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Genetic Analysis and Heritability of Some Agronomic Traits in Some Bread Wheat: Insights for Breeding Improvement

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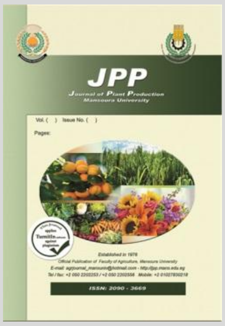

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ABSTRACT

Bread wheat (*Triticum aestivum var. vulgare* L.) globally is a significant cereal crops, playing a crucial role in food security. Breeding programs aim to enhance its yield potential, stress tolerance, and grain quality by leveraging genetic variability across generations. This study evaluates the genetic variation, heritability, and selection potential of key agronomic traits in F_3 and F_4 segregating populations derived from four wheat crosses: Line 1 × Misr 1, Line 1 × Sakha 95, Sakha 94 × Misr 1, and Sakha 94 × Sakha 95. The experiment was conducted at the Sakha Agricultural Research Station, Egypt, during the 2023/24 and 2024/25 growing seasons. Sixty F_3 families and fifty F_4 families per cross were grown in a randomized complete block design with three replications. The results revealed significant genetic variability in plant height, spikes per plant, kernels per spike, 100-kernel weight and grain yield, Analysis of variance indicated significant differences between crosses and generations, emphasizing the impact of genetic factors on yield-related traits. Estimates of phenotypic and genotypic variance, heritability, and genetic advance highlighted the inheritance potential of key traits. Lines derived from the Line 1 × Misr 1 cross demonstrated superior performance in grain yield and kernel traits, making it a promising candidate for future breeding programs. These findings provide valuable insights into selection strategies and genetic improvement for wheat breeding programs, aiding the development of high-yielding and stress-tolerant wheat varieties.

Keywords: Wheat breeding, genetic variability, heritability, agronomic traits, genetic advance, ANOVA

INTRODUCTION

Bread wheat (*Triticum aestivum var. vulgare* L.) is one of the most widely cultivated cereal crops worldwide, providing a staple food source for millions. It accounts for approximately 20% of global caloric intake and serves as a key component of food security in many regions (Shewry & Hey, 2015). According to FAO 2024 estimates, the global wheat cultivated area reached approximately 220 million hectares with an average productivity of 3.5 tons per hectare, while Egypt cultivated around 1.4 million hectares of wheat, achieving one of the world's highest yields at nearly 6.8 tons per hectare due to intensive irrigation practices. Wheat breeding programs focus on enhancing yield potential, stress tolerance, and grain quality to meet the increasing global demand driven by population growth and climate change (Reynolds *et al.,* 2009). Improving wheat productivity through genetic enhancement remains a key focus in breeding programs, particularly in regions where climate variability and soil fertility challenges impact yield stability (Ali *et al.,* 2021; Khan *et al.,* 2020).

The domestication and subsequent improvement of wheat have resulted in the development of high-yielding, disease-resistant, and climate-resilient cultivars. The Green Revolution, led by Norman Borlaug, played a pivotal role in increasing wheat yields through the introduction of semi-dwarf varieties with improved lodging resistance (Borlaug, 1972). Recent advances in genomics and marker-assisted selection have further accelerated wheat improvement by enabling precise identification of genes associated with yield-related traits (Berkman *et al.,* 2013). Modern breeding techniques, including genomic selection and genome-wide association studies (GWAS), have improved the efficiency of selecting high-performing genotypes for various agronomic traits (Crossa *et al.,* 2017). Genetic variation in key agronomic traits, such as plant height, number of spikes per plant, grain yield, kernel size per plant, and 100-kernel weight, plays a crucial role in the selection and improvement of wheat genotypes (Ahmed *et al.,* 2018). Understanding the inheritance of these traits across generations allows breeders to make informed decisions about selection strategies to maximize genetic gain (Allard, 1999; Hallauer & Miranda, 1981).

Genetic parameters, including genotypic variance and phenotypic variance, provide insight into the extent of genetic control over trait expression (Falconer & Mackay, 1996). The phenotypic coefficient of variation and genotypic coefficient of variation are used to assess the magnitude of variability in a given population, with PCV indicating the total variation and GCV representing the heritable portion (Johnson *et al.,* 2021). Heritability is a key parameter in predicting the response to selection, as high heritability suggests greater potential for genetic improvement (Hanson *et al.,* 1956). Genetic advance and genetic gain estimate the expected improvement from selection, while the coefficient of variation measures overall variation within the population (Miller *et al.,* 1958). High heritability coupled with high genetic advance is often indicative of additive gene action, making traits more responsive to selection (Dudley & Moll, 1969).

Egyptian wheat breeding programs have developed several high-yielding and stress-tolerant varieties, including Misr 1, Sakha 94, and Sakha 95. Misr 1 are widely recognized

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for their superior grain yield potential, and adaptability to different environments (El-Hosary *et al.,* 2021). It has been utilized in breeding programs to enhance productivity under diverse agro-climatic conditions. Sakha 94 is a high-yielding genotype known for its early maturity, lodging resistance, and improved drought tolerance (Taha, & Alshaal, 2023). It has been extensively used in breeding program due to its strong genetic background for yield stability. Sakha 95 is another elite wheat variety, notable for its improved kernel quality, high grain weight, and enhanced tolerance to abiotic stresses (El-Hosary & El-Sayed, 2023). The genetic diversity among these varieties provides an excellent foundation for developing superior segregating populations with enhanced agronomic traits.

