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Identifying the Genes of Blast Resistance in Rice (*Oryza sativa* L.) Using Line X Tester Analysis

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ABSTRACT

The present study investigation was carried out at the Experimental Farm of Rice Research and Training Center (RRTC), Sakha, Kafr El-Sheikh, Egypt, during the three successive growing seasons of 2014, 2015 and 2016. Four rice genotypes namely; Sakha 101, Sakha 102, Sakha103 and Sakha 104 were used as Lines and four monogenic lines; i.e., IRBLKS-S, IRBL3-CP4, IRBL5-M and IRBL7-M, were used as Testers, which cried blast resistance genes Pik-s, Pi3, Pi5(t) and Pi7(t). Under field condition, the results showed that the varieties Sakha 102 and Sakha 103 were resistant to blast under the three locations, Sakha, Gemmiza and Zarzoura. On the contrary, the other two Egyptian varieties Sakha 101 and Sakha104 were susceptible. Moreover, the monogenic lines (IRBLKS-S, IRBL3-CP4, IRBL5-M and IRBL7-M) were blast resistant under natural infection conditions. On the other hand, under five artificial inoculations races IA-77, IG-1, ID-15, IC-17 and IB-45 of *Magnaporthe grisea,* the results revealed that Sakha 102 and Sakha 103 variety were resistant to all races, except IB-45 race, which were susceptible. While, the two Egyptian varieties, Sakha 101 and Sakha 104 were susceptible to blast of the five races. For monogenic rice genotypes, results showed that IRBLKS-S, IRBL3-CP4 and IRBL5-M which carried (Pik-s, Pi3 and Pi5) blast resistance genes were resistant to all races, except EG-5 race, which were susceptible and the other rice monogenic line IRBL7-M which carry Pi7(t) was resistant against IG-1, 367 and 374 races and susceptible under EG-5 and IB-45 races of *M. grisea*. The results also suggested that the six major genes; Pi-i, Pi-sh, Pik-s, Pi3, Pi5, Pi7 (t) were effective under Egyptian conditions and can be used for improving blast resistance character in breeding program. The results of the inheritance of blast resistance using sixteen F_1 and F_2 rice populations showed that all F_1s were resistant to blast. Among the F_2 segregating generation eight populations showed resistant and non-segregation ratio, four rice crosses gave segregations 15 resistant (R) : 1 susceptible (S), while the segregating ratio of another four crosses were 3 R : 1 S for blast. In addition, the analysis of variance revealed significant differences among genotypes, lines, testers and line x tester interactions for blast reaction, duration, plant height, panicle length and weight, flag leaf area, number of panicles/plant and primary branches/panicle, 1000-grain weight and spikelet fertility % traits, indicated that the genotypes had wide genetic diversity for the studied traits. However, significant differences due to interactions of line x tester for the above mentioned traits, indicating the importance of both additive and non-additive gene action in the inheritance of these traits. Highly significant and desirable heterosis and heterobeltiosis were recorded in Sakha 103 X IRBL5-M for improving blast resistance, plant height, flag leaf area, number of panicles/plant and spikelet fertility %. In addition, Sakha 102 X IRBLKS-S rice hybrid was the best cross combinations for early maturity, shortness, area of flag leaf, number of panicles/plant and 1000-grain weight traits and it could be used in breeding program to improving these characters in rice

Keywords: rice, blast reaction, combining ability, heterosis, genetic parameters, and line x tester design.

INTRODUCTION

Rice blast disease is a serious caused by a fungal *Pyricularia oryzae* Cavara of rice (*Oryza sativa* L.). It causes considerable damage to rice and crop loss in rice growing regions worldwide. The controlling of this by fungicides can be used to control rice blast, they generate additional costs in rice production and chemical contamination of environment and foods. Therefore, the use of resistant varieties is the best economic way and environmentally efficient ways of crop protection from the disease Yohei *et al*. (2009). The inheritance of host resistance to rice blast studied and they found about 70 genes and 347 quantitative trait loci (QTLs) have been detected by Ballini *et al*. (2008).

Since 1984 in Egypt, after breakdown Rehio variety which had exporting from Japan and growing in large area the new races from blast infected this variety and the damage of this area was more than 60%, then the scientists of Rice Research & Training Center (RRTC) stared to produce resistant varieties (Giza 177, Giza 178, Giza 181, Giza 182, Sakha 101, Sakha 102, Sakha 103, Sakha 104, Sakha 105 and Sakha 106) RRTC (2006). These varieties produced through classical breeding from hybridization between blast resistance varieties as a donor like Japanese Differential Varieties (JDV) with local varieties. Also, monogenic resistant lines can be utilized as donor varieties for blast resistance with different resistance genes Fukuta *et al*. (2004), Telebanco *et al*. (2008) which were used in this investigation. The blast races were identified by reactions to 26 Lijianxintuanheigu (LTH) monogenic lines for targeting 23 resistance genes Mary *et al*. (2010). Relations between races and resistance genes were deliberated by Hinako *et al.* (2009) and were understood by identifying resistance genes in Kasalath variety using monogenic lines as differential varieties carrying 24 kinds of resistance genes.

Success of breeding programs depends on the magnitude of genetic variability and the extent to which the advantageous characters. Therefore, the study of genetic variability in rice is not only essential for selecting variable genotypes and predicting that affect of selecting best genotypes but it will also aid breeders in simultaneous improvement of characters through selection Patil *et al*. (1983). Exploitation of hetrosis in self-pollinated crops, especially rice, is required. The exploitation of heterosis depends mainly on general (GCA) and specific (SCA) combining ability of genotypes in the hybrids. The Line x Tester analysis provides very useful information to plant breeders in marking decisions concerning the type of breeding system and selecting breeding materials that show the greatest promise for successful selection. Analysis of variance for line x tester was carried out as designed by Wynne *et al*. (1970). This investigation aimed to: 1) study the inheritance of blast resistance genes through cross between monogenic lines and some Egyptian rice varieties. 2) study the general and specific combining ability effects for some agronomic traits, and 3) estimate the heterosis and heterobeltiosis percentage.

MATERIALS AND METHODS

This study was carried out at the Experimental Farm of Rice Research and Training Center (RRTC), Sakha, Kafer El-Sheikh, Egypt, during the three successive growing seasons of 201٤, 201٥ and 201٦.

A line x Tester mating design was used, involving four Egyptian cultivars; Sakha 102, Sakha 101, sakha103 and Sakha 104 used as "Lines" and the four monogenic lines; i.e., IRBLKS-S, IRBL3-CP4, IRBL5-M and IRBL7-M, used as "testers". Seeds of the parental lines were obtained from genetic stock of the Rice Research and Training Center (RRTC), Agricultural Research Center (ARC), Egypt. While, the monogenic lines were received from the International Rice Research Institute (IRRI), Philippines (Table 1). These monogenic lines were identifying the type of resistance genes according to Fukuta *et al.* (2004).

Table 1. Parentage, origin, and blast disease reaction for rice genotypes under study.

No.	Entries	Parentage	Origin	Blast reaction	Resistance Gene
1	Sakha 102	(Gz4096-7-1 / Giza177)	Egyptian	R*	*Pi-ta*^{2}* + *Pi-i, Pi-sh*
2	Sakha 101	(Giza 176/Milyang 79)	Egyptian	S	*Pi-ta*^{2}*
3	Sakha 103	(Giza177 / Suwwon349)	Egyptian	R	Unknown
4	Sakha104	(GZ 4096/GZ 4100)	Egyptian	S**	Unknown
5	IRBLKS-S	(IRRI LINES)	IRRI	R	Pik-s
6	IRBL3-CP4	(IRRI LINES)	IRRI	R	Pi3
7	IRBL5-M	(IRRI LINES)	IRRI	R	Pi5(t)
8	IRBL7-M	(IRRI LINES)	IRRI	R	Pi7(t)

Evaluation under field conditions:

Eight parental varieties were evaluated for their reaction against *Magnaporthe grisea* at the blast nursery test at three locations Sakha (Kafr Elsheikh governorate), Gemmiza (Gharbia governorate) and Zarzora (Behera governorate) during 201٤, 201٥ and 201٦ seasons for blast resistance at seedling stage. The varieties were left exposed for natural blast infection at seedling stage. About forty-days from sowing date, the typical blast lesions were scored, according to the Standard Evaluation System using 0-9 scales IRRI (1996) as follow: 1-2 = resistant (R), 3 = moderately resistant (MR), 4-6 = susceptible (S), 7-9= highly susceptible (HS).

