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Estimates of Genetic Parameters, Combining Abilities and Heterosis for some Genotypes of Bread Wheat

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ABSTRACT

Plant breeders are dedicated to comprehending the intricacies of variation to devise efficient breeding strategies. The research was carried out at the Experimental Farm of the Faculty of Agriculture, Suez Canal University, Ismailia Governorate, Egypt, spanning two growing seasons (2021/2022 and 2022/2023), epitomizes this pursuit. Six bread wheat genotypes, chosen for their variability, were subjected to all possible half-diallel crosses among the parents, yielding 15 F_1 hybrids. Results unveiled substantial variation among the studied genotypes across all traits, except the number of spikelets. General combining ability mean squares were significantly high for most traits, except for the number of effective tillers and spikes, the results revealed that the best combiners were Sids 12, Giza 171 and Gemmeiza 11 (good combiners) for the important yield components, and they considered to be promising parents. While, specific combining ability mean squares were significant across all traits. The variance of general combining ability and specific combining ability among parental varieties indicated their significant contribution to enhancing most traits. Most crosses exhibited substantial positive heterosis (significant or highly significant) over both mid and better parent values for most of the studied traits. Estimates of heritability and genetic parameters further substantiated the influence of non-additive gene action on the inheritance of these economic traits. The results indicated the possibility of benefiting these genotypes used in this study in different hybridization programs to produce hybrids distinguished in terms of economic traits which contribute to improving productivity of bread wheat.

Keywords: Bread wheat, Half-Diallel Crosses, General and Specific Combining Ability and Heterosis

INTRODUCTION

Wheat (Triticum aestivum L.), a globally crucial strategic crop, reigns supreme as a staple food for a large portion of the world's population and a preferred choice for many (Al-Juthery *et al.*, 2018). Though ranked third in global cereal production behind maize and rice, wheat holds the top spot in terms of cultivated area (FAO, 2020). Earning its titles as "King of Cereals" and "Stuff of Life," wheat's importance transcends prevalence and productivity. It's a foundational food source, critical for global food security, poverty alleviation, and sustaining livelihoods (Rahul, 2017 and Sharma *et al.*, 2019). In Egypt, wheat reigns supreme among grain crops, accounting for nearly 10% of the total agricultural production value and roughly 20% of all agricultural imports. Breeding high-yielding varieties hinges on selecting parents with superior genetics. This is achieved by evaluating their combining ability, which assesses how well their traits combine in offspring. Successful breeding programs also require recognizing diverse traits in potential parents. Simply relying on a plant's outward appearance (phenotype) can be misleading, as lines exhibiting superior traits might yield poorly when crossed. Therefore, choosing parents based on their underlying genetic value is essential (Kumar *et al.*, 2015). Combining ability analysis is a powerful tool for breeders. By estimating variances and effects, it provides insights into the genetic makeup of parents, allowing breeders to make targeted crosses instead of relying on chance. This approach acts as a roadmap, guiding the selection of superior parents and promising cross combinations for a structured breeding program, ultimately accelerating crop improvement (Kalhoro *et al.*, 2015). Understanding heterosis is crucial for wheat breeders to assess the potential of parents to produce superior offspring and determine their value in breeding programs. Research on heterosis allows breeders to identify and eliminate ineffective hybrids early on. By discarding crosses that lack heterosis, breeders can efficiently focus their efforts on a smaller pool of crosses with a higher likelihood of producing high-yielding varieties. The level of heterosis observed in a crop ultimately dictates the feasibility, application, and economic viability of developing hybrid seed varieties (Tiwari *et al.*, 2024). The aim of this study was to assess general and specific combining ability (GCA and SCA) as well as various genetic parameters, to reveal the type of gene action involved and identify top-performing single-cross hybrids that exhibit significant heterosis across multiple traits. By understanding these factors, breeders can select the most appropriate breeding methods to enhance bread wheat production.