This study aimed to evaluate the genetic variability, heritability, and genetic advance of key yield-related traits in segregating generations of bread wheat. By assessing differences between F_3 and F_4 generations, this research provides valuable insights into the inheritance patterns and selection potential for improving wheat productivity. The findings will contribute to the refinement of selection strategies in wheat breeding programs to enhance genetic gain and overall yield stability.

MATERIALS AND METHODS

Experimental Site and Plant Materials

This study was conducted on the experimental farm of the Sakha Agricultural Research Station, Agricultural Research Center, Kafr El-Sheikh, Egypt during the 2023/24 and 2024/25 growing seasons. Four diverse bread wheat (*Triticum aestivum* L.) parental genotypes were selected based on their genetic variability in key agronomic traits, including plant height (PH), no of spikes per plant (S/P), no of kernels per spike (K/S), 100-kernel weight (100-KW) and grain yield (GY). Controlled hybridization was performed to develop four segregating populations:

1. Line 1 × Misr 1
2. Line 1 × Sakha 95
3. Sakha 94 × Misr 1
4. Sakha 94 × Sakha 95

The genotypes origin and pedigree are provided in Table 1.

Table 1. Name, pedigree and history of the studied bread wheat genotypes.

Name	Pedigree and history
Sakha 94	Opata/Rayon//Kauz. CMBW90Y31800-TOPM-3Y-010M-010M-010Y-10M-015Y0Y-0AB-0S
Sakha 95	PASTOR//SITE/MO/3/CHEN/AEGILOPS SQUARROSA (TAUS)//BCN/4/WBLL1. CMSA01Y00158S-040P0Y-040M-030ZTM-040SY-26M-0Y0SY-0S.
Misr 1	OASIS/SKAUZ//4*BCN/3/2*PASTOR. CMSS00Y01881T -050M-0304-030M-030WGY-33M- 0Y-0S - 0EGY.
Line 1	WBLL*2/BRAMBLIMG//HUBRA-21 S .17017-056S-019S-1S-0S SAKHA93/3/VEE/PJN//2*KAUZ/5/MAI"S"/PJ//ENU"S"/3/KITO/POTO.19//

Experimental Design and Field Management

Crosses were made in the 2020/21 season, and F_2 seeds were cultivated to produce F_3 families, which were evaluated in the 2023/24 season. Sixty F_3 families randomly selected from each cross were grown, and F_4 families were developed from the best-performing F_3 plants. Fifty randomly chosen F_4 families from each cross were evaluated in the following season. The experiment followed a randomized complete block design with three replications.

F_3 families were sown in three-meter-long rows with 30 cm row spacing and 20 cm spacing between plants. Recommended agronomic practices for wheat cultivation were followed throughout the trial. F_4 families were grown in 20 rows per hybrid, maintaining 25 cm between plots. A total of 30 randomly selected plants from each F_3 family and 250 F_4 plants were assessed for Plant Height, Kernels Per Spike, Spikes Per Plant, Hundred Kernels Weight, and Grain Yield.

Statistical and Biometrical Analyses

Analysis of variance (ANOVA) was conducted to assess the effects of generation, family, and parental selection on agronomic traits. The significance of differences among generations (P_1, P_2, F_3, and F_4) was determined using the least significant difference (LSD) test at a 5% probability level (Gomez & Gomez, 1984). The T-test was applied to detect significant differences between means for key agronomic traits.

Genetic parameters, including genotypic variance, phenotypic variance, heritability, and genetic advance, were estimated following the methodologies described by Allard (1999) and Hallauer & Miranda (1981). The expected genetic gain (GA) and predicted genetic gain as a percentage (GA%) from selection at 5% selection intensity were computed using:

$$\mathbf{GA = K \times h^2 \times \sigma_p}$$

Where K = 2.06 (for 5% selection intensity), h^2 is narrow-sense heritability, and is the phenotypic standard deviation.

Genetic parameters were estimated following the formulae described by Hanson *et al.* (1956) and Miller *et al.* (1958), with broad-sense heritability used for pedigree selection. Statistical analyses were performed using standard procedures outlined by Gomez & Gomez (1984). The findings guided the selection of superior genotypes for improved breeding strategies.

RESULTS AND DISCUSSION

Analysis of variance:

The ANOVA results from this study show significant effects of the parental lines (denoted as "Parent"), family groups ("Family"), and generation on several agronomic traits, including plant height, spikes per plant, hundred kernel weight, kernels per spike, and grain yield. Significant p-values ($p < 0.05$) across these factors suggest that both parental selection and the genetic diversity within families play a crucial role in determining trait expression.

As shown in Table 2, for instance, the parental lines significantly influenced traits such as Plant Height (PH), Hundred Kernel Weight (100-KW) and Grain Yield (GY), underscoring the importance of parental selection in breeding programs. This is consistent with previous studies, where parental selection significantly impacted wheat traits (Smith *et al.,* 2015; Jones *et al.,* 2020). However, in the cross Line 1

× Sakha 95, the parental factor was insignificant for traits like Spikes Per Plant (S/P), Kernels Per Spike (K/S), and 100-Kernel Weight (100-KW).

