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Original Article

Trait-Based Evaluation of Bread Wheat Genotypes (*Triticum aestivum* L. em. Thell) Under Terminal Heat Stress

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Abstract

Terminal heat stress is a major constraint on wheat productivity in India's Northwestern Plains Zone, adversely impacting grain yield. This study aimed to identify heat-tolerant genotypes and the key morphological traits associated with resilience. Fifty diverse wheat genotypes were evaluated over two consecutive *Rabi* seasons (2020-22) under timely sown (TS) and late-sown (HS) conditions, the latter inducing terminal heat stress. Grain yield exhibited a strong positive correlation with the harvest index, biological yield per plot, and number of effective tillers per meter. Moderate associations were observed for several traits, such as spike length, spikelets per spike, grains per spike, 1,000-grain weight, flag leaf length, peduncle length, peduncle extrusion, spike weight, and grain weight per spike across both environments. Principal component analysis revealed that biological yield, grain yield, flag leaf length, and effective tillers were the primary contributors to variability under stress, accounting for most of the explained variance. Multiple regression analysis (R^2 = 0.815 and 0.685 for TS and HS, respectively) confirmed the importance of biological yield per plot, harvest index, and tiller number in maintaining yield under heat stress. Selection via a multi-trait genotype-ideotype distance index, combined with high heritability estimates, identified genotypes G2, G3, G9, G22, G35, and G37 as superior performers with enhanced thermotolerance. These genotypes represent valuable genetic resources for breeding programs. The study concludes that simultaneous selection for high biological yield, harvest index, and fertile tiller number is critical for enhancing wheat productivity under terminal heat stress, providing a clear framework for developing climate-resilient varieties.

Categories: Plant genetic resources, Sustainable climate smart agriculture, Trait genetics & breeding of crops

Keywords: wheat, heat stress, correlation, path, pca, regression, mgidi

Introduction

Abiotic stresses are the primary cause of crop losses worldwide, reducing the yields of crops, including wheat, by more than 50% [1,2]. Wheat production is challenged by unpredictable variability in various biotic and abiotic stresses, particularly heat stress and erratic rainfall, especially in dry, semi-arid, tropical, and subtropical regions of the world [3]. Owing to global climate change, wheat yields are projected to decline by 6% for every 1°C increase in temperature. Consequently, global wheat production must increase by 60% by 2050 to meet the food demand of the growing global population [4]. Heat stress in wheat occurs when the average temperature exceeds 31°C during the growth period, negatively affecting plant phenology, growth, and development, and influencing various physiological and biochemical processes. Heat stress during the flowering stage causes pollen and anther sterility, resulting in undeveloped embryos by affecting pollination and fertilization. It also accelerates spikelet development, resulting in the formation of sterile spikelets [5]. Additionally, it leads to a significant decrease in relative growth rate, dry weight, internode size, the number of productive tillers, and biomass, as well as a reduction in cell size, while accelerating senescence. Heat stress during the early grain-filling stage decreases grain weight and the number of grains per spike, thereby severely reducing yield [6-8].

With ongoing climatic changes, it is imperative to focus on maintaining wheat yields by identifying genotypes that are tolerant to heat stress and promoting breeding techniques and management practices that can protect wheat production from heat stress [9]. This necessitates rethinking and redesigning breeding strategies, specifically to target key component traits and identify genotypes with higher productivity and better tolerance to stresses posed by the changing climate. However, wheat yield is a multifaceted quantitative trait arising from the interactions among several component traits [10]. Wheat pre-breeding and breeding programs should shift their focus to utilizing secondary traits, such as the number of grains per spike, grain weight, grain size, and grain-filling rate under heat stress [11]. In addition, an improved understanding of the complex correlations among morphological features linked to heat stress tolerance has important implications for identifying several tolerance mechanisms that will assist in ameliorating the adverse effects of heat stress on wheat. Hence, the adoption of multivariate analysis techniques is a better option, not only for selecting potential genotypes but also for identifying vital traits that principally govern tolerance mechanisms under high-temperature conditions. Moreover, selecting superior genotypes with higher genetic gains and desirable traits is crucial for successful breeding programs. The introduction of newer tools, such as the multi-trait genotype-ideotype distance index (MGIDI), can assist in such identification, as this index considers multiple traits simultaneously, allowing researchers to assess both the strengths and weaknesses of the tested genotypes relative to an ideal breeding target [12]. While earlier studies have largely focused on individual traits or single analytical methods, the present approach combines multiple statistical frameworks to capture complex trait interactions and identify superior genotypes more effectively. This integrated strategy provides a more reliable and holistic basis for selection in wheat breeding programs. In view of this, this study aimed to highlight the intricate relationships among the examined phenological traits under heat stress conditions and their potential to support grain yield, offering insights into the development of heat-resilient wheat genotypes.

Materials And Methods

This study was carried out at the Wheat and Barley Section, CCSHAU, Hisar (29.09°N, 75.43°E, 215.2 m a.s.l.), located in the subtropical region of the Northwestern Plains Zone of India, over two growing seasons (2020-21 and 2021-22). The experiments were conducted under irrigated conditions at the research farm. Fifty bread wheat genotypes, along with two checks, HD3086 (timely sown (TS), irrigated conditions) and WH1124 (late sown (HS), irrigated conditions), were used in this study. Under TS conditions, the sowing dates were 11 November 2020 and 8 November 2021. Under HS conditions, the sowing dates were 6 December 2020 and 10 December 2021. The experiment was conducted in triplicate using a randomized complete block design under two conditions, resulting in 300 experimental units per season. Each plot (3.6 m^2) comprised three rows of 6 m length, with a row-to-row distance of 20 cm. The TS and HS experiments were irrigated 5-6 times to avoid the effects of drought on the tested material. Recommended agronomic practices for this region, in terms of fertilization, weeding, and crop protection, were adopted to grow healthy wheat crops. HS was used as a standard and widely accepted approach to impose terminal heat stress, as it exposes the crop to higher temperatures during the grain-filling stage, thereby simulating natural stress conditions.

Data collection

Data on yield and 16 phenological traits, including days to heading (DH), days to maturity (DM), plant height (PH), spike length (SL), number of spikelets per spike (NS/S), flag leaf length (FL), peduncle length (PL), peduncle extrusion length (PEL), tillers per meter (TL/M), biological yield per plot (BY/P), grain yield per plot (GY/P), harvest index (HI), spike weight

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(SW), grain weight per spike (GW), thousand-grain weight (TGW), and number of grains per spike (NGS/S), were recorded from five randomly selected plants or on a plot basis for each entry across three replications. DH was recorded on a plot basis when 50% of the plants reached heading, and DM was recorded when the entire plot reached physiological maturity. BY/P and GY/P were recorded in kilograms per plot for each genotype, and TGW was estimated by weighing 1,000 grains (g).

Statistical analysis

The analysis was conducted using pooled data across two seasons to ensure robustness and minimize year-to-year variability. A stepwise analytical framework was adopted in which analysis of variance (ANOVA) was first used to assess variability, correlation, and path analysis to examine trait relationships. Principal component analysis (PCA) was employed for dimensionality reduction, regression was used for predictive modelling, and MGIDI was applied for multi-trait genotype selection. Genetic variation was assessed using ANOVA [13]. The genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and broad-sense heritability (h^2) were estimated. Correlation coefficients among traits were calculated following the method suggested by Al-Jibouri et al. [14]. Path coefficient analysis was carried out using phenotypic correlation coefficients as described by Dewey and Lu [15] and Wright [16]. Multiple stepwise regression and PCA were conducted according to the procedures described by Draper and Smith [17], Snedecor and Cochran [18], Gewers et al. [19]. The MGIDI index was used to rank genotypes based on their proximity to an ideal ideotype using the '*metan*' package [12]. It was calculated according to the methodology proposed by Olivoto and Nardino [12] as follows:

$$MGIDI_i = \left[\sum_{j=1}^{f} (Y_{ij} - Y_j)^2 \right]^{0.5}$$

where MGIDI is the multi-trait genotype-ideotype distance index for the i^{th} genotype, Y_{ij} is the j^{th} score of the i^{th} genotype, and Y_j is the j^{th} score of the ideotype ($i = 1, 2, \ldots, t$; $j = 1, 2, \ldots, f$), where t and f denote the number of genotypes and traits, respectively.

The strengths and weaknesses of individual genotypes were assessed by calculating the proportion of the MGIDI of the i^{th} genotype explained by the j^{th} trait (ω_{ij}) as follows:

$$\omega_{ij} = \frac{\sqrt{D_{ij}^2}}{\sum_{j=1}^{f} \sqrt{D_{ij}^2}}$$

For MGIDI analysis, each trait was assigned a specific direction of selection according to the desired ideotype for heat stress tolerance. Traits related to plant architecture and phenology, such as DH, DM, and PH, were defined with a decreasing direction. Reduced DH promotes early flowering, enabling plants to escape heat stress during the highly sensitive reproductive stage. Lower DM shortens the crop duration, allowing completion of the life cycle before the onset of terminal heat stress. Decreased PH contributes to improved resource allocation and reduced transpirational demand, thereby enhancing plant stability and performance under high-temperature conditions. Yield-contributing traits (SL, NS/S, FL, PL, PEL, TL/M, BY/P, HI, SW, GW, TGW, and NGS/S) were set with an increasing direction to favor genotypes with superior reproductive performance. This trait-specific orientation ensured that MGIDI ranked genotypes by their proximity to the ideal phenotype optimized for heat-stress conditions. All statistical analyses were performed using R software (version 4.4.0).

Meteorological parameters

Weather data for the two seasons are presented in Appendix Figure 7 (2020-21) and Appendix Figure 8 (2021-22). The data indicated that the average minimum temperature in 2020-21 was lowest (2.4°C) during 21-27 December, whereas the average maximum temperature (37.3°C) was observed during 12-18 April. The average minimum temperature in 2021-22 was lowest (2.6°C) during 15-21 December, whereas the average maximum temperature (41.1°C) was observed during 10-16 April. The maximum sunshine duration (8.8 hours) was recorded during 12-18 April in the 2020-21 *Rabi* season, whereas the maximum sunshine duration (9.2 hours) was recorded during 24-30 April 2021-22. The pooled range of daily minimum temperatures from anthesis to maturity of the wheat genotypes was 7.1-19.2°C and 12.4-23.0°C, with averages of 13.4°C and 15.6°C under TS and HS conditions, respectively. The pooled range of daily maximum temperatures from anthesis to maturity of the wheat genotypes was 25.5-40.2°C and 28.4-42.4°C, with overall averages of 32.3°C and 34.8°C under TS and HS conditions, respectively. The observations and other weather parameters recorded during both seasons indicated the presence of heat stress during the grain-filling stage of the wheat crop.

