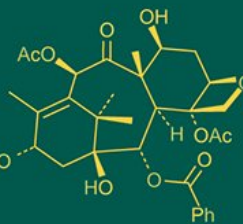


International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2026): 5.29
IJABR 2026; SP-10(6): 1428-1436
www.biochemjournal.com
Received: 27-05-2026
Accepted: 28-06-2026

Meghana Singh Rajotia
Department of Genetics and
Plant Breeding, College of
Agriculture, Chaudhary
Charan Singh Haryana
Agricultural University (CCS
HAU), Hisar, Haryana, India

Om Parkash Bishnoi
Department of Genetics and
Plant Breeding, College of
Agriculture, Chaudhary
Charan Singh Haryana
Agricultural University (CCS
HAU), Hisar, Haryana, India

Yogender Kumar
Department of Genetics and
Plant Breeding, College of
Agriculture, Chaudhary
Charan Singh Haryana
Agricultural University (CCS
HAU), Hisar, Haryana, India

Corresponding Author:
Meghana Singh Rajotia
Department of Genetics and
Plant Breeding, College of
Agriculture, Chaudhary
Charan Singh Haryana
Agricultural University (CCS
HAU), Hisar, Haryana, India

Genetic variability for yield and physiological traits associated with early heat stress tolerance in bread wheat (*Triticum aestivum* L.)

Meghana Singh Rajotia, Om Parkash Bishnoi and Yogender Kumar

DOI: <https://www.doi.org/10.33545/26174693.2026.v10.i6Sq.8849>

Abstract

Early heat stress is an important constraint affecting wheat growth and productivity, particularly under changing climatic conditions. The present investigation was conducted to assess genetic variability, heritability and genetic advance for phenological, morphological, physiological and yield-related traits in bread wheat (*Triticum aestivum* L.) under early heat-stress and normal environments. Six wheat crosses were evaluated under two sowing environments, designated as early heat stress (E₁) and normal condition (E₂), using a randomized complete block design with three replications. Observations were recorded for days to heading, days to anthesis, days to maturity, plant height, spike length, peduncle length, spikelets per spike, NDVI-I, NDVI-II, SPAD chlorophyll content, canopy temperature, tillers per plant, grains per spike, thousand grain weight, grain weight per spike, biological yield per plant, harvest index and grain yield per plant. Phenotypic coefficient of variation was higher than genotypic coefficient of variation for all traits, indicating environmental influence on trait expression. However, narrow differences between these estimates for several traits suggested an appreciable genetic contribution. NDVI-I and NDVI-II showed high genotypic variability, very high heritability and high genetic advance as percentage of mean under both environments. Peduncle length, number of grains per spike, grain weight per spike and grain yield per plant also showed useful variability parameters, particularly under early heat-stress conditions. The results indicate that NDVI-I, NDVI-II, peduncle length and selected yield-related traits may be useful selection criteria for improving wheat performance under early heat-stress environments.

Keywords: Early heat stress, genetic advance, genetic variability, grain yield, heritability, *triticum aestivum*

Introduction

Bread wheat (*Triticum aestivum* L.) is one of the most important cereal crops worldwide and serves as a major source of calories and protein for a large proportion of the global population. Sustaining wheat productivity is essential for ensuring food security under changing climatic conditions. However, increasing temperatures have emerged as a major constraint to wheat production, particularly in regions where crops are exposed to elevated temperatures during the vegetative and reproductive growth phases. Heat stress adversely affects crop growth, accelerates phenological development, reduces photosynthetic activity and ultimately leads to substantial reductions in grain yield.

The development of heat-tolerant wheat cultivars remains one of the most effective approaches for minimizing yield losses under high-temperature conditions. The success of such breeding programmes largely depends upon the availability and exploitation of genetic variability present in the breeding material. Genetic variability constitutes the basic prerequisite for selection and provides opportunities for genetic improvement of economically important traits. In self-pollinated crops such as wheat, the magnitude of variability available for different characters determines the efficiency of selection and the extent of genetic gain that can be achieved through breeding. Recent studies conducted in wheat have demonstrated the existence of substantial variability for agronomic, physiological and yield-related traits, emphasizing the importance of variability assessment in crop improvement programmes (Patil *et al.*, 2024; Ali *et al.*, 2024; Chauhan *et al.*, 2023) [2, 5, 12].

The assessment of genetic variability is commonly achieved through the estimation of genotypic coefficient of variation (GCV) and phenotypic Coefficient of variation (PCV). Burton (1952) [3, 4] proposed that these parameters provide valuable information regarding the magnitude of variability present in a population. While PCV measures the overall phenotypic variation, GCV estimates the proportion attributable to genetic causes. A narrow difference between PCV and GCV indicates relatively lower environmental influence on trait expression and suggests that phenotypic selection may be effective. Therefore, the simultaneous estimation of GCV and PCV is useful for understanding the relative contribution of genetic and environmental factors to observed variation.

Although variability estimates provide an indication of the extent of genetic diversity, they alone are insufficient for predicting response to selection. Heritability estimates indicate the proportion of phenotypic variance that is heritable and therefore transmissible to subsequent generations. However, Johnson *et al.* (1955) [8, 9] emphasized that heritability should be considered together with genetic advance for reliable prediction of selection response. High heritability associated with high genetic advance generally indicates the predominance of additive gene effects and greater effectiveness of direct selection, whereas high heritability coupled with low genetic advance may suggest the involvement of non-additive gene action. Consequently, the combined evaluation of variability parameters, heritability and genetic advance has become a standard approach in wheat breeding programmes for identifying traits amenable to genetic improvement.