Evaluation under artificial inoculation:

The parents were tested under artificial infection at greenhouse at Rice Pathology Department. Five *M. grisea* races were collected from infected rice varieties at different locations of rice growing area during the previous seasons; were used for artificial infection in the trays. The isolates used were identified according to Atkins *et al.* (1967) as virulent races IA-77, IG-1, ID-15, IC-17 and IB-45. The isolates were grown and multiplied on banana medium (200g Banana, 10g Dextrose, and 20g Agar, 1L water) at 28 ^{o}C. Seeds of each parent were seeded in plastic trays (30 x 20 x15 cm.). The trays were kept in the greenhouse at 25-30^{o}C, and fertilized with Urea 46.5% N (5 g/tray). Rice seedlings at 3-4-leaf stage were ready for inoculation by spraying with spore suspension (100 ml) adjusted to 5 x 10^{4} spores/ml. The inoculated seedlings were kept in a moist chamber with at least 90% R.H. and 25-28 ^{o}C for 24 hr, and then moved to the greenhouse. Seven days after inoculation, blast reaction was recorded according to the Standard Evaluation System using 0-9 scales, IRRI (1996).

Hybridization technique:

A line x tester cross was conducted among the eight parents to produce sixteen crosses using hybridization technique of Jodon (1938) and modified by Butany (1961). The studied characters were; blast reaction at seedling stage, duration (day), plant height (cm), number of tillers/plant, number of panicles/plant, number of filled grains/panicle, number of unfilled grains/panicle, 1000- grain weight (g), grain yield /plant (g), panicle weight (g), panicle length (cm) and number of primary branches/panicle, it were evaluated according to Standard Evaluation System IRRI (1996).

The parental varieties and F_1s crosses arranged for evaluation in a Randomized Complete Block Design (RCBD) experiment with three replications. While, the F_2 materials were planted and evaluated for blast reaction as individual plants for each populations. Each F_2 populations ranged from 200 to 300 individual plants. Analysis of variance for line X tester was carried out as designed by Wynne *et al*. (1970) While, estimates of heterosis were completed as done by Mather (1949) and Mather and Jinkes (1982). All recommended cultural practices were applied for the permanent rice field. Weeds were chemically controlled by 2 litters Saturn.

Analysis of variance was computed for each season assuming that the cultivars under study are random. As the error variances of the experiments were statistically homogeneous, the two experiments were statistically combined over the two seasons, according to Le Clerg *et al.* (1962), then, it was subjected to analysis of variance, which was used to partition the gross phenotypic variability into the components due to genetic (hereditary) and non-genetic (environmental) factors and to estimate the magnitude of them. Genotypic variance is the part of the phenotypic variance, which can be attributed to genotypic differences among the phenotypes. Similarly, phenotypic variance is the total variance among phenotypes, when grown over the range of environments of interest, Dudley and Moll (1969). Hence, variance components, genotypic (Vg), phenotypic (Vp) and error (Ve) variances were estimated using the formula of Wricke and Weber

(1986) and Prasad *et al*. (1981). While, broad-sense heritability (h^2B), expressed as the percentage of the ratio of the genotypic variance (Vg) to the phenotypic variance (Vph) was estimated on genotypic mean basis, as described by Allard (1999). Genetic advance (GA) and expected GA as percent of the mean, assuming selection of the superior 5% of the genotypes were estimated in accordance the methods, illustrated by Fehr (1987) and the phenotypic correlation coefficients were computed, according to the method of Dewey and Lu (1959). Combining ability analysis was done using line x tester method, Kempthorne (1957). The variances for general combining ability and specific combining ability were tested against their respective error variances derived from ANOVA reduced to mean level. Significance test for GCA and SCA effects were performed using t-Test. The heterosis were estimated as the deviation of the F_1 mean value from the mid- and better-parent mean values as suggested by Matzinger *et al*. (1962) and Fonsecca and Patterson (1968), respectively.

RESULTS AND DISCUSSION

1-Evaluation under field condition:

Eight rice genotypes were evaluated against *Magnaporthe grisea* infection under field conditions (natural infection) at three locations (Sakha, Gemmiza and Zarzoura).

The results in Table (2) revealed that the varieties Sakha 102 and Sakha 103 were resistant under the three locations, while the other two Egyptian varieties Sakha 101 and Sakha104 were susceptible. Also, the monogenic lines (IRBLKS-S, IRBL3-CP4, IRBL5-M and IRBL7-M) were resistant under natural infection.

Table 2. Blast reaction of four Egyptian varieties and four monogenic lines under blast nursery test in Sakha, Gemmiza and Zarzoura locations.

Genotypes	Locations			Resistance gene
	Sakha	Gemmiza	Zarzoura	
Sakha 102	2	2	2	Pi-ta^2* + Pi-i, Pi-sh
Sakha 101	6	5	6	Pi-ta^2*
Sakha 103	2	2	2	Unknown
Sakha104	5	6	6	Unknown
IRBLKS-S	1	1	1	Pik-s
IRBL3-CP4	1	1	1	Pi3
IRBL5-M	1	1	1	Pi5(t)
IRBL7-M	1	1	1	Pi7(t)

*** Resistance gene according to (Imbe 1998).**

2- Evaluation under artificial inoculation:

Five virulent races; IA-77, IG-1, ID-15, IC-17 and IB-45 of *M. grisea*, were used to contaminated the eight genotypes under artificial inoculation. The data in Table (3) showed that sakha 102 rice variety, which carry genes Pi-ta^2 + Pi-i, Pi-sh Imbe (1998) was resistant to all blast races, except IB-45 race, which was susceptible and the same result were observed with Sakha 103. While, the other two Egyptian varieties, Sakha 101 (Pi-ta^2) and Sakha 104 were susceptible by the five blast races. On the other hand, for monogenic genotypes results showed that IRBLKS-S, IRBL3-CP4 and IRBL5-M which carry (Pik-s, Pi3 and Pi5 (t)) were resistant to all blast races, except EG-5 race which were susceptible. IRBL7-M carry Pi7 (t) was resistant against IG-1, 367 and 374 races, while it was susceptible by EG-5 and IB-45 races of *M. grisea*. The results suggested that the six major genes; Pi-i, Pi-sh, Pik-s, Pi3, Pi5, Pi7 (t) were effective under Egyptian conditions and can be used for improving resistance character in breeding program. While, Pi-ta^2 gene under Egyptian conditions was not effective for the crossing to improve the resistance character.

Table 3. Blast reaction of four Egyptian varieties and four monogenic lines under artificial inoculation in greenhouse.

NO.	Genotypes	IB-45	374	367	IG-1	EG-5
1	Sakha 102	6	2	2	2	2
2	Sakha 101	6	5	4	5	7
3	Sakha 103	4	2	2	2	2
4	Sakha104	5	6	4	4	6
5	IRBLKS-S	2	2	2	2	4
6	IRBL3-CP4	2	2	2	2	5
7	IRBL5-M	2	2	2	2	4
8	IRBL7-M	4	2	2	2	6

3. Inheritance of blast resistance genes:

Eight varieties were chosen to study the resistance and infection type or inheritance of major genes. Four monogenic lines are known to contain specific blast resistance genes; (Pik-s, Pi3, Pi5 and Pi7 (t), and four Egyptian varieties namely; Sakha102, Sakha101, Sakha 103 and Sakha104. Line x tester crossing technique for eight genotypes was used. The F_1 and F_2 generations of sixteen crosses were performed for studying the inheritance of resistance to leaf blast disease under field conditions. The results in Table (4) showed that 16 crosses produced between resistance by resistance and resistances by susceptible parents were resistance in F_1. These results indicate that the resistance parents used carried dominant genes for resistance and that resistance was completely dominant over susceptibility for blast. As for F_2 generation, eight crosses showed resistant and non-segregation ratio, which produced from Resistance x Resistance, which indicate that the resistance genes in those parents could be the same or allelic.

