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Combining Graphical and Diallel Analyses to Identify Elite Bread Wheat (*Triticum aestivum* L.) Genotypes for Grain Yield and Its Component Traits

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Abstract Enhancing grain yield and its components through understanding of genetic parameters remains a central challenge in wheat breeding due to the complexity of improving multiple agronomic traits simultaneously. This study utilized numerical and graphical Hayman diallel analyses to investigate the inheritance of grain yield and related traits in seven bread wheat (*Triticum aestivum* L.) genotypes and their

F₁ progenies, evaluated under a randomized complete block design with three replications. Morley–Jones analysis revealed significant differences ($p < 0.05$ or 0.01) for grain yield and most traits. Inheritance was predominantly governed by both additive and dominant gene effects, with nonadditive action, particularly overdominance, playing a substantial role in grain yield per plant (GY/P) and most traits. Parental genotypes exhibited higher frequencies of dominant than recessive alleles, and favorable alleles outnumbered unfavorable ones. Regression analysis indicated the absence of nonallelic interactions for plant height (PH), spike length (SL), spike weight (SW), number of grains per spike (NGS), spike grain weight (SGW), and number of spikelets per spike (NSP), while epistatic interactions were detected for number of tillers (NT), number of spikes (NS), and GY/P. Low $W_r + V_r$ values suggested that dominant alleles primarily controlled SD, SGW, SW, and SL. Graphical analysis revealed partial dominance for PH, SL, NT, NS, and GY/P; overdominance for SGW, SD, NGS, and SW; and complete dominance for NSP. Genotypes P6 and P7 carried more recessive alleles, whereas P2 and P3 had higher dominant allele frequencies, suggesting potential hybridization to develop superior lines. GGE biplot analysis identified P2 (Sakha 93) as the top performer for SD, NS, NT, and NSP, while P2, P3, and P5 combined high stability and grain yield, positioning them near the ideal genotype.

Keywords: Hayman diallel analysis, numerical methods, graphic approaches, GGE biplot, genetic structure, wheat (*Triticum aestivum* L.)

1. Introduction

The history of wheat domestication and utilization is deeply intertwined with humanity's long-standing efforts to alleviate hunger and ensure sustainable food security. Today, wheat stands as one of the most widely cultivated and essential staple crops worldwide (Greja and Branlard, 2020). During the 2025/2026 season, global wheat statistics indicated a cultivated area of approximately 220.12 million hectares, an average grain yield of 3.71 metric tons per hectare, and a total production of about 816.20 million metric tons. In comparison, Egypt recorded a planted area of 1.43 million hectares, an average yield of 6.50 metric tons per hectare, and a production of 9.30 million metric tons (USDA, 2025).

Egypt remains the world's largest wheat importer, producing only 50% of its annual requirement of 20 million tons. With the national population projected to grow by 1.94% annually, the country's wheat demand is expected to nearly double by 2050 (Abdalla et al., 2023).

For plant breeders, the identification of key genetic traits is a prerequisite for developing effective breeding and selection strategies. In most breeding programs, hybridization remains a fundamental approach for generating new crop varieties with desirable attributes. Among the various analytical tools available, diallel mating design analysis serves as an essential method for elucidating genetic relationships and enhancing the development of improved cultivars. Johnson (1963) described the diallel approach as a systematic and analytical framework for comprehensive genetic evaluation, facilitating the identification of promising parental combinations for early-generation selection.

Diallel crossing has played a pivotal role in examining the genetic behavior of sets of homozygous lines. Two prominent analytical approaches are commonly employed: those proposed by Hayman and Griffing (Salem et al. 2022; Motawei et al. 2025; Elsherbini et al. 2025). Griffing's method allows the estimation of general combining ability (GCA), specific combining ability (SCA), and reciprocal effects, whereas Hayman's method focuses on analyzing gene action, partitioning genetic components, and estimating heritability (Hayman, 1954). Compared with Griffing's approach, Hayman's statistical and graphical procedures can uncover additional genetic information and offer deeper insights into the behavior of genotypes when applied to the same dataset (Arrauveau, 1989).

Diallel cross experiments are fundamental tools for analyzing polygenic systems. Evidence suggests that, under a simplified genetic model, the diverse statistics derived from progeny performance can provide estimates of the overall degree of dominance, the relative dominance levels of parental lines, and the symmetry or asymmetry of gene distribution among them. These relationships can also be illustrated graphically. Hayman (1954) further expanded this approach to explore complexities such as genetic interactions.

Using Hayman's diallel analysis, several key genetic parameters can be estimated, including gene interactions, additive and dominance effects, the distribution of genes among parents, degree of dominance, deviations of F_1 means from parental means, the direction and hierarchy of dominance, the number of genes governing a particular trait, and both broad- and narrow-sense heritability (Hayman, 1954). A thorough understanding of gene action underlying specific traits is essential for effective breeding program management, particularly when selecting appropriate parental genotypes (Undang et al., 2024).

