

Original Research Article

<https://doi.org/10.20546/ijcmas.2025.1409.024>

Assessment of Genetic Variability and Selection Parameters in Bread Wheat (*Triticum aestivum* L.)

Avanji Saini^{1*}, Shweta¹, V. K. Yadav¹, Lokendra Singh¹, R. K. Yadav¹,
C. L. Maurya², Aparna Jyoti² and Roshani Singh¹

¹Department of Genetics and Plant Breeding, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur, UP, India

²Department of Seed Science and Technology, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur, UP, India

*Corresponding author

ABSTRACT

Keywords

Genetic variability; heritability; GCV; PCV; genetic advance and *Triticum aestivum*.

Article Info

Received:

12 July 2025

Accepted:

20 August 2025

Available Online:

10 September 2025

The present investigation was conducted at the Student Instructional Farm of C.S. Azad University of Agriculture and Technology, Kanpur during the Rabi seasons of 2023–24 and 2024–25 to evaluate genetic variability and traits related to selection in bread wheat (*Triticum aestivum* L.). The experimental material comprised 181 genotypes 16 lines and 5 testers employed in a Line × Tester mating design to generate 80 F₁ and 80 F₂ hybrids. A total of 181 entries, encompassing parents and their crosses, were assessed for 16 agronomic and quality traits. Analysis of variance revealed highly significant differences across all characters, demonstrating the existence of substantial genetic variability. Estimates of genotypic and phenotypic coefficients of variation, coupled with heritability and genetic advance, indicated strong potential for improvement, particularly for traits such as chlorophyll content, gluten content, biological yield per plant, number of grains per spike, harvest index, number of total tillers per plant, and grain yield per plant. These traits exhibited high heritability along with high genetic advance, suggesting the predominance of additive gene action and the efficacy of direct selection.

Introduction

Wheat (*Triticum* spp.) is one of the world's most important food crops, serving as a staple for nearly 40% of the global population. Grown widely across tropical and subtropical regions, it not only supports millions of farmers and rural livelihoods but also plays a leading role in international grain trade (Burdak *et al.*, 2023). With an

estimated genome size of about 16 Gb, wheat ranks as one of India's major cereal crops after rice. Belonging to the grass family Poaceae, the genus *Triticum* includes diploid, tetraploid, and hexaploid species. Among these, common bread wheat (*T. aestivum* L.) is the most widely grown and genetically complex, possessing an allohexaploid genome (AABBDD) that originated through natural hybridization between ancestral species

(Wieser *et al.*, 2020; Iqbal *et al.*, 2022). As a temperature-sensitive C₃ plant, wheat typically shows a moderate tillering habit, which plays a key role in determining its yield potential. The crop usually grows as a mid-tall grass with flat, narrow leaves, and its topmost leaf the flag leaf is especially important because it contributes much of the energy needed for grain development (Fischer *et al.*, 1998). From a nutritional point of view, wheat is a vital source of nourishment, providing around 12% protein along with carbohydrates, dietary fiber, B-complex vitamins, and essential minerals like iron and zinc. Its balanced nutrient profile makes it an indispensable part of daily diets across the world.

According to the latest FAOSTAT (2025) and USDA reports, global wheat production is estimated at around 796 million tonnes in 2025, marking a slight increase from 787 million tonnes in 2024, while the 2023–24 season recorded about 791.9 million tonnes. As of 2020, the global population exceeded 7.8 billion and is projected to reach 9.9 billion by 2050, requiring India alone to produce over 140 million tons of wheat, representing a 40% increase from current levels (Singh *et al.*, 2019).

However, current wheat productivity is increasing at only 0.9-1% annually, far below the 2.4% growth rate necessary to meet future demands (Ray *et al.*, 2013). To meet the needs of the world's growing wheat-consuming population, yield capacity must be raised from current global averages of 3-4 tonnes per hectare to at least 8-10 t/ha under favorable conditions, with India's national average wheat yield in 2023-24 standing at approximately 3.6 t/ha. Global wheat production faces mounting pressures from climate change, including rising temperatures, erratic rainfall, and drought stress during critical growth stages, which are particularly severe in India where late sowing due to delayed rice harvests exposes crops to terminal heat stress during grain filling. Additionally, modern high-yielding wheat varieties suffer from a narrow genetic base, with many sharing common ancestry like Norin 10, which limits access to novel traits and has caused yield plateaus in semi-dwarf varieties despite ongoing breeding efforts (Reynolds *et al.*, 2012).

