

# Heterosis and the combining ability of a two-line system in hybrid wheat production as a hybrid wheat technology in Egypt

Sedhom A.M. Abdelkhalik \* , Adel A. Hagrass, Khaled E. Ragab

**Address:**

Wheat Research Department, Field Crops Research Institute (FCRI), Agricultural Research Centre, Giza, Egypt

\*Corresponding author: **Sedhom A. M. Abdelkhalik:** [sedhom\\_aiaad@yahoo.com](mailto:sedhom_aiaad@yahoo.com)

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## ABSTRACT

This study was carried out at the experimental farm of Sakha Agricultural Research Station, ARC, Egypt, to identify the best parents with high combining ability and superior hybrid cross combinations under Egyptian conditions. Three thermo-photosensitive genic male sterile (TPSGMS) lines as female parents and 49 restorer lines as males were crossed according to the line tester hybridization method. The ratio of general combining ability (GCA) to specific combining ability (SCA) variances showed values less than unity for all studied traits, indicating predominantly non-additive gene effects in controlling their inheritance. The GCA values for sterile line S1 were higher than those of lines S2 and S3 in seven out of ten characters. The restorer line R16 and both lines R31 and R34 had a significantly positive GCA in eight and seven characters, respectively. The crosses S1/R8 and S3/R42 had the highest positive SCA values in three characters, including grain yield. In this study, heterosis over the Sakha 95 check variety reached 80.63, 71.27, 55.16, 26.07, and 24.49% for KS, SW, GY, TKW, and SP-1, respectively. The crosses S2/R34 and S1/R16 showed the highest significant positive heterosis estimates (55.16 and 54.43%, respectively) over the standard check for grain yield. Also, the crosses of S1/R16 and S1/R37 had the highest significant positive heterosis estimates over both the better parent (65.81 and 46.64%, respectively) and the mid parent (70.75 and 52.55%, respectively) for grain yield. The results showed a significant increase in heterosis over Sakha 95 check in twelve hybrids, and we recommend evaluating these hybrids in multiplications representing environmental conditions to benefit from them in raising wheat productivity in wide areas in Egypt.

**Keywords:** Hybrid wheat, TPSGMS, Combining ability, Heterosis

## INTRODUCTION

Wheat (*Triticum aestivum* L.) is the most widely consumed and grown cereal food crop in the world. The current annual production level is more than 769 million tons from a total production area of about 222 million hectares (Foreign Agricultural Service/USA, 2022). By the year 2050, the world population is estimated to be 9 billion and the demand for wheat will exceed 900 million tons (Tadesse *et al.*, 2013). The Egyptian wheat production is not enough for domestic local consumption and the gap between production and consumption reached about 50% (Kishk *et al.*, 2019). Egypt's wheat production for the marketing year 2021-22 was 9.8 million tons while the total country's consumption of wheat is 21 million tons. Therefore, Egypt's wheat imports for the 2021-22 market year are forecast at 11 million tons (Foreign Agricultural Service / USDA Economics, Statistics and Market Information System., 2022). Increasing total wheat production could be possible via increasing the wheat cultivated area but there are many challenges, especially water shortages. Therefore, developing new cultivars having high yield potential is the best and most available option to decrease the gap. Hybrid wheat is being recognized as a preferred approach to improve wheat yield (Whitford *et al.*, 2013). The application of hybrid wheat will greatly increase yield production and make a significant contribution to food security in the increasing of population increase, climate change-associated threats and diminishing natural resources (Longin *et al.*, 2012). During 2009 to 2012, the new wheat hybrids were grown on about 66,700 hectares for demonstration with an average yield increase of 15.7 % in 11 provinces in China (Zhao, 2013). Heterosis use in wheat is regarded as one of the most efficient methods for increasing yield, improving stress tolerance, and fostering stability by enriching the genetic base of wheat varieties (Murai and Tsunewaki, 1993; Kempe *et al.*, 2014; Mühleisen *et al.*, 2014; Singh *et al.*, 2015; Tucker *et al.*, 2017; Wang *et al.*, 2017; Yang *et al.*, 2017; Abdelkhalik *et al.*, 2019; Li *et al.*, 2020). Male sterility is an important characteristic in hybrid seed development for self-pollinated crops such as wheat and rice. In hybrid wheat seed production, Cytoplasmic Male Sterile lines (CMS) or thermos-photo sensitive genic male sterile (TPSGMS) lines are recommended as female parents. One of the novel approaches for utilizing wheat heterosis is the "two-line"

strategy using the TPSGMS line. The expression of the TPSGMS character is influenced by both hereditary and environmental factors (temperature and daylight). Low-temperature and short-day induced sterility, as well as high-temperature and long-day induced fertility, characterize the TPSGMS lineages. As a result, this strategy does not require maintainer lines, a large restorer resource, or complicated seed manufacturing procedures (Ji *et al.*, 2004; Song *et al.*, 2005; Zhao, 2010). Between 2002 and 2018, 20 hybrid wheat varieties were released in China (Xiao, 2014), 14 of which were produced using a TPSGMS-based two-line system, with yield increases of 10- 15%, particularly on marginal soils. (Xiao, 2014 and Wang, 2019). Hybrid varieties performed much better than local inbred cultivars in yield, drought tolerance and fertilizer input (Chen, 2015). The knowledge of combining ability influencing yield and its components is useful to assess differences among the genotypes and also, elucidate the nature and magnitude of gene actions involved (Salgotra *et al.*, 2009; Fasahat *et al.*, 2016). Information of general and specific combining abilities influencing yield and its components has become increasingly important for plant breeders to select appropriate parents while developing hybrids (Rasheda *et al.*, 2014). Line x tester analysis is one of the most powerful tools for predicting the general combining ability of parents and selecting suitable parents and crosses with high specific combining ability (Saeed *et al.*, 2001; Rashid *et al.*, 2007; Krystkowiak *et al.*, 2008; Jain and Sastry, 2012). Thus, the main goal of hybrid breeding is to systematically exploit heterosis. The heterosis of a hybrid is expected to increase with the genetic divergence between its parents (Melchinger, 1999). This study, thus, aimed to identify desirable wheat germplasm for superior hybrid combinations and assess the grain yield superiority of the best wheat crosses.

## MATERIALS AND METHODS

The present investigation was conducted on the Experimental Farm of Sakha Agricultural Research Station, ARC, Kafrelsheikh, Egypt, during the two wheat growing seasons, 2019/2020 and 2020/2021. The geographical position of the station is 31° 5' N latitude, 30° 56' E longitude and 7 m above sea level, in North Delta, Egypt.

### Plant materials:

Three sterile TPSGMS lines (S1, S2 and S3 as lines) and 49 restorer elite and yellow rust resistance bread wheat genotypes (R1 to R49 as a testers) from Sakha Crossing Block (SCB), Wheat Research Program, Field Crops Research Institute, ARC were used in this study. The cross name and selection history of the restorer line are presented in Supplementary Table S1. In March 2020, the three TPSGMS lines as female and 49 restorer genotypes as male were crossed to produce 147 wheat crosses according to line x tester matting design developed by Kempthorne (1957).

### Field experiment:

The yield evaluation trial was conducted during the 2020/2021 growing season. In the November 2020 season, parents (males and females) and their 147 F<sub>1</sub>s were sown on the field in triplicate in a randomized complete block pattern. Each genotype was cultivated in a single row that was 3 m long and 30 cm apart, with plants spaced 20 cm apart. A protective row around the experiment. All of the recommended cultural practices for wheat production in the Delta region were implemented on time.

### Recorded Data:

Data of ten biometrical traits including the number of days to heading (DH), number of days to maturity (DM), grain filling period (GFP), grain filling rate (GFR, gday<sup>-1</sup> plant<sup>-1</sup>), plant height (PH, cm), number of spikes per plant (SP<sup>-1</sup>), number of kernels per spike (KS<sup>-1</sup>), spike grain weight (SW, g), thousand kernel weight (TKW, g), and grain yield per plant (GY, g) were recorded. The sterile line grain yield is the outcrossing.

