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### Genetic Analysis of Yield Related Characteristics Using Line × Tester Mating Design in Rice (*Oryza sativa* L.)

Elshenawy, M. M.\*; W. H. Elgamal; Fatma A. Hussein and Neama El-kholly



Rice Research Department, Field Crops Research Institute, Agricultural Research Center, 33717, Sakha, Kafr Elsheikh, Egypt.

#### ABSTRACT

This research was conducted at the Agricultural Research Center, Egypt. Rice Research Department, Sakha Research Station, Kafr El-Sheikh. Five of the most significant local varieties and lines: Giza 177, Sakha104, Sakha105, Sakha106 and GZ 6296-12-1-2-1-1. The following seven introduced genotypes are identified: IRI 367, Namyang 6, IR 10K153, IR 11K 305, IR 12K 269, HANGANGCHAL1, and IR68333-R-R-B-19. Five lines were crossed by seven testers to create 35 F<sub>1</sub> cross. The data recorded on characters showed significant and highly significant differences among genotypes; parents, parents vs. crosses, crosses, lines, testers and line×tester for all studied traits except parents vs. crosses for grain yield /plant was non-significant. Preponderance of non-additive gene effect was shown by estimates of the ratio of general to specific combining ability, and degree of dominance for each characteristic. For the majority of the variables under study, the maternal genotypes GZ6296-12-1-2-1-1 and Sakha 106 had the best general combining ability effects. For the majority of the characteristics under study, Hangangchal1, IRI367and Namyang 6 were found to be effective general combiners. The cross combinations of Giza 177x HANGANGCHAL1 and Sakha 105 x IRI 367 were observed to be good specific combinations for grain yield and most of related traits due to highly significant specific combining ability effects and heterotic effects.

**Keywords:** Rice, GCA, SCA, Heterosis, Yield and Line × tester.



#### INTRODUCTION

For more than half of the world's population, rice is the main diet. About 20% of all calories consumed globally come from rice, which is the second-largest source of calories in the human diet after wheat (Babaei *et al.*, 2011). Given that over 50% of Egyptians eat rice for meals, rice is a major food and field crop in Egypt (Elmoghazy and Elshenawy 2018 and Abd El-Hadi, *et al* 2018).

The expanding population both now and in the future will be a major problem for rice breeders, with developing nations experiencing a greater growth in population (Abd El-Hadi *et al.*, 2018). Over the past 50 years, remarkable progress has been made in rice productivity (Ghidan *et al.*, 2019). One of the biggest challenges of the twenty-first century is ensuring food security. By 2050, there will be 943.6 million tons of rice needed worldwide, which means that production levels must increase by almost 5.8 million tons annually (FAO, 2017).

According to Patil and Mehta (2014), combining ability analysis is a potent technique for differentiating between good and poor combiners as well as for choosing the best hybrid combinations and suitable parental material. Given its simplicity, accuracy, and applicability to a large number of genotypes under study, the line-by-tester approach is one of the most often used to evaluate combining ability as the foundation of crop breeding (Singh and Chaudhary, 1985).

There are three ways to communicate heterosis, depending on how one compares a hybrid's performance (Gupta, 2000). Mid-parent heterosis, better parent heterosis (heterobeltiosis), and conventional heterosis are these three distinct approaches. Standard heterosis is prioritized over

the other two degrees of heterosis from a practical standpoint since it is intended to produce desirable hybrids that are superior to the current, higher yielding commercial varieties (Chaudhary, 1984). Heterosis breeding is a powerful genetic strategy that can increase many other desirable quality features in crops and promote yield upgrades of between 30 and 40% (Srivastava, 2000). Hybrid production-based breeding techniques demand a high degree of heterosis in addition to a particular cross's capacity for combining traits. The selection of suitable good parents and crosses is one of the basic problems faced by plant breeders in their efforts to improve high yielding varieties.

The mating designs provide reliable information on the parents' and hybrids' specific and general combining abilities. Additive gene action is primarily responsible for the differences in general combining ability, whereas non-additive gene effects are responsible for the differences in specific combining ability (Abdalla *et al.*, 2021a). Breeders can identify parents who may be crossed to take advantage of heterosis by using the estimate of general combining ability (Fasahat *et al.*, 2016). Breeders can thus create an efficient breeding strategy for the genetic upgrading of yield and its constituent parts by using the knowledge on combining ability, which provides data on the kind and degree of gene effects that organize grain production and yield attributes (Dar *et al.*, 2014). Previous studies found that optimal heterosis for characteristics including the number of spikelets per plant, the area of the flag leaf, and the number of filled grains per panicle increased grain yield (Vanaja and Babu 2004).

Therefore, the search's objectives were to identify genetic variation in rice, crossings that were feasible, as well

\* Corresponding author.

E-mail address: [mostafarrtc2@gmail.com](mailto:mostafarrtc2@gmail.com)

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as the interplay between general and specific combining abilities. Furthermore, the evaluation of several genetic factors such as additive and dominance among the genotypes of rice under investigation.

## MATERIALS AND METHODS

The study was conducted in the two summer seasons of 2021 and 2022 at the Rice Research and Training Center (RRTC), Sakha Agricultural Research Station Experimental Farm, Kafr El-sheikh, Egypt

### Experimental design and parental lines

Twelve parental genotypes and their thirty-five F1 crosses made during the 2021 and 2022 rice growing seasons,

based on the line × tester mating design, made up the experimental material. For yield and its components, four Egyptian variety and one promising line Sakh 104, Sakha 105, Sakha 106 and GZ 6296-12-1-2-1-1 were chosen. Table 1 lists seven different genotypes that were previously developed and utilized as male testers: HANGANGCHAL 1, IR 68333-R-R-B-19, IR 10K153, IR 11K 305, IR 12K 269, YEONGSAN, and Namyang 6. As a result, a randomized full block design with three replications was used to assess the 35 resulting crosses in addition to their parents. Every suggested practice in the package was followed.

