# Genetic diversity and variability analysis for yield and its components in wheat (*Triticum aestivum* L.)

**Abstract**

Ninety genotypes along with four checks of wheat were studied for creating scientific information on nature and magnitude of genetic diversity and variability at MES of Acharya Narendra Deva University of Agriculture and Technology in 2023. The experiment was conducted in Augmented Block Design. The data were recorded on Days to 50% flowering, Days to maturity, Plant height, Effective tillers per plant, Spike length, Spikelets per spike, 1000-grain weight, Biological yield per plant, Grain yield per plant. Analysis of variance showed significant differences among the genotypes for all characters and variance due to treatments were highly significant, whereas the variation due to blocks were not significant. The highest estimate of genotypic and phenotypic variation is due to plant height the highest estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded for 1000- grain weight. Low PCV values (<10%) were obtained for almost all the characters. High heritability was observed for all the traits and moderate genetic advance observed for 1000- grain weight, genetic advance of grain yield per plant observed was 10.41%. Variability in the genotypes and heritability in the tested traits of the genotypes under study have generally been noted. Thus, hybridization and selection on those genotypes based on the characteristic with high heritability and GCV and genetic advancement might be suggested for further bread wheat yield increase at the appropriate place.

**Key words:** Heritability, genetic advance, phenotypic, genotypic coefficient of variation

**INTRODUCTION**

Wheat (*Triticum aestivum* L.) is one of the most extensively cultivated cereal crops, contributes to both economic security and the world's food supply. It is the world's principal cereal crops, which are a reliable source of food in many areas, are cultivated using both rain and irrigation. Wheat accounts for 17% of global agricultural land and is widely produced in temperate climates. For 40% of people worldwide, it is their basic diet **(Goyal and Prasad, 2010; Peng *et al.,* 2011)**. Due to its importance, it is currently also one of the most significant grains cultivated on a wide scale (**Fassil *et al.,* 2000**). Wheat covers area globally is 220.7 million hectares (545 million acres) **(2021)**. In India, more than 179 million hectares of agricultural land were reported to be under cultivation in the fiscal year 2023, out of which 31.8 million hectares of wheat were harvested in India in 2024–2025. In contrast, over 31.4 million hectares of land were harvested for wheat in 2023–2024 **(STATISTICA 2024).** More than 4.5 billion people worldwide rely on wheat for 20% of their protein and 21% of their overall caloric intake, second only to rice in 94 underdeveloped nations **(Braun *et al.,* 2010)**. Breeders face a difficult challenge in increasing current output levels since the nation's expanding population will need far more food than the current needs. There is no way to expand the producing area. Therefore, the only way to meet the growing demand for food is to boost productivity through the development of better crop types and improved agricultural production management. The continuous development of the best available genotypes for further expansion of their yield potential, either directly or through improvement of many aspects that contribute indirectly to high yield, is a key source of concern for plant breeders. Therefore, the breeding approach needed to be such that it could essentially include the advantageous modifications either by hybridizing better genotypes or by selection. In this sense, knowledge on the kind and extent of genetic diversity is crucial for initiating any organized crop breeding effort. Significant genetic variety in the starting material increases the likelihood that desirable plant kinds will evolve **(Sabharwal and Lodhi, 1995)**. Several studies have highlighted specific traits—such as high tillering potential, increased grain weight, efficient spike fertility, greater spike density, higher grain count per spike, and rapid ground coverage—as being positively associated with yield stability and heat stress tolerance in wheat. In recent years, elevated temperatures have emerged as a critical constraint on wheat productivity, particularly in arid and semi-arid regions. With global temperatures continuing to rise, temperature extremes at both the beginning and end of the growing season increasingly limit wheat cultivation. Given that plant tolerance to heat stress is a heritable trait, it is amenable to genetic improvement through targeted breeding efforts.

However, breeding for enhanced thermal tolerance poses significant challenges. These include an incomplete understanding of the genetic and physiological mechanisms underlying heat resistance, the interactive effects of concurrent stresses such as drought, uncertainty regarding the optimal developmental stages for selection, and the absence of reliable, high-throughput screening methods for physiological traits associated with heat tolerance (cite). Elucidating the interrelationships among morphological and physiological traits linked to heat resilience is essential for establishing effective selection criteria. Correlation analyses at both genotypic and phenotypic levels can offer valuable insights into these trait associations. The strength and direction of such correlations can inform breeding strategies aimed at improving heat tolerance. Accordingly, the present study was undertaken to explore these associations and contribute to the development of more resilient wheat genotypes.

