



Line x Tester Analysis to Estimate Combining Ability and Heterosis in Bread Wheat (*Triticum aestivum* L.)

H.M. Fouad[#], A.M. El. Mohamed

Agronomy Department, Faculty of Agriculture, Minia University, El-minia, Egypt.



COMBINING ability and heterosis were determined in bread wheat through line x tester analysis during two successive seasons: 2020/2021 and 2021/2022 at the Experimental Farm of Faculty of Agriculture, Minia University, Egypt. The two lines, Sids 14 (L3) and Misr 2 (L5) were a good donor for biological yield/plant BY/P in g, no. spikes/plant NS/P and grain yield/plant GY/P in g. Significant positive general combining ability effects estimated for NS/P, GY/P, weight of grains per spike WG/S in g and 1000 grains weight 1000GW in g for line 4 (Misr 1) and line 5 (Misr 2). Sids 12 (T1) was a good donor for BY/P, NS/P, GY/P and 1000GW. Cross L4 × T2 showed significant negative (desirable) specific combining ability for days to heading. Four crosses, L2 × T3, L3 × T1, L3 × T2 and L4 × T1 exhibited significant positive specific combining ability effects for grain yield/plant. For days to heading, cross L3 × T2 showed significant negative heterosis relative to mid-parents and better parent. Six crosses, L3 × T1, L3 × T2, L4 × T1, L4 × T3, L5 × T1 and L5 × T3 showed significant positive heterosis for grain yield/plant over the mid-parents.

Keywords: Bread wheat, Heterosis, Line x tester, Mid-parents, Specific combining ability.

Introduction

Wheat is one of the most important food crops in the world and the main source of energy and protein for human daily nutritional needs. Due to the continuous increase in the number of the population in the world and in Egypt in particular, it was necessary to work to provide the nutritional needs of the population. In Egypt, there is a gap (50.11%) between production (9.00 million tons) and consumption (18.04 million tons) of wheat of season 2020 (FAO, 2022), so work must be done to obtain new agreements of wheat varieties to contribute to raise the productivity per unit area (vertical expansion) in addition to increase the agricultural area (horizontal expansion). The main objective of plant breeders is increasing the productivity of unit area. Therefore, working on finding new genetic combinations that bear high

yield characteristics is considered the desired goal to meet the food gap.

In the early stages of a breeding program, plant breeders need general knowledge about gene action and the genetic system that governs traits. Plant breeders always seek to search for the best genotypes with a high general combining ability so that they can cross between them to be able to get the best hybrids with specific combining ability, and therefore these hybrids can be used to conduct selection in the segregating generations to obtain superior genetic segregants (Rajput & Kandalkar, 2018; Chaudhary et al., 2022). The combining ability gives important information regarding the selection of parents on the basis of their performance in their crosses, and also helps breeders to determine the best parents that are crossed together to exploit the heterosis

[#]Corresponding author e-mails: hassanfouad2009@yahoo.com, hassan.mostafa@mu.edu.eg

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or to combine and stabilize the desired genes. Line × tester analysis is one of the most important tools that plant breeders can use in predicting the effects of general combining ability of parents and specific ability combining of crosses for yield and its components and other traits in wheat. General and specific combining ability consider the main tool used by the breeders to select the superior parents and crosses (El-Gammaal & Morad, 2018; Kutlu & Sirel, 2019; Abro et al., 2021). The objectives for this study are to determine the general, specific combining ability and heterosis for yield and its components in bread wheat.

Materials and Methods

Experimental procedures

The current investigation was carried out during two successive seasons; 2020/2021 and 2021/2022 at the Experimental Farm of Faculty of Agriculture, Minia University, Egypt. Eight Egyptian bread wheat cultivars, five of them were used as lines and the other three cultivars were used as testers to apply crossing by line × tester design. Codes and pedigree of eight bread wheat cultivars are listed in Table 1.

During the winter season of 2020/2021, the five lines (used as females) were crossed by the three testers (as males) to produce fifteen F_1 crosses by line × tester design according to Kempthorne (1957). In season 2021/2022, the 15 F_1 crosses in addition to the 5 lines and 3 testers were sown on 20th November in randomized complete block design with three replications. The plot size was one row 1.5m a long, 20cm. space between rows and 10cm. apart within row. The recommended cultural practices were adopted throughout the two seasons. Days to 50% heading (DH) was recorded. At end of season the following studied traits were recorded on average of 10 guarded plants: Plant height in cm. (PH), Spike length in cm. (SL), Biological yield per plant in g. (BY/P), Number of spikes/plant (NS/P), Grain yield per plant in g. (GY/P), Number of grains per spike (NG/S), Weight of grains per spike in g. (WG/S) and 1000 grains weight in g. (1000 GW). Analysis of variance of the data taken was done according to Steel & Torri (1980). The variances of general σ^2_{gca} , specific σ^2_{sca} combining ability, additive σ^2_A , dominance σ^2_D were determined by line × tester analysis according to Singh & Chaudhury (1979) as in analysis of variance format in Table 2.