Results And Discussion

Throughout the crop season, the minimum and maximum temperatures and rainfall were recorded daily (Appendix Figures 7-8, respectively). The observations and other weather parameters recorded for both seasons indicated the presence of heat stress at the grain-filling stage of the wheat crop. The pooled ANOVA revealed that variances due to genotypes were highly significant ($p < 0.01$), whereas the variance due to replication was non-significant across the environments for all traits studied (Appendix Tables 3-4). This indicates a high magnitude of variability among genotypes for all traits studied. The evaluated wheat genotypes exhibited wide variation in all the assessed traits across all tested environments. High temperature significantly reduced the overall crop development period and traits such as DH (8.3%), DM (12.08%), PH (13.8%), TL/M (17.62%), SL (13.7%), NS/S (10.55%), FL (15.98%), PL (15.65%), PEL (1.93%), TGW (13.3%), SW (14.04%), GW (4%), and NGS/S (9.20%) under HS conditions. Figure 1 illustrates a frequency plot of various phenological traits of wheat genotypes, depicting their distribution and variability under TS and HS conditions. Mean values along with their standard errors (SE) were also calculated for all traits under TS and HS conditions (Figure 2). This provides a comparative assessment of trait performance and the precision of estimates under contrasting environments. The visual representation aids in understanding the range and distribution of phenological characteristics under optimal sowing and stress conditions.

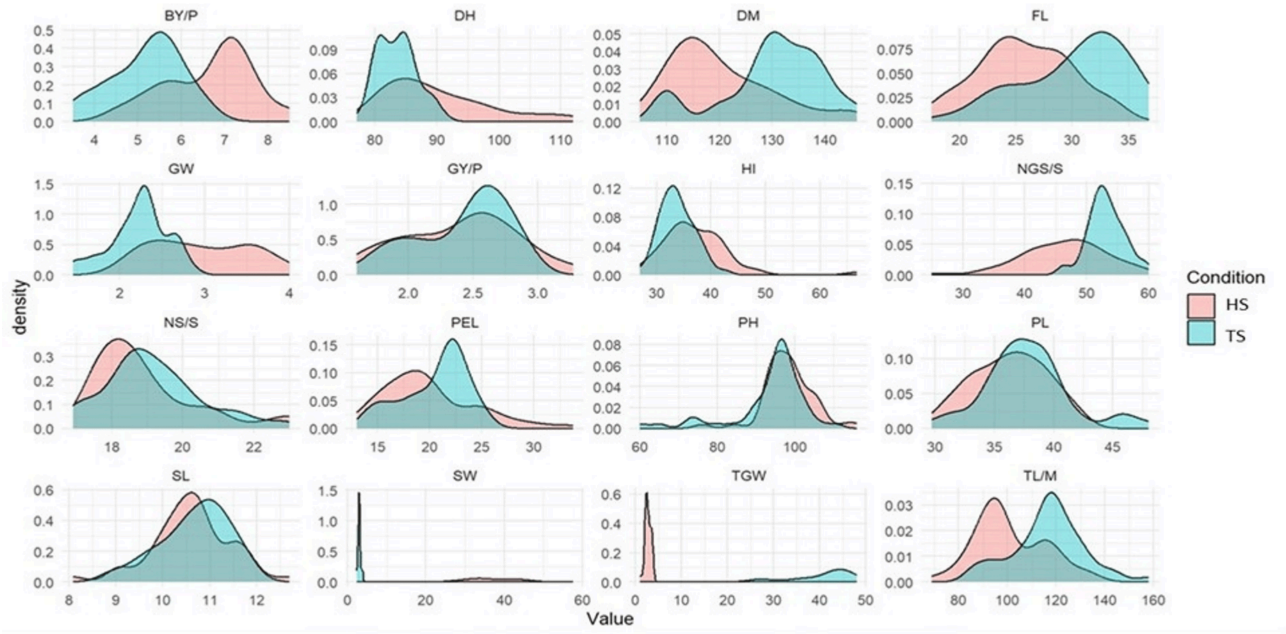

FIGURE 1: Density distribution of agronomic and yield-related traits of wheat genotypes under TS and HS conditions, depicting shifts in trait distributions under HS and reflecting the effect of heat stress on growth and yield components

DH, Days to Heading; DM, Days to Maturity; PH, Plant Height; SL, Spike Length; NS/S, Number of Spikelets per Spike; FL, Flag Leaf Length; PL, Peduncle Length; PEL, Peduncle Extrusion Length; TL/M, Tillers per Meter; BY/P, Biological Yield per Plot; GY/P, Grain Yield per Plot; HI, Harvest Index; SW, Spike Weight; GW, Grain Weight per Spike; TGW, Thousand Grain Weight; NGS/S, Number of Grains per Spike; TS, Timely Sown; HS, Late Sown

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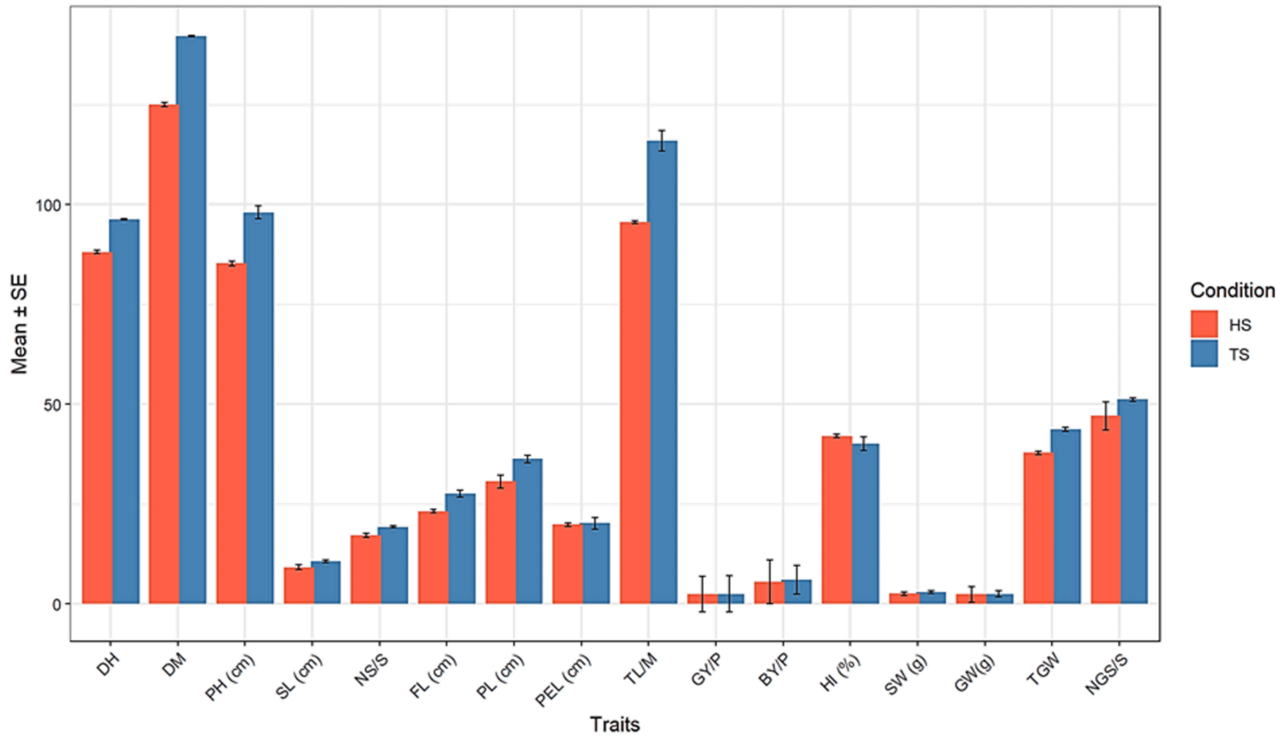

FIGURE 2: Mean performance (±SE) of wheat genotypes for different traits under TS and HS conditions, highlighting the reduction in key agronomic and yield-related traits under HS compared to TS conditions

DH, Days to Heading; DM, Days to Maturity; PH, Plant Height; SL, Spike Length; NS/S, Number of Spikelets per Spike; FL, Flag Leaf Length; PL, Peduncle Length; PEL, Peduncle Extrusion Length; TL/M, Tillers per Meter; BY/P, Biological Yield per Plot; GY/P, Grain Yield per Plot; HI, Harvest Index; SW, Spike Weight; GW, Grain Weight per Spike; TGW, Thousand Grain Weight; NGS/S, Number of Grains per Spike; TS, Timely Sown; HS, Late Sown; SE, Standard Error

Genetic parameters, heritability, and genetic advance

The present study indicated that in both environments, moderate (10-20%) GCV and PCV were observed for most traits, such as GY/P, BY/P, TGW, HI, TL/M, GW, SW, FL, PL, and PEL. The estimates of h^2 ranged from 52.26% to 91.86% and 33.03% to 95.08% under TS and HS conditions, respectively. High h^2 was observed for traits such as DH, DM, SL, FL, PH, and GW. These traits can be improved directly through selection, as they are least influenced by the environment, and there is a high correspondence between genotype and phenotype. Similarly, the expected genetic advance as a percentage of the mean ranged from 4.8% to 31.43% and 7.8% to 40.44% under TS and HS conditions, respectively. High expected genetic advance was observed for TGW, BY/P, GY/P, and TL/M in all environments (Figure *3*).