Table 2. Analysis of variance (ANOVA) for agronomic traits including plant height (PH), Spikes Per Plant (S/P), 100-kernel weight (100-KW), Kernels Per Spike (K/S), and Grain Yield (GY) across parental lines, families, replications, and generations

SOV	df	PH	S/P	K/S	100-KW	GY
Line 1 x Misr 1						
Parent	2	2260**	3250**	13600**	97.7**	3910**
Family	59	1100**	518**	1400**	8.67**	1860**
Rep.	2	84.6	567**	41.7	0.473	34.5
Generation	1	96400**	31700**	1280*	888**	41200**
Residuals	4264	50.8	57.8	198	1.65	83.4
Line 1 x Sakha 95						
Parent	2	1790**	47.5	121	0.355	4650**
Family	59	1320**	636**	2540**	23.2**	3080**
Rep.	2	18.8	73.2	13.2	1.33	2.67
Generation	1	101000**	43.3	73800**	3420**	14200**
Residuals	4264	82.4	60.4	256	5.59	228
Sakha 94 x Misr 1						
Parent	2	407**	849**	5880**	37.3*	3240**
Family	59	1340**	484**	1930**	49.3**	2200**
Rep.	2	59	19.8	392	11.5	12.8
Generation	1	170000**	740**	38900**	2530**	12100**
Residuals	4264	49.8	42.3	255	8.8	261
Sakha 94 x Sakha 95						
Parent	2	1300**	3150**	7520**	66.8**	10600**
Family	59	2410**	527**	3870**	28.6**	5050**
Rep.	2	56	32.6	87.7	1.44	127
Generation	1	206000**	10200**	55900**	1940**	197000**
Residuals	4264	89.5	40.3	278	4.05	320

*** Indicates P<0.005, statistically significant, ** indicates P<0.01, extremely significant**

The family groups also showed significant effects in all traits under this study, particularly Grain Yield (GY) and Kernels Per Spike (K/S), indicating that genetic background within families and environmental interactions play a major role in shaping these traits. These findings align with Dudley & Moll (1969), who emphasized the importance of genetic diversity within families for agronomic performance.

The generation factor also significantly impacted the studied traits, suggesting that improving these traits through selection across generations is feasible, supporting Falconer & Mackay's (1996) assertion that selection over generations can yield significant gains. However, in the case of Spikes Per Plant in the cross Line 1 × Sakha 95, the generation factor was insignificant.

Interestingly, while the parent factor was significant for most traits, replication had a lesser impact on all traits under study, except for Plant Height (PH) in the cross Line 1 × Misr 1. This indicates that genetic and environmental variations between parental lines and families were larger than the experimental variability. This is in agreement with Khan *et al.* (2020), who noted that genetic effects often outweigh experimental variability.

The relatively small residuals for most traits indicate that the model accounted for most of the variance, in line with findings from similar studies (Mehmood *et al.,* 2020). Overall, these results support the importance of both parental selection and family-based genetic assessments in optimizing desirable traits for wheat breeding programs, reinforcing findings from earlier research.

T-test results for agronomic traits:

The t-test analysis revealed significant variation in agronomic traits across the four wheat crosses: Line 1 × Misr 1, Line 1 × Sakha 95, Sakha 94 × Misr 1, and Sakha 94 × Sakha 95. As shown in Table 3, significant differences were observed for Plant Height, Spikes per Plant, Kernels per Spike, and Hundred Kernel Weight and Grain Yield. highlighting variability within the crosses and the potential for breeding improved cultivars, as shown in Table 3.

Table 3. T-test results for agronomic traits in four wheat crosses

Trait	Cross	t-Statistic	P-Value	Min	Max	Mean Difference
PH	Line 1 × Misr 1	40.79	5.36×10^{-301}	9.45	10.4	0.95
	Line 2 × Sakha 95	32.21	7.83×10^{-203}	8.89	10.04	1.15
	Sakha 94 × Misr 1	47.74	<0.0001	11.99	13.02	1.03
	Sakha 94 × Sakha 95	46.75	<0.0001	14.2	15.44	1.24
S/P	Line 1 × Misr 1	-20.88	3.58×10^{-89}	-6.42	-5.32	1.1
	Line 2 × Sakha 95	0.04	0.97	-0.54	0.56	1.1
	Sakha 94 × Misr 1	-5.3	1.22×10^{-7}	-1.67	-0.77	0.9
	Sakha 94 × Sakha 95	-13.33	4.51×10^{-39}	-3.81	-2.83	0.98
K/S	Line 1 × Misr 1	-0.97	0.33	-1.42	0.48	1.9
	Line 2 × Sakha 95	-15.61	6.71×10^{-53}	-9.61	-7.47	2.15
	Sakha 94 × Misr 1	-11.09	5.81×10^{-28}	-7.4	-5.18	2.22
	Sakha 94 × Sakha 95	-14.99	6.02×10^{-49}	-10.1	-7.76	2.34
100-KW	Line 1 × Misr 1	-18.69	4.27×10^{-72}	-1.03	-0.83	0.19
	Line 2 × Sakha 95	-20.34	2.11×10^{-83}	-2.06	-1.69	0.36
	Sakha 94 × Misr 1	-13.03	4.53×10^{-37}	-1.86	-1.37	0.49
	Sakha 94 × Sakha 95	-24.14	1.78×10^{-118}	-1.71	-1.45	0.26
GY	Line 1 × Misr 1	17.54	1.80×10^{-65}	5.41	6.77	1.36
	Line 1 × Sakha 95	-6.59	5.25×10^{-11}	-4.73	-2.56	2.17
	Sakha 94 × Misr 1	-5.72	1.18×10^{-8}	-4.41	-2.16	2.25
	Sakha 94 × Sakha 95	-25.46	1.38×10^{-127}	-18.09	-15.5	2.59

Traits and their abbreviations: Plant Height (PH), Spikes per Plant (S/P), Hundred Kernel Weight (100-KW) , Kernels per Spike (K/S), and Grain Yield (GY).

