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ASSESSMENT OF GENETIC PARAMETERS OF BREAD WHEAT (*Triticum aestivum L.*) HYBRIDS UNDER SPEED BREEDING CONDITIONS

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ABSTRACT

As an increasing world population and changing environmental conditions constrain food security, it is inevitable that the current rate of development of many strategic crops will be insufficient to meet future food demand. Depending on the generation time of plants, this rate of development varies. This study was carried out in speed breeding system greenhouses of Dicle University, Turkey in 2023-2024. In the study, genetic parameters and heterosis effects of F_1 bread wheat hybrids (*Triticum aestivum* L.) developed under speed breeding conditions were investigated. Agronomic, physiological, and yield-related traits were evaluated using three bread wheat cultivars (Adana-99, Alada, and Lucilla) and their F1 hybrids, arranged in a completely randomized design (CRD). In study, heterosis over mid-parent and better-parent, potence ratio, genotypic and phenotypic variance, heritability and genetic advance based on days to heading, days to anthesis, heading time SPAD value, anthesis time SPAD value, plant height, spike length, number of grains per spike, grain weight per spike and total grain weight per plant were analyzed. The results revealed significant genetic variability among the hybrids, with the Alada × Adana-99 (P2 × P1) hybrid showing the highest gains in yield related traits such as total grain weight per plant and grain weight per spike. Especially, broad sense heritability (H^2) and genetic advance (GA) values were high for days to heading (H^2:0.87 and GA:5.16) and number of grains per spike (H^2:0.66 and GA:5.32). High broad sense heritability and genetic advance values for these traits further confirm their relevance in breeding programs aimed at improving wheat productivity and resistance under speed breeding conditions. These findings highlight the usefulness of heterosis breeding and genetic parameter assessment in developing high-yielding and stress-tolerant wheat varieties.

Keywords: Wheat, speed breeding, hybrid breeding, heritability, genetic advance

INTRODUCTION

Wheat (*Triticum aestivum* L.), one of the most important cereals globally, plays a critical role in human nutrition and is one of the most widely grown crops. It serves as the primary source of carbohydrates for energy and also contains essential nutrients such as proteins, vitamins, minerals and fibre (Shewry and Hey, 2015).

Global warming induces both biotic and abiotic stresses in plants, it also negatively affects food security (Lobell *et al.*, 2011; Hatfield *et al.*, 2011; Ipekesen *et al.*, 2023). To overcome these challenges, plant breeders are investigating new breeding programs as well as traditional approaches to develop new lines that can adapt to biotic and abiotic stresses (Rivera-Amado *et al.*, 2020). Selecting appropriate breeding methods to improve desired traits and focusing on the development of high-potential wheat lines as the primary goal in wheat breeding programs should be prioritized as the basis of genetic improvement efforts (Zhang *et al.*, 2017).

In contrast to traditional breeding techniques, speed breeding programs enable the development of new genotypes in much shorter time periods (Jähne *et al.*, 2020). While traditional breeding methods require 10-12 years to develop a new cultivar, speed breeding systems can reduce this time to 2-3 years (Hickey *et al.*, 2017). Such systems accelerate the efficient use of genetic resources (Ahmar *et al.*, 2020), the application of gene editing technologies accelerates the process of genetic improvement for specific traits (Watson *et al.*, 2018), and facilitates the rapid development of resistant lines as an urgent response to unpredictable climate shocks (Miner *et al.*, 2022).

Controlled growing conditions outside the growing season and in greenhouses accelerate breeding cycles and increase genetic gain. Currently, the annual genetic gain of wheat is about 1% per year, which is below the required growth rate of 1.7% per year (Batista *et al.*, 2024). This trajectory is required to reach a production peak of 1 billion metric tonnes globally in 2050 (Tadesse *et al.*, 2019). To achieve this goal and ensure food security, a solution may be to consider alternatives other than the growing season. Shortening the duration of the breeding cycle in breeding programmes accelerates genetic improvement, resulting in faster acquisition of beneficial traits and greater genetic gains in less time.

Estimation of genetic parameters in F1 bread wheat populations serves as an important cornerstone for effective breeding strategies aimed at improving stress tolerance, productivity, and environmental adaptation. By analyzing heritability, genetic diversity, and trait correlations, plant breeders gain insight into the genetic potential of the population and facilitate the selection of superior genotypes (Falconer and Mackay, 1996; Lynch and Walsh, 1998; Rashid *et al*., 2025). Furthermore, understanding heterosis and combining ability is a major goal to identify promising parental lines and produce hybrids with desired traits (Griffing, 1956; Sewore and Abe, 2024). Such assessments not only optimize the utilization of genetic resources but also shorten the breeding cycle through improved methodologies including gene editing and marker-assisted selection (Hickey *et al*., 2017; Watson *et al*., 2018). However, this approach helps develop resilient wheat lines to address the challenges posed by climate variability and supports sustainable agricultural practices and improves food security worldwide (Marsh *et al*., 2021; Senapati *et al*., 2022).

For most crops, developing new cultivars with desired traits is a long and labour-intensive process. After crossing the selected parental lines, the evaluation of agro-morphological traits and the development of genetically stable lines can take at least 4-6 generations for field crops, which are limited to only 1-2 generations per year. In this study, the potential for genetic improvement of wheat hybrids was assessed at an early stage under speed breeding conditions using long photoperiod to reduce the developmental rate and generation time of bread wheat (Watson *et al*., 2018). This study aimed to evaluate the effects of heterosis and detect significant improvements in wheat yield by analyzing F1 hybrid bread wheat lines obtained from crosses conducted under speed breeding conditions.

MATERIALS AND METHODS

Plant material and experimental design: This study was carried out in greenhouses suitable for the speed breeding system at Dicle University in Turkey in 2023-2024. During the growing period of F1 hybrids, the greenhouse average temperature and humidity values were in 21.95 °C and 48.20%, respectively (Figure 1). The generation time was recorded as 85 days.

