Yield And Its Components Of Some Half Diallel Bread Wheat Crosses

Nassar, M. A. A., M. N. Elbnna, G. A.I. Elsorady and M. E. A. Nofal
Plant Production Department, Faculty of Agriculture, Saba Basha, Alexandria University, Egypt
*E-Mail : mohamednofal345@yahoo.com

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ABSTRACT

Two field experiments were conducted at Naguib Mahfouz village, Housh Eisa, El Beheara Government, Egypt. During 2019 and 2020 seasons, to study yield and its components of some half-diallel wheat bread crosses. A randomized complete block design (RCBD) with three replications was used. Each replicate consisted of 33 rows, 3 m. long and 30 cm in width. apart with 15 cm. between plants. Twenty grains were sown in each row.

Where the 7 parental genotypes (Sakha 94, Misr 1, Giza 168, Misr 2, Giza171, Sids 14 and Shandweil 1) were sown in the first season 2019, and crossbreeding took place among them together to obtain 21 hybrids resulting from that process. During the second season2020 , parental genotypes and their 21 F1's were also cultivated, and both parents and their 21 F1's were evaluated in terms of the crop and its components under the natural conditions of the field experiment.

The obtained results revealed that half diallel bread crosses between the seven Egyptian affected significantly for days of maturity (DM) , spikes number /plant (S/P), 1000 kernel weight (KW), grain yield/ row (GY/P), biological yield/ row (BY/R), and Protein content (PC) .and the wheat cross (Sakha 94(P1) x Giza 168(P3)) recorded the highest means values of above-mentioned characters and gave the highest yield and its components under this study.

INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is one of the most important crops providing one-fifth of the total calories for the world's population according to Sehgal *et al.*, (2015).

Wheat is an edible grain, one of the oldest and most important cereal crops in Egypt. The production of wheat grains in Egypt is about 8.8 million tons in an area of about 3.2 million feddan. The production of wheat grains in the world is about 734.1 million tons in an area of about 514.3 million feddan (Food and Agricultural Organization 201*8*).

Wheat production can be increased through the development of productive genotypes/varieties for various agro-climatic conditions. One of the important breeding strategies is crossing the good general combining lines for grain yield and selecting transgressive segregants from its resulting segregating generations. Information, regarding

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the general and specific combining ability of wheat genotypes, is a prerequisite to launching a successful wheat-breeding programme as reported by Anwar *et al.*, (2011) .In wheat where the final objective of breeding is to obtain homozygous lines, the assessment of general combining ability is very important because it expresses the additive genes effect and the additive x additive interaction effect, which can be fixed in future generations, while the specific combining ability represents the dominant epistasis, (Joshi *et al.*, 2004)

Wheat production is likely to be increased by developing new varieties of the wider genetic base with improved characteristics in various environmental conditions. Various methods for the analysis of all possible crosses and genotypes were developed by earlier researchers as recorded by Kumar *et al.*, (2011)

Wheat growers developed new varieties with the desired genetic structure to overcome the consumption pressure of an ever-growing population with the intention of increasing the yield potential of wheat as showed by Rind *et al.*, (2019)

Grain yield is basically a complex trait being the consequence of several genes and their interaction in a particular environment. The main effort of the wheat breeder is the detection of genes and to merge them in a particular genotype using the most suitable combination. As the wheat is predominantly a self-pollinated crop and due to its autogamous nature it attains homozygosity at many loci as indicated by Ullah *et al.*, (2010)

Information about the general combining ability (GCA) and specific combining ability (SCA) in the breeding material is a prerequisite for launching an effective wheat breeding program. The diallel analysis is one of the breeding strategies for assessing the combined effects of the ability of genotypes, and also provides information about the genetic mechanisms controlling various traits as stated by Ahmad *et al.*, (2013)

The objective of this investigation was to study the yield and its components of some half diallel bread crosses.

MATERIALS AND METHODS

The experimental fieldwork of this investigation was carried out at Naguib Mahfouz village, Housh Eisa, El Behera Government, Egypt during 2018/2019 and 2019/2020 seasons. Based on the results of previous experiments conducted by the Wheat Research Department of the ARC, seven bread wheat (*Triticum aestivum, L.*) cultivars, showing yield and its components of some half diallel bread crosses were used as parents of this study (Table 1).

The seven genotypes presented in Table (1) were chosen as parents for this study were grown in 2018/2019 season at the field Naguib Mahfouz village, Housh Eisa, El Beheara, Egypt. All possible diallel crosses (excluding reciprocals) were made among the seven parents and grains of 21 direct F_1 straight crosses were obtained. Since the produced hybrid grains were not enough to start the evaluation experiment, the seven parents were repeatedly sown in 2018/2019 season in the same field at the field Naguib Mahfouz village, Housh Eisa, Elbehearah Government, Egypt of the same 21 F_1s` were produced in sufficient quantities. Grains of the seven parents were also increased in the same season (2019/2020).

