International Journal of Advanced Biochemistry Research

ISSN Print: 2617-4693
ISSN Online: 2617-4707
IJABR 2025; 9(2): 494-498
www.biochemjournal.com
Received: 03-12-2024
Accepted: 06-01-2025

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Estimation of genetic variability parameters and heritability in bread wheat (*Triticum aestivum* L.) over generations

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DOI: https://doi.org/10.33545/26174693.2025.v9.i2g.3851

Abstract
Wheat plays a crucial role in global food security, particularly in India, where it is the second most cultivated cereal. Enhancing wheat productivity requires a thorough understanding of the relationships among yield-contributing traits. This study assessed 67 wheat genotypes (27 F_1s, 27 F_2s, 9 lines, 3 testers, and 1 check) developed using a Line × Tester mating design. The experiment, conducted at BRDPG College, Deoria, followed a randomized block design with three replications, evaluating 14 agronomic traits. Except for number of effective tillers per plant, which was 0.51 in F_1 and 0.83 in F_2, and grain weight per spike, which was 0.70 in F_1 and 0.77 in F_2, the mean squares resulting from the treatments were very significant for every trait studied. The high estimates of phenotypic coefficient of variation (>35%) are found for harvest index (37.10) and no. of grain per spike (35.29) in F_1. And high estimates of phenotypic coefficient of variation (>35%) are found for no. of grain per spike (38.48) in F_2. The high estimate of heritability in broad sense (>90%) was recorded for characters like- grain weight per spike (97.59), harvest index (%) (96.15), number of grain per spike (95.85), number of effective tiller per plant (95.59), peduncle length (93.53), test weight (92.59), grain yield per plant (92.19) and flag leaf area (cm2) (90.19) in F_1 and a similar pattern was also noted inF_2. The high estimates of Genetic Advance as percent of Mean were found in the characters like harvest index and no. of grain per spike in F_1 and F_2. High heritability and genetic advance for key traits like harvest index and grain number indicate strong potential for yield improvement.

Keywords: Genetic variability, heritability, genetic advance, *Triticum aestivum*, grain yield

1. Introduction

Wheat (*Triticum aestivum* L.) is a staple cereal crop globally, renowned for its adaptability and significant contribution to human nutrition. In India, wheat holds a pivotal role in ensuring food security and is the second most cultivated cereal after rice (Anonymous, 2022) [2]. According to the latest data from the Ministry of Agriculture & Farmers Welfare, Government of India, during the 2022-2023 agricultural year, wheat was cultivated over an area of approximately 31.45 million hectares, yielding a production of about 110 million tonnes, with an average productivity of 3.5 tonnes per hectare (Anonymous, 2024) [3].

The prominence of wheat in India's agrarian economy is underscored by its contribution to the national food grain basket and its role in sustaining the livelihoods of millions of farmers. Enhancing wheat yield is thus a critical objective in agricultural research and development (Anonymous, 2022) [2].

Grain yield in wheat is a complex trait influenced by various yield-contributing factors. To enhance grain yield, quality, and other characteristics through breeding, it is essential for breeders to understand the genetic variability associated with yield-related traits and quality parameters. When working with a breeding population, assessing heritability and genetic advance is crucial for tracking genetic improvements (Falconer, 1981) [9]. The success of a breeding program depends on the nature and extent of genetic variability, heritability, and the amount of inherited variation present in the population. These factors play a key role in selecting genotypes with desirable traits (Dudley and Mall, 1969) [8]. Genetic advance is another important parameter in selection, as high genetic advance combined with high heritability provides a reliable prediction of selection outcomes for yield-related traits

(Hanson *et al*., 1956) [12]. For effective yield improvement, breeders must analyze the heritability and genetic advancement of agronomic traits. Heritability refers to the proportion of phenotypic variation that is genetically inherited (Hanson *et al*., 1956) [12], while genetic advance represents the improvement in the average genetic value of selected plants compared to the original population. The relationship between heritability and response to selection, known as genetic advance, is a key factor in breeding success. A combination of high heritability and high genetic advance offers the best conditions for effective selection (Larik *et al*., 2000) [17].

