



Genetic analysis of yield and some related traits in rice (*Oryza Sativa* L.) Using Line x Tester Design

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Abstract

Study was jointly done at Sustainable Development of Environment and Management its Projects Department, Environmental Studies and Research Institute, University of Sadat City and Rice Research and Training Center (RRTC), Sakha Research Station, Kafr EL-Sheikh, Agricultural Research Center (ARC), Egypt during 2018 and 2019. Four of the most important local varieties and lines were selected for yield and quality, i.e, Sakha 101, Sakha 104, and GZ 9461-4-2-3-1 and Giza 178 were used as lines and 4 testers. They are IRBL 7-M, IR12N245, IR12G3239 and Sakha Super300 in Line X Tester mating design. Sixteen new combinations developed from crossing four lines by four testers were assessed for the extent of combining ability effects, heterosis and genetic parameters for yield and related traits. The data recorded on seven yield characters showed highly significant differences among genotypes; parents, parents vs. crosses, crosses, lines, testers and line \times tester for the yield and its components. Estimates of the variance, ratio of general and specific combining ability and degree of dominance indicated the importance of non-additive gene effect for all studied traits. Within lines; Sakha 101, GZ 9461-4-2-3-1 and Giza 178 recorded the best general combining ability effects (GCA) for most of the studied traits. Among testers; IR12G3239 and Sakha Super300 were observed to be good general combiners for most of the studied characters. The cross combinations of GZ 9461-4-2-3-1 \times IR12G3239, Giza178 \times IR12G3239 and Sakha101 \times IRBL 7-M were observed to be good specific cross combinations for grain yield and most of its related traits due to highly significant specific combining ability effects (SCA) and heterotic effects. High broad and narrow sense heritability estimates were observed for most studied traits. Correlation estimates revealed that yield per plant correlated positively and significantly with each of number of panicles per plant, panicle length, panicle weight and number of filled grains per panicle.

Keywords: rice, GCA, SCA, Heterosis, Heritability, correlation, and line x tester

Introduction:

Rice (*Oryza sativa* L.) is the staple food source for more than half of the world's population. After wheat, rice is the second largest source of calories in the human diet and provides approximately 20% of the total calories consumed worldwide

(**Babaei et al., 2011**). In Egypt, rice is very important field crop, since more than half of Egyptians depend on it at their meals.

By the year 2025, about 756 million tonnes of paddy, which is 70 percent, more than the current production, will be needed to meet the growing demand (**Duwayri et al 1999**). Rice (*Oryza sativa* L.) is one of the major staple food crops for Egyptians (**Elmoghazy and Elshenawy 2018 and Abd El-Hadi, et al 2018**). Amazing advancement has been accomplished in rice productivity during the previous 50 years (**Ghidan et al., 2019**). The national yield average had exceeded 9.57 ton/ha during 2011 (**RRTC, 2012**). Food security is among the greatest difficulties of the 21st century. Worldwide rice request is evaluated to ascend from 676 million tons in 2010 to 763 million tons in 2020 and further increment to 852 million tons in 2035 (**Khush, 2013**). The world rice necessity by 2050 will be 943.6 million tons, which requires a yearly increment of about 5.8 million tons from the present degree of creation (**FAO, 2017**). Population increase will be more in developing countries (**Abd El-Hadi, et al 2018**).

Combining ability analysis is a powerful tool to discriminate good as well as poor combinors and selecting out appropriate parental material and best hybrid combinations (**Patil and Mehta, 2014**).

Heterosis is communicated in three different ways, contingent upon the criteria used to compare the performance of a hybrid (**Gupta, 2000**). These three different ways are mid-parent heterosis, better parent heterosis (heterobeltiosis) and standard heterosis. From a practical point of view, standard heterosis is a higher priority than the other two degrees of heterosis because it is planned for creating desirable hybrids superior to the existing better yielding commercial varieties (**Chaudhary, 1984**). Heterosis breeding is a significant genetic tool that can encourage yield upgrade from between 30 to 400% and improves numerous other desirable qualitative traits in crops (**Srivastava, 2000**). Breeding methodologies based on hybrid production require an elevated level of heterosis as well as the specific combining ability of crosses. One of the fundamental issues of plant breeders for improving high yielding varieties is to choose acceptable good parents and crosses.