In the second season, 2019/2020, the experiment was designed in a randomized complete block design (RCBD) with three replications. Each replicate consisted of 33 rows, 3 m. long and 30 cm in width. Apart from 15 cm between plants. Twenty grains were sown in each row. The eight parental genotypes and their 21 F1's were sown in the same place. Moreover, all the other treatments were kept constant for the whole experiment. All agricultural practices were conducted according to the Ministry of agriculture and land

reclamation recommendation The commercial names, source, cross name, and pedigree of the parents used in this study are presented in Table (1).

Table 1. Name and pedigree of seven Egyptian cultivars and lines of bread wheat used as parents in this study.

No	Genotype	Pedigree	Source
1	Sakha 94	Opata / Rayon// Kauz CMBW90Y31800-TOPM-3Y-010M-010M-010Y-1 OM-O15Y-OY-OAP-OS	Egypt
2	Misr 1	OASIS/SKAUZ//4*BCN/3/2*PASTOR CMSSOOYO11YO1881T-05OM-O3OY-O3OM-O3OWGY-33M-OY-OS	Egypt
3	Giza 168	MIL/BUC//Seri CM930468-M-OY-OM-2Y-OB	Egypt
4	Misr 2	SKAUZ / BAV92 CMSSOOYO1881T-O5OM-O3OY-O3OM-O3OWGY-O5OAP-OSD	Egypt
5	Giza 171	SAKHA 93/GEMMEIZA 9 S.6-1GZ-4GZ-1GZ-2GZ-0S	Egypt
6	Sids 14	Bow"s"/Vee"s"//Bow's'/Tsi/3/BANI SUEF 1 SD293-1SD-2SD-4SD-0SD	Egypt
7	Shandaweel 1	SITE/MO/4/NAC/TH.AC//3*PVN/3/MIRLO/BUC CMSS93B00567S-72Y-010M-010Y-010M-3Y-0M-0HTY-0SH	Egypt

The collected data were subjected to the normal analysis of variance of the randomized complete blocks design according to Snedecor and Cochran, (1989). The least significant was used at 5 and 1 % level of probability to test the differences among values. Genotypes degrees of freedom were partitioned into parents, crosses, and parents vs crosses (Table, 2).

Table 2. Analysis of variance for Modle l Method 2 expectation of mean square.

S.O. V	df	Expected mean square
Reps.	(B-1)	2
Genotypes	(G-1)	27
Parents(P)	(P-1)	6
Crosses(C)	(C-1)	20
P vs C		1
Error	(B-1) (G-1)	54
Total	BG-1	83

General (GCA) and specific (SCA) combining ability variances and effects were estimated for all studied traits under each irrigation regime according to Griffing, (1956)) Method II Model I where Table (3) shows the partitioning of genotype degrees of freedom into general (GCA) and specific (SCA) combining abilities for each cross. Analysis of the data was done with the Mstatic program package as stated by Burow and Coors, (1994).

    The heterosis values were estimated as the deviation of F1 value from the mid-parent and better parent mean values as suggested by Matzinger *et al.*, (1962).

S.O. V	D.F>	S. S	M.S	E.M. S
Genotypes	(g-1) = 24	Sg	M_G	
GCA	(p-1) = 7	Sp = M_g/ Me	M_g	$\delta^2_e + 2\delta^2_s + (n+2)\, \delta^2._i$
SCA	[p(p-1)]/2 = 28	Ss = Ms/ Me	Ms	$\delta^2_e + 2\delta^2_s$
Error	(r-1) (g-1) = 48	Se	Me	M^2e

RESULTS AND DISCUSSION

    Presented data in Table (3) showed the mean square of variance for bread wheat parents and their straight crosses of agronomic traits, yield, and yield components

    Highly significant differences were recorded for all studied genotypes of agronomic characters, yield and yield components among 2019/2020 season for days of maturity (DM), spikes number /plant (S/P), 1000 kernel weight (KW), grain yield/ row (GY/R), biological yield/ row (BY/R) and Protein content (PC). These findings agreed with Farooq *et al.*, (2010), Yao *et al.*, (2011), Khodadadi *et al.*, (2012), Khan, (2016), Khokhar *et al.*, (2019).

Table 3. Mean squares of days of maturity (DM), spikes number /plant (S/P), 1000 kernel weight(KW), grain yield/ row (GY/R), biological yield/ row (BY/R), and Protein content (PC). in wheat parents and F1's crosses at 2019/2020 season.

S.O. V	d.f	DM	S/P	1000 KW	GY/P	BY/P	PC
Blocks	(B-1) 2	1.48ns	.04 ns	7.09 ns	0.00ns	0.01ns	0.21 ns
Genotypes	(G-1) 27	3.20**	2.38 **	172.59**	0.03**	0.23**	2.13**
Parent	(p-1) 6	5.43**	1.43*	115.76**	0.01**	0.22**	1.63**
crosses	(c-1) 20	2.69**	2.75**	196.73**	0.03**	0.20**	2.37**
Parent versus crosses	1	0.00ns	0.67ns	30.59*	0.06**	0.75**	0.22**
GCA	6	4.42 **	2.38**	121.83 **	0.02**	0.35**	2.12 **
SCA	21	2.84 **	0.035 ns	187.08**	0.02**	0.18**	0.21 ns
Error	(B-1) (G-1) 54	0.92	0.52	6.85	0.00	0.03	0.38
Total	(B x G)-1 83			0.65	1.00	1.94	10.10
GCA/SCA	-	1.56	68.00	1000 KW	GY/P	BY/P	PC

N.S. = Not significant difference, * and ** = significant and highly significant difference at 0.05 and 0.01 probability.

