

Identification and Evaluation of Some New Hybrids of Rice Under Egyptian Conditions

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ABSTRACT

The present study was carried out at the Experimental Farm of Sakha Agricultural Research Station, Sakha, Kafr El-Sheikh, Egypt, during 2013 and 2014 rice growing seasons to identify the restoring ability and evaluation of some new rice hybrids, as well as extent combining ability, gene action and three types of heterosis for the yield and its components. The experiment comprised 22 cross progenies derived from two cytoplasmic male sterile lines namely; G46A and IR69625A as female parents with 11 lines as pollinated parents (testers) Giza178, Giza179, GZ5121, Millie, IR25571-31, TNAU6464, TNAU831358, TNAU831399, MTU-1010, IR62164-32-2-2-2-1 and CT6510-24-1-2, were evaluated in a Randomized Complete Block Design (RCBD) with three replications. The results showed that the analysis of variance for combining ability revealed significant and highly significant differences among parents, crosses and Line x Tester interaction for all the studied traits. The ratio of K^2 GCA / K^2 SCA was more than unity for all studied traits, indicated the preponderance of additive gene effects in the expression of these traits. The rice hybrids; G46A X TNAU831399, IR69625A X Giza178, IR69625A X Millie, G46A X Giza178 and IR69625A X TNAU831358 were the best specific combiner for grain yield and G46A X CT6510-24-1-2, IR69625A X TNAU831358, G46A X Millie and IR69625A X Giza179 for 1000-grain weight. Concerning grain yield, the eight rice hybrids showed values for standard heterosis more than 15% over the check variety. These hybrids were; IR69625A X Millie (47.1%), G46A X MTU-1010 (36.7%), G46A X Giza179 (30%), G46A X CT6510-24-1-2 (28.3%), IR69625A X CT6510-24-1-2 (22.8%), G46A X IR62164-32-2-2-2-1 (22.4%), G46A X Giza178 (22%), G46A X IR25571-31 (19.7%), IR69625A X MTU-1010 (19.2%) and IR69625A X IR62164-32-2-2-2-1 (16%) and could be utilized to develop hybrid rice varieties.

Keywords: Hybrid rice, grain yield, heterosis, pollen and spikelet fertility, yield components, *Oryza sativa* L

INTRODUCTION

Rice (*Oryza sativa* L.) is an important cereal crop in the world and it is a staple food for more than half of the world's population (Marathi *et al.*, 2012). The increasing population pressure, the demand of cereal is increasing day by day. In Egypt, rice is the second important cereal crop. Development of high yield potential hybrid variety is one of the ways to save the future demand. Hybrid rice offers an opportunity to boost the yield potential of rice. It has a yield advantage of 15-20% over conventional high yielding variety. The breeders try, with the help of suitable quantitatively genetic method to combine the desired properties of different varieties, Rahaman (2016). Hybrid technology is one of the most feasible options to full-fill the demands of increasing population by developing new high yielding hybrids and improved lines/varieties with stable performance for different agro-climatic conditions, Soni *et al.*, (2016). The most common, easy and effective means for developing and identifying new hybrids depends on strong wide combining ability and usefulness to assess nicking ability in crops. At the same time, elucidate the nature and magnitude of gene actions involved, provides breeders about insight of nature and relative magnitude of fixable and non-fixable genetic variances; dominance or epistatic components, Sundaram *et al.*, (2010) according by Soni *et al.*, (2016). Wider combining ability provides useful information for the selection of donor parents for effective breeding programme. Such information are required to design efficient breeding strategy for rapid dynamic crop improvement Sundaram *et al.*, (2010). Pradhan and Singh, (2008) showed that, the combining ability analysis is one of the powerful tools available to estimate the combining ability effects and aids in selecting the desirable parent and crosses for the exploration of heterosis. There is a bright scope to study the combining ability that is prerequisite for developing

hybrid rice varieties with good quality in Egypt. Combining ability is a powerful tool in identifying the best combiners that may be used in crosses either to exploit heterosis or to accumulate fixable genes and obtain desirable segregates Rahaman (2016). It will help to understand the genetic base of various characters that enable the breeder to design effective breeding plan for future up gradation of the existing materials. The line X tester analysis in rice is used principally to determine the general and specific combining ability of the quantitative properties. Hybridization program would be efficient and effective if the genotypes are selected on the basis of their genetic value i.e. additive and non-additive value, Rahaman (2016). The main objective of this investigation was to identify the best restorer lines which show strong heterosis and good restoration for CMS lines to develop new hybrid combinations with high yielding ability under Egyptian conditions. As well as to determine the general and specific combining ability of different male sterile and restorer lines.