### Statistical analysis:

All studied characters were statistically analyzed on a plot mean basis according to Steel and Torrie (1980) to test the significance of differences among the 199 genotypes. Mean squares for genotypes (parents and F<sub>1</sub>s) were partitioned into parents, crosses and parents' vs crosses (Kearsey and Pooni, 1996). Line x tester analysis was performed for all the studied characters. Combining ability (CA) and gene effects were studied following Singh and Chaudhary (1985). The t-test was used to test whether CA effects were different from zero. These analyses were done using Excel and Agrobases 99 computer program (Anonymous, 1999).

### Heterosis estimates:

Generally, the expression of increased vigor of the F<sub>1</sub> hybrid over its parents is called heterosis as proposed by Mather (1949) and Mather and Jinks (1982). However, the following three approaches are usually used for estimation of heterosis:

- 1- Mid-parent heterosis or heterosis over the mean parents (MP). The amount of heterosis as proposed by Mather (1949) and Mather and Jinks (1982) was determined as the increase of the F<sub>1</sub> hybrid means over the average of its two parents as follows: MP % = [(F<sub>1</sub> - MP) / MP] × 100.
- 2- Heterobeltiosis or heterosis over the better parent (BP). The heterosis of an individual cross was

determined as the increase of the F<sub>1</sub> hybrid means over its better parent, as follows: BP % = [(F<sub>1</sub> - BP) / BP] × 100.

3- Standard heterosis or heterosis over the best check cultivar (SH). Sakha 95 was used as the best check. The percentage of F<sub>1</sub> hybrids increase or decrease over the best check was calculated to estimate possible heterotic effects on the above-mentioned parent (Fonseca and Patterson, 1968) as follows: SH% = [(F<sub>1</sub> - SH) / SH] × 100.

LSD values were calculated to test the significance of the heterotic effects over MP, BP and SH according to the formula suggested by Wynne *et al.* (1970).

## RESULTS

### Analyses of variance:

For each attribute under study, the genotypes (parents and hybrids) differed significantly in the analysis of variance (Table 1). For most of the qualities under study, parents and crossings mean squares were extremely significant, showing the diversity of the parents for these traits and the possibility that these diversities could be passed on to the progeny. Except for KS<sup>-1</sup> and GY, all characters have notable variances between the parents and crossovers.

Mean squares of lines, testers, and their interactions were highly significant for all traits under study, indicating that lines and testers significantly contributed to the variance components of general combining ability (GCA) and hybrids significantly contributed to the variance components of specific combining ability (SCA). The populations' GCA and SCA were computed. For all examined qualities, the ratio of GCA to SCA variance estimates was less than unity, indicating that the inheritance of these traits was governed mostly by non-additive gene effects.

**Table 1.** Mean squares of ten agronomic characters in wheat Line × Tester analysis.

S.O.V	d.f	DH	DM	GFP	GFR	PH	SP <sup>-1</sup>	KS <sup>-1</sup>	SW	TKW	GY
Reps	2	8.33	71.42	7.29	0.0018	62.69	13.59	57.2	0.42	10.76	27.12
Genotypes	198	19.8**	33.78**	39.07**	0.0708**	116.2**	15.47**	359.57**	1.275**	72.47**	265.13**
Parents (P)	51	25.41**	28.85**	26.46**	0.0499**	140.7**	5.82*	126.05**	0.468**	48.9**	154.42**
Crosses (C)	146	17.81**	33.59**	42.65**	0.0784ns	102.5**	15.41**	442.59**	1.387**	52.33**	305.51**
P vs C	1	25.25**	312.52**	160.1**	0.0415*	868.8**	516.18**	148.73ns	26.089**	4215**	15.67
Lines (L)	2	165.59**	7.79**	117.23**	0.6987**	2387.8**	52.86**	5012.16**	21.842**	128.05**	2712.03**
Testers (T)	48	26.95**	65.57**	76.64**	0.1181**	138.4**	23.88**	487.38**	1.819**	85.11**	512.84**
L × T	96	10.16**	18.14**	24.1**	0.0456**	3552.1**	10.39**	324.99**	0.745**	34.36**	151.71**
Error	396	0.5202	0.3295	0.7022	0.0196	8.396	4.4129	70.1791	0.2626	15.9608	66.7867
GCA		0.0308	0.0621	0.0746	0.0001	0.2636	0.0202	0.473	0.0026	0.0723	0.6186
SCA		3.208	5.9483	7.7696	0.0082	9.7174	2.1825	82.2234	0.1477	5.0217	27.0528
GCA/SCA var. ratio		0.0096	0.0104	0.0096	0.0122	0.02712	0.0093	0.0058	0.0176	0.0144	0.0229

ns; not significant, \* and \*\*; significant differences at 5% and 1% levels of probability, respectively. DH; days to heading, DM; days to maturity, GFP; grain filling period, GFR; grain filling rate, PH; plant height, SP<sup>-1</sup>; spikes plant<sup>-1</sup>, KS<sup>-1</sup>; kernel spike<sup>-1</sup>, SW; spike grain weight, TKW; thousand kernel weight and GY; grain yield plant<sup>-1</sup>. GCA; general combining ability and SCA; specific combining ability.

### Contribution of lines, testers, and their interactions

The proportional contribution of lines, testers, and their interactions to total variances for the studied traits revealed that maximum contribution was due to tester followed by line × tester, for all traits except KS<sup>-1</sup> (Table 2).

**Table 2.** Proportional contribution of lines, testers, and their interactions to total variance for the ten studied traits.

Genotype	DH	DM	GFP	GFR	PH	SP <sup>-1</sup>	KS <sup>-1</sup>	SW	TKW	GY
Lines	12.74	0.32	3.77	12.22	31.9	4.7	15.51	21.58	3.35	12.16
Testers	49.74	64.18	59.08	49.56	44.38	50.95	36.2	43.12	53.47	55.19
Line × tester	37.52	35.51	37.16	38.23	23.72	44.36	48.28	35.3	43.18	32.65

Note: characters DH represents days to heading, DM days to maturity, GFP grain filling period, GFR grain filling rate, PH plant height, SP<sup>-1</sup> spikes per plant, KS<sup>-1</sup> kernel per spike, SW spike grain weight, TKW thousand kernel weight and GY grain yield per plant.

**Combining ability:**

Combining ability is an estimation of the value of genotypes on the basis of their offspring performance in some definite mating design (Allard, 1960). Average performance of the parental line in a series of cross combinations is generally referred to as GCA and is mainly attributed to additive and additive× additive gene effects. The GCA effect values of the ten studied agronomic traits of wheat parents Table (3) indicated that TPSGMS line S1 is the best combiner comparing to the other two TPSGMS lines with respect to DH, DM, GFR, PH, KS<sup>-1</sup>, SW and GY.

**Table 3.** General combining ability value of ten agronomic traits for three TPSGMS sterile and 49 restorer lines (R1-R49)