2. Materials and Methods

The experimental materials for this study consisted of 67 (27 F_1s + 27 F_2s + 9 lines + testers + 1 check) wheat genotypes. The crosses were generated through crossing 9 lines and 3 testers in Line X Tester mating design in 2019-20. Further F_1s were grown to raise F_2s in 2020-21. The final experiment was conducted during rabi 2021-22 at departmental Research Farm of BRD PG College, Deoria (Affiliated with DDU Gorakhpur University, Uttar Pradesh) in three replications in randomized block design. All the necessary packages and practices were followed to raise a good crop health. The data were observed for fourteen metric traits as Days to 50% flowering (DFF), Days to maturity (DM), Plant Height (PH), No of effective tillers per plant (TPP), Flag leaf area (FLA), Spike length (SL), No. of spikletes per spike (SPS), Peduncle length (PL), No of grains per spike (GPS), Grain Weight per spike (GWPS), Test weight (TW), Biological yield per plant (BYPP), Harvest index (HI) and Grain yield per plant (GYPP). The observations were noted on plot basis for DFF and DM while rest were calculated from 5 randomly selected plants based on their phenotypic superiority. Genetic variability was measured and subjected to statistical analyses as: Analysis of variance suggested by Panse and Shukhatme (1967) [19], Heritability (Broad sense) suggested by Hanson (1963) [11], Genetic advance as per cent over mean suggested by Johnson *et al*. (1955) [14].

3. Results and Discussion

3.1 Analysis of variance for experimental design

Table 1 presents the result of the variance analysis for the Randomized Block Design concerning fourteen characters in wheat.

Quantitative assessment of a crop's variability is necessary because effective management and characterization of genetic variability are crucial for crop development. The degree of fixable and non-fixable variation determines how much genetic diversity may be exploited. In addition to the kind of gene activity, the degree of genetic diversity also affects how the traits are expressed, which is crucial when choosing a breeding strategy. The investigation of plants with more variety is always favoured by nature. Therefore, it is necessary to investigate novel plants with more variety and assess their suitability for various agroclimatic conditions and management techniques. Except for No of effective tillers per plant, which was 0.51 in F_1 and 0.83 in F_2, and Grain Weight per spike, which was 0.70 in F_1 and 0.77 in F_2, the mean squares resulting from the treatments were very significant for every feature examined.

3.2 Mean and range of parents, hybrids, and checks for different characters

The data on mean and range for various traits in both the generations have been presented in Table 2. The table depicts that traits DFF, DM, BYPP and HI possessed high range in both the generations. Rest of the traits showed comparatively less range in the values.

3.3 Coefficient of variation

The phenotypic, and genotypic coefficients of variability for all the twelve characters under both F_1 and F_2 have been given in Table 2. In general, the magnitude of phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the traits in both F_1 and F_2. The high estimates of phenotypic coefficient of variation (>35%) are found for harvest index (37.10) and no. of grain per spike (35.29) in F_1. The moderate estimates (10 - 35%) of PCV recorded for the characters, test weight (g) (21.44) followed by peduncle length (17.02), Days to 50% flowering (12.70) in F_1. And the low estimates of PCV were recorded in plant height (cm) (09.6), followed by Days to maturity (09.57), Flag leaf area (cm^2) (4.98), biological yield per plant (04.87), no. of spikelets per spike (g) (4.14), and spike length (1.76), grain yield per plant (1.23) in F_1. And high estimates of phenotypic coefficient of variation (>35%) are found for no. of grain per spike (38.48) in F_2. The moderate estimates (10 - 35%) of PCV recorded for the characters, harvest index (31.87), test weight (19.51), Days to maturity (18.52), harvest index (%) (18.33), peduncle length (17.55), days to 50% flowering (17.12) and plant height (12.92) in F2. And the low estimates of PCV were recorded in biological yield per plant (06.52), no. of spikelets per spike (04.42), Flag leaf area (cm^2) (4.27) & spike length (2.29).