MATERIALS AND METHODS

The present study was carried out at the Experimental Farm of Sakha Agricultural Research Station, Sakha, Kafr El-Sheikh, Egypt, during 2013 and 2014 rice growing seasons. The experiment comprised cross progenies derived from the two cytoplasmic male sterile lines namely; G46A and IR69625A as female parents with 11 lines as pollinated parents (testers) Giza178, Giza179, GZ5121, Millie, IR25571-31, TNAU6464, TNAU831358, TNAU831399, MTU-1010, IR62164-32-2-2-2-1 and CT6510-24-1-2. At flowering time, hybridization between parents (Line x Tester) was carried out following the technique proposed by Virmani *et al.*, (1997), twenty two crosses combinations generated through line x tester mating design of the two lines as female parents with 11 lines as pollinated parents in 2013 rice growing season. The F_1 hybrid

combinations along with their respective parents were grown in the nursery during the second week of May 2014. Seedlings at 30-days old for all genotypes were individually transplanted in a Randomized Complete Block Design (RCBD) with three replications. Each replicate consisted of 35 genotypes, while each genotype grown in one row. Each row were five meters length with 20 x 20cm between rows/plants, each row had 25 plants. The package of recommendations was applied as recommended by RRTC (2011).

The entire grain yield and its contributing traits were estimated according to Standard Evaluation System for Rice (SES) of IRRI (2002). The studied traits were:

days to 50% of heading, plant height (cm), number of panicles/plant, panicle length (cm), number of spikelets/panicle, pollen fertility (%), spikelets fertility (%), number of filled grains/panicle, panicle weight (g), 1000 – grain weight (g) and grain yield / plant (g).

Statistical analysis: The data were analyzed using the analysis of variances for RCBD as suggested by Panse and Sukhatme (1954) to test the significance of differences among the genotypes. The genetic analysis was performed using line x tester analysis according to Kempthorne (1957). Additionally, the procedures described by Singh and Chaudhary (1977) were used to estimate general combining ability (GCA) effects for each female and male parent and specific combining ability (SCA) effects for hybrid combinations.

Genetic Components: The genetic components were estimated based on the expectations of mean squares according to El-Rouby (2009).

Estimation of heterosis: In general, the heterosis was determined as the percentage for increase or decrease in the performance of the hybrid over better parent (BP), over mid-parents (MP) and standard heterosis (SH), (Mather 1949 and Mather and Jinks 1982). Appropriate L.S.D. values were calculated to test the significance of the heterosis effects for better-parent and mid-parent heterosis, according to the method, suggested by Wyanne *et al.*, (1970).

RESULTS AND DISCUSSION

The mean performances of the morphological and yield characters of the studied genotypes are presented in Table 1. For days to 50% heading the data revealed that G46A was the earliest and the number of the days to 50% of heading was 79 days. The two testers, IR25571-31 and Giza179 were the earliest and the number of the days to 50% heading recorded 88 and 95 days, respectively. The three crosses of IR69625A X MTU-1010, IR69625A X Giza179 and IR69625A X TNAU831358 were earlier, and the number of the days to 50% heading were 92, 94 and 94 days, respectively, these results were in agreement with Awad-Allah (2011) and Elixon *et al.*, (2015). Concerning plant height, G46A showed the shortest plant height (desirable) and gave the lowest mean value (87.2cm). However, the two testers; Giza179 and IR25571-31 gave the lowest values of 88.3 and 99.2cm, respectively.