On the other hand, four crosses (No.7, 8, 13 and 14) gave segregation 15 resistant (R): 1 susceptible (S). This indicated the presence of two resistance genes of leaf blast segregating in these crosses and each gene can express resistance in the genetic background. Also, each parent in these crosses contained one of these genes and the allelic relationship was complete dominance. This data suggested that, if the first parent is AAbb the second shouled be aaBB. These results are compatible with Hammoud (2004), El-Malky *et al.* (2008) and El Sherif (2011). While, four crosses (No. 5, 6, 15 and 16) gave segregated ratio of 3 R : 1 S. These results indicated the presence of one dominant major resistance gene transferred from these resistant parents to their offspring that control the resistant against blast (Table 4). These results were in agreement with those of Mackill and Bonman (1992); Shi *et al*. (1994); Pan *et al.* (1996); Nagaty *et al*. (2006); El-Malky and Elamawi (2013) and El-Malky *et al.* (2014).

Table 4. Sixteen F_1 crosses and phenotypic ratio and expected ratio of F_2 populations, χ^2 test for blast incidence during 2015 and 2016 seasons.

Genotypes	F_1	Phenotypic ratio in F_2 R : S	Expected ratio R : S	χ^2	P. value
1-Sakha 102 X IRBLKS-S	R	294 : 0	1 : 0	-	
2-Sakha 102 X IRBL3-CP4	R	214:0	1 : 0	-	
3-Sakha 102 X IRBL5-M	R	189:0	1 : 0	-	
4-Sakha 102 X IRBL7-M	R	196 :0	1 : 0	-	
5-Sakha 101 X IRBLKS-S	R	174 : 66	3 : 1	1.331	0.622
6-Sakha 101 X IRBL3-CP4	R	203:71	3 : 1	1.211	0.614
7-Sakha 101 X IRBL5-M	R	221: 29	15 : 1	1.122	0.235
8-Sakha 101 X IRBL7-M	R	252 : 21	15 : 1	0.893	0.623
9-Sakha 103 X IRBLKS-S	R	139:0	1 : 0	-	
10-Sakha 103 X IRBL3-CP4	R	156:0	1 : 0	-	
11-Sakha 103 X IRBL5-M	R	167 :0	1 : 0	-	
12-Sakha 103 X IRBL7-M	R	119:0	1 : 0	-	
13-Sakha 104 X IRBLKS-S	R	243: 20	15 : 1	0.933	0.638
14-Sakha 104 X IRBL3-CP4	R	233: 21	15 : 1	0.911	0.624
15-Sakha 104 X IRBL5-M	R	192 : 75	3 : 1	1.33	0.345
16-Sakha 104 X IRBL7-M	R	190:63	3 : 1	0.314	0.612

R= Resistant S= susceptible

4- Inheritance of Quantitative traits:

Analysis of variance for all studied characters:

The recorded data on different characteristics were subjected to analysis of variance to confirm the differences among rice genotypes. Mean squares from analysis of variance of all studied traits of rice are presented in Table (5). The Table depicted highly significant differences among rice genotypes for all the studied traits. Sum of squares of rice genotypes for traits were further portioned into parents, crosses and parents vs. crosses, which revealed highly significant differences among genotypes for all studied traits, except panicle weight. The significant component of variance due to parents vs. crosses indicated prevalence of heterosis for all studied traits. The sum of squares calculated for rice crosses were further portioned into lines, testers and line x tester components. Highly significant ($P \leq 0.01$) differences were displayed among line x tester interaction for most of the studied traits. However, non-significant differences existed among lines and testers and line x tester components for blast reaction and panicle weight traits. The mean squares due to GCA as well as SCA were significant for all the studied traits, except blast reaction and panicle weight traits. Thus, the significance of GCA (variances due to lines and testers) and SCA (variances due to lines x testers) implied that both additive and non-additive types of variation was available for all the traits, yet additive genes were more important than the dominant genes, because variance due to GCA was higher than that of SCA for all mentioned traits. Moreover, the ratio of GCA and SCA variances was greater than unity for all the studied traits that revealed the preponderance of additive gene action over the non-additive gene action for all studied traits. The results suggest that improvement in these traits may be obtained via heterosis breeding or by single plant selection in later segregating generations following hybridization or intermating of selected segregants through recurrent selection.

Table 5. Mean squares from line x tester analysis for yield and its related traits during 2015 growing season.

S.O.V	d.f	Blast reaction	Duration (day)	Plant height (cm)	Flag leaf area (cm^2)	No. of panicles/ plant
Replications	2	0.04	0.54	0.88	0.93	0.10
Genotypes	23	3.76**	132.13**	529.05**	52.64**	108.58**
Parents	7	10.33**	152.95**	731.24**	44.57**	36.18**
Parents vs. Crosses	1	9.00**	33.06**	1139.06**	43.34**	1715.34**
Crosses	15	0.35	129.01**	394.03**	57.02**	35.24**
Lines (gca, L)	3	0.31	171.24**	215.13**	37.08**	51.47**
Testers (sca, T)	3	0.58	181.47**	556.02**	82.19**	17.74**
Lines x Testers (sca)	9	0.29	97.45**	399.67**	55.28**	35.67**
Error	46	0.20	3.54	4.28	3.45	2.30
GCA / SCA		1.25	1.17	1.08	1.10	1.09

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

Table 5. Continuous

S.O.V	d.f	Panicle length (cm)	No. of primary branches	Panicle weight (g)	1000-grain weight (g)	Spikelet fertility %
Replications	2	0.18	0.01	0.12	0.10	1.40
Genotypes	23	18.86**	7.47**	1.68	17.86**	203.22**
Parents	7	15.71**	12.90**	0.95	28.06**	233.84**
Parents vs.Crosses	1	215.11**	37.01**	21.24**	29.98**	184.96**
Crosses	15	7.24**	2.97*	0.72	12.30**	190.15**
Lines (gca, L)	3	18.06**	1.74	0.79	21.69**	320.46**
Testers (sca, T)	3	0.72	4.08*	0.30	4.07*	282.49**
Lines x Testers (sca)	9	5.81**	3.00*	0.84	11.91**	115.93**
Error	46	1.27	1.17	0.11	0.99	4.17
GCA / SCA		1.16	1.05	1.09	1.05	1.10

Similar results also were reported previously by Basbag *et al*. (2007), Viswanathan and Thiyagarajan, (2008), Hassan *et al*. (2013) and Zeinab Montazeri1 *et al*. (2014), they exhibited that high magnitude of specific combining ability (SCA) variance revealed the predominance of non-additive gene action for all characters, viz., duration (day), plant height, number of productive tillers/plant, panicle length, number of unfilled grains/panicle, spikelet fertility %, 100-grain weight and grain yield/plant, which offer scope for exploitation of hybrid vigor through heterosis breeding.

Performance of the studied rice genotypes

Conspicuously, Table (6) shows that the resistant to blast were detected for IRBL3-CP4 followed by IRBL5-M and IRBL7-M, on the other hand, the susceptible to infection were observed on Sakha 101 and Sakha 104. Moreover, the tallest plants were observed in IRBL5-M followed by IRBL3-CP4 and IRBL7-M, while, the shortest ones were exhibited in Sakha 101, Sakha 103 and IRBLKS-S rice varieties. IRBL5-M followed by Sakha 103 and IRBLKS-S, were the earliest rice cultivars. Otherwise, Sakha 101, Sakha 104 and IRBL7-M were the latest rice cultivars comparing with other rice cultivars. The highest number of panicles/plant were detected for Sakha 101 followed by Sakha 104. In addition, Sakha 104 has a longest panicle (25.00 cm). The superior panicle weight (٣.٤٧ g) was obtained for Sakha 102. Sakha 102 was found to be the heaviest grains rice cultivar (28.33 g/1000 grains). High spikelet fertility % with the lowest spikelet sterility % was observed for Sakha 103, Sakha 102 and Sakha 104 rice genotypes comparing with the other cultivated parents. The parental mean values of flag leaf area were ranged between 31.67 and 41.33 cm^2/plant for Sakha 102 and IRBL3-CP4, respectively. Moreover, Sakha 101 was recorded the highest number of primary branches/panicle, so, rice breeders should be use it as donors to improving new rice variety in their breeding program.