MATERIALS AND METHODS

Genetic materials and experimental procedures:

A two-year experiment (2021/2022 and 2022/2023) was conducted at the Experimental Farm of the Faculty of Agriculture, Suez Canal University, Ismailia, Egypt. Six diverse bread wheat genotypes were selected (details in Table 1) from the Wheat Research Section of the Agriculture Research Center, Giza, Egypt. During the 2021/2022 winter season, all possible combinations were made according to half-diallel crosses among the six parents, which generated seeds of 15 F1 hybrids.

Table 1. Plant materials and their sources.

No.	Genotype name	Pedigree	Selection history
P1	Sids 12	BUC//7C/ALD/5/MAYA74/ON//1160. 147/3/BB/GLL/4/CHAT"S"/6/MAYA/VUL//CMH74A.630/4*SX	SD7096-4SD-1SD-1SD-0SD.
P2	Shandaweel 1	SITE/MO/4/NAC/TH.AC//3*/PVN/3/MIRLO/BUC SIDS1/ATTILA//GOUMIRA-17	CMSS93B00567S-72Y-010M-010Y-010M-3Y-0M-0HTY-0SH.
P3	Giza 171	SAKHA 93/GMMEIZA 9	GZ2003-101-1GZ-4GZ-1GZ-2GZ-0GZ.
P4	Sakha 95	PASTOR//SITE/MO/3/CHEN/AEGILOPS/SQUARROSA(TUAS)//B CN/4/WBLLI	CMSA01Y00158S-040POY-040M-030ZTM-040SY-26M-0Y-0SY-0S.
P5	Misr 3	ATTILA*2/PBW65/*2/KACHU	CMSS06Y00582T-099TOPM-099Y-099ZIM-099Y-099M-10WGY-0B-0EGY.
P6	Gemmeiza 11	BOW"S"/KVZ"S"//7C/SER182/3/GIZA168/SAKHA61	GM7892-2GM-1GM-2GM-1GM-0GM

In the following year (2022/2023 season), Six parents and their 15 F_1 seeds were planted in a 3 m² (3 x 1 m). The plot was divided into five rows spaced 20 centimeters apart, both between and within rows. Standard agricultural practices for wheat were followed throughout the growing season, from planting to harvest.

Experimental design and data recorded

To evaluate plant performance, ten plants were randomly selected from each plot and their average values were recorded for the following agronomic traits: Plant height at harvest (cm), measured as plant length from the soil surface to the top of the main spike without awns, Number of effective tillers, Number of spikes, Number of spikelets/spike, Spike length (cm), Spike length without awn (cm), 1000-grain weight (g), Grain yield/plant (g) and Soil and Plant Analyzer Development (SPAD)meters which use to determine the chlorophyll content. A Randomized Complete Block Design with three replicates was employed for the experiment.

Statistical analysis and genetic parameters

The collected data were analyzed using Analysis of Variance (ANOVA) [Steel & Torrie, 1980] to assess the significance of differences between genotypes, crosses, parental lines, and crosses compared to parents. Heterosis, or the superiority of hybrid offspring over parental lines, was estimated for mid-parent (MP) and better parent (BP) using mean values and methods by Matzinger et al. (1962) and Fonseca and Patterson (1968). For traits where genotype variations were statistically significant, Griffing's Method 2 Model 1 (fixed model) [Griffing, 1956] was applied to estimate the general combining ability (GCA) of the six

parent lines and the specific combining ability (SCA) of their hybrids.

RESULTS AND DISCUSSION

Mean performance

Table 2 presents the average performance of parents and F1 hybrids for all studied traits. The results revealed a wide range of average performance among the parents. Notably, Gemmeiza 11 exhibited the highest mean performance in terms of spike length, spike length without awn, SPAD values, 1000-grain weight (g), and grain yield per plant (g). Additionally, Parent 5 had the highest mean performance for plant height and number of spikelets. Furthermore, parents Shandaweel 1, Sakha 95, Misr 3, and Gemmeiza11 displayed the highest mean performance for the Number of effective tillers. On the other hand, the best combinations for the Number of effective tillers were hybrids (1 x 5) and (3 x 4), each with an average of 6 branches per plant. For plant height, hybrid (1 x 3) exhibited the best performance, with an average of 31.11 cm. Regarding the number of spikes, hybrids (1 x 5), (3 x 4), and (3 x 6) were the most favorable, with a mean value of 6 spikes. The best combinations for spike length without awn were (1 x 5) and (3 x 6), with an average of 15.00 cm. For spike length, the best performing combination was (3 x 6), with an average of 19.67 cm. For the number of spikelets, the top combinations were (1 x 2), (1 x 3), (2 x 3), and (4 x 5), with a mean of 25 spikelets. For Soil and Plant Analyzer Development (SPAD) value, hybrid (1 x 4) exhibited the best performance, with an average of 58.43. The hybrid (5 x 6) was the best for 1000-grain weight, with an average of 65.17 gm. Regarding grain yield per plant, the best combination was (1 x 6), with an average of 20.62 g.