Hayman's method, widely recognized for its effectiveness in identifying additive, dominance, and epistatic gene actions, has been extensively applied in diallel mating design studies in wheat (Afridi et al., 2017; El-Said, 2018; Al-Timimi et al., 2020; Hassan and Al Jubouri, 2023; Neupane et al., 2024). Findings from these studies consistently demonstrate that the additive–dominance model adequately explains the inheritance patterns of most traits. For biological yield per plant, allelic interactions often exhibit overdominance, whereas other traits typically display a combination of partial dominance and overdominance effects. Generally, the predominance of nonadditive genetic influences contributes to greater phenotypic expression of desirable traits (Fellahi et al., 2015).

According to Hayman's analysis of variance, all wheat traits—except grain yield and grain weight per spike, which are primarily governed by additive gene effects—were found to be heritable. These traits are particularly suitable for direct selection and can be effectively exploited in breeding programs due to their typically high partial dominance and moderate narrow-sense heritability (Khahani et al., 2018). Hayman's analysis also revealed the concurrent influence of additive and nonadditive genetic components on trait expression. Estimates of the average degree of dominance and accompanying graphical representations indicated overdominance for peduncle length, number of seeds per plant, spike length, and 1000-grain weight, while additive effects predominated for grain yield and plant height (Abdi and Fotokian, 2018).

In comparison to additive effects, dominance gene actions were found to exert stronger and more pronounced influences on wheat grain yield and most other traits examined. This pattern was reflected in elevated dominance degree values, high broad-sense heritability, and medium to low narrow-sense heritability—suggesting that the majority of genetic variance in these studies was attributable to dominance effects (Al-Timimi et al., 2020).

Data generated from diallel crosses can be effectively analyzed using principal component (PC) biplot techniques as described by Yan and Hunt (2001). The GGE biplot methodology, when applied to diallel cross datasets, serves as a powerful tool for identifying potential heterotic patterns among genotypes (Dehghani et al., 2005). Hybrid vigor is typically maximized when parental lines exhibit substantial genetic divergence or lack close genetic relationships, leading to hybrids that are heterozygous at multiple loci across the genome (Krishnamoorthy, 2005).

Several studies have successfully used GGE biplot analysis to investigate combining ability and the genetic basis of yield and related agronomic traits in bread wheat diallel crosses (Farshadfar & Hasheminasab, 2012, 2013; Farshadfar et al., 2012). Malla et al. (2010) employed the GGE biplot approach to evaluate combining ability for *Fusarium* head blight resistance in a wheat diallel mating design. Similarly, Dehghani et al. (2013) used biplot analysis to examine diallel cross data associated with stripe rust resistance. Mostafavi and Zabet (2013) analyzed diallel datasets of bread wheat using biplot techniques to elucidate the genetic determinants of yield and agronomic characteristics, ultimately identifying the most promising general and

specific combiners. GGE biplot analysis provides a basis for selecting wheat genotypes that balance high yield and stability, informing breeding strategies for sustainable crop production (Al-Ghumaiz et al. 2025). The present study aimed to elucidate the genetic architecture and inheritance patterns of grain yield and associated wheat traits. This was accomplished by estimating Hayman's genetic parameters using a half-diallel mating design. In addition, the adaptability and stability of grain yield among seven wheat genotypes were visually assessed, and the traits illustrated in the GGE biplot were employed to facilitate a comparative evaluation of the varieties.

2. Materials and Methods

Plant Materials

The study was conducted at the Experimental Farm of the Faculty of Agriculture, Menoufia University, Egypt, over two consecutive wheat-growing seasons. Seven wheat (*Triticum aestivum* L.) genotypes were evaluated, including five local cultivars, Sakha 69, Sakha 93, Gemmiza 3, Gemmiza 7, and Seds 5, sourced from the Agricultural Research Center (ARC), Giza, Egypt, and two exotic genotypes, Baviacora and Miriam. Table 1 summarizes the names, pedigrees, origins, and key agronomic characteristics of the seven parental genotypes.

Field Experiments

This study investigated seven bread wheat (*Triticum aestivum* L.) genotypes under field conditions, sown at fifteen-day intervals to assess variation in heading date during the wheat-growing season. Seeds of each genotype were sown separately in four rows, every 3 meters in length, with 30 cm between rows and 10 cm between plants within rows. A half-diallel cross (excluding reciprocals) among the seven parents was performed during the first growing season using Hayman's technique in combination with hand emasculation.

A total of twenty-eight F₁ hybrids were generated, and the resulting F₁ seeds were planted during the second week of November of the same season. The experimental design for the F₁ generation followed a randomized complete block design (RCBD) with three replications. Each replication consisted of one row per parent and F₁ hybrid, with rows 3 meters long and containing 30 individual plants. All recommended agronomic practices were applied consistently throughout the study in accordance with standard wheat cultivation protocols.

Phenotypic Data Collection

Data were recorded at the individual plant level for both parental lines and their F₁ hybrids. Following CIMMYT guidelines, ten randomly selected plants per plot, excluding border plants, were used for phenotypic

evaluation. The assessed traits included: plant height (PH, cm), spike length (SL, cm), number of tillers (NT), number of spikes (NS), spike weight (SW, g), number of grains per spike (NG/S), spike grain weight (SGW, g), number of spikelets per spike (NSP), spike density (SD), and grain yield per plant (GY/P, g).