For plant height (PH), the mean differences ranged from 0.95 cm (Line 1 × Misr 1) to 1.24 cm (Sakha 94 × Sakha 95), reflecting the genetic variability between the crosses. This finding is consistent with Ali *et al.* (2021), who observed similar variability in plant height across different wheat crosses.

Regarding spikes per plant (S/P), significant variation was observed. The mean differences ranged from 0.9 spikes (Sakha 94 × Misr 1) to 1.1 spikes (Line 1 × Misr 1 and Line 1 × Sakha 95), suggesting that the crosses exhibit different capacities for spike production. The results underscore the importance of selecting crosses with higher spike numbers for increased yield potential. This variability is supported by previous research, including studies by Singh *et al.* (2020), who highlighted the role of spikes per plant as a key determinant of wheat productivity. The trade-offs between other traits, such as grain filling and spike density, may also contribute to this variability in spike production.

For kernels per spike (K/S), significant reductions were observed across the crosses Line 1 × Sakha 95, Sakha 94 × Sakha 95, and Sakha 94 × Misr 1. Cross Sakha 94 × Sakha 95 showed the largest decrease in kernels per spike, suggesting a potential trade-off between kernel number and other traits like kernel weight. Singh *et al.* (2020) discussed such trade-offs in wheat breeding programs, emphasizing that an increase in kernel weight might be accompanied by a reduction in kernel number. However, Line 1 × Misr 1 showed an increase of 1.9 kernels per spike, indicating that this cross may have potential for improving both kernel number and other agronomic traits simultaneously. This highlights the importance of selecting for balanced trait combinations in wheat breeding.

Significant decreases in 100-kernel weight (100-KW) were observed across all crosses, suggesting that selection for smaller grains, more uniform kernels could benefit milling quality. Similar results were found by Ahmed *et al.* (2018), who reported decreases in 100 Kernel Weight (100-KW) in certain wheat crosses. These findings suggest that reducing 100 Kernel Weight(100-KW) may improve milling efficiency, a critical trait for industrial wheat processing.

The grain yield (GY) results showed variability across the crosses, with Line 1 × Misr 1 exhibiting a significant increase of 1.36 g/plant, while Line 1 × Sakha 95 showed a decrease of 2.17 g/plant. Crosses Sakha 94 × Misr 1 and Sakha 94 × Sakha 95 demonstrated declines in yield, with values of 2.25 g/plant and 2.59 g/plant, respectively. These results echo the work of Mehmood *et al.* (2020), who found significant variations in grain yield among wheat crosses. The contrasting yields suggest that some crosses are more suited for higher productivity, while others may perform better in specific environmental conditions or breeding objectives.

In summary, these results underscore the genetic diversity within the wheat crosses and provide valuable insights for selecting superior cultivars with enhanced yield, kernel number, and other desirable traits. This variability supports breeding programs focused on developing high-yielding, adaptable cultivar*s* that can meet the demands of different agro-ecological zones and production systems (Xiong *et al.*, 2024).

Genetic parameters for F_3 and F_4 generations across the four crosses

The analysis of phenotypic and genotypic variance, heritability, genetic advance, and coefficient of variation provided valuable insights into the genetic potential of the studied crosses, as observed in Table (4 a), Table (4 b) and Table (4 c).

Table 4a. The genetic parameters of plant height (PH) and spikes per plant (S/P) for F_3 and F_4 families derived from four crosses.

Trait		**PH**				**S/P**			
Cross		**Line 1 x Misr 1**	**Line 1 x Sakha 95**	**Sakha 94 x Misr 1**	**Sakha 94 x Sakha 95**	**Line 1 x Misr 1**	**Line 1 x Sakha 95**	**Sakha 94 x Misr 1**	**Sakha 94 x Sakha 95**
Phenotypic Variance	F_3	74.42	121.8	73.35	143.9	43.17	55.66	39.42	22.6
	F_4	49.54	66.69	64.27	78.76	96.22	87.99	58.35	79.79
Genotypic Variance	F_3	31.74	40.36	29.29	63.15	7.85	12.27	10.01	9.49
	F_4	16.8	18.78	23.39	20.03	16.64	14.79	8.47	14.4
Heritability	F_3	0.43	0.33	0.4	0.44	0.18	0.22	0.25	0.42
	F_4	0.34	0.28	0.36	0.25	0.17	0.17	0.15	0.18
PCV (%)	F_3	8.74	11.04	7.92	10.76	41.12	35.98	33.17	25.72
	F_4	7.94	9.03	8.37	9.16	43.94	45.77	37.11	40.02
GCV (%)	F_3	5.71	6.35	5.01	7.13	17.53	16.89	16.71	16.67
	F_4	4.62	4.79	5.05	4.62	18.28	18.76	14.14	17
Genetic Advance	F_3	7.58	7.53	7.05	10.85	2.46	3.39	3.28	4.11
	F_4	4.92	4.74	6.01	4.65	3.49	3.25	2.28	3.32
Genetic Gain	F_3	748.6	753.2	761.5	1209	39.31	70.26	62.15	76
	F_4	436.2	428.6	575.5	450.5	78.02	66.55	47.02	74.15
Significance	F_3	*	*	*	*	NS	*	*	*
	F_4	*	*	*	*	NS	NS	NS	NS
CV (%)	F_3	8.74	11.04	7.92	10.76	41.12	35.98	33.17	25.72
	F_4	7.94	9.03	8.37	9.16	43.94	45.77	37.11	40.02