**Table 1. List of the paternal genotypes type, name, origin, and pedigree.**

No.	Parents	Origin	Pedigree	Type
1	Giza177	Egypt	Giza171/Yamji No.1//Pi No.4	Japonica
2	Sakha 104	Egypt	GZ4096-8-1/GZ4100-9	Japonica
3	Sakha 105	Egypt	GZ5581/GZ4316	Japonica
4	Sakha 106	Egypt	Giza177/Hexi30	Japonica
5	GZ 6296-12-1-2-1-1	Egypt	AC1225/Hun Lien Yu 202	Indica Japonica
6	HANGANGCHAL1	South Korea	-	Japonica
7	IR 68333-R-R-B-19	IRRI	JINMIBYEO/CHEOLWEON46	Japonica
8	IR 10K153	IRRI	HR24580-15-1/IR03K105	Japonica
9	IR 11K 305	IRRI	IR07K125/IR83265-1-1-13-26-3//IR05K109	Japonica
10	IR 12K 269	IRRI	IR07K142/IR84233-11-3-3	Japonica
11	YEONGSAN	IRRI	JINJUBYEO/HR1590-92-4	Japonica
12	Namyang 6	Korea	-	Japonica

### Data collection

Every agricultural practice was carried out in accordance with the RRTC's 2020 recommendations for rice. The Standard Evaluation System (SES), of the International Rice Research Institute (IRRI 2014) states that observations on yield attributes were made using five plants per genotype in each replication. Each genotype was grown in a single row plot of five meters long, with a 20 by 20-centimeter divide. For randomly chosen plants from each replication, the following six yield and yield component traits were examined: harvest index (%), number of panicles plant<sup>-1</sup>, panicle length (cm), panicle weight (g), spikelets fertility percentage (%), 1000-grain weight (g), and grain yield plant<sup>-1</sup> (g).

### Statistical analysis

Analysis of variances was performed on the data for a randomized complete block design (RCBD) with three reps, as recommended by Panse and Sukhatme (1954). Analysis of variance (ANOVA) was applied to the mean values of each attribute in order to assess significant differences between parents and crosses, as suggested by Steel and Torrie (1980). The use of the line × tester mating design determined the general combining ability (GCA) impacts of the parents and the specific combining ability (SCA) effects of the hybrids (Kempthorne, 1957). According to Fehr (1987), the evaluation of heterosis of an individual cross for each attribute was determined by measuring the rise of the F1 hybrid mean over either the mid-parent or the better parent. The t-test was used to test heteroscedastic and combining ability effects using the least significant differences (LSD) test at the 0.05 and 0.01 levels of probability.

## RESULTS AND DISCUSSION

### Analysis of variance:

Table 2 displays the analysis of variance for every

trait that was investigated. The findings showed that significant variations in the genotypes of rice for every character under study. In crop development initiatives, the selection of dominant genotypes requires the existence of genetic heterogeneity. To determine the amount of improvement that may be made in breeding material for different features, it is crucial to evaluate the degree of variety that exists in the genetic material. Parents, crosses, and parents vs. crosses were the additional divisions made in the genotypic mean squares.

The results of the analysis of variance show that there were highly significant variations all the traits under study's genotypes, crosses, lines, testers, and line × tester. As shown in Table 2, variation between parents and parent vs cross comparisons was significant and highly significant for every characteristic under study. Non-additive variances were significant for the most of these traits, as demonstrated by the instant test provided by the significance of the line × tester for all the traits. This indicates a high degree of genetic diversity, offering a wide range of opportunities for selection of various quantitative features. Additionally, Bekele et al. (2013), Sandhya et al. (2014), and Foda (2021) revealed a considerable variation for a several of quantitative features. For every variable, the estimates of variation attributed to general combining ability ( $\sigma^2_{gca}$ ) were less than those attributed to specific combining ability ( $\sigma^2_{sca}$ ), suggesting that dominance genes were crucial in the inheritance of these traits. For every characteristic, the ratio of variation resulting from general to specific combining ability ( $\sigma^2_{gca}/\sigma^2_{sca}$ ) was smaller than unity. It revealed a very excellent chance for the exploitation of non-additive genetic variation for these qualities through hybrid breeding and suggested a greater significance of non-additive gene action in its expression (Ramalingam et al. 1997; Annadurai Nadarajan 2001 and Abdalla et al. 2021a).

**Table 2. Estimates of the mean square of line×tester analysis for yield and its component characteristics during the 2022 growing season.**

Source of variance	df	Days to maturity	Number of panicles/plants	Panicle length	Panicle weight	1000 grain weight	Fertility %	Grain yield /Plant	Harvest index
Reps	2	3.84*	0.65	0.88	0.23	6.60	3.24	5.44*	1.39
Genotypes	46	52.06**	31.95**	6.13**	1.33**	6.73**	22.85**	58.54**	54.63**
Crosses	34	50.51**	27.28**	5.45**	1.67**	6.56**	28.77**	67.55**	64.65**
Line (C)	4	149.56**	40.60**	23.08**	2.86**	5.86**	37.62**	63.09**	155.80**
Tester (C)	6	92.15**	26.52**	2.38*	0.63**	5.00*	5.58**	91.83**	37.36**
L×T	24	23.58**	25.25**	3.28**	1.74**	7.07**	33.09**	62.22**	56.28**
Parents	11	57.03**	28.96**	5.28**	0.25*	7.58**	3.20**	35.78**	14.23**
Line(p)	4	58.07**	4.77**	3.29**	0.16**	9.11**	2.08**	25.27**	4.20**
Tester(p)	6	16.30**	4.49**	1.56**	0.32**	3.90**	4.48**	14.69**	16.29**
Par VS Cros.	1	50.42**	223.49**	38.48**	1.46**	2.79*	37.52**	2.71	158.62**
Error	92	1.21	1.37	0.90	0.11	0.70	1.14	1.49	1.56
GCA	11	0.526	0.0397	0.0424	0.0012	0.0099	0.0844	0.1041	0.1635
SCA	34	7.493	7.983	0.7541	0.538	2.1322	10.637	20.246	18.238
G/C		0.070	0.005	0.056	0.002	0.005	0.008	0.005	0.009

\* and \*\* significant at 0.05 and 0.01 levels, respectively.

