

INHERITANCE OF GRAIN YIELD AND ITS COMPONENTS IN THREE BREAD WHEAT CROSSES (*TRITICUM AESTIVUM* L.)

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ABSTRACT

Bread wheat (*Triticum aestivum* L.) is a major staple in Egypt, yet domestic production remains insufficient to meet growing demand. This study was carried out to evaluate the genetic control of grain yield, its components, heritability, and genetic gains across segregating generations. Five diverse wheat cultivars (Sids 14, Misr 3, Sakha 93, Gemmeiza 12, and Giza 171) were used to develop three hybrid combinations (Sids 14 × Sakha 93, Misr 3 × Giza 171, Gemmeiza 12 × Giza 171). Experiments were conducted over four consecutive seasons (2019/2020–2022/2023) using a randomized complete block design with three replications. Evaluated traits included spikes/plant, kernels/spike, 100-kernel weight, and grain yield/plant. Significant variability was observed among parental and segregating populations. Positive heterosis was recorded for most traits, especially spikes/plant and kernels/spike, while inbreeding depression in F₂ populations indicated partial loss of hybrid vigor. Genetic analysis revealed substantial contributions of both additive and dominance effects, with epistatic interactions affecting key yield traits. Broad-sense heritability was high for kernels/spike and grain yield, whereas narrow-sense heritability varied across traits. Expected and realized genetic gains were highest for grain yield and kernels/spike, confirming the effectiveness of selection. These results suggest that targeted breeding focusing on traits with high heritability and favorable additive effects, while considering non-additive interactions, can enhance wheat productivity. The findings provide guidance for developing high-yielding cultivars to help close the production-consumption gap in Egypt.

Key Words: *Triticum aestivum* L., Genetic behavior, Hybrid vigor, Heritability estimates, Inbreeding effects, Gene action

INTRODUCTION

Wheat (*Triticum aestivum* L.) is a crucial cereal crop in Egypt, serving as the main staple for the majority of the population. Despite its economic and nutritional importance, a significant gap remains between domestic production and the rising consumption demand, mainly due to rapid population growth and limited arable land. This scenario underscores the need to develop high-yielding wheat cultivars capable of narrowing this gap (Almas and Usman2021).

Grain yield in wheat is a quantitatively inherited trait, influenced by multiple yield components and environmental conditions. Its polygenic nature makes direct selection for yield challenging, particularly in early segregating generations. Therefore, traits such as spike number, kernel weight, and kernels/spike are commonly used as indirect selection criteria. A thorough understanding of the genetic mechanisms underlying these traits is essential for designing effective breeding programs (Zhou *et al.*, 2019).

Knowledge of genetic diversity among breeding materials is fundamental in crop improvement, assisting breeders in identifying promising parental combinations. Generation mean analysis (GMA) is a practical tool for dissecting the gene action controlling quantitative traits. This method allows estimation of additive and dominance effects, as well as detection of epistatic interactions, including additive \times additive, dominance \times dominance, and additive \times dominance effects (Mather and Jinke, 1982).

Recent studies have indicated that traits such as No of kernels/spike, kernel weight, and grain yield are often influenced by dominance and epistatic effects, suggesting that effective selection is more successful in advanced generations. On the other hand, reports of high heritability combined with substantial expected genetic advance for certain yield components indicate that early-generation selection can also be promising (Memon *et al.*, 2005; Memon *et al.*, 2007 and Erkul *et al.*, 2010). Because heritability reflects the extent to which traits are transmitted from parents to progeny, considerable efforts have been made to incorporate favorable alleles into wheat germplasm to maximize productivity.

Accordingly, the current study was aimed to: (i) examine the genetic control underlying grain yield and its key components, (ii) assess heritability in both broad and narrow senses, and (iii) evaluate the expected versus actual genetic gains across segregating generations within a five-population framework.