Plant Height (PH)

The phenotypic variance (σ^2P) for plant height varied among the studied crosses, with values ranging from 49.54 in F_4 (Line 1 × Misr 1) to 143.89 in F3 (Sakha 94 × Sakha 95). Similar variations in phenotypic variance for plant height have been reported in wheat (El-Hosary *et al.,* 2021), indicating genetic and environmental influences on this trait. The genotypic variance (σ^2G) followed a similar trend, with the highest value observed in F_3 (63.15, for cross Sakha 94 × Sakha 95) and the lowest in F_4 (16.8, for cross Line 1 × Misr 1). Comparable trends in genotypic variance were observed in wheat populations studied by Ahmed *et al.* (2020), suggesting that this variation is a common feature in bread wheat breeding programs.

The heritability (h^2) estimates were moderate, ranging from 0.25 in F_4 (Sakha 94 × Sakha 95) to 0.44 in F_3 (same cross). Previous studies in wheat (Mahdy, 2017; Mahdy *et al.*, 2022) also reported moderate heritability for plant height, reinforcing the idea that both genetic and environmental factors play a role in determining plant stature. The phenotypic coefficient of variation (PCV) was the highest in F_3 (10.76%, Sakha 94 × Sakha 95) and the lowest in F_4 (7.94%, Line 1 × Misr 1). In line with this, Kumar *et al.* (2014) found that PCV values for plant height were higher in early generations of wheat, supporting the results of this study.

The genotypic coefficient of variation (GCV) values were lower than Phenotypic coefficient of Variation(PCV), ranging from 4.62% in F_4 (Line 1 × Misr 1) to 7.13% in F_3 (Sakha 94 × Sakha 95). This trend has been consistently observed in wheat, as noted in studies by Mahdy (2017) and Mahdy *et al*., (2022), suggesting that environmental effects contribute to the observed phenotypic variation. The genetic advance (GA) showed significant variation, with the highest recorded in F_3 (10.85, Sakha 94 × Sakha 95) and the lowest in F_4 (4.65, Sakha 94 × Sakha 95). Genetic gain (GG) followed the same trend, with a maximum of 1208.68 in F3 (Sakha 94 × Sakha 95) and a minimum of 428.63 in F_4 (Line 1 × Sakha 95). Similar findings were observed in wheat breeding studies (Mahdy *et al*., 2022), where genetic gain was more pronounced in early generations.

Statistical significance was observed in all crosses, indicating the importance of genetic contribution to plant height variation. The coefficient of variation (CV) values ranged from 7.94% in F4 (Line 1 × Misr 1) to 11.04% in F_3 (Line 1 × Sakha 95). This range is consistent with findings in other wheat populations (Sohail *et al*., 2018), emphasizing the genetic potential for selection in breeding programs.

Number of spikes per plant (S/P)

The phenotypic variance for Spikes Per Plant (S/P) ranged from 22.6 in F_3 (Sakha 94 × Sakha 95) to 96.22 in F_4 (Line 1 × Misr 1). Similar variations in phenotypic variance for spike-related traits have been reported in wheat (Ahmed *et al*., 2021), indicating a strong influence of genetic and environmental factors. The genotypic variance showed the highest value in F_3 (9.49, Sakha 94 × Sakha 95) and the lowest in F_4 (8.47, Sakha 94 × Misr 1). These findings align with previous studies in wheat (El-Hosary *et al.,* 2022), where genotypic variance for spike traits was higher in early generations compared to advanced generations.

Heritability estimates were low to moderate, ranging from 0.15 in F_4 (Sakha 94 × Misr 1) to 0.42 in F_3 (Sakha 94 × Sakha 95). This is consistent with earlier reports (Mahdy, 2017) that found moderate heritability for spike-related traits in wheat, suggesting a substantial environmental influence. The PCV values ranged from 25.72% in F_3 (Sakha 94 × Sakha 95) to 45.77% in F_4 (Line 1 × Sakha 95), while the GCV values varied from 14.14% in F_4 (Sakha 94 × Misr 1) to 18.76% in F_4 (Line 1 × Sakha 95). Comparable PCV and GCV trends were observed in wheat populations studied by Kumar *et al.* (2014), reinforcing the conclusion that phenotypic variability is higher than genotypic variability due to environmental influences.