**Genotype performance on average:**

Table 3 shows the mean performance of the parents for the five investigated attributes. For the most studied characteristics, testers recorded higher values than lines. GZ 6296-12-1-2-1-1 had the longest panicle length (23.70 cm), panicle weight (3.81 g), and production of grains per plant (40.00 g). Giza177 was best 1000-grain weight (28.00 g), fertility percentage (96.00%), and harvest index (32.62%). While the line Sakha 104 had the highest number of panicles plant<sup>-1</sup> values (22.00). With a value of 124 days, the line Sakha105 had the shortest maturity time of all the parental genotypes investigated.

The Namyang 6 performed well among the tests getting the highest values of panicle plant<sup>-1</sup> (27.33), panicle length (25.43 cm), and fertility percentage (97.17%). Days to maturity (129 days), panicle weight (4.17 g), and grain yield per plant (45.37 g), while the tester YEONGSAN had the greatest harvest index (36.55%). During their studies of line × tester analysis on rice attributes, Satyanarayana *et al.* (2000), Kumar *et al.* (2004) and Abdalla *et al.* (2021b) reported similar results.

Although no hybrid combination had the optimum values for all analyzed traits (Table 4), the results revealed certain excellent hybrid combinations that showed desirable values for two or more traits. The cross combination GZ 6296-12-1-2-1-1Namyang 6 produced good results for four attributes studied: number of panicles per plant (32.33), panicle weight (4.96 g), fertility percentage (97.74%) and

harvest index (48.53%). GZ 6296-12-1-2-1-1 and IR 68333-R-R-B-19 produced high values for three traits: number of panicles per plant (31.67), panicle length (27.33cm), and panicle weight (5.95 g). Days to maturity (126 days), 1000-grain weight (26.97 g) and grain production per plant (47.27 g) were all favorable for the cross combination Giza177 × HANGANGCHAL 1. The hybrid Sakha 105 × IRI367 (YEONGSAN) produced an acceptable number of panicles per plant (31.00) and grain yield per plant (48.00 g). Sakha 106 × Namyang 6 produced high and desirable 1000-grain weight (27.21 g) and grain yield per plant (47.47 g) values. According to earlier research, cross combinations outperformed parental genotypes for most examined variables (Kumar and Singh 2004, Ahmadikhah 2008, Rahimi *et al.* 2010, and Abdalla 2021a), which could be attributed to heterosis and SCA.

**Combining ability analysis:**

The general combining ability recognizes outstanding parents, whereas the specific combining ability assists in the differentiation of good hybrid combinations, which may eventually lead to hybrid improvement (Shiva *et al.* 2013).

Table 5 shows the general combining ability effects of some yield traits. GZ 6296-12-1-2-1-1, one of the female parents (lines), was a good general combiner for all traits studied because it had high significant positive GCA impacts on all traits studied, with the exception of days to maturity, which had high significant negative GCA values.

**Table 3. The mean performance of all tested attributes for the parental genotypes throughout the 2022 season.**

Parents	Days to Maturity (day)	Number of Panicles/plant	Panicle Length (cm)	Panicle Weight (g)	1000 grain Weight (g)	Fertility (%)	Grain yield /Plant (g)	Harvest Index (%)
Giza177	125.00	19.00	21.13	3.44	28.00	96.00	33.18	32.62
Sakha 104	134.67	22.00	23.13	3.30	24.37	95.28	38.27	29.55
Sakha 105	123.67	19.00	21.67	3.23	27.40	95.92	39.33	31.27
Sakha 106	125.67	20.00	22.57	3.51	26.43	94.78	40.00	31.00
GZ 6296-12-1-2-1-1	125.67	20.67	23.70	3.81	24.17	94.00	40.00	32.13
HANGANGCHAL 1	129.33	24.67	23.67	4.17	24.37	95.38	45.37	31.67
IR 68333-R-R-B-19	134.33	27.00	24.43	3.66	24.40	94.32	42.92	32.22
IR 10K153	135.33	26.00	25.37	3.80	24.27	94.27	41.33	31.83
IR 11K 305	133.33	26.00	23.63	3.70	24.23	95.00	39.00	30.98
IR 12K 269	129.67	25.00	24.33	3.25	26.73	93.76	44.52	35.59
YEONGSAN	133.33	24.00	24.33	3.23	24.13	96.35	43.50	36.55
Namyang 6	134.00	27.33	25.43	3.58	22.90	97.17	44.57	35.69
LSD 0.05	1.78	1.89	1.53	0.54	1.35	1.73	1.97	2.02
LSD 0.01	2.36	2.51	2.04	0.71	1.80	2.29	2.62	2.68