Statistical Analysis

Analysis of variance (ANOVA) was performed following the procedure described by Morley-Jones (1965). The coefficient of variation (CV%) was categorized according to Gomes et al. (2009) as very high ($CV \geq 21\%$), high ($15\% \leq CV \leq 21\%$), moderate ($10\% < CV \leq 15\%$), or low ($CV < 10\%$). Parental lines and one set of F_1 hybrids were analyzed using Hayman's model (Hayman, 1954), with calculations carried out manually in Microsoft Excel 2019 based on the formulas provided by Singh and Chaudhary (1979). Data entry and preliminary processing were conducted using Microsoft Office 2010. In addition, GGE biplot analysis was performed to evaluate grain yield stability among the wheat genotypes using GGE biplot software, version 6.3 (Yan, 2001).

3. Results

Analysis of Variance

The total sum of squares for the Morley-Jones ANOVA components, namely a , b_1 , b_2 , b_3 , and b , was calculated and is presented in Table 2. Highly significant differences were observed for all traits with respect to additive genetic variance (a), dominance genetic variance (b), and the second dominance component (b_2), which reflects the accumulation of dominant alleles in a single parent. For most traits, except spike length (SL), spike weight (SW), and grain yield per plant (GY/P), the first dominance component (b_1), indicative of the average dominance variance and heterosis, was statistically significant at $p \leq 0.01$. The third component (b_3), representing specific combining ability and the allocation of dominance alleles to parental lines, was significant ($p \leq 0.05$ or $p \leq 0.01$) for all traits except the number of spikelets per spike (NSP).

For all examined traits, additive variance (a) exceeded dominance variance (b), with the exceptions of spike density (SD) and GY/P. The Baker ratio ranged from 0.58 for GY/P to 0.96 for SL, indicating varying degrees of predominance of additive effects. Most traits exhibited low coefficients of variation ($CV < 10\%$), except for spike grain weight (SGW) and SD, which showed moderate to high variability ($15\% \leq CV \leq 21\%$).

Hayman Genetic Parameters

197

198 Table 3 presents the genetic parameters estimated for the studied traits, all of which exhibited positive values.
199 Additive effects (D) were highly significant ($p \leq 0.01$) for most traits, except for number of tillers (NT),
200 number of spikes (NS), spike density (SD), and grain yield per plant (GY/P). Dominance effects (H_1) and the
201 proportion of dominance attributed to positive and negative gene effects (H_2) were statistically significant
202 ($p \leq 0.05$ or $p \leq 0.01$) for all traits. For NT, NS, number of grains per spike (NG/S), spike grain weight
203 (SGW), SD, and GY/P, H_1 and H_2 exceeded the corresponding D values, with H_1 consistently greater than H_2
204 across all traits. F values were significant for spike length (SL), spike weight (SW), NG/S, SGW, and number
205 of spikelets per spike (NSP).

206 Dominance components (h^2) were highly significant for NT, NS, NSP, and SD, but not for GY/P.
207 Environmental variance (E) was significant for SL and SD ($p \leq 0.05$) and for NSP ($p \leq 0.01$). The mean
208 degree of dominance ($\sqrt{(H_1/D)}$) exceeded one (>1) for all traits except plant height (PH, 0.94) and SL (0.71).
209 The $H_2/4H_1$ ratio was consistently below 0.25, while the KD/KR ratio was greater than one (>1) for all traits,
210 ranging from 1.02 for NT to 2.91 for NG/S. The h^2/H_2 ratio exceeded one for NT, NS, NSP, and SD but was
211 less than one for the remaining traits.

212 Broad-sense heritability (h^2_{bs}) was high for all traits, ranging from 0.76 for NSP to 0.97 for NT and
213 NS. Narrow-sense heritability (h^2_{ns}) varied from 0.19 to 0.68, being high for PH and SL, moderate for NT,
214 NS, SW, SGW, and NSP, and low for NG/S, SD, and GY/P. In all cases, h^2_{bs} values exceeded h^2_{ns} values.
215 The correlation coefficients (r) between $W_r + V_r$ and parental values (Y_r) were positive for NS, SW, NG/S,
216 and SGW but negative for the remaining traits.

217

218 ***Regression Analysis***

219 The t^2 values indicated significant differences for the number of tillers (NT, $p \leq 0.05$), number of spikes (NS),
220 and grain yield per plant (GY/P, $p \leq 0.01$), while the remaining traits did not show significant variation.
221 Regression coefficient analysis revealed values significantly different from zero, but not from unity, for plant
222 height (PH), spike length (SL), spike weight (SW), number of grains per spike (NG/S), spike grain weight
223 (SGW), and number of spikelets per spike (NSP). In contrast, NT, NS, and GY/P exhibited regression
224 coefficients significantly different from unity. Spike density (SD) exhibited non-significant regression
225 coefficients in the F_1 generation.

The $W_r + V_r$ values were highly significant for all traits, whereas the $W_r - V_r$ values were significant ($p \leq 0.05$ or $p \leq 0.01$) for all traits except PH and SL. The $W_r + V_r$ and $W_r - V_r$ values were classified as low for SD, SGW, SW, and SL; moderate for NSP, NS, and NT; and high for NG/S, PH, and GY/P, reflecting varying degrees of genetic variability and dominance across the measured traits.