Parents	DH	DM	GFP	GFR	PH	SP <sup>1</sup>	KS <sup>-1</sup>	SW	TKW	GY
Sterile Line 1 (S1)	-1.22**	-0.2**	1.03**	0.05**	4.3**	-0.2ns	4.39**	0.22**	-0.56ns	3.52**
Sterile Line 2 (S2)	0.53**	-0.06ns	-0.59**	0.03*	-0.6**	-0.48**	2.23**	0.22**	1.08**	1.27ns
Sterile Line 3 (S3)	0.69**	0.25**	-0.44**	-0.08**	-3.7**	0.67**	-6.63**	-0.45**	-0.52ns	-4.79**
R 1	-1.37**	-2.83**	-1.46**	-0.16**	-3.89**	-1.54*	-5.69ns	-0.61**	-4.56**	-9.87**
R 2	-1.37**	-1.49**	-0.12ns	-0.1*	-2.78**	-2.76**	7.53*	0.76**	3.77*	-5.59*
R 3	1.97**	-2.38**	-4.35**	-0.08ns	-0.56ns	-1.09ns	-1.58ns	-0.25ns	-2.57ns	-7.5**
R 4	3.63**	-1.27**	-4.9**	-0.13**	-0.56ns	-0.87ns	-14.58**	-0.77**	2.35ns	-10.6**
R 5	-0.03ns	-0.49**	-0.46ns	-0.19**	-1.11ns	-0.43ns	-10.25**	-0.55**	1.27ns	-10.78**
R 6	2.97**	0.73**	-2.24**	-0.1*	6.11**	-0.87ns	-11.47**	-0.62**	1.27ns	-6.89*
R 7	1.97**	0.95**	-1.01**	0.07ns	13.33**	0.46ns	11.09**	0.59**	-0.4ns	2.76ns
R 8	-1.03**	1.62**	2.65**	-0.07ns	5.56**	-0.43ns	-1.69ns	-0.34ns	-3.18*	-1.67ns
R 9	-0.7**	-1.05**	-0.35ns	-0.11*	-1.67ns	-0.43ns	-6.91*	-0.66**	-4.68**	-6.73*
R 10	1.63**	0.73**	-0.9**	-0.02ns	-0.56ns	0.68ns	-3.36ns	-0.42*	-3.57*	-2.14ns
R 11	-0.03ns	1.51**	1.54**	-0.16**	2.78**	-1.32*	-8.14**	-0.62**	-2.49ns	-8.2**
R 12	-0.03ns	3.84**	3.88**	-0.18**	1.11ns	-0.65ns	-3.58ns	-0.45*	-3.96**	-7.99**
R 13	-2.03**	0.95**	2.99**	-0.04ns	1.67ns	0.68ns	-1.47ns	-0.39*	-4.26**	-0.03ns
R 14	-0.03ns	1.84**	1.88**	0.08ns	2.22*	1.68*	-0.69ns	-0.45*	-5.99**	6.23*
R 15	2.97**	2.51**	-0.46ns	-0.1*	3.89**	-0.2ns	2.42ns	-0.34ns	-6.86**	-6.29*
R 16	-1.03**	1.51**	2.54**	0.23**	3.33**	1.91**	8.09**	0.45*	-0.32ns	15.86**
R 17	-0.37ns	1.06**	1.43**	0.07ns	1.67ns	1.24ns	6.75*	0.66**	3.22*	5.27ns
R 18	0.63**	1.95**	1.32**	0.07ns	-3.89**	1.57*	6.31*	0.28ns	-1.33ns	5.23ns
R 19	1.63**	-0.27ns	-1.9**	0.04ns	0.56ns	-0.32ns	2.75ns	0.23ns	0.68ns	0.19ns
R 20	1.3**	0.06ns	-1.24**	-0.09ns	-5**	-1.09ns	-3.02ns	-0.3ns	-1.59ns	-6.29*
R 21	2.3**	-1.49**	-3.79**	-0.1*	0ns	0.8ns	-10.91**	-0.62**	0.08ns	-8.62**
R 22	1.63**	-4.49**	-6.12**	-0.16**	-3.89**	-2.2**	-0.02ns	-0.08ns	-0.42ns	-13.07**
R 23	-2.37**	-5.71**	-3.35**	-0.07ns	-1.67ns	-2.54**	8.98**	0.2ns	-4.27**	-6.53*
R 24	0.3ns	-3.38**	-3.68**	-0.01ns	1.67ns	0.46ns	-5.14ns	-0.21ns	0.62ns	-3.73ns
R 25	-2.7**	-8.6**	-5.9**	0.05ns	3.33**	-1.32*	-0.36ns	0.12ns	1.69ns	-2.03ns
R 26	-1.48**	-3.6**	-2.12**	-0.16**	-1.11ns	-3.87**	5.86*	0.4*	0.91ns	-10.9**
R 27	-1.15**	-5.27**	-4.12**	0.05ns	3.33**	-3.2**	10.2**	0.48**	-1.5ns	-0.55ns
R 28	-0.59*	-5.38**	-4.79**	0.04ns	-0.56ns	-2.43**	9.42**	0.46*	-0.26ns	-1.88ns
R 29	0.63**	-2.38**	-3.01**	0.06ns	-1.11ns	-0.65ns	3.86ns	0.51**	2.39ns	0.68ns
R 30	1.3**	0.17ns	-1.12**	0.17**	3.89**	0.57ns	2.2ns	0.6**	6.06**	8.27**
R 31	0.63**	1.62**	0.99**	0.22**	2.22*	-0.54ns	-2.58ns	0.09ns	3.75*	13.34**
R 32	-0.37ns	1.84**	2.21**	0.05ns	-2.78**	-1.98**	18.42**	0.69**	-3.27*	4.58ns
R 33	-1.48**	1.73**	3.21**	-0.04ns	-5.56**	-1.87**	16.42**	1.01**	1.42ns	0.19ns
R 34	-2.03**	1.95**	3.99**	0.18**	3.33**	-0.09ns	8.09**	0.61**	1.59ns	14.01**
R 35	3.63**	4.62**	0.99**	0.04ns	-1.11ns	1.24ns	6.31*	0.38*	0.07ns	2.9ns
R 36	-0.03ns	3.51**	3.54**	0.02ns	-2.78**	1.68*	-11.14**	-0.22ns	6.96**	3.75ns
R 37	-4.15**	1.17**	5.32**	0.19**	-2.22*	3.24**	1.53ns	0.21ns	1.38ns	15.82**
R 38	1.3**	2.29**	0.99**	0.06ns	0.56ns	0.8ns	-3.58ns	0.13ns	4.8**	4.08ns
R 39	-1.37**	1.51**	2.88**	-0.04ns	-0.56ns	1.46*	-6.69*	-0.23ns	2.04ns	0.34ns
R 40	-2.81**	1.62**	4.43**	-0.12*	-1.67ns	1.13ns	-7.58*	-0.2ns	3.9**	-4.03ns
R 41	0.3ns	1.73**	1.43**	0.13**	1.67ns	1.68*	1.86ns	0.07ns	-0.51ns	8.97**
R 42	-1.03**	1.17**	2.21**	0.02ns	2.78**	1.8**	-5.36ns	-0.15ns	2.15ns	2.95ns
R 43	-1.48**	0.73**	2.21**	-0.05ns	-4.44**	0.13ns	-3.8ns	-0.22ns	0.29ns	-0.96ns
R 44	-1.15**	0.51**	1.65**	0.13**	-1.11ns	2.24**	3.53ns	0.06ns	-2.18ns	8.95**
R 45	1.3**	-0.16ns	-1.46**	0ns	1.11ns	-0.09ns	-2.02ns	-0.24ns	-1.65ns	-1.25ns
R 46	1.63**	0.29ns	-1.35**	-0.08ns	2.22*	1.02ns	-2.36ns	0.11ns	3.58*	-5.64*
R 47	-1.03**	2.62**	3.65**	0.03ns	-5**	1.57*	-6.91*	-0.29ns	2.22ns	4.27ns
R 48	-1.03**	-0.38*	0.65*	0.22**	-2.22*	1.68*	5.42ns	0.39*	0.79ns	13.34**
R 49	0.63**	2.29**	1.65**	0.11*	-0.56ns	3.02**	-6.14*	-0.29ns	0.6ns	7.75**

ns; not significant, \* and \*\*; significant differences at 5% and 1% levels of probability, respectively. DH; days to heading, DM; days to maturity, GFP; grain filling period, GFR; grain filling rate, PH; plant height, SP<sup>-1</sup>; spikes plant<sup>-1</sup>, KS<sup>-1</sup>; kernel

spike<sup>-1</sup>, SW; spike grain weight, TKW; thousand kernel weight and GY; grain yield plant<sup>-1</sup>.

Twenty-one restorer lines recorded negative significant GCA effects for DH, among which R37 recorded the lowest negative significant GCA effect (-4.15) followed by R40 (-2.81), R25 (-2.7), R23 (-2.37), R13 (-2.03), R34 (-2.03), R26 (-1.48), R33 (-1.48), R43 (-1.48), R1 (-1.37), R2 (-1.37), R39 (-1.37), R27 (-1.15), R44 (-1.15), R8 (-1.03), R16 (-1.03), R42 (-1.03), R47 (-1.03), R48 (-1.03), R9 (-0.7) and R28 (-0.59) indicating that they were good general combiners for early heading. On the other hand, R35, R4 and R3 recorded the highest positive GCA for DH. Regarding DM, sixteen restorer lines recorded negative significant GCA effects (R1-R5, R9, R21-R29 and R48), among them R25 recorded the lowest GCA effect (-8.6) followed by R23 (-5.71) and R28 (-5.27). Meanwhile, R35, R12 and R36 recorded the highest positive GCA for DM.