**Table 4. The mean performances of all studied traits for all derived crosses during 2022 season.**

Crosses	Days to maturity (day)	Number of panicles	Panicle length (cm)	Panicle weight (g)	1000 grain Weight (g)	Fertility (%)	Grain yield /Plant (g)	Harvest index (%)
Giza177× HANGANGCHAL1	126.00	28.33	25.87	4.29	26.97	93.39	47.27	34.75
Giza177× IR 68333-R-R-B-19	129.00	25.67	25.33	3.31	25.25	96.44	44.34	35.08
Giza177× IR 10K153	130.33	22.33	24.67	3.21	24.40	94.36	36.52	32.32
Giza177× IR 11K 305	132.00	24.67	23.00	3.34	23.30	93.17	39.38	36.06
Giza177× IR 12K 269	133.33	22.33	23.67	3.11	25.27	96.16	42.33	35.57
Giza177×YEONGSAN	129.00	21.33	23.00	3.24	23.63	95.25	34.67	31.17
Giza177× Namyang 6	134.33	24.00	24.40	3.57	25.33	96.92	46.33	34.88
Sakha104×HANGANGCHAL1	134.00	23.33	23.33	3.18	24.42	95.00	41.17	39.15
Sakha104× IR 68333-R-R-B-19	134.33	30.00	22.83	3.54	24.60	95.38	36.78	30.15
Sakha104× IR 10K153	140.00	32.33	24.47	5.30	20.47	94.72	40.50	33.17
Sakha104× IR 11K 305	133.67	25.33	23.00	3.29	26.13	96.61	41.45	32.48
Sakha104× IR 12K 269	134.67	26.67	24.33	3.39	24.07	94.19	35.32	30.02
Sakha104×YEONGSAN	138.67	27.00	23.80	3.97	23.77	85.45	34.97	31.87
Sakha104× Namyang 6	139.00	29.00	25.23	2.78	24.30	86.94	33.63	26.39
Sakha105× HANGANGCHAL1	124.33	23.33	25.33	3.58	24.30	89.46	39.43	29.49
Sakha105× IR 68333-R-R-B-19	129.00	25.67	23.83	2.73	23.83	86.69	33.97	27.43
Sakha105× IR 10K153	133.33	26.67	23.55	3.58	24.60	89.01	40.02	29.90
Sakha105× IR 11K 305	134.33	23.33	23.83	3.25	26.83	92.93	39.50	34.80
Sakha105× IR 12K 269	127.33	29.00	23.27	4.57	23.50	95.44	38.83	35.09
Sakha105×YEONGSAN	126.00	31.00	24.33	3.35	24.73	96.32	48.00	37.33
Sakha105× Namyang 6	132.00	24.00	24.67	3.65	25.17	97.76	46.28	40.19
Sakha106× HANGANGCHAL1	124.33	24.33	24.93	4.82	24.63	95.11	46.35	37.80
Sakha106× IR 68333-R-R-B-19	127.33	29.00	23.67	3.40	25.00	94.59	34.10	39.31
Sakha106× IR 10K153	132.67	26.67	24.60	3.66	24.90	95.54	39.03	38.90
Sakha106× IR 11K 305	134.33	26.33	26.67	3.63	21.67	94.97	36.23	35.62
Sakha106× IR 12K 269	129.00	24.00	25.00	3.59	23.81	94.42	44.53	30.27
Sakha106×YEONGSAN	133.33	24.33	27.57	4.60	27.93	95.88	46.53	38.22
Sakha106× Namyang 6	137.00	28.67	26.27	4.57	27.21	96.20	47.47	37.23
GZ 6296-12-1-2-1-1×HANGANGCHAL1	130.33	29.67	26.67	4.50	25.67	96.23	47.00	36.52
GZ 6296-12-1-2-1-1 × IR 68333-R-R-B-19	128.33	31.67	27.33	5.95	25.93	94.91	45.17	38.53
GZ 6296-12-1-2-1-1 × IR 10K153	125.67	25.33	27.00	3.14	26.40	93.01	40.18	29.43
GZ 6296-12-1-2-1-1 × IR 11K 305	130.33	24.33	25.93	3.55	23.57	91.22	35.48	34.85
GZ 6296-12-1-2-1-1 × IR 12K 269	134.67	24.33	25.67	4.72	24.33	92.44	33.83	39.83
GZ 6296-12-1-2-1-1 × YEONGSAN	132.00	23.33	24.70	3.34	25.87	96.20	42.03	43.48
GZ 6296-12-1-2-1-1 × Namyang 6	135.67	32.33	26.77	4.96	26.00	97.74	45.77	48.53
LSD 0.05	1.78	1.89	1.53	0.54	1.35	1.73	1.97	2.02
LSD 0.01	2.36	2.51	2.04	0.71	1.80	2.29	2.62	2.68

**Table 5. Estimates of GCA effects of the studied parents for Maturity and yield studied traits during 2022 season.**

Parents	Days to maturity	Number of panicles/plants	Panicle length	Panicle weight	1000grain weight	Fertility	Grain yield /plant	Harvest index
Giza177	-1.13**	-2.18**	-0.54*	-0.35**	0.09	1.1**	0.85**	-0.76**
Sakha 104	4.63**	1.39**	-0.96**	-0.15*	-0.83**	-1.39**	-3.01**	-3.13**
Sakha 105	-2.23**	-0.13	-0.7**	-0.26**	-0.08	-1.49**	0.16	-1.56**
Sakha 106	-0.56*	-0.09	0.71**	0.24**	0.23	1.24**	1.34**	1.74**
GZ 6296-12-1-2-1-1	-0.7**	1.01**	1.48**	0.51**	0.6**	0.54*	0.65*	3.72**
HANGANGCHAL 1	-3.9**	-0.48	0.41	0.28**	0.4	-0.16	3.55**	0.52
IR 68333-R-R-B-19	-2.1**	2.12**	-0.21	0.01	0.13	-0.4ns	-1.83**	-0.92**
IR 10K153	0.7*	0.39	0.04	-0.01	-0.64**	-0.67*	-1.45**	-2.28**
IR 11K 305	1.23**	-1.48**	-0.33	-0.38**	-0.49*	-0.22	-2.29**	-0.26
IR 12K 269	0.1	-1.01**	-0.43	0.09	-0.6**	0.53	-1.73**	-0.87**
YEONGSAN	0.1	-0.88**	-0.13	-0.09	0.39	-0.18	0.54	1.39**
Namyang 6	3.9**	1.32**	0.65*	0.11	0.81**	1.11**	3.2**	2.42**
LSD 0.05 Line	0.48	0.51	0.41	0.14	0.36	0.46	0.53	0.54
LSD 0.01	0.63	0.67	0.54	0.19	0.48	0.61	0.70	0.72
LSD 0.05 Tester	0.56	0.60	0.48	0.17	0.43	0.55	0.62	0.64
LSD 0.01	0.75	0.79	0.64	0.23	0.57	0.73	0.83	0.85

\* and \*\* Significant at 0.05 and 0.01 levels, respectively.

Additionally, the majority of the variables that were studied—such as panicle length, panicle weight, fertility %, grain yield per plant, and harvest index showed high values of GCA effects for the Sakha 106 line. These findings are consistent with (Raju *et al.* 2014, Sathya and Jebaraj 2015 and

Foda 2021). While the male parent Namyang6 was the best combiner among testers, recording high positive and significant GCA values for most of the traits that were evaluated, including number of panicles per plant, panicle

length, 1000 grains weight, fertility percentage, grain yield per plant and harvest index.