In recent years, greater emphasis has been placed on evaluating physiological traits along with conventional yield attributes under heat stress environments. Traits such as normalized difference vegetation index (NDVI), chlorophyll content and canopy-related characteristics have been recognized as useful indicators of plant vigour, photosynthetic efficiency and adaptation to adverse environments. Simultaneously, yield-contributing traits such as number of grains per spike, thousand grain weight and grain yield per plant remain the primary targets of wheat improvement programmes. Understanding the magnitude of genetic variability and inheritance of these traits under both normal and heat stress conditions can facilitate the identification of reliable selection criteria for breeding heat-resilient wheat cultivars. Similar approaches have been adopted in recent variability studies in wheat under contrasting environments (Thapa *et al.*, 2023; Patil *et al.*, 2024; Akbar *et al.*, 2025) [1, 12].

Analysis of variance (ANOVA) was performed separately for each environment to assess the significance of variation among the studied genotypes following the procedure described by Panse and Sukhatme (1985) [11]. Genotypic variance and phenotypic variance were estimated from the analysis of variance components. The genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV) were calculated according to the method proposed by Burton (1952) [3, 4]. Broad-sense heritability (h^2) was estimated following Hanson *et al.* (1956) [6, 7]. Genetic advance (GA) and genetic advance as percentage of mean (GG) were computed according to Johnson *et al.* (1955) [8, 9]. The magnitude of variability was interpreted based on the classification suggested by Sivasubramanian and

Madhavamenon (1973) [15], wherein GCV and PCV values were categorized as low (<10%), moderate (10-20%) and high (>20%). Heritability estimates were classified as low (<30%), moderate (30-60%) and high (>60%) following Robinson *et al.* (1949) [14]. Genetic advance as percentage of mean was categorized as low (<10%), moderate (10-20%) and high (>20%) according to Johnson *et al.* (1955). All variability parameters were estimated separately under E_1 (early heat stress) and E_2 (normal) environments.

Material and methods

The experimental material comprised six bread wheat (*Triticum aestivum* L.) crosses, namely DBW 187 × WH 1270, DBW 187 × DBW 327, PBW 872 × DBW 327, WH 1184 × WH 1270, WH 1156 × WH 1270 and DBW 173 × WH 1270. The parental lines and their respective generations were evaluated during the *Rabi* season 2024-25 under two sowing environments. The first environment (E_1) consisted of early sowing and represented the early heat-stress environment, in which the crop was exposed to elevated temperatures during the early stages of growth. The second environment (E_2) consisted of timely sowing and represented the normal environment. The contrasting environments facilitated the assessment of genetic variability and selection parameters under both stress and favourable growing conditions. The experiment was conducted in a randomized complete block design with three replications.

Observations were recorded on phenological, morphological, physiological and yield-related traits. Phenological traits included days to heading, days to anthesis and days to maturity. Morphological traits comprised plant height, spike length, peduncle length and number of spikelets per spike. Physiological observations included normalized difference vegetation index at initiation of anthesis (NDVI-I), normalized difference vegetation index recorded 15 days after anthesis (NDVI-II), SPAD chlorophyll content and canopy temperature. Yield and yield-attributing traits included number of tillers per plant, number of grains per spike, thousand grain weight, grain weight per spike, biological yield per plant, harvest index and grain yield per plant.

Analysis of variance was performed separately for each environment to assess the significance of variation among the studied genotypes. Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV) were estimated according to the procedure suggested by Burton (1952). Broad-sense heritability (h^2) was calculated following Hanson *et al.* (1956) [6, 7], while genetic advance (GA) and genetic advance as percentage of mean (GG) were estimated according to Johnson *et al.* (1955). The magnitude of variability was interpreted based on GCV and PCV estimates, whereas heritability together with genetic advance was used to assess the effectiveness of selection and to infer the nature of gene action governing different traits. All variability parameters were estimated separately under E_1 (early heat stress) and E_2 (normal) environments.

Results

Genetic variability in phenological and morphological traits

In general, the phenotypic coefficient of variation (PCV) was slightly higher than the corresponding genotypic

coefficient of variation (GCV) for all traits, indicating the influence of environmental factors on trait expression. However, the relatively narrow differences between PCV and GCV suggested that the observed variation was predominantly genetic in nature.

Among the phenological traits, days to anthesis exhibited the highest GCV (3.35 and 2.76%) and PCV (3.80 and 3.37%) under E_1 and E_2 , respectively, whereas days to maturity recorded the lowest variability with GCV values of 2.27 and 2.39% (Figure 2). Heritability estimates for phenological traits ranged from 60.24 to 77.63%, while genetic advance as percentage of mean (GG) remained low (3.80-6.08%), indicating limited scope for improvement through direct selection.

Among the morphological traits, peduncle length exhibited the highest variability with GCV values of 8.08 and 9.36% and PCV values of 8.99 and 10.18% under E_1 and E_2 , respectively. The trait also recorded high heritability (80.81 and 84.57%) and moderate GG (14.97 and 17.73%) (Figure 5). Plant height showed moderate variability but high heritability, particularly under E_2 (84.58%), with a GG of 10.87% (Figure 4).

Genetic variability in physiological traits

Among all the studied traits, NDVI-I and NDVI-II exhibited the highest magnitude of genetic variability and heritability under both environments. NDVI-II recorded the highest GCV (18.33% under E_1 and 17.67% under E_2) and PCV (18.97 and 18.10%), coupled with very high heritability estimates of 93.39 and 95.35%, respectively. The trait also exhibited the highest GG values of 36.50 and 35.55% (Figure 7)

Similarly, NDVI-I recorded high GCV (14.55 and 14.86%) and PCV (15.20 and 15.28%), along with very high heritability estimates of 91.63 and 94.64% and GG values of 28.69 and 29.78% under E_1 and E_2 , respectively (Figure 6).

The narrow differences between PCV and GCV for both NDVI traits indicated minimal environmental influence on their expression.