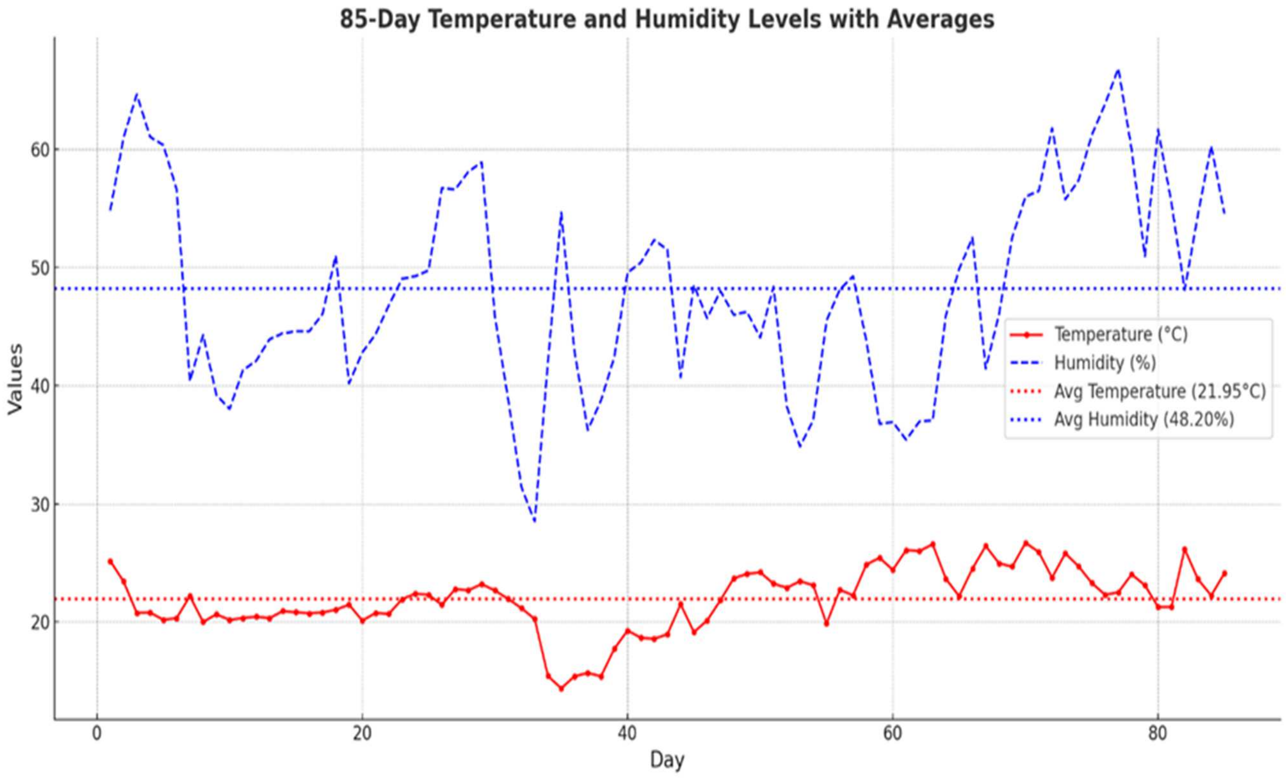

Figure 1. Greenhouse temperature and humidity values during the growing period of F1 hybrids.

Three bread wheat genotypes, Adana-99 (P1), Alada (P2) and Lucilla (P3), were included in the parental crossbreeding program to produce the F1 hybrid generation (seed was provided from elite spikes of proven correctness). The parents' crossbreeding program was conducted using the smart diallel method (Table 1).

Table 1. Used smart diallel method in experiment (Kempthorne, 1957).

			♂	
		1	2	3
♀	1	.	x	x
	2	x	.	.
	3	x	.	.

Due to the heat-sensitive nature of parents P2 and P3, crossing between these two was avoided. Consequently, the smart dial method was employed for the genetic analysis.

Table 2. Genotypes used as parents and their origins.

Parent Genotypes	Heat Stress	Origin
Adana-99 (P1)	Resistant	Eastern Mediterranean Agricultural Research Institute 1999 – Adana/Türkiye
Alada (P2)	Sensitive	Maize Research Institute 2015 – Sakarya/Türkiye
Lucilla (P3)	Sensitive	ProGen Seed 2014 – Türkiye

The seeds of the parental lines were sown under greenhouse conditions using a speed breeding system on November 11, 2023. In the crossing nursery, parents were sown in every three days for a total of six periods, and two pots were used for each parent in each period, with six plants in each pot. The experiment was conducted in 6-liter plastic pots filled with soil at a 1:1 ratio, under a photoperiod of 22 hours of light and 2 hours of darkness. The color range of the LED lights used was 450-730 nm, and the photosynthetic photon flux density at the plant canopy height was 352-400 µmol m^{-2} s^{-1} (Ghosh *et al.*, 2018). Female parent plants were emasculated during the Zadoks 50-55 period, which corresponds to 45-55 days after sowing, just before the flowering stage. After emasculation, crossbreeding was performed (Zadoks 61-65) (Zadoks *et al.*, 1974).

The F1 hybrids obtained (P1 × P2, P2 × P1, P1 × P3, and P3 × P1) and their parental genotypes were planted in 6-liter pots under greenhouse conditions on April 17, 2024, using a speed breeding system. Four seeds were sown in each pot, and the experiment was arranged in a completely randomized design with three replicates (each pair of pots was accepted as one replicate). All hybrid combinations included a total of 24 plants. During the plant growth period, standard agricultural practices and plant protection measures were applied. Harvesting was performed at the Zadoks 92 (85 days after sowing) stage according to the Zadoks scale (Zadoks *et al.*, 1974).

