Plant Archives Vol. 26, Supplement 1, 2026 pp. 2894-2897 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org
DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2026.v26.supplement-1.389

GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR DIFFERENT CHARACTERS IN WHEAT (*TRITICUM AESTIVUM L.)*

Prakrati Saraswat[1*], Sachchidanand Tripathi[1], Alok Kumar Singh[2], Anuj Shakya[3], Vishal Singh[1] and Neeraj Singh[4],

[1]Department of Genetics and Plant Breeding, Kamla Nehru Institute of Physical & Social Sciences, Sultanpur, U.P., India
[2]Principal, Kamla Nehru Institute of Physical & Social Sciences, Sultanpur, U.P., India
[3]Department of Agriculture, Invertis University, Bareilly, U.P., India
[4]Department of Agril. Statistics, Kamla Nehru Institute of Physical & Social Sciences, Sultanpur, U.P., India
*Corresponding author E-mail: saraswatprakrati21@gmail.com
(Date of Receiving : 07-11-2025; Date of Acceptance : 13-01-2026)

ABSTRACT

This investigation, " Studies on Genetic Variability and Path Coefficient of Grain Yield and its Contributing Traits in Wheat (*Triticum aestivum* L.)," evaluated 20 indigenous wheat genotypes during the *Rabi* season of 2024-25 at Kamla Nehru Institute of Physical and Social Science, Sultanpur, India. The study aimed to study genetic variability for different characters in the wheat population across nine quantitative traits: days to 50% flowering, days to maturity, plant height, number of fertile tillers per plant, peduncle length, 1000-grain weight, harvest index, biological yield per plant, and grain yield per plant. Significant variability was observed among genotypes for all traits. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all traits, indicating environmental influence. Grain yield per plant (GCV: 22.3923, PCV: 25.2120), biological yield per plant (GCV: 11.9421, PCV: 22.8399), and peduncle length (GCV: 20.6156, PCV: 21.3224) showed high PCV and GCV. In contrast, the traits days to 50% flowering (GCV: 5.2921; PCV: 5.9403) and days to maturity (GCV: 5.2195; PCV: 5.3949) exhibited the lowest values for both genotypic and phenotypic coefficients of variation, indicating relatively limited variability for these characteristics. High broad-sense heritability was observed for days to maturity, days to 50% flowering, and plant height. Furthermore, high genetic advance was noted for peduncle length, grain yield per plant, plant height, and 1000-grain weight. These findings provide crucial insights into the genetic architecture and potential for improvement of these traits within the indigenous wheat genotypes.

Keywords : Wheat, *Triticum aestivum* L., Genetic variability, Heritability, Genetic advance, Quantitative traits, Genotypes.

Introduction

Wheat (*Triticum aestivum* L.), an annual, self-pollinating cereal belonging to the Poaceae family, holds paramount importance as a global staple crop. Wheat originated in the "Fertile Crescent," a region widely regarded as the cradle of agriculture, where its domestication significantly influenced the development of early human societies and the rise of civilization (Wang *et al.*, 2021; Peng *et al.*, 2011). Widely acclaimed as the "King of Cereals" and "Golden Grain" due to its broad adaptability, high yield potential, and central role in the global food economy, wheat forms the dietary backbone for millions, supplying substantial daily caloric and protein intake through diverse food products (Mohan *et al.*, 2006). The strategic significance of wheat has led to continuous global efforts aimed at enhancing its yield, bolstering resistance to biotic and abiotic stressors, and improving grain quality to meet evolving end-user demands in an increasingly dynamic agricultural landscape.

The cultivation of wheat dates back to the Neolithic period, around 5000 B.C., with its early spread from the Nile Valley to ancient civilization hubs like the Indus Valley, Euphrates basin, and parts of

China, eventually reaching Europe (Reddy *et al.,* 2023). Wheat, which traces its origins to Asia Minor, has played a significant role in shaping the cultural and economic progress of civilizations across the globe. Its adaptability to diverse growing conditions has helped it become one of the most important staple food crops worldwide across varied climatic and soil conditions.