In projects aimed at developing potentially high-yielding rice cultivars, the positive values of the GCA mean increased for the grain yield/plant values (Shiva *et al.* 2013), Thirumalai *et al.* (2018) and Zewdu (2020).

**Specific combining ability effects (SCA):**

Table 6 indicates the estimated SCA effects of the 35 hybrids. Among studied cross combinations seven crosses recorded significant positive values of SCA for three or more studied traits. The cross combinations namely, Giza177 × HANGANGCHAL1 possess significant and highly significant positive SCA effects for No. of panicle

per plant, panicle length, panicle weight, 1000 grain weight and grain yield per plant. Whereas, Sakha105× IR 12K 269 exhibited positive and highly significant SCA effects for No. of panicle per plant, panicle weight, spikelets Fertility percentage and harvest index with, while recorded negative high significant value of days to maturity. The similar results were obtained from the cross combinations Sakha104× IR 10K153, Sakha104× IR 11K 305, Sakha105×YEONGSAN and GZ 6296-12-1-2-1-1 × Namyang 6 where recorded high significant and positive estimates of SCA for most studied traits. However, the results confirm the findings of Roy and Mandal, (2001), Sarker *et al.*, (2002) and Abdalla *et al.*, (2021b).

**Table 6. Estimates of SCA effects (S<sub>ij</sub>) of hybrid combinations for all studied traits during 2022 season.**

Crosses	Days to maturity	Number of panicles/plants	Panicle length	Panicle weight	1000grain weight	Fertility	Grain yield /plant	Harvest index
Giza177× HANGANGCHAL1	-0.67	4.71**	1.18*	0.57**	1.69**	-1.54*	2.17**	-0.03
Giza177× IR 68333-R-R-B-19	0.53	-0.55	1.27*	-0.12	0.24	1.74**	4.62**	1.74*
Giza177× IR 10K153	-0.93	-2.15**	0.35	-0.21	0.16	-0.07	-3.58**	0.34
Giza177× IR 11K 305	0.2	2.05**	-0.95	0.28	-1.09*	-1.7**	0.12	2.06**
Giza177× IR 12K 269	2.67**	-0.75	-0.18	-0.42*	0.99*	0.53	2.51**	2.17**
Giza177×YEONGSAN	-1.67**	-1.89**	-1.14	-0.11	-1.64*	0.33	-7.42**	-4.49**
Giza177× Namyang 6	-0.13	-1.42*	-0.53	0.01	-0.35	0.71	1.59*	-1.80*
Sakha104× HANGANGCHAL1	1.57*	-3.86**	-0.94	-0.74**	0.05	2.55**	-0.07	6.74**
Sakha104× IR 68333-R-R-B-19	0.10	0.21	-0.81	-0.09	0.51	3.17**	0.92	-0.81
Sakha104× IR 10K153	2.97**	4.28**	0.57	1.68**	-2.86**	2.78**	4.26**	3.56**
Sakha104× IR 11K 305	-3.9**	-0.86	-0.53	0.03	2.66**	4.22**	6.05**	0.85
Sakha104× IR 12K 269	-1.76**	0.01	0.9	-0.33	0.70	1.05*	-0.64	-1.00
Sakha104×YEONGSAN	2.24**	0.21	0.08	0.42*	-0.59	-6.98**	-3.27**	-1.41
Sakha104× Namyang 6	-1.23*	0.01	0.72	-0.97**	-0.47	-6.78**	-7.25**	-7.92**
Sakha105× HANGANGCHAL1	-1.24*	-2.33**	0.8	-0.23	-0.81	-2.89**	-4.97**	-4.49**
Sakha105× IR 68333-R-R-B-19	1.63**	-2.6**	-0.07	-0.79**	-1.01*	-5.43**	-5.07**	-5.11**
Sakha105× IR 10K153	3.16**	0.13	-0.61	0.06	0.53	-2.83**	0.6	-1.28
Sakha105× IR 11K 305	3.63**	-1.33*	0.04	0.10	2.62**	0.64	0.93	1.6*
Sakha105× IR 12K 269	-2.24**	3.87**	-0.42	0.95**	-0.61	2.4**	-0.3	2.5**
Sakha105×YEONGSAN	-3.57**	5.73**	0.35	-0.09	-0.37	3.99**	6.6**	2.48**
Sakha105× Namyang 6	-1.37*	-3.47**	-0.10	0.01	-0.35	4.13**	2.22**	4.3**
Sakha106× HANGANGCHAL1	-2.9**	-1.38*	-1.01	0.5*	-0.79	0.03	0.77	0.52
Sakha106× IR 68333-R-R-B-19	-1.7**	0.69	-1.65**	-0.64**	-0.15	-0.26	-6.11**	3.47**
Sakha106× IR 10K153	0.83	0.09	-0.97	-0.37	0.52	0.97	-1.55*	4.41**
Sakha106× IR 11K 305	1.96**	1.62*	1.47*	-0.03	-2.86**	-0.06	-3.51**	-0.88
Sakha106× IR 12K 269	-2.24**	-1.18	-0.1	-0.53**	-0.62	-1.36*	4.22**	-5.63**
Sakha106×YEONGSAN	2.1**	-0.98	2.17**	0.65**	2.52**	0.81	3.96**	0.07
Sakha106× Namyang 6	1.96**	1.15	0.09	0.41*	1.38*	-0.15	2.23**	-1.96**
GZ 6296-12-1-2-1-1 × HANGANGCHAL1	3.24**	2.86**	-0.04	-0.09	-0.13	1.85**	2.1**	-2.74**
GZ 6296-12-1-2-1-1 × IR 68333-R-R-B-19	-0.56	2.26**	1.25*	1.64**	0.41	0.78	5.64**	0.71
GZ 6296-12-1-2-1-1 × IR 10K153	-6.03**	-2.34**	0.66	-1.16**	1.65**	-0.85	0.28	-7.03**
GZ 6296-12-1-2-1-1 × IR 11K 305	-1.90**	-1.48*	-0.03	-0.38	-1.33**	-3.1**	-3.58**	-3.63**
GZ 6296-12-1-2-1-1 × IR 12K 269	3.57**	-1.94**	-0.2	0.33	-0.46	-2.62**	-5.79**	1.96**
GZ 6296-12-1-2-1-1 × YEONGSAN	0.9	-3.08**	-1.46*	-0.88**	0.08	1.85**	0.14	3.35**
GZ 6296-12-1-2-1-1 × Namyang 6	0.77	3.72**	-0.18	0.54**	-0.2	2.09**	1.22	7.37**
LSD 0.05	1.26	1.34	1.08	0.38	0.96	1.22	1.40	1.43
LSD 0.01	1.67	1.78	1.44	0.50	1.27	1.62	1.85	1.90

\* and \*\* Significant at 0.05 and 0.01 levels, respectively.