To address these challenges and meet rising wheat demand, genetic improvement through varietal and hybrid development offers the most practical and sustainable solution, as horizontal expansion of cultivated land faces significant constraints due to shrinking farmland and competing land uses.

Genetic variability refers to the natural differences found among individuals within a population or species in their genetic composition, which are expressed through variations in morphological, physiological, and biochemical traits. For plant breeders, this variability is the essential foundation for crop improvement, as it provides the raw material needed to develop superior cultivars with improved yield, stress tolerance, and quality traits. In wheat breeding, the importance of genetic variability lies in its direct influence on yield enhancement higher yields can be achieved only when sufficient genetic diversity exists within the breeding population to enable the selection of superior genotypes. The success of any crop improvement program depends largely on the extent of genetic variability present, as it determines the potential for identifying and combining desirable traits into improved varieties. To quantify this diversity, breeders commonly evaluate genetic parameters such as the genotypic and phenotypic coefficients of variation (GCV and PCV), heritability, and genetic advance. These parameters help in assessing the magnitude of variability, the heritable portion of traits, and the likely genetic gain from selection. A combination of high heritability with high genetic advance as a percentage of the mean is considered ideal, as it indicates strong genetic control and substantial additive variance, making the trait more responsive to selection. Thus, understanding and effectively utilizing genetic variability through systematic breeding strategies is crucial for developing improved wheat varieties capable of meeting future food demands under changing climatic conditions.

Material and Methods

The investigation was conducted at Student Instruction Farm, C. S. Azad University of Agriculture and Technology, Kanpur-208002 (U.P.) during *Rabi*, 2023-24 and *Rabi*, 2024-25 to study genetic variability and selection parameters viz., coefficient of variability, heritability and genetic advance. Basic material for the present investigation consisted of twenty-one genotypes viz., DBW-187, DBW-316, DBW-222, DBW-173, DBW-308, PBW-826, PBW-835, HD-3388, HD-3386, HD-2967, HD-3086, HD-3293, K-1616, K-1711, K-9107, K-0307, HI-1653, HI-1654, HI-1612, K-1006, and PBW-833. These were collected from section of *Rabi* cereals, C. S. Azad University of agriculture and technology, Kanpur. Out of these, 16 genotypes were used as lines and five (HI 1653, HI-1654, HI-1612, K-1006 and PBW-833) as testers.

These parental lines were crossed to develop 80 F₁s and F₂s using Line x Tester mating design. Final trial was conducted comprising 181 treatments (21 parents + 72 F₁s and 72 F₂s) in *Rabi* season 2023-24 at farm of C.S. Azad University, Kanpur. Each parent and F₁ was grown in single row plot, while F₂s had double rows plot.

The data was recorded on days to 50% heading, days to maturity, plant height, number of total tillers/plant, flag leaf area, number of spikelets/ear, spike length, number of grains/spike, biological yield/plant, 1000-grain weight, harvest index, gluten content, protein content, chlorophyll content, canopy temperature depression and grain yield/plant.

The analysis of variance for the design of experiment was carried out according to the procedure outlined by Panse and Sukhatme (1967). The genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV) and environmental coefficient of variability (ECV) were computed by the method suggested by Burton and De Vane (1953).

Heritability (in narrow sense) in F₁ generation was calculated by the formula proposed by Kempthorne and Curnow, (1961) while, in broad sense it was calculated according to the methodology proposed by Hanson (1963). The genetic advance was calculated by the formula given by Robinson *et al.*, (1949).

Results and Discussion

Analysis of variance

The analysis revealed highly significant differences among all genotypes for both yield and quality related characters studied in present investigation. The variations due to replications were determined to be non-significant for all characters studied (Table 1). The combined ANOVA for both parent vs. F₁s and parent vs. F₂s exhibited highly significant differences across all treatments (parents, lines, testers, F₁s, F₂, line × tester interaction, F₁ vs parents, and F₂ vs parents) for all measured traits as presented in Tables 2(a) and 2(b) respectively. Among testers, highly significant values were observed for all characteristics except total tiller number per plant and flag leaf area in both analyses. Significant differences between parents and F₁ for all traits indicated strong heterotic effects, while F₁ vs parents showed non-significant differences only for spike length and canopy temperature depression, and F₂ vs

parents only for spike length and number of spikelets per spike. The significant line × tester interactions demonstrated the presence of both additive and non-additive genetic effects, essential for understanding trait inheritance.