    Recorded data at Table (4) cleared the mean performances of days of maturity (DM) (days), spikes number /plant (S/P), and 1000 kernel weight (KW) (g), grain yield/row (GY/R), biological yield/row (BY/R) and protein content (PC) for wheat parents and f1,s crosses at 2019/2020 season.

    Regarding the genotype Misr 2 (P4), recorded the maximum days of maturity (153.33days) whereas the genotype Giza 168(P3) was earlier parent where the value was (149.33days). Concerning, the cross (P2 X P5) revealed the late genotype from all studies

crosses where the value was (152.66 days) whereas there were nine crosses revealed the early maturity in days to maturity where the range was (148.66 to 150.00 days).

As mention before that, all genotypes differed significantly in all studied characters. It is obvious, that Giza 168(P3) and Shandweil 1 (P7) recorded the maximum spikes number /plant (8.33) whereas, the two genotypes parents Sakha 94(P1) and Misr 2(P4) gave the lower spikes number/plant where the value was (6.66).

On the other side, nine crosses (P1 X P2) (P1 X P3) (P1 X P5) (P1 X P7) (P2 X P6) (P3X P5) (P3 X P7) (P4 X P7) and (P6X P7) showed the highest values of spikes number / plant .These values were 7.66;8.33;8.33;7.66;8.00;8.33;8.00;8.66; and 8.66 (s/p),respectively without significant differences between them . In contrary, (P2 X P5) and (P5X P7) obtained the lowest values of spikes number / plant (5.66).

Regarding the 1000 kernels weight (g) for bread weight and f1,s crosses, Giza 171(P5) and sides 14(P6) attained the heaviest weight where were (61.16 g) and (60.83 g), respectively, without significant differences between them.With regard to bread, wheat crosses 6 crosses from 21 revealed the desirable 1000 k w ranged from 60.73 to 65.50 g. These crosses were(P1 X P3) (P1 X P5) (P2 X P5) (P2 X P7) (P3 X P6) and (P5X P6). So, these crosses are considered promise crosses in order to increase grain yield /plant and crop yield /Fadden.

All studied genotypes differed significantly in all studied characters, it is obvious to say the genotypes Misr 1(P2), Misr 2(P4), and Giza 171(P5) recorded the maximum grain yield/row where were (.99;.96 and .96 kg), respectively without significant differences between them .whereas the Shandweil 1 (P7) gave the minimum one, where the values were (.80 kg).

On the other side, the crosses (P3X P5) and (P2 X P3) revealed the highest values in all studies crosses for graining yield where were (1.07) and (1.06 kg). In the contrary the crosses (P1X P7) , (P2 X P5) , (P2 X P6) , (P3 X P4) , (P3 X P6) , (P3 X P7) , (P4 X P5) and (P5 X P7) gave the lowest row where were (0.74 ; 078 ; 0.77 ; 0.76 ; 0.79 ; 0.77 ; 0.76 and 0.78) respectively without significant differences between them.

Also, Misr 1(P2) recorded the maximum biological yield/row (3.10 kg) whereas the genotypes Giza 168(P3), Giza 171(P5), Sids 14(P6), and Shandweil 1 (P7) gave the minimum where the values were (2.40 kg) for all studied parents.Respecting the crosses (P1 X P2), (P1 X P3) and (P2X P3) revealed the highest values in all studies crosses for biological yield where were (2.70; 2.80 and 2.80 kg), on the contrary, the crosses (P4 X P5) and (P5X P7) obtained the lowest (2.00 kg).Protein content (%) for wheat parents and F1,s crosses at 2019/2020 season presented in Table (4). Each of Sakha 94(P1), Giza 168(P3), and Misr 2(P4) recorded the highest values of protein content (13.68,13.98and 13.27%), respectively, whereas the Sids 14(P6) gave the lowest one where it's value was (11.73%).

Concerning the bread wheat crosses, it was noticed that the 7 crosses from 21 revealed the highest protein contents without significant differences between them. These crosses were (P1X P6, 13.87%); (P1X P7, 13.97%); (P2X P4, 13.33%) (P3X P4, 14.06%); (P3X P7, 14.32%) (P4X P5, 14.28%) and (P4X P6, 13.36%).So, it can be improved the protein content in bread wheat thought introducing from these crosses in breeding wheat program.

These results are in the same trend as those obtained by Gallandt *et al.*, (2001), Padhar *et al.*, (2013; Singh *et al.*, (2014), Kumar *et al.*, (2015), Farhat and Darwish, (2016).