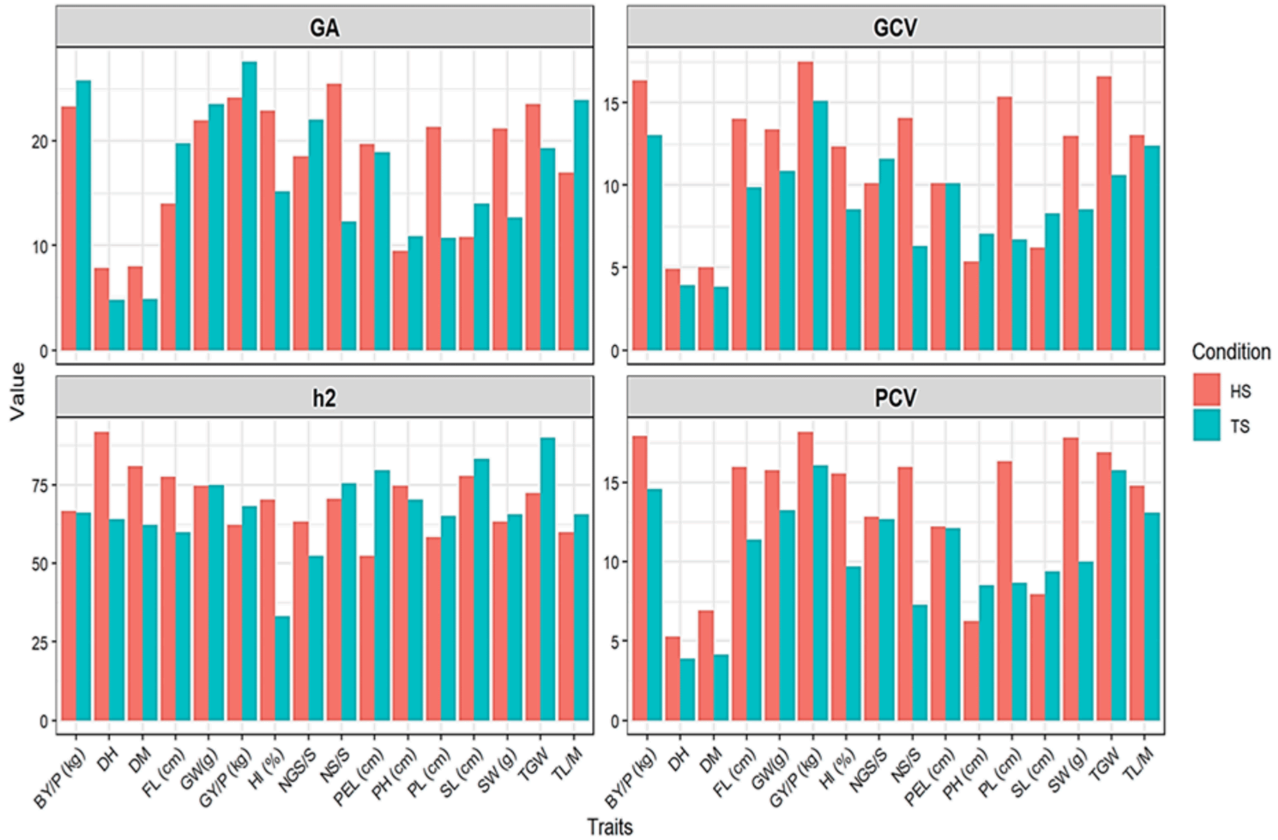

FIGURE 3: Comparison of GCV, PCV, h2 (broad sense), and GA (5% of mean) in wheat genotypes for phenological traits under TS and HS conditions

DH, Days to Heading; DM, Days to Maturity; PH, Plant Height; SL, Spike Length; NS/S, Number of Spikelets per Spike; FL, Flag Leaf Length; PL, Peduncle Length; PEL, Peduncle Extrusion Length; TL/M, Tillers per Meter; BY/P, Biological Yield per Plot; GY/P, Grain Yield per Plot; HI, Harvest Index; SW, Spike Weight; GW, Grain Weight per Spike; TGW, Thousand Grain Weight; NGS/S, Number of Grains per Spike; TS, Timely Sown; HS, Late Sown; GA, Genetic Advance; GCV, Genotypic Coefficient of Variation; PCV, Phenotypic Coefficient of Variation

Inter-trait correlation patterns under variable sowing environments

Under TS conditions, GY/P showed high positive correlations with BY/P, NS/S, SL, TL/M, PH, and SW. Moderate associations were observed between FL, PL, PEL, GW, TGW, and NGS/S. In contrast, the harvest index exhibited a low but significant positive correlation. A similar pattern was evident under HS conditions, where GY/P maintained strong associations with GW, TL/M, NS/S, SW, BY/P, FL, and PEL. Moderate relationships were noted with PH, PL, NGS/S, and HI, whereas TGW and SL showed weaker associations. Across both environments, DH and DM were negatively and significantly correlated with grain yield, indicating that early phenology favoured yield stability under stress (Appendix Tables *5*-*6*). Path analysis further clarified these associations by partitioning the direct and indirect effects (Appendix Tables *7*-*8*). Under TS conditions, BY/P exerted the highest positive direct effect on GY/P (0.7843), followed by HI, NS/S, SW, TL/M, GW, FL, PL, NGS/S, SL, and TGW. Similarly, under HS conditions, BY/P (0.4928) and HI (0.4853) contributed the most, whereas NS/S, SW, TL/M, GW, FL, PL, NGS/S, SL, TGW, and PH also showed positive direct effects, albeit of lower magnitude. Conversely, DH and DM exerted negative direct effects, reinforcing the importance of early flowering and maturity in stress adaptation. As all direct effects were less than 1, multicollinearity was negligible. These traits, along with early phenology (DH and DM), have the potential to serve as effective selection criteria in breeding programs aimed at enhancing heat tolerance.

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Multivariate trait differentiation under different environmental conditions

Under TS conditions, the first seven principal components (PCs) explained 71.5% of the total data variance. PC-1 was mainly associated with GY/P, BY/P, FL, TL/M, and SL. PC-2 was dominated by PEL, whereas PC-3 to PC-7 captured the variations in GW, TGW, DM, PH, and NGS/S. Under HS conditions, the first five PCs explained 73.36% of the total variance. PC-1 highlighted GW, GY/P, TL/M, PEL, FL, and HI, whereas PC-2 was dominated by TGW. PC-3 to PC-5 explained the variation in DH, DM, NGS/S, SL, and BY/P. The biplot (PC-1 and PC-2: 50% variance) indicated that yield and spike-related traits contributed positively, whereas DH and DM were negatively correlated with the other traits (Appendix Tables *9*-*11*). The PCA biplot is a method for further analysing the results from PC, as it combines the PC scores and loading vectors in a biplot graph (Figures *4*-*5*). The plot depicts the original variables as vectors (i.e., arrows). The longer the arrow, the more information it contributes to the PC, and hence, it shows a high variability. When the two vectors form an acute angle, the respective variables are positively correlated. If they form an obtuse angle, the respective traits are negatively correlated. The PCA biplot, which integrates the PC scores and loading vectors, revealed key trait associations and genotypic diversity. The biplots based on PC-1 and PC-2 explained 57.2% and 47.1% of the total variation under TS and HS conditions, respectively, effectively distinguishing the genotypic diversity. The biplot of the genotypes describes their diversity in terms of spatial distance vectors, with greater length (GY/P, BY/P, TL/M, NS/S, PEL, NGS/S, and GW) contributing strongly to the first two PCs under both TS and HS conditions. Traits such as DH, DM, and PH formed obtuse angles with most parameters, indicating negative correlations with the grain yield.

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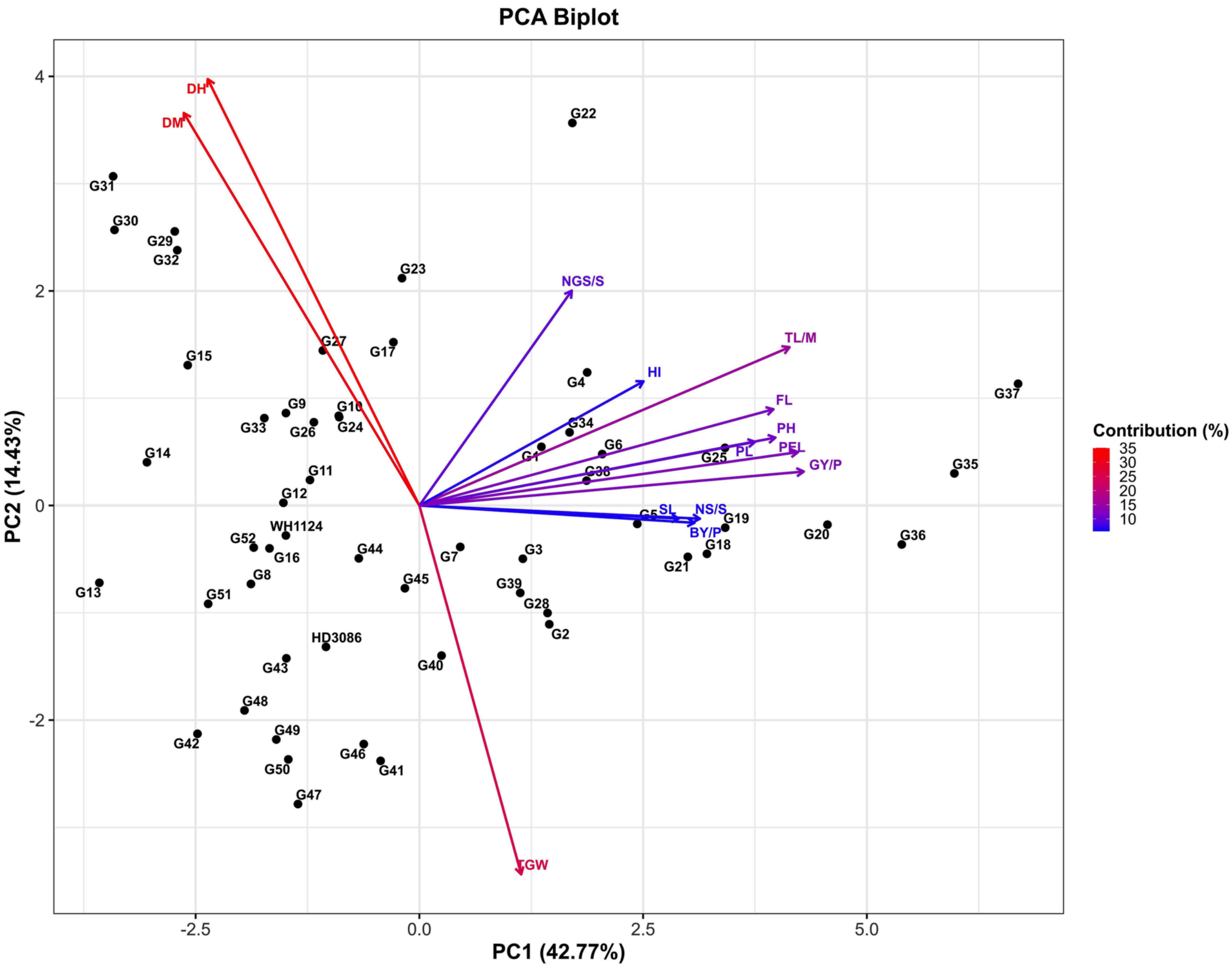

FIGURE 4: Principal component biplot under TS conditions

The plots represent original variables as vectors (arrows) and genotypes as points. The length of each vector indicates the magnitude of its contribution to the principal components, with longer arrows denoting higher variability. Acute angles between vectors indicate positive correlations, while obtuse angles indicate negative correlations among traits.
PCA, Principal Component Analysis; TS, Timely Sown