Graphical Analysis

Figure 1 illustrates the graphical representation of $W_r - V_r$, along with the corresponding regression coefficients and standard errors for the parental genotypes and assessed traits. The intersection of the regression line above the origin in the $W_r - V_r$ plot indicates partial dominance for plant height (PH), spike length (SL), number of tillers (NT), number of spikes (NS), and grain yield per plant (GY/P). In contrast, the regression line intersected below the origin for spike grain weight (SGW), spike density (SD), number of grains per spike (NG/S), and spike weight (SW), suggesting overdominance for these traits. The number of spikelets per spike (NSP) exhibited a regression line intersecting the origin, indicating complete dominance.

For individual parental contributions, P7 was closest to the origin for PH; P2 and P3 for SL; P2 and P7 for NT and NS; P5 and P3 for SW and SGW; P3 and P2 for NG/S and GY/P; P1 and P2 for NSP; and P2 for SD. These positions indicate a predominance of dominant alleles controlling the respective traits. Conversely, P1 for PH, SW, NG/S, and SGW; P5 for SL; P3 for NT and NS; P4 for NSP and SD; and P7 for GY/P were located furthest from the origin, suggesting a higher proportion of recessive alleles. Parental genotypes positioned along intermediate points of the regression line reflected a balanced combination of dominant and recessive genes influencing the traits.

GGE Biplot Analysis

The GGE biplot analysis was subsequently employed to assess genotype performance and stability across the measured traits.

A) Which-won-where model

The GGE biplot polygon was constructed by connecting the outermost genotypes from the center, ensuring that all remaining points were enclosed within the polygon boundaries. As illustrated in Figure 2, the seven wheat genotypes were distributed across three sectors, while the ten evaluated traits were arranged into two

sectors within the polygon. Sakha 69 (P1) exhibited the highest performance for spike length (SL) and grain yield per plant (GY/P), whereas P6 (Baviacora) showed the tallest plant height (PH). Genotype P2 (Sakha 93) demonstrated superior performance for spike density (SD), number of spikes (NS), number of tillers (NT), and number of spikelets per spike (NSP). In contrast, P4 (Gemmiza 7) and P5 (Seds 4) exhibited the lowest performance across all traits, indicating that these genotypes were the least productive among the studied varieties.

B) Mean vs. stability

When the “which–won–where” pattern identifies superior wheat lines in specific environments, it is crucial to evaluate the overall performance and stability of all elite genotypes to guide selection decisions. The GGE biplot provides a robust framework for visualizing performance and stability by employing average environment coordinates (AECs). This approach integrates both yield potential and consistency across traits, allowing identification of the most efficient and reliable genotypes, as indicated by the arrowhead. The horizontal axis (abscissa) represents genotype productivity, with higher-yielding genotypes positioned to the right of the origin and lower-yielding genotypes to the left. The vertical axis (ordinate) reflects the interaction between genetic traits and environmental influences, where greater lengths indicate increased variability and reduced stability, and shorter lengths indicate higher stability.

As depicted in Figure 3, genotypes P3 and P6 exhibited above-average performance but low stability, whereas P2, P3, and P5 demonstrated below-average performance with high stability. Genotypes P1 and P4 showed moderate yields and inconsistent performance. Overall, P2, P3, and P5 combined favorable stability with substantial grain yields, identifying them as the most advantageous genotypes for selection.

C) Discriminativeness vs. representativeness

The concept of the theoretically ideal genotype, though practically unattainable, is represented by the arrowhead in the GGE biplot. Two coordinate axes are defined: the first extends from the arrowhead to the origin, while the second is perpendicular to the first at the origin. By examining the concentric circles around the arrowhead, genotypes can be categorized based on their proximity to the arrowhead along the vertical axis and their placement within the circles. In this study, cultivars P2, P3, and P5 were positioned near the ideal line, serving as reference points for genotype evaluation, as illustrated in Figure 4.

4. Discussion

Morley–Jones (1965) proposed a model that emphasizes variation rather than direct estimation of genetic parameters (Singh et al., 1990). In the present study, significant differences were observed for both the additive (a) and dominance (b) effects across all traits, indicating that inheritance was primarily governed by a combination of additive and dominance gene actions. In most traits, the additive effect (a) exceeded the dominance effect (b), suggesting that additive gene action plays a more prominent role, consistent with the findings of El-Karamity et al. (2025) and Neupane et al. (2024). In breeding terminology, estimates of general and specific combining ability correspond to (a) and (b) effect estimates, respectively (Farshadfar et al., 2012).

Except for spike length (SL), spike weight (SW), and grain yield per plant (GY/P), the b1 component was highly significant for all traits, indicating the presence of directional dominance, where dominance effects at multiple loci act predominantly in one direction (Farshadfar et al., 2013). The b2 component was highly significant across all traits, revealing asymmetry in gene distribution among parents, where some parents possess a greater proportion of dominant alleles than others (Hayman, 1954). The b3 component, which evaluates residual dominance interactions arising from additive $\times$ additive, additive $\times$ dominance, and dominance $\times$ dominance effects specific to each F1 cross (Singh and Narayanan, 1993; Farshadfar et al., 2013), was significant for GY/P and several other traits, highlighting the influence of epistatic interactions in their genetic architecture (El-Said, 2018).