MATERIALS AND METHODS

1. Selection of Parental Lines and Crosses

Five genetically diverse bread wheat (*Triticum aestivum* L.) cultivars were selected as parental lines for the development of experimental populations (Table 1). These cultivars-Sids 14, Misr 3, Sakha 93, Gemmeiza 12, and Giza 171-were chosen based on their agronomic performance and genetic variability. Three hybrid combinations were established: (1) Sids 14 \times Sakha 93, (2) Misr 3 \times Giza 171, and (3) Gemmeiza 12 \times Giza 171.

Table 1. Pedigree and origin of the parental wheat genotypes

Parent	Pedigree and selection history	Origin
Giza 171	Sakha 93/Gemmeiza 9 G6Z2003-101-1GZ-4GZ-1GZ-2GZ-0GZ	Egypt
Gemmeiza 12	OTUS/3/SARA/THB/VEE CMSS97Y00227S-5Y-010M-010Y-010M-2Y-1M-0Y-0GM	Egypt
Sids 14	Bow"s"/Vee"s"/Bow"s"/TSI/3/Bani Sewef 1 SD293-1SD-2SD-4SD-0sd	Egypt
Misir 3	ATTILA2/ABW652/KACHU CMSS06Y00258 2T-099TOPM-099Y-099ZTM-099Y-099M-10WGY-0B-0GZ	Egypt
Sakha 93	SAKHA92/TR810328 S.8871-1S-2S-1S-0S	Egypt

2. Experimental Design and Field Procedures

The experiment was carried out at the Sakha Agricultural Research Station, Agricultural Research Center (ARC), Kafr El-Sheikh, Egypt, over four consecutive growing seasons (2019/2020 to 2022/2023). In the first season (2019/2020), F₁ seeds were generated through half-diallel crosses among the parental lines. During 2020/2021, F₁ plants were cultivated and self-pollinated to produce F₂ seeds, with backcrossing performed as needed to maintain seed viability. Portions of both F₁ and F₂ seeds were stored under cold conditions. In the 2021/2022 season, F₁ and F₂ plants were again selfed to produce additional F₂ and F₃ seeds, respectively. Final evaluations involving five generations-P₁, P₂, F₁, F₂, and F₃-were conducted in the 2022/2023 season.

A randomized complete block design (RCBD) with three replications was used. Each row was 4 m long, with 20 cm between rows and 10 cm between plants.

3. Data Collection and Statistical Analysis

Data were collected from individual guarded plants for four yield-related traits: number of spikes per plant, number of kernels per spike, 100-kernel weight (g), and grain yield per plant (g). Variance components were estimated only when significant variability was observed in the F₂ generation. Heterosis was expressed as the percentage superiority of F₁ over the better parent (heterobeltiosis), and inbreeding depression was calculated as the proportional reduction in F₂ performance relative to F₁. The significance of heterosis and inbreeding depression, as well as their standard errors, were determined following **Singh and Chaudhary (1985)**.

The potence ratio (P) was calculated according to **Petr and Frey (1966)**, while deviation components (E₁ and E₂) were estimated as suggested by **Mather and Jinks (1971)**. Gene effects, including additive (d), dominance (h), and epistatic interactions (i, l), were partitioned

following **Hayman (1958)**, and their standard errors and significance were computed according to **Singh and Chaudhary (1985)**.

Broad-sense heritability was estimated following **Mather (1949)**, whereas narrow-sense heritability was obtained through parent–offspring regression as described by **Sakai (1960)**. Expected genetic gain (Δg) from selection was predicted using the formula of **Johanson et al. (1955)** and expressed as a percentage of the F_2 mean ($\Delta g\%$). Realized genetic gain was estimated by comparing the response in the F_3 generation relative to the F_2 mean following **Miller et al. (1958)**.

RESULTS AND DISCUSSION

1. Mean performance:

Significant differences were observed among the parental genotypes for most of the studied traits, as well as in the F_2 genetic variances of the three bread wheat crosses, confirming the presence of sufficient genetic variability for further analysis. Table 2 presents the means (\bar{X}) and variances (S^2) of the five populations (P_1 , P_2 , F_1 , F_2 , and F_3) for the three crosses.