Table 4. Mean performance of days of maturity (DM) (days), spikes number /plant (S/P), and 1000 kernel weight (KW) (g), grain yield/row (GY/R), biological yield/row (BY/R) and Protein content (PC) in wheat parents and F1's crosses at 2019/2020 season.

Genotypes	DM (days)		S/P		1000 KW (g)		GY/P (g)		BY/P (g)		Pc %	
Sakha 94(P1)	150.66	cdef	6.66	defg	50.53	fghi	0.93	cdef	2.60	d	13.68	abcde
Misr 1(P2)	149.66	efgh	7.66	abcd	48.76	ghij	0.99	b	3.10	a	12.81	efgh
Giza 168(P3)	149.33	fgh	8.33	ab	52.46	efgh	0.92	ef	2.40	e	13.98	abc
Misr 2(P4)	153.33	a	6.66	defg	50.20	fghi	0.96	bcde	2.80	c	13.27	bcdef
Giza 171(P5)	149.66	efgh	7.33	bcde	61.16	bc	0.96	bcde	2.40	ef	12.85	efgh
sods 14(P6)	150.66	cdef	7.33	bcde	60.83	bc	0.89	fgh	2.40	e	11.73	i
Shandweil1(P7)	150.33	cdefg	8.33	ab	44.50	j	0.80	jkl	2.40	e	12.71	efghi
(P1 X P2)	149.00	Gh	7.66	abcd	51.93	efghi	0.90	fg	2.70	d	12.37	fghi
(P1 X P3)	150.00	defgh	8.33	ab	64.63	ab	0.97	bc	2.80	c	12.89	defgh
(P1 X P4)	151.33	bcd	7.33	bcde	56.10	de	0.84	ij	2.20	jkl	12.69	efghi
(P1 X P5)	149.66	efgh	8.33	ab	60.73	bc	0.86	ghi	2.30	ghijk	12.89	defgh
(P1 X P6)	151.33	bcd	7.33	bcde	44.83	j	0.85	hi	2.30	efghi	13.87	abcd
(P1 X P7)	151.66	bc	7.66	abcd	54.00	ef	0.74	m	2.40	ef	13.97	abc
(P2 X P3)	149.66	efgh	7.33	bcde	40.13	k	1.06	a	2.80	a	11.72	i
(P2 X P4)	149.66	efgh	6.33	efg	55.30	e	0.97	bcd	3.00	b	13.33	abcdef
(P2 X P5)	152.66	ab	5.66	g	64.53	ab	0.78	lm	2.20	ijk	12.21	ghi
(P2 X P6)	150.00	defgh	8.00	abc	52.66	efg	0.77	lm	2.30	hijk	13.27	bcdef
(P2 X P7)	151.00	cde	6.66	defg	61.70	abc	0.84	ij	2.40	ef	11.75	i
(P3 X P4)	151.00	cde	6.66	defg	47.77	ij	0.76	lm	2.20	kl	14.06	abc
(P3 X P5)	148.66	h	8.33	ab	48.30	hij	1.07	a	2.80	a	12.00	hi
(P3 X P6)	151.00	cde	7.00	cdef	64.07	abc	0.79	kl	2.40	efg	12.02	hi
(P3 X P7)	151.00	Cde	8.00	abc	56.13	de	0.77	lm	2.10	lm	14.32	a
(P4 X P5)	150.00	defgh	6.00	fg	48.73	ghij	0.76	lm	2.00	m	14.28	ab
(P4 X P6)	150.66	cdef	6.66	defg	37.16	k	0.83	ijk	2.30	fghij	13.36	abcdef
(P4 X P7)	151.33	bcd	8.66	a	52.63	efg	0.86	ghi	2.40	efgh	13.06	cdefg
(P5 X P6)	150.33	cdefg	6.33	efg	65.50	a	0.92	def	2.40	ef	13.11	cdefg
(P5 X P7)	150.33	cdefg	5.66	g	47.90	ij	0.78	lm	2.00	m	11.71	i
(P6 X P7)	150.00	defgh	8.66	a	59.90	cd	0.93	def	2.40	e	11.73	i
LSD at 0.05	1.58.00		1.18		4.28		0.05		0.11		1.01	

Means within the same letter within each column are not significant differences at 0.05 level of probability

Heterosis is the better performance of a hybrid relative to the parents and is the outcome of the genetic and phenotypic variation. The heterosis values were measured based on mid-parents (MP) and better parents (BP) values. Heterosis is expressed as the percentage deviation of F1 performance from its mid parent's average value and the deviation of F1 performance from the better parent for agronomic characters, yield and yield component are presented in Table (5). Significant positive and negative heterotic effects would be of interest for agronomic characters yield component.

For days of maturity, it could be noticed that four crosses (P1 X P2), (P2 X P4), (P4 X P5), and (P4 X P6) gave the desirable negative and significant values of heterosis relative mid- parents, these values were -0.78, -1.21, -0.99 and 0.88 %, respectively.It's interesting to say that nine crosses from 21 crosses recorded the desirable and highly significant values of heterosis relative mid- parents for spikes number /plant and ranged from 4.29% for the cross (P1X P6) to 18.57% for the cross (P1 X P5).

