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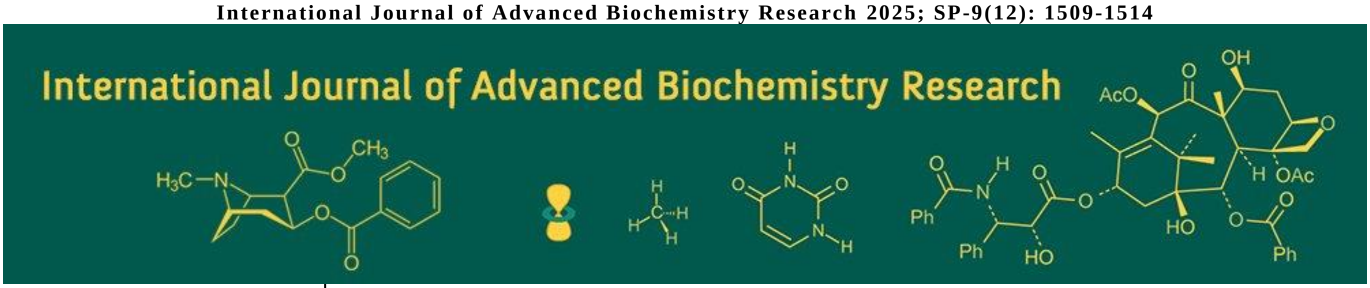

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Studies on genetic variability and character association in wheat [*Triticum aestivum* L.]

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Abstract
The current research was conducted in a bid to determine genetic variation and association to character in relation to twelve quantitative traits in regards to the growth and yield of 18 wheat genotypes (*Triticum aestivum* L.). A randomized block design was used in the experiment to conduct it three times. Statistical conclusion showed that there was a significant difference among genotypes in most of the traits, which shows that there were considerable variability. There was the influence of the environment through higher phenotypic coefficients of variation as compared to the lower genotypic coefficients. Estimates of heritability were high in plant height, peduncle length, ear length and days to 50% flowering indicating that they were well controlled genetically. The yield attributes are complex as evidenced by moderate heritability. The research establishes the possibility of using the genetic variability in the successful selection in wheat improvement schemes.

Keywords: Wheat, genetic variability, heritability, genetic advance, quantitative traits, yield components

Introduction

Wheat (*Triticum aestivum* L.) is a principal staple grain crop globally and a vital source of calories and protein, particularly in developing nations, so enhancing its yield is a priority for plant breeding initiatives. The efficacy of any wheat enhancement program primarily relies on the presence of adequate genetic diversity for yield and associated characteristics within the breeding stock (Gaur, 2019) [1].

Background

Genetic diversity enables breeders to identify superior genotypes and to generate novel combinations of advantageous alleles for intricate quantitative variables, including grain production, harvest index, and stress tolerance. In bread wheat, characteristics such as plant height, days to heading and maturity, spike length, number of spikelets, grains per spike, and 1000-grain weight exhibit significant variability, hence allowing for successful selection (Meena *et al.*, 2014) [4].

Requirement for investigations into genetic variability

“Quantitative traits are significantly affected by environmental factors; therefore, it is crucial to decompose the observed variance into genetic and environmental components utilizing metrics such as phenotypic and genotypic coefficients of variation, heritability, and genetic gain. The elevated heritability and significant genetic progress for traits like grain count per spike, efficient tillers, and 1000-grain weight signify the dominance of additive gene action, implying that straightforward selection might provide considerable enhancement.

Character correlation and output

The grain yield in wheat is a multifaceted trait influenced by the cumulative impact of various yield components that frequently exhibit correlations among themselves. Understanding character association (phenotypic and genotypic correlations) and path coefficients facilitates the identification of traits with significant positive associations and direct impacts on grain yield, including effective tillers per plant, grains per spike, and biological yield (Mundiyara *et al.*, 2024) [6].