The mating designs give solid data about general combining ability and specific combining ability of the parents and hybrids. The differences in general combining ability are mainly due to additive gene action, while the differences in the specific combining ability are attributed to non-additive gene effects (**Ghidan et al., 2019**). Estimation of general combining ability helps the breeder to identify parents with the superior combining ability that maybe crossed to utilize heterosis (**Fasahat et al., 2016**). In this way, the information on combining ability gives data on the nature and extent of gene effects that organize grain yield and yield traits, hence enabling the breeder to design an effective breeding method for genetic upgrading of yield and its components (**Dar et al., 2014**). Past investigations revealed an

expansion in grain yield because of ideal heterosis for traits such as number of spikelets per plant, flag leaf area and number of filling grains per panicle (**Vanaja and Babu 2004**).

Line x tester is helpful in choosing the proportional ability of female and male lines to deliver desirable hybrid combinations. It additionally gives data on genetic components and enables the breeder to choose appropriate strategies for development breeding programs (**Ghidan et al., 2019**). Data on general and specific combining ability for characters will demonstrate valuable in the determination of appropriate parents for the improvement of superior hybrids. The information on heritability and genetic advance might be useful in some promising material selection from the current population, which would be of most significance (**Kemphorne, 1957**). The present research work was done with the targets to evaluate combining ability dependent on mean performance, genetic components, heterosis and heterobeltiosis for some vegetative and yield traits in rice. Broad and narrow-sense heritability and phenotypic correlation coefficient were estimated for all studied traits. The data got in this way will be utilized in the selection of suitable parents and choice of appropriate breeding tools to upgrade high yielding rice genotypes.

Materials and Methods

This study is carried out at Sakha Agricultural Research Station experimental farm and Rice Research and Training Center (RRTC), Sakha, Kafr Elsheikh, Egypt, during the two successive summer seasons 2018 and 2019.

Experimental design and plant materials

The experimental material consisted of eight parental genotypes and their sixteen F1 crosses according to the line x tester mating design during the 2018 and evaluated during 2019 rice growing seasons. Four Egyptian genotypes i.e., the three commercial varieties; Sakha 101, Sakha 104, Giza 178 and the promising line GZ 9461-4-2-3-1 were used as females (lines) and were crossed with four diverse genotypes i.e., IRBL 7-M, IR12N245, IR12G3239 and Sakha Super300 which used as males (testers). Thus, the resultant sixteen crosses along with their parents were evaluated in a randomized complete block design with three replications.

Data collection

All agricultural practices are made according to rice recommendations of **RRTC (2015)**. According to Standard Evaluation System, SES of **IRRI (2014)**. observations on yield traits were recorded based on five plants in every genotype in each replication. Every genotype was raised in 2.5 m long single row plot, keeping 20 x 15 cm dividing. Seven yield traits were studied for randomly selected plants from every replication viz., Number of panicles plant¹, panicle length (cm), panicle weight (g), Number of filled

grains panicle⁻¹, spikelets fertility percentage (%), 1000-grain weight (g) and grain yield plant⁻¹ (g).

Statistical analysis

The data is subjected to analysis of variances for a randomized complete block design as suggested by **Panase and Sukhatme (1954)**. The mean data of each trait was exposed to analysis of variance (ANOVA), to estimate significant differences among crosses and parents as proposed by **Steel and Torrie (1980)**. The general combining ability (GCA) effects of the parents and the specific combining ability (SCA) effects of the hybrids were dictated by the utilization of the line x tester mating design (**Kemphorne, 1957**). The estimation of heterosis of an individual cross for every characteristic was resolved as the increase of the F1 hybrid mean over either mid-parent and better parent. Heterotic and combining ability effects were tested by the least significant differences (LSD) test at the 0.05 and 0.01 levels using the t-test. Correlation coefficients (r) among every considered trait were registered to utilize the SPSS statistical package according to **Gomez and Gomez (1984)**. Some important genetic parameters such as additive variance, non-additive variance, broad sense heritability (h^2_b), narrow sense heritability (h^2_n) and genetic advance were also estimated according to **Falconar and Mackey (1996)**.