**Heterosis:**

One of the key elements that contributes to the development of heterozygosity and yield is hybrid vigor, which results from the possibility of a superior gene content in a hybrid that can be supplied by both parents (Mather, 1955). Tables 7 and 8, respectively, show the heterotic respoes of hybrids above the mid-parent (average) and better parent (heterobeltiosis) for the eight variables under study.

Positive heterosis is preferred for every characteristic under study, with the exception of days to maturity. Significant positive and negative heterosis was seen in the traits under investigation. None of the hybrids in this investigation had demonstrated the most extreme

heterosis for all studied traits. Regardless, a desirable level and a significant of heterosis over mid-parent and better parent were gotten in several crosses. The crosses Giza177 × HANGANGCHAL1, Sakha105 × YEONGSAN, Sakha106 × HANGANGCHAL1, Sakha106 × YEONGSAN, Sakha106 × Namyang 6, GZ 6296-12-1-2-1-1 × HANGANGCHAL1 and GZ 6296-12-1-2-1-1 × Namyang 6 recorded a desirable level and positive significant and high significant values of heterotic for most studied traits including grain yield /plant Table 7. In previous similar studies, Ahmadikah 2008, Rahimi *et al.*, 2010, Ghidan *et al.*, 2019, and Foda 2021 found a high heterosis for rice grain yield and several yield components.

**Table 7. Heterosis relative to mid parent for days to maturity, yield and its component traits during 2022 season.**

Crosses	Days to maturity	Number of panicles/plants	Panicle length	Panicle weight	1000grain weight	Fertility	Grain yield/plant	Harvest index
Giza177× HANGANGCHAL1	-0.92	29.77**	15.48**	12.83*	3	-2.4**	20.35**	8.11**
Giza177× IR 68333-R-R-B-19	-0.51	11.59**	11.19**	-6.62	-3.63	1.35	16.54**	8.19**
Giza177× IR 10K153	0.13	-0.74	6.09*	-11.27	-6.63**	-0.81	-1.99	0.28
Giza177× IR 11K 305	2.19**	9.63*	2.76	-6.35	-10.78**	-2.43**	9.12**	13.41**
Giza177× IR 12K 269	4.71**	1.52	4.11	-7.08	-7.67**	1.34	8.97**	4.29
Giza177× YEONGSAN	-0.13	-0.78	1.17	-2.9	-9.34**	-0.96	-9.58**	-9.88**
Giza177× Namyang 6	3.73**	3.6	4.8	1.61	-0.46	0.35	19.19**	2.13
Sakha104× HANGANGCHAL1	1.52*	0.01	-0.28	-14.95*	0.21	-0.34	-1.55	27.91**
Sakha104× IR 68333-R-R-B-19	-0.12	22.45**	-3.99	1.87	0.89	0.62	-9.38**	-2.37
Sakha104× IR 10K153	3.7**	34.72**	0.89	49.23**	-15.83**	-0.05	1.76	8.07**
Sakha104× IR 11K 305	-0.25	5.56	-1.64	-6.1	7.54**	1.55	7.3**	7.32*
Sakha104× IR 12K 269	1.89**	13.48**	2.53	3.56	-5.81*	-0.35	-14.66**	-7.81**
Sakha104× YEONGSAN	3.48**	17.39**	0.28	21.53**	-1.99	-10.81**	-14.47**	-3.55
Sakha104× Namyang 6	3.47**	17.57**	3.91	-19.09**	2.82	-9.65**	-18.79**	-19.09**
Sakha105× HANGANGCHAL1	-1.71**	6.87	11.76**	-3.2	-6.12**	-6.47**	-6.89**	-6.29*
Sakha105× IR 68333-R-R-B-19	0.01	11.59**	3.4	-20.58**	-7.98**	-8.86**	-17.41**	-13.6**
Sakha105× IR 10K153	2.96**	18.52**	0.14	1.85	-4.77*	-6.4*8	-0.79	-5.22
Sakha105× IR 11K 305	4.54**	3.7	5.22	-6.26	3.94	-2.65**	0.85	11.82**
Sakha105× IR 12K 269	0.53	31.82**	1.16	41.09*8	-13.18*8	0.64	-7.37**	4.98
Sakha105× YEONGSAN	-1.95**	44.19**	5.8*	3.72	-4.01	0.2	15.9**	10.11**
Sakha105× Namyang 6	2.46**	3.6	4.74	7.15	0.07	1.26	10.32**	20.04*8
Sakha106× HANGANGCHAL1	-2.48**	8.96*	7.86**	25.61**	-3.02	0.03	8.33**	20.65**
Sakha106× IR 68333-R-R-B-19	-2.05**	23.4**	0.71	-5.12	-1.64	0.04	-17.95**	24.36**
Sakha106× IR 10K153	1.66**	15.94**	2.64	0.01	-1.78	1.08	-4.25*	23.81**
Sakha106× IR 11K 305	3.73**	14.49**	15.44	0.79	-14.47**	0.08	-8.5**	14.95**
Sakha106× IR 12K 269	1.04	6.67	6.61	6.36	-10.45**	0.15	5.13*	-9.1**
Sakha106× YEONGSAN	2.96**	10.61**	17.56	36.53**	10.48**	0.33	11.19**	13.18**
Sakha106× Namyang 6	5.52**	21.13**	9.44	28.82**	10.31**	0.24	11.99**	11.65**
GZ 6296-12-1-2-1-1 × HANGANGCHAL1	2.22**	30.88**	12.6	12.65*	5.77*	1.62*	10.11**	14.48**
GZ 6296-12-1-2-1-1 × IR 68333-R-R-B-19	-1.28*	32.87**	13.57	59.3**	6.79**	0.8	8.94**	19.73**
GZ 6296-12-1-2-1-1 × IR 10K153	-3.7**	8.57*	10.05	-17.55**	9.02**	-1.19	-1.19	-7.97**
GZ 6296-12-1-2-1-1 × IR 11K 305	0.64	4.29	9.58	-5.59	-2.62	-3.47**	-10.18**	10.44**
GZ 6296-12-1-2-1-1 × IR 12K 269	5.48**	6.57	6.87	33.81**	-4.39	-1.53	-19.94**	17.64**
GZ 6296-12-1-2-1-1 × YEONGSAN	1.93**	4.48	2.85	-5.2	7.11**	1.08	0.68	26.63**
GZ 6296-12-1-2-1-1 × Namyang 6	4.49**	34.72**	8.96	34.08**	10.48**	2.26**	8.24**	43.12**
LSD0.05	1.54	1.64	1.33	0.46	1.17	1.49	1.71	1.75
LSD0.01	2.05	2.18	1.76	0.62	1.56	1.99	2.27	2.32