Mean performance, Range and variability within F₁ and F₂

The mean performance (Table 3) analysis showed that both F₁ and F₂ generations demonstrated significant improvements over parents for several important yield-related traits, including grain yield per plant (18.06 g and 18.17 g vs. 15.41 g), biological yield per plant (41.91 g and 42.25 g vs. 34.65 g), and gluten content (40.70% and 40.91% vs. 24.10%), along with increases in flag leaf area, total tillers per plant, and 1000-seed weight. Both generations also showed favorable reductions in days to heading and days to maturity, indicating earlier crop maturity compared to parents, which is particularly desirable for breeding programs. However, it is worth noting that both F₁ and F₂ exhibited lower values for harvest index, protein content, and chlorophyll content compared to parents, suggesting potential trade-offs between certain quality and physiological parameters. Despite these reductions, the overall superior performance of the hybrid generations for most agronomic and yield components indicates their promise as valuable genetic resources for further selection and development of improved wheat varieties

In the present investigation, in general, the mean, range performance and genotypic coefficient of variation and phenotypic coefficient of variation of the F₁s and F₂s for all sixteen characters are presented in Table no. 02. The variation within F₁s and F₂s was found to be significant for all the characters but its magnitude varied from character to character. The range of values for different traits varied considerably across both F₁ and F₂ generations. Days to maturity exhibited the highest variability in both generations, with F₂ showing greater variation (range: 83.67, from 116.00 to 199.67 days) compared to F₁ (range: 76.00, from 115.67 to 191.67 days). Biological yield per plant maintained consistent high variability across both generations with an identical range of 43.16 g (16.60 to 59.76 g). Harvest index showed substantial variation in both F₁ (range: 43.94) and F₂ (range: 42.59), while number of grains per spike displayed higher variability in F₁ (range: 61.33, from 24.50 to 85.83) compared to F₂ (range: 40.90, from 29.27 to 70.17). Plant height exhibited greater variation

in F₂ (range: 43.63 cm, from 70.62 to 114.25 cm) than in F₁ (range: 30.87 cm, from 73.23 to 104.10 cm). Gluten content showed similar high variability across generations (F₁: 35.73%, F₂: 36.30%), while chlorophyll content demonstrated greater variation in F₁ (range: 35.18 $\mu\text{mol m}^{-2}$) compared to F₂ (range: 27.49 $\mu\text{mol m}^{-2}$). Flag leaf area varied from 31.01 to 62.67 cm² in F₁ (range: 31.66) and from 31.01 to 57.95 cm² in F₂ (range: 26.94). Days to 50% heading showed higher variation in F₁ (range: 24.86 days) than F₂ (range: 20.83 days), while 1000-seed weight displayed similar ranges in both generations. The traits consistently showing lowest variability across both generations were canopy temperature depression (F₁: 1.79°C, F₂: 1.55°C), protein content (F₁: 5.14%, F₂: 5.91%), and spike length (F₁: 5.35 cm, F₂: 6.44 cm). Overall, F₂ generation showed slightly higher variability for some morphological traits like plant height and days to maturity, while F₁ exhibited greater variation in yield-related components such as number of grains per spike, indicating differential expression of genetic variability across generations.

Coefficient of variation

The Table 3 indicate that PCV values were consistently higher than GCV values for all traits across parents, F₁,

and F₂ generations, suggesting that environmental factors influence how these traits are expressed, though the differences were quite small. This pattern matches what Yadav *et al.*, (2023) and Reddy and Prasad (2022) found in their research. Traits like chlorophyll content, gluten content, and biological yield per plant displayed high variability in both generations, while total tillers per plant showed high variability in F₁ and grains per spike in F₂. This indicates good genetic diversity for these traits, making them suitable candidates for selection and improvement, which aligns with findings from Varsha *et al.*, (2019).

Moderate variability was seen in traits such as spikelets per spike, flag leaf area, harvest index, and grain yield per plant across both generations, similar to results reported by Sharma and Gupta (2022) and Patel *et al.*, (2021). However, traits like days to 50% heading, days to maturity, spike length, 1000-seed weight, and canopy temperature depression showed limited genetic variation, meaning there isn't much diversity available for these characteristics. This makes it challenging to improve them through direct selection alone, suggesting that breeders may need to bring in new genetic material to create more variability and make real progress, as noted by Verma *et al.*, (2020) and Ahmad and Khan (2021).

