The Journal of Agricultural Sciences - Sri Lanka
Vol. 21 No 2, May 2026. pp 317-330
https://doi.org/10.4038/jas.v21i2.11191

RESEARCH

Selection of High-yielding Genotypes and Phenotypic Correlations of F_2 Wheat (*Triticum aestivum* L.) During the Late Planting Season in Field Conditions of Bangladesh

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Received: 06th September 2024 / Accepted: 27th September 2026

ABSTRACT

Purpose: *Around the globe, wheat is a significant cereal crop, used for food, feed, and raw materials. Terminal heat stress threatens wheat production, notably in subtropical countries like Bangladesh. An experiment was conducted to select heat-tolerant, high-yielding transgressive segregants using the F_2 populations from several biparental crosses of elite wheat varieties in Bangladesh.*

Research Method: *A total of ten thousand F_2 seeds (1000 from ten crosses) were evaluated in the field of Bangladesh under late sown conditions to induce terminal heat stress and assess eight yield and yield-related traits. Statistical analysis was conducted using R-studio software among the transgressive segregants and their respective parents.*

Findings and Values: *A total of 100 F_2 genotypes obtained from biparental crosses of five elite wheat varieties were selected based on yield and related traits under late sown conditions imposing terminal heat stress. Significant differences were observed for most of the traits between the segregating lines and their five parents. Traits such as flag leaf length, hundred-grain weight, number of grains per plant, spike length, and yield per plant showed high heritability and genetic advance, making them suitable for breeding programs. Terminal heat-tolerant genotypes H10, J9, J4, E2, F2, and G7, grouped in cluster 4, are promising for developing advanced heat-tolerant wheat lines in Bangladesh. The work involved selecting promising terminal heat stress-tolerant transgressive segregants using an elite vs elite crosses approach to plant breeding.*

Keywords: *F_2 population, Genetic analysis, Terminal heat tolerance, Transgressive segregants.*

INTRODUCTION

Wheat (*Triticum aestivum* L.) is known as the universal cereal of old-world agriculture and a prominent crop cultivated globally across various agroecology (Abhinandan *et al*. 2018). The three main components of wheat grain are carbohydrates (60–75%), proteins (7–18%), lipids (1.5–2%), and other minor vitamins and minerals components (Guzmán *et al*. 2022). As a major staple food, wheat contributes to around 35% of the global food intake and provides approximately 20% of the total calories consumed worldwide. However, abiotic stresses like heat, drought, salinity, cold, chemical, and water excess common in tropical and subtropical regions and can significantly reduce wheat yields by more than 50% (Rahaie *et al*. 2013, Ohama *et al*. 2017, Buttar *et al*. 2020).

High-temperature stress induces structural and phenotypic modifications in the aerial component of the plant, including stem elongation and leaf expansion (Patel & Franklin 2009). In addition, vegetative growth

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was extended, whereas the green leaf area and the number of productive tillers significantly declined at day/night temperatures of 30/25°C (Djanaguiraman *et al*. 2010). Even a slight temperature rise (1–2°C) has been shown to reduce wheat yield significantly (Nahar *et al*. 2010).

A considerable decrease in ear length, the number of spikelets, and the number of fertile florets due to delayed sowing of wheat (Prasad *et al*. 2011). Exposure to heat stress at the early growth stages affects later stages, such as dough and maturity, was also reported, where the shortening of the kernel desiccation period has associated with grain yield losses (Hasanuzzaman *et al*. 2013). High temperatures can reduce wheat grains' zinc and iron content (Panigrahi *et al*. 2022). Also, the development of diseases like wheat blast is favored by higher temperatures (18–30°C) and high humidity when plants are wet for at least 10 hours due to rain or dewfall (Cardoso *et al*. 2008). From seedling to harvest, high temperatures threaten almost every wheat growth and development stage, potentially reducing yield and seed quality (Rezaei et al. 2018, Buttar *et al*. 2020, Fleitas *et al*. 2020). To improve wheat yields under heat stress, researchers should focus on traits such as plant height, flag leaf length, and grain number (Farooq et al. 2011) because yield per plant is a complex variable (Cossani & Reynolds 2012) to identify as a heat tolerance plant. At International Wheat and Maize Improvement Center (CIMMYT) and International Center for Agricultural Research in the Dry Areas (ICARDA), extensive use is made of crosses between spring and winter wheat, as well as elite lines crossed with synthetic wheats, to create high-yielding genotypes. These genotypes are designed to have broad adaptation and resistance to significant biotic and abiotic stresses, aiming to mitigate the impacts of climate change (Tadesse *et al*. 2019). The used elite varieties - BARI Gom-20, BARI Gom-25, BARI Gom-26, BARI Gom-32, and BARI Gom-33 - exhibit moderately heat tolerance for late sowing. Through the crossbreeding of these varieties, it is feasible to generate genotypes with enhanced heat tolerance, while upholding high yields during late sowing. Transgressive segregation becomes apparent in the F_2 generation and subsequent generations. Hence, employing pedigree selection in this fashion is imperative for cultivating promising lines.

While traditional breeding has achieved advancements, identifying desirable genotypes combining heat tolerance and high yields remains challenging. This study employs a phenotypic approach in an F_2 field trial to evaluate multiple morphological traits associated with heat tolerance and yield potential, including plant height, flag leaf length, spike length, number of grains per plant, hundred-grain weight, tiller number per plant, and spikelets per spike. By analyzing these traits in the segregating population and their parents, we aim to select terminal heat-tolerant and high-yielding F_2 genotypes from various crosses, compare the performance of selected lines under heat stress conditions with parental lines, and investigate the association between different morphological traits and heat tolerance/high yield under field conditions. Ultimately, this research seeks to identify heat-tolerant and high-yielding segregant genotypes in F_2 generations and phenotypic correlations during the late planting season in the field conditions of Bangladesh.

MATERIALS AND METHODS

Plant materials

Seeds from various cross progeny, F_2 seeds of *BG32/BG33* (A); *BG33/BG32* (B); *BG26/BG33* (C); *BG33/BG26* (D); *BG25/BG33* (E); *BG33/BG25* (F); *BG20/BG33* (G); *BG33/BG20* (H); *BG20/BG26* (I); *BG26/BG20* (J) and their respective parents having high yield potential and moderately tolerant to terminal heat stress (*BARI Gom-33, BARI Gom-32, BARI Gom-26, BARI Gom-25*, and *BARI Gom-20*) were used for the study. Elite wheat varieties were obtained from Bangladesh Agricultural Research Institute (BARI), and F_1 progenies were generated using mating among them at Plant Molecular Genetics Laboratory, Dept. of Genetics Plant Breeding. A thousand (5000) seeds were sown from 10 cross progenies and five parental lines.