R22 recorded the lowest negative significant GCA impact (-6.12), followed by R25 (-5.9) and R4 (-4.9), showing that they were good general combiners for GFP. Twenty restorer lines (R1, R3, R4, R6, R7, R10, R19-R30, R45, and R46) showed negative significant GCA effects for GFP. With regard to GFP, R37, R40, and R34 had the greatest positive GCAs. Only nine restorer lines for GFR showed substantial positive GCA effects; R16 had the strongest effect (0.23), followed by R31 (0.22), R48 (0.22), R37 (0.19), R34 (0.18), R30 (0.17), R41 (0.13), R44 (0.13), and R49 (0.11). R25, R23, and R28 had the lowest negative GCA for GFR, however. Six restorer lines (R1, R23, R25, R26, R27, R28, R29, and R48) generally showed strong negative GCA effects for each of DH, DM, and GFP, demonstrating that they were effective general combiners for earliness traits.

For PH, 14 restorer lines had positive significant GCA effects and were effective general combiners. Of these, R7 had the highest positive significant GCA impact (13.33), followed by R6 (6.11), R8, R15, and R30, R16, R25, R27, and R34, R11 and R42, and R14, R31, and R46 (2.22).

Twelve restorer lines had statistically significant positive GCA effects for SP-1; of these, R37 had the highest positive GCA effect (3.24), followed by R49 (3.02), R44 (2.24), R16 (1.91), R42 (1.80), R14, R36, R41 and R48 (1.68), R18 and R47 (1.57), and R39 (1.46), indicating that they were effective general combiners for SP-1. R2, R27, and R22, on the other hand, had the lowest SP-1 negative GCA values. The highest GCA effect was observed by R32 (18.42), followed by R33 (16.42), R7 (11.09), R27 (10.2), R28 (9.42), R23 (8.98), R16 (8.09), R34 (8.09), R2 (7.53), R17 (6.75), R18 (6.31), R35 (6.31), and R26 (5.86). For KS-1, R4, R6, and R36 had the lowest negative GCA readings.

The largest GCA effect for the 14 restorer lines was observed by R33 (1.01), followed by R2 (0.76) and R32 (0.69), showing that they were effective general combiners for SW. R4, R9, and R21 reported the lowest negative significance GCA impacts. Nine restorer lines produced GCA effects for TKW that were both positive and significant, proving they were effective general combiners for this character. The largest GCA effect was recorded by R36 (6.96), which was followed by R30 (6.06), R38 (4.8), R40 (3.9), R2 (3.77), R31 (3.75), R46 (3.58), R17 (3.22), and R29 (2.39), whereas R15, R14, R9, and R1 had the lowest negative GCA for TKW.

Ten restorer lines for GY had positive significant GCA effects and were good general combiners; of these, R16 had the highest effect (15.86), followed by R37 (15.82), R34 (14.01), R31 (13.34), R48 (13.34), R41 (8.97), R44 (8.95), R30 (8.27), R49 (7.75), and R14 (6.23). The least negative GCA was observed for GY by R22, R26, R5, and R4. As it recorded positive significant GCA effects for eight characters (DM, GFP, GFR, PH, SP-1, KS-1, SW, and GY) and preferred negative significant effects for DH, we can conclude that R16 was the best general combiner restore. Seven characters in R31 and R34 have a significant positive GCA (DH, DM, GFP, GFR, PH, TKW, GY, and DM, GFP, GFR, PH, KS-1, SW, and GY, respectively). In six characters, R30 and R49 demonstrated strong positive GCA (DH, GFR, PH, SW, TKW, GY, and DH, DM, GFP, GFR, SP-1, GY, respectively). The GCA effects of R7, R14, R17, R18, R35, R37, R41, R44, and R48 were all highly significant in five characters. Specific combining ability (SCA), or the non-additive portion, is the term used to describe variations in the performance of a cross expected based on the average performance of the parental lines. These variations are mostly related to dominant and epistatic effects. To regulate characteristics, a non-additive component must be present, which forces wheat breeding plans to make use of hybrid vigor.

The SCA effects of the 147 hybrids for all studied characters were estimated and the highest 10 values for each character are presented in Table 4. The best crosses for DH which had the lowest negative and significant SCA effects were S3/R33, S2/R37, S2/R44, S2/R38, S2/R45, S3/R27, S1/R12, S3/R43, S2/R10, and S1/R22, while for DM were S2/R44, S1/R33, S1/R30, S2/R45, S1/R22, S2/R48, S3/R3, S3/R2, S1/R29 and S3/R32. The crosses S1/R34, S2/R18, S3/R2, S3/R13, S2/R48, S2/R7, S1/R30, S1/R31, S3/R12 and S1/R29 recorded the lowest negative and significant SCA effects for GFP. Only seven from 147 crosses recorded positive significant SCA for GFR (S2/R7, S3/R48, S3/R42, S3/R38, S1/R8, S1/R33 and S2/R12).



The best crosses for PH were S3/R13, S3/R17, S1/R43, S1/R44, S2/R19, S1/R42, S2/R3, S3/R39, S1/R24 and S3/R21. The best four crosses for SP<sup>-1</sup> were S3/R42, S3/R35, S1/R8 and S3/R39. The crosses S3/R32, S3/R26, S3/R28, S3/R33, S3/R27, S1/R22, S2/R5, S1/R40 and S1/R39 had positive and significant SCA values for both characters; KS<sup>-1</sup> and SW. Three crosses recorded positive and significant SCA values for TKW. Seven crosses recorded positive and significant SCA values for GY (S3/R48, S3/R42, S1/R8, S1/R13, S2/R12, S2/R7 and S2/R34).

In general, the crosses S1/R22, S1/R33, S1/R8, S2/R7, S3/R27, S3/R32, S3/R33, and S3/R42 recorded desirable and significant SCA values in three characters each. The two crosses S1/R8 and S3/R42 had the highest positive SCA values in the three characters GFR, SP-1, and GY. Meanwhile, the S2/R7 cross recorded significant positive SCA values for GY and GFR and significant negative SCA values for GFP.

**Table 4.** Specific combining ability effect estimates of the studied traits for the top 10 of 147 wheat crosses.

DH	DM	GFP	GFR	PH	SP <sup>-1</sup>	KS <sup>-1</sup>	SW	TKW	GY
S1/R22 -4.33**	S3/R32 -4.7**	S1/R29 -6.36**	S2/R7 0.25**	S3/R13 12.6**	S3/R42 3.99**	S3/R32 33.07**	S3/R26 1.2**	S1/R32 6.34*	S3/R48 15.08**
S2/R10 -3.76**	S1/R29 -4.69**	S3/R12 -5.45**	S3/R48 0.23**	S3/R17 7.59**	S3/R35 3.88**	S3/R26 32.29**	S3/R33 1.14**	S3/R43 6.17*	S3/R42 13.8**
S3/R43 -3.13**	S3/R2 -4.37**	S1/R31 -5.36**	S3/R42 0.21*	S1/R43 5.7**	S1/R8 3.09**	S3/R28 27.74**	S3/R32 1.01**	S2/R41 5.13*	S1/R8 11.98*
S1/R12 -2.67**	S3/R3 -4.14**	S1/R30 -4.25**	S3/R38 0.18*	S1/R44 5.7**	S3/R39 2.99**	S3/R33 20.74**	S3/R28 0.97**	S3/R4 4.83ns	S1/R13 10.7*
S3/R27 -2.47**	S2/R48 -3.83**	S2/R7 -4.07**	S1/R8 0.17*	S2/R19 5.6**	S2/R32 2.92*	S3/R27 18.29**	S1/R39 0.85**	S1/R26 4.74ns	S2/R12 10.69*
S2/R38 -2.42**	S1/R22 -3.58**	S2/R48 -3.74**	S1/R33 0.17*	S1/R42 5.15**	S3/R37 2.88*	S1/R22 15.83**	S2/R5 0.8*	S1/R28 4.66ns	S2/R7 9.84*
S2/R45 -2.42**	S2/R45 -3.39**	S3/R13 -3.56**	S2/R12 0.17*	S2/R3 5.05**	S2/R34 2.7*	S1/R23 15.83**	S3/R27 0.78*	S1/R25 4.12ns	S2/R34 9.7*
S2/R37 -2.31**	S1/R30 -3.25**	S3/R2 -3.45**	S1/R13 0.16ns	S3/R39 4.81**	S1/R10 2.64*	S2/R5 13.88**	S1/R40 0.7*	S3/R7 3.93ns	S3/R43 9.49ns
S2/R44 -2.31**	S1/R33 -3.14**	S2/R18 -3.41**	S3/R43 0.16ns	S1/R24 4.59**	S2/R19 2.59*	S1/R40 12.38*	S3/R1 0.68*	S1/R10 3.83ns	S1/R36 9.26ns
S3/R33 -2.13**	S2/R44 -3.05**	S1/R34 -3.36**	S1/R36 0.15ns	S3/R21 4.25**	S1/R33 2.53*	S1/R39 11.83*	S1/R22 0.62ns	S3/R13 3.8ns	S2/R30 8.99ns