The significance of a, b, b2, and b3 components has been corroborated in wheat studies by Afridi et al. (2017) and Neupane et al. (2024). For most traits examined, Baker's ratio approached unity, indicating that additive gene effects are more influential than nonadditive effects (Baker, 1978), a result consistent with Darwish et al. (2024).

Positive D, H1, and H2 values were observed for grain yield per plant and other studied traits, highlighting the importance of both additive and nonadditive gene actions in their inheritance. For NT, NS, NG/S, SGW, SD, and GY/P, H1 and H2 exceeded D, indicating the predominance of nonadditive gene action (overdominance), whereas for other traits, D values were greater than H1 and H2, emphasizing the role of additive gene effects. Overall, overdominance was prominent for most traits, although both additive (D) and dominance (H1, H2) variance components were significant (Afridi et al., 2017). Higher dominance values than additive components increased the degree of average dominance (>1) for all evaluated traits (Al-Timimi

et al., 2020), and H1 consistently exceeded H2, suggesting a greater number of positive alleles than negative alleles (Neupane et al., 2024).

For PH, SL, SW, NG/S, SGW, and GY/P, H2 estimates were not significant, indicating that the average F1 deviation from parents was minimal. Positive F values and KD/KR ratios >1 for GY/P and other traits further confirmed the prevalence of dominant alleles. Potency ratios >1 suggested overdominant effects, consistent with Elsherbini et al. (2025) and Hassan and Jubouri (2023), and individuals with heterozygous alleles performed better than homozygotes (Sukrutha et al., 2023). H2/4H1 ratios were <0.25, indicating a symmetrical distribution of positive and negative alleles (Farshadfar et al., 2013; Chaudhari et al., 2023), while h2/H2 ratios <1 implied the presence of at least one group of genes with dominant action.

Broad-sense heritability (h^2_{bs}) values exceeded 60% for all traits, demonstrating the strong influence of genetic components, whereas narrow-sense heritability (h^2_{ns}) was low to moderate, reflecting a relatively weaker contribution of additive gene effects, particularly for GY/P. The higher h^2_{bs} relative to h^2_{ns} indicates the prominent role of nonadditive effects in inheritance (Al-Timimi et al., 2020; Bagherikia et al., 2022; Elsherbini et al. 2025; Hassan and Jubouri, 2023). Negative correlation coefficients (r) for GY/P and most traits suggest that dominant alleles primarily contribute to trait improvement. The Hayman analysis confirmed that dominant genetic variance exceeded additive variance for most traits, supporting selection and genetic improvement in advanced generations (Bagherikia et al., 2022; Chaudhari et al., 2023 and Mohamad et al. 2025). Over time, selection may plateau, dominance effects may decline, and transgressive segregants may appear, underscoring the need for integrated breeding strategies with delayed selection to maximize wheat population improvement (Afridi et al., 2017).

According to Chaudhari et al. (2023), the significance of the t^2 parameter indicates that certain assumptions underlying diallel analysis may not be fully met. These assumptions include diploid segregation, absence of differences in reciprocal crosses, independent action of nonallelic genes (i.e., no epistasis), homozygous parents, and independent gene distribution between parents (i.e., no linkage or multiple allelism). Traits such as PH, SL, SW, NG/S, SGW, and NSP were significantly different from zero but not from unity, suggesting minimal influence of nonallelic interactions in their inheritance. In contrast, NT, NS, and GY/P exhibited regression coefficients significantly differing from unity but not from zero, indicating the presence of epistatic or nonallelic gene interactions, consistent with the genetic composition of the parents.

For most traits, nonsignificant t^2 values supported the validity of Hayman's assumptions (Hayman, 1954) by satisfying the uniformity of covariance and variance (W_r-V_r), as reported by Al-Mamun et al. (2022). The dominance order of the parents, inferred from $W_r + V_r$ values, reflected the composition of their dominant alleles. High W_r+V_r and W_r-V_r values were observed for NG/S, PH, and GY/P; moderate values for NSP, NS, and NT; and low values for SD, SGW, SW, and SL. Lower W_r+V_r values indicate a higher proportion of dominant genes controlling the trait, with parents closest to the origin possessing the most dominant alleles and those farthest away containing the most recessive alleles (Al-Timimi et al., 2020). The association between V_r and W_r further confirms the dominance hierarchy among the parental genotypes.

The positions of the parents along the regression line in the V_r-W_r graph reflect the dominance order of genes controlling the studied traits. Partial dominance, overdominance, and complete dominance were inferred from the W_r -axis intercepting the regression line above, below, or at the origin, respectively. Parents closest to the origin possessed the greatest number of dominant alleles, whereas those farthest from the origin carried the most recessive alleles. Intermediate positions indicated a balanced mix of dominant and recessive alleles. Parents located farther from the origin also exhibited increased genotype $\times$ environment interactions (Chaudhari et al., 2023). For most traits, including grain yield, the proportions of dominant and recessive alleles were approximately equal (Bagherikia et al., 2022).

In the present study, PH, SL, NT, NS, and GY/P exhibited partial dominance, SGW, SD, NG/S, and SW showed overdominance, and NSP displayed complete dominance. Graphical analysis revealed that incomplete dominance governed plant height, peduncle length, number of grains per spike, and biological yield, whereas dominant gene action controlled grain yield, 100-kernel weight, and biological yield (Bagherikia et al., 2022). Overall, the parents carried more dominant alleles for GY/P and most other traits. Specifically, P2 and P3 had predominantly dominant genes, while P6 and P7 harbored excessive recessive genes. The close genetic similarity between P6 and P7 suggests their potential use in crosses to develop new varieties with enhanced grain yield.