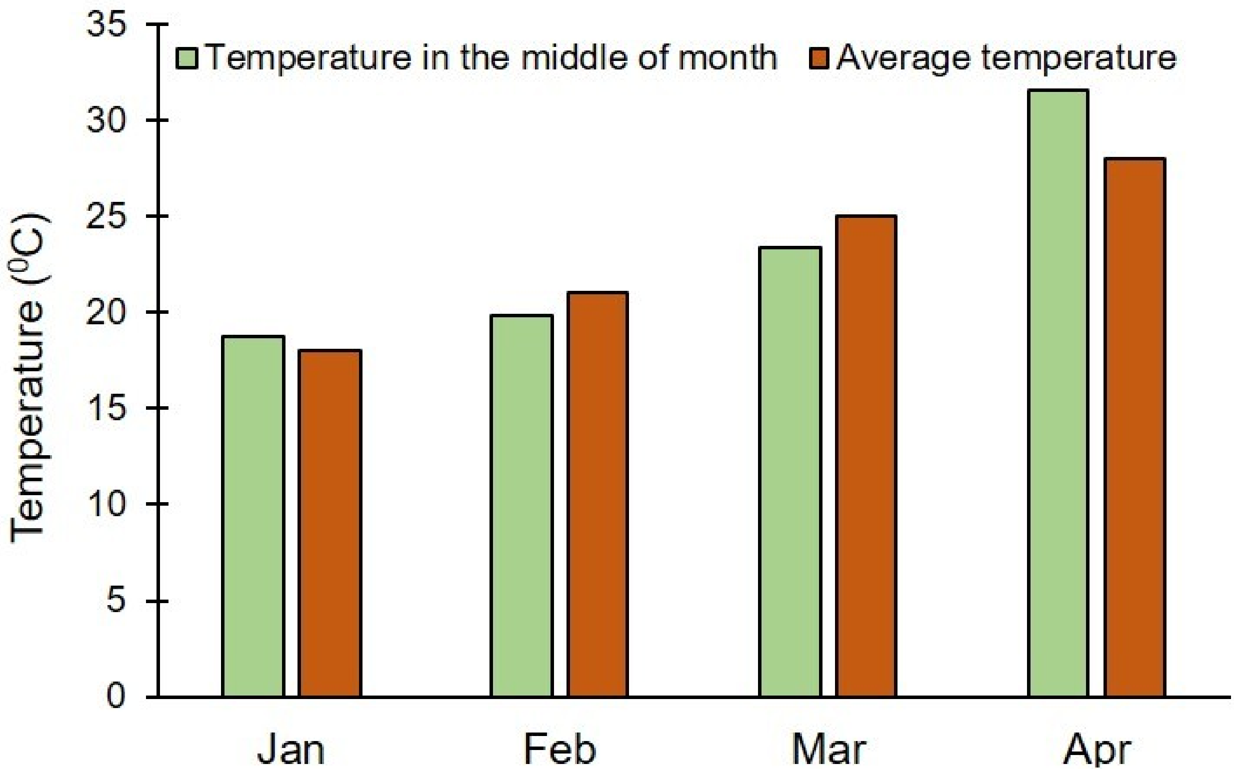


Figure 1. Average monthly temperature during the experimental period.

Experimental site, duration and design

The experiment was conducted at the Farm Lab of Bangladesh Agricultural University during the period from November 2022 to April 2023. The field is situated at 24°75 N and 90°50 E, 18 meters above sea level, with sandy loam soil having a pH of 6.5. 500 seeds from each cross and 20 seeds of their respective parents were planted in 15 plots, each consisting of 7 rows, 2 meters long, with a row spacing of 30 cm and a plant spacing of 10 cm within rows. Terminal heat stress was applied using a late sown condition (January 5th) due to delayed planting and elevated temperatures (Fig. 1).

Observation recorded and selection of F_2 genotypes

From the check varieties, 10 random plants were selected and phenotypic data were collected on several agronomic traits, including plant height (PH), flag leaf length (FLL), spike length (SL), number of spikelets per spike (NSPS), number of tillers per plant (NTPP), grain number per plant (NGPP), yield per plant (YPP), and 100-grain weight (HGW). For F_2 independent line selection, the pedigree method was employed to study heat stress in field conditions. The selected line was named A, B, C, D, E, F, G, H, I, and J for 10 different crosses, accordingly.

Statistical analysis

Statistical analysis was performed using R software (version 4.3.3). Analysis of variance (ANOVA) was conducted to determine the effects of genotypes and their interaction on measured traits. Means were compared using the Least Significant Difference (LSD) test at $p < 0.05$.

RESULTS AND DISCUSSION

Analysis of variance (ANOVA) for different studied traits

ANOVA revealed significant genetic differences among parents, crosses, and reciprocal crosses of F_2 in traits like plant height, flag leaf length, spike length, number of spikelets per spike, number of grains per plant, hundred-grain weight, and yield per plant, all at the 0.001 significance level (Table 1). No significant difference was found in the number of tillers

Table 1. Analysis of variance (mean squares) for F_2 population and parents.

SOV	df	PH	FLL	SL	NSPS	NTPP	NGPP	HGW	YPP
Genotype	14	694.***	75.096***	24.253***	36.539***	6.7638	31160.0***	4.859***	17.055***
Error	126	116.14	6.701	1.035	7.025	6.3649	7027.6	0.5073	5.2289

Note: *** indicate significant at 0.1% levels of probability Legends: df= degrees of freedom; PH= Plant height; FLL= Flag leaf length; SL= Spike length; NTPP= Number of tillers per plant; NSPS= Number of spikelets per spike; NGPP= Number of grains per plant; HGW= Hundred grain weight; YPP= Yield per plant.

per plant.Mostafa *et al.* (2014) found strong significance in plant height, spike length, number of spikelets per spike, number of grains per plant, yield per plant, and hundred-grain weight. Irshad *et al.* (2012) observed highly significant genotypic differences for all traits under various temperature regimes, indicating diverse heat tolerance mechanisms in wheat.