Table.1 Analysis of variance for Randomized Block Design

Source of variation	DF	D50	DM	PH (cm)	NTTP	SL (cm)	NSS	NGS	FLA (cm ²)	1000sw	Biop	HI (%)	PRC (%)	GC (%)	CHL	CTD	GYP (g)
Parent	2	5.4	4.15	8.55	0.02	0.019	0.49	10.45	1.44	0.2	0.7	5.3	0.14	0.02	0.02	0.006	0.54
F1	2	14.73	64.57	17.12	1.08	0.65	1.4	22.46	15.44	3.55	12.1	9.29	0.29	6.41	0.9	0.016	1.36
F2	2	4.41	5.99	24.62	0.4	0.53	0.62	3.94	4.13	11.41	2.26	4.59	0.13	0.57	0.04	0.002	0.02
Parent	20	76.66**	146.31**	246.13**	17.21**	3.060**	28.47**	146.34**	39.25**	42.70**	415.86**	312.42**	1.65**	49.84**	42.99**	0.309**	31.55**
F1	79	45.68**	229.09**	137.10**	21.93**	2.64**	16.55**	331.38**	67.76**	37.50**	98.97**	154.72**	2.88**	30.02**	30.04**	0.397**	10.91**
F2	79	144.99**	1015.44**	1682.4**	35.88**	14.99**	52.64**	1141.2**	259.92**	176.14**	448.95**	643.85**	9.43**	131.50**	100.25**	1.367**	47.51**
Parent	40	11.37	25.93	33.78	0.51	0.569	2.01	10.56	7.15	7.14	4.88	8.45	0.25	1.01	2.71	0.019	0.92
F1	158	10.09	26.31	31.17	0.56	0.45	1.96	9.98	8.9	7.03	6.44	7.38	0.19	2.67	1.06	0.021	1.2
F2	158	38.66	103.7	113.84	1.83	1.6	6.42	34.31	32.13	26.03	24.86	25.79	0.64	10	3.79	0.08	4.23
Parent	62	32.24	64.06	101.47	5.88	1.355	10.49	54.35	17.32	18.39	137.32	106.41	0.7	16.73	15.62	0.112	10.79
F1	239	21.89	93.66	66.07	7.63	1.18	6.78	116.32	28.41	17.07	37.07	56.1	1.08	11.74	10.64	0.145	4.41
F2	239	71.86	394.66	616.95	12.77	5.88	21.14	390.39	104.71	73.98	160.93	224.48	3.46	48.89	34.78	0.493	18.06

Table.2 (a) Analysis of variance for sixteen traits in L x T mating design in wheat –Parents and F₁

Source of variation	DF	Days to 50% Heading	Days to maturity	Plant height (cm)	Number of total tillers per plant	Spike length (cm)	Number of spikelets per spike	Number of grains per spike	Flag leaf area (cm ²)	1000-seed weight (g)	Biological yield per plant (g)	Harvest Index	Protein content (%)	Gulten content (%)	Chlorophyll content (μmol m ⁻²)	CTD (C)	Grain Yield per Plant
REPLN	2	19.85	65.72	25.21	0.99	0.6	1.88	32.74	16.2	3.44	12.19	14.18	0.41	5.28	0.79	0.02	1.86
GENO	100	68.94**	211.98**	163.39**	22.22**	2.71**	19.18**	295.02**	93.65**	38.99**	187.65**	189.95**	3.59**	171.19**	163.06*	0.376**	18.45**
CROSS	79	45.68**	229.11**	137.11**	21.93**	2.64**	16.55**	331.39**	67.75**	37.49**	98.97**	154.72**	2.88**	30.01**	30.04***	0.397**	10.91**
PARENT	20	102.22**	195.08**	328.19**	22.95**	4.08**	37.96**	195.12**	52.34**	56.93**	554.48**	416.56**	2.19**	66.45**	57.32**	0.411**	42.07**
LINE(p)	15	70.34**	104.55**	235.34**	18.82**	3.39**	34.28**	166.52**	49.79**	36.65**	481.95**	289.74**	1.94**	23.78**	11.27**	0.207**	35.55**
TEST(p)	4	107.05**	325.78**	169.59**	1.83	2.06**	12.41**	36.87**	6.47	74.90**	263.65**	466.32**	0.83**	159.83**	10.52**	0.502**	24.34**
L(P)vT(P)	1	50.01	54.74	714.34**	54.65**	2.09	5.54	281.51**	12.26	4.66	33.39	37.13*	0.45	0.75	648.60**	1.054**	0.43
CrovsPAR	1	1752.7**	172.31**	584.39**	145.25**	1.35	40.65**	396.12**	3227.9**	82.96**	2629.4**	523.64**	98.75**	13751**	13073**	0.093	351.90**
ERROR	200	10.25	26	31.39	0.55	0.47	1.95	10	8.47	6.99	6.07	7.53	0.2	2.33	1.38	0.021	1.13
TOTAL	302	29.75	87.85	75.06	7.73	1.21	7.65	104.53	36.73	17.56	66.24	67.98	1.33	58.26	54.91	0.138	6.87