Data collection: Physiological traits (days to heading, days to anthesis, SPAD value at heading and anthesis time), morphological traits (plant height, spike length), and yield-related traits (grain weight per plant, grain number per spike, grain weight per spike) were collected from the genotypes. The average of data collected from each plant in a pot was used. Heading and anthesis times were calculated as the number of days from the emergence date until the ears emerged from the flag leaf sheath. Plant height was measured from the ground to the tip of the main spike of the plant. SPAD value in leaves of wheat from the flag leaf were measured by Minolta 502-SPAD during heading and anthesis stages. Spike length was measured from the lowest node of the plant on the main spike axis to the tip of the top spikelet (excluding the awn). The number of grains spike^{-1} was counted. Grain weight plant^{-1} was recorded by weighing the grains obtained from the spike sample on a 0.01 g sensitive scale (Koc and Genc 1990).

Statistical analysis and estimation of genetic parameters: Data related to agronomic traits were analyzed using variance analysis with JMP 17 statistical software to test significant differences between parental genotypes and F1 hybrids. Heat map matrix based on pairwise correlation coefficients of traits were performed in JMP 17 software (Ipekesen and Bicer, 2025). Additionally, genetic progress estimation of the F1 hybrid lines was performed using the heritability package in RStudio (Xposit, 2025). Biplot analysis technique was performed in Genstat 12th software (Payne 2009).

Heterosis was estimated according to Fonseca and Patterson (1968), using their method for calculating the percentage increase or decrease of the F1 hybrid relative to the mid-parent and better-parent values.

1. Heterosis over mid parent (HMP) (%) = $\frac{F1-\bar{MP}}{\bar{MP}}*100$
2. Heterosis over better parent (HBP) (%) = $\frac{F1-\bar{BP}}{\bar{BP}}*100$

Where: F1 is the mean performance of the F1 hybrid, $\bar{MP}$ is the average of the two parental means, and $\bar{BP}$ is the mean performance of the better-performing parent.

3. Potence Ratio (P) = $\frac{F1-\bar{MP}}{|P1-P2|}$

Where: F1: Mean value of the F1 hybrid for a trait. $\bar{MP}$: Mid-parent value, calculated as the average of the two parental means, P1 and P2: Mean values of the two parents for the trait. |P1−P2|: Absolute difference between the parental means, Fonseca and Patterson (1968).

$P>1$: Indicates overdominance,
$P=1$: Indicates complete dominance,
$0<P<1$: Indicates partial dominance,
$P=0$: Indicates no dominance (additive gene action),
$P<0$: Indicates negative dominance, Mather and Jinks (1971).

4. Genotypic Variance (*GV*) (σ^2g) = $\frac{MSg-MSe}{r}$
5. Phenotypic Variance *(PV)* (σ^2p) = $GV+Mse$

Where: MSg: Mean square for genotypes (from ANOVA table), MSe: Mean square for error (environmental variance (σ^2e)) and r: Number of replications, Falconer and Mackay (1996).

6. Genotypic Coefficient of Variation (*GCV*) (%) = $\frac{\sqrt{GV}}{\bar{X}}*100$
7. Phenotypic Coefficient of Variation (*PCV*) (%) =$\frac{\sqrt{PV}}{\bar{X}}*100$

Where: $\sqrt{GV}$: The square root of the genotypic variance (*GV*), $\sqrt{PV}$ The square root of the phenotypic variance (*PV*) $\bar{X}$: The population mean of the trait Burton (1952), Falconer and Mackay (1996).

8. Broad-Sense Heritability (H^2) = $\frac{GV}{PV}$

$H^2=1$: All variation is genetic (high heritability),
$H^2=0$: All variation is environmental (low heritability),
$0<H^2<1$: Both genetic and environmental factors contribute to variation, Singh and Chaudhary (1981), Falconer and Mackay (1996).

9. Genetic Advance (*GA*) = $k*H^2*\sigma p$

Where: *k*: Selection differential, based on the proportion of individuals selected (commonly k=2.06 for 5% selection intensity), H^2: Broad-sense heritability of the trait, σp: Phenotypic standard deviation, calculated as the square root of the phenotypic variance ($\sigma p=\sqrt{PV}$), (Falconer and Mackay, 1996: Singh and Chaudhary, 1981).

10. Genetic Advance as Percentage of Population Means (*GAM*) (%) = $\frac{GA}{\bar{X}}*100$

It was calculated according to the method of Johnson et al. (1955).

The strength of correlation coefficients (r) was classified according to Cohen (1988) and Mukaka (2012) as follows: very weak (0.00–0.19), weak (0.20–0.39), moderate (0.40–0.59), strong (0.60–0.79), and very strong (0.80–1.00).

Broad-sense heritability (H^2) estimates were categorized following Johnson et al. (1955) and Singh and Chaudhary (1981) as low (<30%), moderate (30–60%), and high (>60%). These thresholds were used to describe and interpret the results in this study.

RESULTS

Phenotypic performance: The assessment of agronomic traits in F1 hybrids and parental wheat genotypes revealed substantial variability, highlighting their genetic potential for breeding programs. Among the genotypes, P2 required the longest duration for days to heading (51.0 days), whereas the hybrid P1 × P3 reached this stage the earliest (43.7 days), with an average of 46.7 days and a low coefficient of variation (CV) of 2.22%. Days to anthesis (DF) ranged from 48.3 days in P3 to 54.3 days in P1, with an average of 50.1 days and a CV of 2.30%. The highest SPAD value at both heading and anthesis was recorded in P2, with values of 59.84 and 63.14, respectively, while P1 exhibited the lowest levels.

Plant height (PH) varied from 42.67 cm in P2 to 52.33 cm in the hybrid P1 × P3, with a mean of 49.11 cm and a CV of 5.55%. Spike length (SL) showed notable variation, with P1 and its hybrid P1 × P2 achieving the longest spikes (8.4 cm), whereas P2 recorded the shortest (6.9 cm). The number of grains per spike (NG) was highest in P2 × P1 (32.3 grains) and lowest in P3 (21.2 grains), resulting in a mean of 26.6 grains and a CV of 8.58%. Grain weight per spike (GW) ranged from 0.42 g in P3 to 0.96 g in P1, with an average of 0.76 g and a CV of 18.10%.