Table 2. Mean performance of Parents and its F_1 hybrids for studied traits.

	Plant height	Number of effective tillers	Number of spikes	Spike length	Spike length without awn	Number of spikelets	SPAD value	1000-grain weight(g)	grain yield/plant (g)
P1	28.06	2	2	15.17	10.67	23	45.60	52.67	6.31
P2	26.39	3	3	17.67	11.00	23	51.20	61.73	9.81
P3	29.44	2	2	15.67	10.83	24	50.70	64.07	5.55
P4	28.89	3	3	15.33	12.33	24	47.69	50.57	9.54
P5	32.78	3	3	18.33	11.67	25	47.69	53.60	11.02
P6	29.33	3	3	19.67	15.33	22	57.17	66.13	11.16
1 x 2	27.22	4	4	19.00	12.00	25	50.00	54.37	13.70
1 x 3	31.11	4	4	18.67	12.67	25	53.13	64.40	16.69
1 x 4	27.78	4	4	15.67	9.67	23	58.43	64.10	15.72
1 x 5	27.22	6	6	19.33	15.00	22	53.93	54.50	18.59
1 x 6	29.44	5	5	18.33	13.33	23	51.43	61.17	20.62
2 x 3	30.00	5	5	18.67	13.00	25	46.83	60.87	14.02
2 x 4	26.67	5	5	17.00	11.50	23	50.13	48.23	13.20
2 x 5	27.67	3	3	16.33	12.00	24	48.35	51.80	8.50
2x6	27.72	4	4	18.00	12.00	23	51.57	55.93	10.52
3 x 4	28.78	6	6	17.00	10.33	24	47.13	55.30	16.53
3 x 5	27.67	5	5	17.67	11.33	21	55.27	51.57	10.21
3 x 6	29.11	6	6	19.67	15.00	20	52.73	64.47	15.83
4 x 5	27.67	5	5	17.00	11.67	25	56.80	53.20	12.09
4 x 6	27.89	3	3	18.00	11.00	22	51.57	57.53	7.16
5 x 6	28.33	5	5	19.33	12.67	22	50.30	65.17	16.86
LSD $_{0.05}$	1.68	0.273	0.276	0.478	0.481	0.623	0.179	0.962	0.768
LSD $_{0.01}$	2.25	0.365	0.369	0.640	0.643	0.834	0.240	1.287	1.027

Analysis of variance

This study sought to identify and promote superior bread wheat genotypes by evaluating several economically important traits. To achieve this, a set of half diallel crosses was conducted among six different bread wheat varieties. Results from evaluating these half diallel crosses were used to Investigate how the genetic makeup of each variety influences the characteristics of their offspring and to break down the total genetic variation into its constituent parts. Understanding the genetic basis of these traits was key to developing a targeted breeding strategy for improved bread wheat varieties.

The highly significant differences in genotype mean squares across all studied traits except number of spikelets (Table 3) indicate substantial genetic variation. This validates our planned comparisons to understand the nature of this variation and estimate heterosis. Consequently, partitioning the genetic variance into its components was feasible. Furthermore, the analysis revealed significant variations between parents and crosses for most traits, indicating both their inherent diversity and a strong heterotic response in the studied materials. These findings are consistent with previous reports by El-Borhamy (2004), Rahul and Kandalkar (2018), and Haridy *et al.* (2021).