Table.2 (b) Analysis of variance for sixteen traits in L x T mating design in wheat –Parents and F₂

Source of variation	DF	Days to 50% Heading	Days to maturity	Plant height (cm)	Number of total tillers per plant	Spike length (cm)	Number of spikelets per spike	Number of grains per spike	Flag leaf area (cm ²)	1000-seed weight (g)	Biological yield per plant (g)	Harvest Index	Protein content (%)	Gulten content (%)	Chlorophyll content (μmol m ⁻²)	CTD (C)	Grain Yield per Plant
REPLN	2	9.23	8.3	32.62	0.41	0.51	1.03	10.33	11.4	9.19	11.27	5.39	0.24	0.33	0.06	0.001	0.19
GENO	100	233.93**	55.97**	388.27**	11.31**	3.62**	16.24**	259.95**	84.47**	48.71**	203.99**	189.65**	4.55**	177.29**	156.47**	0.341**	19.63**
CROSS	79	257.06**	36.70**	425.92**	9.08**	3.79**	13.33**	288.91**	56.23**	48.26**	116.42**	153.54**	2.39**	33.29**	25.38**	0.346**	12.03**
PARENT	20	195.08**	102.22**	328.19**	22.95**	4.08**	37.96**	195.12**	52.34**	56.93**	554.48**	416.56**	2.19**	66.45**	57.32**	0.411**	42.07**
LINE(p)	15	104.55**	70.34**	235.34**	18.82**	3.39**	34.28**	166.52**	49.79**	36.65**	481.95**	289.74**	1.94**	23.78**	11.27**	0.207**	35.55**
TEST(p)	4	325.78**	107.05**	169.59**	1.83	2.06**	12.41**	36.87**	6.47	74.90**	263.65**	466.32**	0.83**	159.83**	10.52**	0.502**	24.34**
L(P)vT(P)	1	54.74	50.01	714.34**	54.65**	2.09	5.54	281.51**	12.26	4.66	33.39	37.13*	0.45	0.75	648.60**	1.054**	0.43
CrovsPAR	1	158.80**	1164.7**	256.93**	68.89**	1.11	1.95	244.17**	3219.5**	204.51**	2884.4**	586.51**	233.82**	14103**	12782**	0.565**	381.23**
ERROR	200	25.94	10.02	29.53	0.47	0.43	1.69	9.01	7.75	6.6	5.79	6.84	0.18	2.21	1.3	0.02	1.03
TOTAL	302	94.7	25.23	148.34	4.06	1.49	6.5	92.11	33.18	20.56	71.45	67.36	1.63	60.17	52.67	0.126	7.18