TABLE 1. Codes and pedigree of the bread wheat cultivars used in the study

Genotypes	Codes	Pedigree
Lines		
Gemmeiza 11	L1	BOW''S''/KZ''S''//7C/AERY 82/3/GIZA 168/SAKHA 61 GM78922-GM-1GM-2GM-1GM-0GM
Sids 1	L2	HD2172/Pavon''S''1158.57/Maya74''S''Sd46-4Sd-2Sd-1Sd-0Sd.
Sids 14	L3	BOW''S''/VEE''S''//BOW''S''/TSI/3/ BANI SEWEF1 SD293-1SD-2SD-4SD-0SD OASIS/KAUZ//4*BCN/3/2*PASTOR.
Misr 1	L4	CMSS00Y01881T-050M-030Y-030M-030WGY-33M-0Y-0S SKAUZ / BAV92
Misr 2	L5	CMSS96M03611S-1M-010SY-010M-010SY-8M-0Y-0S
Testers		
Sids 12	T1	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
Sakha 94	T2	Opata / Rayon // KAUZ CMBW90Y3180-0TOPM-3Y-010M-010M010Y-10M-015Y- 0Y-0AP-0S.
Giza 171	T3	SAKHA 93/GEMMEIZA 9

TABLE 2. Analysis of variance for line × tester design

S.O.V.	D. F.	Mean square (MS)
Replication (<i>r</i>)	<i>r</i> -1	
Genotypes (<i>g</i>)	<i>g</i> -1	MS _g
Parents (<i>p</i>)	<i>p</i> -1	
Parents vs. Crosses	1	
Crosses (<i>c</i>)	<i>c</i> -1	
Lines (<i>l</i>)	<i>l</i> -1	M <i>l</i>
Testers (<i>t</i>)	<i>t</i> -1	M <i>t</i>
Lines x testers	(<i>l</i> -1)(<i>t</i> -1)	M <i>lxt</i>
Error	(<i>r</i> -1)(<i>t</i> -1)	MS _e

Results and Discussion

Analysis of variance

Significant (P<0.05 or 0.01) difference were found among the genotypes for all studied traits (Table 3). Indicating presence of sufficient genetic variation among the lines, testers and their crosses. Obvious differences were observed between the minimum and maximum of mean values of the genotypes for the studied traits were 11.00 days, 33.67cm, 8.67cm, 86.56g, 7.57 spikes, 28.24g, 37.67 grains, 2.81g, 12.85g, and 10.87% for DH, PH, SL, BY/P, NS/P, GY/P, NG/S, WG/S, 1000-GW and HI%, respectively (Table 4). These differences were higher than the values of LSD at 5% or 1% by 3 to 5 times. Parents and crosses exhibited significant (P<0.05 or 0.01) differences for all traits. Significant (P<0.05 or 0.01) differences found for the contrast parents vs. crosses for all traits except days to heading and plant height. Indicating the considerable amount of average heterosis was reflected in their crosses for most traits (Table 3). Partitioning mean squares of crosses (line × tester) revealed that variance due to both of lines and testers were significant for most traits of lines and testers and days to heading of testers. The variance due to line × tester was significant for all traits studied indicating that the five lines did express effective role with the three testers according to their crosses performance (Table 3). These consequences are in arrangement with those reported by Abd El-Aty, (2016), El-Gammaal & Morad (2018), Rajput (2018), El-Gammaal (2019), Abro (2021), Roy et al. (2021a), Alhossary (2020), Shah et al. (2020) and Fouad et al. (2022).