While, the most desirable mean values towards tallness as restorer lines were found in the restorers GZ5121 (114.7cm), TNAU6464 (114.7cm), TNAU831399 (114.7cm), MTU-1010 (114.7cm), IR62164-32-2-2-2-1 (114.7cm) and CT6510-24-1-2 (114.7cm) for the CMS line G46A, on the contrary the restorers GZ5121 (114.7cm), CT6510-24-1-2 (118.3cm) and IR62164-32-2-2-2-1 (156cm) for the CMS line IR69625A. The most desirable mean values towards shortness were found for the three hybrids IR69625A X MTU-1010 (98cm), IR69625A X TNAU6464 (99.4cm) and IR69625A X TNAU831399 (99.4cm), these results were similar with the results were obtained by Sanghera and Hussain (2012) and Elixon *et al.*, (2015). Concerning number of panicles/plant the three genotypes IR62164-32-2-2-2-1, CT6510-24-1-2 and MTU-1010 gave the highest mean values and their values were 18.7, 18.3 and 17.3 panicles/plant, respectively. The three hybrids IR69625A X TNAU831358, IR69625A X IR62164-32-2-2-2-1 and IR69625A X TNAU6464 gave the highest mean values (27.3, 27.3 and 25 panicles/plant, respectively), these findings were in agreement with their obtained by Awad-Allah (2011), Bhuiyan *et al.*, (2014) and Elixon *et al.*, (2015). Number of productive tillers are an important yield component in rice. For number of panicle bearing tillers/ plant is believed to be closely associated with high grain yield/plant so, the hybrids with more number of panicles bearing tillers/plant to be identified. For the mean values of panicle length; the three genotypes CT6510-24-1-2, MTU-1010 and IR25571-31 gave the highest mean values of the panicle length (26.2, 25.7 and 25.6cm), while the two hybrids G46A X IR25571-31 and IR69625A X Millie gave the highest mean values for panicle length (28.3 and 28.1cm), these results were similar with the obtained by Sanghera and Hussain (2012), Bhuiyan *et al.*, (2014) and Elixon *et al.*, (2015). For number of spikelets/panicle, the highest mean value was recorded in G46A (161.5). The two testers; IR62164-32-2-2-2-1 and IR25571-31 gave the highest mean values (246.8 and 213.6, respectively) for the number of spikelets/panicle. The hybrids of G46A X IR25571-31 (367.8), G46A X Giza178 (313), G46A X IR62164-32-2-2-2-1 (281) and G46A X CT6510-24-1-2 (264.5) gave the highest mean values for number of spikelets/panicle, these results were similar with the obtained by Awad-Allah (2011), Sanghera and Hussain (2012) and Elixon *et al.*, (2015). For pollen fertility percentage the genotypes; TNAU831358, Giza178 and TNAU831399 gave the highest mean values. These values were 97.8, 97.1 and 96.9%, respectively. The hybrids IR69625A X Giza178 and G46A X Giza178 gave the highest mean values. These values were 98.4 and 97.6%, respectively. These results were in agreement with that reported by Awad-Allah (2011) and Sanghera and Hussain (2012). For the mean values of spikelet fertility percentage; the genotypes CT6510-24-1-2 and TNAU831358 gave the highest mean values (96.5 and 95.7%, respectively), while the three hybrids IR69625A X Giza178, G46A X IR62164-32-2-2-2-1 and IR69625A X MTU-1010 gave the highest mean values of the panicle length (96.3, 96.2 and 94.6%,

respectively), these results were in agreement with that obtained by Awad-Allah (2011) and Sanghera and Hussain (2012). Concerning the number of filled grains/panicle, G46A (G46B) showed the highest mean value (134.4). The two testers IR62164-32-2-2-2-1 and IR25571-31 gave the highest mean values for the same trait (216.3 and 192.7). The hybrids G46A X IR25571-31, G46A X Giza178 and G46A X IR62164-32-2-2-2-1 gave the highest mean values of 345.4, 290.9 and 270.3, respectively, these findings were in agreement with that recorded Bhuiyan *et al.*, (2014) and Elixon *et al.*, (2015). Concerning the panicle weight, the lines G46A (G46B) and IR69625A (IR69625B) gave the values of 3.4 and 3.6 g, respectively for the panicle weight. The two testers IR62164-32-2-2-2-1 (6.9g) and IR25571-31 (5.1g) gave the highest mean values. While, the hybrids G46A X IR25571-31, G46A X Giza178 and G46A X Giza179 gave the highest mean values. These values were 8.8, 8.1 and 7.6g, respectively, these findings were in agreement with that recorded by Awad-Allah (2011). For 1000–grain weight. The highest value was recorded for IR69625A (24.1g). The three testers; Giza179, Millie and IR62164-32-2-2-1 gave the highest mean values of the 1000–grain weight. These values were 27.6, 27.5 and 26.8g, respectively. The five hybrids of IR69625A X GZ5121, G46A X Giza179, G46A X Millie, G46A X TNAU831358 and IR69625A X IR25571-31 gave the highest mean values of the 1000–grain weight. These values were 28, 27.9, 27, 27 and