Mean performance of F_2 genotypes and their parents

Detailed comparisons of various characters among the F_2 genotypes and its parents presented in Table 2 and Fig. 2 showed that plant height ranges from 102.64 cm to 74.10 cm, with a mean of 92.09 cm. The highest values were observed in crosses involving *BARI Gom-33*, the lowest in *BARI Gom-20* and *BARI Gom-32*. Flag leaf length ranged from 15.693 cm to 25.110 cm, averaging 20.11 cm. The largest flag leaf was observed in *BARI Gom-25* and *BG32* × *BG33*, while lowest values in *BARI Gom-33* and *BARI Gom-32*. Average spike length is 10.93 cm, ranging from 8.23 cm to 13.227 cm. The longest spikes were in *BG25* × *BG33* and *BG26* × *BG33*, while shortest in parent genotypes *BARI Gom-25*, *BARI Gom-20*, *BARI Gom-32*, and *BARI Gom-26*. No significant difference was found in the number of tillers per plant. The highest seed count was observed in *BARI Gom-20*, followed closely by *BG26* × *BG20*. Conversely, the lowest seed count was noted in *BARI Gom-26* and *BG26* × *BG33*. The hundred-grain weight varied from 4.28 g to 1.38 g, with an average of 2.53 g, where *BG20* × *BG33* and *BG33* × *BG32* were top performers, and *BARI Gom-26*, *BARI Gom-25*, and *BARI Gom-20* had the lowest weights. The yield per plant among the genotypes varied from 6.50 g to 1.63 g, with an average of 4.47 g, where *BG26* × *BG20*, *BG33* × *BG25*, *BG20* × *BG26*, and *BG25* × *BG33* had the highest yields, and *BARI Gom-26*and *BARI Gom-25* had the lowest yields. The F_2 population exhibited significant variability in plant height and this diversity is essential for breeding progress. Heat stress likely reduced plant height (Ford & Thorne 1975, Mattas *et al.* 2011). According to Pask (2012), high-temperature stress reduced flag leaf length. Yield traits like spike length, number of spikelets per spike, number of grains per plant, and hundred-grain weight were higher in F_2 lines under stress compared to their parents (Salous *et al.* 2014). Most traits in the segregated population displayed transgressive segregation under stressful conditions (Putri *et al.* 2020). A few lines from crosses appeared transgressive, suggesting that parents contributed different genes for heat tolerance (Paliwal *et al.* 2013). The highest hundred-grain weight (HGW) was observed in selected genotypes, surpassing their parents (Table 2). A high yield per plant was noted in several genotypes, exceeding their parent lines (Fouad *et al.* 2022). Pedigree selection yielded higher gains compared to indirect selection (Fellahi *et al.* 2018).

Estimation of genetic parameters using parents and F_2 population

The genotypic analysis presented in Table 3 shows that for every trait the phenotypic co-efficient of variation (PCV) was higher than genotypic co-efficient of variation (GCV). The higher GCV and PCV values were observed in case of yield per plant and number of grains per plant. Highest heritability was observed in spike length (69%) and the lowest value in number of tillers per plant (1%). Number of grains per plant have high genetic advance, where as other trait showed moderate genetic advance except for number of tillers per plant, which have the lowest value (0.03). Genetic variability is critical for crop breeding because it helps determine the

Table 2. Comparison of mean performance among selected F_2 genotypes and their parents.

Gen	PH	FLL	SL	NSPS	NTPP	NGPP	HGW	YPP
BG33	83.96d	16.15gh	11.04ef	18.00abc	6.0ab	140.9ef	2.795bc	3.934bcd
BG32	74.10e	15.693h	8.97g	13.60e	8.1a	162.6def	2.818bc	4.579abcd
BG26	88.55cd	20.90cde	9.08g	16.90cd	7.3a	118.8f	1.384d	1.634e
BG25	89.83bcd	25.11a	8.23g	14.60de	7.0ab	168.4cdef	1.585d	2.672de
BG20	82.23de	17.47fgh	8.61g	20.10a	7.2ab	313.3a	1.598d	5.022abc
BG33/BG32	90.32bcd	23.73ab	11.13def	17.66bc	7.9a	136.1ef	2.466c	3.238cde
BG32/BG33	102.64a	21.82bc	11.99bcd	18.63abc	6.5ab	115.0f	3.134b	3.539cde
BG26/BG33	97.70abc	21.46bc	12.61ab	19.88ab	6.0ab	178.1cdef	2.425c	4.427bcd
BG33/BG26	99.99a	18.82def	11.88bcde	18.79abc	6.2ab	175.6cdef	2.489c	4.433bcd
BG25/BG33	95.72abc	18.25fg	13.27a	19.51ab	6.7ab	237.6bc	2.444c	5.651ab
BG33/BG25	99.92a	21.06cd	12.30bc	19.95ab	6.8ab	227.1bcd	2.647bc	5.794ab
BG20/BG33	99.33ab	21.33c	11.68cde	19.71ab	5.0b	139.9ef	4.281a	5.247abc
BG33/BG20	98.46ab	18.50f	11.80bcde	18.64abc	6.5ab	176.8cdef	2.705bc	4.709abc
BG20/BG26	83.17de	18.66ef	10.31f	18.25abc	6.1ab	207.2bcde	2.795bc	5.753ab
BG26/BG20	95.54abc	22.81bc	11.16def	19.06abc	7.6a	259.3ab	2.447c	6.509a

Legends: PH = Plant height; FLL = Flag leaf length; SL = Spike length; NTPP = Number of tillers per plant; NSPS = Number of spikelets per spike; NGPP = Number of grains per plant; HGW = Hundred grain weight; YPP = Yield per plant.

Table 3. Estimation of genetic parameters for morphological traits using parents and F_2 population.

Traits	GV	PV	GCV	PCV	h^2b (%)	GA	GAM (%)
PH	57.80	173.94	8.26	14.32	33	9.03	9.80
FLL	6.84	13.54	13.00	18.29	51	3.83	19.03
SL	2.32	3.36	13.93	16.75	69	2.61	23.87
NTPP	0.04	6.40	2.97	37.62	1	0.03	0.48
NSPS	2.95	9.98	9.43	17.33	30	1.92	10.56
NGPP	2413.24	9440.86	26.73	52.87	26	51.16	27.84
YPP	1.18	6.41	24.29	56.56	18	0.96	21.49
HGW	0.43	0.94	26.03	38.30	46	0.92	36.43

Legends: GV = Genotypic variance; PV = Phenotypic variance; GCV = Genotypic coefficient of variation; PCV = Phenotypic coefficient of variation; h^2b = Heritability (broad sense); GA = Genetic advance; GAM = Genetic advance as percent of mean.