**Materials and Methods**

A total of ninety along with four checks (DBW14, DBW187, NW1014, and HD3086) of wheat genotypes were evaluated to estimate direct selection parameters—such as genetic variability, heritability, and genetic advance in relation to heat tolerance. The study was conducted at the MES of Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, during the Rabi seasons of 2023-2024. An Augmented block design was employed for the field trials. The experimental field will be separated into 6 blocks, with each block housing 19 plots (15 genotypes and 4 checks). Each plot has two 3 m-long rows with a 5 cm plant-to-plant spacing inside each row and a 20 cm distance between rows. Standard agronomic practices were uniformly applied throughout the experimental period.

Data collection focused on grain yield and associated agronomic traits, including days to 50% flowering; plant height; spike length; spikelets per spike; days to maturity; flag leaf area; number of grains per spike; 1000-grain weight; biological yield per plant; grain yield per plant; harvest index. Measurements for all traits were based on five randomly selected plants from each genotype. The measurement of flag leaf was done manually by using scale and applying mathematical formula to get result. The collected data were analysed through analysis of variance, and further subjected to biometrical techniques to compute genotypic and phenotypic coefficients of variation, along with heritability in broad sense.

The mean values of all traits were subjected to analysis of variance following the statistical model outlined by **Panse and Sukhatme (1969)**. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated based on the method described by **Searle (1961)**. Estimates of broad-sense heritability [h²/(b)] and genetic advance as a percentage of the mean were derived using the formulas proposed by **Allard (1960).**

**Results and Discussion**

Genetic Variability:

Analysis of variance demonstrated highly significant differences among the genotypes for all the traits evaluated (Table 1), indicating the presence of considerable genetic variability within the population. This substantial variation suggests a strong potential for future genetic improvement through selection. These findings are consistent with those reported by **Tanzeen *et al.* (2009)**. The observed diversity may be attributed to the utilization of genetically diverse breeding materials and the influence of environmental factors on phenotypic expression.

Table 1: Analysis of variance (ANOVA) for all the evaluated traits

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

1000 grain weight and Effective tillers per plant were among the characteristics with the highest phenotypic variance values, although other traits also displayed a similar pattern. This implies that these variables have a good range of selection. For every characteristic, the phenotypic coefficient of variance was greater than the corresponding genotypic coefficient of variation. The highest phenotypic coefficient of variation was seen in the 1000 grain weight and effective tillers per plant. Table 2 displays the range, mean, phenotypic and genotypic coefficients of variation (PCV, GCV), broad-sense heritability, and genetic advancement estimates. The range of heritability was 89.32 to 99.87 percent among them the highest is for biological yield per plant (99.87%) followed by 1000- grain weight (99.65%), plant height (99.54%), spikelets per spike (99.53), days to maturity (98.11), flag leaf area (98.06), spike length (97.67) all showed high heritability estimates. The heritability of the none of the characteristics was modest.

Compared to genotypic variance ($σ^{2}g$) estimates of phenotypic variance ($σ^{2}p$) were larger (Table 2). Plant height,1000-grain grains per spike, days to maturity, days to 50% flowering, flag leaf area showed a broad range of phenotypic variance ($σ^{2}p$), although effective tillers per plant, spike length and spikelets per spike indicated a small range of variance. The phenotypic coefficient of variation showed that the plant height had the greatest coefficient of variation (6.61) while 1000-grain weight at second place (5.2). For plant height, the genotypic coefficient of variation was highest (6.58) followed by 1000- grain weight (5.19). Additionally, the genotypic coefficient of variation for other feature was moderate to low and effective tillers per plant showed the lowest genotypic variation value.

 Table 2: Genetic variability parameters for different agronomic traits

The parameters such as 1000-grain weight (13.05), biological yield per plant (11.10), effective tillers per plant (10.65), grain yield per plant (10.41), spike length (8.24) had the greatest estimate of genetic progress as a percentage of mean. High genetic advancement and high heritability were combined to show that selection was successful in improving these qualities, as seen by the percent mean for 1000 grain weight and biological yield per plant, effective tillers per plant, and grain yield per plant. Heritability is the percentage of variability passed on from parents to children (**Lush, 1949**). All characters showed high estimates of heritability, none of the characters showed low or moderate estimates (Table 2). High heritability was also noted by **Yadav *et al.* (2014**) for test weight, tillers per plant, grain per spike, days to 50% blooming, days to maturity, and grain yield per plant. This indicates that there is an additive gene impact and that these qualities may be improved by selection. Even while low heritability showed that environmental factors had a significant impact on the traits, it will be challenging to enhance genetics through selection because of the environment's influence. According to **Johanson *et al.* (1955**), a trait with high heritability may not always translate into great genetic advancement. It can be determined more precisely when heredity is combined with is examined in relation to genetic advancement **(Dudley and Moll, 1969**). Consequently, it is more beneficial to estimate heritability in conjunction with genetic advancement in order to comprehend the sort of gene activity implicated in the manifestation of several polygenic traits.