Results and Discussion

Analysis of variance:

The analysis of variance for all studied traits are presented in Table 1. The results dedicated highly significant differences among the rice genotypes for all the studied characters. The presence of genetic variability is pre-essential for the selection of predominant genotypes during crop improvement programs. Therefore, the assessment of the extent of variation present in the genetic material is important to estimate the magnitude of improvement that can be achieved in breeding material for various characters (**Ghidan *et al.*, 2019**). Genotypic mean squares were further partitioned into parents, crosses and parents vs. crosses. The analysis of variance uncovered highly significant differences among genotypes, crosses, lines, testers, and line x tester were observed in all studied characters. Variation among parents and parent vs. crosses were highly significant for most of the studied traits except panicle length and panicle weight, which were non-significant as present in Table 1. The significance of line x tester for all the traits gave an immediate test, showing that non-additive variances were significant for most of these traits. This reveals high variability among the genotypes providing abundant scope of selection for different quantitative traits. A significant variation for various quantitative traits was also reported (**Bekele *et al.*, 2013; Sandhya *et al.*, 2014 and Ghidan *et al.*, 2018**). Estimates of variance due to general combining

ability (σ^2_{gca}) were lower than those of variance due to specific combining ability (σ^2_{sca}) for all the traits indicate that the dominance genes were played important role in the inheritance of these traits. The ratio of variance due to general to specific combining ability ($\sigma^2_{gca}/\sigma^2_{sca}$), were less than unity for all the traits and degree of dominance being greater than unity. It suggested greater importance of non-additive gene action in its expression and indicated very good prospect for the exploitation of non-additive genetic variation for these traits through hybrid breeding (**Ramalingam *et al*, 1997; Annadurai and Nadarajan, 2001**).

Mean performance of genotypes:

The mean performance of the parents and their F_1 crosses for yield traits are presented in Table 2. There were significant differences between the lines for all the measured traits, the line Sakha 101 recorded the desirable values for the panicle length, panicle weight, fertility percentage % and 1000 grain weight. The Giza178 showed the desirable value for No. of panicles plant¹, filled grain per panical and grain yield per plant.

For testers, the Sakha Super 300 gave the desirable values panicle weight, filled grain per panical, 1000 grain weight and grain yield per plant. Among the hybrid combinations, Giza178×IR12G3239 showed the desirable value for No. of panicle per plant, filled grain per panical and grain yield per plant. The hybrid combination GZ 9461-4-2-3-1×IR12G3239 showed th

e desirable value for panicle weight and 1000 grain weight. The hybrid combination.

Table (1): Estimates of the mean square of line x tester analysis for yield and its component traits during 2019 season.

Sources of variation	D f	Mean square						
		No. of panicle plant ⁻¹	Panicle length (cm)	Panicle weight (g)	Filled grain panical ⁻¹	Fertility percentage (%)	1000- grain weight (g)	Grain yield plant ⁻¹
Replication	2	1.21	0.35	0.01	0.20	0.07	0.24	0.53
Genotypes	23	624.68**	724.62**	13.90**	23162.31**	7594.15**	767.41**	2843.22**
Parents (p)	7	300.59**	355.22**	7.20**	14902.46**	5738.74**	458.13**	1327.30**
Crosses (c)	15	816.42**	945.18**	17.95**	28169.29**	8483.96**	957.68**	3736.89**
P vs C	1	17.10**	2.02	0.01	5876.43**	7234.85**	78.27**	49.55**
Lines	3	1772.03**	2081.76**	38.85**	62408.34**	18689.26**	2116.72**	8302.17**
Testers	3	1792.92**	2103.67**	39.20**	62534.96**	18887.03**	2115.70**	8263.59**
L x T	9	172.39**	180.15**	3.90**	5301.06**	1614.50**	185.33**	706.22**
Error	46	0.66	0.62	0.01	2.09	0.65	0.44	0.69
δ^2_{gca}		22.36	26.56	0.49	794.04	238.52	26.82	105.23
δ^2_{sca}		57.24	59.84	1.30	1766.32	537.95	61.63	235.18
$\delta^2_{gca} / \delta^2_{sca}$		0.039	0.044	0.038	0.045	0.044	0.043	0.045

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

Table (2): The mean performances of yield and its component traits for studied genotypes during 2019 season.