Respecting, 1000 kernel weight, 13 crosses from 21 crosses recorded the desirable positive and highly significant values of heterosis relative mid- parents and ranged from 4.60% for the cross (P1 X P2) to 32.31% for the cross (P2 X P7). With regard to grain yield/ row, there were four crosses from 21 crosses that revealed the positive, highly significant and desirable values for heterosis relative mid-parents i.e. (P1 X P3) , (P2 X P3), (P3 X P5), and (P6 X 7). These crosses showed values (5.42, 11.19, 14.18, and 9.88%), respectively.

For biological yield/row, both crosses (P1 X P3) and (P3 X P5) recorded the highest, positive, and highly significant values of heterosis relative mid-parents (10.17 and 14.64 %), respectively.It's obvious to reveal that 9 crosses from 21 crosses recorded the desirable, significant, and highly significant values of heterosis relative mid-parents for protein content and ranged from 2.20% for the cross (P2X P4) to 9.31% for the cross (P4 X P5).

Table 5. Estimates of heterosis (%) relative to mid-parents for days of maturity (DM), spikes number /plant (S/P), 1000 kernel weight (KW), grain yield/ row (GY/R), biological yield/ row (BY/R), and Protein content (PC) in wheat parents and F1's crosses at 2019/2020 season.

Crosses	DM	S/P	1000 KW	GY/P	BY/P	PC
(P1 X P2)	-0.78	6.94	4.60	-5.57	-7.04	-6.58
(P1 X P3)	0.00	10.67	25.50	5.42	10.17	-6.84
(P1 X P4)	-0.44	8.96	11.38	-11.11	-19.51	-5.87
(P1 X P5)	-0.33	18.57	8.74	-8.83	-10.27	-2.80
(P1 X P6)	0.44	4.29	-19.49	-6.42	-8.30	9.16
(P1 X P7)	0.78	2.67	13.64	-14.12	-5.93	5.90
(P2 X P3)	0.11	-8.75	-20.71	11.19	0.30	-12.48
(P2 X P4)	-1.21	-12.50	11.75	-0.85	-0.34	2.20
(P2 X P5)	2.00	-24.00	17.40	-19.86	-18.23	-4.78
(P2 X P6)	-0.11	6.67	-3.89	-18.29	-18.31	8.12
(P2 X P7)	0.67	-16.25	32.31	-5.79	-13.11	-7.92
(P3 X P4)	-0.22	-10.67	-6.95	-19.65	-18.07	3.14
(P3 X P5)	-0.56	6.41	-14.99	14.18	14.64	-10.57
(P3 X P6)	0.67	-10.26	13.09	-12.71	-2.34	-6.54
(P3 X P7)	0.78	-3.61	15.78	-10.68	-12.69	7.28
(P4 X P5)	-0.99	-14.29	-12.48	-20.97	-23.28	9.31
(P4 X P6)	-0.88	-4.29	-33.05	-10.43	-13.09	6.82
(P4 X P7)	-0.33	16.00	11.16	-2.65	-10.82	0.56
(P5 X P6)	0.33	-13.70	7.38	-0.54	-0.62	6.64
(P5 X P7)	0.22	-26.92	-9.34	-11.57	-15.71	-8.32
(P6 X P7)	-0.33	11.54	13.73	9.88	0.00	-3.98
Average	-0.01	-2.50	3.12	-6.64	-8.22	-0.84
LSD at 0.05	0.52	1.04	3.79	2.26	4.05	1.89
LSD at 0.01	0.64	1.39	5.11	4.35	6.06	2.20

Results in Table (6) cleared that the heterosis (%) relative to the better parent for plant height (PH), days to heading (DH), days of maturity (DM), kernels number /spike (K/S)in wheat parents and F1's crosses at 2019/2020 season.For days of maturity, it could be noticed that the cross (P3 X P7) was the only cross that recorded the desirable, negative and highly significant values of heterosis relative better parent, the value was -1.52%.It's interesting to say that both crosses (P1 X P4) and (P1X P5) recorded the highest, positive and highly significant values of heterosis relative to better parents (8.96 and 13.70 %), respectively, for spikes number /plant.

Respecting 1000 kernel weight, ten crosses from 21 crosses recorded the desirable and highly significant values of heterosis relative better parent and ranged from 4.85% for the cross (P4 X P7) to 26.52% for the cross (P2 X P7). With regard to grain yield/ row, three crosses from 21crosses revealed the positive, highly significant, and desirable values for heterosis relative better parent i.e. (P1 X P3), (P2 X P3) and (P3 X P5). These crosses showed values (5.04, 7.43, and 11.81%), respectively.

For biological yield/row, both crosses (P1 X P3) and (P3 X P5) recorded the highest, positive, and highly significant values of heterosis relative better parent (5.44 and 14.25 %) respectively.For Protein content, it could be noticed that the cross (P4 X P5) was the only

cross that recorded the desirable, positive and highly significant values of heterosis relative better parent, the value was 7.56%. These results were in a line with those Hussain *et al.*, (2007), Erkul *et al.*, (2010), Gite *et al.*, (2014), El-Hosary and Nour El-Deen, (2015).