Total grain weight per plant (TGW) exhibited the greatest variation, with P2 × P1 achieving the highest value (2.38 g) and P3 the lowest (0.61 g), resulting in a mean of 1.41 g and a CV of 7.09%. These results underscore significant genetic variability among genotypes, with hybrids such as P2 × P1 showing remarkable advantages, particularly for yield-related traits.

Genetic parameters estimation: The analysis of genetic parameters revealed significant insights into the heterotic effects and genetic potential of wheat hybrids across various traits. For days to heading and days to anthesis, most hybrid combinations exhibited negative heterosis values, indicating earlier flowering compared to the parental means and better parent. Notably, the P1 × P3 hybrid showed the most pronounced reduction in days to heading (HMP = -7.96, HBP = -12.47), suggesting its potential for breeding programs aimed at early flowering. This trait is particularly valuable in environments with shorter growing seasons or limited water availability.

For SPAD value, hybrids displayed variable responses during both heading and anthesis stages. The P3 × P1 combination demonstrated the highest heterotic effects, with positive HMP values for heading (5.06) and anthesis SPAD value (6.06). This result indicates that this hybrid retains superior photosynthetic capacity compared to parental genotypes, making it a promising candidate for improving photosynthetic efficiency and stress tolerance.

Table 3. Mean values and standard deviation for evaluating F1 hybrid and their parent of wheat genotypes for traits.

Genotypes		DH	DA	H-SPAD	A-SPAD	PH (cm)	SL (cm)	NG	GW (g)	TGW (g)
Adana-99 (P1)		45.00 ^{bcd}	48.00 ^{b}	51.43 ^{d}	53.96 ^{bc}	49.56 ^{a}	8.44	26.78 ^{b}	0.96 ^{a}	1.55 ^{b}
Alada (P2)		51.00 ^{a}	54.33 ^{a}	59.84 ^{a}	63.14 ^{a}	42.67 ^{b}	6.89	29.00 ^{a}	0.45 ^{b}	1.13 ^{d}
Lucilla (P3)		49.89 ^{a}	52.67 ^{a}	53.50 ^{cd}	53.07 ^{c}	49.11 ^{a}	7.22	21.22 ^{c}	0.42 ^{b}	0.61 e
P1 × P2		46.00 ^{bc}	49.33 ^{b}	57.41 ^{ab}	62.93 ^{a}	48.33 ^{a}	8.44	25.33 ^{b}	0.85 ^{a}	1.51 ^{b}
P1 × P3		43.67 ^{d}	48.33 ^{b}	54.72 ^{bcd}	57.49 ^{b}	52.33 ^{a}	7.67	25.22 ^{bc}	0.85 ^{a}	1.29 ^{cd}
P2 × P1		46.67 ^{b}	49.67 ^{b}	57.89 ^{ab}	62.20 ^{a}	49.67 ^{a}	7.89	32.33 ^{a}	0.93 ^{a}	2.38 ^{a}
P3 × P1		44.67 ^{cd}	48.67 ^{b}	55.12 ^{bc}	56.76 ^{bc}	52.11 ^{a}	8.00	26.33 ^{b}	0.88 ^{a}	1.44 ^{bc}
Means		46.7	50.14	55.7	58.51	49.11	7.79	26.6	0.76	1.41
Coefficient Variation		2.22	2.30	3.46	3.79	5.55	7.79	8.58	18.10	7.09
LSD		1.85	2.05	3.43	3.95	4.85	1.08	4.06	0.25	0.18
	D.F.				**Mean Square**		**(F values)**			
Replications	2	0.577	1.000	0.816	5.048	6.894	0.196	1.815	0.001	0.002
Genotypes	6	22.687**	17.428**	24.614**	54.576**	31.012*	1.029^{NS}	35.578**	0.155**	0.851**
		(21.071)	(13.071)	(6.634)	(11.094)	(4.177)	(2.794)	(6.821)	(8.117)	(84.798)
Error	12	1.077	1.333	3.71	4.920	7.425	0.369	5.216	0.019	0.01003

*, ** = significant at P≤ 0.05 and P≤ 0.01, respectively. Levels not connected by same letter are significantly different. Where; DH: Days to heading, DA: Days to anthesis, H-SPAD: Heading time SPAD value, A-SPAD: Anthesis time SPAD value, PH: Plant height, SL: Spike length, NG: Number of grains per spike, GW: Grain weight per spike, TGW: Total grain weight per plant.

In terms of plant height, the hybrid P2 × P1 exhibited the highest positive heterosis over the mid-parent (7.71), reflecting significant hybrid vigor. However, HBP values were generally closer to zero, indicating that these hybrids only moderately surpassed their better parent. For spike length, only P1 × P2 showed a positive potence ratio (1), while other combinations had negative HBP values, highlighting limited improvement for this trait.

The analysis of yield-related traits showed promising results. For number of grains per spike, the P2 × P1 hybrid showed superior heterosis with a HMP of 15.92 and a positive potence ratio (2), making it a strong candidate for selection. Furthermore, grain weight per spike showed significant hybrid vigour and the P2 × P1 combination achieved the highest HMP value (31.91), indicating significant yield potential. In addition, total grain weight per plant was another prominent trait for the P2 × P1 hybrid, reinforcing its dominance for yield-related traits with a superior HMP value of 77.57 and a positive potency ratio (2).

On the other hand, some combinations showed limited genetic potential. For example, spike length in the P1 × P3 hybrid had a negative HBP value (-9.12), suggesting that this trait may require more pure parental selection and breeding strategies. Similarly, traits such as SPAD value in certain combinations such as P1 × P2 showed negative heterosis (-4.06 at heading) relative to the better parent, indicating areas where improvements were required.

Overall, the findings highlight that hybrids such as P2 × P1 exhibit superior performance across multiple traits, particularly for yield-related characteristics. These results emphasize the importance of targeted hybridization strategies to capitalize on heterotic effects for improving wheat productivity. Traits with strong hybrid vigor, such as grain weight per spike and total grain weight per plant, offer substantial opportunities for enhancing yield potential, while traits with negative heterosis values require careful consideration of genetic and environmental interactions.