In contrast, SPAD chlorophyll content and canopy temperature exhibited relatively low variability. SPAD recorded GCV values of 4.07 and 3.89% with heritability estimates close to 60%, while canopy temperature exhibited GCV values of 3.06 and 2.53% and heritability estimates of 66.96 and 61.30% under E_1 and E_2 , respectively (Figure 8). Both traits showed low GG values, ranging from 4.09 to 6.49%.

Genetic variability in yield and yield-contributing traits

Under E_1 , grain yield per plant exhibited high variability with GCV and PCV values of 14.55 and 16.06%, respectively. The trait also recorded high heritability (82.06%) and GG (27.15%). Under E_2 , GCV, heritability and GG decreased to 8.69%, 64.62% and 14.38%, respectively.

Grain weight per spike recorded high variability under E_1 , with GCV and PCV values of 13.12 and 15.12%, respectively, coupled with high heritability (75.29%) and GG (23.44%). However, under E_2 , the corresponding estimates declined substantially, with heritability decreasing to 40.31% and GG to 8.06% (Figure 11). Number of grains per spike exhibited moderate to high variability and heritability under E_1 (GCV = 8.61%, h^2 = 82.62% and GG = 16.12%), whereas lower estimates were observed under E_2 (GCV = 5.21%, h^2 = 63.11% and GG = 8.52%) (Figure 10). Overall, the results indicated that NDVI-I, NDVI-II, grain yield per plant, grain weight per spike, peduncle length and number of grains per spike possessed substantial genetic variability coupled with moderate to high heritability and genetic advance, suggesting their potential usefulness as selection criteria for improving wheat performance under early heat stress conditions.

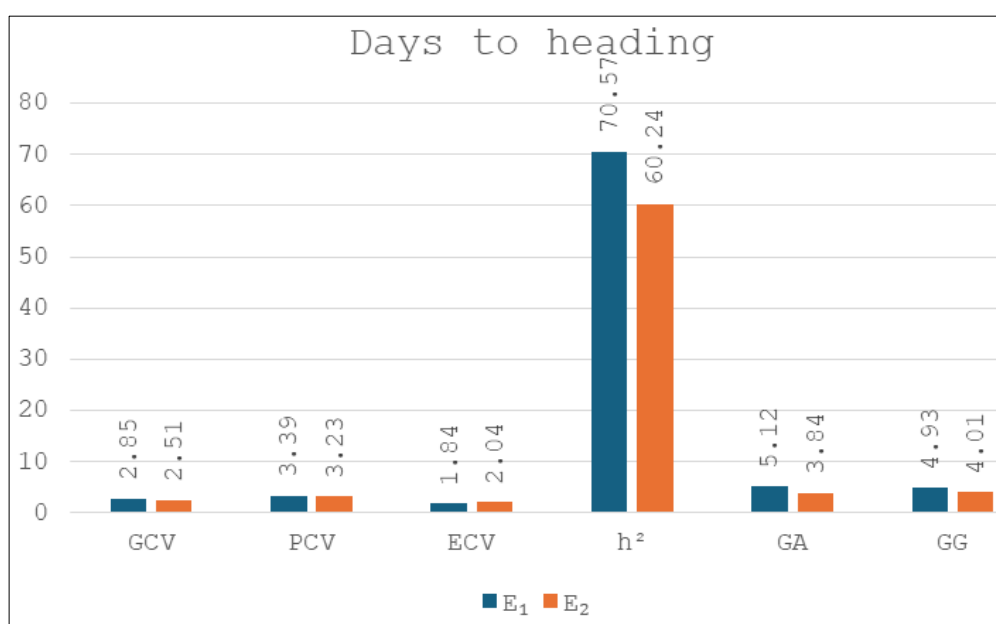


Fig 1: Estimates of variability parameters for days to heading under early heat stress (E_1) and normal (E_2) environments

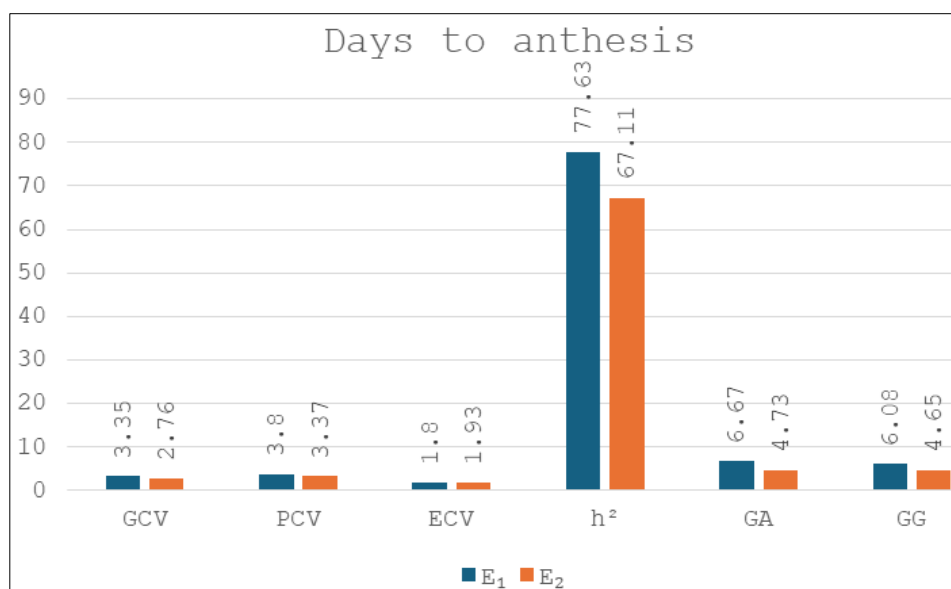


Fig 2: Estimates of variability parameters for days to anthesis under early heat stress (E₁) and normal (E₂) environments