TABLE 3. Mean squares for line × tester design for the studied traits

S.O.V.	df	DH	PH	SL	BY/P	NS/P	GY/P	NG/S	WG/S	1000GW
Rep	2	44.39	8.65	5.23	1450.37	4.54	42.31	4.48	0.02	24.56
Genotypes	22	28.77**	256.60**	17.44**	1930.51**	14.07**	213.04**	288.36**	1.51**	48.92**
Parents P	7	30.48**	406.48**	7.24**	817.97**	11.00**	103.27**	221.33**	0.81**	46.83**
Crosses C	14	27.74**	169.51**	15.14**	2391.16**	15.70**	271.04**	274.42**	1.42**	41.68**
P vs C	1	0.81	20.30	113.87**	2451.28**	1.87*	66.19**	731.46**	6.88**	118.18**
Lines	4	59.52*	198.17**	10.14**	4659.10**	27.55**	524.302**	353.59**	1.64**	21.69**
Testers	2	5.76	228.29**	58.16**	1816.44**	10.61**	207.37**	399.36**	2.31**	120.42**
L × T	8	17.34**	140.48**	6.88**	1400.88**	11.04**	160.32**	203.61**	1.09**	31.99**
Error	44	4.71	33.35	1.79	56.56	0.52	GY/P	15.30	0.02	3.01

*, **, *** significant at 0.5 and 0.01 levels of probability, respectively.

For lines, Misr 1 (L4) recorded the earliest line in days to 50% heading by 88.67 days and the lowest line in each of plant height (76.33cm), number of spikes/plant (2.77), grain yield/plant (11.22g) and 1000 grains weight (42.88g) (Table 4). Moreover, Misr 1 gave the highest values for each of spike length (13.00cm), number of grains/spike (76.00) and weight of grains/spike (3.65g) but its grain yield showed decline because of the reduction in the number of spikes/plant. The line 5 (Misr 2) gave the highest values for each of plant height (110.00cm), number of spikes/plant (6.09) and grain yield/plant (22.18g). Line 2 (Sids 1) recorded the highest 1000 grain weight (55.73g) (Table 4).

For testers, Sakha 94 (T2) gave the highest values for each of plant height (102.33cm), biological yield/plant (77.25g), number of spikes/plant (9.75), and grain yield/plant (30.30g) (Table

4). Sids 12 (T1) gave the highest values for each of spike length (14.33cm), number of grains/spike (74.67) and weight of grains/spike (3.83g). Giza 171 (T3) recorded the highest values for 1000 grains weight (53.31g) (Table 4). Similar findings are in line with conclusions of Baloch et al. (2016), Abro et al. (2021), and Roy et al. (2021a).

Concerning crosses, cross L4 × T2 recorded the earliest cross 89.33 days. L2 × T3 recorded the highest values for plant height (102.67cm). L3 × T1 gave the highest values for each of BY/P (117.47g), NS/P (10.33) and grain yield/plant (37.70g). L4 × T1 gave the highest values for each of WG/S (5.20g) and 1000GW (55.58g). L4 × T3 recorded the highest NG/S (87.67 grains). For spike length, L5 × T3 gave the tallest spike (17.67cm). Three crosses L3 × T1, L4 × T1 and L5 × T1 recorded the highest grain yield by 37.70, 30.78 and 35.67g, respectively.

TABLE 4. Mean performance for the studied traits of the 5 lines, 3 testers and their 15 F₁s crosses

Genotypes	DH	PH (cm)	SL (cm)	BY/P (g)	NS/P	GY/P (g)	NG/S	WG/S (g)	1000GW (g)
L1	96.00	106.00	9.00	37.79	5.53	13.90	54.33	2.39	45.80
L2	96.00	82.33	11.67	59.57	5.14	21.67	64.33	3.29	55.73
L3	97.67	101.33	12.33	71.40	5.89	20.53	66.67	3.39	50.42
L4	88.67	76.33	13.00	31.55	2.77	11.22	76.00	3.65	42.88
L5	99.00	110.00	10.67	56.42	6.09	22.18	68.33	2.91	44.99
T1	95.00	86.33	14.33	66.48	6.73	22.20	74.67	3.83	46.89
T2	99.00	102.33	10.67	77.25	9.75	30.30	50.00	2.41	47.53
T3	93.33	86.67	12.67	34.52	4.05	13.28	70.00	3.57	52.31
L1 x T1	93.33	91.00	17.00	50.41	5.39	15.07	56.67	2.84	54.43
L1 x T2	95.33	84.00	11.00	37.23	3.49	11.02	77.33	3.58	44.32
L1 x T3	93.00	84.00	17.33	42.36	3.83	13.44	74.00	4.02	53.72
L2 X T1	98.33	90.67	13.33	30.90	3.05	9.46	63.33	3.19	52.59
L2 X T2	97.67	99.67	11.33	42.51	4.50	13.04	58.33	3.15	52.90
L2 X T3	97.67	102.67	14.00	60.82	6.00	19.56	70.67	3.60	50.78
L3 x T1	94.00	94.67	13.33	117.47	10.33	37.70	75.00	4.21	53.33
L3 x T2	92.67	106.67	14.67	94.32	8.70	29.92	64.00	3.48	51.28
L3 x T3	97.33	90.00	16.00	39.50	3.50	12.53	74.67	4.21	54.70
L4 x T1	96.67	82.67	14.33	87.05	7.42	30.78	84.33	5.20	55.58
L4 x T2	89.33	92.67	11.00	54.36	5.03	15.23	62.33	2.83	43.82
L4 x T3	90.67	99.00	17.00	64.23	5.59	23.23	87.67	4.81	50.90
L5 x T1	98.00	85.67	15.00	112.09	9.00	35.67	76.00	4.13	52.98
L5 x T2	99.67	100.67	14.33	76.47	7.25	25.52	78.00	4.06	48.32
L5 x T3	96.67	87.67	17.67	93.59	8.24	29.81	83.33	4.34	46.33
LSD 5%	3.58	9.53	2.21	12.41	1.19	4.32	6.45	0.21	2.86
LSD 1%	4.79	12.75	2.96	16.60	1.59	5.78	8.63	0.28	3.83