The genetic parameters evaluated in this study provide critical insights into the variation and heritability of traits in wheat, which are essential for guiding breeding programs. Days to heading exhibited high broad sense heritability (0.87), indicating a strong genetic influence and making it a prime candidate for improvement through selection. Similarly, days to anthesis demonstrated moderate broad sense heritability (0.65), accompanied by a genetic advance (4.39) and genetic advance as a percentage of the mean (7.88), suggesting that this trait could respond favourably to breeding efforts, albeit to a lesser degree compared to days to heading.

Table 4. Heterosis over mid parent (HMP), heterosis over better parent (HBP), and potence ratio (PR), for phenological, physiological, and yield-related traits in F1 hybrids of bread wheat derived from three parental genotypes (P1, P2, P3).

Genotypes	**Days to heading**			**Days to anthesis**			**Heading time SPAD value**		
	HMP	**HBP**	**PR**	**HMP**	**HBP**	**PR**	**HMP**	**HBP**	**PR**
P1 × P2	-4.17	-9.80	0	-3.59	-9.20	0	3.19	-4.06	0
P1 × P3	-7.96	-12.47	-1	-3.98	-8.24	0	4.30	2.28	1
P2 × P1	-2.78	-8.50	0	-2.92	-8.58	0	4.05	-3.26	0
P3 × P1	-5.85	-10.47	-1	-3.31	-7.59	0	5.06	3.03	1
	Anthesis time SPAD value			**Plant height**			**Spike length**		
	HMP	**HBP**	**PR**	**HMP**	**HBP**	**PR**	**HMP**	**HBP**	**PR**
P1 × P2	7.48	-0.33	0	4.80	-2.48	0	10.11	0.00	1
P1 × P3	7.43	6.54	4	6.07	5.59	7	-2.04	-9.12	0
P2 × P1	6.23	-1.49	0	7.71	0.22	1	2.94	-6.52	0
P3 × P1	6.06	5.19	4	5.62	5.15	6	2.17	-5.21	0
	Number of grains per spike			**Grain weight per spike**			**Total grain weight per plant**		
	HMP	**HBP**	**PR**	**HMP**	**HBP**	**PR**	**HMP**	**HBP**	**PR**
P1 × P2	-9.18	-12.66	-1	20.57	-11.46	0	12.92	-2.47	0
P1 × P3	5.08	-5.83	0	23.19	-11.46	0	19.22	-17.00	0
P2 × P1	15.92	11.48	2	31.91	-3.12	0	77.57	53.37	2
P3 × P1	9.71	-1.68	0	27.54	-8.33	0	33.23	-7.25	0

SPAD value during heading and anthesis stages showed substantial genetic control, with broad sense heritability values of 0.80 and 0.77, respectively. These findings, coupled with genetic advance percentages of 8.51% and 12.58%, underscore the potential of these traits to contribute to enhanced photosynthetic efficiency and, ultimately, improved yield stability. The high broad sense heritability of these traits suggests their reliability as selection criteria in breeding programs aimed at increasing stress tolerance and productivity.

Plant height displayed moderate broad sense heritability (0.51), reflecting a balance between genetic and environmental influences. The relatively modest genetic advance percentage (8.43) indicates a limited potential for substantial genetic gains in this trait.

Grain related traits such as number of grains per spike and grain weight per spike stood out as promising targets for genetic improvement. The number of grains per spike showed moderate broad sense heritability (0.66) and significant genetic advance percentage (20.01), indicating potential for selection. The grain weight per spike stood out with the highest genetic coefficient of variation (27.88) and genetic advance percentage (48.19) and was considered important as the main determinant of yield and a priority for future breeding initiatives.

Total grain weight per plant exhibited superior broad sense heritability (0.97), reflecting almost complete genetic control. The genetic advance percentage (75.84) further highlighted its significant potential for genetic gain. This trait represents a highly promising target for maximizing yield potential through selection.

In conclusion, traits with high broad sense heritability and genetic advance percentages, such as grain weight per spike and total grain weight per plant, offer important implications for genetic improvement and should be prioritized in breeding programs, whereas traits with lower broad sense heritability, such as spike length, may benefit more from strategies that integrate genetic improvements with environmental interventions. These findings provide a clear roadmap for the targeted selection of traits to enhance the productivity and resilience of wheat under diverse environmental conditions.

In this study, a classical CRD design was used to calculate aggregate genotypic variance (σ^2g) and phenotypic variance (σ^2p). However, narrow-sense heritability (h^2) values could not be obtained because designs that separate additive (σ^2a), dominant, and epistatic components (e.g., diallel, parent–offspring, or half/full sibling analyses) were not used (Lynch and Walsh, 1998; Nyquist and Baker, 1991).

Therefore, Genetic Advancement (GA) and Genetic Advancement Percentage (GAM) calculations were based on broad-sense heritability (H^2). H^2 is a broader parameter encompassing all genetic components and indicates the general potential for selection (Visscher *et. al.*, 2008). In the literature, the use of H^2 is accepted as a temporary but valid alternative in cases where h^2 cannot be calculated (Bernardo, 2002). However, this approach should be interpreted with the understanding that GA and GAM results may include not only additive genetic effects but also dominant and epistatic effects (Jafar *et al.*, 2023).