Table 2. Descriptive statistics (mean \bar{X} and variance S^2) for the parental, hybrid, and segregating populations across three bread wheat crosses for the assessed traits.

Character	Cross	Parameter	P_1	P_2	F_1	F_2	F_3
No of spikes/plant	1	\bar{X}	15.70	17.90	22.60	21.40	21.10
		S^2	8.90	9.20	9.70	73.80	60.50
	2	\bar{X}	18.27	15.63	21.16	19.85	16.77
		S^2	4.88	6.63	3.34	22.81	17.53
	3	\bar{X}	17.60	15.75	18.15	17.30	16.17
		S^2	3.70	6.80	4.20	8.50	7.60
No of kernels/spike	1	\bar{X}	53.40	60.90	63.40	62.80	60.90
		S^2	22.90	24.50	16.90	120.80	70.80
	2	\bar{X}	79.66	76.07	77.19	68.55	58.9
		S^2	14.06	21.36	27.53	112.27	75.07
	3	\bar{X}	49.90	53.50	60.10	69.70	58.00
		S^2	18.90	21.00	22.80	226.8	169.00
100 kernels/weight (g)	1	\bar{X}	4.90	5.33	5.15	5.10	4.95
		S^2	0.13	0.18	0.07	0.37	0.30
	2	\bar{X}	4.09	4.47	4.63	5.03	5.07
		S^2	0.02	0.02	0.02	0.23	0.13
	3	\bar{X}	5.60	4.92	5.40	5.33	5.26
		S^2	0.01	0.10	0.09	0.33	0.27
Grain yield /plant (g)	1	\bar{X}	39.00	47.50	54.85	50.90	49.82
		S^2	25.90	28.40	31.45	231.50	155.70
	2	\bar{X}	52.91	65.70	57.90	52.53	50.80
		S^2	10.12	19.53	12.46	184.46	114.29
	3	\bar{X}	48.90	38.80	50.70	46.90	44.30
		S^2	18.00	26.00	24.50	170.90	113.70

For **No of spikes/plant**, the F_1 means were higher than those of both parents in the first and second crosses (22.6 and 21.16,

respectively), indicating the presence of positive heterotic effects. The highest variance was recorded in the F₂ populations (73.8 in Cross 1 and 22.8 in Cross 2), reflecting segregation and recombination. In contrast, the third cross showed relatively lower differences between generations, with F₁ (18.15) being close to the parental means.

For **No of kernels/spike**, the F₁ mean of Cross 1 (63.4) exceeded both parents (53.4 and 60.9), while Cross 3 showed a considerable increase in the F₁ mean (60.1) compared with the parents (49.9 and 53.5). On the other hand, the second cross exhibited a decline in the F₂ and F₃ means (68.55 and 58.9), suggesting negative heterotic expression. Notably, F₂ variances were highest in Cross 3 (226.8), indicating strong genetic segregation for this trait.

Regarding **100-kernel weight**, Cross 2 displayed gradual improvement from parents (4.09 and 4.47) to F₂ (5.03) and F₃ (5.07), reflecting additive effects. By contrast, Crosses 1 and 3 showed slight reductions in F₁ means compared with the better parent, implying negative heterosis.

For **grain yield/plant**, Cross 1 showed the highest F₁ mean (54.85) compared to parents (39.0 and 47.5), accompanied by a large F₂ variance (231.5). Cross 2 showed lower F₁ yield (57.9) than the higher parent (65.7), with reduced F₂ and F₃ means. Cross 3 maintained moderate F₁ yield (50.7), but F₂ and F₃ declined slightly. These results confirm that yield performance is mainly dependent on spikes/plant, kernels/spike, and kernel weight.

These findings align with recent studies by **Schmitz & Ransom (2021)** ; **Zhang et al.(2024)** who emphasized the critical role of yield components in explaining hybrid wheat performance.