ns; not significant, \* and \*\*; significant differences at 5% and 1% levels of probability, respectively. DH; days to heading, DM; days to maturity, GFP; grain filling period, GFR; grain filling rate, PH; plant height, SP<sup>-1</sup>; spikes plant<sup>-1</sup>, KS<sup>-1</sup>; kernel spike<sup>-1</sup>, SW; spike grain weight, TKW; thousand kernel weight and GY; grain yield plant<sup>-1</sup>.

#### Heterosis effects:

The use of heterosis % as a crucial criterion to assess hybrids has received significant attention from researchers. Therefore, choosing the ideal cross combination would be aided by being aware of the degree of heterosis. For each of the 10 traits under study, the heterosis percent over mid-parents (MP), better parents (BP), and over-check variety Sakha 95 (standard heterosis; SH) was calculated. From one hybrid to the next and from character to character, the degree of heterosis fluctuated. The number of hybrids showing significant heterosis in the intended direction for the ten variables under study is summarized in Table (5). Out of the 147 crossings examined, 80, 90, and 51 crosses, respectively, displayed preferable SH heterosis for the Earliness Characters DH, DM, and GFP. In addition, for SW, TKW, and GY, respectively, 68, 60, and 12 crosses demonstrated desirable SH heterosis.

**Table 5.** Number of crosses showing significant and desirable heterosis over mid-parent (MP), better parent (BP) and standard heterosis (SH) out of 147 crosses for ten traits in wheat.

Character	Number of crosses showing significant and desirable heterosis		
	MP	BP	SH
Days to heading	53	29	80
Days to maturity	82	60	90
Grain filling period	69	41	51
Grain filling rate	30	11	8
Plant height	140	40	70
Number of spikes per plant	8	2	2
Number of kernels per spike	20	9	36
Spike grain weight	43	27	68
Thousand kernel weight	97	59	60
Grain yield per plant	28	13	12

Significant positive, as well as negative heterosis for MP, BP and SH % were observed for all characters **Tables (6 and 7)**. Negative heterosis was desirable for DH, DM and GFP but positive estimates were desirable for the rest of the characters. The highest twelve combinations of heterosis for earliness characters and plant height are presented in **Table (6)**.

The earliest heading crosses were S1/R22 and S1/R23, which exhibited the highest significant heterosis over MP (-6.93 and -5.97%) and over BP (-4.14 and -5.26%). Fortunately, these two hybrids recorded significant negative heterosis for DM as well. The highest SH estimates (-9.78%) were for the S1/R37 and S2/R37 combinations. The crosses S1/R29, S3/R4, and S3/R3 recorded the shortest GFP, which recorded the highest negative significant heterosis over MP (-15.52, -15.36, and -14.37%), over BP (-12.5, -14.62, and -14.37%), and SH (-14.04, -14.62, and -12.87%).

The highest combination for GFR heterosis over BP and MP was S1/R16, while the hybrid S3/R48 recorded the highest positive heterosis over SH (45.61%). The S3/R13 combination recorded the highest positive heterosis over MP (27.93%) and BP (16.39%). The S1/R7 combination recorded the highest positive heterosis for PH over SH (22.58%).

**Table 6.** Heterosis estimates using various approaches of earliness characters and plant height for top 12 crosses of 147 hybrid wheat crosses.

DH	MP	S1/R22	S1/R23	S3/R26	S2/R45	S3/R27	S2/R37	S2/R40	S1/R24	S1/R26	S2/R5	S2/R10	S2/R17
	BP	S1/R23	S1/R22	S2/R5	S2/R10	S2/R17	S1/R12	S3/R43	S1/R2	S2/R14	S2/R38	S2/R45	S1/R25
	SH	S1/R37	S2/R37	S1/R13	S1/R23	S1/R25	S1/R12	S1/R22	S1/R33	S1/R40	S2/R40	S3/R43	S1/R2
DM	MP	S1/R22	S1/R24	S3/R3	S1/R23	S2/R45	S1/R26	S3/R1	S2/R1	S1/R25	S1/R28	S1/R27	S2/R23
	BP	S1/R22	S1/R24	S1/R26	S3/R3	S1/R27	S2/R27	S3/R2	S1/R23	S3/R26	S3/R27	S2/R1	S2/R22
	SH	S1/R25	S2/R25	S1/R22	S1/R23	S1/R28	S1/R29	S2/R23	S3/R25	S3/R3	S1/R24	S3/R2	S1/R26
GFP	MP	S1/R29	S3/R4	S3/R3	S2/R3	S1/R28	S2/R22	S3/R1	S3/R5	S2/R1	S1/R30	S1/R31	S2/R25
	BP	S3/R4	S3/R3	S1/R29	S2/R3	S2/R22	S1/R31	S2/R4	S1/R28	S1/R30	S1/R9	S3/R2	S3/R5
	SH	S3/R4	S1/R29	S2/R22	S2/R25	S3/R3	S2/R3	S1/R28	S2/R23	S2/R27	S3/R22	S2/R4	S2/R7
GFR	MP	S1/R16	S1/R33	S1/R44	S2/R7	S1/R31	S3/R38	S1/R37	S3/R37	S2/R16	S1/R34	S2/R34	S1/R36
	BP	S1/R16	S1/R44	S2/R7	S1/R33	S1/R37	S2/R16	S1/R10	S1/R28	S3/R37	S1/R39	S1/R36	S1/R25
	SH	S3/R48	S1/R16	S2/R7	S2/R34	S1/R31	S2/R30	S1/R34	S2/R16	S3/R37	S2/R19	S2/R48	S1/R41
PH	MP	S3/R13	S1/R7	S1/R30	S1/R44	S1/R31	S1/R12	S1/R24	S1/R4	S2/R38	S1/R34	S1/R46	S1/R42
	BP	S3/R13	S2/R38	S1/R12	S1/R44	S1/R30	S1/R29	S1/R4	S1/R31	S1/R32	S1/R38	S2/R29	S1/R34
	SH	S1/R7	S1/R42	S1/R24	S1/R30	S1/R31	S2/R7	S3/R7	S3/R13	S1/R6	S1/R8	S1/R15	S1/R16

Note: " \* ", " \*\* " and "ns" represent significant differences at P<5%, P<1% levels and not significant, respectively. For characters DH represents days to heading, DM days to maturity, GFP grain filling period, GFR grain filling rate and PH plant height. MP (mid parent), BP (better parent) and SH (check).

The highest twelve combinations of heterosis for yield and its components are presented in Table 7. For SP-1, significant positive heterosis over BP was recorded by eight crosses: S3/R35, S3/R39, S3/R49, S3/R48, S3/R41, S3/R38, S3/R37, and S3/R42. Meanwhile, significant positive heterosis estimates were observed in only two crosses (S3/R37 and S3/R42) in SH and BP. S3/R32, S3/R26, S3/R28, S3/R33, and S1/R23 combinations recorded the highest significant positive heterosis over MP, BP, and SH for KS-1 (ranging from 80.63 to 38.53%). For SW, highly significant positive heterosis estimates were observed in SH. This showed the tendency of superiority in S3/R33, S2/R2, S2/R30, S2/R17, S3/R32, S1/R29, S3/R26, S2/R7, S1/R34, and S1/R17 in this trait. However, the BP and MP heterosis was significant to highly significant positive in many crosses, and the best one was S3/R33.

**Table 7.** Heterosis estimates using various approaches for yield and yield components for the top 12 of 147 wheat crosses.