Table 5. Genetic parameters estimated from the combined analysis of three parental genotypes and four F1 hybrids of bread wheat

Traits	σ^2g	σ^2p	GCV (%)	PCV (%)	H^2	GA	GAM (%)
Days to heading	7.20	8.28	5.75	6.16	0.87	5.16	11.04
Days to anthesis	6.97	10.68	4.74	5.87	0.65	4.39	7.88
Heading time SPAD value	5.36	6.70	4.62	5.16	0.80	4.27	8.51
Anthesis time SPAD value	16.55	21.47	6.95	7.92	0.77	7.36	12.58
Plant height (cm)	7.86	15.29	5.71	7.96	0.51	4.14	8.43
Spike length (cm)	0.22	0.59	6.02	9.85	0.37	0.59	7.59
Number of grains per spike	10.12	15.34	11.96	14.72	0.66	5.32	20.01
Grain weight per spike (g)	0.05	0.06	27.88	33.23	0.70	0.37	48.19
Total grain weight per plant (g)	0.28	0.29	37.47	38.13	0.97	1.07	75.84

Where; σ^2g: genotypic variance, σ^2p: phenotypic variance, GCV: symbol of genotype coefficient of variation, PCV: symbol of phenotypic coefficient of variation H2: symbol of broad sense heritability, GA: indicates the genetic advance, GAM %: genetic advance as percentage of population means.

Biplot and Correlation analysis: In the GGE biplot analysis conducted using the mean values of the obtained data, the total variation (79.33%) was represented by PC1 (45.08%) and PC2 (34.25%). In the polygon (which-won-where) graph, which illustrates the performance of hybrids and parents in terms of traits, a total of four sectors (green lines) were formed. In the first sector, the hybrid P1 × P3 and its reciprocal P3 × P1, along with the parent P1, stood out in terms of PH, DA, SL, and GW.

In the second sector, the hybrid P2 × P1 and its reciprocal P1 × P2,which were located at the vertices of the polygon, showed the highest averages for A-SPAD and TGW. The parent P2, located in the third sector, stood out in terms of H-SPAD and DH. The parent P3 was positioned in the fourth sector and exhibited below-average values for all traits. Additionally, the traits located on the left side of the coordinate plane were found to be negatively correlated with those on the right side.

Phenotypic correlation analysis identifies significant relationships between agronomic and physiological traits, providing awareness of their potential roles in breeding strategies. The strong positive correlation (r^2 = 0.93) between SPAD value and antes during heading indicates that genotypes with high photosynthetic capacity during heading retain this trait during antes. This relationship highlights the genetic or physiological continuity between these growth stages, which is crucial for biomass production and yield stability. Similarly, the strong correlation (r^2 = 0.87) between spike length and grain weight per spike highlights the importance of spike structure in influencing grain weight, making SL an important target for yield-oriented breeding programs.

Moderate positive correlations provide more actionable insights. For example, grain weight per spike and total grain weight per plant (r^2 = 0.76) indicate that heavier spikes significantly increase total grain yield. This direct relationship can guide selection strategies for developing high-yielding cultivars. In addition, the number of grains per spike shows a significant relationship with anthesis SPAD value (r^2 = 0.65), indicating that maintaining high photosynthetic efficiency during antes can positively impact grain production. However, the correlation between plant height and spike length (r^2 = 0.52) indicates that taller plants may have longer spikes, although this relationship may be influenced by environmental factors such as lodging resistance.

On the other hand, strong negative correlations determine meaningful trade-offs. The inverse relationship between days to heading and plant height (r^2 = -0.83) indicates that earlier-heading genotypes are generally shorter and follow a path that prioritizes reproductive development over vegetative growth. Similarly, the negative correlation between days to heading and grain weight (r^2 = -0.89) indicates that earlier-heading genotypes tend to produce heavier grains, a desirable trait for environments with short growing seasons.

Weak or insignificant correlations, such as between number of grain per spike and plant height (r^2 = -0.25) or between total grain weight per plant and headding time SPAD value (r^2 = 0.26), indicate that these traits are independent. This independence allows breeders to improve these traits without sacrificing others and offers flexibility in selection programs.

Overall, this analysis highlights the complex interaction of traits that affect the performance of the genotype. The findings highlight the importance of integrating trait-based selection strategies to optimize genetic gain.

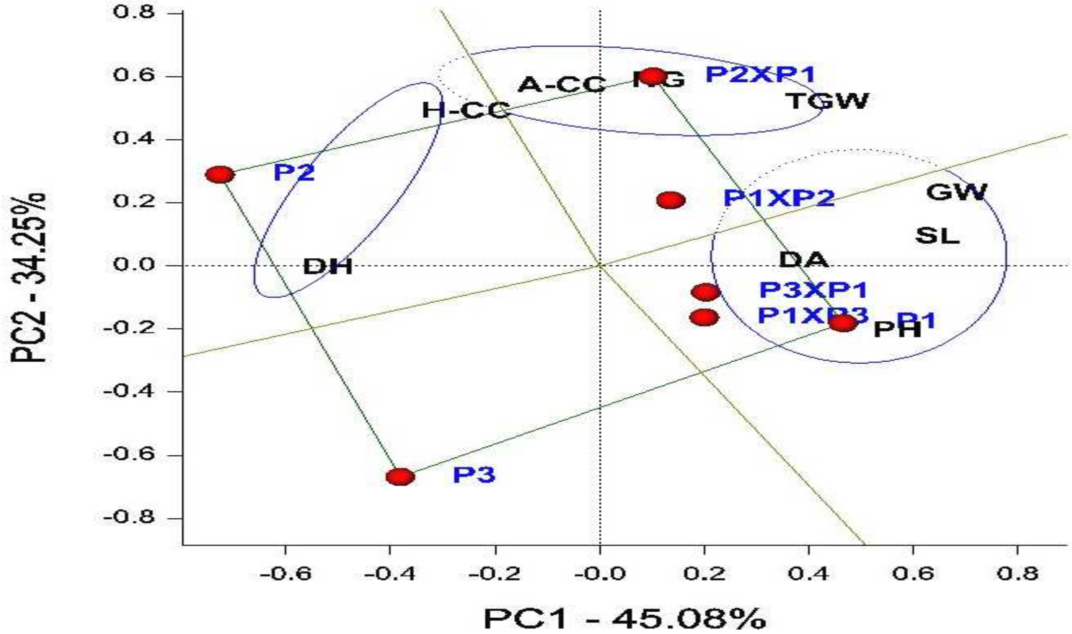

Figure 2. Biplot analysis of F1 hybrids and parents' performance based on traits using polygon and sectors (Which-Won-Where)