Additionally, the graphical analysis indicated nonrandom gene distribution at several loci and possible interallelic interactions among the parents. Such correlated gene distributions may explain discrepancies between the results from genetic component analyses and the W_r-V_r graph (Chaudhari et al., 2023).

Analyzing the contributions of genetics, the environment, and their interactions is essential for effective crop breeding. The GGE biplot provides a robust tool for interpreting genotype–environment interactions, visually representing interaction patterns, identifying “which-won-where” scenarios, and delineating mega-environments across test locations (Saeidnia et al., 2023). The polygon view of the GGE biplot efficiently summarizes genotype performance and genotype–environment interaction, clearly illustrating the which-won-where pattern in multienvironment datasets (Yan and Kang, 2003). Neisse et al. (2018) evaluated genotypes based on mean performance versus stability using a GGE biplot, successfully identifying high-yielding and stable genotypes via the average environment coordinate (AEC). Similar findings regarding genotype stability were reported using AEC techniques by Yan (2001), Yan and Hunt (2001), Singh et al. (2019), and Poudel et al. (2020b). Strategies for selecting genotypes that combine high yield with stability across multiple environments align with the approaches described by Yan and Kang (2003) and Yan and Tinker (2006). Additionally, the attractiveness of a genotype, determined by its proximity to the theoretical ideal genotype, corroborates the conclusions of Yan (2001), and has been similarly observed in studies by Akther et al. (2015) and Bishwas et al. (2021). The most stable wheat genotypes are identified using the GGE biplot (Abd El-Aty et al. 2025; Brković et al. 2025; Sood et al. 2025).

5. Conclusions

The Hayman diallel analysis is widely employed to investigate the quantitative inheritance of plant traits and the genetic composition of populations. Examination of genetic parameters using the Morley–Jones and Hayman methods indicated that wheat grain yield, along with other analyzed traits, was governed by both additive and dominant gene effects. However, dominant gene effects were particularly significant for the inheritance of grain yield per plant and several other traits. Hayman’s graphical analysis revealed that parents P6 and P7, as well as P2 and P3, possess an excess of recessive and dominant genes, respectively, controlling the studied traits. The close proximity of P6 and P7, coupled with their shared recessive genes, presents a valuable opportunity for crossing to develop new high-yielding wheat varieties. Breeding and selection for dominant genes are typically more effective in later generations, once homozygosity and genetic fixation are achieved, allowing for the dilution of dominance and the identification of transgressive segregants, thereby clarifying gene functions and interactions. According to the GGE biplot analysis, genotype P2 (Sakha 93)

exhibited superior performance in spike density (SD), number of spikes (NS), number of tillers (NT), and number of spikelets per spike (NSP). In contrast, genotypes P4 (Gemmiza 7) and P5 (Seds 4) showed suboptimal performance across all measured traits. Genotypes P2, P3, and P5 combined high stability with notable grain yields and were positioned near the ideal line based on discriminativeness versus representativeness, highlighting their potential as reference cultivars for wheat breeding programs.

Statements & Declarations:

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Data Availability

All data generated or analyzed during this study are included in this article and its supplementary information files. and its supplementary information files.

Ethical Approval and Consent to Participate

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Consent for Publication

Not applicable.

Competing Interests

The authors have no relevant financial or non-financial interests to disclose.