Wheat (*Triticum aestivum* L.) is a genetically intricate allohexaploid species (2n = 6x = 42), possessing extensive genetic variability. Within India, bread wheat (*T. aestivum*) dominates national cultivation, contributing nearly 88% of total wheat output, while *Triticum durum* accounts for about 10%, and *Triticum dicoccum* makes up less than 2% of the production (Grewal *et al*., 2015). Wheat is well adapted to the cool and dry climate typical of the Rabi season and needs particular temperature ranges throughout its growth stages. It grows optimally in well-drained soils such as loamy and clay-loam types. It is widely cultivated in diverse agro-climatic regions throughout India (Britannica, 2021). From a nutritional perspective, wheat is a vital source of both macro and micronutrients, comprising around 60–68% carbohydrates, 8–15% protein, and essential minerals. Its high gluten content plays a crucial role in dough elasticity, making it a cornerstone in the baking industry and a key contributor to nutritional security worldwide (Rathore, 2001; Heyne, 1987).

On a global scale, wheat stands as the second-most produced cereal crop after maize, with an estimated production of 785 million metric tons recorded during the 2023–2024 period. Countries such as China, India, and Russia are among the top wheat producers, with the global cultivation area reaching approximately 215.48 million hectares. In the Indian context, wheat was cultivated on 31.86 million hectares during the 2022–2023 season, producing 107.45 million tons, with Uttar Pradesh emerging as the leading state in production (Statistics at a Glance, 2023). The wheat industry worldwide is undergoing transformation due to technological innovations in agriculture, changing dietary trends favoring processed foods, and increasing demand for specific grain quality characteristics (Pingali, 2012).

To fulfil the escalating demand for wheat, it is essential to integrate improved agricultural methods with the development of high-yielding and stress-tolerant varieties. Grain yield in wheat is a complex quantitative trait governed by multiple genes and influenced by various genetic, environmental, morphological, and pathological components. Gaining a clear understanding of the genetic basis of yield and associated traits is fundamental to breeding resilient and high-performing genotypes (Sukumaran *et al*., 2018). The cornerstone of any wheat improvement program lies in the availability of substantial genetic variation within the breeding material, which enables efficient selection. Evaluating both genotypic and phenotypic correlations among yield-related traits helps in elucidating their interdependencies and their direct or indirect contributions to grain yield (Olivera *et al*., 2019, 2022). Furthermore, traits exhibiting high heritability coupled with significant genetic advance are of paramount importance in selection strategies. High heritability reflects additive gene effects and ensures selection reliability, while genetic advance estimates the potential improvement achievable through selection, thereby assisting breeders in designing effective strategies for developing improved wheat cultivars (Girma & Sisay, 2021).

Materials and Methods

The experiment was conducted during the *Rabi* season of 2024-25 at the Experimental Field of the Department of Genetics and Plant Breeding, Kamla Nehru Institute of Physical and Social Sciences, Sultanpur, Uttar Pradesh, India (26.30°N latitude, 82.11°E longitude). The site features a moist subtropical climate with summer temperatures ranging from 32-46°C and winter temperatures from 5-15°C. Average annual rainfall is approximately 1110 mm, primarily received between July and September, with a mean relative humidity of 67%. The soil type at the experimental farm is sandy loam with a pH of 7.0–7.4.

The study utilized 20 indigenous genotypes of bread wheat (*Triticum aestivum L.*) as the experimental material. These genotypes were evaluated in a Randomized Block Design (RBD) with three replications. Each genotype was sown on November 20, 2024, in plots consisting of three 4-meter-long rows. Spacing was maintained at 20 cm between rows and 15 cm between plants, with a 50 cm gap between plots. All recommended agronomic practices and necessary plant protection measures were consistently applied to ensure optimal crop growth.

Observations were recorded on nine quantitative traits from five randomly selected plants in each plot. The average data from these selected plants were used for subsequent statistical analyses. The recorded traits included: number of days to 50% flowering, number of days to maturity, plant height (cm), number of fertile tillers per plant, peduncle length (cm), and 1000-grain weight (g).

The statistical analysis of the data was averaged per replication by taking mean of 5 plants per replication. Analysis of variance (ANOVA) for a

Randomized Block Design was performed following Panse and Sukhatme (1961, 1967) to test genotypic differences using the F-test. Genetic variability parameters, including Genotypic and Phenotypic Coefficients of Variation (GCV and PCV), were assessed as per Lush (1940) and Burton and De Vane (1953). Broad-sense heritability (h^2b) was estimated following Hanson *et al.* (1956), and genetic advance as percent of mean (GAM) by Lush (1949), Johnson *et al.* (1955), and Allard (1960). Categorization scales for GCV/PCV, heritability, genetic advance, were also applied.