2. Analysis of Heterosis, Inbreeding Effects, and Genetic Parameters

The estimates of heterobeltiosis, potence ratio (P), inbreeding depression, and gene action parameters for the evaluated crosses are presented in **Table 3**. Heterobeltiosis was calculated to assess the superiority of F₁ hybrids over the better-performing parent, providing insight into the potential of hybrid vigor. Inbreeding depression, expressed as the proportional decline in mean performance of F₂ relative to F₁, was determined to evaluate the stability of hybrid traits in subsequent generations.

The potence ratio (P) was used to quantify the degree and direction of dominance in the expression of yield-related traits. Gene action was further dissected into additive, dominance, and epistatic components, including additive × additive, dominance × dominance, and additive × dominance interactions. These parameters collectively help to elucidate the genetic control of key yield traits, thereby guiding selection strategies for improving wheat productivity.

Table 3: Analysis of genetic effects on yield components, covering heterobeltiosis, potence ratio, and inbreeding depression.

character	Cross	Hetero- beltiosis %	Potence ratio	Inbreeding depression %	Gene action parameters						
					m	d	h	i	I	E1	E2
No of spikes/plant	1	26.26**	5.27	5.31	21.4**	-1.1**	1.6	-6.4*	1.6	1.7*	2.8*
	2	15.89**	3.22	6.25**	19.83**	3.686**	9.034**	12.2**	2.51**	-17.14**	-9.586**
	3	3.13	1.59	4.68*	17.3**	0.93**	3.58*	3.96**	-3.76	-0.11	-2.49**
No of kernels/spikes	1	4.11*	1.67	0.95	62.8**	-3.75**	5.47	-8.28*	-8.53	2.53**	1.25
	2	-3.09**	-0.362	-15.91**	68.54**	1.8**	31.49**	-28.32**	35.71**	-8.986**	-37.27**
	3	12.34**	4.67	0.67	69.7**	-1.8**	3.2	-8.8	-4.8	3.8**	5.4*
100 kernels weight	1	-3.38**	0.18	0.97	5.10**	-0.22**	0.43	-0.03	-0.67	-0.03	-0.37**
	2	3.59**	1.865	-8.44**	5.01**	-0.185*	-0.393**	-0.773*	-1.109	0.563**	1.225**
	3	-3.57**	0.41	1.3	5.33**	0.34**	0.23	0.77**	-0.19	0.00	-0.14
Grain yield /plant	1	15.47**	2.73	7.2**	50.9**	-4.25**	5.51	-14.59**	4.77	1.85	1.54
	2	-11.73**	-0.22	9.293**	52.52**	-5.86**	8.45*	4.65	-2.42**	-5.806**	-15.26**
	3	3.68*	1.36	7.5**	46.9**	5.05*	9.47	12.72**	-3.73	-0.38	-5.95**

In the first cross (**Sids 14** × **Sakha 93**), notable positive heterosis was observed for spikes/plant (26.26%) and grain yield (15.47%). Similarly, kernels/spike increased by 4.11%. However, 100-kernel weight showed negative heterosis (−3.38%). The potence ratios ($P > 1$) indicated over-dominance in spikes/plant and grain yield, while kernel weight ($P = 0.18$) suggested partial dominance. Inbreeding depression was significant for grain yield (7.2%), confirming the expected decline from F1 to F2.

In the second cross (**Misr 3** × **Giza 171**), positive heterosis was observed for the number of spikes per plant (15.89%) and 100-kernel weight (3.59%), whereas negative heterosis occurred for the number of kernels per spike (−3.09%) and grain yield per plant (−11.73%). The potence ratios for grain yield (−0.22) and kernels/spike (−0.36) indicated partial dominance with negative effects toward the lower parent. Inbreeding depression was significant for most traits, especially kernels/spike (−15.91%), supporting the influence of recessive alleles.

In the third cross (**Gemmeiza 12** × **Giza 171**), heterosis was positive and significant for kernels/spike (12.34%) and grain yield (3.68%), while kernel weight showed negative heterosis (−3.57%). The potence ratios indicated partial dominance (0.41 for kernel weight and 1.36 for grain yield). Inbreeding depression was significant for spikes/plant (4.68%) and grain yield (7.5%).