In addition, the F_1 mean values of blast reaction were ranged between 1.60 for cross No. 1 (Sakha 102 X IRBLKS-S) and 2.67 for cross No. 6 (Sakha 101 X IRBL3-CP4). Blast reaction was found to be lower than the lowest parent for three rice crosses, indicating that over-dominance was played a remarkable role in the inheritance of these traits in these counted or mentioned crosses. Moreover, blast reaction was controlled by partial dominance in seven crosses; their F_1 mean values were located between the values of their parental lines. Moreover, the F_1 mean values of duration were ranged between 117.00 day for cross No. 10 (Sakha 103 X IRBL3-CP4) and 143.33 day for cross No. 8 (Sakha 101 X IRBL7-M). Plant height of seven rice crosses was ranged between 101.33 -114.00 cm, which agrees with the target of rice breeders for selected ideal plant height under normal conditions for resistance to lodging and suitable for mechanical harvesting. Flag leaf area was found to be higher than the highest parent for two rice crosses, namely cross No. 2 and No. 5, indicating that over-dominance was played a remarkable role in the inheritance of these traits in these counted or mentioned crosses. The highest number of panicles/plant were exhibited for cross No. 2 (Sakha 102 X IRBL3-CP4), No. 16 (Sakha 104 X IRBL7-M), No. 8 (Sakha 101 X IRBL7-M) and No. 13 (Sakha 104 X IRBLKS-S). Moreover, cross No. 6 (Sakha 101 X IRBL3—CP4) followed by cross No. 16 (Sakha 104 X IRBL7-M) and No. 15 (Sakha 104 X IRBL5-M) were found to be the longest panicle, their estimated values of panicle length were ranged between 28.33 cm and 26.67 cm. On the other hand, cross No. 16 (Sakha 104 X IRBL7-M) followed by cross No. 7 (Sakha 101 X IRBL5-M and No. 13 (Sakha 104 X IRBLKS-S) were the heaviest panicle. High percent of spikelet fertility were observed for cross No. 13 (Sakha 104 X IRBLKS-S), No. 2 (Sakha 102 X IRBL3-CP4), No. 1 (Sakha 102 X IRBLKS-S) and No. 11 (Sakha 103 X IRBL5-M), but, their estimated values were lower than the value of the highest parent (Sakha 103).

Table 6. Mean performance of crosses, lines and testers for the studied traits during 2015 growing season.

Genotype	Blast reaction	Duration (day)	Plant height (cm)	Flag leaf area (cm^2)	No. of panicles/ plant
Parents					
1-Sakha 102	2.00	126.00	105.00	31.67	21.00
2-Sakha 101	5.67	142.67	93.67	41.00	26.00
3-Sakha 103	2.00	124.00	98.00	35.33	23.33
4-Sakha 104	5.67	135.00	105.00	33.67	24.00
5-IRBLKS-S	2.00	125.00	98.00	32.33	20.33
6-IRBL3-CP4	1.00	126.00	122.67	41.33	17.00
7-IRBL5-M	1.67	121.00	140.33	37.00	18.33
8-IRBL7-M	1.67	132.33	114.67	39.67	16.33
F_1- Crosses					
1-Sakha 102 X IRBLKS-S	1.60	123.00	102.00	41.33	33.00
2-Sakha 102 X IRBL3-CP4	1.67	127.00	112.00	44.00	38.67
3-Sakha 102 X IRBL5-M	2.00	128.00	141.33	30.33	28.67
4-Sakha 102 X IRBL7-M	2.00	131.67	135.00	38.00	31.67
5-Sakha 101 X IRBLKS-S	1.67	133.67	101.33	48.33	31.33
6-Sakha 101 X IRBL3-CP4	2.67	130.00	110.00	39.00	31.00
7-Sakha 101 X IRBL5-M	2.33	122.00	118.67	34.00	28.67
8-Sakha 101 X IRBL7-M	2.00	143.33	120.00	36.00	33.67
9-Sakha 103 X IRBLKS-S	1.67	129.00	122.33	37.67	24.67
10-Sakha 103 X IRBL3-CP4	2.00	117.00	117.67	33.00	32.00
11-Sakha 103 X IRBL5-M	1.67	117.67	122.33	35.00	30.33
12-Sakha 103 X IRBL7-M	2.00	128.33	108.67	36.67	26.00
13-Sakha 104 X IRBLKS-S	1.67	134.00	114.00	37.00	33.67
14-Sakha 104 X IRBL3-CP4	2.00	128.67	132.67	39.00	28.67
15-Sakha 104 X IRBL5-M	2.67	124.67	124.00	39.67	31.33
16-Sakha 104 X IRBL7-M	1.67	123.00	107.67	41.33	35.00
L.S.D. 0.05	0.74	3.10	3.41	3.06	2.50
0.01	0.99	4.15	4.56	4.10	3.34

Table 6. Continued.

Genotype	Panicle length (cm)	No. of primary branches/ panicle	Panicle weight (g)	1000-grain weight (g)	Spikelet fertility%
Parents					
1-Sakha 102	24.00	11.00	3.47	28.33	98.00
2-Sakha 101	24.00	13.00	3.20	26.37	92.10
3-Sakha 103	21.33	11.00	3.10	25.33	99.47
4-Sakha 104	25.00	12.00	3.30	25.90	95.17
5-IRBLKS-S	18.33	8.00	1.93	24.37	91.20
6-IRBL3-CP4	21.00	8.00	2.63	26.33	73.03
7-IRBL5-M	21.00	10.00	2.73	22.33	87.17
8-IRBL7-M	20.00	7.33	2.10	18.43	82.00
F_1- Crosses					
1-Sakha 102 X IRBLKS-S	25.00	11.00	4.10	26.60	94.17
2-Sakha 102 X IRBL3-CP4	24.33	12.00	3.90	28.17	95.33
3-Sakha 102 X IRBL5-M	26.00	10.33	4.20	29.40	84.17
4-Sakha 102 X IRBL7-M	26.66	11.00	4.10	26.37	81.13
5-Sakha 101 X IRBLKS-S	26.33	10.00	4.20	26.23	90.90
6-Sakha 101 X IRBL3-CP4	28.33	13.00	3.80	22.50	85.03
7-Sakha 101 X IRBL5-M	24.00	12.00	4.73	25.63	80.27
8-Sakha 101 X IRBL7-M	25.00	11.67	3.07	23.57	83.13
9-Sakha 103 X IRBLKS-S	23.67	13.00	3.57	26.37	91.67
10-Sakha 103 X IRBL3-CP4	23.00	11.00	3.30	25.50	90.00
11-Sakha 103 X IRBL5-M	25.00	10.00	3.30	27.50	94.17
12-Sakha 103 X IRBL7-M	23.67	12.00	4.27	26.67	92.03
13-Sakha 104 X IRBLKS-S	26.00	12.00	4.30	27.13	97.17
14-Sakha 104 X IRBL3-CP4	26.33	13.00	3.90	24.70	71.17
15-Sakha 104 X IRBL5-M	26.67	11.00	3.80	22.10	76.33
16-Sakha 104 X IRBL7-M	28.00	12.00	4.83	28.27	75.20
L.S.D. 0.05	1.86	1.79	0.55	1.64	3.37
0.01	2.48	2.39	0.74	2.19	4.50

Estimates of general and specific combining ability effects

General combining ability effects:

The estimates of general combining ability effects consider an important indicator of the potential of parental lines for generating superior breeding populations. A negligible or negative combining ability effect indicates a poor ability to transfer its genetic superiority to hybrids. The largest significant positive values have the largest effects. On the other hand, the largest significant negative values have the smallest effects, except in case of duration (days) and plant height traits. Obviously, Table (7) indicated that Sakha 102 was found to be an overall good general combiners for five traits under consideration including Blast reaction, no of panicles/plant, Panicle weight, 1000-grain weight and spikelet fertility%. Moreover, Sakha 101 was the good general combiners for plant height, flag area and Panicle length traits. Sakha 103 was good general combiners for blast reaction, heading date, 1000-grain weight and spikelet fertility% traits. Sakha 104 was the best general combiners for flag leaf area, No. of panicles/plant, panicle length,

Table 7. Estimates of general combining ability effects for the studied traits during 2015 growing season.