Days to 50% flowering, plant height, number of spikelets per spike, number of grains per spike, 1000 grain weight, biological yield per plant, and grain yield per plant all showed strong heritability and high genetic advancement as a percentage mean**. Nagireddy** and **Jyothula (2009)** and **Khokhar *et al*. (2011**) reported similar results. This suggests that additive gene activity had a significant role in the characters' expression. Therefore, it would be more beneficial to pick for such characters directly.

**Conclusion**

Significant genetic variation was found among the studied genotypes, and heritability for many parameters supported the idea that wheat productivity may be raised in the target area. To effectively boost grain output, attention should be paid to characteristics with moderate to high heritability and genetic advancement. Therefore, for further bread wheat yield enhancement at the appropriate area, selection and hybridization on genotypes based on the characteristic with high GCV, heritability, and genetic advancement can be advised.

**References:**

Allard, R.W. (1960). Principle of Plant Breeding. John Wiley and sons, NewYork. p. 185.

Braun HJ, Atlin G, Payne T (2010). Multi-location testing as a tool to identify plant response to global climate change. In: Reynolds MP, ed. Climate Change and Crop Production. Surrey: CABI. pp. 115 138.

Dudley, J.W. and Moll, R.H. (1969). Interpretation and uses of estimates of heritability and genetic advance in plant breeding. Crop Sci. (9): 257-262.

FAO (2024) FAO Statistical Yearbook 2024, Statistical Division, Food and Agricultural Organization, Rome, https://www.fao.org/worldfoodsituation/csdb/en.

Fassil K, Teklu E, Teklu T, Assefa G (2000). On farm demonstration of improved durum wheat varieties under enhanced drainage on Vertisols in central highlands of Ethiopia. In: Eleventh Regional Wheat Workshop for Eastern, Central and Southern Africa. CIMMYT, Addis Ababa, Ethiopia.

Goyal A, Prasad R (2010). Some important fungal diseases and their impact on wheat production. In: Arya A, PerellóAEV (eds) Management of fungal plant pathogens. CABI (H ISBN 9781845936037). P 362.

Johnson, H.W., Robinson, H.F. and Comstock, R.F. (1955). Estimates of genetic and environmental variability in soybean. Agron. J. 47: 314-318.

Khokhar, M.I., Hussain, M., Zulkiffal, M., Sabir, W., Mahmood, S. and JamilAnwar, M.W. (2010). Studies on genetic variability and inter-relationship among the different traits in wheat (Triticum aestivum L.) Krmiva. 52: (2) 77-84.

Lush, J.L. (1949). Heritability of quantitative characters in farms animals. Proceedings of 8th Congress of Genetics and Hereditas. 35: 356-375.

Nagireddy, A.V. and Jyothula, D.P.B. (2009). Heritability and interrelationship of yield and certain agronomic traits in wheat. Research on Crops. 10(1): 124-127

Panse, V.G. and Sukhatme, P.V. (1969). Statistical methods for agricultural workers. Indian Council of Agricultural Research, New Delhi.

Peng J, Sun D, Nevo E (2011). Wild emmer wheat, Triticum dicoccoides, occupies a pivotal position in wheat domestication. Agricultural Journal of Crop Science 5:1127-1143.

Sabhrawal, P.S. and Lodhi, G.P. (1995). Germplasm evaluation for different traits in wheat (Triticum aestivum L.). HAU, J. of Agri. Res. 25 (4): 207 - 210.

Searle, S.R. (1961). Phenotypic, Genotypic and environmental correlations. Biometrics 47: 474-480.

Tazeen, M. and Naqvi., F.N. (2009). Heritability, phenotypic correlation and path coefficient studies for some agronomic characters in synthetic elite lines of wheat. J. of Food Agri. and Environ. 7(3/4):278-282

Yadav, S.K., Singh, A.K., Baghel, S.S., Jarman, M. and Singh, A.K. (2014). Assessment of genetic variability and diversity for yield and its contributing traits among CIMMYT based wheat germplasm. J. of Wheat Res. 6(2): 154-159.