26.9g, respectively. These results were similar to that reported by Awad-Allah (2011) and Elixon *et al.*, (2015). Concerning the grain yield/plant, the results indicated that the genotypes/line IR69625A (IR69625B) showed the highest mean value (40.5g) of grain yield/plant. The four testers; CT6510-24-1-2, IR62164-32-2-2-2-1 and MTU-1010 showed the highest mean values of 47, 45.8 and 44.4g, respectively. The nine hybrids IR69625A X Millie (68.3), G46A X MTU-1010 (63.5), G46A X Giza179 (60.4), G46A X CT6510-24-1-2 (59.6), IR69625A X CT6510-24-1-2 (57), G46A X IR62164-32-2-2-2-1 (56.8), G46A X Giza178 (56.6), G46A X IR25571-31 (55.6) and IR69625A X MTU-1010 (55.3) gave the highest mean values of the grain yield/plant, these results were in agreement with that recorded by Awad-Allah (2011), Sanghera and Hussain (2012) and Elixon *et al.*, (2015).

With regarding to contributing traits and grain yield for the genotypes CT6510-24-1-2, IR62164-32-2-2-2-1, MTU-1010, IR25571-31, GZ5121, IR69625A X Millie, G46A X MTU-1010, G46A X Giza179, G46A X CT6510-24-1-2, recorded good desirable traits such as earliness, shortness, number of panicles/plant, panicle length, number of spikelets/panicle, number of filled grains/panicle, panicle weight, 1000 – grain weight and grain yield. So, we can use some of these genotypes as a new hybrids and a source for developing new restorer lines in rice breeding program, under Egyptian conditions.

Table 1 : Mean performance for morphological and yield traits of the studied genotypes during 2014 season.

Genotypes	Traits Days to heading (day)	Plant height (cm) *	No. of panicles /plant*	Panicle length (cm)*	No. of spikelets/ panicle*	Pollen fertility (%)*
G46A (L1)	79.4	87.2	11.2	20.4	161.5	86.3
IR69625A (L2)	99.3	100.7	14.8	22.5	136.7	93.3
Giza178 (T1)	100.8	104.3	13.7	23.1	165.2	97.1
Giza179 (T2)	95.0	88.3	15.0	20.7	135.1	90.0
GZ5121 (T3)	98.0	114.7	17.0	23.3	148.9	91.2
Millie (T4)	102.0	109.8	11.5	20.0	121.0	93.3
IR25571-31 (T5)	88.0	99.2	16.3	25.6	213.6	85.7
TNAU6464 (T6)	106.7	105.7	16.6	22.4	136.3	95.1
TNAU831358 (T7)	107.7	105.4	17.1	23.6	125.1	97.8
TNAU831399 (T8)	105.7	111.1	13.2	23.1	103.3	96.9
MTU-1010 (T9)	98.0	106.3	17.3	25.7	177.9	88.8
IR62164-32-2-2-2-1 (T10)	109.1	156.0	18.7	23.1	246.8	84.1
CT6510-24-1-2 (T11)	101.0	118.3	18.3	26.2	176.3	92.7
G46A X Giza178	102.6	124.2	15.9	26.6	313.0	97.6
IR69625A X Giza178	101.4	107.4	16.9	24.9	192.2	98.4
G46A X Giza179	103.0	108.0	17.2	25.7	245.0	89.6
IR69625A X Giza179	94.0	100.3	20.0	22.7	147.8	86.9
G46A X GZ5121	95.1	111.5	18.2	23.9	192.2	81.6
IR69625A X GZ5121	99.6	113.2	22.2	24.0	136.0	87.8
G46A X Millie	96.0	104.6	14.0	23.0	140.2	71.7
IR69625A X Millie	111.0	126.2	18.6	28.1	248.2	87.6
G46A X IR25571-31	96.0	111.2	21.0	28.3	367.8	90.9
IR69625A X IR25571-31	95.2	102.1	20.4	23.6	176.3	84.4
G46A X TNAU6464	106.0	109.8	15.2	24.0	152.6	88.6
IR69625A X TNAU6464	100.0	99.4	25.0	23.0	139.2	60.8
G46A X TNAU831358	107.0	111.5	15.0	24.4	171.5	77.6
IR69625A X TNAU831358	94.0	110.3	27.3	25.6	182.4	81.0
G46A X TNAU831399	107.0	106.4	14.6	25.1	154.8	85.9
IR69625A X TNAU831399	100.0	99.4	14.8	25.2	183.6	68.9
G46A X MTU-1010	95.0	108.0	20.0	23.1	140.2	89.3
IR69625A X MTU-1010	92.0	98.0	23.8	23.3	135.7	91.0
G46A X IR62164-32-2-2-2-1	125.0	164.0	18.8	23.9	281.0	92.4
IR69625A X IR62164-32-2-2-2-1	110.0	134.7	27.3	24.6	198.2	90.6
G46A X CT6510-24-1-2	104.0	116.3	20.7	23.6	264.5	86.8
IR69625A X CT6510-24-1-2	95.0	106.2	24.7	25.7	168.3	76.7
L.S.D 5%	1.08	3.53	2.23	1.39	10.32	2.90
L.S.D 1%	1.43	4.68	2.96	1.84	13.71	3.85
CV	1.11	3.60	12.74	5.95	5.85	3.53