Genotypes	No. of panicle plant ⁻¹	Panicle length (cm)	Panicle weight (g)	Filled grain panical ⁻¹	Fertility percentage (%)	1000-grain weight (g)	Grain yield per plant ⁻¹ (g)
lines							
Sakha 101 (P1)	21.67	24.33	3.47	153.00	95.83	28.34	44.30
Sakha 104 (P2)	20.67	23.33	3.33	143.67	93.09	25.92	42.41
GZ 9461-4-2-3-1 (P3)	23.00	22.67	3.16	140.33	91.13	27.17	42.83
Giza 178 (P4)	24.00	21.33	2.97	159.33	91.40	22.01	49.38
Mean	22.33	22.92	3.23	149.08	92.86	25.86	44.73
Tester							
IRBL 7-M (P5)	16.33	24.33	2.53	136.67	87.61	23.55	42.45
IR12N245 (P6)	15.00	20.33	2.43	127.00	84.86	21.91	38.28
IR12G3239 (P7)	20.33	23.67	3.47	144.33	93.53	27.18	40.74
Sakha Super300 (P8)	17.67	19.33	3.53	159.67	92.11	26.46	46.79
Mean	17.33	21.92	2.99	141.92	89.53	24.77	42.07
Crosses							
Sakha 101× IRBL 7-M	33.33	28.67	3.07	161.67	87.39	30.02	54.83
Sakha 101× IR12N245	23.67	27.33	3.96	153.33	82.74	31.02	52.45
Sakha 101× IR12G3239	25.33	29.67	4.23	149.67	92.58	28.75	57.96
Sakha 101× Sakha Super300	24.00	27.33	4.18	163.67	89.11	30.07	59.53
Sakha 101× Sakha Super300	24.00	28.33	4.81	148.67	86.27	28.38	52.50
Sakha 101× Sakha Super300	21.00	27.00	3.83	147.00	84.81	27.24	49.85

Sakha 104× IRBL 7-M	25.33	30.67	4.23	151.33	93.42	30.98	56.58
	26.67	27.00	3.92	164.67	81.93	27.27	57.51
Sakha 104× IR12N245	28.00	28.67	3.73	145.33	80.29	28.32	55.37
Sakha 104× IR12G3239	25.33	30.33	3.26	151.00	78.25	28.04	52.38
	28.67	31.67	4.22	159.33	93.00	31.16	55.36
Sakha104× Sakha Super300	25.33	26.33	3.97	159.33	88.03	28.89	57.08
	26.33	30.33	3.23	156.67	73.59	24.45	62.20
GZ 9461-4-2-3- 1× IRBL 7-M	24.67	25.67	3.05	155.67	78.23	25.40	58.83
GZ 9461-4-2-3- 1× IR12N245	31.00	30.00	4.17	165.00	91.50	30.33	64.16
	26.33	27.00	4.03	163.67	83.37	28.27	59.38
GZ 9461-4-2-3- 1×IR12G3239							
GZ 9461-4-2-3- 1× Sakha Super300							
Giza 178×IRBL 7-M							
Giza 178×IR12N245							
Giza178×IR12G 3239							
Giza178× Sakha Super300							
Mean	26.19	28.50	3.87	156.00	85.28	28.66	56.62
G. Mean	24.07	26.47	3.62	152.50	87.25	27.55	52.22
LSD 0.05	1.33	1.29	0.026	2.37	1.32	1.09	1.37
0.01	1.78	1.73	0.035	3.18	1.77	1.45	1.83

Combining ability analysis

The general combining ability recognizes predominant parents while specific combining ability helps in the distinguishing of good hybrid combinations that may at last lead to the improvement of hybrids (**Shiva *et al.*, 2013**).

General combining ability (GCA):

The general combining ability effects of some yield traits are exhibited in Table 3. Among the male (testers) parents, IR12G3239 was a good general combiner for most of the studied traits because it has high positive GCA effects for most characters i.e., number of panicles per plant, panicle length panicle weight, fertility percentage, 1000-grain weight and grain yield per plant. The tester Sakha S 300 had the highest GCA effects for grain yield per plant, also revealed significant and desirable GCA effects for No. of filled grain per panical and panicle weight. Previous studies also announced good general combiners for yield and its component characters in rice genotypes (**Raju *et al.*, 2014; Sathya and Jebaraj, 2015 and Devi *et al.*, 2017**). While, the female (line) GZ 9461-4-2-3-1 recorded high and positive GCA effects for No. of panicle per plant, panicle length and 1000 grain weight, the (line) Giza 178 recorded high and positive GCA effects for No. of panicle per plant, No. of filled grain per panical and grain yield per plant.