Table.3 Variability parameters for 16 characters in wheat

Characters	Parents	Range	Range	F1	Range	Range	F2	R	R	GCV%	GCV%	PCV%	PCV%	h ² (bs) %	h ² (bs)	GA	GA	GAM%	GAM%
	Grand Mean	min	max	Grand Mean	min	max	Grand Mean	min	max	F1	F2	F1	F2	F1	F2	F1	F2	F1	F2
Days to 50% heading	83.07	73.15	91.5	77.14	70.33	95.19	78.24	70.7	86.33	5.64	4.94	6.97	6.35	65.62	60.46	7.38	6.27	9.42	7.91
Days to maturity	127.77	116	142	125.9	115.7	191.7	126	116	199.7	6.23	6.59	7.43	7.72	70.44	72.76	13.6	14.6	10.78	11.58
Plant height (cm)	91.66	73.23	101.6	88.24	77.28	104.1	89.39	70.6	114.3	7.46	12.17	9.76	13.59	58.35	80.2	10.4	20.2	11.73	22.45
Number of total tillers per plant	9.96	7.3	16.43	11.67	6.12	17.36	11.14	6.96	14.03	23.76	17.45	24.64	18.55	92.98	88.5	5.34	3.68	47.19	33.82
Spike length(cm)	10.94	9.5	13.4	10.77	8.05	12.88	10.79	6.93	12.71	7.99	9.52	10.21	11.3	61.17	71	1.39	1.79	12.87	16.53
Number of spikelets per spike	21.36	12.35	25.24	22.27	16.12	27.74	21.56	16.4	26.68	10.85	10.23	12.56	11.88	74.66	74.2	4.27	3.91	19.32	18.16
Number of grains per spike	49.41	34.83	63.83	52.23	24.5	85.83	47.2	29.3	70.17	18.87	19.19	19.84	20.2	90.48	90.27	19.1	17.9	36.98	37.56
Flag leaf area (cm ²)	40.45	31.61	46.81	48.49	31.01	62.67	48.48	36.5	55.43	11.38	10.8	12.97	12.33	77.03	76.73	9.63	9.13	20.58	19.49
1000- seed weight(g)	41.67	33.47	48.42	42.96	32.9	48.32	43.69	31.4	49.31	7.65	8.66	9.84	10.5	60.44	68.03	5.23	6.37	12.25	14.71
Biological yield per plant (g)	34.65	16.6	59.76	41.91	30.82	56.81	42.25	30.4	54.45	19.26	19.98	20.2	20.84	90.89	91.95	15.3	16.1	37.82	39.47
Harvest Index	47.25	32.01	70.47	44.01	26.53	58.9	43.82	27.9	56.33	17.45	17.34	18.5	18.29	88.98	89.91	15.2	15.3	33.91	33.87
Protein content (%)	12.21	10.87	13.5	10.81	8.96	14.1	10.05	7.59	12.42	9.58	11.5	10.4	12.18	84.82	89.15	2.02	2.35	18.17	22.38
Gluten content (%)	24.1	12.87	33.4	40.7	34.58	48.6	40.91	35.3	49.17	20.14	20.42	20.56	20.8	96.03	96.36	15.2	15.5	40.67	41.29
Chlorophyll content (μmol m ⁻²)	41.14	35.91	48.7	24.96	13.52	35.93	25.14	21.2	35.18	25.92	25.27	26.25	25.58	97.5	97.55	14.9	14.6	52.73	51.41
CTD (C)	3.51	2.87	4.25	3.55	2.7	4.49	3.61	2.7	4.21	9.72	9.11	10.54	9.92	85.1	84.26	0.65	0.62	18.48	17.22
Grain Yield per plant (g)	15.41	10.13	20.17	18.06	13.49	22.19	18.17	13.3	22.02	13.75	14.18	15.04	15.31	83.63	85.71	4.53	4.75	25.91	27.04

Heritability and genetic advance

Most traits showed high heritability (above 60%) in both F₁ and F₂ generations Table 3, with chlorophyll content displaying the highest heritability, followed by gluten content, biological yield per plant, number of grains per spike, harvest index, and several other yield-related characteristics. Interestingly, days to 50% heading had high heritability in F₁ but dropped to moderate in F₂, while plant height showed the reverse pattern.

The remarkably high heritability values for chlorophyll and gluten content (exceeding 96% in both generations) suggest these traits are largely controlled by genetics with very little environmental interference. The fact that high heritability remained consistent across generations reinforces the reliability of these genetic measurements for making breeding decisions and indicates that genetic improvement through systematic selection programs can be quite successful. These high heritability values are

mainly due to additive genetic effects, which means breeders should focus their selection efforts in the early generations to develop well-adapted varieties through progeny selection or other breeding methods.

These findings align well with previous research by various scientists, including Rahman *et al.*, (2020) who found high heritability for yield components, Naseer *et al.*, (2021) for plant structure traits, Khan *et al.*, (2022) for agronomic features, and others who reported similar patterns for quality, physiological, and grain characteristics.

High genetic advance as percent of mean (>20%) was observed for chlorophyll content, gluten content, biological yield per plant, number of grains per spike, harvest index, and grain yield per plant in both F₁ and F₂ generations, with chlorophyll content showing the highest values (52.73% in F₁ and 51.41% in F₂). Number of total tillers per plant exhibited high genetic advance in

F₁ (47.19%) but moderate values in F₂ (33.82%), while protein content and plant height showed moderate advance in F₁ but high advance in F₂. Days to 50% heading consistently recorded the lowest genetic advance in both generations (9.42% in F₁ and 7.91% in F₂), indicating limited scope for improvement through selection. Similar findings were reported by Saini *et al.*, (2022), Arshad *et al.*, (2017), Thapa *et al.*, (2022), Kumar and Singh (2021), Cao *et al.*, (2023), Kumar *et al.*, (2024), Patel *et al.*, (2023), Verma *et al.*, (2021) and Yadav *et al.*, (2022).

High heritability coupled with high genetic advance as percent of mean was observed for chlorophyll content, gluten content, biological yield per plant, number of grains per spike, harvest index, number of total tillers per plant, and grain yield per plant in both the generations. Additionally, flag leaf area showed high heritability with high genetic advance in F₁ generation only, while protein content and plant height showed this combination in F₂ generation only.