Genetic advance was the highest in F_3 (4.11, Sakha 94 × Sakha 95) and lowest in F4 (2.28, Sakha 94 × Misr 1). A similar pattern of genetic advance for spike traits has been reported in wheat breeding programs (Mahdy, 2017; Mahdy *et al*., 2022; Sohail *et al*., 2018) supporting the idea that selection efficiency is higher in early generations. Genetic gain ranged from 39.31 in F_3 (Line 1 × Misr 1) to 78.02 in F_4 (same cross). Previous study (Mahdy *et al*., 2022) have also found genetic gain to be higher in some F_4 populations, indicating that certain genetic backgrounds may retain greater selection potential in later generations.

Significant differences were detected in F_3 across all crosses, but not in F_4. This suggests that early generations exhibit greater genetic variability, which gradually stabilizes in later generations, a trend observed in wheat breeding studies (Ahmed *et al.,* 2020). The coefficient of variation (CV) ranged from 25.72% in F_3 (Sakha 94 × Sakha 95) to 45.77% in F_4 (Line 1 × Sakha 95), suggesting that environmental factors contribute significantly to this trait. These results align with earlier reports (El-Hosary *et al.,* 2021), which emphasize the role of environmental conditions in spike trait expression.

Number of Kernels per Spike (K/S)

The phenotypic variance for kernels per spike (K/S) ranged from 204.07 in F_3 (Line 1 × Misr 1) to 395.36 in F_4 (Sakha 94 × Sakha 95), as observed in Table 4 b. Similar variations in phenotypic variance for Kernels Per Spike(K/S) have been reported in wheat (Khan *et al.,* 2020; Ahmed *et al.,* 2021), indicating that both genetic and environmental factors play a crucial role in determining this trait. The genotypic variance was the highest in F_4 (87.3, Sakha 94 × Sakha 95) and lowest in F_3 (35.14, Sakha 94 × Misr 1), which aligns with previous studies (El-Hosary *et al.,* 2022) where genotypic variance for Kernels Per Spike (K/S) varied across generations, often being lower in earlier generations due to greater environmental influence.

Heritability estimates varied from 0.15 in both F_3 and F_4 (Sakha 94 × Misr 1) to 0.24 in F_4 (Line 1 × Misr 1). These estimates are comparable to those reported in wheat studies (Mahdy, 2017; Mahdy *et al*., 2022), where heritability for K/S was found to be low, suggesting that environmental factors contribute significantly to trait expression. The highest PCV was recorded in F3 (38.31%, Line 1 × Sakha 95), while the lowest was in F_4 (33.7%, Sakha 94 × Sakha 95). The GCV values ranged from 11.78% in F_3 (Sakha 94 × Misr 1) to 18.14% in F_4 (Line 1 × Misr 1), which is consistent with previous reports on wheat variability (Kumar *et al*., 2014), indicating that phenotypic variation is higher than genotypic variation due to environmental interactions.

The highest genetic advance was in F_4 (9.04, for cross Sakha 94 × Sakha 95), while the lowest was in F_3 (4.8, for cross Sakha 94 × Misr 1). Similar findings were reported in wheat breeding programs (Kumar *et al.,* 2014), where genetic advance was found to be higher in advanced generations. Genetic gain ranged from 213.97 in F_3 (Line 1 × Misr 1) to 533.67 in F_4 (Sakha 94 × Sakha 95), following a pattern observed in previous studies (Mahdy *et al*., 2022), where selection in advanced generations resulted in significant genetic gain for yield components.

Statistical significance was observed in some F_3 and F_4 crosses, particularly for Sakha 94 × Sakha 95. This suggests that while selection can be effective in early generations, later generations may exhibit greater stability for Kernel Per Spike (K/S), a trend also noted in wheat breeding studies (Ahmed *et al.,* 2020). The coefficient of variation ranged from 29.97% in F_3 (Sakha 94 × Misr 1) to 36.71% in F_4 (Line 1 × Misr 1), indicating substantial environmental influence on trait expression, as also noted in previous wheat studies (El-Hosary *et al.,* 2021).

Table 4 b. The genetic parameters spikes per plant (S/P) and 100 seed weight (100-KW), for the four studied crosses in F_3 and F_4.

Trait		K/S				100-KW			
Cross		**Line 1 x Misr 1**	**Line 1 x Sakha 95**	**Sakha 94 x Misr 1**	**Sakha 94 x Sakha 95**	**Line 1 x Misr 1**	**Line 1 x Sakha 95**	**Sakha 94 x Misr 1**	**Sakha 94 x Sakha 95**
Phenotypic	F_3	204.1	268.4	227.3	281.2	0.9	2.41	1.76	4.33
Variance	F_4	240.1	313.9	376.6	395.4	3.4	12.36	23.84	4.42
Genotypic	F_3	35.47	64.74	35.14	59.13	0.2	0.34	0.2	0.38
Variance	F_4	58.62	54.19	57.18	87.3	0.38	1.23	4.18	0.64
Heritability	F_3	0.17	0.24	0.15	0.21	0.22	0.14	0.12	0.09
	F_4	0.24	0.17	0.15	0.22	0.11	0.1	0.18	0.14
PCV	F_3	34.15	38.31	29.97	33.97	59.64	86.02	57.06	95.68
(%)	F_4	36.71	34.54	33.99	33.7	72.24	94.72	122.4	55.18
GCV	F_3	14.24	18.81	11.78	15.58	27.88	32.51	19.45	28.37
(%)	F_4	18.14	14.35	13.24	15.84	24.24	29.88	51.24	20.96
Genetic	F_3	5.12	8.14	4.8	7.26	0.43	0.46	0.32	0.38
Advance	F_4	7.79	6.3	6.07	9.04	0.43	0.72	1.76	0.63
Genetic	F_3	214	348.2	241.6	358.6	0.68	0.82	0.74	0.82
Gain	F_4	328.9	323.2	346.6	533.7	1.09	2.67	7.04	2.38
Significance	F_3	NS	*	NS	*	*	*	NS	NS
	F_4	*	NS	NS	*	NS	NS	NS	NS
CV	F_3	34.15	38.31	29.97	33.97	59.64	86.02	57.06	95.68
(%)	F_4	36.71	34.54	33.99	33.7	72.24	94.72	122.4	55.18