L1 Gemmeiza 11, L2 Sids 1, L3 Sids 14, L4 Misr 1, L5 Misr 2, T1 Sids 12, T2 Sakha 94 and T3 Giza 171.

Combining ability effects and variances

The general and specific combining ability are the main criteria of rapid genetic assaying of the tested genotypes under line \times tester design.

The effects of general combining ability (\hat{g}_i) of the parents (lines and testers) are useful tools for selecting the cross parents. According to this, the effects of GCA of the parents for the studied traits are presented in Table 5.

Among the five parental lines, two lines Gemmeiza 11 (L1) and Misr 1 (L4) showed significant negative GCA effects for days to 50% heading, hence it considered a good combiner for earliness. Line 2 and 5 (Sids 1 and Misr 2) showed highly significant positive GCA effects for DH while, tester 2 (Sakha 94) showed non-significant negative GCA effect for days to 50% heading. So, the combinations that include these genotypes had relatively lateness in days to 50% heading. The two lines Sids 1 (L2) and Sids 14 (L3) and tester Sakha 94 (T2) showed significant ($P \leq 0.05$ or 0.01) positive GCA effects for plant height hence it was a good combiner for tallness that are desired to straw yield while, the line Gemmeiza 11 (L1) and tester Sids 12 (T2) were a good combiner for shortness that preferred for resistance for lodging. All parents except Gemmeiza 11 and Sids 12 had significant positive or non-significant negative

GCA effects for plant height. Consequently, it can be realized that positive or insignificant negative GCA effects increasing the plant height were more than the significant negative effects. Similarly for spike length except the two parents Sids 1 (L2) and Sakha 94 (T2). For spike length, Misr 2 (L5) and Giza 171 (T3) had highly significant positive GCA effects and considered a good combiner for long spike. The two lines, Sids 14 (L3) and Misr 2 (L5) were a good donor for BY/P, NS/P and GY/P, where it showed high significant positive GCA effects for these traits. Sids 12 (T1) was a good donor for BY/P, NS/P, GY/P and 1000GW where it gave high significant positive GCA effects for them. Significant ($P \leq 0.05$ or 0.01) positive GCA effects estimated for BY/P, NS/P, GY/P, WG/S and 1000GW for line 4 (Misr 1) and line 5 (Misr 2) in addition tester 3 (Giza 171) for traits plant height and spike length. Similar results were in harmony with those reported by Ijaz & Kaukab (2017), Rajput (2018), Hama-Amin & Towfiq (2019), El-Gammaal (2019), Alhossary (2020), Gupta et al. (2020), Abro et al. (2021), Roy et al. (2021a), and Chaudhary et al. (2022).

In self-pollination species, specific combining ability (SCA) effects can be utilizing to select lines with homozygosity that appear transgressive segregation in early generations.

TABLE 5. General combining ability GCA effects for the studied traits of the 5 lines and 3 testers