Genotype	Blast reaction	Duration (day)	Plant height (cm)	Flag leaf area (cm^2)	No. of panicles/ plant
Sakha 102	-0.13*	-0.15	4.48**	0.27	1.85**
Sakha 101	0.21**	4.69**	-5.60**	1.19**	0.02
Sakha 103	-0.13*	-4.56**	-0.35	-2.56**	-2.90**
Sakha 104	0.04	0.02	1.48**	1.10**	1.02**
S.E (gi)	0.13	0.54	0.60	0.54	0.44
S.E (gl-gj)	0.18	0.77	0.84	0.76	0.62
IRBLKS-S	-0.29**	2.35**	-8.19**	2.94**	-0.48*
IRBL3-CP4	0.13*	-1.90**	-0.02	0.60*	1.44**
IRBL5-M	0.21**	-4.48**	8.48**	-3.40**	-1.40**
IRBL7-M	-0.04	4.02**	-0.27	-0.15	0.44*
S.E (gi)	0.13	0.54	0.60	0.54	0.44
S.E (gt-gj)	0.18	0.77	0.84	0.76	0.62

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

No. of primary branches/panicle and panicle weight, while, IRBLKS-S was the greatest general combiner for blast reaction, shortness, flag area, 1000-grain weight and spikelet fertility%. combiner for blast reaction, shortness, flag area, 1000-grain weight and spikelet fertility%. In addition, IRBL3-CP4 rice tester was good general combiners for improving earliness, flag leaf area, No. of panicles and No. of primary branches/panicle. While, IRBL5-M was the best general combiners for earliness. Moreover, IRBL7-M was the best general combiners for No. of panicles/panicle and Panicle weight. However, some parents with high mean values exhibited low GCA effects. Hence, both performances *per se* and GCA effects should be taken into account for parental selection. The parent IRBL3-CP4, was selected as the best one since it had high mean values for blast reaction and was also a good general combiners for the same traits. It is obvious that none of the parents were found to be good for all studied the traits. Hence, it would be desirable to have multiple crosses involving the parents, viz., IRBLKS-S, IRBL3-CP4 and Sakha 102, and practicing a selection in the segregating generations to isolate superior genotypes. Similar results were obtained previously by Soroush and Moumeni (2006). El Abd, *et al*. (2007), Viswanathan satheesh and Thiyagarajan (2008), Muthuramu, *et al*. (2010), Hassan *et al*. (2013) and Zeinab Montazeri1 *et al*. (2014).

Table 7. Continuous

Genotype	Panicle length (cm)	No. of primary branches/pa.	Panicle weight (g)	1000-grain weight (g)	Spikelet fertility%
Sakha 102	-0.01	-0.48**	0.11*	1.59**	2.33**
Sakha 101	0.42*	0.10	-0.01	-1.56**	-1.53**
Sakha 103	-1.67**	-0.06	-0.35**	0.46**	5.60**
Sakha 104	1.25**	0.44**	0.25**	-0.49**	-6.40**
S.E (gi)	0.33	0.31	0.10	0.29	0.59
S.E (gl-gj)	0.46	0.44	0.14	0.41	0.83
IRBLKS-S	-0.25	-0.06	0.08	0.54**	7.11**
IRBL3-CP4	0.01	0.69**	-0.24**	-0.83**	-0.98**
IRBL5-M	-0.08	-0.73**	0.05	0.11	-2.63**
IRBL7-M	0.33	0.10	0.11**	0.17	-3.49**
S.E (gi)	0.33	0.31	0.10	0.29	0.59
S.E (gt-gj)	0.46	0.44	0.14	0.41	0.83

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

Specific combining ability effects

High specific combining ability effects were caused by the dominance and interaction or epistatic effects (non-fixable genes) that existed between the crossed parents. The same can be used as an index to determine the usefulness of a particular cross-combination in the exploitation of heterosis. As shown in Table (8), only one cross out of 16 combinations possessed significant desirable SCA effects for blast reaction involving two kind of combinations between the parents of high and low GCA effects, such as Sakha 103 X IRBL5-M (high x low), where the majority were derived from former cross-combinations. Moreover, the hybrid, Sakha 102 X IRBL3-CP4 was the best cross combinations to improve shortness, flag leaf area, increase number of panicles/plant and increase 1000-grain weight as well as high fertility percentage. While, Sakha 103 X IRBL5-M was the best cross combinations for improving resistance to blast, plant height, flag leaf area, number of panicles/ plant and spikelet fertility%. In addition to, Sakha 102 X IRBLKS-S hybrid was the best cross combinations for early maturity, short plant height, flag leaf area, increase number of panicles/plant and increase 1000-grain weight. Furthermore, On the contrary, Sakha 102 X IRBL7-M and Sakha 104 X IRBL3-CP4 rice hybrids were very poor cross combinations, which showed no significant specific combining abilities effects for all the studied traits. On the other hand, Sakha 103 X IRBL5-M was the greatest cross combinations; it showed significant favorable SCA effects for five traits among them blast reaction, plant height, flag leaf area, number of panicles/ plant and spikelet fertility %. The studied hybrids involved all kinds of parental combinations such as high x high, high x low and low x low. This suggests that either additive x additive, additive x dominance and/or dominance x dominance genetic interactions were predominant. The superiority of these crosses may be due to complementary and duplicate type of gene interactions.

Hence, these hybrids are expected to produce desirable segregants and could be exploited successfully in breeding programs. Similar findings were reported earlier by Pradhan, *et al.* (2006), El Abd, *et al.* (2007), Basbag, *et al.* (2007), Sarma, *et al.* (2007), Viswanathan Satheesh and Thiyagarajan (2008), Muthurama, *et al.* (2010), Hassan *et al.* (2013) and Zeinab Montazeri1 *et al.* (2014).

Table 8. Estimates of specific combining ability effects for the studied traits during 2015 growing season.