Table 6. Estimates of heterosis (%) relative to the better parent for plant height(PH), days to heading (DH), days of maturity (DM), spikes number /plant (S/P), and kernels number /spike (K/S) in wheat parents and F1's crosses at 2019/2020 season.

Crosses	DM	S/P	1000 KW	GY/P	PC
(P1 X P2)	-0.45	0.00	2.77	-8.45	-3.38
(P1 X P3)	0.45	0.00	23.19	5.04	-7.84
(P1 X P4)	0.44	8.96	11.02	-12.80	-7.28
(P1 X P5)	0.00	13.70	-0.71	-10.42	0.36
(P1 X P6)	0.44	0.00	-26.30	-8.27	1.39
(P1 X P7)	0.89	-7.23	6.86	-20.14	2.12
(P2 X P3)	0.22	-12.05	-23.51	7.43	-16.16
(P2 X P4)	0.00	-18.18	10.16	-2.03	0.40
(P2 X P5)	2.00	-25.97	5.50	-20.95	-4.93
(P2 X P6)	0.22	3.90	-13.42	-22.30	3.59
(P2 X P7)	0.89	-19.28	26.52	-14.86	-8.27
(P3 X P4)	1.12	-19.28	-8.96	-21.45	0.52
(P3 X P5)	-0.45	0.00	-21.04	11.81	-14.20
(P3 X P6)	1.12	-15.66	5.32	-14.13	-14.06
(P3 X P7)	-1.52	-3.61	6.99	-16.67	2.38
(P4 X P5)	0.22	-17.81	-20.33	-21.11	7.56
(P4 X P6)	0.00	-8.22	-38.90	-13.84	0.63
(P4 X P7)	0.67	4.82	4.85	-11.07	-1.58
(P5 X P6)	0.67	-13.70	7.08	-4.17	2.02
(P5 X P7)	0.45	-31.33	-21.69	-19.10	-8.82
(P6 X P7)	-0.22	4.82	-1.53	4.12	0.00
Average	0.34	-7.43	-3.15	-10.16	-3.12
LSD 0.05	0.14	4.85	3.10	5.22	3.73
LSD 0.01	0.53	7.14	4.17	8.29	5.98

The analysis of variance for combining ability as outlined by Griffing (1956) method 2 model 1 in the data for the studied agronomic, yield and its component characters are shown in Tables (7and 8). The general combing ability revealed highly significant variations. Specific combining ability revealed significant variations for all the studied characters, as shown in Tables (3 and 4).

Combining ability implies the capacity of a parent to produce progenies when crossed with another parent. An estimate of GCA effects (gi) for individual parental genotype in each trait of yield and its components data are presented in Table (7) general combining ability effects computed here were found to differ significantly from zero in all cases. Parental genotypes which expressed significant positive desirable (gi) effects for these characters could be considered as an excellent parent in breeding programs. Combining ability implies the capacity of a parent to produce progenies when crossed with another parent.For days of maturity, the wheat parent genotype Giza 168(P3) was the only genotype that recorded the desirable, negative, and highly significant values of GCA, the value was -0.455 for days to maturity. So, these negative and significant values indicated that may use these genotypes as good combiners to improve the days of maturity. It's interesting to say the wheat parent genotype Giza 168(P3) was the only genotype that recorded the desirable, positive, and highly significant values of GCA, the value was 0.418. So, these positive and

significant values indicated that may be using this genotype as a good combiner to improve the spikes number /plant.

With regard to 1000 kernel weight, it could be said that there two wheat parent genotypes gave positive and highly significant values of GCA. These genotypes were in Giza 171(P5) (3.174) and sides 14(P6) (1.815) so, these positive and significant values indicated that may be used these genotypes as good combiners to improve the 1000 kernel weight. On the other side, the remain wheat parents revealed non-significant negative GCA values except Misr 2(P4) reach a significant level.

For grain yield/ row, the wheat parent genotype Misr 1(P2) was the only genotype that recorded the desirable, positive, and highly significant values of GCA, the value was 0.215. These positive and highly significant values of GCA revealed that Misr 1(P2) may be a good combiner to improve the grain yield/ row.It's interesting to say that the wheat parent genotypes Sakha 94(P1), Misr 1(P2), Giza 168(P3) and (Giza 171(P5) were the genotypes that recorded positive and non-significant values of GCA for biological yield.

Respecting protein content, it could be said that both wheat parent genotyps Sakha 94 (P1) and Misr 2(P4) gave positive and significant values of GCA, the values were 0.303 for Sakha 94 (P1) and .443 for Misr 2 (P4). So, these positive and significant values indicated that may be used these genotypes as good combiners to improve the protein content. on the other side, the remain wheat parents revealed significant, non-significant, and negative GCA values.

Table 7. Estimates of general combining ability effects of wheat parents for plant height(PH), days to heading (DH), days of maturity (DM), spikes number /plant (S/P), and kernels number /spike (K/S) in wheat parents and F1's crosses at 2019/2020 season.