It could be recommended that through the parental genotypes (lines and testers), each parent recorded the highest value for any trait under study is considered as good combiner for this trait and could be used in breeding programs to develop new promising lines for this trait. In other study by **Rahimi *et al.* 2010** found that, the significance of specific combining ability (SCA) and general combining ability (GCA) for all studied traits revealed that, both additive and non-additive gene effects contributed to the inheritance of the tr

Table (3): Estimates of GCA effects of the studied parents for yield traits studied during 2019 season.

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

Genotypes	Traits						
	No. of panicle plant ⁻¹	Panicle length (cm)	Panicle weight (g)	Filled grain Panical ⁻¹	Fertility percentage (%)	1000- grain weight (g)	Grain yield per plant ⁻¹ (g)
Lines:							
Sakha 101 (P1)	0.40	-0.25	-0.01	1.08*	2.67**	1.30**	-0.43
Sakha 104 (P2)	-1.94	-0.25	0.33**	-3.08	1.32**	-0.19	-2.51
GZ 9461-4-2-3-1 (P3)	0.65**	0.75**	-0.07	-2.25	-0.39	0.44*	-1.58
Giza 178 (P4)	0.90**	-0.25	-0.25	4.25**	-3.61	-1.55	4.52**
Testers:							
IRBL 7-M (P5)	1.73**	0.50*	-0.16	-2.92	-3.40	-0.87	-0.40
IR12N245 (P6)	-2.52	-0.92	-0.34	-4.25	-4.28	-0.74	-3.25
IR12G3239 (P7)	1.40**	2.00**	0.34**	0.33	7.34**	1.65**	1.89**
Sakha Super300 (P8)	-0.60	-1.58	0.16**	6.83**	0.33	-0.04	1.75**
L.S.D. for lines	0.05	0.47	0.46	0.009	0.84	0.47	0.38
	0.01	0.63	0.61	0.012	1.12	0.62	0.51
L.S.D. for testers	0.05	0.47	0.46	0.009	0.84	0.47	0.38
	0.01	0.63	0.61	0.012	1.12	0.62	0.51

Specific combining ability effects (SCA) of F1 Hybrids: The estimates of SCA effects of the 16 hybrids are presented in Table 4. The cross combinations namely, Giza178 x IR12G3239 possess highly significant and positive SCA effects for No. of panicle per plant, panicle weight, No. of filled grain per panical, fertility percentage, 1000 grain weight and grain yield per plant. Whereas, Sakha 101 x IRBL 7-M exhibited positive and highly significant SCA effects for No. of panicle per plant, No. of filled grain per panical, spikelets Fertility percentage and 1000 grain weight. However, the results confirm the findings of **Roy and Mandal, (2001) and Sarker et al., (2002)**. More number of panicles/plant and increased panicle length is also a desirable trait of rice hybrids with increased yield/plant. Yield/plant is an ultimate objective of rice breeding and hybrid development programmes. The high yield potential noticed in the crosses with high x low general combining ability combinations could be attributed to an interaction among positive alleles in the great

combiner and negative alleles in the poor combiner (**Hasan *et al.*, 2015**). High SCA effects of hybrids that started from high x low general combining ability combining parents would be unfixable in subsequent generations and thus cannot be abused by pedigree selection strategy (**Sathya and Jebaraj, 2015**). However, these crosses would deliver desirable transgressive segregates in later generations on change of the conventional breeding methodology approaches to understand both additive and non-additive genetic effects (**Chakraborty *et al.*, 2009**).

Table (4): Estimates of SCA effects (Sij) of hybrid combinations for yield traits studied and its component during 2019 season.