* : These traits were recorded on maintainer lines which was related to CMS lines

Table 1 : Continued

Genotypes	Traits Spikelet fertility (%)*	No. of filled grains/panicle*	Panicle weight (g)*	1000-grain weight (g)*	Grain yield /plant (g)*
G46A (L1)	83.2	134.4	3.4	23.4	29.9
IR69625A (L2)	90.0	123.1	3.6	24.1	40.5
Gizal78 (T1)	94.6	156.2	4.0	20.7	26.9
Gizal79 (T2)	93.2	125.9	3.7	27.6	33.8
GZ5121 (T3)	94.6	141.0	3.6	23.7	40.2
Millie (T4)	88.3	106.6	3.7	27.5	18.3
IR25571-31 (T5)	90.2	192.7	5.1	23.0	40.9
TNAU6464 (T6)	92.6	126.1	3.2	22.8	32.5
TNAU831358 (T7)	95.7	119.8	3.1	23.6	31.6
TNAU831399 (T8)	94.2	102.7	3.3	23.9	28.3
MTU-1010 (T9)	92.9	165.2	4.1	21.7	44.4
IR62164-32-2-2-2-1 (T10)	87.6	216.3	6.9	26.8	45.8
CT6510-24-1-2 (T11)	96.5	170.2	4.2	23.0	47.0
G46A X Gizal78	93.0	290.9	8.1	25.0	56.6
IR69625A X Gizal78	96.3	185.0	4.9	24.8	46.4
G46A X Gizal79	92.6	226.8	7.6	27.9	60.4
IR69625A X Gizal79	90.5	133.7	3.7	24.0	38.3
G46A X GZ5121	82.1	157.8	2.9	23.0	28.7
IR69625A X GZ5121	92.3	125.5	4.6	28.0	38.7
G46A X Millie	67.4	94.6	3.2	27.0	19.8
IR69625A X Millie	85.4	208.1	5.3	22.8	68.3
G46A X IR25571-31	94.0	345.4	8.8	24.0	55.6
IR69625A X IR25571-31	88.7	156.3	4.6	26.9	46.9
G46A X TNAU6464	84.5	128.9	3.7	25.7	33.2
IR69625A X TNAU6464	56.6	78.8	2.4	23.8	30.2
G46A X TNAU831358	72.9	125.1	4.0	27.0	31.1
IR69625A X TNAU831358	76.2	138.9	4.1	22.0	40.6
G46A X TNAU831399	82.7	128.1	3.2	22.1	35.9
IR69625A X TNAU831399	64.8	119.0	3.4	23.6	25.4
G46A X MTU-1010	93.0	130.4	3.6	23.0	63.5
IR69625A X MTU-1010	94.6	128.4	3.4	24.1	55.3
G46A X IR62164-32-2-2-2-1	96.2	270.3	3.7	20.0	56.8
IR69625A X IR62164-32-2-2-2-1	94.5	187.4	5.1	25.2	53.9
G46A X CT 6510-24-1-2	90.0	238.0	3.7	24.0	59.6
IR69625A X CT 6510-24-1-2	78.0	131.3	3.4	22.0	57.0
L.S.D 5%	11.95	10.94	0.47	0.94	5.03
L.S.D 1%	15.86	14.53	0.62	1.25	6.68
CV	14.24	7.05	11.29	4.01	12.43