These results highlight that heterotic expression in key yield components, particularly spikes/plant (Cross 1) and kernels/spike (Cross 3), can substantially improve yield potential. However, the presence of inbreeding depression in F2 indicates that hybrid vigor was not fully transmitted to later generations. Similar findings were reported by (**Abd El-Rahman, 2013, Hammad 2014, Al-Bakry et al. 2017, and Abd El-Hamid and Ghareeb, Zeinab 2018**).

3. Gene Action

The results of the five-parameter genetic model indicated that the mean effect (m) was consistently and highly significant for all evaluated traits, highlighting the substantial influence of overall genetic control. Additive gene effects (d) contributed positively and significantly to spikes/plant and kernels/spike in Cross 2, as well as to spikes/plant, kernel weight, and grain yield in Cross 3. These results suggest that additive gene action could be effectively exploited through selection in these particular crosses. In contrast, most traits in Cross 1 exhibited negative additive estimates, indicating a relatively weak contribution of additive variance.

Dominance effects (h) were significant for spikes/plant in Crosses 2 and 3, kernels/spike and grain yield in Cross 2, and kernel weight in

Cross 2, implying that dominance plays a considerable role in the inheritance of these traits.

Epistatic interactions were also evident, with dominance \times dominance (I) being significant for spikes/plant and grain yield in Crosses 2 and 3, while additive \times additive (i) interactions were significant for spikes/plant and kernels/spike in Cross 2. These findings demonstrate that non-additive genetic interactions substantially influence trait expression and should be considered in breeding strategies.

The current findings align with recent studies (; Schmitz & Ransom, 2021; Li and Wang, 2021 and Zhang *et al.*, 2023), which highlighted the significant contributions of both additive and dominance effects in the genetic enhancement of bread wheat.

4. Heritability and Genetic Gain

Heritability estimates and genetic gain are presented in Table (4).

Table 4. Heritability values and assessment of expected versus achieved genetic progress for the studied agronomic traits in three bread wheat hybrids.

Character	Cross	Heritability %			Expected gain for(F ²)		Actual gain for(F ³)	
		Broad sense	Narrow sense	Parent off spring regression	Δg	%	Ag	%
No of spikes/plant	1	87.45	36.04	61.74	11.31	52.83	5.78	27.40
	2	59.36	35.45	58.86	3.88	19.53	5.075	30.29
	3	44.35	21.18	31.76	2.25	13.03	1.2	7.42
No of kernels/spike	1	82.36	82.00	82.07	32.8	52.23	14.21	23.30
	2	72.113	31.32	78.71	15.739	22.963	13.69	23.24
	3	90.81	50.97	70.88	28.03	46.95	13.65	23.50
100- kernel weight	1	68.38	36.76	51.26	0.82	16.01	0.42	8.48
	2	88.18	80.14	84.55	0.774	15.46	0.635	12.55
	3	84.55	33.33	56.36	0.7	13.12	0.36	6.80
Grain yield/plant	1	87.69	65.49	76.57	36.38	71.47	16.83	33.80
	2	93.26	75.24	83.83	21.07	40.09	18.47	36.41
	3	86.11	66.94	76.79	31.95	68.13	14.7	33.20

Broad-sense heritability was generally high ($\geq 82\%$ for kernels/spike in Cross 1 and 90.8% in Cross 3), while spikes/plant showed lower values in Cross 3 (44.35%).

Narrow-sense heritability was moderate to high in most cases, reaching 82% for kernels/spike in Cross 1, but lower for spikes/plant in Cross 3 (21.18%).

Parent-offspring regression confirmed these trends, indicating that both additive and non-additive gene effects contribute to inheritance.

The **expected genetic gain ($\Delta g\%$ of F2)** and **realized gain ($\Delta g\%$ of F3)** were highest for grain yield in Crosses 1 (71.47% and 33.8%, respectively) and 3 (68.13% and 33.2%), confirming their potential for

effective selection. By contrast, kernel weight showed limited gain across all crosses, suggesting that improvement in this trait may be slower.