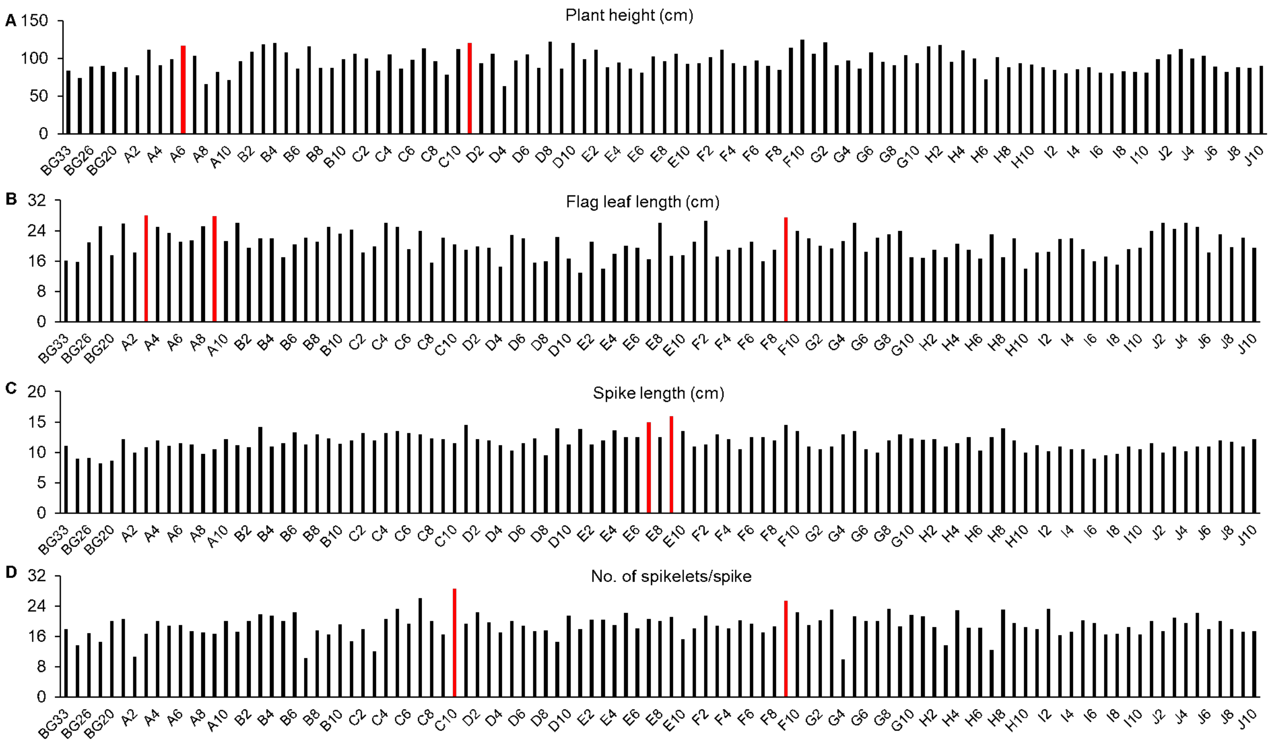


Figure 2. Genotypic variation among 100 F_2 genotypes and their parents for different traits. (Here, black color shows different genotypes, red indicates the genotype that performed best among all. Plant height (A); Flag leaf length (B); Spike length (C); Number of spikelets per spike (D); Number of tillers per plant (E); Number of grains per plant (F); Hundred grain weight (G); Yield per plant (H).

success of selection and genetic improvement. Assessing existing variability is essential for effective breeding programs. Phenotypic and genotypic variances were vast, with the highest observed for the number of grains per plant (2413.24 and 9440.86, respectively). For all the characters studied, the PCV was higher than the GCV, which indicates the influence of environmental factors. A similar result was also found in Anis *et al.* (2016). Traits like number of grains per plant and yield per plant exhibited the highest PCV and GCV (Desheva & Cholakov 2014, El-Areed *et al.* 2023). Variability in yield-attributing traits aids in breeding high-yielding varieties through hybridization and selection. The low difference between PCV and GCV suggests minimal environmental influence or stronger genetic control (Desheva & Cholakov 2014), and in the study, the lowest PCV and GCV values were observed for plant height (14.32% and 8.26%, respectively). High heritability and genetic advance as a percentage were observed in flag leaf length, hundred grain weight, number of grains per plant, spike length, and yield per plant, which indicates additive gene effects and suitability for selection (Ali & Shakor 2012, Kumar *et al.* 2014, Kyosev & Desheva 2015, Bhanu *et al.* 2018). Flag leaf length is a crucial trait for wheat heat tolerance (Wang *et al.* 2016). On the other hand, the number of tillers per plant exhibited the lowest values, aligning with findings by Mishra & Marker (2013). High heritability coupled with substantial genetic advance suggests potential for selection in subsequent generations (Johnson *et al.* 1955).

Evaluation of the selected F_2 genotypes for yield and its attributing traits under late sown conditions

The evaluation of selected F_2 genotypes revealed significant diversity across multiple morphological traits (Fig. 1). Plant height varied notably from 125 cm to 63.5 cm, with F10 displaying the tallest stature at 125 cm, indicating potential for enhancing plant height in breeding programs. Flag leaf length exhibited substantial variation, with genotype 26.50 cm highlighting the lengthiest flag leaf among

F_2 plants, even surpassing the tallest parent. Spike length, essential for yield contribution, displayed a wide range from 16.00 cm to 9 cm, with notable performers such as A3 and B3 exhibiting longer spikes. Similarly, the number of spikelets per spike varied considerably, with some F_2 genotypes surpassing their parent lines. On the other hand, the number of tillers per plant ranged from 18.00 to 2.00, indicating diverse trends within the population. Noteworthy variations were also observed in the number of grains per plant, with F_2 genotypes like E2 and F2 demonstrating substantial seed numbers. Hundred-grain weight ranged from 9.44 g to 1.40 g, highlighting variations in grain quality and development. Finally, yield per plant showed significant diversity, with genotypes like J9 exhibiting high yields and others like B5 displaying minimal yields, emphasizing the variability in yield potential across the F_2 population.

Association among the studied morphological traits of F_2 genotypes

Correlation analysis presented in Fig. 3 reveals that plant height, flag leaf length, and spikelets per spike showed positive correlation with all traits. However, significant positive relationships were observed between plant height and spike length (0.25), as well as between spike length and number of spikelets per spike (0.29). Other traits show less positive association with plant height. Flag leaf length exhibits insignificant positive correlations with spike length and other traits, with spike length showing a small association (0.03). Spike length is significantly positively related to plant height and number of spikelets per spike, but significantly negatively related to number of tillers per plant (-0.20). Yield per plant demonstrates strong positive correlations with number of grains per plant (0.91), number of tillers per plant (0.63), and number of spikelets per spike (0.33), while having small negative correlations with spike length (-0.06). Hundred-grain weight shows moderate positive correlations with most traits except number of grains per plant, which has a significantly negative correlation (-0.22). Overall, the number of tillers per plant and the number of grains per plant exhibit strong correlations with yield per plant. According to Blum (2018), complex traits like grain yield are largely affected by a greater number of genes in the A, B, and D genomes and have lower narrow-sense heritability. As it is highly influenced by the environment, it is hard to rely on grain yield as a unique selection criterion (Dhanda *et al.* 2004). Traits like spikelets per spike, grain number per plant, and tiller number show significant correlations with yield per plant. According to El-Areed *et al.* (2023), these traits should be considered to improve desirable genotypes. Moreover, the number of spikelets per plant has a significant positive correlation with grain number, tiller number, hundred-grain weight, and spike length. Selection for a greater grain number per spike positively affects grain yield per spike (Gupta *et al.* 2015). However, spike length has a negative correlation with yield per plant and tiller number (Semenov 2009). Positive correlations are observed between grain yield per plant, plant height, and the number of productive tillers per plant (Gupta *et al.* 2015).

