.22	4.61	4.75
Plant height (cm)	F ₁	95.66	80.60	120.53	93.22	13.89	14.52	7.30	7.56
	F ₂	94.25	80.60	120.20	92.37	12.98	13.77	6.95	7.24
Chlorophyll content	F ₁	40.32	34.23	48.07	85.62	5.45	13.52	7.09	7.66
	F ₂	40.39	34.98	48.71	81.68	5.54	13.72	7.37	8.15
Number of productive tillers plant	F ₁	8.43	6.00	11.67	78.72	2.67	31.71	17.35	19.56
	F ₂	8.56	6.00	12.67	79.53	2.52	29.46	16.04	17.99
Spike length	F ₁	10.71	8.30	13.47	93.22	2.60	24.30	12.22	12.65
	F ₂	10.63	8.07	13.47	93.13	2.53	23.84	11.99	12.43
Number of spikelets per spike	F ₁	18.18	14.80	21.20	91.81	3.42	18.81	9.53	9.95
	F ₂	18.02	14.87	21.13	90.58	3.38	18.74	9.56	10.05
No. of grains per spike	F ₁	36.46	28.53	41.60	89.19	6.21	17.03	8.75	9.27
	F ₂	35.97	29.13	41.93	89.61	6.68	18.58	9.53	10.06
Weight of grain/ spike(g)	F ₁	1.66	1.30	2.13	79.68	0.34	20.29	11.03	12.36
	F ₂	1.66	1.33	2.27	74.89	0.30	17.97	10.08	11.65
1000 seeds grain weight (g)	F ₁	42.67	38.98	46.12	82.16	3.30	7.74	4.14	4.57
	F ₂	42.78	38.98	46.61	90.43	3.91	9.14	4.66	4.91
Biological yield per plant (g)	F ₁	39.28	20.67	52.07	93.45	13.70	34.87	17.51	18.11
	F ₂	37.59	26.77	57.00	93.96	13.68	36.39	18.22	18.80
Harvest index (%)	F ₁	39.87	30.61	45.64	76.37	4.64	11.63	6.46	7.39
	F ₂	40.03	30.61	45.78	70.77	4.46	11.15	6.44	7.65
Protein content (%)	F ₁	10.18	8.81	11.54	84.32	1.15	11.30	5.97	6.50
	F ₂	10.08	8.89	11.54	78.76	1.06	10.49	5.74	6.46
Grain yield per plant (g)	F ₁	15.66	8.53	23.40	91.84	5.93	37.88	19.19	20.02
	F ₂	15.05	10.87	24.10	92.65	6.05	40.20	20.27	21.06

In F₁ generation, at level of phenotypic coefficient of variation high values of phenotypic coefficient of variation (PCV) were observed for grain yield per plant and exhibited moderate for number of productive tiller per plant, biological yield per plant, spike length and weight of grain per spike. whereas recorded low for number of spikelets per spike, number of grains per spike, chlorophyll content, plant height, harvest index, protein content, days to heading (50 %), days to maturity and 1000 grain weight. At level of genotypic coefficient of variation, high values of genotypic coefficient of variation (GCV) were observed for none of the characters and exhibited moderate for grain yield per plant, biological yield per plant, number of productive tiller per plant, spike length and weight of grain per spike whereas recorded low for number of spikelets per spike, number of grains per spike, plant height, chlorophyll content, harvest index, protein content, days to heading (50 %), days to maturity and 1000 grain weight [22,23,24]

In F₂ generation, at level of phenotypic coefficient of variation high values of phenotypic coefficient of variation (PCV) were observed for grain yield per plant and exhibited moderate for biological yield per plant, number of productive tiller per plant, spike length weight of grain per spike, number of grains per spike and number of spikelets per spike whereas recorded low for chlorophyll content, harvest index, plant height, protein content, days to heading (50 %), 1000 grain weight and days to maturity. At level of genotypic coefficient of variation, high values of genotypic coefficient of variation (GCV) were observed for grain yield per plant and exhibited moderate for biological yield per plant, number of productive tiller per plant, spike length and weight of grain per spike whereas recorded low for number of spikelets per spike, number of grains per spike, chlorophyll content, plant height, harvest index, protein content, days to heading (50 %), 1000 grain weight and days to maturity [25,26,27] .