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Justification for the current research

Research on genetic variability and trait association in wheat seeks to find advantageous genotypes and essential yield-contributing characteristics for use as selection criteria in breeding programs. Evaluating variability, heritability, genetic progress, and relationships among agronomic parameters offers a solid foundation for formulating effective selection techniques aimed at producing high-yielding wheat cultivars suited to particular settings (Poonia *et al.*, 2023) [7].

Literature Review

(Girma Seyoum & Sisay, 2021) [2] Wheat (*Triticum aestivum* L.) is a high-yield crop with extensive adaptability and serves as the primary food source globally and in Ethiopia. In Ethiopia, wheat productivity has, nonetheless, risen in recent years. Due to abiotic factors such as heat, drought, and frost, as well as biotic factors like rusts (stem, yellow, and leaf), Septoria, and Fusarium, production remains relatively low compared to other wheat-producing nations. The aims were to evaluate the variability of genotypic and phenotypic traits, as well as heritability and genetic advancement in bread wheat genotypes. Consequently, this study evaluated 30 bread wheat genotypes for yield and related parameters. A trial was conducted in Holetta, Ethiopia, during the 2018/19 agricultural season. The materials underwent testing with a three-replication alpha lattice design. The yield and related characteristics data were evaluated with SAS software version 9.3. The heritability estimates for 1000 kernel weight were determined to be exceptionally high, at 81.14 percent. The trait of 1000 kernel weight exhibited both strong heritability and a significant genetic advance as a percentage of the mean. It was determined that a kernel weight of 1000 may be established as the selection criterion for enhancing grain yield. Nevertheless, additional research must be undertaken. The future breeding efforts for bread wheat should concentrate on varietal development.

(Mishra *et al.*, 2019) [5] The study of thirty-six wheat genotypes found significant differences among them for all traits, indicating substantial variability in yield and its associated characteristics within the examined material. Among the genotypes evaluated, HI 1610 appears to be the most superior because to its high yield, early flowering, early maturation, large grain size, and dwarf stature. The GCV and PCV for days to heading, 1000 grain weight, and days to maturity were nearly equivalent, suggesting these traits are minimally affected by environmental factors. In contrast, grain yield and plant height demonstrated a significantly higher PCV compared to GCV, indicating that a substantial portion of the variation in these traits is attributable solely to environmental influences. Increased heritability was noted for days to heading, 1000 grain weight, and plant height. Significant heritability along with substantial genetic advancement observed for the traits of 1000 grain weight, plant height, days to heading, and grain yield indicates that these characteristics are influenced by additive gene effects; thus, directional selection for these traits would be more efficacious for achieving desired genetic enhancement.

(Rathwa *et al.*, 2018) [8] The experiment was conducted to evaluate genetic diversity about grain yield and its components for heat tolerance in durum wheat. The phenotypic coefficient of variation values under both sowing conditions were marginally greater than the genotypic coefficient of variation for all examined traits, suggesting a diminished influence of the environment on the expression of the analyzed characteristics. Under D0 conditions, the genetic gain at 5% selection intensity (k = 2.06) was significantly elevated for the number of grains per main spike, harvest index, and biological yield per plant. Under D0 conditions, moderate genetic advancement was noted for days to 50% flowering, plant height, grain filling duration, days to maturity, chlorophyll content at anthesis (CHLa), and grain yield per plant, but under D1 conditions, it was detected for the number of grains per main spike and harvest index. High heritability, along with significant genetic advancement expressed as a percentage of the mean, was noted for all traits except under D0 conditions for days to maturity, plant height, and length of the main spike. Under D1 conditions, this was observed for days to maturity, grain filling period, length of the main spike, and 100-grain weight. This phenomenon may be ascribed to the dominance of additive gene action, which exhibits substantial selective value, thereby indicating that selection pressure could be effectively applied to enhance these traits.