Result and Discussion

The data presented in Table 1 delineate the genetic variability, heritability, and genetic advance of the evaluated traits, offering foundational information for developing effective breeding strategies.

The range of variation for each trait indicated considerable diversity within the studied germplasm. For instance, the number of days to 50% flowering ranged between 72.00 and 92.00 days, while plant height varied from 72.84 cm to 119.60 cm, indicating a wide range of variability and considerable potential for effective selection. The mean values provide a central measure of performance for each character, with Grain Yield per Plant averaging 24.0240 g.

Analysis of the coefficients of variation revealed that the Phenotypic Coefficient of Variation (PCV) was consistently higher than the Genotypic Coefficient of Variation (GCV) for all traits, indicating an influence of environmental factors on trait expression. Traits such as Grain Yield per Plant (GCV: 22.3923, PCV: 25.2120), Biological Yield per Plant (GCV: 11.9421, PCV: 22.8399), and Pod Length (GCV: 20.6156, PCV: 21.3224) exhibited high GCV and PCV values, indicating a substantial genetic influence on their variability and, therefore, a strong scope for genetic enhancement through selection. Conversely, Days to 50% Flowering (GCV: 5.2921, PCV: 5.9403) and Days to Maturity (GCV: 5.2195, PCV: 5.3949) showed lower GCV and PCV, implying relatively less genetic variability for these traits within the population.

Broad-sense heritability estimates indicated the proportion of phenotypic variance attributable to genetic variance. High broad-sense heritability was observed for Days to 50% Flowering (79.73%), Days to Maturity (93.61%), and Plant Height (87.57%), signifying that these traits are largely under genetic control and would respond effectively to direct selection. Moderate heritability was noted for 1000 Grain Weight (70.48%). Traits such as fertile tillers per plant (20.80%), harvest index (35.56%), and biological yield per plant (27.34%) exhibited comparatively low heritability estimates

The genetic advance (GA) quantifies the expected genetic gain from selection. High genetic advance was noted for Pod Length (5.6557), Grain Yield per Plant (9.8425), Plant Height (17.6754), and 1000 Grain Weight (5.4097). When expressed as a percentage of the mean (GAM), Pod Length (41.0607%) and Grain Yield per Plant (40.9694%) showed high expected gains. High heritability coupled with high genetic advance indicates that the trait's expression is predominantly controlled by additive gene action, making selection highly effective and reliable for genetic improvement.

Table 1 : Range mean, coefficient variation, heritability, genetic advance and genetic advance as per cent of mean.

Character	Range		Mean	Coefficient of variation			Heritability (%)	Genetic advance	Genetic advance as %age of mean
	Min.	Max.		GCV	PCV	ECV			
Days to 50% Flowering	72.0000	92.0000	81.5833	5.2921	5.9403	2.6984	0.7973	7.9234	9.7120
Days to maturity	121.0000	149.0000	131.5833	5.2195	5.3949	1.3641	0.9361	13.6884	10.4028
Plant height	72.8400	119.6000	92.7293	9.8882	10.5669	3.7261	0.8757	17.6754	19.0613
Peduncle length	7.6000	19.6300	13.7740	20.6156	21.3224	5.4448	0.9348	5.6557	41.0607
Fertile tillers per plant	7.4000	16.6000	12.9592	8.3816	18.3795	16.3571	0.208	1.0204	7.8740
1000 Grain weight	21.8700	42.5600	33.0878	9.4539	11.2612	6.1186	0.7048	5.4097	16.3495
Harvest index	20.0300	57.9500	35.6428	11.2364	18.8421	15.1251	0.3556	4.9200	13.8036
Biological yield per plant	40.1500	104.0000	67.7217	11.9421	22.8399	19.4691	0.2734	8.7109	12.8628
Grain yield per plant	15.6700	41.3800	24.0240	22.3923	25.2120	11.5857	0.7888	9.8425	40.9694

Conclusion

The study revealed significant genetic variability among the twenty indigenous wheat genotypes for all evaluated traits. This variability presents a substantial opportunity for genetic improvement through breeding. High broad-sense heritability was observed for days to maturity, days to 50% flowering, and plant height, indicating that direct selection for these traits would be highly effective. Furthermore, high genetic advance was noted for peduncle length, grain yield per plant, plant height, and 1000-grain weight, suggesting that significant improvement in these traits can be achieved through selection efforts.