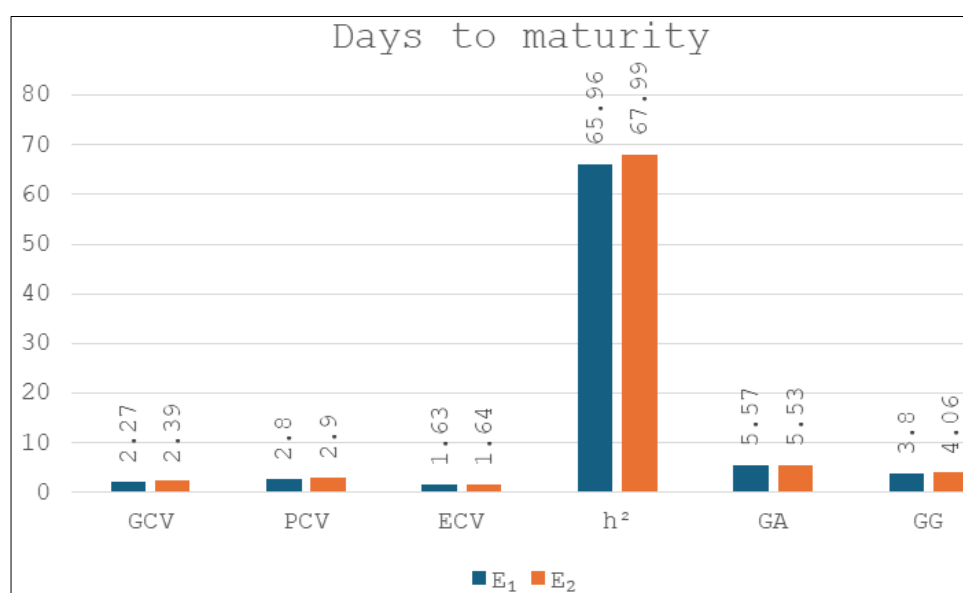


Fig 3: Estimates of variability parameters for days to maturity under early heat stress (E₁) and normal (E₂) environments.

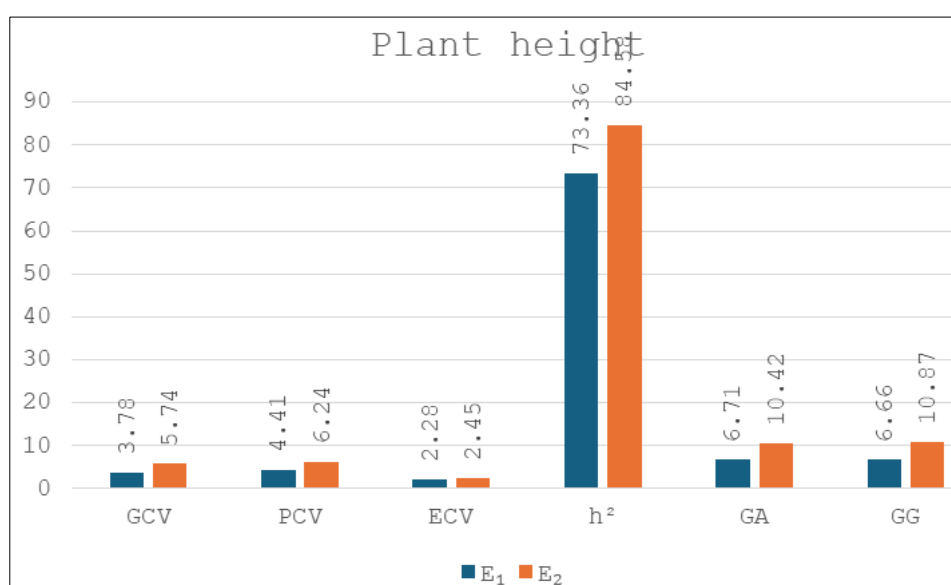


Fig 4: Estimates of variability parameters for plant height under early heat stress (E₁) and normal (E₂) environments

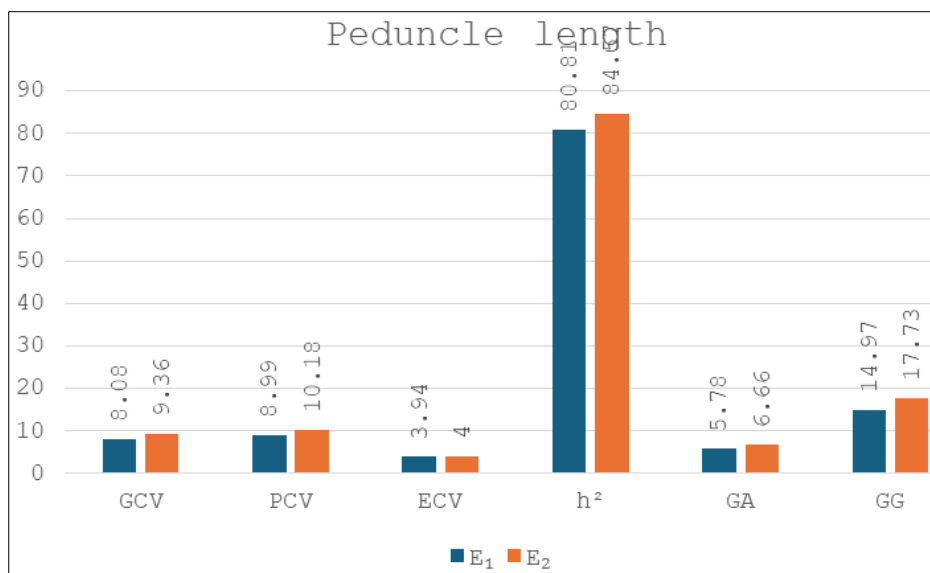


Fig 5: Estimates of variability parameters for peduncle length under early heat stress (E₁) and normal (E₂) environments.