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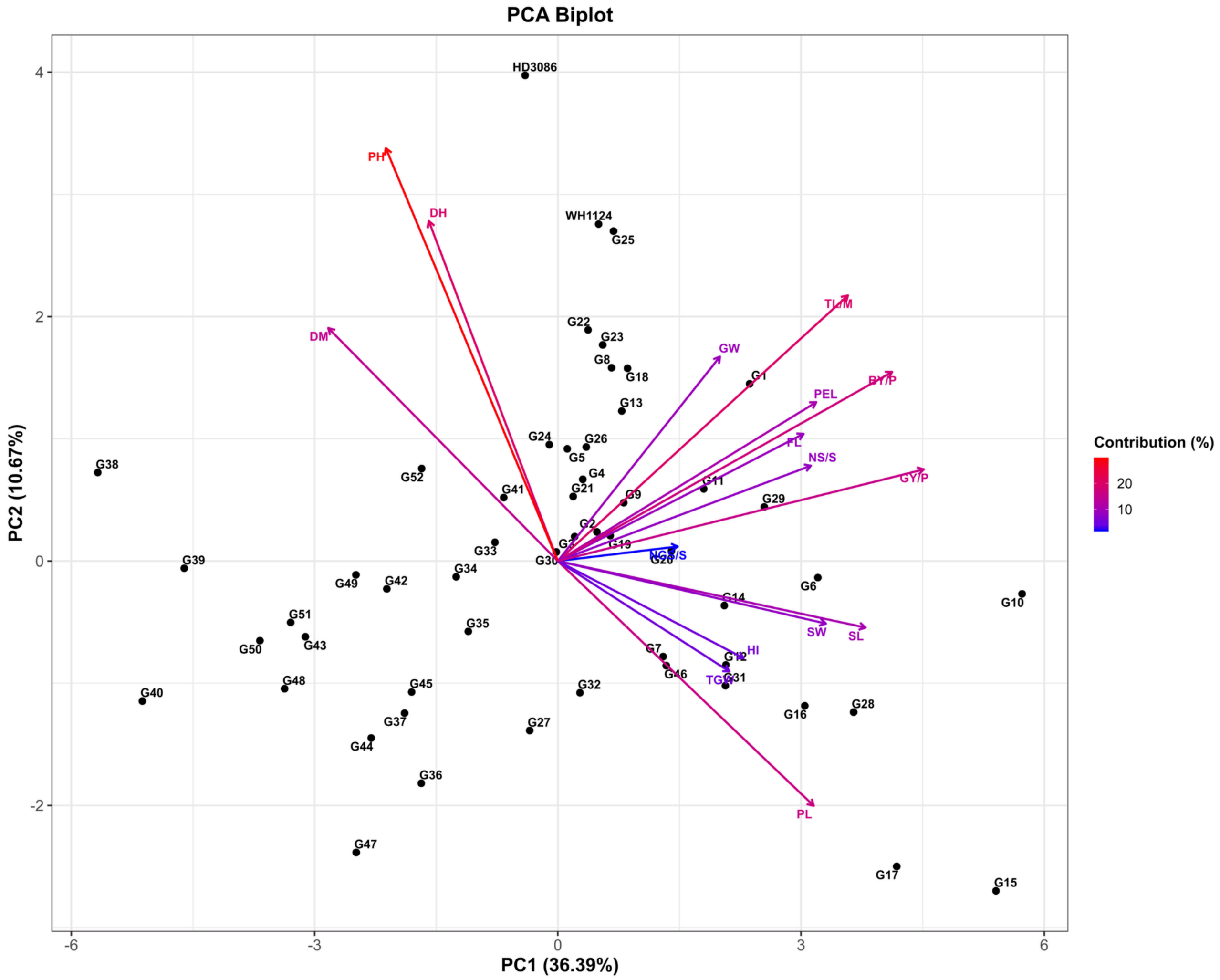

FIGURE 5: Principal component biplot under HS conditions

The plots represent original variables as vectors (arrows) and genotypes as points. The length of each vector indicates the magnitude of its contribution to the principal components, with longer arrows denoting higher variability. Acute angles between vectors indicate positive correlations, while obtuse angles indicate negative correlations among traits.
HS, Late Sown; PCA, Principal Component Analysis

Multi-trait regression for identifying key yield determinants

The phenotypic correlation coefficient was calculated to determine the association among different traits under TS and HS conditions using a scatter diagram. The line of best fit for important phenological traits was GY/P (Y = -0.1304x + 2.7165, R^2 = 0.0253), BY/P (Y = -0.0825x + 7.0119, R^2 = 0.0053), HI (Y = -0.1204x + 40.747, R^2 = 0.1241), and GW (Y = 0.6961x + 0.6585, R^2 = 0.105). The multiple regression model showed higher R^2 values for phenological traits under TS and HS conditions (0.815 and 0.685, respectively), indicating that most of the total variation in the dependent variable (GY/P) was explained by the linear function of the independent variables (Appendix Table 12). The regression coefficient (b) was significantly positive at the 5% level of significance for traits such as BY/P, HI, and TGW under both environments, indicating that these traits contribute more to the variability of the genotypes than the other traits under study. Based on these results, the predictive model equations for grain yield (Y) were formulated as follows:

Traits	Factor	h^2 (broad sense)	SG (%)
PH	FA1	0.896	5.79
TL/M	FA1	0.913	12.9
SL	FA1	0.879	0.316
FL	FA1	0.916	3.88
PEL	FA1	0.94	4.17
DH	FA2	0.969	0.463
DM	FA2	0.926	-0.837
PL	FA3	0.813	2.04
BY/P	FA3	0.805	15.8
TGW	FA3	0.92	7.89
HI	FA4	0.767	6.77
NS/S	FA4	0.807	8.99
NGS/S	FA4	0.885	7.345
SW	FA4	0.889	0.497
GW	FA4	0.901	15.67
GY/P	FA4	0.951	23.5

TABLE 1: Estimated genetic gain for the PCA-selected traits in MGIDI

MGIDI, Multi-Trait Genotype-Ideotype Distance Index; PCA, Principal Component Analysis; SG, Selection Gain; DH, Days to Heading; DM, Days to Maturity; PH, Plant Height; SL, Spike Length; NS/S, Number of Spikelets per Spike; FL, Flag Leaf Length; PL, Peduncle Length; PEL, Peduncle Extrusion Length; TL/M, Tillers per Meter; BY/P, Biological Yield per Plot; GY/P, Grain Yield per Plot; HI, Harvest Index; SW, Spike Weight; GW, Grain Weight per Spike; TGW, Thousand Grain Weight; NGS/S, Number of Grains per Spike

Model for morphological traits under TS conditions:

$$Y = -927.7 - 0.125DH - 2.423DM + 0.023PH + 1.203TL/M + 0.324SL + 0.201FL + 0.714PL + 1.235PEL + 5.688BY/P + 15.230HI + 10.989TGW + 3.245NS/S + 0.785NGS/S + 0.988SW + 0.201GW$$

Model for morphological traits under HS conditions:

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$$Y = -547.03 - 0.086DH - 0.123DM + 2.052PH + 0.970TL/M + 0.256SL + 0.096FL + 1.387PL + 0.975PEL + 3.216BY/P + 12.567HI + 1.852TGW + 1.543NS/S + 0.967NGS/S + 1.029SW + 0.154GW$$

Appendix Table 12 displays the variables that were either added to or deleted from the developed model using stepwise analysis under both TS and HS conditions. It also reports the standard errors of the variables, the significance (P-value) of variables entered or excluded from the model, and the partial and cumulative coefficients of determination (R^2). The stepwise regression model retained five traits - BY/P, HI, DM, SL, and GW - contributing more than 89.8% of the total variation in grain yield per plot under TS conditions, and six phenological traits - BY/P, HI, TL/M, TGW, SW, and PEL - accounted for 81.4% of the variation in GY/P under HS conditions.

Selection of heat stress-tolerant genotype using MGIDI analysis

The MGIDI index was computed using PCA-selected traits to identify superior genotypes under the experimental conditions. A significant genotypic effect ($p < 0.05$) was observed for all selected traits (Table 1). The expected selection gain (SG) varied considerably among traits, ranging from a negative value for DM (−0.837%) to a maximum of 23.5% for GY/P. Traits such as TL/M (12.9%), BY/P (15.8%), TGW (7.89%), and NGS/S (7.35%) exhibited notable gains, highlighting their potential role in improving productivity.

The MGIDI index ranked genotypes based on their proximity to the ideal genotype (ideotype). The selection pressure, defined by the red boundary in the MGIDI ranking plot (Figure 6(a)), identified six genotypes (G2, G3, G9, G35, G37, and G22) as the most promising, as they were positioned closest to the ideotype with the lowest MGIDI values. These genotypes exhibited minimal overall deviation from the desired trait profile, reflecting superior multi-trait performance under heat stress conditions. The strengths and weaknesses view (Figure 6(b)) further elucidated the contribution of each factor (FA1-FA6) to the MGIDI scores. FA1, representing phenological traits (DH and DM), showed lower contributions to G2 and G3, indicating earlier flowering and maturity, thereby improving heat escape. FA2, associated with plant architectural traits (PH, FL, PL, and PEL), contributed more prominently in G22, suggesting suboptimal plant structure requiring improvement. FA3, corresponding to yield component traits (TGW, GW, NGS/S, and SW), remained relatively stable across most selected genotypes, indicating consistent sink capacity. In contrast, FA4, representing productivity traits (GY/P, BY/P, and HI), showed higher contributions in G37, reflecting limitations in yield performance despite selection (Table 2). Genotypes G9 and G35 exhibited relatively balanced and moderate contributions across all factors, indicating stable performance without pronounced weaknesses. Overall, the MGIDI analysis effectively enabled the simultaneous identification of superior and stable genotypes while also highlighting specific trait limitations. Among the selected genotypes, G2, G3, and G9 demonstrated the most desirable combination of early phenology, optimal architecture, and stable yield performance, making them suitable candidates for direct advancement. In contrast, G22 and G37 may serve as valuable donor parents for targeted improvement of plant architecture and yield-related traits, respectively, under heat stress environments.

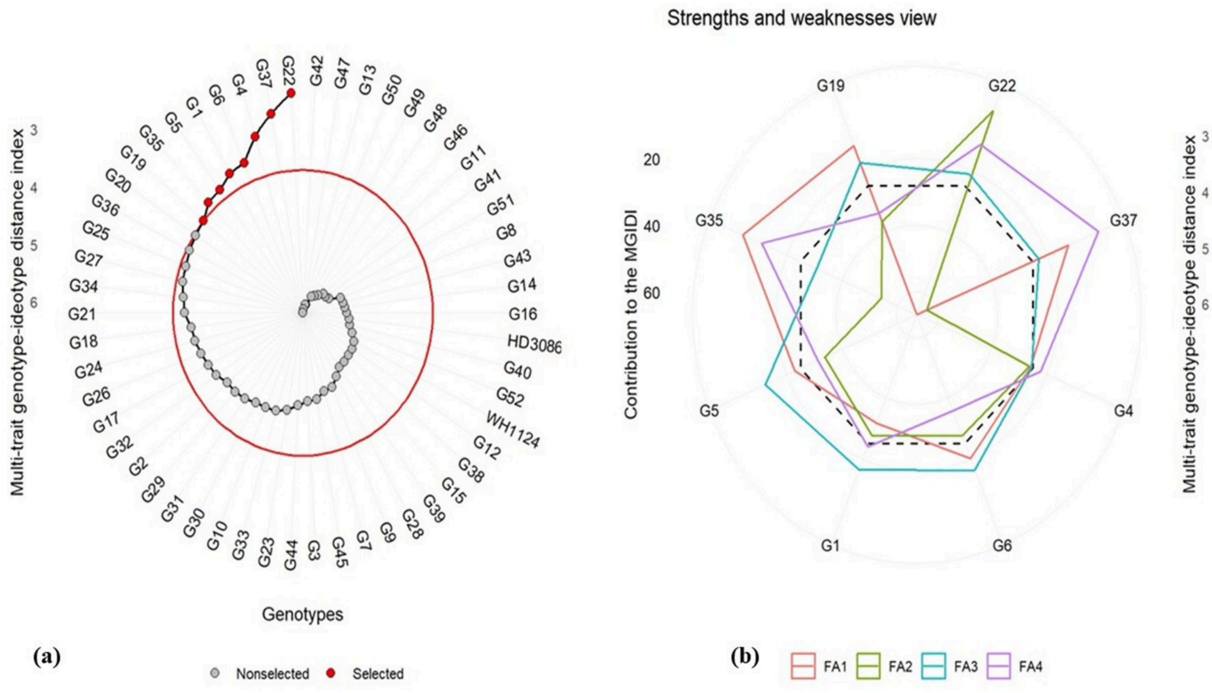

FIGURE 6: (a) MGIDI analysis of genotype ranking. (b) The percentage of each factor on the calculated MGIDI index represents the genotype's strengths and weaknesses

(a) The red color highlights the top-ranked selected genotypes. Based on the selection pressure, the cutoff point is represented by the central red circle. (b) The closer a factor's characteristics are to the ideotype, the lower its proportional contribution (toward the outer border). The theoretical value, assuming equal contribution from all components, is indicated by the dashed line.