\* and \*\* Significant at 0.05 and 0.01 levels, respectively.

**Table 8. Heterosis relative to better parent for days to maturity, yield and its component traits during 2022 season.**

Crosses	Days to maturity	Number of panicles/plants	Panicle length	Panicle weight	1000grain weight	Fertility	Grain yield /plant	Harvest index
Giza177× HANGANGCHAL1	-2.58**	14.86**	9.3**	2.96	-3.68	-2.72**	4.19	6.53*
Giza177× IR 68333-R-R-B-19	-3.97**	-4.94	3.68	-9.39	-9.82**	0.46	3.32	7.53*
Giza177× IR 10K153	-3.69**	-14.1**	-2.76	-15.51*	-12.86**	-1.71	-11.65**	-0.93
Giza177× IR 11K 305	-1.00	-5.13	-2.68	-9.64	-16.79**	-2.94**	0.98	10.56**
Giza177× IR 12K 269	2.83**	-10.67**	-2.74	-9.69	-9.76**	0.16	-4.9*	-0.07
Giza177× YEONGSAN	-3.25**	-11.11**	-5.48	-5.81	-15.6*8	-1.14	-20.31**	-14.72**
Giza177× Namyang 6	0.25	-12.2**	-4.06	-0.37	-9.52**	-0.26	3.96	-2.26
Sakha104× HANGANGCHAL1	-0.50	-5.41	-1.41	-23.82**	0.21	-0.4	-9.26**	23.63**
Sakha104× IR 68333-R-R-B-19	-0.25	11.11**	-6.55*	-3.1	0.82	0.11	-14.29**	-6.42*
Sakha104× IR 10K153	3.45**	24.36**	-3.55	39.35**	-16.01**	-0.58	-2.02	4.19
Sakha104× IR 11K 305	-0.74	-2.56	-2.68	-11.17	7.25*	1.4	6.29*	4.84
Sakha104× IR 12K 269	0.01	6.67	0.01	2.73	-9.98**	-1.14	-20.65**	-15.64**
Sakha104× YEONGSAN	2.97**	12.5**	-2.19	20.3**	-2.46	-11.31**	-19.62**	-12.79**
Sakha104× Namyang 6	3.22**	6.10	-0.79	-22.25**	-0.27	-10.52**	-24.53**	-26.06**
Sakha105× HANGANGCHAL1	-3.87**	-5.41	7.04**	-14.15*	-11.31**	-6.74**	-13.08**	-6.88*
Sakha105× IR 68333-R-R-B-19	-3.97**	-4.94	-2.46	-25.25**	-13.02**	-9.62**	-20.85**	-14.89**
Sakha105× IR 10K153	-1.48*	2.56	-7.16**	-5.87	-10.22**	-7.2**	-3.19	-6.06
Sakha105× IR 11K 305	0.75	-10.26**	0.85	-12.25	-2.07	-3.11**	0.42	11.3**
Sakha105× IR 12K 269	-1.8*	16**	-4.38	40.66**	-14.23**	-0.49	-12.77**	-1.40
Sakha105× YEONGSAN	-5.5**	29.17**	0.01	3.61	-9.73**	-0.03	10.34**	2.15
Sakha105× Namyang 6	-1.49*	-12.2**	-3.01	1.86	-8.15**	0.61	3.84	12.6**
Sakha106× HANGANGCHAL1	-3.87**	-1.35	5.35	15.67*	-6.81*	-0.28	2.16	19.38**
Sakha106× IR 68333-R-R-B-19	-5.21**	7.41*	-3.14	-7.02	-5.42*	-0.2	-20.54**	22**
Sakha106× IR 10K153	-1.97**	2.56	-3.02	-3.86	-5.8**	0.81	-5.56	22.19**
Sakha106× IR 11K 305	0.75	1.28	12.83**	-1.8	-18.03**	-0.03	-9.87**	14.9**
Sakha106× IR 12K 269	-0.51	-4	2.74	2.37	-10.95**	-0.38	0.04	-14.96**
Sakha106× YEONGSAN	0.01	1.39	13.29**	31.15**	5.67*	-0.49	6.97**	4.59
Sakha106× Namyang 6	2.24**	4.88	3.28	27.56**	2.94	-0.99	6.51**	4.31
GZ 6296-12-1-2-1-1×HANGANGCHAL1	0.77	20.27**	12.52**	7.83	5.34	0.89	3.6	13.65**
GZ 6296-12-1-2-1-1×IR 68333-R-R-B-19	-4.47**	17.28**	11.87**	56.03**	6.28*	0.63	5.24*	19.56**
GZ 6296-12-1-2-1-1 × IR 10K153	-7.14**	-2.56	6.44*	-17.66*	8.79**	-1.33	-2.78	-8.39**
GZ 6296-12-1-2-1-1 × IR 11K 305	-2.25**	-6.41	9.42**	-6.99	-2.75	-3.98**	-11.3**	8.46**
GZ 6296-12-1-2-1-1 × IR 12K 269	3.86**	-2.67	5.48	23.86**	-8.98**	-1.66	-24**	11.92**
GZ 6296-12-1-2-1-1 × YEONGSAN	-1.00	-2.78	1.51	-12.41	7.03*	-0.15	-3.37	18.98**
GZ 6296-12-1-2-1-1 × Namyang 6	1.24	18.29**	5.24	29.98**	7.59**	0.59	2.69	35.99**
LSD0.05	1.78	1.89	1.53	0.54	1.35	1.73	1.97	2.02
LSD0.01	2.36	2.51	2.04	0.71	1.80	2.29	2.62	2.68