Parents	DM	S/P	1000 KW	GY/P	BY/P	PC
Sakha 94(P1)	0.026	0.159	0.426	0.04	0.003	0.303
Misr 1(P2)	-0.307	-0.175	-0.63	0.215	0.033	-0.34
Giza 168(P3)	-0.455	0.418	-0.389	0.024	0.03	0.182
Misr 2(P4)	0.73	-0.397	-3.485	0.016	-0.006	0.443
Giza 171(P5)	-0.307	-0.397	3.174	-0.116	0.011	-0.159
sids 14(P6)	0.101	0.011	1.815	-0.07	-0.015	-0.278
Shandweil 1 (P7)	0.212	0.381	-0.911	-0.109	-0.055	-0.152
SE (g$_i$)	0.029	0.016	0.218	0.001	0.001	0.012
SE (g$_i$-g$_j$)	0.068	0.038	0.508	0.002	0.001	0.029
LSD at 0.05	0.343	0.257	0.938	0.064	0.0844	0.222
LSD at 0.01	0.456	0.342	1.245	0.084	0.0636	0.295
CD at 0.05	2.676	3.069	4.025	3.550	4.454	3.140

NS= Not significant difference, *, and **= significant and highly significant difference at 0.05 and 0.01 probability levels of probability, respectively.

Recorded data in Table (8) cleared the estimates of specific combining ability effects of F1's wheat crosses for days of maturity (DM), spikes number /plant (S/P), 1000 kernel weight (KW), grain yield/ row (GY/R), biological yield/ row (BY/R) and protein content in wheat parents and F1's crosses at 2019/2020 season.For days of maturity, the crosses (P1 X P2) (P1 X P5) (P2 X P4) (P3 X P5) (P4 X P5) (P4 X P6) (P6 X P7) recorded the desirable, negative and highly significant values of GCA , the values (-1.231 ; -0.565 ; -1.269 ; -1.083 ; -0.935 ; -0.676 ; -0.824), respectively . So, these negative and significant values indicated that may be used these crosses to improve the days of maturity.Six crosses from 21 crosses recorded the desirable, positive, and significant values of SCA and ranged from 0.361 for the cross

(P1 X P2) to 1.361 for the cross (P4 X P7). So, these positive and significant values indicated that may be used these crosses to improve the spikes number /plant.

　　With concern to 1000 kernel weight, it could be said that 11 crosses from 21 crosses recorded the desirable, positive and significant values of SCA and ranged from 3.346 for the cross (P4 X P7) to 10.913 for the cross (P1 X P3). So, these positive and highly significant values indicated that may be used these crosses to improve the 1000 kernel weight.

　　For grain yield/ row, it could be noticed that there five crosses from 21 crosses recorded the desirable and significant values of SCA. These crosses were (P1 X P3) (0.276), (P2 X P4) (0.289), (P3 X P5) (0.404), (P5X P6) (0.140), and (P6X P7) (0.163) . So, these positive and significant values indicated that may be used these crosses to improve the grain yield/ row.For biological yield/ row it could be said that six crosses from 21 crosses recorded the desirable, positive and significant values of SCA and ranged from .050 for the cross (P5 X P6) to 0.159 for the cross (P3 X P5). So, these positive and significant values indicated that may be used these crosses as good combiners to improve biological yield.

　　With concern to the (PC) it's interesting to reveal that five crosses (P1 X P6), (P1 X P7), (P2 X P6), (P3 X P7), and (P4 X P5) were the crosses that recorded the desirable, positive and significant values of SCA, the values were 0.933; 0.906; 0.969; 1.371; 1.077, respectively. So, these positive and significant values indicated that may be used these crosses as good combiners to improve the Protein content. These results were in the same direction as those obtained by Malik *et al.*, (2005), Farooq *et al.*, (2006), Hasnain *et al.*, (2006), Hassan *et al.*, (2007), Çifci and Yagdi, (2010), Yao *et al.*, (2011), Ismail, (2015; Nagar *et al.*, (2018), H Ayoob, (2020).

Table 8. Estimates of specific combining ability effects of F1's wheat crosses for days of maturity (DM), spikes number /plant (S/P), (K/S)1000 kernel weight(KW), of grain yield/ row (GY/R), biological yield/ row (BY/R) and Protein content (pc) in wheat parents and F1's crosses at 2019/2020 season.