Parents	DH	PH	SL	BY/P	NS/P	GY/P	NG/S	WG/S	1000GW
Lines									
L1	-1.47*	-6.44**	0.62	-23.55**	-1.85**	-8.29**	-3.04*	-0.36**	-0.24
L2	2.53**	4.89**	-1.60**	-22.14**	-1.57**	-7.45**	-8.27**	-0.53**	1.02
L3	-0.69	4.33*	0.18	16.88**	1.42**	5.25**	-1.16	0.12**	2.04**
L4	-3.13**	-1.33	-0.38	1.66	-0.07	1.62*	5.73**	0.44**	-0.97
L5	2.76**	-1.44	1.18**	27.16**	2.08**	8.87**	6.73**	0.34**	-1.85**
se (\hat{g}_i)	0.65	1.72	0.4	2.24	0.21	0.78	1.17	0.04	0.52
Testers									
	DH	PH	SL	BY/P	NS/P	GY/P	NG/S	WG/S	1000GW
T1	0.71	-3.84**	0.11	12.70**	0.95**	4.27**	-1.31	0.07*	2.72**
T2	-0.42	3.96**	-2.02**	-5.91**	-0.29	-2.52**	-4.38**	-0.42**	-2.94**
T3	-0.29	-0.11	1.91**	-6.79**	-0.65**	-1.75**	5.69**	0.35**	0.22
se (\hat{g}_i)	0.46	1.22	0.28	1.59	0.15	0.55	0.82	0.03	0.37

L1 Gemmeiza 11, L2 Sids 1, L3 Sids 14, L4 Misr 1, L5 Misr 2, T1 Sids 12, T2 Sakha 94 and T3 Giza 171, *,** significant at 0.5 and 0.01 levels of probability, respectively.

Table 6 showed the effects of specific combining ability (S_{ij}) of the fifteen crosses for the studied traits. Only one cross $L4 \times T2$ showed significant negative (desirable) SCA for days to 50% heading, indicating this cross could be used to select early heading lines and shorten vegetative growth duration. Four crosses, $L1 \times T1$, $L3 \times T2$, $L4 \times T3$ and $L5 \times T2$ showed significant positive ($P \leq 0.05$ or 0.01) S_{ij} effects for plant height, it could be considered a good combiner for high straw yield. Two crosses, $L1 \times T1$ and $L3 \times T2$ showed highly significant positive S_{ij} effects for spike length. Three crosses, $L2 \times T3$, $L3 \times T1$ and $L3 \times T2$ exhibited highly significant positive S_{ij} effects for biological yield/plant.

For number of spikes/plant, five crosses $L2 \times T2$, $L2 \times T3$, $L3 \times T1$, $L3 \times T2$ and $L5 \times T3$ had significant positive ($P \leq 0.05$ or 0.01) S_{ij} effects. So, these crosses could be used for selecting high tillering ability lines.

Regarding grain yield per plant, four crosses $L2 \times T3$, $L3 \times T1$, $L3 \times T2$ and $L4 \times T1$ exhibited significant positive (0.01) S_{ij} effects. These crosses could be a good combiner for high yielding of grain. For no. of grains/spike, four crosses $L1 \times T2$, $L3 \times T1$, $L4 \times T1$ and $L4 \times T3$ had significant positive ($P \leq 0.05$ or 0.01) S_{ij} effects. Four crosses $L1 \times T3$, $L2 \times T2$, $L4 \times T1$ and $L5 \times T2$ for traits weight of grains/spike and 1000 grains weight in addition two crosses $L1 \times T2$ and $L3 \times T2$ of weight of grains/spike showed significant positive ($P \leq 0.05$ or 0.01) S_{ij} effects, they considered a good donor for these traits. These results are in line with those reported by Sarwar (2016), Ijaz & Kaukab (2017), Rajput (2018), Rajjitha et al. (2018), Shah et al. (2018a), El-Gammaal (2019), Alhossary (2020), Dhoot et al. (2020), Gupta et al. (2020), Kizilgeci (2020), El Nahas & Ali (2021) and Roy et al. (2021b).

TABLE 6. Specific combining ability SCA for the studied traits of the 15 F_1 's crosses