MGIDI, Multi-Trait Genotype-Ideotype Distance Index

Traits	FA1	FA2	FA3	FA4	FA5	FA6	Communality	Uniqueness
DH	-0.88	0.10	-0.05	0.06	0.02	-0.03	0.82	0.18
DM	-0.91	0.08	-0.02	0.04	0.11	-0.01	0.85	0.15
PH	0.05	-0.92	-0.08	0.03	0.12	-0.04	0.87	0.13
SL	0.10	0.21	-0.65	0.40	-0.05	0.02	0.67	0.33
NS/S	-0.03	0.10	-0.72	0.35	-0.02	0.01	0.64	0.36
FL	0.06	0.78	-0.10	0.22	-0.04	-0.05	0.68	0.32
PL	0.08	0.81	-0.06	0.10	0.05	-0.02	0.70	0.30
PEL	0.04	0.76	-0.03	0.15	0.02	-0.06	0.63	0.37
TL/M	-0.02	0.12	0.20	0.05	-0.70	0.30	0.60	0.40
BY/P	0.05	0.18	0.30	0.70	0.22	-0.10	0.72	0.28
GY/P	-0.02	0.10	0.35	0.82	0.12	-0.05	0.80	0.20
HI	-0.10	-0.05	0.15	0.75	-0.08	0.02	0.60	0.40
SW	0.03	0.09	0.65	0.50	-0.02	0.04	0.68	0.32
GW	0.02	0.05	0.78	0.30	-0.01	0.03	0.72	0.28
TGW	0.01	0.04	0.82	0.10	-0.03	0.05	0.69	0.31
NGS/S	-0.04	0.06	0.75	0.20	-0.25	0.02	0.68	0.32

TABLE 2: Pooled factor loadings (FA) after varimax rotation, communalities, and uniqueness from factor analysis of the 16 different traits across the environments

DH, Days to Heading; DM, Days to Maturity; PH, Plant Height; SL, Spike Length; NS/S, Number of Spikelets per Spike; FL, Flag Leaf Length; PL, Peduncle Length; PEL, Peduncle Extrusion Length; TL/M, Tillers per Meter; BY/P, Biological Yield per Plot; GY/P, Grain Yield per Plot; HI, Harvest Index; SW, Spike Weight; GW, Grain Weight per Spike; TGW, Thousand Grain Weight; NGS/S, Number of Grains per Spike

Discussion

Over the past few years, temperature fluctuations have become a major concern in wheat production, as they reduce yield by affecting different growth stages [20]. Terminal heat stress is a critical issue, particularly in the Northwestern Plains Zone of India. In both years, the reproductive stage (late February-March) was affected by moisture stress due to extremely high temperatures, in contrast to the ideal conditions that prevailed throughout the vegetative phase (December-mid-February). From the first week of February to the third week of February, the season's highest temperatures were mild to moderate. Extreme heat, even for a short time, can significantly reduce wheat grain production [21] because of factors such as early senescence induction, accelerated grain-filling activities, reduced grain-filling duration, and reduced carbon absorption [22]. Owing to its effects on reproductive development and grain-filling process, heat stress decreases wheat production [11,20].

Identifying plant traits and developing wheat cultivars with improved adaptation to terminal heat stress are key priorities for plant breeders when breeding for climate resilience. This study demonstrated that HS genotypes exhibited a decrease in yield traits, including SL, NGS/S, TGW, and BY/P, compared to TS conditions, resulting in an overall reduction in grain yield under heat stress conditions. The overall reduction may result from a shorter grain-filling duration, which could impact the grain-filling process, ultimately leading to decreased grain weight and final yield in wheat [11,23]. The decrease in the number of grains per spike is linked to low grain fertility and floral spikelets, which are influenced by a rise in temperature, even by 1°C, during the booting and anthesis stages [24]. The reduction in grain weight might be attributed to shrivelled grains in genotypes under heat stress, which might be due to the formation of structurally abnormal and nonfunctional florets [25] and changes in the structure of the aleurone layer and cell endosperm [26]. Another possible reason for the decrease in yield traits in the present study might be the reduced duration between different crop stages and the lower translocation of biomass to yield [27]. However, a higher number of grains per spike was observed in the tolerant lines in the present study, which might be attributed to the increased availability of stem water-soluble carbohydrates. These tolerant lines had higher thousand-grain weight, total number of productive tillers, and grain yield, and maintained these traits under terminal heat stress. Thus, this study highlights the significance of these traits in critically evaluating the adverse effects of heat stress on the overall development of wheat crops, thereby identifying them as key indices for categorizing superior and stable genotypes in breeding programs.

To explore the intricate relationship between various traits and grain yield, which is a complex trait influenced by a large number of component traits, it is important to study the coefficient of variation and correlation of these traits with grain yield for their effective use in a successful breeding program. High h^2, coupled with high genetic advance, was observed for traits such as DH, DM, SL, FL, PH, GW, and TGW. Overall heritability was higher under HS than under TS conditions. This may be due to variations in gene expression under different environmental conditions and gene-environment interactions [28-30]. Other researchers have reported similar findings in wheat, noting alterations in correlation and heritability estimates as a result of late sowing [31]. A notable negative correlation was identified among DH, DM, and PH under HS conditions. The duration to maturity and early heading mitigates stress during the critical reproductive phase, thereby enhancing productivity before the onset of heat stress [32]. Therefore, DH and DM can be strategically selected to enhance grain yield during periods of extended heat stress, particularly in the late growing season. Furthermore, the path coefficient offers a precise and clear depiction of complex events at the correlation level. In this experiment, path coefficient analysis indicated that BY/P, HI, NS/S, SW, TL/M, GW, FL, PL, NGS/S, SL, and TGW exerted positive direct effects on grain yield per plot under both TS and HS conditions, whereas DH and DM demonstrated negative direct effects on grain yield under these conditions. Similarly, DH, GW, NS/S, HI, and BY/P had favourable direct effects on grain yield under terminal heat stress [33].

To further elucidate heat stress tolerance mechanisms in wheat and select key traits, multivariate approaches were employed. Stepwise and multiple regression analyses were performed to narrow down the traits that contributed significantly to grain yield across environments. The multiple regression model showed higher R^2 values for phenological and quality traits under TS and HS conditions (0.815 and 0.685, respectively), indicating that most of the total variation in the dependent variable (GY/P) is explained by the linear function of the independent variables. The regression coefficient (b) was significantly positive at the 5% level of significance for traits such as BY/P, HI, and TGW under both environments, indicating that these traits contributed more to the genotype variability than other traits under study. The stepwise regression model retained five traits - BY/P, HI, DH, SL, and GW - which explained more than 89.8% of the total variation in grain yield per plot under HS conditions, and six phenological and quality traits - BY/P, HI, TL/M, TGW, SW, and PEL - accounted for 81.4% of the variation in grain yield per plot under HS conditions. Sobhaninan et al. [34] concluded that

94.5% of the total variation in grain yield/m^2 was explained by biological yield/m^2, HI, relative water content, and TGW. However, Nasri et al. [35] stated that stepwise regression was used to remove the effects of ineffective or low impact traits in the regression model. Furthermore, the PCA biplot has emerged as a successful tool for evaluating crop tolerance to various abiotic stresses [36]. Investigating the intrinsic patterns and relationships among variables is a key application of PCA. This capability assists researchers in identifying potential redundancies and irrelevant features in a dataset. In our study, PCA revealed high loading values for BY/P, GY/P, FL, TL/M, and SL under TS conditions, whereas GW, GY/P, TL/M, PEL, PL, FL, and HI had high loading values in PC-1 under both HS and TS conditions. Hence, among all the traits studied, BY/P, HI, TL/M, and TGW can be considered for selecting heat-tolerant genotypes. Previous studies reported similar results [36-38]. The correlation coefficients, regression coefficients, and PCA loadings observed in this study also provide important insights into the underlying physiological mechanisms of heat stress tolerance in wheat. Traits such as BY/P, HI, TL/M, and GW, which exhibited strong positive associations with grain yield and high contributions in PCs, are closely linked with the plant's ability to maintain photosynthetic efficiency, assimilate partitioning, and sink strength under elevated temperature conditions. Maintenance of higher biological yield under heat stress reflects sustained biomass accumulation, indicating better source activity, while a higher harvest index suggests efficient remobilization of assimilates towards grain filling during stress-induced shortened growth duration. Similarly, the strong contribution of TL/M and grain-related traits (GW, TGW, NGS/S) in PCA indicates the importance of reproductive resilience and sink capacity under heat stress. Heat-tolerant genotypes are known to maintain higher tiller fertility and grain set by reducing spikelet sterility and preserving pollen viability under high temperatures. The negative association of DH and DM with yield further supports the heat escape mechanism, where early phenology allows crops to avoid exposure to terminal heat stress during the critical grain-filling stage. These findings are consistent with previous reports [39,40], emphasizing the role of biomass accumulation, efficient assimilate partitioning, and early maturity as key adaptive strategies under heat stress. From a breeding perspective, the integration of correlation and PCA results suggests that indirect selection for traits such as BY/P, HI, TL/M, and TGW can effectively enhance grain yield under heat stress conditions. Therefore, these traits can serve as reliable physiological and agronomic markers for the development of heat-resilient wheat genotypes [41].