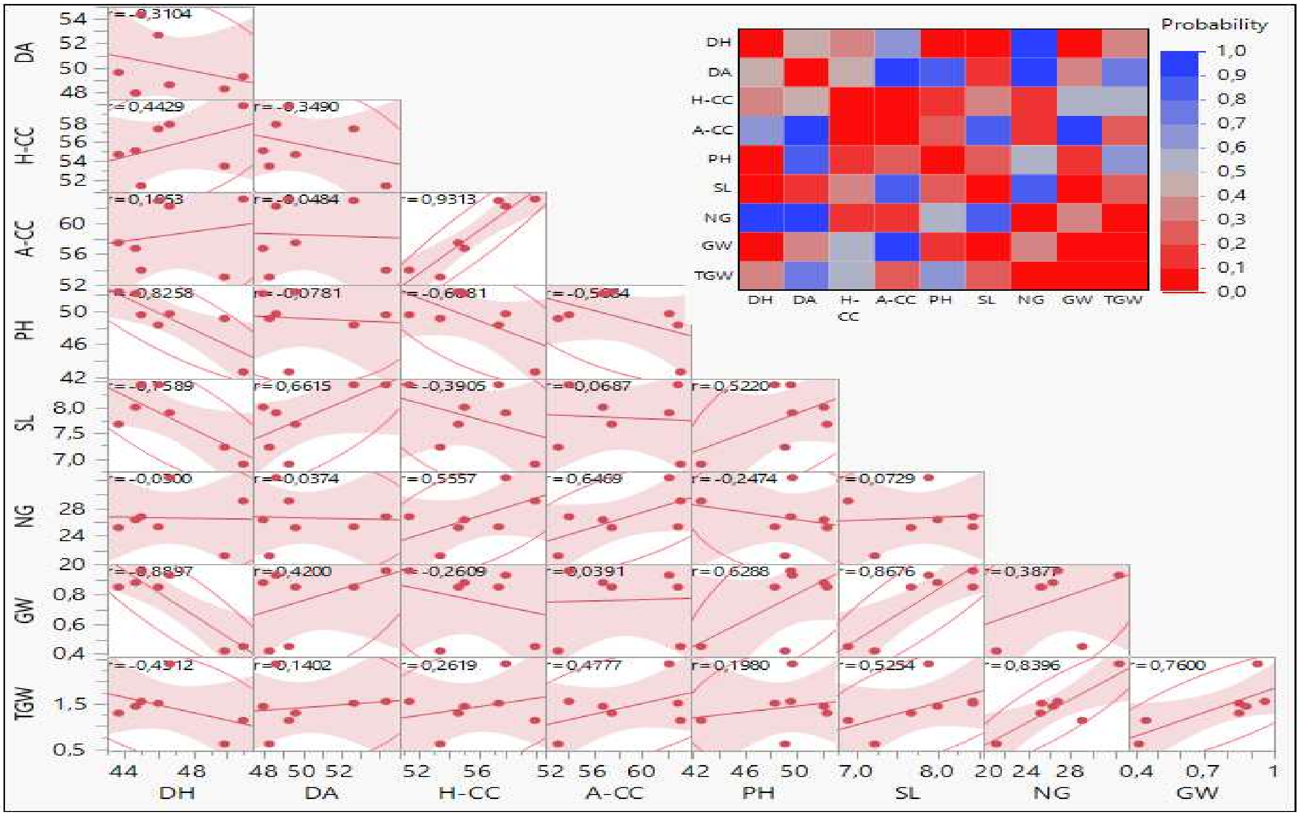

Figure 3. Correlation analysis with scatter plot and heat map using 9 traits of F1 Hybrids and their respective parents.

DISCUSSION

The basis of speed breeding, the effects of artificial lighting on plants, dates back to the early 20th century (Schoen *et al*., 2023). And these ideas have led to the development of specialized protocols for different systems aimed at accelerating genetic gain and generation time in particularly important crops (Watson *et al*., 2018;

Saxena *et al*., 2019; Fang *et al*., 2021). In light of these developments, this study examines the genetic gain of wheat lines developed in the speed breeding system.

In this study, it was determined that heterosis is effective in improving yield-related traits, particularly in wheat. The P2 × P1 hybrid consistently outperformed other genotypes in terms of these traits. These findings are consistent with previous studies emphasizing the contribution of hybrid vigor to yield increases through the accumulation of favourable alleles (Gimenez *et al*., 2021; Hayyat *et al*., 2025; Revell *et al*., 2025). Negative heterosis values in terms of heading and anthesis time, which are characteristics related to flowering, have shown that hybrid individuals develop earlier than their parents. This situation provides an important adaptive advantage in regions where the growing season is limited or where there is a risk of drought, enabling plants to complete their life cycle without yield loss (Blum, 2011; Richards, 2006). The P1 × P3 hybrid, which showed the greatest reduction in heading time, holds potential for breeding programs targeting early physiological maturity. However, given the low coefficient of variation in these traits, careful selection of parents is necessary to achieve reliable genetic gains.

The positive heterosis observed in SPAD value during the heading and anthesis stages indicates that this trait increases photosynthetic efficiency and grain filling capacity under stress conditions. The P3 × P1 hybrid stood out for its high chlorophyll retention, which has been associated with increased tolerance to heat and drought stress and biomass production (Fischer *et al*., 1998; Tuberosa, 2012). Plant height and spike length showed different results in terms of heterosis. The P2 × P1 hybrid showed significant hybrid vigor in plant height, while spike length exhibited low or negative heterosis values in most combinations. This indicates that improving spike length through hybridization alone is limited, and environmental effects play a decisive role in this trait. Therefore, comprehensive strategies incorporating appropriate agricultural practices in addition to genetic improvement are necessary (Lobell and Burke, 2010). The P2 × P1 hybrid showed the highest heterosis values for yield-related traits such as total grain yield and grain weight per ear. In contrast, the P1 × P3 combination exhibited negative heterosis in grain weight per ear, highlighting the importance of parent selection and the need for careful determination of genetic combinations (Cooper *et al*., 2006; Cossani and Reynolds, 2012).