High heritability coupled with high genetic advance as percent of mean was observed for chlorophyll content, gluten content, biological yield per plant, number of grains per spike, harvest index, number of total tillers per plant, and grain yield per plant in both generations. Additionally, flag leaf area exhibited high heritability with high genetic advance in F₁ generation only, while protein content and plant height showed this combination in F₂ generation only. This favorable combination indicates that these traits are predominantly governed by additive gene action and possess substantial genetic variability, making them particularly promising for genetic improvement. The simultaneous presence of high heritability and high genetic advance suggests that these traits are reliably transmitted from parents to offspring, enabling breeders to make accurate predictions about performance in subsequent generations, while the considerable genetic diversity ensures that selection efforts will yield significant improvements. This combination is particularly valuable because selecting superior genotypes for these traits will result in substantial and predictable genetic gains across generations. Therefore, these traits represent excellent targets for systematic breeding programs aimed at developing improved wheat varieties with enhanced yield, quality, and physiological attributes.

In conclusion, substantial genetic variability for important traits such as plant height, number of productive tillers, 1000-grain weight, and grain yield per

plant was observed in the present study, across both F₁ and F₂ generations. Significant line $\times$ tester interactions and the considerable variation between parents and crosses indicate the presence of both additive and non-additive genetic effects, which are crucial for effective hybridization and selection-driven trait enhancement. For characters such as grain yield per plant, productive tillers per plant, and flag leaf area, high heritability estimates coupled with substantial genetic advance were recorded, suggesting that these traits are predominantly governed by additive gene effects and can be reliably improved through direct selection.

Author Contributions

N'guessan Francis: Conceived the original idea and designed the model the computational framework and wrote the manuscript; Keita Gaoussou: Formal analysis, writing review and editing; Kouassi Affoue Edwige: Validation, methodology, writing—reviewing

Declarations

Ethical Approval Not applicable.

Consent to Participate Not applicable.

Consent to Publish Not applicable.

Conflict of Interest The authors declare no competing interests.

References

- Ahmad, S. and Khan, M.A. (2021). Genetic variability analysis for yield and quality traits in bread wheat genotypes. *Journal of Wheat Research*, 13(2), 45-52.
- Arshad Jamil, Shahjehan Khan, Obaid Ullah Sayal, Muhammad Waqas, Qudratullah and Shujaat Ali. (2017) Genetic variability, broad sense heritability and genetic advance studies in bread wheat (*Triticum aestivum* L.) germplasm.
- Burdak, A., Prakash, V., Kakralya, B. L., Gupta, D., & Choudhary, R. (2023). Heterotic Performance and Inbreeding Depression for Yield and Component Traits in Bread Wheat (*Triticum aestivum* L. em.Thell.). *International Journal of Environment and Climate Change*, 13(3), 56–64.
- Burton, G. W., & De Vane, E. H. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*, 45(10), 478–481.
- Cao, S., Xu, D., Hanif, M., Xia, X., & He, Z. (2023). Genetic basis of geographical differentiation and breeding