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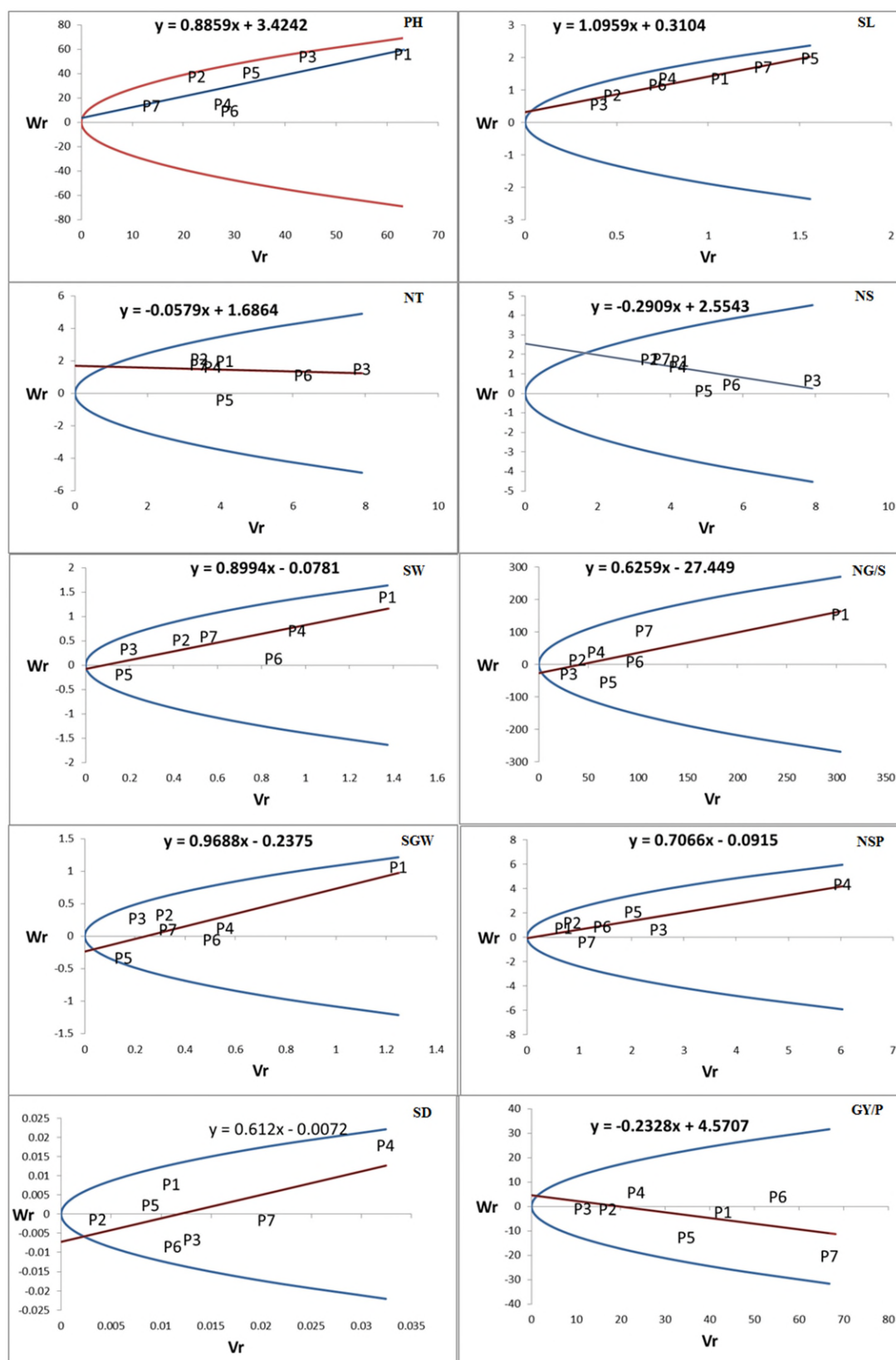


Figure 1 W_r-V_r graph for the diallel of ten traits in wheat.

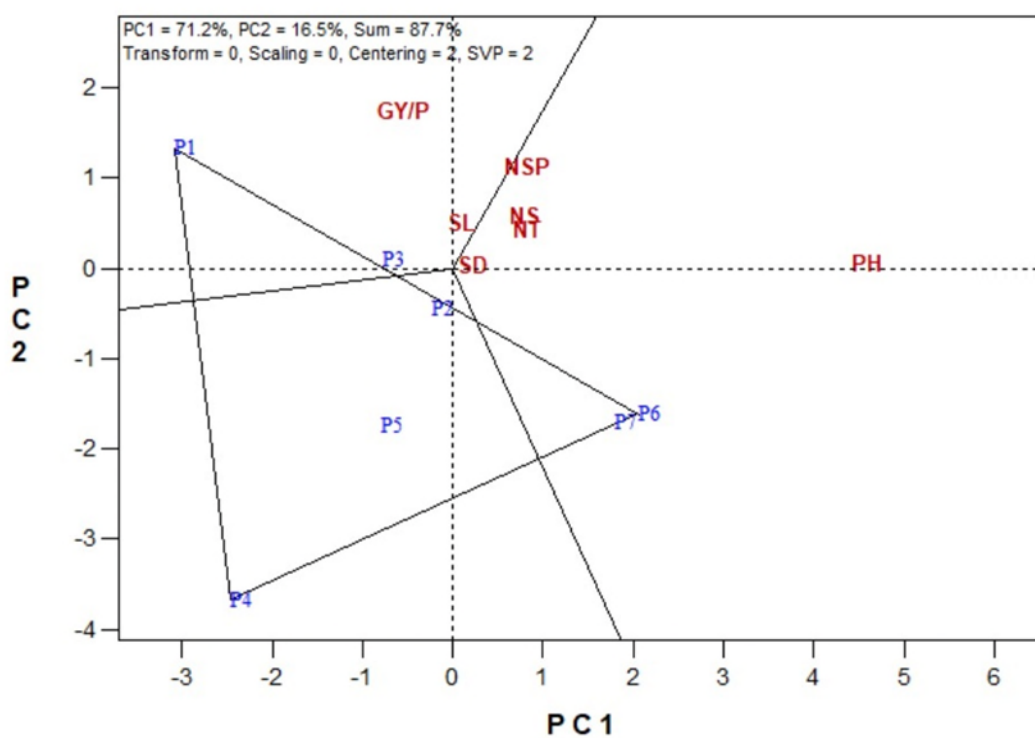


Figure 2 Polygon representation of the GGE biplot (which-won-where model) illustrating seven genotypes of wheat with its studied traits.