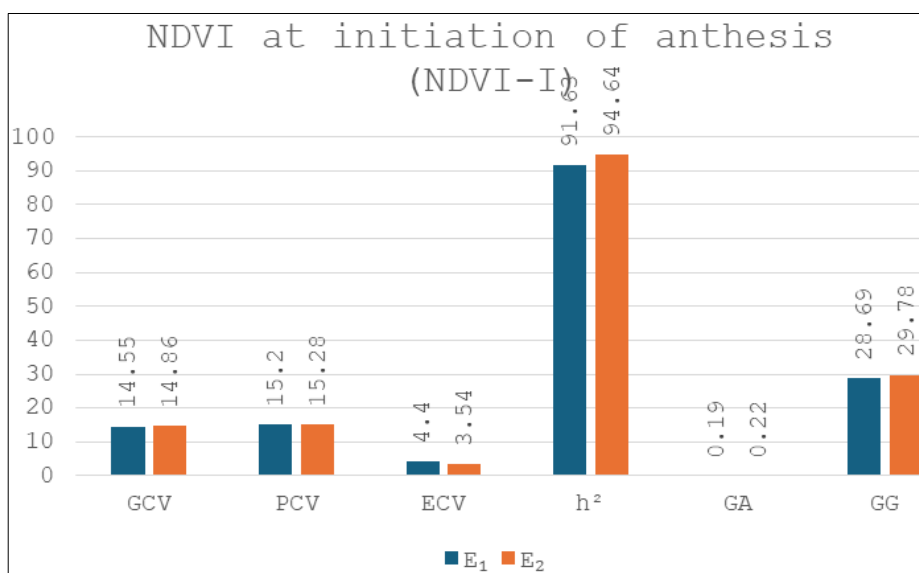


Fig 6: Estimates of variability parameters for NDVI at initiation of anthesis (NDVI-I) under early heat stress (E₁) and normal (E₂) environments

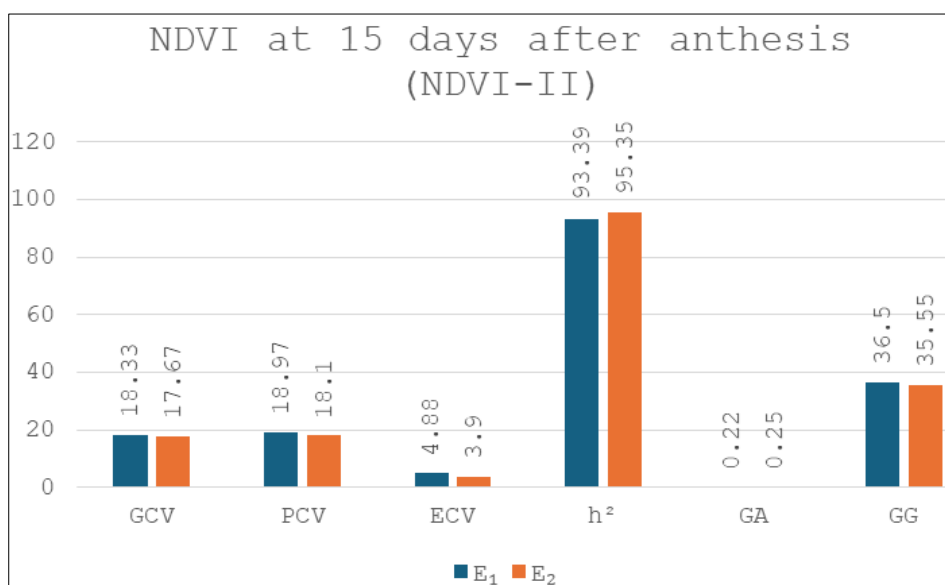


Fig 7: Estimates of variability parameters for NDVI at 15 days after anthesis (NDVI-II) under early heat stress (E₁) and normal (E₂) environments.

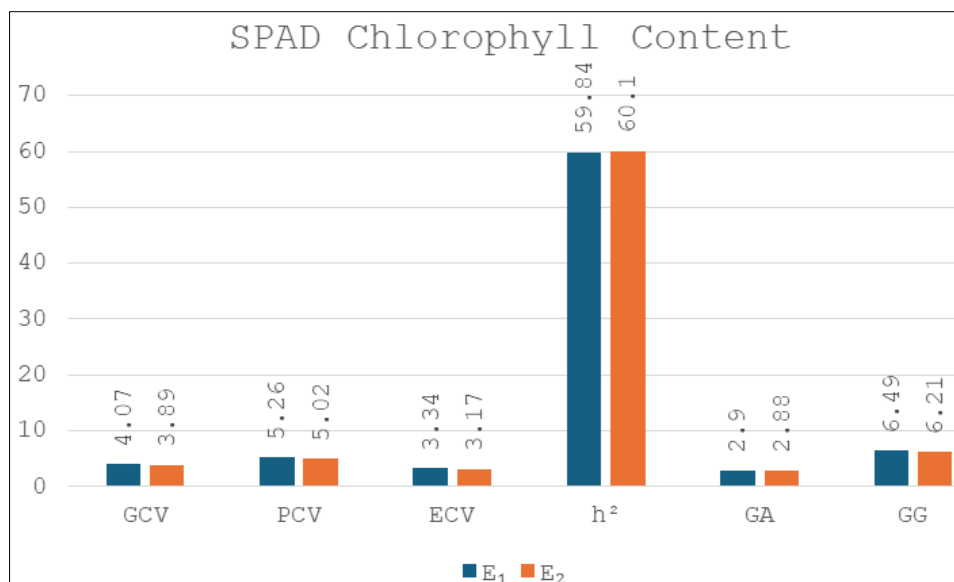


Fig 8: Genetic variability parameters for SPAD chlorophyll content under early heat stress (E₁) and normal (E₂) environments.