Hybrid combination	Traits						
	No. of panicle plant ⁻¹	Panicle length (cm)	Panicle weight (g)	Filled grain panical ⁻¹	Fertility percentage (%)	1000-grain weight (g)	Grain yield per plant ⁻¹ (g)
Sakha 101 x IRBL 7-M	5.02**	-0.08	-0.63	7.50**	2.83**	0.93*	-0.96
Sakha 101x IR12N245	-0.40	0.01	0.44**	0.50	-0.94	1.79**	-0.50
Sakha 101x IR12G3239	-2.65	-0.58	0.03**	-7.75	-2.72	-2.86	-0.13
Sakha101x Sakha Super300	-1.98	0.67	0.16**	-0.25	0.83	0.14	1.58**
Sakha 104x IRBL 7-M	-1.98	-0.42	0.77**	-1.33	3.06**	0.78*	-1.21
Sakha 104x IR12N245	-0.73	-0.33	-0.02	-1.67	2.48**	-0.49	-1.02
Sakha 104x IR12G3239	-0.31	0.42	-0.31	-1.92	-0.53	0.87*	0.58
Sakha104x Sakha Super300	3.02**	0.33	-0.43	4.92**	-5.01	-1.16	1.65**
GZ 9461-4-2-3-1x IRBL 7-M	-0.56	-1.08	0.09**	-5.50	-1.20	0.09	0.72
GZ 9461-4-2-3-1x IR12N245	1.02*	2.00**	-0.19	1.50	-2.37	-0.32	0.58
GZ 9461-4-2-3-1xIR12G3239	0.44	0.42	0.08**	5.25**	0.76	0.42	-1.58
GZ 9461-4-2-3-1x Sakha Super300	-0.90	-1.33	0.02**	-1.25	2.81**	-0.18	0.28
Giza 178xIRBL 7-M	-2.48	1.58**	-0.23	-0.67	-4.69	-1.79	1.45**
Giza 178xIR12N245	0.10	-1.67	-0.23	-0.33	0.83	-0.98	0.93
Giza178xIR12G3239	2.52**	-0.25	0.21**	4.42**	2.48**	1.58**	1.13*

Giza178x Sakha Super300	-0.15	0.33	0.25**	-3.42	1.37**	1.19**	-3.51
LSD 0.05	0.94	0.92	0.018	1.68	0.93	0.77	0.97
0.01	1.26	1.23	0.025	2.25	1.25	1.03	1.29

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

Genetic parameters and heritability: The phenotypic and genotypic coefficients of variance can be utilized for evaluating and contrasting the nature and magnitude of variability contained for different traits in the breeding materials. Heritability in a broad sense measures the extent of heritable genetic variance to total phenotypic change, while heritability in a narrow sense represents the fixable additive genetic variance ratio to total phenotypic change. Estimates of heritability help in assessing anticipated advancement through selection (Devi *et al.*, 2017). The estimates of genetic parameters were computed for seven traits of 16 crosses and their eight parents in Table 5. Additive and non-additive variances were significant for all the studied traits. However, non-additive effects played more important role as confirmed by value of degree of dominance (d). This parameter in all traits were estimated to be more than unity indicating that over-dominance is preponderant in controlling the studied traits. Several researchers also reported the predominance of dominant gene action for a majority of the yield traits Satyanarayana *et al.*, (2000); Kumar *et al.*, (2004), while Vijay Kumar *et al.* (1994) reported that, the predominance of additive gene and must be used in combination with other parameters action. Preponderance of non-additive gene action in the expression of yield and yield-related traits was also reported by Pradhan *et al.* (2006), and Thirumeni *et al.* (2000). The heritability in broad sense (h_2b) was obtained for studied traits over (85%), indicating slight effects of environment on these traits. In all cases, a low narrow sense heritability (h_2n) was obtained. Ahmadikhah (2008) also reported a low specific heritability for yield-related traits and Wu *et al.* (1986) reported a low specific heritability for tillers number and grain yield. Therefore, it seems that hybridization must be a choice for utilizing the putative heterosis in special crosses. Heritability is a valuable quantitative parameter, which finds the role of heredity and the environment, determining the expression of a trait. In the present study, high estimates of heritability in a broad sense were observed for all traits.

Table (5): Estimates of genetic parameters and heritability in broad and narrow senses for yield and its component traits studied during 2019 season.

Genetic parameters and heritability	Traits						
	No. of panicle plant ⁻¹	Panicle length (cm)	Panicle weight (g)	Filled grain panical ⁻¹	Fertility percentage (%)	1000-grain weight (g)	Grain yield per plant ⁻¹ (g)
Additive variance (σ^2A)	44.72	53.13	0.98	1588.07	477.05	53.64	210.46
dominant variance (σ^2D)	57.24	59.84	1.30	1766.32	537.95	61.63	235.18
Genotypic variance (σ^2G)	101.97	112.97	2.28	3354.39	1015.00	115.27	445.64
Environmental variance (σ^2E)	0.66	0.62	0.01	2.09	0.65	0.44	0.69
Phenotypic variance (σ^2P)	102.63	113.59	2.28	3356.49	1015.64	115.71	446.33
Broad sense heritability (h ² b%)	99.36	99.45	99.99	99.94	99.94	99.62	99.84
Narrow sense heritability (h ² n%)	43.58	46.77	42.87	47.31	46.97	46.35	47.15
Relative importance of gca%*	0.44	0.47	0.43	0.47	0.47	0.47	0.47
Relative importance of sca%**	0.56	0.53	0.57	0.53	0.53	0.53	0.53
Dominance of the degree (d)	1.13	1.06	1.15	1.05	1.06	1.07	1.06