Crosses	DM	S/P	1000 KW	GY/R	BY/R	PC
(P1 X P2)	-1.231	0.361	-1.546	-0.032	-0.007	-0.505
(P1 X P3)	-0.083	0.435	10.913	0.276	0.067	-0.514
(P1 X P4)	0.065	0.250	5.476	-0.289	-0.031	-0.975
(P1 X P5)	-0.565	1.250	3.450	-0.107	-0.028	-0.166
(P1 X P6)	0.694	-0.157	-11.091	-0.090	-0.013	0.933
(P1 X P7)	0.917	-0.194	0.802	0.009	-0.082	0.906
(P2 X P3)	-0.083	-0.231	-12.531	0.081	0.123	-1.034
(P2 X P4)	-1.269	-0.417	5.731	0.289	0.066	0.308
(P2 X P5)	2.769	-1.083	8.306	-0.296	-0.138	-0.203
(P2 X P6)	-0.306	0.843	-2.202	-0.332	-0.126	0.969
(P2 X P7)	0.583	-0.861	9.557	-0.149	-0.012	-0.677
(P3 X P4)	0.213	-0.676	-2.043	-0.327	-0.141	0.516
(P3 X P5)	-1.083	0.991	-8.169	0.404	0.159	-0.942
(P3 X P6)	0.843	-0.750	8.957	-0.034	-0.099	-0.803
(P3 X P7)	0.731	-0.120	3.750	-0.245	-0.082	1.371
(P4 X P5)	-0.935	-0.528	-4.639	-0.330	-0.119	1.077
(P4 X P6)	-0.676	-0.269	-14.846	-0.096	-0.023	0.276
(P4 X P7)	-0.120	1.361	3.346	0.003	0.044	-0.144
(P5 X P6)	0.361	-0.602	6.828	0.140	0.050	0.628
(P5 X P7)	-0.083	-1.639	-8.046	-0.184	-0.053	-0.892
(P6 X P7)	-0.824	0.954	5.313	0.163	0.122	-0.752
SE (SIJ)	0.247	0.139	1.840	0.009	0.000	0.103
SE (SIJ-SIK)	0.546	0.307	4.062	0.020	0.001	0.228
LSD 0.05	0.999	0.749	2.727	0.190	0.028	0.646
LSD 0.01	1.328	0.995	3.622	0.252	0.038	0.858
CD 0.05	2.599	2.807	4.480	3.027	4.583	2.964

N.S. = Not significant difference,* and **= significant and highly significant difference at 0.05 and 0.01 probability levels of probability, respectively.

Conclusion

It can be concluded that using the hybrid (Sakha 94 (P1) x Giza 168 (P3)) achieved the highest values of the yield and its components under the conditions of the study

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ARABIC SUMMARY

المحصول ومكوناته لبعض الهجن التبادلية لقمح الخبز

**محمد أحمد عبد الجواد نصار ، محمد نجيب البنا ، جوهرة عبد السلام إسماعيل الصردي ،
محمد السيد أبو اليزيد نوفل**

قسم الأنتاج النباتي – كلية الزراعة سابا باشا – جامعة الأسكندرية – مصر

أقيمت تجربتان حقليتان بمزرعة خاصة بمنطقة حوش عيسي – البحيرة – مصر خلال موسمى الزراعة 2019 و 2020 لدراسة المحصول ومكوناته لبعض الهجن التبادلية لقمح الخبز على سبعة أصناف من القمح المصري . القطاعات كاملة العشوئية (RCBD) بثلاثة مكررات. يتكون كل مكرر من 33 صفًا ، 3 م. طول و 30 سم عرض. بمسافة 15 سم. بين النباتات. تم زرع عشرين حبة في كل صف.

حيث تم زراعة 7 طرز وراثية أبوية (سخا 94 ، مصر 1 ، جيزة 168 ، مصر 2 ، جيزة 171 ، سدس 14 وشندويل 1) في الموسم الأول 2019 ، وتم التهجين بينهم للحصول على 21 هجين ناتج عن تلك العملية. خلال الموسم الثاني 2020 ، تم أيضًا زراعة الأنماط الجينية الأبوية و 21 هجين ، وتم تقييم كلا الأباء و الهجن من حيث المحصول ومكوناته في ظل الظروف الطبيعية للتجربة.

ولخصت أهم النتائج فيما يلي:

- أظهرت الهجن التبادلية لقمح الخبز تأثير معنوي على عدد الأيام حتي النضج و عددالسنابل لكل نبات ومحصول الحبوب و المحصول البيولوجي ومحتوي الحبوب من البروتين ، حيث أن هجين القمح المصري (سخا 94 x جيزة 186) أعطي أعلى قيم لمعطم الصفات المذكورة أعلى خلال موسمي الزراعة2019 و 2020.

- وجد أن هناك اختلاف معنوي بين السبعة أصناف من القمح المصري فى معظم الصفات المدروسة خلال موسمي الدراسة 2019 ، و 2020 ، حيث هجين القمح المصري (سخا 94 x جيزة 186) تفوق على باقي الهجن فى معظم الصفات كما سجل أعلى القيم خلال موسمي الزراعة

- كان تأثير التهجين بين الأصناف السبعة معنوياً على عدد الأيام حتي النضج و عددالسنابل لكل نبات ومحصول الحبوب و المحصول البيولوجي ومحتوي الحبوب من البروتين ، خلال موسمى الزراعة. حيث حقق زراعة الهجين (سخا 94 x جيزة 186) أعلى قيم لهذه الصفات.

التوصية:

من النتائج المتحصل عليها يمكن التوصية بزراعة هجين القمح المصري (سخا 94 x جيزة 186) حيث حقق هذا الهجين أعلى قيم لصفات المحصول ومكوناته تحت ظروف الأراضى الجديدة بمنطقة حوش عيسي – محافظة البحيرة .