Plant breeding programs that aim for initial selection under a single environment with no stress or only a single stress condition may lead to the loss of desirable alleles or genetic variability for additional stresses other than the target stress [42]. The efficiency in the selection of desirable traits could be greater if based on multiple traits, but identifying genotypes that combine high performance and stability across many environments is difficult [43]. Thus, the use of MGIDI is especially important for screening genotypes based on multiple traits, such as secondary traits, along with grain yield under various stress environments. It has been applied to diverse crops, such as bush yam, water yam, barley, cassava, cucumber, guar, lentil, maize, rice, rice bean, soybean, wheat, chickpea, fenugreek, black bean, quinoa, sorghum, black oat, sesame, green gram, and eggplant [44-47]. The integration of MGIDI with conventional statistical analyses (correlation, path analysis, PCA, and regression) offers a significant advantage by enabling simultaneous evaluation of multiple traits along with yield. The multivariate analyses provided clear implications for wheat breeding under heat stress. PCA identified key trait groups, indicating that early phenology (DH, DM) and stable yield components can be effectively targeted for indirect selection of heat tolerance. The MGIDI index enabled simultaneous multi-trait selection, identifying genotypes with optimal trait combinations. This combined analytical framework enhances precision and reliability in selection decisions and provides deeper insights into trait contributions, making it highly valuable for future wheat breeding programs targeting heat stress tolerance. In this study, the MGIDI index proved to be an effective tool for integrating multiple traits and identifying superior genotypes with desirable trait combinations. The high heritability estimates and substantial expected genetic gains for key yield-contributing traits suggest a strong potential for genetic improvement through selection in the future. Overall, genotypes G2, G3, and G9, which exhibited superior and stable multi-trait performance, are suitable for direct advancement and use as parental lines in breeding programs targeting heat tolerance. In contrast, G22 and G37, despite certain limitations, possess specific desirable traits and can serve as donor parents for targeted improvement of plant architecture and yield-related traits, respectively. Genotype G35, showing balanced performance across traits, represents a stable genetic resource and can be effectively utilized in hybridization programs aimed at developing heat-resilient cultivars.

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Conclusions

In conclusion, this study demonstrated that heat stress significantly affects overall performance and ultimately yield. GY/P was positively and significantly correlated with TL/M, SL, FL, PL, PEL, NS/S, NGS/S, BY/P, HI, TGW, SW, and GW under both environmental conditions, suggesting that these traits can be used to enhance grain yield. Multivariate analysis approaches proved to be powerful tools for exploratory investigations. The multiple regression model showed a higher R2 value and positive regression coefficients (b) for traits such as BY/P, HI, and TGW under both environments, which was further validated by the stepwise regression model and PCA, which retained the three most important traits, BY/P, HI, and TL/M, under both environments, contributing the most to total variability. Therefore, BY/P, HI, TL/M, and TGW should be considered when developing heat-tolerant genotypes for breeding. Furthermore, MGIDI analysis identified six promising genotypes, G2, G3, G9, G35, G37, and G22, with stable performance under stress, making them suitable for direct utilization in future breeding programs.

Appendices

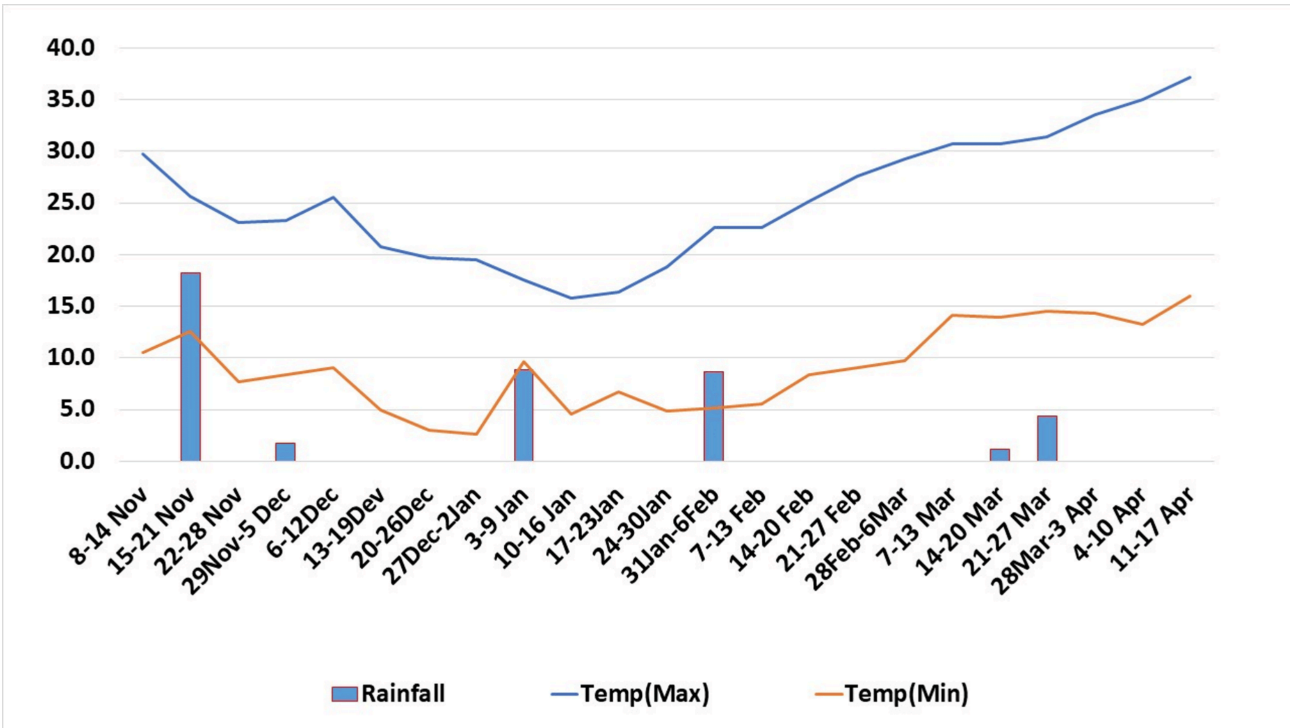

FIGURE 7: Weekly weather parameters 2020-21

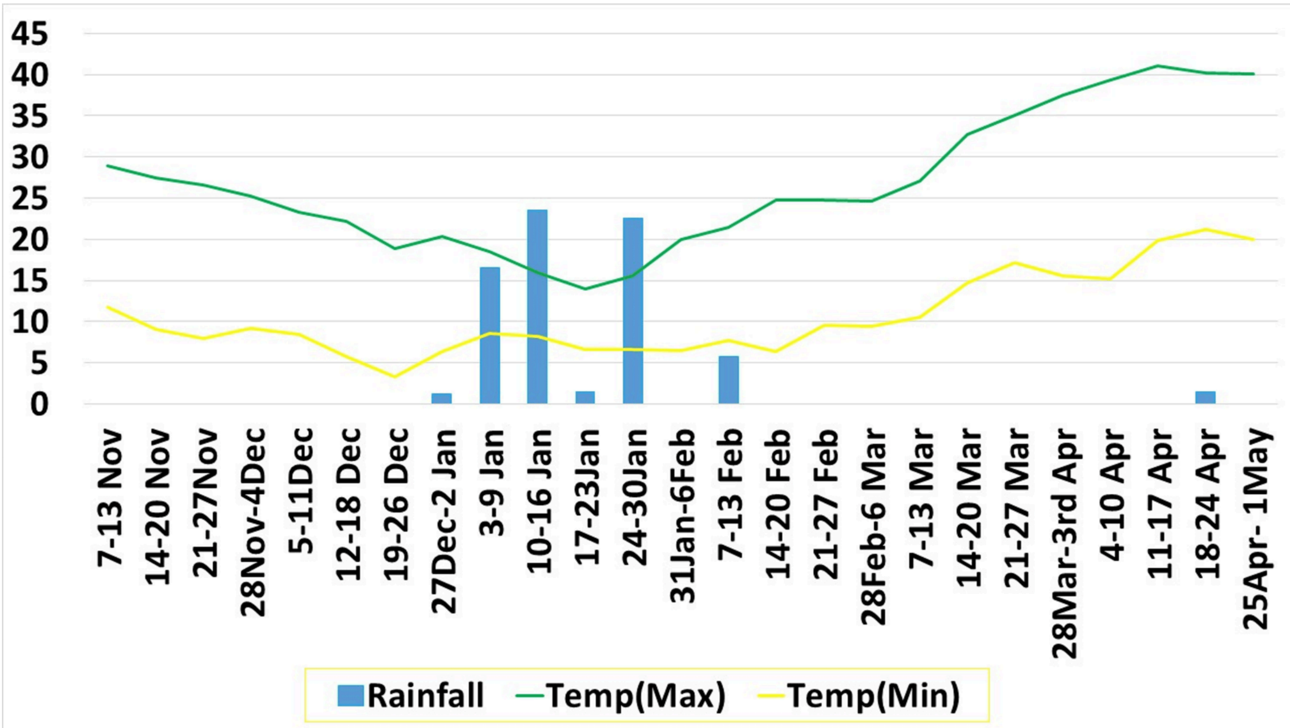

FIGURE 8: Weekly weather parameter 2021-22

Traits	df	DH	DM	PH	TL/M	SL	FL	PL	PEL	BY/P	GY/P	HI	NS/S	NGS/S	TGW	SW	GW
Replication	1	3.276	18.019	18.79	44.024	0.169	3.155	0.357	2.284	0.051	0.029	0.453	2.655	1.112	0.023	0.071	0.251
Genotype	51	199.709**	300.16**	94.141**	560.983**	1.501**	42.366**	19.605**	50.047**	2.44**	0.55**	67.733**	125.306**	103.863**	0.807**	0.931**	0.656**
Error	102	5.727	21.973	9.581	48.722	0.184	3.767	3.754	2.888	0.442	0.028	15.422	14.597	7.904	0.09	0.116	0.009

TABLE 3: Pooled analysis of variance for different traits of wheat genotypes under HS conditions

*, **Significant at 5% and 1% level of significance, respectively.
DH, Days to Heading; DM, Days to Maturity; PH, Plant Height; TL/M, Tillers per Meter; SL, Spike Length; FL, Flag Leaf Length; PL, Peduncle Length; PEL, Peduncle Extrusion Length; BY/P, Biological Yield per Plot; GY/P, Grain Yield per Plot; HI, Harvest Index; NS/S, Number of Spikelets per Spike; NGS/S, Number of Grains per Spike; TGW, Thousand Grain Weight; SW, Spike Weight; GW, Grain Weight per Spike; HS, Late Sown

Traits	df	DH	DM	PH	TL/M	SL	FL	PL	PEL	BY/P	GY/P	HI	NS/S	NGS/S	TGW	SW	GW
Replication	1	5.559	150.891	9.488	59.226	0.117	0.848	0.448	1.795	0.226	0.002	0.076	4.928	0.028	6.501	0.021	0.101
Genotypes	51	21.747**	117.346**	165.648**	586.883**	1.481**	64.108**	23.453**	19.735**	2.287**	0.396**	4.161**	29.9**	0.21**	100.884**	0.675**	0.564**
Error	102	3.44	41.125	34.196	37	0.146	4.361	4.298	3.008	0.181	0.014	0.777	4.359	0.031	10.18	0.083	0.009

TABLE 4: Pooled analysis of variance for different traits of wheat genotypes under TS conditions