Genotypes	Blast reaction	Heading date (day)	Plant height (cm)	Flag leaf area (cm^2)	No. of panicles/ plant
1-Sakha 102 X IRBLKS-S	0.13	-6.77**	-12.40**	-0.02	0.48
2-Sakha 102 X IRBL3-CP4	-0.29	1.48	-10.56**	4.98*	4.23**
3-Sakha 102 X IRBL5-M	-0.04	5.06**	10.27**	-4.69*	-2.94*
4-Sakha 102 X IRBL7-M	0.21	0.23	12.69**	-0.27	-1.77*
5-Sakha 101 X IRBLKS-S	-0.21	-0.94	-2.98*	6.06**	0.65
6-Sakha 101 X IRBL3-CP4	0.38*	-0.35	-2.48*	-0.94	-1.60
7-Sakha 101 X IRBL5-M	-0.04	-5.77**	-2.31	-1.94	-1.10
8-Sakha 101 X IRBL7-M	-0.13	7.06**	7.77**	-3.19*	2.06*
9-Sakha 103 X IRBLKS-S	0.13	3.65*	12.77**	-0.85	-3.10*
10-Sakha 103 X IRBL3-CP4	0.04	-4.10*	-0.06	-3.19*	2.31*
11-Sakha 103 X IRBL5-M	-0.38*	-0.85	-3.90*	2.81*	3.48**
12-Sakha 103 X IRBL7-M	0.21	1.31	-8.81**	1.23	-2.69*
13-Sakha 104 X IRBLKS-S	-0.04	4.06*	2.60*	-5.19**	1.98*
14-Sakha 104 X IRBL3-CP4	-0.13	2.98*	13.10**	-0.85	-4.94**
15-Sakha 104 X IRBL5-M	0.46*	1.56	-4.06*	3.81*	0.56
16-Sakha 104 X IRBL7-M	-0.29	-8.60**	-11.65**	2.23*	2.40*
S.E (Sij)	0.16	1.09	1.19	1.07	0.88
S.E (Sij-Skl)	0.27	1.54	1.69	1.52	1.24
L.S.D 0.05	0.32	2.20	2.40	2.16	1.77
0.01	0.69	4.16	4.56	5.83	3.35

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

Table 8. Continuous

Genotypes	Panicle length (cm)	No. of primary branches	Panicle weight (g)	1000-grain weight (g)	Spikelet fertility%
1-Sakha 102 X IRBLKS-S	-0.25	-0.02	-0.06	-1.57*	-1.64
2-Sakha 102 X IRBL3-CP4	-1.17*	0.23	0.06	1.36*	7.62**
3-Sakha 102 X IRBL5-M	0.58	-0.02	0.08	1.65*	-1.90
4-Sakha 102 X IRBL7-M	0.83	-0.19	-0.08	-1.44*	-4.08*
5-Sakha 101 X IRBLKS-S	0.67	-1.60*	0.17	1.21*	-1.04
6-Sakha 101 X IRBL3-CP4	2.42*	0.65	0.09	-1.16*	1.18
7-Sakha 101 X IRBL5-M	-1.83*	1.06	0.74**	1.04	-1.93
8-Sakha 101 X IRBL7-M	-1.25	-0.10	-0.99**	-1.09	1.79
9-Sakha 103 X IRBLKS-S	0.08	1.56*	-0.12	-0.68	-7.41**
10-Sakha 103 X IRBL3-CP4	-0.83	-1.19	-0.07	-0.18	-0.98
11-Sakha 103 X IRBL5-M	1.25	-0.77	-0.36	0.88	4.83**
12-Sakha 103 X IRBL7-M	-0.50	0.40	0.55*	-0.01	3.56*
13-Sakha 104 X IRBLKS-S	-0.50	0.06	0.01	1.04	10.09**
14-Sakha 104 X IRBL3-CP4	-0.42	0.31	-0.07	-0.02	-7.82**
15-Sakha 104 X IRBL5-M	0.00	-0.27	-0.46*	-3.56**	-1.00
16-Sakha 104 X IRBL7-M	0.92	-0.10	0.52*	2.54**	-1.28
S.E (Sij)	0.65	0.63	0.19	0..57	1.18
S.E (Sij-Skl)	0.92	0.88	0.27	0.81	1.67
L.S.D 0.05	1.31	1.27	0.38	1.15	2.38
0.01	2.48	0.73	2.19	4.51	6.37

Estimates of heterosis and heterobeltiosis:

A large number of crosses exhibited high estimates of heterosis and heterobeltiosis in a desirable direction for different traits under study. The estimates of heterosis and heterobeltiosis for different traits are presented in Table 9. A greater magnitude of heterobeltiosis was observed in four crosses for blast reaction. The availability of sufficient hybrid vigor in several crosses in respect of blast reaction suggests that a hybrid breeding program could profitably be undertaken in rice. The results showed that significant heterosis and heterobeltiosis in desirable negative direction was recorded on cross No. 10 (Sakha 103 X IRBL3-CP4) and No. 16 (Sakha 104 X IRBL7-M) rice crosses for earliness. Moreover, neither heterosis nor heterobeltiosis were observed for plant height in all the studied crosses also. Nine out of 16 crosses had highly significant and positive estimates of heterosis and heterobeltiosis for flag leaf area, the highest estimated values were exhibited in cross No. 5 (Sakha 101 X IRBLKS-S) and No. 1 (Sakha 102 X IRBLKS-S), otherwise, the lowest estimated values were recorded in cross No. 14 (Sakha 104 X IRBL3-CP4) and No. 15 (Sakha 104 X IRBL5-M).

Table 9. Estimates of heterosis as a deviation from mid-parents (MP) and better-parents (BP) for blast reaction, duration, plant height and flag leaf area traits in the studied rice crosses during 2015 growing season.

Genotype	Blast reaction		Duration (day)		Plant height (cm)		Flag leaf area	
	M.P	B.P	M.P	B.P	M.P	B.P	M.P	B.P
1-Sakha 102 X IRBLKS-S	-16.67**	-16.67**	-1.99	-1.60	0.49	4.08*	29.17**	27.84**
2-Sakha 102 X IRBL3-CP4	11.11**	66.67**	0.79	0.79	-1.61	6.67**	20.55**	6.45**
3-Sakha 102 X IRBL5-M	9.09**	20.00**	3.64**	5.79**	15.22**	34.60**	-11.65**	-18.02**
4-Sakha 102 X IRBL7-M	9.09**	20.00**	1.94	4.50**	22.91**	28.57**	6.54**	-4.20**
5-Sakha 101 X IRBLKS-S	-56.52**	-16.67**	-0.12	6.93**	5.74**	8.19**	31.82**	17.89**
6-Sakha 101 X IRBL3-CP4	-20.00**	166.67**	-3.23*	3.17*	1.69	17.44**	-5.26**	-5.65**
7-Sakha 101 X IRBL5-M	-36.36**	40.00**	-7.46**	0.83	1.42	26.69**	-12.82**	-17.07**
8-Sakha 101 X IRBL7-M	-45.45**	20.00**	4.24**	8.31**	15.20**	28.11**	-10.74**	-12.20**
9-Sakha 103 X IRBLKS-S	-16.67**	-16.67**	3.61**	4.03**	24.83**	24.83**	11.33**	16.49**
10-Sakha 103 X IRBL3-CP4	33.33**	100.00**	-6.40**	-5.65**	6.65**	20.07**	-13.91**	-20.16**
11-Sakha 103 X IRBL5-M	-9.09**	0.01	-3.95**	-2.75	2.66	24.83**	-3.23*	-5.41**
12-Sakha 103 X IRBL7-M	9.09**	20.00**	0.13	3.49*	2.19	10.88**	-2.22	-7.56**
13-Sakha 104 X IRBLKS-S	-56.52**	-16.67**	3.08*	7.20**	12.32**	16.33**	12.12**	9.90**
14-Sakha 104 X IRBL3-CP4	-40.00**	100.00**	-1.40	2.12	16.54**	26.35**	4.00**	-5.65**
15-Sakha 104 X IRBL5-M	-27.27**	60.00**	-2.60	3.03**	1.09	18.10**	12.26**	7.21**
16-Sakha 104 X IRBL7-M	-54.55**	2.00**	-7.98**	-7.05**	-1.97	2.54	12.73**	4.20**
L.S.D 0.05	0.64	0.74	2.69	3.10	2.96	3.41	2.65	3.06
0.01	0.86	0.99	3.59	4.15	3.95	4.56	3.55	4.10

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

All studied crosses showed significant and positive heterosis and heterobeltiosis for number of panicles/ plant, their estimated values were ranged between (12.98, 5.71 and 103.5, 84.13 %) in Sakha 103 X IRBLKS-S and Sakha 102 X IRBL3-CP4 rice crosses, respectively. In addition to, fourteen out of 16 crosses had highly significant and positive estimates of heterobeltiosis for panicle length, the highest estimated values (18.06 and 17.19 %) were exhibited in Sakha 101 X IRBL3-CP4 and Sakha 103 X IRBL5-M rice crosses, respectively. While, all studied crosses showed significant and positive heterosis for panicle length. Highly significant and positive estimates of heterosis and heterobeltiosis were obtained in 12 and 4 crosses for number of primary branches, respectively, the most important crosses for reducing number of primary branches were Sakha 102 X IRBL3-CP4, Sakha 103 X IRBLKS-S and Sakha 103 X IRBL7-M.