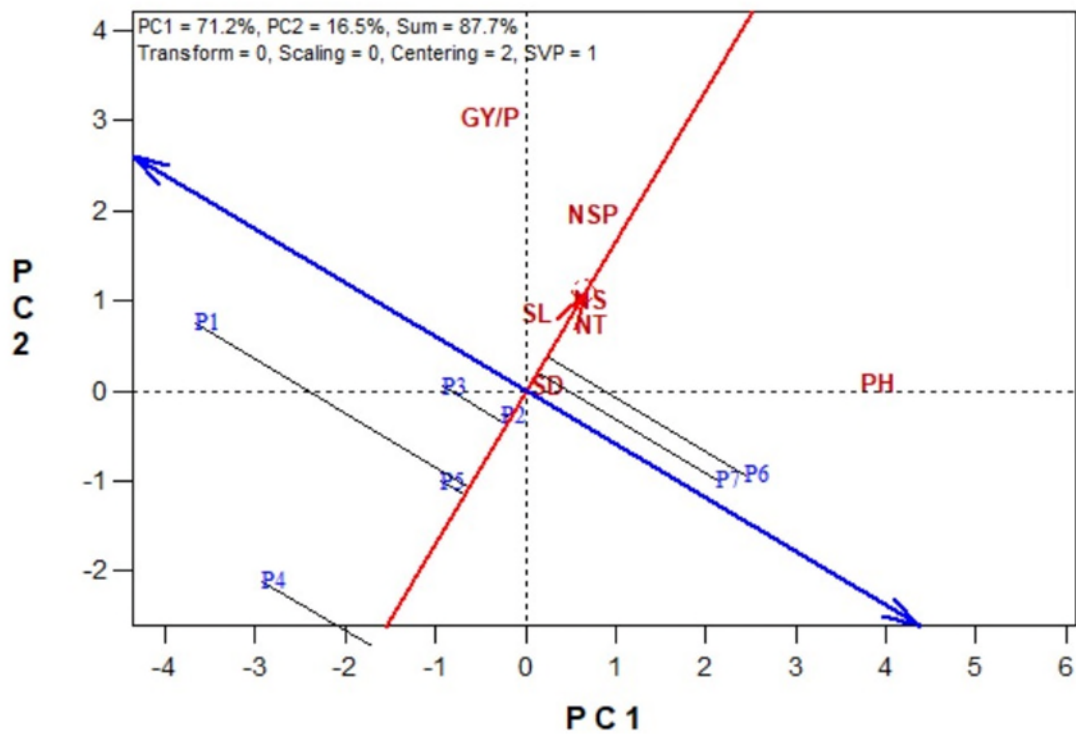


Figure 3 Comparison of the mean and stability in the GGE biplot illustrating the average performance and stability of the analyzed wheat cultivars alongside their traits.

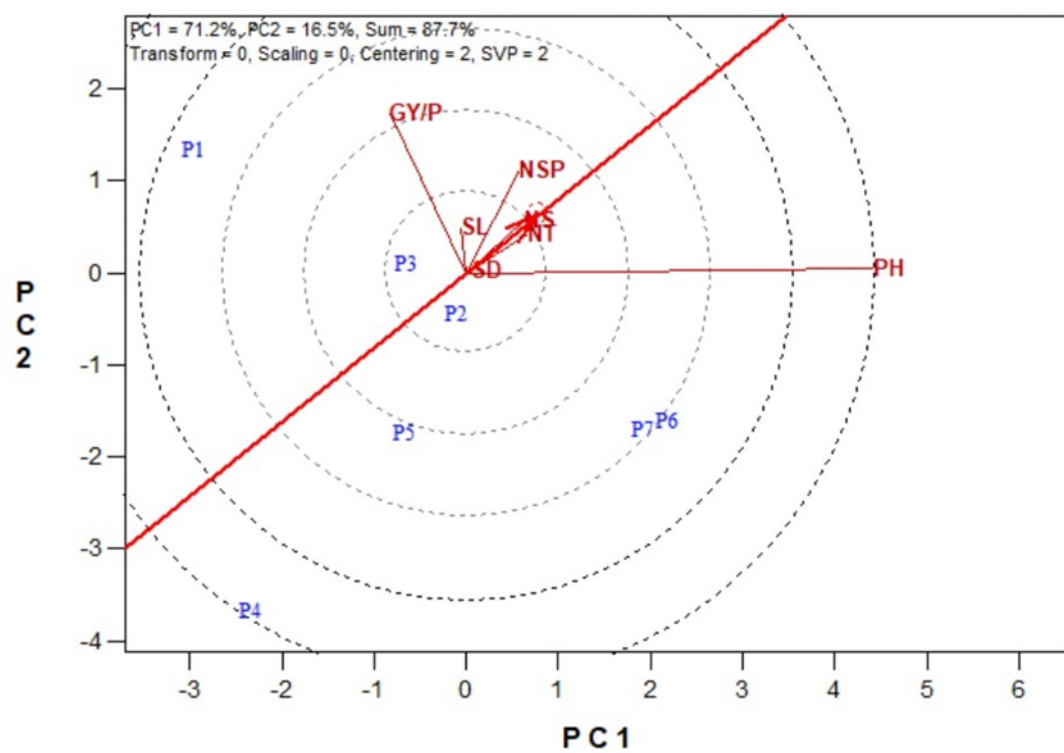


Figure 4 GGE biplot illustrating the ranking of the seven top wheat lines relative to the ideal line.

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