*, **Significant at 5% and 1% level of significance, respectively.
DH, Days to Heading; DM, Days to Maturity; PH, Plant Height; TL/M, Tillers per Meter; SL, Spike Length; FL, Flag Leaf Length; PL, Peduncle Length; PEL, Peduncle Extrusion Length; BY/P, Biological Yield per Plot; GY/P, Grain Yield per Plot; HI, Harvest Index; NS/S, Number of Spikelets per Spike; NGS/S, Number of Grains per Spike; TGW, Thousand Grain Weight; SW, Spike Weight; GW, Grain Weight per Spike; TS, Timely Sown

	DH	DM	PH	TL/M	SL	FL	PL	PEL	BY/P	HI	NS/S	NGS/S	SW	GW	TGW
DH															
DM	0.302**														
PH	0.208**	0.368**													
TL/M	-0.202*	-0.339**	-0.146												
SL	-0.347**	-0.293**	-0.172*	0.383**											
FL	-0.242**	-0.325**	-0.075	0.493**	0.360**										
PL	-0.354**	-0.430**	-0.329**	0.326**	0.438**	0.223**									
PEL	-0.174*	-0.177*	-0.002	0.353**	0.361**	0.406**	0.277**								
BY/P	-0.315**	-0.351**	-0.152	0.665**	0.583**	0.500**	0.390**	0.377**							
HI	-0.072	-0.027	-0.295**	0.127**	0.241**	0.075	0.194*	0.265**	-0.034						
NS/S	-0.305**	-0.314**	-0.152	0.223**	0.359**	0.358**	0.214**	0.253**	0.370**	0.333**					
NGS/S	-0.11	0.019	-0.063	0.108**	0.234**	0.178*	0.157**	0.098	0.327**	0.088	0.151				
SW	-0.172*	-0.505**	-0.289**	0.352**	0.293**	0.297**	0.470**	0.305**	0.326**	0.250**	0.289**	-0.008			
GW	-0.078	-0.123	-0.068	0.308**	0.103NS	-0.048	0.141	0.339**	0.299**	0.136	0.271**	0.026	0.095		
TGW	-0.063	-0.176*	-0.227**	0.239**	0.281**	0.007	0.351**	0.232**	0.251**	0.178*	0.118	-0.044	0.147	0.272**	

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GY/P	-0.360**	-0.350**	-0.268**	0.613**	0.652**	0.542**	0.571**	0.563**	0.877**	0.328**	0.727**	0.425**	0.512**	0.423**	0.404**

TABLE 5: Pooled phenotypic correlation coefficients among grain yield and phenological traits under TS conditions

*, **Significant at 5% and 1% level of significance, respectively.

DH, Days to Heading; DM, Days to Maturity; PH, Plant Height; TL/M, Tillers per Meter; SL, Spike Length; FL, Flag Leaf Length; PL, Peduncle Length; PEL, Peduncle Extrusion Length; BY/P, Biological Yield per Plot; HI, Harvest Index; NS/S, Number of Spikelets per Spike; NGS/S, Number of Grains per Spike; SW, Spike Weight; GW, Grain Weight per Spike; TGW, Thousand Grain Weight; GY/P, Grain Yield per Plot; TS, Timely Sown

	DH	DM	PH	TL/M	SL	FL	PL	PEL	BY/P	HI	NS/S	NGS/S	TGW	SW	GW
DH															
DM	0.891**														
PH	-0.264**	-0.296**													
TL/M	-0.187*	-0.277**	0.592**												
SL	-0.311**	-0.341**	0.514**	0.387**											
FL	-0.155	-0.238**	0.571**	0.596**	0.322**										
PL	-0.129	-0.189*	0.476**	0.529**	0.209**	0.531**									
PEL	-0.261**	-0.369**	0.755**	0.642**	0.488**	0.632**	0.541**								
BY/P	-0.174*	-0.142	0.232**	0.385**	0.253**	0.409**	0.391**	0.312**							
HI	-0.142	-0.218**	0.340**	0.349**	0.210**	0.235**	0.136	0.313**	-0.213**						
NS/S	-0.287**	-0.285**	0.288**	0.515**	0.136	0.391**	0.379**	0.387**	0.268**	0.225**					
NGS/S	0.06	0.014	0.017	0.231**	0.072	0.190*	0.167*	0.115	0.210**	0.235**	0.207**				
TGW	-0.436**	-0.355**	-0.02	0.133	0.029	0.135	0.246**	0.084	0.299**	-0.091	0.096	-0.119			
SW	-0.293**	-0.318**	0.455**	0.645**	0.275**	0.364**	0.269**	0.452**	0.437**	0.298**	0.383**	0.194*	-0.056		

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GW	-0.231**	-0.210**	0.503**	0.570**	0.360**	0.466**	0.496**	0.511**	0.471**	0.310**	0.320**	0.127	0.262**	0.489**	
GY/P	-0.330**	-0.355**	0.678**	0.688**	0.269**	0.626**	0.577**	0.644**	0.633**	0.521**	0.693**	0.403**	0.238**	0.662**	0.755**

TABLE 6: Pooled phenotypic correlation coefficients among grain yield and phenological traits under HS conditions

*, **Significant at 5% and 1% level of significance, respectively.

DH, Days to Heading; DM, Days to Maturity; PH, Plant Height; TL/M, Tillers per Meter; SL, Spike Length; FL, Flag Leaf Length; PL, Peduncle Length; PEL, Peduncle Extrusion Length; BY/P, Biological Yield per Plot; HI, Harvest Index; NS/S, Number of Spikelets per Spike; NGS/S, Number of Grains per Spike; SW, Spike Weight; GW, Grain Weight per Spike; TGW, Thousand Grain Weight; GY/P, Grain Yield per Plot; HS, Late Sown

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	DH	DM	PH	TL/M	SL	FL	PL	PEL	BY/P	HI	NS/S	NGS/S	SW	GW	TGW	r with GY/P
DH	-0.10302	0.003	-0.00571	-0.01908	-0.03505	0.00986	0.01836	0.00052	-0.19041	-0.02134	0.00122	-0.00308	-0.01247	-0.00427	0.00183	-0.35964
DM	-0.01737	-0.1026	-0.0101	-0.03199	-0.02954	0.01328	0.02226	0.00053	-0.16987	-0.00796	0.00125	0.00053	-0.0366	-0.0067	0.00514	-0.36974
PH	-0.01199	0.00367	-0.02742	-0.01381	-0.01734	0.00308	0.01707	0.00001	0.11403	-0.08773	0.00061	-0.00178	-0.02094	-0.00373	0.00663	-0.2677
TL/M	0.01164	-0.00337	0.00401	0.15639	0.03868	-0.0201	-0.01687	-0.00106	0.36908	0.03775	-0.00184	0.00304	0.02548	0.01681	-0.00696	0.61268
SL	0.02	-0.00291	0.00471	0.03618	0.10094	-0.01469	-0.02272	-0.00108	0.43632	0.07152	-0.00143	0.00656	0.02122	0.00563	-0.00818	0.65207
FL	0.01391	-0.00324	0.00207	0.04653	0.03633	0.1223	-0.01157	-0.00122	0.29248	0.02234	-0.00143	0.00499	0.02155	-0.0026	-0.00022	0.54222
PL	0.02041	-0.00427	0.00903	0.03074	0.04426	-0.00911	0.10334	-0.00083	0.29153	0.05768	-0.00086	-0.00197	0.03407	0.0077	-0.01024	0.57148
PEL	0.01003	-0.00176	0.00007	0.0333	0.03646	-0.01657	-0.01435	0.12033	0.28211	0.07884	-0.00101	0.00274	0.02207	0.01845	-0.00676	0.56395
BY/P	0.01815	-0.00349	0.00418	0.06284	0.05885	-0.02039	-0.02018	-0.00113	0.74843	-0.01011	-0.00148	0.00917	0.02361	0.01627	-0.00732	0.8774
HI	0.00413	-0.00027	0.00809	0.01199	0.02428	-0.00307	-0.01005	-0.00079	-0.02546	0.29729	-0.00133	0.00248	0.01812	0.00739	-0.00518	0.32762
NS/S	0.01754	-0.00312	0.00417	0.0436	0.03627	-0.01459	-0.0111	-0.00076	0.27677	0.09885	0.24203	0.00425	0.02091	0.01479	-0.00343	0.72618

NGS/S	0.00632	0.00019	0.00173	0.01023	0.02359	-0.00725	0.00364	-0.00029	0.24452	0.02624	-0.0006	0.11423	-0.00061	0.0014	0.00129	0.42463
SW	0.00991	-0.00503	0.00792	0.03321	0.02956	-0.01213	-0.02436	-0.00091	0.24386	0.07435	-0.00115	-0.00024	0.15644	0.00517	-0.00429	0.51231
GW	0.00451	-0.00122	0.00188	0.02913	0.01042	0.00195	-0.00732	-0.00101	0.22344	0.04031	-0.00108	0.00072	0.00687	0.122	-0.00793	0.42267
TGW	0.00361	-0.00175	0.00623	0.02253	0.02832	-0.00031	-0.0182	-0.0007	0.18774	0.05284	-0.00047	-0.00124	0.01067	0.01481	0.10002	0.4041

TABLE 7: Pooled path coefficient analysis of phenological traits on grain yield under TS conditions

Residual factor: 0.009652
DH, Days to Heading; DM, Days to Maturity; PH, Plant Height; TL/M, Tillers per Meter; SL, Spike Length; FL, Flag Leaf Length; PL, Peduncle Length; PEL, Peduncle Extrusion Length; BY/P, Biological Yield per Plot; HI, Harvest Index; NS/S, Number of Spikelets per Spike; NGS/S, Number of Grains per Spike; SW, Spike Weight; GW, Grain Weight per Spike; TGW, Thousand Grain Weight; GY/P, Grain Yield per Plot; TS, Timely Sown