* : These traits were recorded on maintainer lines which was related to CMS lines

The results of the analysis of variance for morphological, grain yield and their contributing traits, are presented in Table 2. The results showed that the mean squares of the genotypes for grain yield and contributing traits showed highly significant values. This finding indicated that the presence of large variations among them. Similarly, the results cleared that, the mean squares of the parents (except for spikelets fertility percentage), parents Vs crosses, crosses, lines (except for panicle length, 1000-grain weight and grain yield / plant), testers and line x tester are showed significant and highly significant differences. Parents Vs. crosses mean squares is an indication to average heterosis overall crosses. Similar results were obtained by Awad-Allah (2011) and Rahaman (2016).

Estimation of ratio K^2 GCA (additive gene effects) and K^2 SCA (non-additive gene effects) for the grain yield and contributing traits are presented in Table 3. The ratio of K^2 GCA / K^2 SCA was more than unity for contributing traits and grain yield, indicated preponderance of additive gene effects in the expression of these traits. Therefore, the selection procedures based on the accumulation of additive effect would be successful in improving contributing traits and grain yield, agreement with the results were obtained by Saidaiah *et al.*, (2010), Saleem *et al.*, (2010) and Latha *et al.*, (2013). Awad-Allah *et al.*, (2015) they found that the preponderance of additive gene effects in the expression of the traits : grain yield, number of panicles/plant, number of filled grains/panicle, days to heading, spikelets/panicle and spikelets fertility percentage. On the contrary, preponderance of non-

additive gene effects in the expression of the these traits panicle weight and 1000-grain weight. Upadhyay and Jaiswal (2015) for days to heading, plant height and 1000-grain weight, Waza *et al.*, (2015) for days to heading, plant height, number of panicles/plant and 1000-grain weight, Rahaman (2016) for filled grains/panicle and grain/yield plant.

General combining ability (GCA) analysis is presented in Tables 4 and 5. For days to heading the data revealed that the line IR69625A (-2) gave highly significant negative and desirable values. While, highly significantly negative values were shown by six out of the 12 testers, while the two testers MTU-1010 (-7.8) and IR25571-31 (-5.7) were showed the highest negative value. This finding indicated that these lines and testers are considered as good combiners to develop early restorer lines and hybrids. Thus GCA estimate could help in identifying the lines and testers which would give good hybrids and improve parental lines for desirable traits, these findings were in agreement with that recorded by Saidaiah *et al.*, (2010) and Awad-Allah (2011). Concerning plant height, the line IR69625A (-3.6) showed highly significant desirable and negative GCA effects. While, the testers TNAU831399 (-9.5), MTU-1010 (-9.4), Giza179 (-8.2), TNAU6464 (-7.8), IR25571-31 (-5.7), and TNAU831358 (-1.5) showed highly significant negative and desirable values of GCA effects. Moreover, the significant negative value of GCA effects was showed by the tester CT6510-24-1-2 (-1.1). The negative values are indicators of decreased plant height. Therefore, it could be useful to breed short stature rice cultivars, or hybrid combinations. While, the positive values were desirable for the good restorers lines, these results agreed with the results obtained by Saidaiah *et al.*, (2010), Awad-Allah (2011) and Sanghera and Hussain (2012). Concerning the number of panicles/plant, data showed that the line IR69625A (2.3) showed highly significant positive (desirable) value, while the testers; IR62164-32-2-2-2-1 (3.5), CT 6510-24-1-2 (3.1), MTU-1010 (2.3), TNAU831358 (1.6) and IR25571-31 (1.1) showed highly significant positive values of GCA effects, these findings were in agreement with that obtained by Awad-Allah (2011) and Sanghera and Hussain (2012). For panicle length, data showed that non significant positive value for the lines tested. While, for the testers IR25571-31 (1.3), Giza178 (1.1), Millie (0.9) gave the highly significant positive (desirable) values. On the other hand, TNAU831399 (0.5) gave the significant positive value, this means that these genotypes could help to improvement of parental lines of hybrids rice and new rice hybrids, also noted by Sanghera and Hussain (2012). Obviously for number of spikelets/panicle the data illustrated highly significant positive and desirable value of GCA effects for the line G46A (23.4). While the testers IR25571-31 (75.2), Giza178 (55.8), IR62164-32-2-2-2-1 (42.7) and CT6510-24-1-2 (19.5) showed highly significant positive value of general combining ability effects. This means that these genotypes could be good parental combiners in rice hybrids breeding, these findings were in agreement with the recorded by