Table 3. Analysis of variances and mean squares for genotypes, GCA and SCA for traits studies.

S.O. V	d.f	Plant height	Number of effective tillers	Number of spikes	Spike length	Spike length Without awn	Number of spikelets	SPAD value	1000-grain weight(g)	grain yield/ plant (g)
Replicates	2	29.25	0.14	0.25	2.01	0.14	0.89	0.003	18.48	1.78
Genotypes	20	61.18**	3.60**	3.53**	6.19**	3.60**	7.01	37.91**	96.44**	51.28**
Parents(P)	5	119.72**	0.62	0.62	10.35**	3.97**	9.28	49.98**	131.91**	17.27**
Crosses (C)	14	38.49	2.31**	2.27**	4.21*	3.72**	6.65	33.22**	90.31**	43.04**
P vs C	1	86.17*	36.67**	35.71**	13.00**	0.13	0.73	43.17**	4.96	336.74**
Error	40	19.96	0.53	0.54	1.612	0.53	1.63	0.226	6.52	4.16

*,** significant at 0.05 and 0.01 level of probability, respectively

Combining ability analysis.

Table 4 summarizes the mean squares for general (GCA) and specific (SCA) combining ability across all studied traits. The highly significant results for both GCA and SCA mean squares in most traits indicate that both additive and non-additive gene actions contribute to the inheritance of the studied traits. This finding is consistent with previous research by Ahmad et al. (2011), Nazir *et al.* (2014), Abdallah *et al.* (2015), Jatav *et al.* (2017), and Motawea (2017).

Table 4. Analysis of variance and mean squares for combining ability analysis for studied traits.

S.O.V	d.f	Plant height	Number of effective tillers	Number of spikes	Spike length	Spike length without awn	Number of spikelets	SPAD value	1000-grain weight(g)	grain yield/ plant (g)
GCA	5	28.097**	1.20	0.237	4.093**	3.518**	2.743*	89.48**	64.96**	5.72**
SCA	15	17.825**	8.73**	1.490**	1.385**	1.943**	2.143*	193.83**	21.21**	20.88**
Error	40	6.653	0.175	0.179	0.537	0.543	0.912	0.075	2.174	1.386

*,** significant at 0.05 and 0.01 level of probability, respectively

General and specific combining ability effects

Combining ability is a measure that assesses how effectively a genotype can pass on its superior genetic qualities to its offspring when crossed with other genotypes. This analysis provides valuable insights into the genetic worth of inbred lines and aids in identifying the most suitable parents for producing high-performing hybrids. By evaluating the combining ability of different genotypes, plant breeders can make informed decisions about which lines to use in their hybridization programs to maximize the chances of obtaining superior hybrid varieties with desirable traits (Farshadfar *et al.*, 2013). General combining ability effects (g_1) for each parent of all studied traits are presented in Table 5. Parent 1 exhibited significant positive effects on grain yield per plant. Additionally, Parent 3 showed exhibited positive significant impacts for plant height and 1000-grain weight. Furthermore, Parent 6 demonstrated significant positive effects on spike length, spike length without awn, number of spikes, and 1000-grain weight (g).

Table 5. Estimates of general combining ability effects of parents for 9 traits in bread wheat

	Plant height	Number of effective tillers	Number of spikes	Spike length	Spike length without awn	Number of spikelets	SPAD value	1000-grain weight(g)	grain yield/plant (g)
P₁	-0.313	-0.167	-0.194	-0.313	-0.13	0.556	-0.136	0.010	1.257**
P2	-2.875 **	-0.208	-0.194	0.063	-0.31	-0.111	-1.242 **	-1.140*	-1.039**
P3	2.188 *	0.042	0.056	-0.104	-0.13	0.431	-0.341 **	2.618**	-0.435
P4	-1.188	0.208	0.222	-1.063**	-0.77**	-0.361	0.029	-3.036**	-0.513
P5	1.646	0.125	0.139	0.312	0.13	0.431	0.102	-2.544**	0.052
P6	0.542	0.000	-0.028	1.104**	1.21**	-0.944	1.589 **	4.093**	0.679
LSD 0.05	1.68	0.273	0.276	0.478	0.481	0.623	0.179	0.962	0.768
LSD 0.01	2.25	0.365	0.369	0.640	0.643	0.834	0.240	1.287	1.027
SE(gi)	0.832	0.135	0.14	0.237	0.238	0.31	0.089	0.476	0.38
LSD (gi-gj)	7.671	0.202	0.21	0.620	0.627	1.05	0.087	2.506	1.60