Principal component analysis (PCA)

Principal Component Analysis (PCA) reduces data dimensionality by identifying key components explaining most variance (Fig. 4). The first three components (PC1, PC2, and PC3) account for 32.993%, 20.151%, and 12.746% of the variance, respectively, totaling 65.891% (Fig. 4). These components capture the primary patterns in the data, with the remaining components explaining progressively smaller proportions of the variance. The cumulative variance shows the total variance explained by each component and its predecessors. PC1 explains the most variance (32.993%) and is strongly associated with NGPP (0.938), YPP (0.930), and NTPP (0.794), indicating higher yield potential with higher values on Dim.1. PC2 explains 20.151% of the variance and is positively correlated with PH (0.670), NSPS (0.608), and SL (0.667), capturing variation related to spike density and length (Fig. 4). The biplot from PCA of eight traits in 105 plant genotypes shows the first two principal components (PC1: 33%, PC2: 20.1%) in Fig. 4. Yield per plant, number of grains per plant, and tiller number had the most influence, while hundred-grain weight had the least. Genotypes J4, E2, J9, and F2 varied significantly in

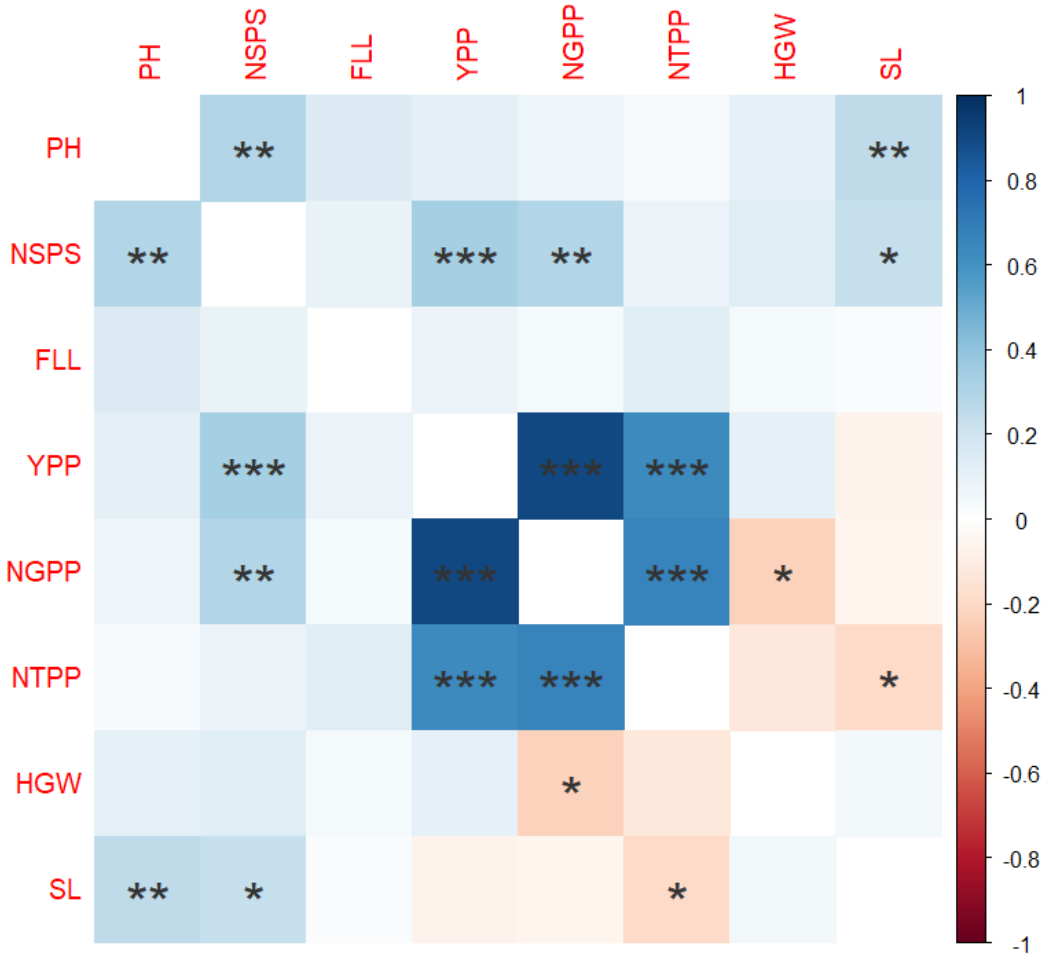


Figure 3. Correlation coefficient matrix for the 8 morphological traits of F_2 genotypes and their parents. (* indicates significance at 5% level, ** indicates significance at 1% level and *** indicates significance at 0.1% level)

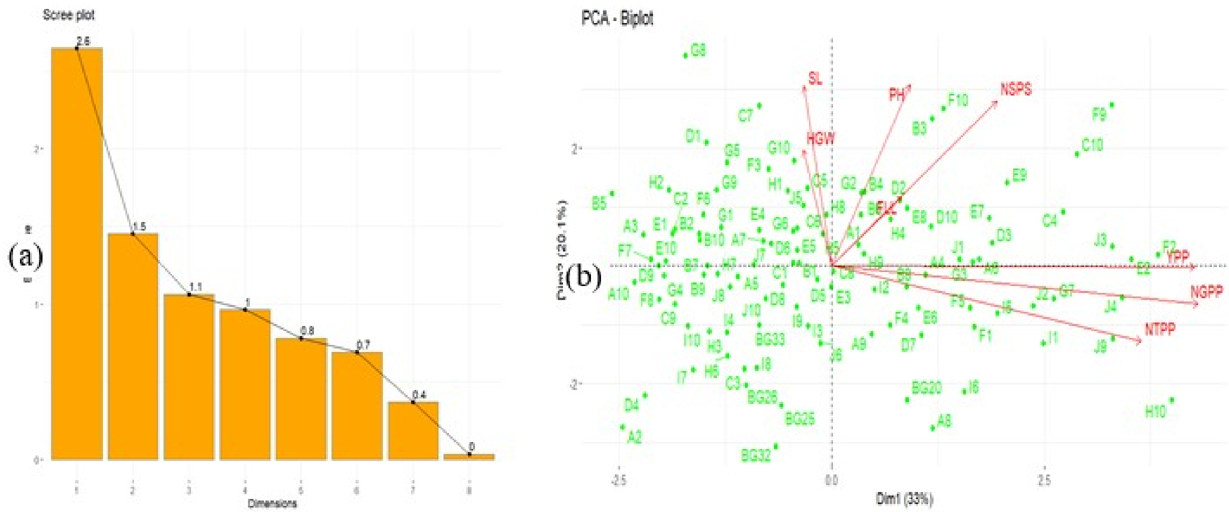
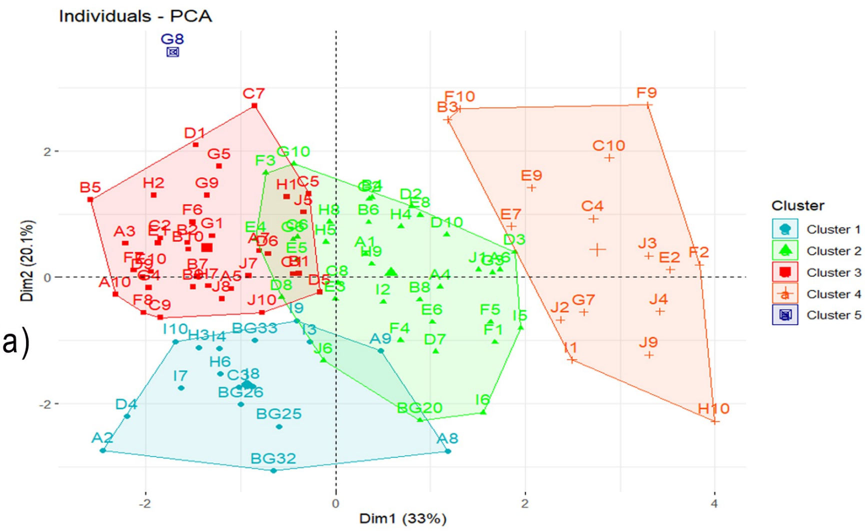