\* and \*\* Significant at 0.05 and 0.01 levels, respectively

Furthermore, some hybrid combinations, i.e., crosses Giza177× HANGANGCHAL1, Sakha104× IR 11K 305, Sakha105× IR 12K 269, Sakha105×YEONGSAN, Sakha106×YEONGSAN and GZ 6296-12-1-2-1-1 × Namyang 6 gave positive significant and highly significant estimates heterosis over better parent (heterobeltiosis) for most studied traits including yield and its components Table 8.

**Percent contribution of population to total variance:**

The proportionate contribution of populations to the total variance indicated that, for the majority of the traits under study, such as the number of panicles per plant (65.34%), panicle weight (73.24%), 1000-grain weight

(76.05%), fertility percentage (81.19%), grain yield per plant (65.02%), and harvest index (61.45%), the interactions between lines and testers contributed significantly to the total variance when compared to lines and testers independently. In contrast, the maternal lines had a significant impact on the overall variance for the length of the panicle (49.82%) and the days to heading (34.84%). The results clearly showed that the lines and lines × testers interactions had highly contributed to the total variance that played essential role in dealing with the variation in the existing studies (Table 9).

**Table 9. The contribution rates of lines, testers and line×tester interaction for hybrid generation (%).**

Genotypes	Days to maturity	Number of panicles/plants	Panicle length	Panicle weight	1000grain weight	Fertility	Grain yield /plant	Harvest index
Line	34.84	17.51	49.82	20.11	10.50	15.38	10.99	28.35
Tester	32.20	17.15	7.70	6.66	13.44	3.42	23.99	10.2
Line × Tester	32.96	65.34	42.48	73.24	76.05	81.19	65.02	61.45

**CONCLUSION**

From the obtained results entire investigation, it can be concluded that based on performance and combining ability effects four genotypes two lines viz., GZ 6296-12-1-2-1-1 and Sakha 106, in addition to two testers HANGANGCHAL 1 and Namyang 6 among the parental genotypes were identified as a good combiner for most of the studied traits. On the other hand, the crosses Giza177 × HANGANGCHAL 1, Sakha 105 × IRI367 (YEONGSAN) and GZ 6296-12-1-2-1-1×Namyang 6 exhibited positive and significant heterosis, heterobeltiosis and SCA effects for grain yield plant-1 and some related studied traits. Hence, they may be extensively used in developing superior genotypes in future breeding programs.

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## التحليل الوراثي لبعض الصفات المتعلقة بالمحصول باستخدام نظام التزاوج السلالة $\times$ الكشاف في الأرز

مصطفى ممدوح الشناوي، وليد حسن الجمل، فاطمة عوض حسين و نعمة كمال الخولي

قسم بحوث الارز، معهد بحوث المحاصيل الحقلية، مركز البحوث الزراعية، مصر

### المخلص

أجريت هذه الدراسة قسم بحوث الأرز محطة بحوث سخا، كفر الشيخ، مركز البحوث الزراعية، مصر خلال علمي 2021 و 2022 و 2022. وتم اختيار خمسة من أهم الأصناف والسلالات المحلية من حيث المحصول والجودة وهم جيزة 177، سخا 104، سخا 105، سخا 106 و IRI 367 (YEONGSAN) و IRI 12K 269 و IRI 11K 305 و IRI 10K153 و IR 68333-R-R-B-19 و HANGANGCHAL 1 و Namyang 6 و IRI 367 (YEONGSAN) خمسة وثلاثين من هجن الجيل الأول الناتجة عن التهجين بين 5 سلالات  $\times$  7 كشافات. تم تقييم التراكيب الوراثية المدروسة لتحديد القدرة العامة و القدرة الخاصة على التآلف وكذلك قوة الهجين للمحصول والصفات المرتبطة به. أظهرت البيانات المسجلة على ثماني صفات، وجود فروق معنوية وعالية المعنوية بين التراكيب الوراثية: الآباء، الآباء مقابل الهجن، الهجن، السلالات، الكشافات و السلالات  $\times$  الكشافات لجميع الصفات تحت الدراسة ما عدا الآباء مقابل الهجن في صفة محصول الحبوب / نبات فردي كانت غير معنوية. أشارت تقديرات التباين ونسبة القدرة العامة و القدرة الخاصة على التآلف ودرجة السيادة إلى التأثير الجيني غير الإضافي لكل الصفات المدروسة. التراكيب الوراثية الأمومية الأبوية (السلالات)؛ سجلت IRI 367 (YEONGSAN) و IRI 12K 269 و HANGANGCHAL 1 و Namyang 6 ذات قدرة عامة على التآلف من بين الكشافات لمعظم الصفات المدروسة. وقد لوحظ أن التراكيب الوراثية جيزة 177  $\times$  HANGANGCHAL 1 و IRI 367 (YEONGSAN)  $\times$  IRI 12K 269 و IRI 11K 305 و IRI 10K153 و IR 68333-R-R-B-19 هي توليفات ذات قدرة خاصة على التآلف (SCA) عالية لمحصول الحبوب ومعظم الصفات المرتبطة بها نتيجة إلى قيمها العالية للقدرة الخاصة على التآلف و قوة الهجين. نسبة عالية من التباين ساهم بها التفاعل بين السلالة و الكشاف من إجمالي التباين الكلي متبوعه بالتباين الراجع للسلالات مقارنة بالكشافات.