(Singh *et al.*, 2020) [9] Sixty advanced wheat lines were cultivated using a randomized complete block design (RCBD) with three replications. An analysis of genetic variability, heritability, and genetic progress for fifteen variables was conducted. The phenotypic coefficient of variation (PCV) exceeded the genotypic coefficient of variation (GCV) in magnitude for all examined traits. Peduncle length exhibited the largest phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), measuring 29.34% and 27.33%, respectively. High broad-sense heritability was noted for 1000-grain weight (97.27%) and plant height (95.27%), while medium heredity was documented for wet gluten percentage (58.41%) and protein percentage (47.13%). The significant genetic gain as a percentage of the mean (at 5% selection intensity) observed for peduncle length is 52.46%. Significant heritability (bs) alongside a substantial genetic progress as a percentage of the mean (at 5% selection intensity) was noted for thousand grain weight (97.27%). This suggests that these characteristics may be governed by additive genetic diversity, which can be leveraged for subsequent breeding operations and crossing nurseries aimed at wheat enhancement. Key Features A comprehensive understanding of many quantitative and qualitative features is essential for the success of any crop development program. m The protein % and wet gluten percentage of each genotype were determined using the micro-Kjeldahl method and an automatic gluten washer, respectively.

(Lone, 2017) [3] The morphological evaluation of the genotypes, conducted in accordance with DUS norms, indicated that over 50% of the genotypes exhibited a lack of coleoptile anthocyanin coloration, green leaves, awned structure, an intermediate growth habit, absence of waxiness, and medium pubescence. The genotypes were assessed for variability factors and relationships for seven quantitative characteristics. Marked genotypic differences were noted for all examined variables, demonstrating substantial diversity among genotypes for each characteristic. The estimations of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were elevated for proline content and grain count per earhead, moderate for earhead length, peduncle length, effective tiller count per plant, and plant height. The heritability estimates were elevated for all examined traits. The anticipated genetic improvement as a percentage of means was substantial for proline content, grains per earhead, earhead length, peduncle length, effective tillers per plant, and plant height, whereas it was moderate for total phenols."

Methodology

Experimental Material

"In the current study, eighteen genotypes of bread wheat (*Triticum aestivum* L.) were used to provide adequate variability in yield and the quantitative characteristics that are associated with yield. To determine the level of genetic variability and character association twelve agronomic characters such as phenological, morphological, and yield-contributing characters were evaluated in these genotypes.

The experimental layout and design was satisfactory, with petri-plates being used to perform the experiment.

The experiment was setup in a Randomized Block Design (RBD) and replicated three times in order to reduce the variation in the environment and provide precision. All the genotypes were cultivated in the same agronomic conditions with the observance of the recommended cultural operations. Five plants of each genotype were randomly chosen in each replication and observations made on them, with the exception of days to 50 percent flowering which was made on a plot basis.

Data Collection

A total of twelve quantitative characteristics were measured, which were days to 50 percent flowering, height of plants, length of the peduncle, length of ear, number of tillers per plant, flag leaf length, flag leaf width, awn length, number of spikelets per ear, weight of the entire plant, 100-grain weight and weight of the grain per plant. The accurate and consistent results were obtained through standard measuring procedures.

Statistical Analysis

Statistical analysis of the recorded data was done to approximate the mean values and ranges. It was analysed using analysis of variance (ANOVA) to check the significance of differences among the genotypes based on standard procedures. Calculation of genotypic, phenotypic and environmental variances were done and coefficients of variation (GCV, PCV, ECV) were estimated. To ascertain the nature and degree of genetic control of traits that were being studied, broad-sense heritability and expected genetic advance were computed.

Statistical Analysis

The following statistical procedures were followed in the present investigation.

Mean

Mean was calculated by usual procedure

$$\bar{X} = \frac{\sum X}{n}$$

Where,
$\bar{X}$ = Mean value
X = Total value of character
n = Number of observations

Range

Range was calculated with the help of treatment means.

Analysis of Variance (ANOVA)

Analysis of variance was carried out according to Panse and Sukhatme (1967).