Traits	Highest combination												
SP <sup>-1</sup>	MP	S3/R42 46.34**	S3/R37 41.86**	S3/R35 38.1**	S3/R39 34.94**	S3/R49 31.76**	S3/R48 30.12**	S3/R41 27.71**	S3/R38 26.58*	S3/R44 19.54ns	S3/R47 19.05ns	S3/R30 13.92ns	S3/R14 13.25ns
	BP	S3/R42 30.43**	S3/R37 22*	S3/R35 20.83ns	S3/R39 19.15ns	S3/R38 16.28ns	S3/R48 14.89ns	S3/R49 14.29ns	S3/R41 12.77ns	S1/R36 8.33ns	S3/R15 5ns	S3/R30 4.65ns	S3/R47 4.17ns
	SH	S3/R37 24.49*	S3/R42 22.45*	S3/R35 18.37ns	S3/R39 14.29ns	S3/R49 14.29ns	S3/R48 10.2ns	S3/R41 8.16ns	S1/R36 6.12ns	S3/R44 6.12ns	S1/R10 2.04ns	S3/R38 2.04ns	S3/R47 2.04ns
KS <sup>-1</sup>	MP	S3/R32 63.9**	S3/R26 44.55**	S3/R28 44.15**	S3/R33 40.79**	S1/R23 40.57**	S3/R27 33.98**	S1/R22 28.44**	S1/R7 27.06**	S1/R34 25.24**	S1/R17 22.03*	S1/R29 22.03*	S1/R37 20.64*
	BP	S3/R32 63.51**	S3/R26 44.55**	S3/R28 43.13**	S1/R23 40.57**	S3/R33 38.53**	S3/R27 30.81**	S1/R22 27.83**	S1/R7 26.76**	S1/R34 21.7*	S1/R17 18.87ns	S1/R29 18.87ns	S1/R16 17.51ns
	SH	S3/R32 80.63**	S3/R26 59.69**	S3/R28 58.12**	S3/R33 58.12**	S1/R23 56.02**	S3/R27 44.5**	S1/R22 41.88**	S1/R7 41.36**	S2/R7 38.74**	S2/R2 35.6**	S1/R34 35.08**	S2/R35 34.03**
SW	MP	S3/R33 53.92**	S1/R23 48.18**	S2/R30 44.25**	S3/R32 44.21**	S2/R17 43.16**	S2/R2 42.41**	S1/R25 42.06**	S1/R16 41.86**	S1/R17 41.19**	S1/R22 41.06**	S3/R26 40.98**	S1/R37 39.52**
	BP	S3/R33 53.25**	S3/R32 42.74**	S1/R23 41.65**	S1/R17 40.55**	S2/R2 40.41**	S3/R26 40.35**	S1/R16 39.45**	S2/R30 38.96**	S2/R17 38.7**	S3/R28 35.75**	S1/R22 34.59**	S1/R40 33.3**
	SH	S3/R33 71.27**	S2/R2 61.47**	S2/R30 59.8**	S2/R17 59.51**	S3/R32 58.14**	S1/R29 55.88**	S3/R26 55.49**	S2/R7 52.65**	S1/R34 51.67**	S1/R17 51.57**	S1/R23 51.37**	S3/R28 50.39**
TKW	MP	S2/R22 28.83**	S2/R17 26.56**	S1/R30 25.05**	S2/R30 24.84**	S2/R38 24.53**	S1/R25 23.21**	S2/R47 23.12**	S2/R41 23.06**	S2/R26 22.94**	S1/R26 22.55**	S3/R4 22.44**	S3/R6 22.44**
	BP	S2/R22 24.19**	S1/R30 22.38**	S3/R4 22.35**	S1/R25 21.9**	S2/R17 21.87**	S2/R30 21.01**	S1/R26 20.9**	S2/R26 20.11**	S2/R6 19.21**	S3/R30 18.84**	S2/R41 18.56**	S3/R5 18.5**
	SH	S1/R36 26.07**	S2/R17 24.06**	S2/R36 24**	S2/R38 23.67**	S1/R30 22.88**	S2/R47 22.76**	S3/R4 22.35**	S3/R31 21.61**	S2/R31 21.6**	S2/R30 21.51**	S2/R46 21.07**	S3/R43 21.02**
GY	MP	S1/R16 70.75**	S1/R37 52.55**	S1/R33 48.09**	S2/R34 47.79**	S1/R44 46.14**	S2/R16 46.07**	S1/R39 44.69**	S1/R36 43.56**	S2/R37 41.17**	S1/R13 40.87**	S3/R37 39.97**	S2/R38 38.6*
	BP	S1/R16 65.81**	S1/R37 46.64**	S1/R33 45.81**	S2/R16 45.56**	S1/R39 44.68**	S1/R44 42.46*	S2/R37 40.2**	S3/R37 38.91*	S2/R7 37.02*	S2/R34 33.55**	S2/R32 33.42*	S1/R36 33.25*
	SH	S2/R34 55.16**	S1/R16 54.43**	S3/R48 52.22**	S1/R34 41.19**	S2/R30 40.94**	S1/R37 39.47**	S1/R36 36.53*	S2/R16 36.52*	S1/R31 35.79*	S2/R31 33.58*	S2/R37 32.34*	S1/R41 32.61*

Note: " \* ", " \*\* " and "ns" represent significant differences at P<5%, P<1% levels and not significant, respectively. For characters SP<sup>-1</sup> represents spikes per plant, KS<sup>-1</sup>kernel per spike, SW spike grain weight, TKW thousand kernel weight and GY grain yield per plant.

The combination S2/R22 recorded the highest positive heterosis over MP and BP in TKW, while S1/R36 had the highest significant positive heterosis estimates over SH. Highly significant heterosis percentage was recorded for GY up to 70.75, 65.81 and 55.16% over MP, BP and check cultivar. The crosses S1/R16 and S1/R37 had the highest heterosis estimates over BP and MP while, the crosses S2/R34 and S1/R16 showed the highest estimates over check cultivar.

## DISCUSSION

### Analyses of variance:

Analysis of variance showed highly significant differences among the genotypes revealing that considerable genetic variation existed among the parents and their hybrids (Fisher and Yates, 1967). A comparison of the parents versus crosses revealed significant differences for all characters except KS<sup>-1</sup> and GY, reflecting a sort of heterosis and hybrid vigor for these characters of the studied wheat genotypes.

For all studied traits, the ratio of GCA to SCA variance estimates was less than unity, indicating that the inheritance of these traits was governed primarily by non-additive gene effects. This finding suggests that it may be possible to select superior cross combinations as hybrid cultivars, and selection for inbred lines would be carried out in late segregating generations using the bulk method. These findings agreed well with those outlining the significant contribution of non-additive genetic diversity to the inheritance of grain yield per plant (El-Borhamy 2005; Abdel Nour et al., 2011; Saren et al., 2018; Farooq et al., 2019); thousand kernel weight (Abdel Nour et al., 2011; Saren et al, 2018; Farooq et al., 2019), grains per spike, spikes per plant (Abdel Nour et al., 2011) and days to heading (Saren et al., 2018).

### Contribution of lines, testers, and their interactions

The proportional contribution was due to tester followed by line x tester, for all traits except KS<sup>-1</sup>, suggests that specific effects are more important in expression than general effects.



**Combining ability:**

The best restorer lines R1, R23, R25, R26, R27, R28, R29 and R48 recorded negative significant GCA effects for each of DH, DM and GFP, indicating that they were good general combiners for earliness characters.

The line R16 was the best general combiner restorer as it recorded positive significant GCA effects in eight characters (GFP, GFR, PH, SP<sup>-1</sup>, KS<sup>-1</sup>, SW and GY) and preferred negative significant effects for DH. R31 and R34 had positive significant GCA in seven characters (DH, DM, GFP, GFR, PH, TKW, GY and DM, GFP, GFR, PH, KS<sup>-1</sup>, SW, GY, respectively). R30 and R49 had positive significant GCA in six characters (DH, GFR, PH, SW, TKW, GY and DH, DM, GFP, GFR, SP<sup>-1</sup>, GY, respectively). Each of R7, R14, R17, R18, R35, R37, R41, R44 and R48 had positive significant GCA effects in five characters.