The analysis of genetic parameters provides important information about the genetic structure of wheat traits. Traits with high heritability, such as heading time (0.87) and total grain weight per plant (0.97), indicate that genetic control is dominant. Therefore, phenotype-based selection can provide meaningful genetic gains in these traits. Traits showing moderate heritability, such as days to anthesis (0.65) and number of grains per spike (0.66), are under the combined influence of genetic and environmental factors. Therefore, multiple environment trials and genotype × environment interaction analyses are necessary to stabilize the performance of these traits under variable environmental conditions (Ceccarelli *et al*., 2007; Blum, 2011; Oner and Akıncı, 2024).

SPAD value during the heading (0.80) and anthesis (0.77) stages showed high heritability values. These traits contribute to yield stability under biotic and abiotic stresses by enhancing photosynthetic efficiency (Özkan *et al*., 2025). Therefore, incorporating these physiological traits into breeding programs is of great importance for the development of stress-tolerant and productive varieties. The grain weight per spike and total grain weight per plant have emerged as the traits related to yield, showing high genetic variation and genetic improvement potential. Grain weight per ear exhibits high genetic variability (27.88%) and genetic advancement rate (48.19%), while total grain weight per plant shows a higher genetic advancement rate (75.84%). The role of these traits in increasing wheat yield is supported by previous studies (Rajaram and van Ginkel, 2001; Cossani and Reynolds, 2012).

In contrast, traits with low heritability, such as spike length (0.37), are more influenced by environmental factors. A holistic approach that includes genetic improvements as well as appropriate agricultural practices is necessary to develop such traits (Lobell and Burke, 2010). This strategy can contribute to better adaptation and performance under different agroecological conditions. The findings are consistent with previous studies emphasizing that heritability and genetic advance potential have a critical role in determining priority traits in breeding programs (Seyoum and Sisay, 2021; Paril *et al*., 2024).

Biplot analysis is widely used in the evaluation of parent and hybrid lines according to many agricultural traits. In this study, PC1 and PC2 components explained 79.33% of the total variance, strongly representing the structure of the data. The polygonal structure formed by the outlier genotypes enabled the identification of genotypes exhibiting superior performance in specific traits; the plane divided into four sectors facilitated genotype classification. As a result of the biplot analysis, it was observed that the P1 × P3 and P3 × P1 hybrids showed superior performance in yield-related traits such as DA, SL, and GW. The P2 × P1 and P1 × P2 combinations were associated with A-SPAD and TGW. The P2 parent was found to be associated with heading duration (DH) and SPAD value during the heading period (H-SPAD), while the P3 parent did not show a significant advantage in the measured traits. These results enable the selection of productive combinations and the development of more balanced breeding strategies by considering the relationships between traits.

Correlation analysis reveals the fundamental relationships between agronomic and physiological traits, providing insights for breeding strategies. The strong positive relationship between SPAD value during heading and anthesis periods indicate the continuity of photosynthetic activity throughout the growing season and is important for yield stability (Yorulmaz *et al.*, 2025). In addition, the positive correlation between spike length and grain weight per spike indicates that optimizing spike characteristics can increase grain yield (Philipp *et al.*, 2018). The fact that early-maturing genotypes generally produce heavier grains indicates that these varieties are suitable for areas with short growing seasons (Takumi *et al.*, 2020). Traits showing weak or insignificant correlations, on the other hand, provide the opportunity for independent development, thereby increasing selection flexibility.

This study was conducted in a greenhouse environment, where environmental conditions are largely controlled. This allowed for clearer observation of physiological responses (e.g., SPAD value, anthesis time). However, these conditions may not fully represent the variability of field environments (temperature, soil, natural light spectrum, etc.), so it is recommended that the results be validated with field trials (Reynolds *et al.*, 1997). The experiment was conducted with a long photoperiod of 22 hours of light. This practice accelerates the selection process, particularly by shortening the heading and anthesis periods. Watson *et al.* (2018) showed that this system enables 4-6 generations to be produced per year, but that some physiological adaptation processes may deviate under these artificial conditions. Voss-Fels *et al.* (2018) highlighted the risks of speed breeding, including narrowing genetic variation, high energy consumption, and limited accessibility in field applications. Therefore, it is necessary to compare the findings obtained under classical field conditions (Voss-Fels *et al.*, 2018; Chaudhary and Sandhu, 2024; Pasala *et al.*, 2024). In future studies, it is recommended that validation be carried out under different environmental conditions and that molecular methods such as genomic selection be used to accelerate hybrid development. This approach could make a significant contribution to the development of high-yielding wheat varieties that are resistant to environmental stresses.

In this study, only three parents were used to create four hybrid combinations. This situation may lead to a limited genetic pool, particularly in adaptation and stability analyses. Cooper *et al.* (2006) reported that broader genetic pools are essential for the accurate assessment of environmental tolerance traits. Therefore, the importance of using parental genotypes from different geographical sources and hybrid analyses supported by genomic selection should be emphasized for future studies (Cooper *et al.*, 2006; Chaudhary and Sandhu, 2024).

Conclusion: This study has demonstrated that F1 wheat hybrids obtained under speed breeding conditions, particularly the P2 × P1 combination, can exhibit superior performance in terms of yield and physiological characteristics. Breeders can more efficiently direct their selection programs by prioritizing traits such as grain number per spike, grain yield, and SPAD value, which have high heritability and genetic progress values. Considering the positive relationship between spike length and grain weight, morphological selection strategies should also be integrated to increase yield. However, since these findings were obtained using limited parental material and under greenhouse conditions, it is important to support breeding programs with multi-environment trials and materials with broader genetic variation. Breeders are advised to use speed breeding methods, which offer speed generation cycles, in conjunction with physiological and agronomic yield criteria.

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