Correction Factor (C.F.)

$$\text{C.F.} = \frac{(G.T.)^2}{N}$$

Where,
G.T. = Grand total
N = Total number of observations

Replication Sum of Squares (R.S.S.)

$$\text{R.S.S.} = \frac{(\sum R_1^2 + \sum R_2^2 + \sum R_3^2)}{\text{Number of treatments}} - \text{C.F.}$$

Treatment Sum of Squares (Tr.S.S.)

$$\text{Tr.S.S.} = \frac{(\sum T_1^2 + \sum T_2^2 + \cdots + \sum T_{18}^2)}{\text{Number of replications}} - \text{C.F.}$$

Total Sum of Squares (T.S.S.)

$$\text{T.S.S.} = \text{Sum of squares of all entries} - \text{C.F.}$$

Error Sum of Squares (E.S.S.)

$$\text{E.S.S.} = \text{T.S.S.} - (\text{R.S.S.} + \text{Tr.S.S.})$$

Analysis of Variance Table (ANOVA)

Source of Variation	Degree of Freedom	Sum of Squares	Mean Sum of Squares	F Value
Replication	r − 1	R.S.S.	R.S.S./(r − 1)	MSR/EMS
Treatment	t − 1	Tr.S.S.	Tr.S.S./(t − 1)	MST/EMS
Error	(r − 1)(t − 1)	E.S.S.	E.S.S./(r − 1)(t − 1)	—
Total	rt − 1	T.S.S.	—	—

Test of Significance

The calculated F-values were compared with the table values. A calculated F-value higher than the table F-value at 0.05 probability level indicated significant differences among treatments. If the calculated F-value exceeded the table F-value at 0.01 probability level, the differences were considered highly significant.

Critical Difference (C.D.)

Critical difference was calculated as:

$$\text{C.D.} = \text{S.E.(d)} \times t$$

Where,

S.E.(d) = Standard error of difference between two treatment means

't' = Table value at error degree of freedom at 0.05 or 0.01 probability level

$$\text{S.E.(d)} = \sqrt{\frac{2 \times \text{M.S.E.}}{\text{Number of replications}}}$$

M.S.E. = Error mean square

Variability and Genetic Parameters

Genotypic Variance (σ_g^2)

$$\sigma_g^2 = \frac{\text{M.S. Treatment} - \text{M.S. Error}}{\text{Number of replications}}$$

Error Variance (σ_e^2)

$$\sigma_e^2 = \text{M.S. Error}$$

Phenotypic Variance (σ_p^2)

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

Coefficient of Variation

Phenotypic Coefficient of Variation (PCV)

$$\text{PCV}(\%) = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

Genotypic Coefficient of Variation (GCV)

$$\text{GCV}(\%) = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

Environmental Coefficient of Variation (ECV)

$$\text{ECV}(\%) = \frac{\sqrt{\sigma_e^2}}{\bar{X}} \times 100$$

Where,

σ_p^2 = Phenotypic variance

σ_g^2 = Genotypic variance

σ_e^2 = Environmental variance

$\bar{X}$ = General mean of the character

Heritability (Broad Sense)

Heritability was calculated according to Hanson, Robinson and Comstock (1956).

$$h^2(\%) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Genetic Advance (G.A.)

Expected genetic advance under selection was calculated following Johnson *et al.* (1955).

$$\text{G.A.} = \frac{\sigma_g^2}{\sigma_p^2} \times \sqrt{\sigma_p^2} \times K$$

Where,

K = Selection differential (constant = 2.06 at 5% selection intensity)