Crosses	DH	PH	SL	BY/P	NS/P	GY/P	NG/S	WG/S	1000GW
$L1 \times T1$	-1.27	8.51**	1.78**	-5.62	0.2	-2.38*	-11.36**	-0.71**	0.89
$L1 \times T2$	1.87	-6.29**	-2.09**	-0.19	-0.45	0.36	12.38**	0.52**	-3.56**
$L1 \times T3$	-0.6	-2.22	0.31	5.81	0.25	2.01	-1.02	0.19**	2.68**
$L2 \times T1$	-0.27	-3.16	0.33	-26.54**	-2.42**	-8.83**	0.53	-0.19**	-2.21**
$L2 \times T2$	0.2	-1.96	0.47	3.68	1.78**	1.54	-1.4	0.26**	3.74**
$L2 \times T3$	0.07	5.11	-0.8	22.86**	2.14**	7.29**	0.87	-0.07	-1.53*
$L3 \times T1$	-1.38	1.4	-1.44*	21.00**	1.87**	6.71**	5.09**	0.17**	-2.49**
$L3 \times T2$	-1.58	5.60*	2.02**	16.47**	1.48**	5.72**	-2.84	-0.07	1.11
$L3 \times T3$	2.96**	-7.00**	-0.58	-37.47**	-3.35**	-12.43**	-2.24	-0.11	1.38
$L4 \times T1$	3.73**	-4.93*	0.11	5.81	0.46	3.43**	7.53**	0.85**	2.76**
$L4 \times T2$	-2.47*	-2.73	-1.09	-8.28*	-0.69*	-5.33**	-11.40**	-1.02**	-3.34**
$L4 \times T3$	-1.27	7.67**	0.98	2.47	0.23	1.9	3.87*	0.18**	0.58
$L5 \times T1$	-0.82	-1.82	-0.78	5.34	-0.11	1.07	-1.8	-0.12*	1.05
$L5 \times T2$	1.98*	5.38*	0.69	-11.67**	-0.62*	-2.30*	3.27	0.31**	2.05**
$L5 \times T3$	-1.16	-3.56	0.09	6.33	0.73*	1.23	-1.47	-0.19**	-3.10**
se (s_{ij})	0.92	2.43	0.56	3.17	0.3	1.1	1.65	0.05	0.73

Gemmeiza 11 (L1), Sids 1 (L2), Sids 14 (L3), Misr 1 (L4), Misr 2 (L5), Sids 12 (T1), Sakha 94 (T2) and Giza 171 (T3), *, ** significant at 0.05 and 0.01 levels of probability, respectively.

Heterosis

Table 7 showed significant mid-parents and better parent heterosis of the 15 F_1 's crosses for the studied traits. For days to heading, cross L3 x T2 showed significant negative heterosis relative to mid-parents (-5.76%) and better parent (-5.12%) in addition cross L4 x T2 relative to better parent by -4.80%. The negative heterosis for days to 50% heading may be desirable for breeding wheat line for earliness. Two crosses, L2 x T3 and L4 x T3 showed significant positive heterosis for plant height relative to mid-parents by 21.5% and 21.47%, respectively. For spike length, seven crosses exhibited significant positive heterosis compared to the mid-parents ranged from (27.54%) of L3 x T2 to (64.52%) of L1 x T1, also relative to the better parent ranged from (26.32%) of L3 x T3 to (45.71%) of L1 x T1. For biological yield/plant, six crosses had significant positive heterosis based on both of mid-parents and better parent. For no. of spikes/plant, for crosses L3 x T1, L4 x T3, L5 x T1 and L5 x T3 showed significant positive heterosis ranged from (40.44%) of L5 x T1 to (64.17%) of L4 x T3 relative to the mid-parents and ranged from (33.73%) of L5 x T1 to (53.54%) of L3 x T1 relative to better parent.

Regarding grain yield/plant, six crosses L3 x T1, L3 x T2, L4 x T1, L4 x T3, L5 x T1 and L5 x T3 showed significant positive heterosis over the mid-parents ranged from (17.73%) of L3 x T2 to (84.22%) of L4 x T1, moreover, five crosses from these crosses except L3 x T2 showed significant positive heterosis relative to the better parent ranged from (34.44%) of L5 x T3 to (69.83%) of L3 x T1. For number of grains/spike, eight crosses had significant positive heterosis relative to mid-parents ranged from (9.27%) of L3 x T2 to (31.83%) of L5 x T2, meanwhile, five crosses expressed significant positive heterosis relative to the better parent ranged from (10.96%) of L4 x T1 to (19.05%) of L5 x T3.

For weight of grains/spike, significant positive heterosis showed relative to mid-parents for eleven crosses ranged from (10.60%) of L2 x T1 to (52.78%) of L5 x T2 and relative to the better parent for eight crosses ranged from (7.97%) of L5 x T1 to (35.82%) of L4 x T1.

Concerning 1000 grains weight, eight crosses had significant positive heterosis compared to the mid-parents ranged from (6.50%) of L3 x T3 to (23.83%) of L4 x T1. Three crosses exhibited significant positive heterosis ranged from (5.77%) of L3 x T1 to (18.54%) of L4 x T1. These results were in agreement with those found by Abd El-Aty et al. (2016), Baloch et al. (2016), Ijaz & Kaukab (2017), Jatav et al. (2017), Shah et al. (2018b), Hama-Amin & Towfiq (2019) and Shah (2020).

Genetic components

Selection of the parents that used for hybridization program and the suitable breeding method depend upon knowledge of gene action. Estimates of the genetic components for the studied traits are presented in Table 8.