The crosses S1/R22, S1/R33, S1/R8, S2/R7, S3/R27, S3/R32, S3/R33 and S3/R42 recorded desirable significant SCA values in three characters each. The two crosses S1/R8 and S3/R42 had the highest positive SCA values in the three characters GFR, SP<sup>-1</sup> and GY. Meanwhile, S2/R7 cross recorded significant positive SCA values for GY and GFR while negative significant SCA values for GFP. This information could be used for estimating and selecting superior cross combinations while exploiting heterosis and selecting homozygous lines in wheat, which is a self-pollinated crop (Istipliler *et al.*, 2015; Kose, 2017)

**Heterosis effects:**

Many researchers have emphasized the utilization of heterosis percent as an important criterion to evaluate hybrids. Therefore, knowledge about the magnitude of heterosis would help in selection of the best cross combination. With respect to GY, the crosses S2/R34 and S1/R16 showed the highest significant positive heterosis estimates over check cultivar (55.16 and 54.43, respectively). Also, the crosses S1/R16 and S1/R37 had the highest significant positive heterosis estimates over BP (65.81 and 46.64, respectively) and MP (70.75 and 52.55, respectively) with respect to GY. Many scientists have observed varying degrees of heterosis for yield and its related characters (Khan and Habib, 2004; Ahmad *et al.*, 2006; Ismail, 2015; Saren *et al.*, 2018; El-Gammaal *et al.*, 2019; Abdelkhalik *et al.*, 2019; Li *et al.*, 2020). This exploitation of heterosis in wheat hybrid development could be of significant economic importance considering the role of wheat in food security around the globe (Hochholdinger and Baldauf, 2018; Abdelkhalik *et al.*, 2019). These promising materials could be utilized for parental line traits improvement and heterosis level enhancement for hybrid wheat breeding program.

**CONCLUSION**

Non-additive gene activity primarily controlled all examined traits. The greatest GCA values for DH, DM, GFR, PH, KS-1, SW, and GY were recorded by TPSGMS Line 1. For the eight characters, DM, GFP, GFR, PH, SP-1, KS-1, SW, and GY, the restorer R16 is a good combiner. In seven characters, R31 and R34 exhibited notably favorable general combining abilities (DH, DM, GFP, GFR, PH, TKW, GY, and DM, GFP, GFR, PH, KS-1, SW, and GY, respectively). In six characters, R30 and R49 displayed significantly positive GCA (DH, GFR, PH, SW, TKW, GY, DM, GFP, GFR, SP-1, and GY, respectively). The GCA effects of R7, R14, R17, R18, R35, R37, R41, R44, and R48 were all highly significant in five characters. The crossings S1/R22, S1/R33, S1/R8, S2/R7, S3/R27, S3/R32, S3/R33, and S3/R42 showed highly desired SCA values in three different characters. The three characters GFR, SP-1, and GY obtained the highest positive SCA values in the crosses S1/R8 and S3/R42. The crosses S2/R34 and S1/R16 had the highest positive heterosis estimations above the check cultivar in terms of GY (55.16 and 54.43, respectively). The most significant positive heterosis estimates across BP (65.81 and 46.64, respectively) and MP (70.75 and 52.55, respectively) regarding GY were also found for the crossings S1/R16 and S1/R37. In hybrid wheat breeding operations, these potential materials might be used to raise heterosis level and improve parental line traits.

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## قوة الهجين والقدرة على التآلف في الهجن بنظام السلالتين كتقنية لإنتاج القمح الهجين في مصر

سيدهم عبدالخالق محمد عبدالخالق\*، عادل عبدالعزيز هجرس ، خالد الدمرداش  
إبراهيم رجب

قسم بحوث القمح - معهد بحوث المحاصيل الحقلية - مركز البحوث الزراعية - مصر  
\*بريد المؤلف المراسل: [sedhom\\_aiad@yahoo.com](mailto:sedhom_aiad@yahoo.com)

أجريت هذه الدراسة في محطة البحوث الزراعية بسخا - مركز البحوث الزراعية - مصر - خلال الموسمين 2020/2019 و2021/2020. وتهدف الدراسة الي تحديد أفضل الآباء ذات القدرة العالية على التآلف وانتخاب أفضل الهجن بناء على تقديرات قوة الهجين. تم استخدام ثلاثة من السلالات العقيمة الحساسة للفترة الضوئية والحرارة كمهات و49 سلالة اخري معيدة للخصوبة كآباء للهجين وفقاً لطريقة تهجين السلالة x الكشاف. كانت النسبة بين تباين القدرة العامة على التآلف الي تباين القدرة الخاصة اقل من الوحدة مما يدل على ان الفعل الجيني غير المضيف له التأثير الأكبر في وراثة الصفات تحت الدراسة. كانت القدرة العامة على التآلف للسلالة العقيمة الاولى S1 أعلى من الأخرتين في سبعة صفات من أصل عشرة. في حين كانت السلالة المعيدة للخصوبة R16 الأعلى قدرة علي التآلف في ثمان صفات و السلالات R31 و R34 سجلت قدرة عامة علي التآلف عالية ومعنوية في سبع صفات. كان الهجينان S1/R8 و S3/R42 الأعلى قيم موجبة للقدرة الخاصة على التآلف في ثلاث صفات محصوليه. سجلا الهجينان S2/R34 و S1/R16 اعلي قيم موجبة ومعنوية لقوة الهجين لصفة محصول الحبوب بالنسبة الي صنف المقارنة (55.16 و 54.43 على التوالي). بينما سجلا الهجينان S1/R37 و S1/R16 اعلي قيم موجبة ومعنوية لقوة الهجين لصفة محصول الحبوب بالنسبة الي الاب الأعلى (46.64 و 65.81 على التوالي) ومتوسط الابوين (52.55 و 70.75 على التوالي). دلت النتائج على وجود زيادة كبية في قوة الهجين مقارنة بالصنف التجارى (سحا 95) في عدد اثنا عشر هجين، ونوصى بتقييم تلك الهجن في مواقع بيئية مختلفة والاستفادة منها في رفع إنتاجية القمح في مصر.