Genetic Gain as Percentage of Mean

$$\text{Genetic Gain}(\%) = \frac{\text{G.A.}}{\bar{X}} \times 100$$

Experimental analysis

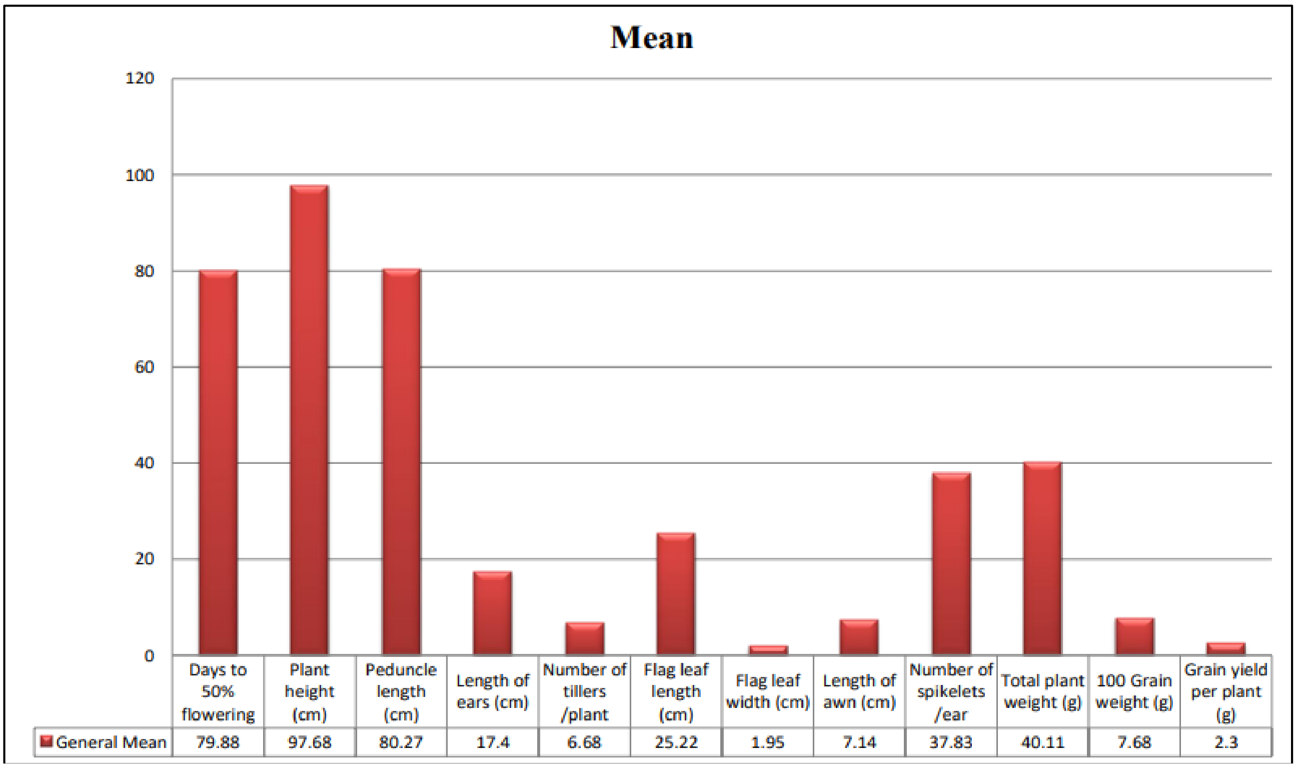
Analysis of Variance

The results of the analysis were used to test the difference between all the twelve quantitative characters and are represented in table 4.1. The mean squares due to treatments were extremely significant at 0.1 percent level of significance of character days to 50 percent flowering. Height of the plants, length of the peduncle, ear length, tillers count/plant, flag leaf width, awn length, number of spikelets/ear and weight of 100 grains were extremely significant at the level of 1 percent of significance. On the same note, flag leaf length, total weight of the plant and the grain yield per plant were significantly different at a 5 percentage level of significance meaning that large degree of dispersion existed in the experimental material of all the characters under the study.

Table 1: Analysis of variance for 12 quantitative characters in wheat (*Triticum aestivum* L.).