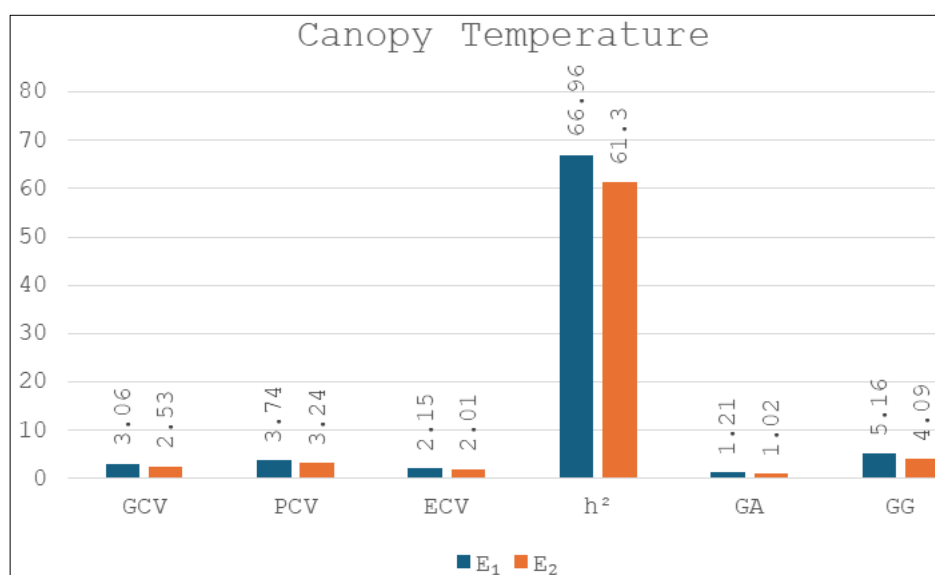


Fig 9: Genetic variability parameters for canopy temperature under early heat stress (E₁) and normal (E₂) environments.

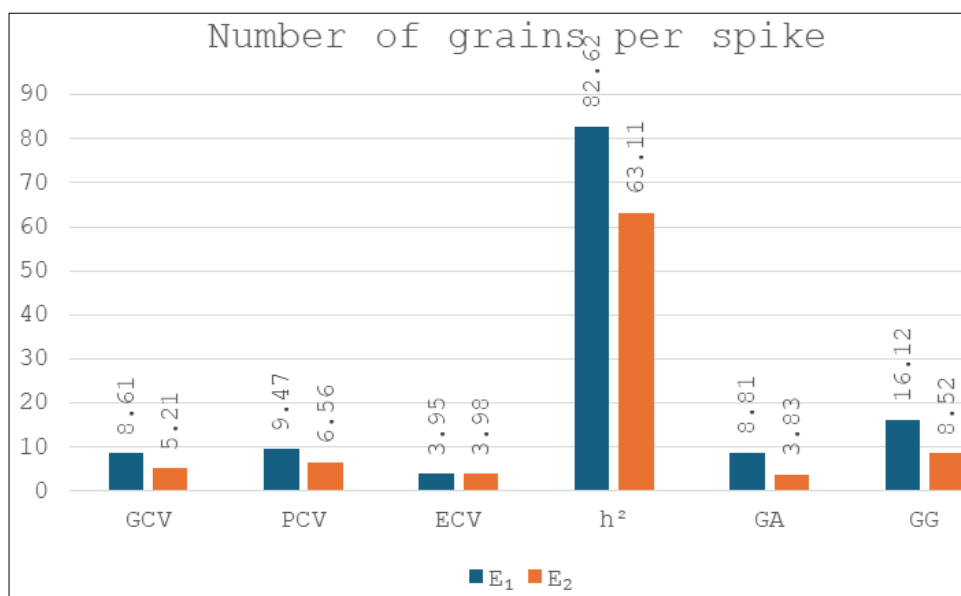


Fig 10: Estimates of variability parameters for number of grains per spike under early heat stress (E₁) and normal (E₂) environments

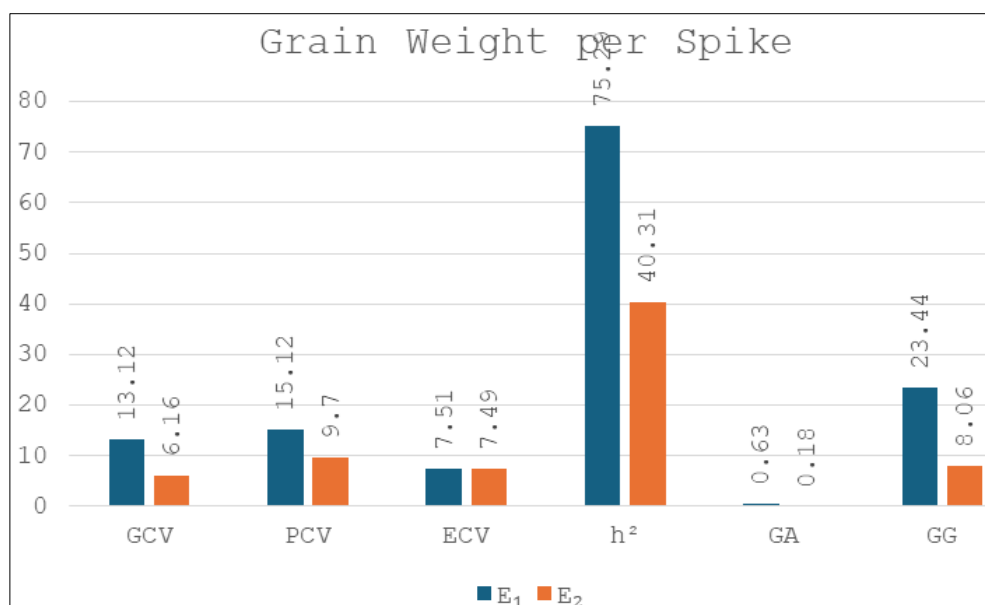


Fig 11: Estimates of variability parameters for grain weight per spike under early heat stress (E₁) and normal (E₂) environments