As noted by (Dixit *et al.* 1970), high heritability alone is insufficient; it must be accompanied by high genetic advance to ensure selection efficiency. In this study, such a combination was evident for grain yield and kernels/spike in Crosses 1 and 3. Similar conclusions were drawn by (Abd El-Hamid and Ghareeb, Zeinab 2018, Gebrel *et al.* 2020, and Mohamed *et al.* 2021).

CONCLUSION

Overall, most biometrical parameters were higher in magnitude for the first (Sids 14 × Sakha 93) and third (Gemmeiza 12 × Giza 171) crosses compared with the second (Misr 3 × Giza 171). This indicates that these two crosses represent promising sources for selecting high-yielding wheat genotypes, owing to the favorable combination of heterosis, additive gene action, and high genetic gain.

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توارث محصول الحبوب ومكوناته في ثلاث هجن من قمح الخبز

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يُعتبر القمح (*Triticum aestivum* L.) الغذاء الرئيسي والأساسي في مصر، إلا أن الإنتاج المحلي لا يكفي لسد احتياجات الطلب المتزايد. تهدف هذه الدراسة إلى تحليل الفعل الجيني وبعض المعايير الوراثية لمحصول الحبوب ومكوناتها، وتقدير معامل التوريث، بالإضافة إلى دراسة قوة الهجين عبر أجيال المتباينة. تم اختيار خمسة أصناف من قمح الخبز (سدس 14، مصر 3، سخا 93، جَمِيْزَة 12، والجيزة 171) لإنتاج ثلاث هجن هي: سدس 14 × سخا 93، مصر 3 × الجيزة 171، وجميْزَة 12 × الجيزة 171. نفذت التجارب خلال أربعة مواسم زراعية متتالية (2023/2022–2020/2019)، باستخدام تصميم القطاعات العشوائية الكاملة بثلاث مكررات. تضمنت الصفات المدروسة عدد السنبال في النبات، وعدد الحبوب في السنبلة، ووزن مئة حبة، بالإضافة إلى إنتاج الحبوب لكل نبات. أظهرت النتائج وجود اختلافات واضحة بين الأصناف الأبوية والأجيال الناتجة منها، حيث ظهرت قوت هجين موجبة في معظم الصفات المدروسة، لاسيما في عدد السنبال للنبات وعدد الحبوب في السنبلة. في المقابل، لوحظ انخفاض في أداء الجيل F_2 نتيجة التدهور في التربية الداخلية، مما يشير إلى فقدان جزئي لقوة الهجين. أوضحت النتائج أن هناك تأثيرات للجينات المضيفة وجينات الغير مضيفة في توريث الصفات، إلى جانب ظهور تفوق (epistasis) الجين التراكمي في الصفات المحصولية. اتضح أن الوراثة بالمعنى الواسع كانت مرتفعة في صفتي عدد الحبوب لكل سنبلة وإنتاجية الحبوب،

بينما أظهرت الوراثة بالمعنى الضيق تفاوتاً بين الصفات المختلفة. وكان معامل التوريث المرتبط بعدد الحبوب في السنبله ومحصول الحبوب مرتفعاً، بينما اختلفت القيم لباقي الصفات. كما حقق محصول الحبوب وعدد الحبوب في السنبله أعلى تحسين وراثي متوقع، مما يدل على أن الانتخاب لهذه الصفات سيكون فعالاً بشكل عام. تشير هذه النتائج إلى أن هدف التربية التركز على الصفات عالية التوريث وذات فعل جيني مضعف، مع الأخذ في الاعتبار التفاعلات الجينية غير المضافة والتي يمكن أن تسهم في رفع إنتاجية القمح. وتعمل هذه الدراسة على إنتاج أصناف قمح عالية المحصول بهدف تخفيض الفجوة بين الإنتاج والاستهلاك في مصر.