Source of Variation	D.F.	Days to 50% flowering	Plant height (cm)	Peduncle length (cm)	Length of ears (cm)	Number of tillers/plant	Flag leaf length (cm)	Flag leaf width (cm)	Length of awn (cm)	Number of spikelets per ear	Total plant weight (g)	100 Grain weight (g)	Grain yield per plant (g)
Replication	2	0.167	1.852	0.667	4.74	0.351	16.167	0.129	4.018	1.5	6.722	0.296	0.68
Treatment	17	76.98***	196.96**	160.55**	10.76**	2.76**	34.66*	0.49**	2.40**	17.65**	7.41*	1.70**	0.35*
Error	34	2.951	0.166	0.235	0.309	0.822	19.814	0.173	0.881	0.715	3.29	0.531	0.185

4.2 Mean Performance



	Days to 50% flowering	Plant height (cm)	Peduncle length (cm)	Length of ears (cm)	Number of tillers /plant	Flag leaf length (cm)	Flag leaf width (cm)	Length of awn (cm)	Number of spikelets /ear	Total plant weight (g)	100 Grain weight (g)	Grain yield per plant (g)
🟥 General Mean	79.88	97.68	80.27	17.4	6.68	25.22	1.95	7.14	37.83	40.11	7.68	2.3

Fig 1: Grand mean performance of 12 quantitative characters in wheat (*Triticum aestivum* L.).

Days to 50% flowering

The overall average of days to 50 percent flowering was 79.88 with a standard deviation of 0.99 days with equal ranges of 73.00 to 88.00 days. The earliest flowering genotypes were PBW154 (73.00), DBW187/Karn Vandana (74.00), MAHIKO GOL (74.33) and SRI RAM INTERNational 303 (74.67) and the late flowering genetics were KW101 (86.00), MANGESH (ANKUR) (86.00) and KEDAR (ANKUR) (88.00).

Plant height (cm)

The average of the plant height was 97.68 = .23 cm with range of 77.33 to 107.67. Genotypes KW101 (77.33), PBW550 (84.00), DBW17 (92.33) and PBW723 (94.33) exhibited lower plant height whereas PBW343 (107.67), HD3226 (107.67), PBW373 (105.33) and HUW234 (104.33) exhibited high plant height.

Peduncle length (cm)

The overall peduncle length mean was 80.27 0.28 cm, with the range of 65.00-93.00 cm. The KW101 (65.00), PBW550 (67.00), PBW154 (75.00) and PBW723 (75.67) genotypes were found to have shorter length of the peduncle and the PBW343 (92.33), HD3226 (89.00), and HUW234 (88.00) were found to have longer length of the peduncle.

Length of ears (cm)

The overall average ear length was 17.40032 cm with a range of 12.33 to 19.67 cm. Lower values were registered in the genotypes KW101 (12.33), DBW17 (15.33), HD2967 (15.33) and PBW343 (15.33) whereas, higher values were registered in MANGESH (ANKUR) (19.67), PBW154 (19.33), KEDAR (ANKUR) (19.33) and MAHIKO GOL (19.00).

Number of tillers per plant

The overall release of the number of tillers per plant was 6.68 with a standard deviation of 0.52 between 5.67 and 9.00. Minimum tillers were observed in PBW373 (5.00), SRI RAM INTER-National 303 (5.00) and MAHIKO GOL (5.67) and KW101 (5.67) genotypes and maximum tillers were observed in PBW343 (9.00), DBW187/Karn Vandana (7.67), HD3226 (7.33) and MANGESH (ANKUR) (7.33) genotypes"

Genetic Variability

Table 4.3 shows the estimates of the grand mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), environmental coefficient of variation (ECV), heritability in broad sense, genetic advance and genetic advance as percentage of mean of all the twelve characters.

The largest GCV was obtained in flag leaf width, then the number of tillers per plant, length of ears, grain yield per plant and length of awn. All characters had higher PCV values than values of GCV, which showed that there was an impact of environmental factors. The flag leaf width recorded the highest ECV then grain yield per plant and grain length of the flag leaf.

Heritability (Broad Sense)

High estimates of heritability were obtained on plant height, length of peduncle, length of ears and days to half flowering. There was moderate heritability of number of spikelets per ear and number of tillers per plant with lower heritability estimates being in the case of 100-grain weight, flag leaf width, length of awn, total plant weight, grain yield per plant and flag leaf length.