These findings suggest that these parents likely carry beneficial genes that could enhance hybrids for these traits. On the other hand, the Specific Combining Ability effects (Sij) for the determined traits were analyzed, and the results, presented in Table 6, indicate that Cross (1x3) displayed significant positive SCA effects for plant height, spike length, spike length without awn, spike values, 1000-grain weight, and grain yield per plant. Additionally, cross (1x5) demonstrated significant positive SCA effects for the Number of effective tillers, number of spikes, spike length, spike length without awn, SPAD values, and grain yield per plant. However, cross (1x6) revealed significant positive SCA effects for plant height, Number of effective tillers, number of spikes, and grain yield per plant. Cross (2x3) exhibited significant positive SCA effects for plant height, Number of effective tillers, number of spikes, spike length, spike length without awn, 1000-grain weight, and grain yield per plant. Furthermore, cross (2x4) showed significant positive SCA effects for the Number of

effective tillers, number of spikes, and grain yield per plant. Cross (2x5) displayed significant positive SCA effects for the number of spikelets. Cross (3x4) revealed significant positive SCA effects for the Number of effective tillers, number of spikes, spike length without awn, and grain yield per plant. Similarly, cross (3x5) demonstrated significant positive SCA effects for the Number of effective tillers and SPAD values. Cross (3x6) showed significant positive SCA effects for the Number of effective tillers, number of spikes, spike length,

spike length without awn, and grain yield per plant. Cross (4x5) exhibited significant positive SCA effects for the Number of effective tillers, number of spikes, and SPAD values. Finally, cross (5x6) revealed significant positive SCA effects for the Number of effective tillers, number of spikes, 1000-grain weight, and grain yield per plant. The findings point to a critical role of non-additive gene action in how these traits are inherited. Results agreed with Chaudhary *et al.,* 2022 and Al-Mafarji and Al-Jubouri 2023.

Table 6. Estimates of specific combining ability effects of parents for 9 traits in wheat (Triticum aestivum L).

	Plant height	Number of effective tillers	Number of spikes	Spike length	Spike length without awn	Number of spikelets	SPAD value	1000-grain weight(g)	grain yield/ plant (g)
1 x 2	-0.741	0.28	0.310	1.560**	0.295	1.333**	0.061	-2.187**	0.928
1 x 3	5.863 **	-0.30	-0.274	1.393**	0.774*	0.792	2.293**	4.088**	3.318**
1 x 4	-0.762	0.20	0.226	-0.649	-1.580**	0.250	7.223**	9.442**	2.425**
1 x 5	-5.262 **	1.61 **	1.643**	1.643**	2.857**	-1.875**	2.650**	-0.649	4.724**
1 x 6	2.509 *	1.07 **	0.810**	-0.149	0.107	0.833	-1.337**	-0.620	6.130**
2 x 3	5.092 **	0.74 **	0.726**	1.018**	1.295**	-1.875**	-2.902**	1.705*	2.941**
2 x 4	-1.533	0.90 **	0.893**	0.310	0.440	0.250	0.029	-5.274**	2.195**
2 x 5	-1.366	-1.01 **	-1.024**	-1.732**	0.045	1.125**	-1.824**	-2.199**	-3.066**
2x6	-0.095	-0.22	-0.190	-0.857*	-1.03**	-1.500**	-0.098	-4.704**	-1.670**
3 x 4	-0.262	1.32 **	0.893**	0.310	0.440	0.250	0.029	-5.274**	2.195**
3 x 5	-6.429 **	0.40 *	0.393	-0.232	-0.810*	0.583	4.188**	-6.191**	-1.957**
3 x 6	-0.991	1.53 **	1.560**	0.976**	1.774**	0.625	0.168	0.071	3.036**
4 x 5	-3.054 *	0.90 **	0.893**	0.060	0.170	-2.292**	5.352**	1.096	-0.006
4X6	-1.283	-0.97 **	-0.940**	0.268	-1.580**	-1.917**	-1.368**	-1.208	-5.560**
5x6	-2.783 *	0.78 **	0.810**	0.226	-0.810*	-0.708	-2.708**	5.934**	3.572**
SE (Sij)	2.286	0.37	0.375	0.65	0.65	0.85	0.24	1.31	1.04
(Sij - Sik)	7.868	1.28	1.291	2.24	2.25	2.91	0.84	4.50	3.59
(Sij - Skl) LSD	7.285	1.18	1.195	2.07	2.08	2.70	0.78	4.16	3.32