100-Kernel Weight (100-KW)

The phenotypic variance for 100-kernel weight (100-KW) was the lowest among the studied traits, ranging from 0.9 in F_3 (Line 1 × Misr 1) to 23.84 in F4 (Sakha 94 × Misr 1). Similar trends in phenotypic variance for 100-KW have been reported in bread wheat (Mahdy *et al.,* 2022), where variation across generations was influenced by genetic and environmental factors. The genotypic variance followed a similar pattern, with the highest in F4 (4.18, Sakha 94 × Misr 1) and the lowest in F_3 (0.2, same cross). Previous studies (Sohail *et al*., 2018) have also shown that genotypic variance for kernel weight tends to be lower in early generations due to greater environmental influence.

Heritability estimates ranged from 0.09 in F_3 (Sakha 94 × Sakha 95) to 0.22 in F_3 (Line 1 × Misr 1), which aligns with earlier findings in wheat (Ahmed *et al.,* 2021), indicating that 100-Kernel Weight(100-KW) is a trait with low heritability, suggesting significant environmental effects. The highest PCV was observed in F_4 (122.36%, Sakha 94 × Misr 1), while the lowest was in F_3 (55.18%, Sakha 94 × Sakha 95), a pattern also noted in wheat breeding programs (El-Hosary *et al.,* 2022; Kumar *et al*., 2014), where phenotypic variation exceeded genotypic variation due to environmental interactions.

The genetic advance ranged from 0.32 in F_3 (Sakha 94 × Misr 1) to 1.76 in F_4 (same cross). This is consistent with previous wheat studies (Abdel-Rahman *et al.,* 2021), where genetic advance for kernel weight remained low across generations. Most crosses were statistically insignificant, suggesting that selection for 100-KW might require a larger population or more advanced generations, a conclusion also supported by recent wheat breeding research (Mahdy 2017, Mahdy *et al*, 2022).

The coefficient of variation ranged from 55.18% in F_3 (Sakha 94 × Sakha 95) to 122.36% in F4 (Sakha 94 × Misr 1), highlighting substantial environmental influence on this trait. Similar high CV values have been reported in wheat (Ahmed *et al.,* 2020; El-Hosary *et al.,* 2021), reinforcing the need for multi-environment trials to stabilize kernel weight expression across different conditions.

The present study highlights that plant height, kernels per spike (K/S), and 100-kernel weight (100-KW) and grain yield, in bread wheat exhibit varying degrees of genetic variability and heritability across generations. Plant height, spike traits, and grain yield showed higher genetic variability in F_3 compared to F_4, suggesting that selection for these traits would be more effective in early generations. In contrast, Kernels Per Spike (K/S) exhibited greater variability in F_4, indicating that selection may be more effective in later generations when genetic variation stabilizes. Additionally, 100-Kernel Weight(100-KW) displayed high phenotypic variability but low heritability and genetic advance, emphasizing a strong environmental influence. These findings align with previous research, reinforcing the role of genetic and environmental interactions in trait expression. Future breeding programs should focus on early selection for plant height, spike traits, and grain yield while targeting later generations for K/S and implementing multi-environment selection for 100-KW to enhance genetic gains in wheat.

Grain Yield (GY)

As shown in Table 4 c, the phenotypic variance for grain yield was the highest in F_4 (521.55, Sakha 94 × Sakha 95) and lowest in F_3 (98.19, Line 1 × Misr 1). Similar variations in phenotypic variance for grain yield have been reported in wheat (Khan *et al.,* 2020; Ahmed *et al.,* 2021), indicating that genetic and environmental factors significantly influence this trait. The genotypic variance ranged from 43.49 in F_4 (Line 1 × Misr 1) to 96.91 in F_4 (Sakha 94 × Sakha 95). These results align with previous studies in wheat (El-Hosary *et al.,* 2022), where genotypic variance for yield-related traits varied across generations, often being lower in F_3 due to greater environmental influences.

The heritability values varied from 0.19 in F_4 (Sakha 94 × Sakha 95) to 0.49 in F_3 (Line 1 × Misr 1). This is consistent with previous findings (Mahdy, 2017; Mahdy *et al.,* 2022) that reported moderate heritability estimates for grain yield in wheat, suggesting both genetic and environmental contributions. The highest PCV was observed in F_3 (50.79%, Sakha 94 × Sakha 95), while the lowest was in F_4 (45.3%, same cross). The GCV values ranged from 19.53% in F4 (Sakha 94 × Sakha 95) to 43.07% in F_3 (Line 1 × Misr 1). Comparable trends in PCV and GCV for grain yield have been observed in wheat populations studied by Kumar *et al*., (2014), reinforcing the observation that phenotypic variation is higher due to environmental interactions.