Discussion

The results indicate that there is a considerable level of genetic variability of the genotypes of wheat on most of the quantitative traits, meaning that there is sufficient room to apply selection and genetic enhancement. The larger magnitude of the phenotypic coefficients of variations over the genotypic coefficients are indicative of environmental effect on the expression of the traits although the disparities were small in a number of characters. Plant height, peduncle length, ear length, and days to 50 percent flowering traits had a high heritability, which implies that they are mainly genetically determined. Yield-related traits were found to have moderate to low heritability due to their complexity. In general, the variability and genetic parameters noticed support the possibility of the traits to be useful as selection indices in wheat breeding programs.

Conclusion

The research conclusively proves that there is indeed high genetic variation within the considered wheat genotypes in terms of yield and related characteristics. The high heritability and the significant genetic progress of specific characters makes it probable that they will be influenced by additive action of genes which are susceptible to direct selection. Intermediate-heritability traits that contribute to yield are the determinants of indirect selection strategies. The findings give a sound genetic foundation into finding the best genotypes and prioritization of important features in breeding programs. Therefore, the research can be of great value in making effective selection strategies that would improve the productivity of wheat, and come up with better high yielding cultivars.

References

1. Gaur SC. Genetic improvement through variability, heritability and genetic advance for grain yield and its contributing traits in wheat (*Triticum aestivum* L. em Thell). International Journal of Pure & Applied Bioscience. 2019;7(1):368-373. doi:10.18782/2320-7051.7368.
2. Girma SE, Sisay A. Genetic variability, heritability and genetic advance study in bread wheat genotypes (*Triticum aestivum* L.). Advances in Bioscience and Bioengineering. 2021;9(3):13-18. doi:10.11648/j.abb.20210903.13.
3. Lone RA. Genetic variability and correlation studies in winter wheat (*Triticum aestivum* L.) germplasm for morphological and biochemical characters. International Journal of Pure & Applied Bioscience. 2017;5(1):82-91. doi:10.18782/2320-7051.2489.
4. Meena HS, Kumar D, Prasad SR. Genetic variability and character association in bread wheat (*Triticum aestivum*). Indian Journal of Agricultural Sciences. 2014;84(4):394-399. doi:10.56093/ijas.v84i4.39462.
5. Mishra U, Sharma AK, Chauhan S. Genetic variability, heritability and genetic advance in bread wheat (*Triticum aestivum* L.). International Journal of Current Microbiology and Applied Sciences. 2019;8(7):2401-2408. doi:10.20546/ijcmas.2019.807.282.
6. Mundiyara R, Yadav GL, Bajiya R, Singh I, Bhardwaj R, Meena V, *et al.* Genetic variability and character association analysis in wheat (*Triticum aestivum* L.) in saline water condition. International Journal of Bio-Resource and Stress Management. 2024;15(7):1-6. doi:10.23910/1.2024.5361.
7. Poonia MK, Kumar A, Kumar V, Bhanu AN, Kumar S. Genetic variability and character association analysis for seed yield and its attributes in wheat (*Triticum aestivum* L.). International Journal of Plant & Soil Science. 2023;35(9):2912-2919. doi:10.9734/ijpss/2023/v35i92912.
8. Rathwa HK, Pansuriya AG, Patel JB, Jalu RK. Genetic variability, heritability and genetic advance in durum wheat (*Triticum durum* Desf.). International Journal of Current Microbiology and Applied Sciences. 2018;7(1):147-153. doi:10.20546/ijcmas.2018.701.147.
9. Singh K, Singh V, Singh T, Tripathi R, Gupta P, Chauhan M, Sharma G. Analysis of variability, heritability and genetic advance of yield, its components and quality traits in wheat. Journal of Pharmacognosy and Phytochemistry. 2020;9(6):12911-12916. doi:10.22271/phyto.2020.v9.i6f.12911.