Nature of gene action:

Understanding gene action is crucial for choosing appropriate breeding programs to enhance specific quantitative traits. Therefore, before initiating a strategic breeding program, the plant breeder needs to grasp the gene action's nature in the development of various quantitative traits. So various genetic parameters were calculated through combining ability analysis, and results are provided in Table 7. For all the traits studied, the ratio σ2g to σ2S was less than one, indicating the significance of non-additive gene effects in these traits, which confirms predominated of dominance gene action in the inheritance of these traits. This can be improved through hybrid production breeding method. The findings indicated that for all the traits studied, the non-additive genetic variances (VD) exceeded the

corresponding estimates of additive genetic variances (VA). This implies that dominance genetic variance had a significant impact on the inheritance of these traits. This observation is further emphasized by the average degree of dominance (D), which was greater than one for all the traits analyzed. Additionally, In all studied traits, broad-sense heritability (h²bs) was higher than narrow-sense heritability (h²ns). Moreover, the broad-sense heritability estimates (h^{2}bs%) exceeded 64.9% and were higher than their corresponding narrow-sense heritability (h^{2}ns%) across all the traits we investigated. These findings confirmed that non-additive gene action predominantly influences the inheritance of these traits. These findings were agreed with Salam *et al.,* (2019), Ayoob (2020) and Tiwari *et al.,* (2021).

Table 7. The relative magnitude of different genetic parameters for all the studied traits

	Plant height	Number of effective tillers	Number of spikes	Spike length	Spike length without awn	Number of spikelets	SPAD value	1000 seed weight	grain yield/plant (g)
σ2g/σ2S	0.24	0.003	0.006	0.524	0.266	0.186	0.057	0.412	0.028
VA	5.36	0.01	0.014	0.889	0.744	0.458	1.666	15.697	1.084
VD	11.17	1.36	1.311	0.848	1.400	1.230	14.525	19.036	19.498
VE	6.65	0.18	0.179	0.537	0. 543	0.912	0.075	2.174	1.386
D	2.04	17.43	13.454	1.381	1.940	2.319	4.176	1.557	5.998
Hb%	71.3	88.62	88.1	76.4	79.8	64.9	99.5	94.1	93.7
Hn%	23.1	0.58	1.0	39.1	27.7	17.6	10.2	42.5	4.9

Heterosis

It is widely accepted that heterosis, or hybrid vigor, is a common phenomenon in both cross-pollinated and self-pollinated crops. This phenomenon is influenced by three major genetic factors: (1) the genetic diversity of the parental organisms, with heterotic effects becoming more pronounced as the genetic divergence in morphological traits increases, particularly when the parents come from different geographical locations, (2) the genetic makeup of the parents, and (3) the broad adaptability of the parents. The genetic basis of heterosis can be attributed to three possible causes: partial dominance, complete dominance, and over-dominance, with

a particular emphasis on the interactions of dominance. (Solieman *et al.,* 2013). From this perspective, heterosis becomes economically beneficial when the F1 hybrid surpasses its superior parent. Therefore, if a breeder were to implement a selection program in the advanced segregating generation based on these exceptional specific hybrids, the anticipated enhancements would yield fruitful results. Table 8 presents the heterosis (performance difference between the F1 generation and the parental lines) for all the studied traits. Significant positive heterosis compared to the mid-parent value was observed for plant height in crosses (1x3) and (2x3). Furthermore, most crosses exhibited substantial