The obtained results indicated that ratios of $\sigma^2_{gca}/\sigma^2_{sca}$ were lower than unity for all traits, indicating the importance role of non-additive (dominance) gene action for controlling in inheritance of traits. This result supported by values of degree of dominance $(\sigma^2_D/\sigma^2_A)^{0.5}$ greater than unity. Low estimates of heritability in narrow sense compared to heritability in broad sense for all traits, indicating presence of partial dominance. The values of narrow sense heritability ranged from (1.24%) of plant height to (8.65%) of spike length, while broad sense heritability ranged from (63.00%) of days to 50% heading to (91.70%) of biological yield/plant. These results revealed that selection plants for these traits should be postponed to the later generations because of predominance of non-additive gene action for all studied traits. These consequences are in arrangement with those of Fellahi et al. (2013), Abd El-Aty et al. (2016), Ali (2019), El-Gammaal (2019), Dhoot et al. (2020), Roy et al. (2021b) and Chaudhary et al. (2022).

Contribution of lines was higher than testers and line x tester interaction for days to 50% heading, biological yield/plant, no. of spikes/plant and grain yield/plant. Tester's contribution was the highest source of variation compared to testers and line x tester interaction for spike length. While, for plant height, no. of grains/spike, weight of grains/spike and 1000 grains weight, contribution of line x tester interaction was the highest compared to the total variation.

TABLE 7. Significant mid-parents (H MP %) and better parent (H BP %) heterosis for the studied traits of the 15 F1's crosses

Cross	H%	DH	PH	SL	BY/P	NS/P	GY/P	NG/S	WG/S	1000GW
L1 x T1	MP			64.52**						7.22**
	BP		-14.15**	45.71**			-30.47**	-11.92*	-13.68**	
L1 x T2	MP		-18.97**		-31.81**	-38.85**	-35.97**	27.82**	23.81**	-7.87**
	BP		-20.75**		-47.86**	-40.71**	-46.32**	16.00**		-12.10**
L1 x T3	MP		-12.80**	60.00**				19.03**	35.01**	9.51**
	BP		-20.75**	36.84**		-30.75**		12.61**		
L2 x T1	MP	3.22*			-45.87**	-42.77**	-51.65**	-9.52*	-6.64*	9.16**
	BP				-53.52**	-54.74**	-57.39**	-15.18**	-16.70**	-5.62*
L2 x T2	MP				-37.86**	-39.59**	-49.81**		10.60*	
	BP				-44.97**	-53.88**	-56.95**			-5.08
L2 x T3	MP	3.17*	21.50**		29.27**	30.65**				-6.00*
	BP	4.64*	18.46**							-8.88**
L3 x T1	MP				70.38**	63.75**	76.45**		16.56**	9.61*
	BP				64.51**	53.54**	69.83**		9.93**	5.77*
L3 x T2	MP	-5.76**		27.54**	26.90**		17.73*	9.71*		
	BP	-5.12**		18.92*	22.10**					
L3 x T3	MP	4.29*	-11.18*	28.00**	-25.41*	-29.48**	-25.88*	9.27*	20.98**	6.50**
	BP	5.26**		26.32**	-44.67**	-40.52**	-38.97**		17.93**	
L4 x T1	MP	9.02**			77.59**	56.27**	84.22**	11.95**	39.00**	23.83**
	BP	-4.80*			30.94**		38.67**	10.96**	35.82**	18.54**
L4 x T2	MP					-19.62*	-26.63**		-6.52*	
	BP		-9.45*		-29.64**	-48.41**	-49.73**	-17.98**	-22.47**	-7.80**
L4 x T3	MP		21.47**	32.47**	94.42**	64.17**	89.62**	20.09**	33.10**	6.94**
	BP		14.23**	30.77**	86.07**	38.24**	74.90**	15.35**	31.64**	
L5 x T1	MP		-12.73**	20.00**	82.40**	40.44**	60.78**		22.64**	15.33**
	BP		-22.12**		68.60**	33.73**	60.70**		7.97**	13.00**
L5 x T2	MP			34.38**				31.83**	52.78**	
	BP		-8.48*	34.38**		-25.66**	-15.77*	14.15**	39.52**	
L5 x T3	MP		-10.85**	51.43**	105.83**	62.69**	68.16**	20.48**	33.95**	
	BP		-20.30**	39.47**	65.88**	35.41**	34.44**	19.05**	21.57**	-11.43**

L1 Gemmeiza 11, L2 Sids 1, L3 Sids 14, L4 Misr 1, L5 Misr 2, T1 Sids 12, T2 Sakha 94 and T3 Giza 171, *, ** significant at 0.05 and 0.01 levels of probability, respectively.