Figure 4. (a) Eigenvalue index and Variance (%) for 8 characters of 105 wheat genotypes. (b) PCA biplot for eight traits of F_2 genotypes and their parents studied under heat stress. In the figure, A-J stands for the selected line on 10 different crosses.

(a)



(b)

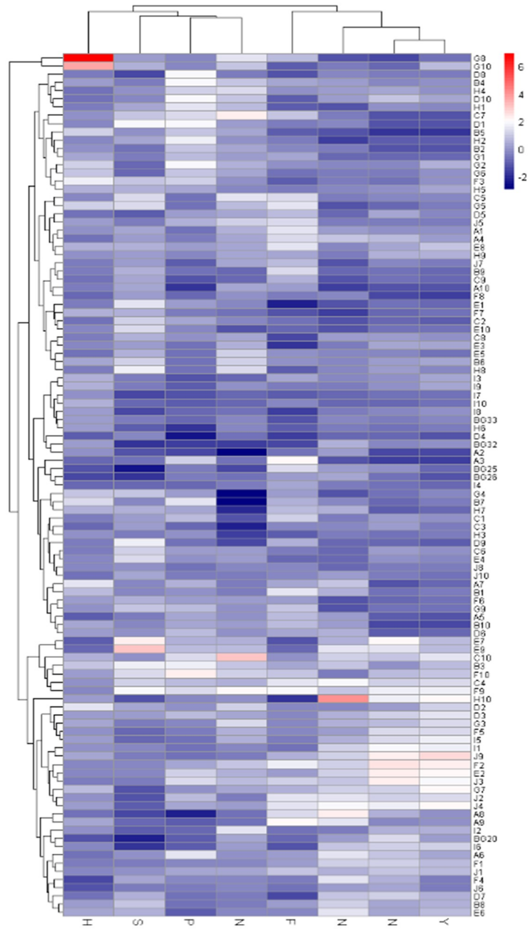


Figure 5. (a) Five clustering group loading in PCA-Biplot of selected 100 F_2 genotypes with their parents. (b) Heatmap displaying the clustering pattern of 100 F_2 wheat genotypes and their parents. The heatmap's color intensity represents loading values for traits on the first three principal components (PCs), with darker colors indicating stronger associations. PC1 is positively associated with NGPP, YPP, and NTPP, suggesting genotypes F2, J3, J2, J9, I5, G3, D2, and C4 score higher on PC1. PC2 is positively associated with NSPS and negatively with SL, indicating genotypes E9, F10, B4, G8, and D9 have higher scores on PC2. PC3 is positively associated with PH and HGW, suggesting genotypes G8 and H5 score higher on PC3 (Figure 5b).

Table 4. Distance between cluster centroids.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	0				
Cluster II	6.755	0			
Cluster III	6.561	6.523	0		
Cluster IV	8.272	6.820	8.560	0	
Cluster V	9.240	9.248	8.473	10.153	0

The plot visually identifies five distinct clusters, each containing genotypes positioned closely together, indicating potential groupings based on their shared trait profiles (Fig. 4).

these traits. Genotypes near the origin (e.g., A1, B1, C8) showed less variation. Parents *BG33, BG32,* and *BG26* clustered negatively for all traits in the third quadrant. PCA-biplot analysis integrates traits and objects into multiple dimensions, minimizing overlapping variations for better selection clarity (Arzu *et al.* 2018). PC1, PC2, and PC3 collectively account for 65.891% of the variance; similar findings were reported by Fellahi *et al.* (2018) and Bhatti *et al.* (2022). NGPP and YPP show maximum positive loadings on PC1, spike length on PC2, and HGW on PC3. These findings are partly supported by previous studies (Fellahi *et al.* 2018; Bhatti *et al.* 2022; Singh *et al.* 2022). Notably, YPP, NGPP, NSPS, SL, PH, and NTPP contribute significantly to variation between F_2 segregation lines and their parents. Khan *et al.* (2023) found that yield per plant had the highest variability with the maximum length of the vector compared to the rest of the parameters; however, in this study, the NGPP vector had the highest length compared to other traits. Genotypes like H10, J9, J4, E2, F2, and G7 exhibit potential for heat-tolerant line development, while those closer to the biplot center are more heat-susceptible.

Cluster analysis of different groups of selected F_2 lines

Table 4 presents the pairwise distances between five clusters comprising 105 genotypes. Each cell in the matrix represents the distance measure, unveiling the dissimilarity between clusters based on specific features relevant to the genotypes. The varying distances indicate different levels of dissimilarity among the clusters. The distances between Cluster I and Cluster IV (9.24) and Cluster IV and Cluster V (10.15) are relatively high, suggesting substantial dissimilarities. In contrast, the distances between Cluster I and Cluster II (6.76) and Cluster II and Cluster III (6.52) are comparatively lower, indicating moderate dissimilarity. These pairwise distances offer valuable insights into relationships among genotypic clusters, providing a foundation for understanding genetic or phenotypic variation within the studied population. Cluster-wise biplots and Euclidean heatmap clustering are essential tools in plant breeding for analyzing multidimensional data (Mumtaz *et al.* 2019; Khalid *et al.* 2020). The biplot visualizes samples and variables simultaneously, while the heatmap clusters individuals based on Euclidean distances (Wolde *et al.* 2016). Major clusters, such as Cluster 1 (red), contain most individuals and their parents, while Clusters 2 (green) and 5 (blue) appear distinct (Fig. 5). Cluster 4 contains genotypes associated with yield variables, while Cluster 2 shows less variation and may not be ideal for further development (Ajmal *et al.* 2013).