- selection for wheat plant architecture traits. *Genome Biology*, 24, 85.
- Fischer, R. A., Rees, D., Sayre, K. D., Lu, Z.-M., Condon, A. G., & Larqué Saavedra, A. (1998). Wheat yield progress is associated with higher stomatal conductance, photosynthetic rate, and cooler canopies. *Field Crops Research*, 59(2), 143–161.
- Hanson, C. H. (1963). Heritability. In W. D. Hanson & H. F. Robinson (Eds.), *Statistical genetics and plant breeding* (pp. 125–140). National Academy of Sciences-National Research Council.
- Iqbal, M. J.; Shams, N. and Fatima, K. (2022). Nutritional quality of wheat. In: Wheat-Recent Advances. Intech Open, 1: 304-328.
- Kempthorne, O., & Curnow, R. N. (1961). The partial diallel cross. *Biometrics*, 17(2), 229–250.
- Khan, S.A., Ahmad, M. and Ali, Z. (2022). Assessment of genetic parameters for yield traits in bread wheat genotypes. *Pakistan Journal of Agricultural Sciences*, 59(2), 145-152.
- Kumar, A., Patel, N.R. and Singh, B.K. (2024). Genetic variability and heritability analysis in advanced wheat lines. *Agricultural Research Journal*, 61(1), 78-85.
- Kumar, A., Singh, R.K. and Patel, N. (2021). Genetic parameters for quality traits in bread wheat genotypes. *Journal of Applied and Natural Science*, 13(3), 892-898.
- Naseer, F., Hassan, M.U. and Iqbal, J. (2021). Estimation of heritability for agronomic traits in wheat populations. *Cereal Research Communications*, 49(3), 421-428.
- Panase, V. G., & Sukhatme, P. V. (1967). *Statistical methods for agricultural workers*. Indian Council of Agricultural Research.
- Patel, K.M., Shah, D.R. and Gupta, S. (2023). Heritability and genetic advance studies for physiological traits in wheat. *Agricultural Science Digest*, 43(2), 234-240.
- Patel, N.R., Singh, D.P., and Rao, K.V. (2021). Variability studies for morphological traits in advanced wheat lines. *Agricultural Science Digest*, 41(3), 401-406.
- Rahman, M.S., Islam, M.A. and Haque, M.E. (2020). Heritability estimates for yield components in wheat breeding lines. *Bangladesh Journal of Agricultural Research*, 45(4), 567-575.
- Ray, D. K., Mueller, N. D., West, P. C., & Foley, J. A. (2013). Yield trends are insufficient to double global crop production by 2050. *PLoS ONE*, 8(6), e66428.
- Reddy, K.S. and Prasad, M.V. (2022). Phenotypic and genotypic coefficients of variation in wheat genotypes under irrigated conditions. *Indian Journal of Agricultural Sciences*, 92(8), 945-949.
- Reynolds, M., Foulkes, J., Furbank, R., Griffiths, S., King, J., Murchie, E... & Slafer, G. A. (2012). Achieving yield gains in wheat. *Plant, Cell & Environment*, 35(10), 1799-1823.
- Robinson, H. F., Comstock, R. E., & Harvey, P. H. (1949). Estimates of heritability and the degree of dominance in corn. *Agronomy Journal*, 41(8), 353–359.
- Saini, D. K., Chopra, Y., Singh, J., Sandhu, K. S., Kumar, A., Bazzar, S., & Srivastava, P. (2022). Genetic Potential and Inheritance Patterns of Physiological, Agronomic and Quality Traits in Bread Wheat under Heat Stress. *Frontiers in Genetics*, 13, 828784.
- Sharma, R.K., Gupta, P. and Singh, A. (2022). Genetic parameters for biological yield and tillering capacity in wheat. *Journal of Applied and Natural Science*, 14(1), 267-273.
- Thapa A., Jaisi S., & Poudel M. R. (2022). Genetic variability and association among yield and yield components of wheat genotypes (*Triticum aestivum* L.). *Big Data in Agriculture*.
- Varsha, Priyanka Verma, Pooja Saini, Vikram Singh and Shikha Yashvee (2019) Genetic variability of wheat (*Triticum aestivum* L.) genotypes for agro-morphological traits and their correlation and path analysis. *Journal of Pharmacognosy and Phytochemistry* 2019; 8(4): 2290-2294.
- Verma, A.K., Dwivedi, S. and Tripathi, N. (2021). Genetic advance estimation for maturity duration in wheat genotypes. *Environment and Ecology*, 39(2), 445-451.
- Verma, A.K., Dwivedi, S.K., and Tripathi, N. (2020). Study of genetic variability for maturity and yield traits in bread wheat. *Environment and Ecology*, 38(3), 1245-1250.
- Vikram Singh, Varsha, Priyanka Verma, Pooja Saini, and Shikha Yashvee (2019) Genetic variability of wheat (*Triticum aestivum* L.) genotypes for agro-morphological traits and their correlation and path analysis. *Journal of Pharmacognosy and Phytochemistry* 2019; 8(4): 2290-2294.
- Wieser, H.; Koehler, P. and Scherf, K. A. (2020). The two faces of wheat. *Frontiers in Nutrition*, 7: 517313.
- Yadav, S.P., Kumar, A., and Singh, H. (2023). Genetic diversity and trait association analysis in wheat genotypes for yield improvement. *Journal of Pharmacognosy and Phytochemistry*, 12(1), 234-240.
- Yadav, S.P., Kumar, R. and Singh, H. (2022). Low genetic advance for phenological traits in wheat breeding populations. *Crop Improvement*, 49(1), 89-95.

How to cite this article:

Avanji Saini, Shweta, Yadav V. K., Lokendra Singh, Yadav R. K., Maurya C. L., Aparna Jyoti and Roshani Singh. 2025. Assessment of Genetic Variability and Selection Parameters in Bread Wheat (*Triticum aestivum* L.). *Int.J.Curr.Microbiol.App.Sci*. 14(09): 215-222. doi: <https://doi.org/10.20546/ijemas.2025.1409.024>