TABLE 8. Genetic components and proportional (%) contribution of lines, testers and their interaction to total variation for the studied traits

ItemS	DH	PH	SL	BY/P	NS/P	GY/P	NG/S	WG/S	1000GW
σ^2_{gca}	0.22	0.67	0.30	24.39	0.10	2.72	1.86	0.01	0.36
σ^2_{sca}	4.21	35.71	1.70	448.11	3.51	51.16	62.77	0.36	9.66
$\sigma^2_{gca}/\sigma^2_{sca}$	0.05	0.02	0.18	0.05	0.03	0.05	0.03	0.03	0.04
σ^2_A	0.44	1.34	0.61	48.78	0.20	5.44	3.73	0.02	0.73
σ^2_D	4.21	35.71	1.70	448.11	3.51	51.16	62.77	0.36	9.66
$(\sigma^2_D/\sigma^2_A)^{0.5}$	3.09	5.16	1.67	3.03	4.19	3.07	4.10	4.24	3.64
H ns%	3.47	1.24	8.65	7.16	4.04	7.20	3.50	3.53	3.97
H bs%	63.00	69.05	74.42	91.70	89.70	90.94	85.61	96.80	83.57
Cont. lines	61.30	33.40	19.14	55.67	50.15	55.27	36.81	33.08	14.87
Cont. testers	2.96	19.24	54.87	10.85	9.66	10.93	20.79	23.28	41.27
Cont. L x T	35.72	47.36	25.97	33.48	40.18	33.80	42.40	43.86	43.86

Conclusion

Line \times tester analysis is use in predicting the effects of general combining ability of parents and specific ability combining of their crosses. The lines L3 and L5 were a good donner for biological yield/plant, no. spikes/plant and grain yield/plant. Tester 1 was a good donner for these traits in addition 1000 grains weight. Four crosses, L2 \times T3, L3 \times T1, L3 \times T2 and L4 \times T1 exhibited excellent combiners for specific combining ability for grain yield/plant. It's recommended to use these genotypes in programs of wheat breeding by selection to achieve transgressive segregation.

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تحليل السلالة × الكشاف لتقدير القدرة على الانتلاف وقوة الهجين في قمح الخبز

حسن محمد فؤاد، احمد محمد المهدي محمد
قسم المحاصيل - كلية الزراعة - جامعة المنيا - المنيا - مصر.

تهدف الدراسة إلى تقدير القدرة على الانتلاف وقوة الهجين في قمح الخبز باستخدام تحليل السلالة × الكشاف خلال موسمين متتاليين 2020/2021 و2021/2022 في المزرعة التجريبية لكلية الزراعة - جامعة المنيا - مصر. وأظهرت النتائج ان السلالتين سدس 14 ومصر 2 كانوا سلالات ذات قدرة عالية على توريث صفاتها لنسلها لصفات المحصول البيولوجي/نبات وعدد السنابل/نبات ومحصول الحبوب/نبات، ووجدت تأثيرات موجبة معنوية للقدرة العامة على الانتلاف لصفات عدد السنابل/نبات ومحصول الحبوب/نبات ووزن حبوب السنبل ووزن الالف حبة للسلالة 4 مصر 1 والسلالة 5 مصر 2، وكان الصنف الكشاف 1 سدس 12 معطى جيد لصفات المحصول البيولوجي/نبات وعدد السنابل/نبات ومحصول الحبوب/نبات ووزن الالف حبة، كما اظهر الهجين سلالة 4 × كشاف 2 قدرة خاصة على الانتلاف سالبة مرغوبة معنوية لصفة عدد ايام طرد السنابل، كما اظهرت اربعة هجن هي سلالة 2 × كشاف 3، سلالة 3 × كشاف 1، سلالة 3 × كشاف 2، سلالة 4 × كشاف 1 قدرة خاصة على الانتلاف موجبة معنوية لصفة محصول الحبوب/نبات، واطهر الهجين سلالة 3 × كشاف 2 قوة هجين سالبة مرغوبة ومعنوية لصفة ميعاد طرد السنابل بالنسبة لكلا من متوسط الابوين والاب الاعلى، كما اظهرت ستة هجن هي سلالة 3 × كشاف 1، سلالة 3 × كشاف 2، سلالة 4 × كشاف 1، سلالة 4 × كشاف 3، سلالة 5 × كشاف 1، سلالة 5 × كشاف 3 قوة هجين موجبة معنوية لصفة محصول الحبوب/نبات بالنسبة لمتوسط الابوين.