References

Allard, R.W. (1960). *Principles of Plant Breeding.* John Wiley & Sons, New York, USA.

Britannica. (2021). *Wheat.* Encyclopaedia Britannica Inc., Chicago, USA.

Burton, G. W., & DeVane, E. H. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*, **45**, 478–481.

Dewey, D. R., & Lu, K. H. (1959). A correlation and path-coefficient analysis of components of crested wheatgrass seed production. *Agronomy Journal*, **51**, 515–518.

Falconer, D. S. (1964). *Introduction to Quantitative Genetics.* Oliver and Boyd, Edinburgh, UK.

Fisher, R. A., & Yates, F. (1963). *Statistical Tables for Biological, Agricultural and Medical Research.* Oliver and Boyd, Edinburgh, UK.

Girma, A., & Sisay, T. (2021). Genetic variability, heritability and genetic advance in wheat. *Ethiopian Journal of Agricultural Sciences*, **31**(2), 45–58.

Grewal, R. P. S., Singh, R., & Sharma, R. K. (2015). Genetic variability and character association in wheat. *Indian Journal of Genetics and Plant Breeding*, **75**(4), 478–484.

Hanson, C. H., Robinson, H. F., & Comstock, R. E. (1956). Biometrical studies of yield in segregating populations of Korean lespedeza. *Agronomy Journal*, **48**, 268–272.

Heyne, E. G. (1987). *Wheat and Wheat Improvement* (2nd ed.). American Society of Agronomy, Madison, USA.

Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, **47**, 314–318.

Lenka, D., & Mishra, B. (1973). Path coefficient analysis of yield in rice varieties. *Indian Journal of Agricultural Sciences*, **43**, 376–379.

Li, C. C. (1975). *Path Analysis: A Primer.* Boxwood Press, Pacific Grove, USA.

Lush, J. L. (1940). Intra-sire correlations or regression of offspring on dam as a method of estimating heritability. *Journal of Animal Science*, **1**, 293–301.

Lush, J. L. (1949). Heritability of quantitative characters in farm animals. *Proceedings of the 8th International Congress of Genetics*, 356–375.

Mohan, M., Gupta, R., & Sharma, I. (2006). Wheat improvement in India: Achievements and challenges. *Indian Journal of Agricultural Sciences*, **76**(5), 261–273.

Olivera, C. S., Santana, F. M., & Costa, L. C. (2019). Genetic parameters and trait associations in wheat. *Crop Science*, **59**, 1234–1245.

Olivera, C. S., Santana, F. M., & Costa, L. C. (2022). Path coefficient analysis for grain yield in wheat. *Theoretical and Applied Genetics*, **135**, 987–998.

Panse, V. G., & Sukhatme, P. V. (1967). *Statistical Methods for Agricultural Workers* (2nd ed.). ICAR, New Delhi, India.

Peng, J., Sun, D., & Nevo, E. (2011). Domestication evolution, genetics and genomics in wheat. *Molecular Breeding*, **28**, 281–301.

Pingali, P. L. (2012). Green revolution: Impacts, limits, and the path ahead. *Proceedings of the National Academy of Sciences*, **109**(31), 12302–12308.

Rathore, P. S. (2001). *Techniques and Management of Field Crop Production.* Agrobios, Jodhpur, India.

Reddy, V. R., Kumar, S., & Singh, P. (2023). Historical evolution and spread of wheat cultivation. *Journal of Crop History*, **12**(1), 15–28.

Searle, S. R., Casella, G., & McCulloch, C. E. (1965). *Variance Components.* Wiley, New York, USA.

Statistics at a Glance. (2023). Directorate of Economics and Statistics, Ministry of Agriculture & Farmers Welfare, Government of India.

Subramanian, S., & Menon, M. P. (1973). Genotypic and phenotypic variability in crop plants. *Agricultural Research Journal of Kerala*, **11**, 23–27.

Sukumaran, S., Reynolds, M. P., & Sansaloni, C. (2018). Genome-wide association studies for grain yield in wheat. *Frontiers in Plant Science*, **9**, 179.

Wang, J., Liu, Y., & Zhang, L. (2021). Genomic insights into wheat evolution and domestication. *Nature Genetics*, **53**, 142–150.

Wright, S. (1921). Correlation and causation. *Journal of Agricultural Research*, **20**, 557–585.