Table 9. Estimates of heterosis as a deviation from mid-parents (MP) and better-parents (BP) for No. of panicles/plant, panicle length and No. of primary branches/panicle traits in the studied rice crosses during 2015 growing season.

Genotype	No. of panicles/plant		Panicle length (cm)		No. of primary branches/ panicle	
	M.P	B.P	M.P	B.P	M.P	B.P
1-Sakha 102 X IRBLKS-S	59.68**	57.14**	18.11**	4.15**	15.79**	0.00
2-Sakha 102 X IRBL3-CP4	103.51**	84.13**	8.15**	1.39	26.32**	9.09**
3-Sakha 102 X IRBL5-M	45.76**	36.51**	15.56**	8.33**	-1.59*	-6.06**
4-Sakha 102 X IRBL7-M	69.64**	50.79**	21.21**	11.11**	20.00**	0.00
5-Sakha 101 X IRBLKS-S	35.25**	20.51**	24.41**	9.72**	-4.76**	-23.08**
6-Sakha 101 X IRBL3-CP4	44.19**	19.23**	25.93**	18.06**	23.81**	0.00
7-Sakha 101 X IRBL5-M	29.32**	10.26**	6.67**	0.00	4.35**	-7.69**
8-Sakha 101 X IRBL7-M	59.06**	29.49**	13.64**	4.17**	14.75**	-10.26**
9-Sakha 103 X IRBLKS-S	12.98**	5.71**	19.33**	10.94**	36.84**	18.18**
10-Sakha 103 X IRBL3-CP4	58.68**	37.14**	8.66**	7.81**	15.79**	0.00
11-Sakha 103 X IRBL5-M	45.60**	30.00**	18.11**	17.19**	-4.76**	-9.09**
12-Sakha 103 X IRBL7-M	31.09**	11.43**	14.52**	10.94**	30.91**	9.09**
13-Sakha 104 X IRBLKS-S	51.88**	40.28**	20.00**	4.00**	20.00**	0.00
14-Sakha 104 X IRBL3-CP4	39.84**	19.44**	14.49**	5.33**	30.00**	8.33**
15-Sakha 104 X IRBL5-M	48.03**	30.56**	15.94**	6.67**	0.01	-8.33**
16-Sakha 104 X IRBL7-M	73.55**	45.83**	24.44**	12.00**	24.14**	0.00
L.S.D 0.05	2.17	2.50	1.61	1.86	1.55	1.79
0.01	2.90	3.34	2.15	2.48	2.07	2.39

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

Table 9. Continuous

Genotype	Panicle weight (g)		1000-grain weight (g)		Spikelet fertility%	
	M.P	B.P	M.P	B.P	M.P	B.P
1-Sakha 102 X IRBLKS-S	51.85**	18.27**	0.95	-6.12**	-0.46	-3.91*
2-Sakha 102 X IRBL3-CP4	27.87**	12.50**	3.05**	-0.59	11.48**	-2.72
3-Sakha 102 X IRBL5-M	35.48**	21.15**	16.05**	3.76**	-9.09**	-14.12**
4-Sakha 102 X IRBL7-M	47.31**	18.27**	12.76**	-6.94**	-9.85**	-17.21**
5-Sakha 101 X IRBLKS-S	63.64**	31.25**	3.42**	-0.51	-0.82	-1.30
6-Sakha 101 X IRBL3-CP4	30.29**	18.75**	-14.61**	-14.66**	2.99*	-7.67**
7-Sakha 101 X IRBL5-M	59.55**	47.92**	5.27**	-2.78**	-10.45**	-12.85**
8-Sakha 101 X IRBL7-M	15.72**	-4.17**	5.21**	-10.62**	-4.50**	-9.74**
9-Sakha 103 X IRBLKS-S	41.72**	15.05**	6.10**	4.08**	-3.85*	-7.84**
10-Sakha 103 X IRBL3-CP4	15.12**	6.45**	-1.29	-3.16**	4.35**	-9.52**
11-Sakha 103 X IRBL5-M	13.14**	6.45**	15.38**	8.55**	0.91	-5.33**
12-Sakha 103 X IRBL7-M	64.10**	37.63**	21.86**	5.26**	1.43	-7.47**
13-Sakha 104 X IRBLKS-S	64.33**	30.30**	7.96**	4.76**	4.27**	2.10
14-Sakha 104 X IRBL3-CP4	31.46**	18.18**	-5.42**	-6.20**	-15.38**	-25.22**
15-Sakha 104 X IRBL5-M	25.97**	15.15**	-8.36**	-14.67**	-16.27**	-19.79**
16-Sakha 104 X IRBL7-M	79.01**	46.46**	27.52**	9.14**	-15.11**	-20.98**
L.S.D 0.05	0.48	0.55	1.42	1.64	2.92	3.37
0.01	0.64	0.74	1.90	2.19	3.90	4.50

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

Obviously, (Table 9) shows that All the studied crosses showed significant and positive heterosis and heterobeltiosis for panicle weight, the cross, Sakha 104 X IRBL7-M exhibited highest estimate of heterosis (79.01%) for panicle weight followed by Sakha 104 X IRBLKS-S (64.33%), while, the highest estimate of heterobeltiosis was recorded on Sakha 101 X IRBL5-M (47.92%) for the same trait. Furthermore, highly significant and positive estimates of heterosis and heterobeltiosis were recorded on 11 and 6 rice crosses, the highest estimated values were reported on Sakha 104 X IRBL7-M (27.52%) and (9.14%) for 1000-grain weight, respectively. four rice crosses exhibited highly significant and positive heterosis, when it was measured as a deviation from mid-parent for spikelet fertility %, the highest estimated value was recorded on Sakha 102 X IRBL3-CP4 (11.48%), on the other hand, no heterobeltiosis were recorded for spikelet fertility % in all the studied crosses. Similar results were reported by several scientists such as, Khoyumthem, *et al.* (2005), Basbag, *et al.* (2007), El Abd, *et al.* (2007), Ganapathy and Ganesh (2008), Amudha, *et al.* (2010), Muthuramu, *et al.* (2010), Hassan *et al*. (2013) and Zeinab Montazeri1 *et al*. (2014).

Estimates of genetic parameters for the studied traits:

It is evident from Table (10) that the dominance genetic variance was greater than additive genetic variance for all the studied traits. The highest estimated values of environmental variance were recorded for plant height and spikelet fertility% traits. On the other hand, high heritability coupled with moderate to high expected genetic advance were noted for panicle weight followed by number of panicles/plant, flag leaf area, blast reaction, 1000-grain weight and number of primary branches/panicle traits, revealing substantial contribution of additive variance in phenotypic expression, and indicating the effectiveness of selection in early generation to improve these traits. Falconer and Mackay (1996) demonstrated that the lower narrow sense heritability was caused by low additive effects and high dominant gene action. Low genetic advance as percent mean was observed for duration (3.69%), plant height (6.05%), panicle length (6.51%), and spikelet fertility% (5.75%), indicating the involvement of non-additive gene action in controlling these traits and heterosis breeding may be useful for further generation of variability for these traits, hence in this case selection may not be effective. These results are in harmony with the combining ability analysis. The lowest estimated values of narrow sense heritability were exhibited for all studied traits.

Table 10. Estimates of genetic parameters for the studied traits during 2015 growing season.