الكلمات المفتاحية: القمح الهجين ، سلالات عقيمة ، القدرة علي التآلف ، قوة الهجين

**Table S1.** Names and selection history of the studied bread wheat genotypes.

Abbreviation	Cultivar or Line name & Selection history
S1	Sterile line 1
S2	Sterile line 2
S3	Sterile line 3
R1	GIZA 168 CM93046-8M-0Y-0M-2Y-0B
R2	GIZA 171 S.6-1GZ-4GZ-1GZ-2GZ-0GZ
R3	SAKHA 94 CMBW90Y3180-0TOPM-3Y-010M-010M-010Y-10M-015Y-0Y-0AP-0S.
R4	SAKHA 95 CMA01Y00158S-040POY-040M-030ZTM-040SY-26M-0Y-0SY-0S.
R5	MISR 3 CMSS06Y00582T-099TOPM-099Y-099ZTM-099Y-099M-10WGY-0B-0EGY
R6	FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ*2/5/BOW/URES//2*WEAVER/3/CROC_1/AESQUAR ROSA (213)//POG CGSS05B00144T-099TOPY-099M-099NJ-099NJ-7WGY-0B-5Y-0B
R7	QUAIU/5/FRET2*2/4/SNT/TRAP#1/3/HAUZ*2/TRAP//... CMSS06B00109S-0Y-099ZTM-099NJ-099NJ-13WGY-0B-0SH
R8	WH 542 / GIZA 168 // GEMMIZA 11 S.2012-11-010S-010S-5S -0S
R9	WH 542 / GIZA 168 /3/ CHAPIO//2*SERI/RAYON S.2012-13-017S-020S-6S -0S
R10	CHEN / AEGILOPS SQUARROSA (TAUS) // FCT /3/ 2*WEAVER /4/ HUBARA-1 /5/ KAUZ/PASTOR//BAV92/RAYON S.2012-17-017S-024S-1S -0S
R11	CHEN / AEGILOPS SQUARROSA (TAUS) // FCT /3/ 2*WEAVER /4/ HUBARA-1 /5/ TIMBA/ELVIRA S.2012-18-026S-025S-5S -0S
R12	SAKHA 12 /5/ KVZ // CNO 67 / PJ 62 /3/ YD "S" / BLO "S" /4/ K 134 (60) / VEE /6/ CROC 1 / AEGILOPS.SQUARROSA (205) // KAUZ /3/ SITE /7/ MISR 2 S.2012-41-017S-08S-2S -0S
R13	PASTOR // SITE / MO /3/ CHEN / AEGILOPS SQUARROSA (TAUS) // BCN /4/ WBL1/5/ SKAUZ *2 / SRMA S.2012-62-018S-013S-3S -0S
R14	PASTOR // SITE / MO /3/ CHEN / AEGILOPS SQUARROSA (TAUS) // BCN /4/ WBL1/5/ WHEAR / KUKUNA / WHEAR S.2012-67-050S-025S-1S -0S
R15	SAKHA 93 /4/ WHEAR/VIVITSI/3/C80.1/3*BATAVIA//2* WBL1 S.2011-4-014S-07S-1S-1S-0S
R16	MISR 2 // WON-D22/SAFI-1 S.2013-33-033S-01S-1S-0S
R17	SAKHA 94 // KAUZ / PASTOR /8/ CHIBIA//PRLII/CM65531 /7/ BUC // 7C / ALD /5/ MAYA74 / ON // 1160.147 /3/ BB / GLL /4/CHAH"S" /6/ MAYA / VUL // CMH74A.630 /4*SX S.2013-44-04S-018S-11S -0S
R18	GALVEZ / WEAVER /3/ VORONA / CNO79 // KAUZ /4/ SAKHA 93 /5/ UP2338*2/KKTS*2//YANA S.2013-48-040S-026S-12S -0S
R19	PASTOR // SITE / MO /3/ CHEN / AEGILOPS SQUARROSA (TAUS) // BCN /4/ WBL1 /8/ KVZ /4/ CC / INIA /3/ CNO // ELGAU / SON 64 /5/ SPARROW "S" / BROCHIS "S" /6/ BAYA "S" / IMU /7/ HUBARA-2 S.2013-61-023S-07S-19S -0S
R20	BABAX / LR42 // BABAX*2 /4/ SNI / TRAP/3/ KAUZ*2 / TRAP // KAUZ /5/ UP2338*2/KKTS*2//YANA S.2013-69-056S-08S-6S -0S
R21	BABAX / LR42 // BABAX*2 /4/ SNI / TRAP/3/ KAUZ*2 / TRAP // KAUZ /6/ ALTAR 84/AE.SQUARROSA (221) // 3*BORL95 /3/ URES / JUN // KAUZ /4/ WBL1 /5/ MILAN/S87230//BAV92 S.2013-70-042S-08S-14S -0S
R22	KIRITATI//SERI/RAYON /5/ CAZO / KAUZ // KAUZ /4/ PJN / BOW // OPATA*2 /3/ CROC-1 / AE.SQUARROSA (224) // OPATAS S.2013-117-016S-03S-12S -0S
R23	KAMB1*2 / KIRITATI /5/ ATTILA*2 / PBW65 /4/ CHEN / AEGILOPS SQUARROSA (TAUS) // BCN /3/ 2*KAUZ

	S.2013-141-014S-014S-6S -0S
R24	KAMB1*2 / KIRITATI /7/ SAKHA 94 /6/ GIZA 158 /5/ CFN /CNO "S" // RON /3/ BB / NOR 67 /4/ TL /3/ FN / TH // NAR 59*2 S.2013-143-013S-03S-7S -0S
R25	FRET2*2/BRAMBLING /4/ CHIBIA // PRLII /CM65531/3/ SKAUZ *2 / SRMA S.2013-172-020S-02S-14S -0S
R26	FRET2*2/BRAMBLING /6/ ALTAR 84/AE.SQUARROSA (221)//3*BORL95 /3/ URES/JUN//KAUZ/4/WBLL1/5/MILAN /S87230//BAV92 S.2013-174-043S-020S-11S -0S
R27	FRET2*2/BRAMBLING // WAXWING*2/HEILO S.2013-175-027S-04S-8S -0S
R28	CROC_1/AE.SQUARROSA (205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2/5/CIRO16 CMSS10Y00023S-099Y-099M-099NJ-099NJ-4WGY-0B
R29	SUP152/QUAIU #2//BECARD/QUAIU #1 CMSS11B00405S-099M-099NJ-099NJ-26WGY-0M
R30	CIRO16/2*BORL14 CMSS12B00569T-099TOPY-099M-0SY-53M-0WGY
R31	CNO79//PF70354/MUS/3/PASTOR/4/BAV92*2/5/HAR311/6/BECARD/QUAIU #1/7/BECARD/QUAIU #1 CMSS12B00640T-099TOPY-099M-0SY-14M-0WGY
R32	KACHU//WBLL1*2/BRAMBLING*2/3/KACHU/KIRITATI CMSS12B00801T-099TOPY-099M-0SY-36M-0WGY
R33	ONIX/KBIRD//BORL14/3/ONIX/KBIRD CMSS12B00825T-099TOPY-099M-0SY-17M-0WGY
R34	FRET2*2/BRAMBLING//BECARD/3/WBLL1*2/BRAMBLING*2/4/BECARD/QUAIU #1 CMSS12B00944T-099TOPY-099M-0SY-33M-0WGY
R35	MUU/KBIRD//2*KACHU/KIRITATI CMSS12Y01082T-099TOPM-099Y-099M-099NJ-099NJ-4Y-0WGY
R36	ATTILA/3*BCN//BAV92/3/TILHI/4/SUP152/5/SUP152/6/KFA/2*KACHU/7/ATTILA/3*BCN//BAV92/3/P ASTOR/4/TACUPETO F2001*2/BRAMBLING/5/PAURAQ CMSS12B00841T-099TOPY-099M-099NJ-099NJ-36Y-0WGY
R37	FRET2/KUKUNA//FRET2/3/PARUS/5/FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ*2/6/WBLL1/KU KUNA//TACUPETO F2001/3/UP2338*2/VIVITSI CMSS10B01093T-099TOPY-099M-099NJ-099NJ-23WGY-0B-0S
R38	MUCUY//MUTUS*2/TECUE #1 CMSS11B00372S-099M-099NJ-099NJ-19WGY-0B-0S
R39	CHIBIA/PRILL/CM65531/3/FISCAL/4/DANPHE#1/5/CHIBIA//PRL11/CM65531/3/SKAUZ/BAV92 CMSS08B00657T-099TOPY-099M-099NJ-099NJ-17WGY-0B-0EG
R40	FRET2*2/SHAMA//PARUS/3/FRET2*2/KUKUNA*2/4/TRCH/SRTU//KACHU CMSS10B01084T-099TOPY-099M-099NJ-099NJ-38WGY-0B
R41	TRCH/SRTU//KACHU*2/4/WBLL1/KUKUNA//TACUPETO F2001/3/UP2338*2/VIVITSI CMSS10B01108T-099TOPY-099M-099NJ-099NJ-26WGY-0B
R42	BAJ#1/3/TRCH/SRTU//KACHU CMSS10Y00030S-099Y-099M-11WGY-0B
R43	BAJ #1/KISKADEE #1 CMSS08Y00406S-099Y-099M-099NJ-39WGY-0B
R44	CROC_1/AE.SQUARROSA(205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2/5/SNI/TRAP#1/3/KAUZ*2/ TRAP//KAUZ/4/PARUS/PASTOR CMSA10M00466S-050ZTM-0SY-30M-0WGY
R45	GOUMRIA-17 /3/ MILAN / KAUZ // CHIL / CHUM18 S. 16508-063S-08S-2S-1S -0S
R46	KACHU*2/BECARD CMSS09Y00815T-099TOPM-099Y-099ZTM-099NJ-099NJ-5WGY-0B
R47	KACHU/3/WHEAR//2*PRL/2*PASTOR CMSS10Y00016S-099Y-099M-4WGY-0B
R48	KACHU/SAUAL/3/TACUPETO F2001/BRAMBLING//KIRITATI CMSS10Y00372S-099Y-099M-3WGY-0B
R49	KACHU/SAUAL/8/ATTILA*2/PBW65/6/PVN//CAR422/ANA/5/BOW/CROW//BUC/PVN/3/YR/4/TRAP# 1/7/ATTILA/2*PASTOR CMSS10Y00374S-099Y-099M-1WGY-0B