The high estimates of genotypic coefficient of variation (>35%) are found for plant height (cm) (65.73) and biological yield per plant (g) harvest index (35.67), in F_1. The moderate estimates (10 - 35%) of GCV recorded for the characters, grain per spike (33.82), test weight (19.86), and peduncle length (15.92) in F_1. And the low estimates of GCV were recorded in days to 50% flowering (7.94), days to maturity (6.59) plant height (5.15), flag leaf area (4.49) and biological yield per plant (4.87), number of spikelets per spike (3.52), spike length (cm) (1.56) and grain yield per plant (1.13). A high estimate of genotypic coefficient of variation (>35%) are found for no of spikelets per spike (37.21), in F_2. The moderate estimates (10 - 35%) of GCV recorded for the characters, harvest index (%) (30.26), test weight (17.88) peduncle length (16.33) and days to 50% flowering (12.34) in F_2. And the low estimates of GCV were recorded in days to maturity (8.50) followed by biological yield per plant (g) (5.53), flag leaf area (cm^2) (3.89), spike length (2.04), plant height (cm) (3.81), panicle length (cm) (9.54), days to maturity (8.50), grain yield per plant (g) (6.80) number of spikelets per spike (3.88), number of spikelets per spike (3.88) and grain yield per plant (g) (2.03). In their studies, Tarkeshwar *et al*. (2019) [21] and Chaudhary *et al*. (2022) [6] have also noted high GCV and PCV for various metric traits attributed to grain yield.

These results align with previous studies on genetic variability in cereal crops, where researchers have reported higher PCV than GCV for yield-related traits, indicating substantial environmental influence (Kumar *et al*., 2022) [15]. Traits with high GCV and PCV are considered ideal for selection in breeding programs, as they offer greater scope for improvement through selection. The high variability observed in traits such as the number of grains per spike and harvest index suggests their potential utility in breeding programs aimed at improving grain yield. The moderate and low GCV estimates for other traits highlight the necessity of hybridization and advanced breeding techniques to enhance their genetic gain. Observations on higher PCV and GCV for number of grains per spike and harvest index are in close agreement with the results of Sabit *et al.* (2017) [20], Bayisa *et al*. (2020) [5], Vaghela *et al.* (2021) [23], Kumar *et al*. (2022) [16], Chaurasia *et al*. (2023) [7] and Gautam *et al*. (2025) [10] in wheat.

3.3 Heritability and genetic advance

In the present investigation, heritability and genetic advance are presented in Table 2. The high estimate of heritability in broad sense (>90%) was recorded for characters like- grain weight per spike (97.59), harvest index (%) (96.15), number of grain per spike (95.85), number of effective tiller per plant (95.59), peduncle length (93.53), test weight (92.59), grain yield per plant (92.19) and flag leaf area (cm2) (90.19) and low estimate of heritability in broad sense (>40) was recorded in spike length (cm) (88.44) followed by no. of spikelets per plant (85.00), Biological yield per plant (g) (84.86), Days to maturity (68.83), Days to 50% flowering (62.52), and Plant height (cm) (53.79) in F_1. And the high estimate of heritability in a broad sense (>90%) in F_2 for all characters like- grain weight per spike (97.59) followed by number of grains per spike (96.70), Number of effective tillers per plant (96.39), Harvest index (%) (94.96), Grain yield per plant (g) (94.88), peduncle length (93.05), test weight (91.62), Flag leaf area (cm2) (91.11), Biological yield per plant (g) (90.97), and low estimate of heritability in a broad sense (>40%) in spike length (cm) (89.04), Number of spikelets per spike (87.74), Days to 50% flowering (72.07), and Days to maturity (45.86).