positive heterosis (significant or highly significant) over both mid-parent and better parent values for traits such as the number of effective tillers, number of spikes, spike length (with and without awns), number of spikelets, SPAD value, 1000 seed weight, and grain yield per plant. These results indicate that most crosses produced significantly higher yields than their parents, highlighting the importance of non-additive gene action in these traits. These findings are consistent with those reported by Bilgin *et al.* (2011), Yao *et al.* (2014), and Abas *et al.* (2018).

Table 8. F$_1$ Generation Heterosis (%): Mid-Parent and Better-Parent for All Studied Traits

Crosses	Plant height		Number of effective tillers		Number of spikes		Spike length		Spike length without awn	
	M.P.	B.P.	M.P.	B.P.	M.P.	B.P.	M.P.	B.P.	M.P.	B.P.
1x2	0.00	-2.97	41.2**	20.0**	41.2**	20.0**	15.74**	7.55**	10.77**	9.09**
1x3	8.21*	5.66	57.1**	57.1**	57.1**	57.1**	21.08**	19.15**	17.83**	16.92**
1x4	-2.44	-3.85	52.9**	30.0**	52.9**	30.0**	2.73**	2.17*	-15.94**	-21.62**
1x5	-10.50**	-16.95**	112.5**	88.9**	112.5**	88.9**	15.42**	5.45**	34.33**	28.57**
1x6	2.61	0.38	87.5**	66.7**	75.0**	55.6**	5.26**	-6.78**	2.56**	-13.04**
2x3	7.46*	1.89	64.7**	40.0**	64.7**	40.0**	12.00**	5.66**	19.08**	18.18**
2x4	-3.52	-7.69**	50.0**	50.0**	50.0**	50.0**	3.03**	-3.77**	-1.43	-6.76**
2x5	-6.48*	-15.59**	-5.3**	-10.0**	-5.3**	0.0	-9.26**	-10.91**	5.88**	2.86**
2x6	-0.50	-5.49	15.8**	10.0**	15.8**	10.0**	-3.57**	-8.47**	-8.86**	-21.74**
3x4	-1.33	-2.26	100.0**	70.0**	100.0**	70.0**	9.68**	8.51**	-10.79**	-16.22**
3x5	-11.07**	-15.59**	75.0**	55.6**	75.0**	55.6**	3.92**	-3.64**	0.74	-2.86**
3x6	-0.95	3.76	112.5**	88.9**	112.5**	88.9**	11.32**	0.00	14.65**	-2.17*
4X5	-10.27**	-15.59**	68.4**	77.8**	68.4**	77.8**	0.99	-7.27**	-2.78**	-5.41**
4x6	-4.20	-4.92	5.3**	0.00	5.3**	0.0	2.86**	-8.47**	-20.48**	-28.26**
5x6	-8.77**	-13.56**	66.7**	66.7**	66.7**	66.7	1.75	-1.69	-6.17**	-17.39**
LSD 0.05	6.38	7.37	1.04	1.20	1.05	1.21	1.81	2.10	1.82	2.11
LSD 0.01	8.54	9.86	1.39	1.60	1.40	1.62	2.43	2.80	2.44	2.82

Table 8. Continued F$_1$ Generation Heterosis (%): Mid-Parent and Better-Parent for All Studied Traits