* Relative importance of gca% = σ^2A/σ^2G

** Relative importance of sca% = σ^2D/σ^2G

Heterosis

Heterosis is the reason for the development of harvest yield and heterozygosity, which is because of superior gene content possible in a contributed hybrid by both the parents (Mather, 1955). The heterotic responses of hybrids over mid-parent (average) and better parent (heterobeltiosis) for the eleven studied traits are presented in Tables 6 and 7, respectively.

For the all studied traits, positive heterosis is desirable. It was seen that a significant positive and negative heterosis in the studied traits. None of the hybrids in this investigation had demonstrated the most extreme heterosis for all the traits. In any case, a desirable level and a significant of heterosis over mid-parent and better parent were gotten in several crosses.

In addition, all hybrid combinations gave positive significant and highly significant heterotic effects. As well, the better parent was found to be highly significant and positive heterotic effects in the all hybrids for the same trait.

For Fertility percentage (%), the maximum significant and positive mid-parent heterosis and heterobeltiosis were exhibited in hybrid GZ 9461-4-2-3-1xIR12G3239, also most hybrids were negative for this trait.

The all hybrids had the positive and high significant mid-parent heterosis and heterobeltiosis effect for traits namely number of tillers plant⁻¹, number of panicles plant⁻¹, panicle length, panicle weight, Filled grain panical⁻¹, 1000- grain weight and grain yield per plant⁻¹ traits.

Table (6): Heterosis relative to mid parent for yield and its component traits studied during 2019 season.

Hybrid combination	Traits						
	No. of panicle plant ⁻¹	Panicle length (cm)	Panicle weight (g)	Filled grain panical ⁻¹	Fertility percentage (%)	1000-grain weight (g)	Grain yield per plant ⁻¹ (g)
Sakha 101/ IRBL 7-M	75.44**	17.81**	2.39**	11.62**	-4.72	15.68**	26.41**
Sakha 101x IR12N245	29.09**	22.39**	33.97**	9.52**	-8.42	23.45**	27.03**
Sakha 101x IR12G3239	20.63**	23.61**	21.81**	0.67	-2.22	3.55**	36.32**
Sakha101x Sakha Super300	22.03**	25.19**	19.37**	4.69**	-5.17	9.74**	30.70**
Sakha 104x IRBL 7-M	29.73**	18.88**	64.16**	6.06**	-4.52	14.71**	23.74**
Sakha 104x IR12N245	17.76**	23.66**	33.02**	8.62**	-4.68	13.91**	23.55**
Sakha 104x IR12G3239	23.58**	30.50**	24.37**	5.09**	0.12	16.69**	36.10**

Sakha104x Sakha Super300	39.13**	26.56**	14.38**	8.57**	-11.53	4.13**	28.95**
GZ 9461-4-2-3-1x IRBL 7-M	21.74**	26.47**	17.81**	3.56*	-11.89	4.21**	29.27**
GZ 9461-4-2-3-1x IR12N245	10.14**	33.82**	2.95**	7.60**	-14.14	3.20**	22.29**
GZ 9461-4-2-3-1xIR12G3239	24.64**	39.71**	33.30**	13.54**	2.06*	14.68**	29.26**
GZ 9461-4-2-3-1x Sakha Super300	10.14**	16.18**	25.61**	13.54**	-3.40	6.31**	33.26**
Giza 178xIRBL 7-M	30.58**	32.85**	17.40**	5.86**	-17.78	7.31**	35.46**
Giza 178xIR12N245	26.50**	23.20**	12.84**	8.73**	-11.23	15.66**	34.22**
Giza178xIR12G3239	39.85**	33.33**	29.53**	8.67**	-1.04	23.34**	42.40**
Giza178x Sakha Super300	26.40**	32.79**	24.06**	2.61	-9.13	16.64**	23.49**

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

Table (7): Heterosis relative to better parent for yield traits and its component studied during 2019 season.