CONCLUSION

Due to global climate change in the past few decades, the impact of rising temperatures on wheat production has gained concern worldwide, especially in subtropical countries like Bangladesh. In this study, an attempt was made to select heat-tolerant high-yielding plants and analyze phenotypic correlations of the F_2 population from several crosses and their reciprocal crosses under late planting conditions in Bangladesh. From each 10-cross combination, a total of 100 genotypes were selected based on their performance under terminal heat stress conditions using phenotypic evaluation. BARI Gom-20 stood out as a promising parental line for overall trait performance. High phenotypic and genotypic coefficients of variation were observed for number of seeds per plant (52.87 and 26.73, respectively) and yield per plant (56.56 and 24.29, respectively), indicating their potential as selection criteria. The selected terminal heat-tolerant genotypes H10, J9, J4, E2, F2, and G7 were grouped in a single cluster along with others, which can be further used and advanced to develop heat-tolerant wheat breeding lines in Bangladesh for sustainable food production.

Acknowledgements

Bangladesh Agricultural University Research System (BAURES) is acknowledged for funding the project BAURE/2024/47/AU-GC to GHMS.

REFERENCES

Abhinandan K, Skori L, Stanic M, Hickerson NMN, Jamshed M, Samuel MA (2018) Abiotic Stress Signaling in Wheat – An Inclusive Overview of Hormonal Interactions During Abiotic Stress Responses in Wheat. *Frontiers in Plant Science*, 9, 734–739. https://doi.org/10.3389/fpls.2018.00734.

Ajmal SU, Minhas NM, Hamdani A, Shakir A, Zubair M, Ahmad Z (2013) Multivariate analysis of genetic divergence in wheat (*Triticum aestivum*) germplasm. *Pakistan Journal of Botany*, 45(5), 1643–1648.

Ali IH, Shakor EF (2012) Heritability, variability, genetic correlation and path analysis for quantitative traits in durum and bread wheat under dry farming conditions. *Mesopotamia Journal of Agriculture*, 40(4), 27–39. https://doi.org/10.33899/magrj.2012.59640.

Anis G, Sabagh AE, Ghareb A, Rewainy IEL (2016) Evaluation of promising lines in rice (*Oryza sativa* L.) for agronomic and genetic performance under Egyptian conditions. *International Journal of Agronomy and Agricultural Research*, 8(3), 52–57.

Arzu K, Onder O, Bilir O, Kosar F (2018) Application of multivariate statistical analysis for breeding strategies of spring safflower (*Carthamus tinctorius* L.). *Turkish Journal of Field Crops*, 23(1), 12–19. https://doi.org/10.17557/tjfc.413818.

Bhanu AN, Arun B, Mishra VK (2018) Genetic variability, heritability and correlation study of physiological and yield traits in relation to heat tolerance in wheat (*Triticum aestivum* L.). *Biomedical Journal of Scientific & Technical Research*, 2(1), 2112–2116. https://doi.org/10.26717/BJSTR.2017.01.000636.

Bhatti N, Dalal MS, Phougat D, Devi S (2022) Multivariate analysis of morpho-physiological traits in bread wheat genotypes under terminal heat stress. *Electronic Journal of Plant Breeding*, 13(4), 1180–1186. https://doi.org/10.37992/2022.1304.170.

Blum A (2018) Plant breeding for stress environments. CRC Press. https://doi.org/10.1201/9781351075718.

Buttar ZA, Wu SN, Arnao MB, Wang C, Ullah I, Wang C (2020) Melatonin suppressed the heat stress-induced damage in wheat seedlings by modulating the antioxidant machinery. *Plants*, 9(7), 809–813. https://doi.org/10.3390/plants9070809.

Cardoso C, Reis EM, Moreira EN (2008) Development of a warning system for wheat blast caused by *Pyricularia grisea*. *Summa Phytopathologica*, 34, 216–221. https://doi.org/10.1590/S0100-54052008000300002.

Cossani CM, Reynolds MP (2012) Physiological traits for improving heat tolerance in wheat. *Plant Physiology*, 160(4), 1710–1718. https://doi.org/10.1104/pp.112.207753.

Desheva G, Cholakov T (2014) Variability, heritability and genetic progress for some yield components in common winter wheat genotypes (*Triticum aestivum* L.). *Genetics and Plant Physiology*, 4(3–4), 191–200.

Dhanda SS, Sethi GS, Behl RK (2004) Indices of drought tolerance in wheat genotypes at early stages of plant growth. *Journal of Agronomy and Crop Science*, 190(1), 6–12. https://doi.org/10.1111/j.1439-037X.2004.00592.x.

Djanaguiraman M, Prasad PVV, Seppanen M (2010) Selenium protects sorghum leaves from oxidative damage under high temperature stress by enhancing the antioxidant defense system. *Plant Physiology and Biochemistry*, 48(12), 999–1007. https://doi.org/10.1016/j.plaphy.2010.09.009.

El-Areed SR, Shawky M, Elmoselhy O (2023) Selection by independent culling levels method in bread wheat under normal and heat stress conditions. *Egyptian Journal of Plant Breeding*, 27, 289–308.

Farooq M, Bramley H, Palta JA, Siddique KHM (2011) Heat stress in wheat during reproductive and grain-filling phases. *Critical Reviews in Plant Sciences*, 30(6), 491–507.

Fellahi ZEA, Hannachi A, Bouzerzour H (2018) Analysis of direct and indirect selection and indices in bread wheat (*Triticum aestivum* L.) segregating progeny. *International Journal of Agronomy*, 1–11. https://doi.org/10.1155/2018/8312857.

Fleitas MC, Mondal S, Gerard GS, Hernández-Espinosa N, Singh RP, Crossa J et al. (2020) Identification of CIMMYT spring bread wheat germplasm maintaining superior grain yield and quality under heat-stress. *Journal of Cereal Science*, 93, 102981. https://doi.org/10.1016/j.jcs.2020.102981.

Ford MA, Thorne GN (1975) Effects of variation in temperature and light intensity at different times on growth and yield of spring wheat. *Annals of Applied Biology*, 80(3), 283–299. https://doi.org/10.1111/j.1744-7348.1975.tb01634.x.

Fouad H, Mohamed M, Salim M, Mohiy M, Abd El-Mageed M (2022) Half diallel analysis and heat stress tolerance indices for grain yield in bread wheat. *Journal of Plant Production*, 13(10), 763–773. https://doi.org/10.21608/jpp.2022.161348.1168.

Gupta M, Chawla V, Dhanda SS, Saharan RP, Munjal R, Garg P (2015) Effect of terminal heat stress on yield and yield components of bread wheat genotypes. *Research on Crops*, 16(1), 42–45. https://doi.org/10.5958/2348-7542.2015.00006.6.