The high estimates of Genetic Advance as percent of Mean (>10%) were found in these characters- harvest index (%) (12.06), and no. of grain per spike (11.73) in F_1. The moderate estimates (05 - 10%) of genetic advance as percent of mean recorded for the characters, 1000-grain weight (g) (8.83), grain per spike (10.85), & days to maturity (7.12) harvest index (%) (06.48), and peduncle length (cm) (7.95), in F_1. And the low estimates (<5) of genetic advance as percent of mean were recorded in days to 50% flowering (4.59), days to maturity (4.39), flag leaf area (cm^2) (04.14), biological yield per plant (g) (3.86), number of spikelets per spike (03.56), plant height (cm) (3.43), spike length (2.42), grain yield per plant (2.10), grain weight per spike (0.98) and number of effective tillers per plant (0.82), in F_1. Earlier Tarkeshwar *et al*. (2019) [21] and Chaudhary *et al*. (2022) [6] have also noted high heritability along with high genetic advance for number of effective tillers per plant, harvest index, grain yield per plant, and biological yield per plant. And high estimates of Genetic Advance as a percent of Mean (>10%) are found in F_2 for number of grains per spike (12.36) and harvest index (11.04) exhibited. And moderate estimates (05 - 10%) of genetic advance as percent of mean recorded for the characters, in F_2, 1000-grain weight (g) (8.34) followed by peduncle length (cm) (8.03) and days to 50% flowering (6.14). And the low estimates (<5) of genetic advance as percent of mean were recorded in biological yield per plant (g) (4.78) followed by days to maturity (4.07), flag leaf area (cm2) (03.88), number of spikelets per spike (03.80), spike length (2.78), grain yield per spike (2.86), plant height (cm) (2.18), number of effective tillers per plant (1.06), and grain weight per spike (g) (1.03) in F_2. The findings indicate that heritability in the broad sense was generally high (>90%) for most of the traits, suggesting a strong genetic influence with limited environmental variability. High heritability estimates were recorded for traits such as grain weight per spike (97.59%), harvest index (96.15%), number of grains per spike (95.85%), number of effective tillers per plant (95.59%), and peduncle length (93.53%) in F_1. Similarly, in F_2, high heritability values were found for grain weight per spike (97.59%), number of grains per spike (96.70%), and number of effective tillers per plant (96.39%). In contrast, traits such as spike length, number of spikelets per plant, days to maturity, and plant height showed comparatively lower heritability values, indicating a greater environmental influence on their expression.

Genetic advance as a percentage of the mean provides insights into the expected genetic gain from selection. The high estimates (>10%) for genetic advance in F_1 were observed for harvest index (12.06%) and the number of grains per spike (11.73%), indicating the potential for selection to enhance yield-related traits. Moderate genetic advance (5-10%) was recorded for test weight, days to maturity, and peduncle length, while low genetic advance (<5%) was observed for days to 50% flowering, plant height, biological yield per plant, and grain yield per plant. In F_2, high genetic advance was found for the number of grains per spike (12.36%) and harvest index (11.04%), while moderate and low estimates followed a similar trend as observed in F_1.

These findings are consistent with previous studies conducted by Balkan (2018) [4], Bayisa *et al*. (2020) [5] and Tiwari and Singh (2024) [22] who reported high heritability and genetic advance for key yield-contributing traits in wheat. Similar research by Nageshwar *et al*. (2023) [18] indicated that traits with high heritability and moderate to high genetic advance are more amenable to selection-based improvement. The results of the present study reaffirm that selection for traits with high heritability and genetic advance, such as grain weight per spike and harvest index, can effectively enhance genetic gain in breeding programs. However, for traits with low heritability and genetic advance, hybridization and advanced breeding techniques may be required to achieve significant improvements. In earlier studies, high genetic advance in per cent of mean coupled with high heritability have also been reported by Jaiswal *et al.* (2020) [13], Ammar *et al.* (2022) [1], Kumar *et al.* (2022) [15], Nageshwar *et al*. (2023) [18], Tiwari and Singh (2024) [22] and Gautam *et al*. (2025) [10].

Table 1: Analysis of variance (ANOVA) for fourteen metric traits of wheat in F_1 and F_2