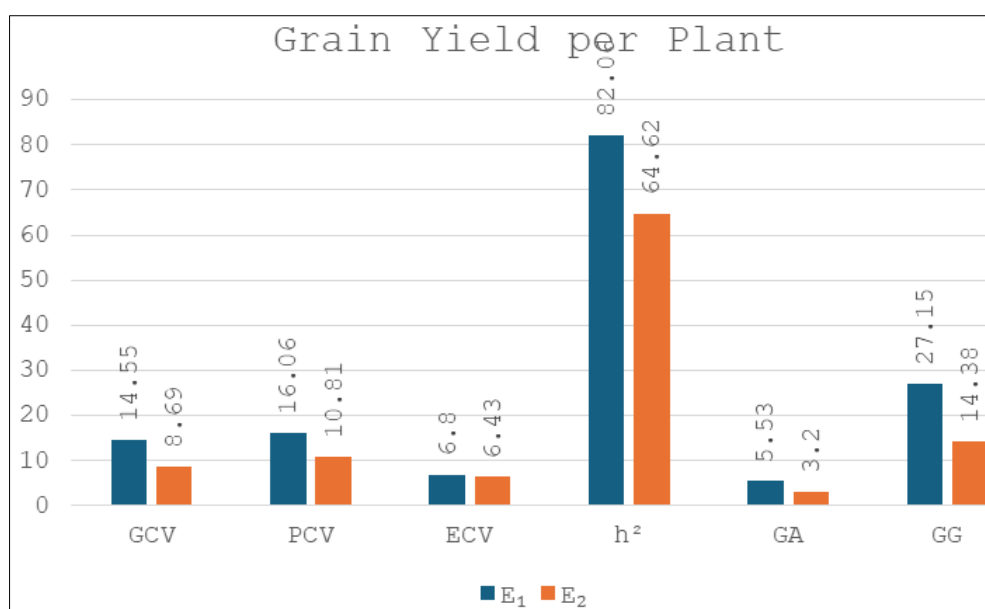


Fig 12: Estimates of variability parameters for grain yield per plant under early heat stress (E₁) and normal (E₂) environments

Discussion

The magnitude of genetic variability present in a breeding population determines the effectiveness of selection and the potential for genetic improvement. In the present study, phenotypic coefficient of variation (PCV) estimates were consistently higher than the corresponding genotypic coefficient of variation (GCV) values for all studied traits under both early heat stress (E₁) and normal (E₂) environments, indicating the influence of environmental factors on trait expression. However, the relatively narrow differences between PCV and GCV for most characters suggested that a substantial proportion of the observed variation was genetically controlled and that phenotypic selection would be reasonably reliable. Similar observations in bread wheat have been reported by Ali *et al.* (2024) [2], Patil *et al.* (2024) [12], Chauhan *et al.* (2023) [5] and Akbar *et al.* (2025) [1], who also observed slightly higher PCV than GCV values for most agronomic and yield-related traits. Among the phenological traits, days to heading, days

to anthesis and days to maturity exhibited low GCV and PCV values under both environments. Heritability estimates were moderate to high, whereas genetic advance as percentage of mean (GG) remained low. Such a combination generally indicates limited genetic variability and restricted scope for substantial improvement through direct selection. The low genetic advance despite moderate heritability may be attributed to the involvement of non-additive gene effects and the relatively conserved nature of phenological traits in adapted wheat germplasm. Similar findings were reported by Chauhan *et al.* (2023) [5], Ali *et al.* (2024) [2] and Patil *et al.* (2024) [12], who observed low variability and low expected genetic gain for flowering and maturity traits in wheat populations.

Among the morphological traits, plant height and peduncle length showed comparatively greater genetic variability than phenological traits. Peduncle length exhibited moderate to high GCV and PCV along with high heritability and moderate genetic advance under both environments. High

heritability coupled with appreciable genetic advance generally indicates the predominance of additive gene action and suggests that improvement through direct phenotypic selection would be effective. Plant height also exhibited high heritability, particularly under the normal environment, although the corresponding genetic advance was relatively lower than that observed for peduncle length. Similar associations of high heritability and moderate genetic advance for plant height and peduncle length have been reported by Thapa *et al.* (2019) ^[16], Chauhan *et al.* (2023) ^[5] and Patil *et al.* (2024) ^[12].

Considerable variation was observed among physiological traits. NDVI-I and NDVI-II recorded the highest GCV and PCV values among all studied characters and also exhibited exceptionally high heritability estimates exceeding 90 per cent under both environments. Furthermore, both traits expressed high genetic advance as percentage of mean, indicating the predominance of additive gene effects and strong genetic control. The narrow difference between GCV and PCV further demonstrated minimal environmental influence on trait expression. NDVI is widely recognized as an indicator of canopy vigour, biomass accumulation and photosynthetic efficiency under stress environments. Lopes *et al.* (2012) ^[10] reported that NDVI-based measurements were strongly associated with biomass production and grain yield in wheat breeding populations. Reynolds *et al.* (2017) ^[13] also emphasized the usefulness of canopy spectral traits as indirect selection tools for improving adaptation and productivity under stress environments. The present findings suggest that NDVI-I and NDVI-II may serve as reliable selection criteria for improving wheat adaptation to early heat stress conditions.

In contrast, SPAD chlorophyll content and canopy temperature exhibited comparatively low GCV and PCV values, moderate heritability and low genetic advance. The low magnitude of genetic advance suggests limited exploitable variability within the studied material and indicates that direct selection for these traits may be less effective. Similar observations have been reported by Thapa *et al.* (2019) ^[16], who found relatively lower variability and expected genetic gain for physiological traits associated with chlorophyll content and canopy temperature under heat stress conditions.