Hybrid combination	Traits						
	No. of panicle plant	Panicle length (cm)	Panicle weight (g)	Filled grain panical ⁻¹	Fertility percentage (%)	1000-grain weight (g)	Grain yield per plant-1 (g)
Sakha 101 x IRBL 7-M	53.85**	17.81**	-11.52	5.66**	-8.81	5.90**	23.77**
Sakha 101x IR12N245	9.23**	12.33**	13.92**	0.22	-13.66	9.43**	18.40**
Sakha 101x IR12G3239	16.92**	21.92**	21.69**	-2.18	-3.39	1.42*	30.83**
Sakha101x Sakha Super300	10.77**	12.33**	18.41**	2.51*	-7.01	6.09**	27.22**
Sakha 104x IRBL 7-M	16.13**	16.44**	44.44**	3.48**	-7.33	9.48**	23.68**
Sakha 104x IR12N245	1.61	15.71**	15.12**	2.32	-8.90	5.09**	17.54**
Sakha 104x IR12G3239	22.58**	29.58**	21.92**	4.85**	-0.11	13.99**	33.42**
Sakha104x Sakha Super300	29.03**	15.71**	11.14**	3.13*	-11.99	3.07**	22.91**
GZ 9461-4-2-3-1x IRBL 7-M	21.74**	17.81**	17.81**	3.56**	-11.89	4.21**	29.27**

GZ 9461-4-2-3-1x IR12N245	10.14**	33.82**	2.95**	7.60**	-14.14	3.20**	22.29**
GZ 9461-4-2-3-1xIR12G3239	24.64**	33.80**	21.63**	10.39**	-0.56	14.67**	29.26**
GZ9461-4-2-3-1xSakha Super300	10.14**	16.18**	12.56**	-0.21	-4.43	6.31**	21.98**
Giza 178xIRBL 7-M	9.72**	24.66**	8.76**	-1.67	-19.48	3.79**	25.96**
Giza 178xIR12N245	2.78**	20.31**	2.70**	-2.30	-14.41	15.39**	19.14**
Giza178xIR12G3239	29.17**	26.76**	20.19**	3.56**	-2.16	11.62**	29.94**
Giza178x Sakha Super300	9.72**	26.56**	14.16**	2.51*	-9.49	6.84**	20.26**

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

Phenotypic correlation coefficient:

Complete information of the interrelationship of plant traits like grain yield with different characters is of fundamental significance to the plant breeder for improving in complex quantitative traits like grain yield for which direct choice is not a lot of compelling. Hence, investigation was attempted to decide the direction of selection and number of traits to be considered in developing grain yield. **Ghidan et al., 2019** stated that correlations are measures of the intensity of association between traits. The selection for one trait results in progress for all characters that are positively correlated and retrogress for traits that are negatively correlated **Steel and Torrie (1984)**. The phenotypic correlation coefficient among the seven studied traits was assessed and presented in Table 8.

Grain yield plant⁻¹ was highly significantly and positively correlated with number of panicles plant⁻¹, panicle length, panicle weight and number of filled grain/panical indicating the importance of these traits as selection criteria in yield enhancement programs. **Hallauer and Miranda (1988)** in a similar study reported that plant vigour is positively correlated to yield suggesting that during selection emphasis should be placed on plant with vigour as this would be translated with good yield. At last, 1000- grain weight exhibited a significant and positive phenotypic correlation with the, number of panicles plant⁻¹, Panicle length and panicle weight. These findings were in full compatible with the past announced by (**Ghidan et al., 2019**).

Table (8): Phenotypic correlation coefficients among yield and its component traits of some rice genotype during 2019 season.

Trait	NOP	PAL	PAW	FGP	FEP%	TGW	GYP ¹
NOP	1.00	0.739**	0.437*	0.673**	-0.166	0.605**	0.776**
PaL		1.00	0.573**	0.379	-0.277	0.662**	0.743**
PaW			1.00	0.480*	0.177	0.757**	0.561**
FGP				1.00	-0.035	0.469*	0.752**
Fe.P%					1.00	0.219	-0.371
TGW						1.00	0.489*
GYP-1							1.00

* Significant at 0.05 level, ** Significant at 0.01 level

Abbreviation No. of panicle/ plant= PAP : Panicle length= PAL; Panicle weight= PAW;; Filled grain/panical= FGP: Fertility percentage (%)=FEP%: Thousand grain weight= TGW: Grain yield / plant = GYP¹

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