	DH	DM	PH	TL/M	SL	FL	PL	EL	BY/P	HI	NS/S	NGS/S	TGW	SW	GW	r with GY/P
DH	-0.13648	0.09396	0.01575	-0.02259	0.00184	-0.01667	-0.00796	-0.0228	-0.08475	-0.06978	0.00659	0.00544	-0.04701	-0.04058	-0.0053	-0.33034
DM	-0.12167	-0.1054	0.01766	-0.03341	0.00201	-0.02568	-0.01171	-0.0322	-0.06898	-0.10736	0.00654	0.00122	-0.03834	-0.04405	-0.00482	-0.35539
PH	0.036	-0.03118	0.10052	0.07138	-0.00303	0.06158	0.02947	0.06595	0.11261	0.16736	-0.00661	0.00155	-0.00212	0.06305	0.01155	0.67808
TL/M	0.02557	-0.02921	-0.03536	0.12054	-0.00229	0.0643	0.03272	0.05601	0.18726	0.17163	-0.01182	0.02076	-0.0144	0.08934	0.01309	0.68814
SL	0.04246	-0.03591	-0.03067	0.0467	0.12265	0.03471	0.0129	0.04257	0.12291	0.10342	-0.00312	0.00648	0.00315	0.03815	0.00827	0.26937
FL	0.02109	-0.02509	-0.03407	0.07182	-0.0019	0.10791	0.03282	0.05519	0.19862	0.11564	-0.00897	0.01712	0.01461	0.05046	0.0107	0.62595
PL	0.01757	-0.01995	-0.02844	0.06376	-0.00123	0.05726	0.10256	0.0472	0.18988	0.06704	-0.0087	0.01504	0.02656	0.03722	0.01139	0.57716
EL	0.03564	-0.03887	-0.0451	0.07733	-0.00288	0.06822	0.03344	0.1256	0.15172	0.15422	-0.00888	0.0103	0.00904	0.06261	0.01175	0.64414
BY/P	0.02381	-0.01496	-0.01384	0.04646	-0.00149	0.04411	0.02417	0.02726	0.48586	-0.10476	-0.00616	0.0189	0.03224	0.06056	0.01082	0.63298
HI	0.01936	-0.023	-0.02031	0.04205	-0.00124	0.02536	0.00843	0.02736	-0.10344	0.49203	-0.00516	0.02111	-0.00986	0.04121	0.00713	0.52103
NS/S	0.03915	-0.03004	-0.0172	0.06207	-0.008	0.04216	0.02345	0.03376	0.13024	0.11062	0.21105	0.01861	0.01035	0.05303	0.00735	0.6938

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NGS/S	-0.00826	0.00143	-0.00103	0.02785	-0.00043	0.02055	0.01035	0.01001	0.10215	0.11559	-0.00476	0.1125	-0.01281	0.02691	0.00291	0.40296
TGW	0.05944	-0.03744	0.00117	-0.01608	-0.00017	0.01461	0.01522	0.00731	0.14514	-0.04496	-0.0022	-0.01067	0.10793	-0.00779	0.00602	0.23753
SW	0.03999	-0.03352	-0.02718	0.07775	-0.00163	0.03931	0.01662	0.03947	0.21243	0.14639	-0.00879	0.01746	-0.00607	0.13851	0.01123	0.66197
GW	0.0315	-0.02212	-0.03002	0.06868	-0.00213	0.05027	0.03066	0.04464	0.22867	0.15271	-0.00734	0.0114	0.02828	0.0677	0.10256	0.75546

TABLE 8: Pooled path coefficient analysis of phenological traits on grain yield under HS conditions

Residual factor: 0.01225

DH, Days to Heading; DM, Days to Maturity; PH, Plant Height; TL/M, Tillers per Meter; SL, Spike Length; FL, Flag Leaf Length; PL, Peduncle Length; PEL, Peduncle Extrusion Length; BY/P, Biological Yield per Plot; HI, Harvest Index; NS/S, Number of Spikelets per Spike; NGS/S, Number of Grains per Spike; SW, Spike Weight; GW, Grain Weight per Spike; TGW, Thousand Grain Weight; GY/P, Grain Yield per Plot; HS, Late Sown

Principal component	Eigenvalue	% of variance	Cumulative % of variance	Eigenvalue	% of variance	Cumulative % of variance
PC 1	6.2	28.3	28.3	7.726	35.117	35.117
PC 2	2.2	10.0	38.3	3.278	14.900	50.017
PC 3	2.0	9.3	47.6	2.440	11.090	61.106
PC 4	1.5	7.0	54.6	1.627	7.396	68.502
PC 5	1.4	6.2	60.8	1.064	4.834	73.336
PC 6	1.3	5.8	66.6	0.957	4.349	77.685
PC 7	1.1	4.9	71.5	0.855	3.886	81.572
PC 8	0.9	4.2	75.7	0.697	3.170	84.741
PC 9	0.8	3.8	79.5	0.629	2.857	87.598
PC 10	0.8	3.4	83.0	0.517	2.349	89.947
PC 11	0.7	3.3	86.2	0.498	2.264	92.211
PC 12	0.6	2.8	89.0	0.374	1.700	93.911
PC 13	0.5	2.1	91.1	0.314	1.426	95.337
PC 14	0.4	2.0	93.1	0.227	1.030	96.367
PC 15	0.4	1.7	94.9	0.197	0.896	97.263
PC 16	0.3	1.5	96.3	0.188	0.856	98.119
PC 17	0.3	1.2	97.6	0.156	0.708	98.827
PC 18	0.2	1.1	98.7	0.113	0.515	99.341
PC 19	0.1	0.7	99.3	0.075	0.342	99.683
PC 20	0.1	0.6	99.9	0.046	0.209	99.892
PC 21	0.0	0.0	100.0	0.023	0.105	99.996
PC 22	0.0	0.0	100.0	0.001	0.004	100.000

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TABLE 9: Principal component (PC), eigenvalue, percentage of total variation, and cumulative percentage of phenological traits under TS and HS conditions

TS, Timely Sown; HS, Late Sown

	PC1	PC2	PC3	PC4	PC5	PC6	PC7
DH	-0.430	-0.351	0.332	0.167	0.437	0.002	0.197
DM	-0.448	-0.137	0.174	0.691	-0.175	0.025	0.192
PH	-0.161	-0.481	-0.363	0.483	0.078	0.161	-0.050
TL/M	0.529	0.168	0.082	-0.175	0.210	0.160	0.508
SL	0.572	0.078	-0.313	0.395	-0.188	-0.056	-0.157
FL	0.603	0.283	-0.480	-0.102	0.270	-0.024	-0.082
PL	0.534	0.437	0.148	0.272	0.055	0.264	-0.115
PEL	0.619	-0.243	0.100	0.139	0.084	0.199	-0.295
BY/P	0.867	0.126	-0.002	0.029	-0.106	0.149	0.034
HI	0.213	-0.310	0.445	0.445	0.187	-0.282	0.071
NS/S	0.721	0.249	0.194	0.037	0.162	-0.086	0.171
NGS/S	0.603	0.164	-0.144	0.293	-0.105	0.009	0.287
TGW	0.143	0.203	0.566	0.066	0.102	0.523	-0.354
SW	0.350	0.107	0.015	0.020	0.630	-0.248	0.191
GW	0.492	-0.220	0.693	-0.148	-0.192	-0.009	-0.022
GY/P	0.894	0.091	0.093	0.141	-0.076	-0.017	0.001

TABLE 10: PCA loading matrix for yield and yield-related traits in wheat under TS conditions

DH, Days to Heading; DM, Days to Maturity; PH, Plant Height; TL/M, Tillers per Meter; SL, Spike Length; FL, Flag Leaf Length; PL, Peduncle Length; PEL, Peduncle Extrusion Length; BY/P, Biological Yield per Plot; HI, Harvest Index; NS/S, Number of Spikelets per Spike; NGS/S, Number of Grains per Spike; SW, Spike Weight; GW, Grain Weight per Spike; TGW, Thousand Grain Weight; GY/P, Grain Yield per Plot; PC, Principal Component; TS, Timely Sown

	PC1	PC2	PC3	PC4	PC5
DH	-0.430	-0.351	0.332	0.167	0.437
DM	-0.448	-0.137	0.174	0.691	-0.175
PH	-0.161	-0.481	-0.363	0.483	0.078
TLM	0.529	0.168	0.082	-0.175	0.210
SL	0.572	0.078	-0.313	0.395	-0.188
FL	0.603	0.283	-0.480	-0.102	0.270
PL	0.534	0.437	0.148	0.272	0.055
PEL	0.619	-0.243	0.100	0.139	0.084
BY/P	0.867	0.126	-0.002	0.029	-0.106
HI	0.213	-0.310	0.445	0.445	0.187
NS/S	0.721	0.249	0.194	0.037	0.162
NGS/S	0.603	0.164	-0.144	0.293	-0.105
TGW	0.143	0.203	0.566	0.066	0.102
SW	0.350	0.107	0.015	0.020	0.630
GW	0.492	-0.220	0.693	-0.148	-0.192
GY/P	0.894	0.091	0.093	0.141	-0.076

TABLE 11: PCA loading matrix for yield and yield-related traits in wheat under HS conditions

DH, Days to Heading; DM, Days to Maturity; PH, Plant Height; TL/M, Tillers per Meter; SL, Spike Length; FL, Flag Leaf Length; PL, Peduncle Length; PEL, Peduncle Extrusion Length; BY/P, Biological Yield per Plot; HI, Harvest Index; NS/S, Number of Spikelets per Spike; NGS/S, Number of Grains per Spike; SW, Spike Weight; GW, Grain Weight per Spike; TGW, Thousand Grain Weight; GY/P, Grain Yield per Plot; PC, Principal Component; HS, Late Sown

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Sr. no.	Traits	TS	HS
	Constant	-927.7±56.43**	-547.03±71.29**
1	DH	-0.125±0.239	-0.086±1.08
2	DM	-2.423±4.20	-0.123±5.23
3	PH	0.023±2.09	2.052±5.35
4	TL/M	1.203±7.39	0.970±7.34
5	SL	0.324±0.25	0.256±0.54
6	FL	0.201±0.26	0.096±0.*
7	PL	0.714±0.78	0.387±0.83
8	PEL	1.235±0.45	0.975±0.35
9	BY/P	5.688±0.023	3.216±0.15
10	HI	15.23±0.04**	12.563±0.04**
11	NS/S	10.989±0.25**	1.852±0.25**
12	NGS/S	3.245±1.32	1.543±0.91
13	TGW	0.785±12.31	0.967±10.23
14	SW	0.988±0.512	1.029±56.23
15	GW	0.201±21.03	0.154±2.13

TABLE 12: Multiple regression analysis of different phenological and quality components under TS and HS conditions

*, **Significant at 5% and 1% level of significance, respectively.
DH, Days to Heading; DM, Days to Maturity; PH, Plant Height; TL/M, Tillers per Meter; SL, Spike Length; FL, Flag Leaf Length; PL, Peduncle Length; PEL, Peduncle Extrusion Length; BY/P, Biological Yield per Plot; HI, Harvest Index; NS/S, Number of Spikelets per Spike; NGS/S, Number of Grains per Spike; SW, Spike Weight; GW, Grain Weight per Spike; TGW, Thousand Grain Weight; TS, Timely Sown; HS, Late Sown

Additional Information

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Disclosures

Plant subjects: All authors have confirmed that this study did not involve any herbarium specimen. **Human subjects:** All authors have confirmed that this study did not involve human participants or tissue. **Animal subjects:** All authors have confirmed that this study did not involve animal subjects or tissue. **Conflicts of interest:** In compliance with the ICMJE uniform disclosure form, all authors declare the following: **Payment/services info:** All authors have declared that no financial support was received from any organization for the submitted work. **Financial relationships:** All authors have declared that they have no financial relationships at present or within the previous three years with any organizations that might have an interest in the submitted work. **Other relationships:** All authors have declared that there are no other relationships or activities that could appear to have influenced the submitted work.

Data Availability Statements

The datasets (and/or code) supporting this study are available from the corresponding author upon reasonable request. All data generated or analyzed during this study are included in this published article and/or its appendices.

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