Guzmán C, Ibba MI, Álvarez JB, Sissons M, Morris C (2022) Wheat quality. In: Springer International Publishing, pp. 177–193. https://doi.org/10.1007/978-3-030-90673-311.

Hasanuzzaman M, Nahar K, Alam M, Roychowdhury R, Fujita M (2013) Physiological, biochemical, and molecular mechanisms of heat stress tolerance in plants. *International Journal of Molecular Sciences*, 14(5), 9643–9684. https://doi.org/10.3390/ijms14059643.

Irshad M, Khaliq I, Khan AS, Ali A (2012) Genetic studies for some agronomic traits in spring wheat under heat stress. *Pakistan Journal of Agricultural Sciences*, 49(1), 11–20.

Johnson H, Robinson HF, Comstock RE (1955) Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, 47(7), 314–318. https://doi.org/10.2134/agronj1955.00021962004700070009x.

Khalid MU, Akhtar N, Arshad M, Yousaf MI (2020) Characterization of maize inbred lines for grain yield and related traits under heat stress conditions. *International Journal of Biology and Biotechnology*, 17(2), 367–375.

Khan MA, Ayyub MU, Bashir A, Alam B (2023) Characterization of bread wheat genotypes using morpho-phenological attributes related to yield under terminal heat stress. *Gesunde Pflanzen*, 75(6), 2377–2385. https://doi.org/10.1007/s10343-023-00883-8.

Kyosev B, Desheva G (2015) Study on variability, heritability, genetic advance and associations among characters in emmer wheat genotypes (*Triticum dicoccon* Schrank). *Journal of Bioscience and Biotechnology*, 221–228.

Mattas KK, Uppal RS, Singh RP (2011) Effect of varieties and nitrogen management on growth, yield and nitrogen uptake of durum wheat. *Research Journal of Agricultural Sciences*, 2(2), 376–380.

Mishra R, Marker S (2013) Evaluation of wheat genotypes for heat stress under late sown conditions of Allahabad region. *Trends in Biosciences*, 6(5), 625–627.

Mostafa M, Ismail A, Abo-Elwafa A, Tawfelis M (2014) Genetical studies of yield and its components in durum wheat under heat stress. *Assiut Journal of Agricultural Science*, 45(5), 53–78. https://doi.org/10.21608/ajas.2014.3522.

Mumtaz A, Hussain D, Saeed M, Arshad M, Yousaf MI (2019) Stability and adaptability of sorghum hybrids elucidated with genotype–environment interaction biplots. *Turkish Journal of Field Crops*, 24(2), 155–163. https://doi.org/10.17557/tjfc.631130.

Nahar K, Ahamed KU, Fujita M (2010) Phenological variation and its relation with yield in wheat (*Triticum aestivum* L.) cultivars under normal and late sowing heat stress. *Notulae Scientia Biologicae*, 2(3), 51–56. https://doi.org/10.15835/nsb234723.

Kumar N, Markar S, Kumar V (2014) Studies on heritability and genetic advance estimates in timely sown bread wheat (*Triticum aestivum* L.). *Bioscience Discovery*, 5(1), 64–69.

Ohama N, Sato H, Shinozaki K, Yamaguchi-Shinozaki K (2017) Transcriptional regulatory network of plant heat stress response. *Trends in Plant Science*, 22(1), 53–65. https://doi.org/10.1016/j.tplants.2016.08.015.

Paliwal R, Arun B, Srivastava J, Joshi A (2013) Inheritance of terminal heat tolerance in two spring wheat crosses. *Cereal Research Communications*, 41(3), 400–408. https://doi.org/10.1556/CRC.2013.0013.

Panigrahi S, YK Pankaj, Kumar V, Kumar R, Singh SK (2022) Effects of terminal heat stress on yield stability, grain iron and zinc content in wheat (*Triticum aestivum* L.). *Indian Journal of Genetics and Plant Breeding*, 82(3), 289–298. https://doi.org/10.31742/ISGPB.82.3.3.

Pask A (Ed.) (2012) *Physiological Breeding: A field guide to wheat phenotyping*. CIMMYT.

Patel D, Franklin KA (2009) Temperature-regulation of plant architecture. *Plant Signaling & Behavior*, 4(7), 577–579. https://doi.org/10.4161/psb.4.7.8849.

Prasad PVV, Pisipati SR, Momčilović I, Ristic Z (2011) Independent and combined effects of high temperature and drought stress during grain filling on plant yield and chloroplast EF-Tu expression in spring wheat. *Journal of Agronomy and Crop Science*, 197(6), 430–441. https://doi.org/10.1111/j.1439-037X.2011.00477.x.

Putri NE, Sutjahjo SH, Nur A, Suwarno WB, Wahyu Y (2020) Wheat transgressive segregants and their adaptation in the tropical region. *SABRAO Journal of Breeding & Genetics*, 52(4), 506.

Rahaie M, Xue GP, Schenk PM (2013) The role of transcription factors in wheat under different abiotic stresses. *Abiotic Stress–Plant Responses and Applications in Agriculture*, 2, 367–385. https://doi.org/10.5772/54795.

Rezaei EE, Siebert S, Manderscheid R, Müller J, Mahrookashani A, Ehrenpfordt B et al. (2018) Quantifying the response of wheat yields to heat stress: The role of the experimental setup. *Field Crops Research*, 217, 93–103. https://doi.org/10.1016/j.fcr.2017.12.015.

Salous MS, El-Morshidy MA, Kheiralla KA, Moshref MK (2014) Selection for grain yield in bread wheat (Triticum aestivum L.) under normal and heat stress conditions. *Assiut Journal of Agricultural Science*, 45(2), 1–18. https://doi.org/10.21608/ajas.2013.731.

Semenov MA (2009) Impacts of climate change on wheat in England and Wales. *Journal of the Royal Society Interface*, 6(33), 343–350. https://doi.org/10.1098/rsif.2008.0285.

Singh V, Poonia MS, Verma A, Tyagi BS (2022) Multivariate biplot analysis for the diversity in bread wheat genotypes (Triticum aestivum L.). *International Journal of Bio-resource and Stress Management*, 13(3), 219–225.

Tadesse W, Sanchez-Garcia M, Assefa SG, Amri A, Bishaw Z, Ogbonnaya FC et al. (2019) Genetic gains in wheat breeding and its role in feeding the world. *Crop Breeding, Genetics and Genomics*, 1(1), e190005.

Wang F, Liu J, Chen M, Zhou L, Li Z, Zhao Q et al. (2016) Involvement of abscisic acid in PSII photodamage and D1 protein turnover for light-induced premature senescence of rice flag leaves. *PLOS ONE*, 11(8), e0161203. https://doi.org/10.1371/journal.pone.0161203.

Wolde T, Eticha F, Alamerew S, Assefa E, Dutamo D (2016) Multivariate analysis of some metric traits in durum wheat (*Triticum durum* L.) accessions. *Advances in Crop Science and Technology*, 74, 26–31.