D. Heritability and Genetic Advance

Estimates of heritability (narrow sense) and genetic advance for 14 characters, both in F₁ and F₂ generations, are presented in Table-5. There are three categories for the expression of heritability viz., high (above 30%), moderate (above 10 and below 30%) and low (below 10%) and genetic advance viz., high (above 20%), moderate (above 10 and below 20%) and low (below 10%).

(a) Heritability

“In F₁ generation, high heritability estimates were recorded for all characters namely days to heading (50%), days to maturity, plant height (cm), number of productive tillers per plant, chlorophyll content (%), spike length (cm), number of spikelets per spike, number of grains per spike, weight of grain per spike(g), 1000 grain weight (g), biological yield (g), harvest index (%),protein content (%) and grain yield per plant (g)” [28,29].

“In F₂ generation, high heritability was observed for all characters namely days to heading (50 %), days to maturity, plant height (cm), number of productive tillers/plant, chlorophyll content (%), spike length (cm), number of spikelets per spike, number of grains per spike, weight of grain per spike(g), 1000 grain weight (g), biological yield (g), harvest index (%),protein content (%) and grain yield per plant (g)” [30,31].

(b) Genetic advance:-

“Estimates of genetic advance in per cent over mean ranged from 7.74 (1000 grain weight) to 37.88 (grain yield per plant) in F₁ generation. High genetic gain was observed for grain yield per plant followed by biological yield per plant, number of productive tiller per plant, spike length and weight of grain per spike. Moderate genetic advance was recorded for number of spikelets per spike followed by number of grains per spike, plant height, chlorophyll content, harvest index and protein content and low for days to heading followed by days to maturity and 1000 grain weight” [32,33].

“Estimates of genetic advance in per cent over mean ranged from 9.14 (1000 grain weight) to 40.20 (grain yield per plant) in F₂ generation. High genetic gain was observed for grain yield per plant followed by biological yield per plant, number of productive tiller per plant, and spike length. Moderate genetic advance was recorded for number of spikelets per spike followed by number of grains per spike, weight of grain per spike, plant height, chlorophyll content, harvest index, protein content and days to heading. Low for days to maturity followed by 1000 grain weight” [34,35].

ACKNOWLEDGEMENTS

This work was done by author for the doctoral program thesis at C S Azad University of

Agriculture and Technology, Kanpur, UP. The author highly grateful for the research facilities provided by the university and sincerely acknowledge the support of Dr. S V Singh, Assistant Professor and wheat breeder and advisor for the support during whole research work.

4. CONCLUSIONS

The present study generally indicated there was plenty of genetic variability among the genotypes. Thus, there is vast opportunity in the improvement of protein content and grain yield in bread wheat genotype. Therefore the result and information generated from current study need to be used by interested plant breeders. These results showed the major involvement of additive genetic component and marginal role of non-additive component in controlling the inheritance of these characters. Similarly reported for plant height, number of productive tillers per plants, number of grain per spike by Dhonde et al. [36] days to maturity, plant height, number of productive tillers per plant, number of grain per spike, biological yield per plant, 1000 grain weight, harvest index, protein content and grain yield per plant. Studies revealed that the days to maturity with high heritability and low genetics advance over mean followed by biological yield per plant and grain yield per plant high heritability and low genetics advance over mean in both generation F₁s and F₂s. plant height, chlorophyll content, number of spikelets per spike, number of grain per spike, harvest index and protein content were the major yield attributing characters coupled with moderate genetic advance over mean in both generation F₁s and F₂s, so emphasis should be given for these characters at the time of sample selection.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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