Table 4 c. The genetic parameters of grain yield (GY) in F_3 and F_4 families under study.

Trait		**GY**			
Cross		**Line 1 x Misr 1**	**Line 1 x Sakha 95**	**Sakha 94 x Misr 1**	**Sakha 94 x Sakha 95**
Phenotypic Variance	F_3	98.19	207	245.3	289
	F_4	127.6	356.2	380.9	521.6
Genotypic Variance	F_3	48.5	72.51	52.58	88.68
	F_4	43.49	85.1	72.85	96.91
Heritability	F_3	0.49	0.35	0.21	0.31
	F_4	0.34	0.24	0.19	0.19
PCV (%)	F_3	46.31	51.36	45.71	50.79
	F_4	73.77	59.02	52.14	45.3
GCV (%)	F_3	32.54	30.4	21.16	28.14
	F_4	43.07	28.85	22.8	19.53
Genetic Advance	F_3	10.08	10.38	6.92	10.75
	F_4	7.93	9.29	7.69	8.74
Genetic Gain	F_3	215.8	290.9	237	359.6
	F_4	121.4	297.1	287.8	440.7
Significance	F_3	*	*	*	*
	F_4	*	*	NS	NS
CV (%)	F_3	46.31	51.36	45.71	50.79
	F_4	73.77	59.02	52.14	45.3

The genetic advance was the highest in F_3 (10.75, Sakha 94 × Sakha 95) and the lowest in F_4 (7.93, Line 1 × Misr 1). A similar pattern of genetic advance for yield traits has been documented in wheat breeding programs (Kumar *et al.,* 2014), supporting the concept that selection efficiency is greater in early generations. The genetic gain followed a similar trend, with values ranging from 215.78 in F_3 (Line 1 × Misr 1) to 440.69 in F4 (Sakha 94 × Sakha 95). Previous studies (Mahdy, 2017) have found higher genetic gain in some F_4 populations, suggesting that selection for grain yield may still be effective in advanced generations.

Significant variation was detected across most crosses in F_3, but not in all F_4 crosses. This suggests that early generations exhibit greater genetic variability, which stabilizes in later generations, a trend that has been observed in wheat breeding studies (Ahmed *et al.,* 2020). The coefficient of variation ranged from 45.3% in F_4 (Sakha 94 × Sakha 95) to 73.77% in F_4 (Line 1 × Misr 1), indicating that environmental factors contribute significantly to yield variability. These findings align with previous studies (El-Hosary *et al.,* 2021), emphasizing the role of environmental influences on grain yield expression in wheat.

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التحليل الوراثي ودرجة التوريث لبعض الصفات المحصولية في بعض قمح الخبز : رؤى لتحسين التربية

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الملخص

قمح الخبز (*Triticum aestivum var. vulgare* L.) من اهم محاصيل الحبوب الرئيسية ويعتبر ذو أهمية عالمية، ويلعب دورًا مهم في الأمن الغذائي. تهدف برامج التربية إلى تعزيز إمكاناته الإنتاجية وتحمله للإجهاد وجودة الحبوب من خلال الاستفادة من التباين الوراثي عبر الأجيال. تقيم هذه الدراسة التباين الوراثي ودرجة التوريث وإمكانية الاختيار للصفات المحصوليةالرئيسية في مجموعات منفصلة من الجيلين الثالث والرابع ناتجة من أربعة تهجينات قمح: سلالة ١ × مصر ١، سلالة ١ × سخا ٩٥، وسخا ٩٤ × مصر ١، وسخا ٩٤ × سخا ٩٥. أجريت التجربة في محطة بحوث سخا الزراعية، مصر، خلال موسمي النمو ٢٠٢١/٢٢ و٢٠٢٢/٢٣. تمت زراعة ستين عائلة من الجيل الثالث وخمسين عائلة من الجيل الرابع لكل تهجين في تصميم قطاعات كاملة العشوائية فى ثلاث مكررات. كشفت النتائج عن تباين وراثي كبير في طول النبات، وعدد السنابل لكل نبات، ومحصول الحبوب، وعدد الحبوب لكل سنبلة، ووزن ١٠٠ حبة. أشار تحليل التباين (ANOVA) إلى فروق معنوية بين الهجن والأجيال، مؤكدًا تأثير العوامل الوراثية على الصفات المرتبطة بالمحصول. وقد اظهرت تقديرات التباين الظاهري والجيني، والتوريث، والتقدم الوراثي، إمكانات توريث الصفات الرئيسية. وقد أظهر هجين سلالة ١ × مصر ١ أداءً متفوقًا في صفات محصول الحبوب ومكوناتة، مما يجعله مرشحًا واعدًا لبرامج التربية المستقبلية. وتوفر هذه النتائج رؤى قيّمة حول استراتيجيات الانتخاب والتحسين الوراثي لبرامج تربية القمح، مما يساعد على تطوير أصناف قمح عالية الغلة ومقاومة للامراض والاجهاد.