Yield and yield-contributing traits exhibited considerable variability, particularly under the early heat stress environment. Number of grains per spike recorded moderate to high GCV, high heritability and moderate genetic advance under E₁ environment, indicating the presence of substantial additive genetic variance. Grain weight per spike also exhibited high variability and favourable heritability estimates under early heat stress. However, the reduction in heritability and genetic advance under E₂ environment suggested a comparatively greater environmental influence under normal growing conditions. Similar results were reported by Ali *et al.* (2024) ^[2] and Akbar *et al.* (2025) ^[1], who observed substantial genetic variability and favourable heritability estimates for grain number and grain weight traits in bread wheat populations.

Grain yield per plant exhibited one of the highest levels of variability among the yield-related traits. Under early heat stress, grain yield showed high GCV, high heritability and high genetic advance as percentage of mean, indicating the existence of considerable exploitable genetic variation. The comparatively lower estimates observed under the normal

environment suggest that stress conditions may have enhanced the expression of genetic differences among genotypes. High heritability associated with high genetic advance generally reflects additive genetic control and indicates that effective progress can be achieved through selection. Similar findings have been reported by Patil *et al.* (2024), Ali *et al.* (2024) and Akbar *et al.* (2025) ^[1], who identified grain yield as a highly variable and selectable trait in wheat breeding populations.

Overall, the present investigation demonstrated that NDVI-I, NDVI-II, peduncle length, number of grains per spike, grain weight per spike and grain yield per plant possessed favourable combinations of genetic variability, heritability and genetic advance. These traits exhibited substantial genetic control and therefore represent promising selection criteria for the development of wheat genotypes adapted to early heat stress environments.

Conclusion

The study revealed the presence of genetic variability for several physiological and yield-related traits in bread wheat under early heat-stress and normal environments. Phenotypic coefficient of variation was higher than genotypic coefficient of variation for all traits, showing that environmental factors influenced trait expression. However, relatively narrow differences between these estimates for several characters indicated that genetic factors also contributed substantially to the observed variation. Among the physiological traits, NDVI-I and NDVI-II showed high genotypic coefficient of variation, very high heritability and high genetic advance as percentage of mean under both environments. These results suggest that NDVI-based traits may be useful indicators for selection in the studied material. Peduncle length, number of grains per spike, grain weight per spike and grain yield per plant also showed favourable variability parameters, especially under the early heat-stress environment. In contrast, phenological traits, SPAD chlorophyll content and canopy temperature showed comparatively lower genetic advance. Overall, the findings indicate that NDVI-I, NDVI-II and selected yield-contributing traits can be considered useful selection criteria for wheat improvement under early heat-stress conditions.

References:

1. Akbar A, Ahmad I, Jehan A, Ali I, Haris M. Genetic variability among advanced wheat lines for yield and yield related traits. *Sarhad Journal of Agriculture*. 2025; 41(1):154-164.
2. Ali A, Javed M, Ali M, Rahman SU, Kashif M, Khan SU. Genetic variability, heritability, and genetic gain in F3 populations of bread wheat (*Triticum aestivum* L.) for production traits. *Sabrao Journal of Breeding and Genetics*. 2024; 56(2):505-518.
3. Burton GW. Quantitative inheritance in grasses. *Proceedings of the 6th International Grassland Congress*. 1952; 1:277-283.
4. Burton GW. Quantitative inheritance in grasses. *Proceedings of the 6th International Grassland Congress*. 1952; 1:277-283.
5. Chauhan S, Gupta A, Tyagi SD, Singh S. Genetic variability, heritability and genetic advance analysis in bread wheat (*Triticum aestivum* L.) genotypes. *International Journal of Plant & Soil Science*. 2023; 35(19):164-172.

6. Hanson CH, Robinson HF, Comstock RE. Biometrical studies of yield in segregating populations of Korean lespezea. *Agronomy Journal*. 1956; 48(6):268-272.
7. Hanson CH, Robinson HF, Comstock RE. Biometrical studies of yield in segregating populations of Korean lespezea. *Agronomy Journal*. 1956; 48(6):268-272.
8. Johnson HW, Robinson HF, Comstock R. Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*. 1955; 47(7):314-318.
9. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*. 1955; 47(7):314-318.
10. Lopes MS, Reynolds MP, Manes Y, Singh RP, Crossa J, Braun HJ. Genetic yield gains and changes in associated traits of CIMMYT spring bread wheat in a “historic” set representing 30 years of breeding. *Crop Science*. 2012; 52(3):1123-1131.
11. Panse VC, Sukhatme PV. Statistical methods for agricultural workers. New Delhi: Indian Council of Agricultural Research; 1985. p. 145.
12. Patil P, Shrivastav SP, Patil K, Landge R, Gurjar D. Genetic variability, heritability, genetic advance and divergence analysis in wheat (*Triticum aestivum* L.). *Indian Journal of Agricultural Research*. 2024; 58(2):209-214.
13. Reynolds MP, Pask AJ, Hoppitt WJ, Sonder K, Sukumaran S, Molero G, Joshi AK. Strategic crossing of biomass and harvest index-source and sink-achieves genetic gains in wheat. *Euphytica*. 2017; 213(11):257.
14. Robinson HF, Comstock RE, Harvey PH. Estimates of heritability and the degree of dominance in corn. *Agronomy Journal*. 1949; 41(8):353-359.
15. Sivasubramanian S, Madhavamenon P. Genotypic and phenotypic variability in rice. *Madras Agricultural Journal*. 1973; 60:1093-1096.
16. Thapa RS, Sharma PK, Pratap D, Singh T, Kumar A. Assessment of genetic variability, heritability and genetic advance in wheat (*Triticum aestivum* L.) genotypes under normal and heat stress environment. *Indian Journal of Agricultural Research*. 2019; 53(1):51-56.