Genetic Parameter	Blast reaction	Duration (day)	Plant height (cm)	Flag leaf area(cm^2)	No. of panicles/ plant
Dominance Variance	0.03	31.30	131.79	17.27	11.12
Additive Variance	0.01	5.24	11.55	1.70	0.97
Genetic Variance	0.03	36.53	143.35	18.98	12.10
Environment Variance	0.20	3.54	4.28	3.52	2.30
Phenotypic Variance	0.48	6.33	12.15	4.73	3.79
Ratio of gca Var. to sca Var.	1.25	1.17	1.08	1.10	1.09
Narrow sense heritability	3.11	13.06	7.82	7.58	6.79
Broad sense heritability	15.19	91.16	97.10	84.61	84.03
Expected Genetic Advance	9.89	3.69	6.05	10.09	12.17

Table 10. Continued.

Genetic Parameters	Panicle length (cm)	No. of primary branches	Panicle weight (g)	1000-grain weight (g)	Spikelet fertility%
Dominance Variance	1.52	0.61	0.24	3.64	37.25
Additive Variance	0.25	0.05	0.01	0.36	9.01
Genetic Variance	1.76	0.66	0.25	4.00	46.26
Environment Variance	1.27	1.17	0.11	0.99	4.17
Phenotypic Variance	1.74	1.35	0.61	2.23	7.10
Ratio of gca Var. to sca Var.	1.16	1.09	1.05	1.10	1.24
Narrow sense of Heritability	8.12	2.86	3.60	7.22	17.86
Broad sense of Heritability	58.15	36.08	69.32	80.15	91.72
Expected Genetic Advance	6.51	7.82	31.08	9.64	5.75

Moreover, the ratio of GCA and SCA variances was greater than unity for all the traits revealed the preponderance of non-additive gene action over the additive gene action for all studied traits. The results suggest that improvement in these traits may be obtained via heterosis breeding or by single plant selection in later generations following hybridization or intermating of selected segregants through recurrent selection. Similar results were observed previously by Saxena, *et al.* (2005), Manickavelu, *et al.* (2006), Pradhan, *et al*. (2006), Sarma, *et al.* (2007), Hassan *et al*. (2013) and Zeinab Montazeri1 *et al*. (2014).

4. Proportional Contribution of Lines, Testers and L. x T. to Total Variances:

Line x testers contributed more to the total sum square for all studied traits. The contribution of lines was lower compared to the testers and lines × testers interaction for all traits under study, except number of panicles/plant, panicle length, panicle weight and 1000-grain weight. All three sources of variation contributed equally for the spikelet fertility %. Contribution of tester was slightly greater than that of lines for blast reaction, duration, plant height, flag leaf area and number of primary branches/panicle (Table١١). These results showed that lines, testers and the interaction lines × testers brought much variation in the expression of the studied traits. Similar results were observed previously by Mushonga (1991).

Table 11. Contribution of Lines, Tester and Lines x Tester for the studied traits during 2015 growing season.

% of contribution	Blast reaction	Duration (day)	Plant height (cm)	Flag leaf area	No. of panicles/ plant
Contribution of Lines	17.82	26.55	10.92	13.00	29.21
Contribution of Tester	33.45	28.13	28.22	28.83	10.07
Contribution of LinexTester	48.64	45.32	60.86	58.17	60.73

Table 11. Continuous

% of contribution	Panicle length (cm)	No. of primary branches	Panicle weight (g)	1000-grain weight (g)	Spikelet fertility%
Contribution of Lines	49.85	11.76	22.03	35.27	33.71
Contribution of Tester	1.99	27.49	8.38	6.62	31.71
Contribution of LinexTester	48.16	60.75	69.59	58.10	33.58

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تحديد جينات المقاومة لمرض اللفحة فى الأرز باستخدام تحليل السلالة X الكشاف

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أجريت هذه الدراسة فى قسم بحوث الأرز – سخا – كفر الشيخ – مصر، خلال مواسم ٢٠١٤، ٢٠١٥ و ٢٠١٦ . استخدمت اربعة تراكيب وراثية وهى: سخا ١٠١ ، سخا ١٠٢، سخا ١٠٣ و سخا ١٠٤ كسلالات وأربعة اصناف أرز (وحيدة الجين للفحة) وهى: IRBLKS-S ، IRBL3- CP4 ، IRBL5- M و IRBL7- M ككشافات والتى تحمل الجينات المعرفة لمرض اللفحة (Pi5(t)، Pi3 ، Pik-S و (t) Pi7). وذلك بهدف دراسة توارث المقاومة لمرض لفحة الأوراق في الأرز والمتسبب عن الفطر *Magnaporthe grisea*. أظهرت النتائج تحت الظروف الحقلية ان الأصناف سخا ١٠٢ و سخا ١٠٣ كانت مقاومة للفحة تحت ظروف المواقع الثلاث سخا، جميزة وزرزورا، بينما كانا الصنفين سخا ١٠١ و سخا ١٠٤ حساسيين للاصابة تحت ظروف نفس المواقع. أيضا كانت سلالات الارز وحيدة الجين IRBLKS-S ، IRBL3- CP4 ، IRBL5- M و IRBL7- M مقاومة للفحة تحت ظروف الإصابة الطبيعية. على الجانب الاخر اوضحت البيانات ان الصنفين سخا ١٠٢ وسخا ١٠٣ كانا مقاومين للفحة لسلالات الفطر الخمسة المستخدمة ماعدا سلالة الفطر IB-45 كانا حساسيين لها. بينما الصنفين المصريين سخا ١٠١ و سخا ١٠٤ كانا حساسين للإصابة لسلالات الخمسة للفطر. بينما اوضحت النتائج ان السلالات وحيدة الجين للفحة IRBLKS-S ، IRBL3- CP4 و IRBL5- M والتى تحمل جينات المقاومة (Pi5(t)، Pi3 و Pik-S) كانت مقاومة لكل سلالات الفطر ماعدا سلالة الفطر EG-5 كانت حساسة لها. اوضحت النتائج ان ستة جينات رئيسية Pi-i ، Pi-sh ، Pi5(t)، Pi3 ، Pik-S و Pi7 (t) كانت فعالة تحت الظروف المصرية واستطاعت ان تحسن جينات المقاومة لمرض اللفحة في برنامج التربية. نتائج التوريث لمقاومة اللفحة باستخدام ستة عشر تركيبا وراثيا من الجيل الأول والجيل الثاني أوضحت أن جميع تركيب الجيل الاول كانت مقاومة، بينما أعطي الجيل الانعزالي ثمانية مجاميع اظهرت مقاومة وعدم مقاومة. أربعة هجن اعطت نسب انعزالات ١٥ مقاوم الى ١ حساس، بينما نسبة الانعزال للاربعة هجن الاخرى كانت ٣ مقاوم الى ١ حساس للصفات المحصولية، اوضح تحليل التباين اختلافات معنوية لمعظم التراكيب الوراثية السلالات، الكشافات، تفاعل السلالة x الكشاف لصفات مرض اللفحة، نضج المحصول، ارتفاع النبات، طول ووزن السنبلة، مساحة ورقة العلم، عدد السنابل/نبات، عدد الفروع الاولية/سنبلة، وزن ال ١٠٠٠حبة والنسبة المؤية للعقم موضحة ان التراكيب الوراثية تمتلك تنوع جينى واسع للصفات المدروسة،فضلا عن ذلك اختلافات وراثية ترجع لتفاعل السلالة xالكشاف للصفات المذكورة سابقا موضحة اهمية كلا من التفاعل الجيني المضيف وغير المضيف فى توريث هذه الصفات. وجدت اختلافات معنوية مرغوبة لقوة الهجين مقارنة بمتوسط الابوين والاب الافضل فى الهجين سخا ١٠٣ x IRBLKS-S كافضل التراكيب لتحسين صفات المقاومة لمرض اللفحة، إرتفاع النبات، مساحة ورقة العلم، عدد السنابل/نبات و النسبة المؤية للعقم. اضافة الى ذلك كان الهجين سخا ١٠٢ x IRBLKS-S افضل التراكيب الوراثية لصفات التبكير في النضج، القصر، مساحة ورقة العلم، زيادة عدد السنابل/نبات زيادة وزن ال ١٠٠٠ حبة، وعلية من الممكن استخدامه في برنامج التربية لتحسين هذه الصفات فى الارز.