Crosses	Number of spikelets		SPAD value		1000 seed weight		grain yield/plant (g)	
	M.P.	B.P.	M.P.	B.P.	M.P.	B.P.	M.P.	B.P.
1x2	6.47**	5.71**	3.31**	-2.34**	-4.95**	-11.93**	5.64**	39.63**
1x3	4.96**	4.23**	10.35**	4.80**	10.34**	0.52	10.76**	164.76**
1x4	-1.41	-2.78*	25.27**	22.52**	24.18**	21.71**	7.80**	64.81**
1x5	-9.59**	-13.16**	15.62**	13.08**	2.57	1.68	9.92**	68.61**
1x6	2.19	0.00	0.10	-10.03**	2.97	-7.51**	11.89**	84.82**
2x3	-8.57**	-9.86**	-8.08**	-8.53**	-3.23	-4.99*	6.34**	42.89**
2x4	-3.55**	-5.56**	1.39**	-2.08**	-14.10**	-21.87**	3.52**	34.50**
2x5	0.69	-3.95**	-2.21**	-5.56**	-10.17**	-16.09**	-1.92	-22.89**
2x6	-10.29**	-11.59	-4.83**	-9.80**	-12.51**	-15.42**	0.04	-5.68**
3x4	-3.50**	-4.17**	-4.19**	-7.03**	-3.52	-13.68**	8.98**	73.24**
3x5	-0.68	-3.95**	12.34**	9.01**	-12.35**	-19.51**	1.93	-7.35**
3x6	0.00	-2.82*	-2.22**	-7.76**	-0.97	-2.52	7.48**	41.92**
4X5	-16.22**	-18.42**	19.09**	19.09**	2.14	-0.75	1.81	9.65**
4x6	-15.11**	-18.06**	-1.65**	-9.80**	-1.40	-13.00**	-3.19*	-35.82**
5x6	-9.09**	-14.47**	-4.06**	-12.01**	8.85**	-1.46	5.77**	51.09**
LSD 0.05	2.36	2.73	0.68	0.78	3.65	4.21	2.91	3.36
LSD 0.01	3.16	3.65	0.91	1.05	4.88	5.64	3.90	4.50

CONCLUSION

In conclusion, the considerable genetic diversity seen across all studied traits, along with the significant impact of both GCA (general combining ability) and SCA (specific combining ability), underscores the dominant role of non-additive gene action in their inheritance. Additionally, the cultivars Sids 12, Giza 171, and Gemmeiza 11 are identified as a good combiner, with most cross combinations showing highly positive and significant heterosis values for most studied traits compared to their parents. These results emphasize the importance of non-additive gene action in breeding strategies for these traits and indicate the potential for further yield improvement by leveraging this genetic component.

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تقدير القيم الوراثية والقدرة على التآلف وقوة الهجين لبعض التراكيب الوراثية الجديدة في قمح الخبز

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الملخص

أجريت هذه الدراسة في مزرعة كلية الزراعة بجامعة قناة السويس في الإسماعيلية، مصر، خلال الموسمين الشتويين 2022/2021 و2023/2022 بهدف تقدير القدرات الائتلافية وقوة الهجين والفعل الجيني لستة آباء من القمح وهجنها الفردية. تمت دراسة الصفات المورفوفسيولوجية مثل طول النبات، عدد الأفرع النشطة، طول السنبلة، طول السنبلة بدون سفا، عدد السنابل، عدد السنيبلات بالسنبلة، وزن الألف حبة، ومحصول حبوب النبات. أظهرت النتائج تبايناً وراثياً كبيراً بين التراكيب الوراثية في جميع الصفات المدروسة باستثناء عدد السنيبلات. أظهر اختبار القدرة العامة على التآلف أن أفضل الآباء لمعظم صفات مكونات المحصول كانت سدس 12، جيزة 171، وجميزة 11 (ملقحات جيدة). بينما أظهرت قيم القدرة الخاصة على التآلف وجود اختلافات معنوية لمعظم الصفات المدروسة. أظهرت النتائج أيضاً أن التباين الناتج عن القدرة العامة على التآلف كان أكبر من التباين الناتج عن القدرة الخاصة، مما يؤكد أهمية القدرة العامة في توريث معظم الصفات المدروسة. كذلك كانت قوة الهجين لجميع الهجن الفردية موجبة ومعنوية لمعظم الصفات المدروسة، أنتجت معظم الهجن محصولاً مرتفعاً مقارنة بالآباء، مما يشير إلى أهمية الجينات غير المضيفة في توريث المحصول ومكوناته وإمكانية استخدام هذه الهجن في برامج التربية والتحسين لإنتاج سلالات جديدة من قمح الخبز ذات إنتاجية عالية.

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