Saidaiah *et al.*, (2010) and Rahaman (2016). For pollen fertility percentage, data indicated that the line G46A (1.7) and five testers Giza 178 (13.2), IR62164-32-2-2-1 (6.7), MUT1010 (5.3), Giza 179 (3.4), and IR25571-31 (2.8) showed highly significant positive values of GCA effects. This means that these genotypes could be utilized as parents for breeding genotype with more fertile pollen grains per panicle for developing maintainer, restorer lines and hybrids, these results were in agreement with the results were obtained by Awad-Allah (2011), Sanghera and Hussain (2012) and Latha *et al.*, (2013). Concerning the spikelets fertility percentage, data indicated that the line G46A (1.7) and five testers; Giza178 (13.2), IR62164-32-2-2-2-1 (6.7), MTU-1010 (5.3), Giza179 (3.4) and IR25571-31 (2.8) showed highly significant positive and desirable values of GCA effects. It means that these genotypes could be utilized as parents for breeding genotype with more fertile grains per panicle for developing maintainer, restorer lines and hybrids, these findings were in agreement with that recorded by Saidaiah *et al.*, (2010), Sanghera and Hussain (2012) and Latha *et al.*, (2013). Regarding the number of filled grains/panicles data revealed that the line G46A (24.7) and the testers IR25571-31 (81.4), Giza178 (68.5), IR62164-32-2-2-2-1 (59.3), CT6510-24-1-2 (15.2) and Giza179 (10.8) showed highly significant positive values, so these genotypes could be identified as the best combiners for this trait, these findings were in agreement with the results were obtained by Saidaiah *et al.*, (2010) and Sanghera and Hussain (2012). Concerning panicle weight, the data indicated that the line G46A (0.3) and the three testers IR25571-31 (2.3), Giza178 (2.1) and Giza179 (1.2) showed highly significant positive values of GCA effects for panicle weight, these results were similar to the results obtained by Rahaman (2016). Consequently, the former genotypes can be used in the hybrid rice program as good combiners for heavier panicle weight. Furthermore, the values of GCA effects for 1000-grain weight, were non significant positive for the lines. While, the testers; Giza179 (1.6), GZ5121 (1.1), IR25571-31 (1.1), Giza178 (0.5) and Millie (0.5) showed highly significant positive values of general combining ability effects, moreover, the tester TNAU6464 (0.4) showed significant positive values of general combining ability effects, these results were in agreement with other results obtained by many investigators among them Awad-Allah (2011) and Latha *et al.*, (2013). It means that these genotypes could be considered as good combiners for heavy grain weight. The grain yield/plant, were non significant positive for the lines. On the other hand, for the testers; MTU-1010 (13.8), CT6510-24-1-2 (12.7), IR62164-32-2-2-2-1 (9.8), Giza178 (6), IR25571-31 (5.7) and Giza179 (3.8) the recorded data showed highly significant positive values of general combining ability effects. These genotypes appeared to be good combiners to improve yield components, these findings were in agreement with those reported by Saidaiah *et al.*, (2010), Awad-Allah (2011) and Latha *et al.*, (2013).

Table 2 : Analysis of variance and combining ability for the morphological and yield traits for the studied genotypes during 2014 rice growing season.