	Characters	df	Days to 50% flowering	Days to maturity	Plant Height (cm)	No of effective tillers per plant	Flag leaf area (cm)	Spike length (cm)	No.of spikletes per spike	Peduncle length (cm)	No of grains per spike	Grain Weight per spike (g)	Test weight (g)	Biological yield per plant (g)	Harvest index (%)	Grain yield per plant (g)
F_1	Replication	2	7.85	6.92	1.47	0.00	0.61	0.11	0.85	1.40	1.56	0.01	1.12	1.52	2.00	0.08
	Treatment	39	28.59**	22.75**	19.90**	0.51**	13.95**	4.89**	11.19**	48.86**	102.93**	0.70**	61.15**	13.15**	108.44**	3.49**
	Error	78	4.76	2.98	4.44	0.01	0.49	0.20	0.62	1.10	1.47	0.01	1.59	0.74	1.43	0.10
	Total	119	12.62	9.53	9.46	0.17	4.90	1.74	4.09	16.76	34.72	0.23	21.10	4.82	36.51	1.21
F_2	Replication	2	6.68	14.65	5.94	0.01	0.27	0.45	0.33	1.85	1.09	0.01	1.49	0.31	2.79	0.13
	Treatment	39	41.80**	35.51**	20.54**	0.83**	12.06**	6.37**	12.18**	50.20**	112.90**	0.77**	55.27**	18.38**	92.39**	6.19**
	Error	78	4.78	10.03	9.10	0.01	0.38	0.25	0.54	1.22	1.27	0.01	1.64	0.59	1.61	0.11
	Total	119	16.94	18.46	12.80	0.28	4.21	2.26	4.35	17.28	37.85	0.26	19.21	6.41	31.38	2.10

Table 2: Overall mean, range, heritability, GA and GCV and PCV in F_1 including parents and in F_2

Characters	Gen.	Mean	Range		Coefficient of variation		Heritability (%)	GA (%)
			Min	Max	var (g)	var (p)		
Days to 50% flowering	F_1	77.88	72.22	84.27	7.94	12.70	62.52	4.59
	F_2	77.25	71.24	84.27	12.34	17.12	72.07	6.14
Days to maturity	F_1	120.59	115.96	125.57	6.59	9.57	68.83	4.39
	F_2	119.78	113.63	125.57	8.50	18.52	45.86	4.07
Plant Height (cm)	F_1	112.36	104.86	116.64	5.15	9.60	53.69	3.43
	F_2	111.98	106.22	117.48	3.81	12.92	29.51	2.18
No of effective tillers per plant	F_1	3.51	2.53	4.21	0.17	0.18	95.59	0.82
	F_2	3.83	2.53	4.43	0.27	0.28	96.39	1.06
Flag leaf area (cm)	F_1	24.29	19.17	28.12	4.49	4.98	90.19	4.14
	F_2	24.23	19.17	28.02	3.89	4.27	91.11	3.88
Spike length (cm)	F_1	16.69	13.78	19.35	1.56	1.76	88.44	2.42
	F_2	17.04	13.78	19.69	2.04	2.29	89.04	2.78
No.of spikletes per spike	F_1	27.67	24.12	31.55	3.52	4.14	85.00	3.56
	F_2	27.53	24.12	31.79	3.88	4.42	87.74	3.80
Peduncle length (cm)	F_1	38.94	31.80	45.26	15.92	17.02	93.53	7.95
	F_2	39.09	31.80	44.82	16.33	17.55	93.05	8.03
No of grains per spike	F_1	41.62	30.38	49.49	33.82	35.29	95.85	11.73
	F_2	41.84	30.38	49.53	37.21	38.48	96.70	12.36
Grain Weight per spike (g)	F_1	2.90	2.15	4.39	0.23	0.24	97.59	0.98
	F_2	2.87	1.72	3.64	0.26	0.26	97.24	1.03
Test weight (g)	F_1	46.61	35.01	60.08	19.86	21.44	92.59	8.83
	F_2	46.77	35.01	53.38	17.88	19.51	91.62	8.34
Biological yield per plant (g)	F_1	28.50	24.82	32.01	4.14	4.87	84.86	3.86
	F_2	28.30	23.09	32.16	5.93	6.52	90.97	4.78
Harvest index (%)	F_1	42.39	30.66	50.31	35.67	37.10	96.15	12.06
	F_2	42.27	30.66	48.14	30.26	31.87	94.96	11.04
Grain yield per plant (g)	F_1	11.83	9.50	14.08	1.13	1.23	92.19	2.10
	F_2	11.45	7.44	13.65	2.03	2.13	94.88	2.86

Conclusion

In a nutshell, the study confirms substantial genetic variability in wheat traits, with significant differences in both F_1 and F_2 generations. High heritability and genetic advance for key traits like harvest index and grain number indicate strong potential for yield improvement, while traits with lower values may require advanced breeding techniques for effective selection.

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