Sources of variance (SOV)	d.f	Days to heading	Plant height (cm)	No. of Panicles/ plant	Panicle length (cm)	No. of spikelets/ panicle	Pollen fertility (%)	Spikelets fertility (%)	No. of filled grains /panicle	Panicle weight (g)	1000-grain weight (g)	Grain yield /plant (g)
Replications	2	0.1 ^{ns}	17.4 ^{ns}	0.03 ^{ns}	0.5 ^{ns}	34.9 ^{ns}	3.3 ^{ns}	114.4 ^{ns}	53.5 ^{ns}	0.02 ^{ns}	0.4 ^{ns}	7.8 ^{ns}
Genotypes	34	184.8**	715.2**	50.1**	10.3**	10265.7**	209.8**	362.3**	10197**	6.6**	12.9**	510.6**
Parents	12	204.9**	862.2**	17.9**	11.4**	4687.1**	61.7**	43.5 ns	3438.7**	3.1**	13.4**	218.3**
P. vs. Crosses	1	102.4**	426.4**	427.1**	63.1**	37935.2**	1165**	1684.6**	15163.7**	4.5**	3.2**	2531**
Crosses	21	177.3**	645**	50.5**	7.2**	12135.8**	248.9**	481.6**	13822.3**	8.7**	13.0**	581.4**
Lines	1	269.6**	834.3**	348.2**	0.1 ^{ns}	36145.5**	194.4**	472.1*	40324.7**	8**	0.27 ^{ns}	0.00004 ^{ns}
Tester	10	237.9**	1037**	46.4**	4.9**	11566.3**	294.3**	784.6**	15429**	9.9**	8.2**	710.2**
Lines xTesters	10	107.5**	234.1**	24.9**	10.1**	10304.5**	208.9**	179.5*	9565.4**	7.5**	19.2**	510.8**
Error	68	0.6	6.2	2.5	1.0	53.5	4.2	71.7	60.2	0.1	0.4	12.7

** : Highly significant at 1% * : significant at 5% ns : Non significant.

Table 3 : Ratio between K2 GCA and K2 SCA for the morphological and yield traits for the studied genotypes during 2014 rice growing season.

Genetic components	Traits Days to heading	Plant height (cm)	No. of Panicles/ plant	Panicle length (cm)	No. of spikelets/ panicle	Pollen fertility (%)	Spikelets fertility (%)	No. of filled grains /panicle	Panicle weight (g)	1000-grain weight (g)	Grain yield /plant (g)
K ² GCA	8.2	25.1	10.5	-0.03	1093.7	5.8	12.1	1220.1	0.2	-0.01	-0.4
K ² SCA	39.6	171.8	7.3	0.7	1918.8	48.3	118.8	2561.5	1.6	1.29	116.2
K ² GCA / K ² SCA	35.7	75.9	7.5	3.0	3417	68.2	36.0	3168.4	2.4	6.25	166.0

Table 4 : General combining ability effects of the lines for the morphological and yield traits during 2014 rice growing season.

Lines	Traits Days to heading	Plant height (cm)	No. of Panicles/ plant	Panicle length (cm)	No. of spikelets/ panicle	Pollen fertility (%)	Spikelets fertility (%)	No. of filled grains /panicle	Panicle weight (g)	1000-grain weight (g)	Grain yield /plant (g)
G46A	2.02**	3.6**	-2.3**	0.03 ^{ns}	23.4**	1.7**	2.7**	24.7**	0.3**	0.06 ^{ns}	-0.001 ^{ns}
IR69625A	-2.02**	-3.6**	2.3**	-0.03 ^{ns}	-23.4**	-1.7**	-2.7**	-24.7**	-0.3**	-0.06 ^{ns}	0.001 ^{ns}
L.S.D 5%	0.13	0.4	0.3	0.17	1.3	0.4	1.5	1.4	0.06	0.12	0.621
L.S.D 1%	0.19	0.6	0.4	0.24	1.8	0.5	2.1	1.9	0.08	0.16	0.878

** : Highly significant at 1% * : significant at 5% ns : Non significant

Table 5 : General combining ability effects of the tester lines for the morphological and yield traits during 2014 rice growing season.

Testers	Traits Days to heading	Plant height (cm)	No. of Panicles/ plant	Panicle length (cm)	No. of spikelets/ panicle	Pollen fertility (%)	Spikelets fertility (%)	No. of filled grains /panicle	Panicle weight (g)	1000-grain weight (g)	Grain yield /plant (g)
Gizal78	0.7**	3.4**	-3.2**	1.1**	55.8**	13.2**	11.1**	68.5**	2.1**	0.5**	6.0**
Gizal79	-2.8**	-8.2**	-1.0**	-0.4*	-0.4 ^{ns}	3.4**	8.0**	10.8**	1.2**	1.6**	3.8**
GZ5121	-3.9**	-0.1 ^{ns}	0.6 ^{ns}	-0.7**	-32.7**	-0.1 ^{ns}	3.7*	-27.8**	-0.7**	1.1**	-11.8**
Millie	2.2**	3.0**	-3.3**	0.9**	-2.7 ^{ns}	-5.2**	-21.4**	-18.1**	-0.2**	0.5**	-1.5*
IR25571-31	-5.7**	-5.7**	1.1**	1.3**	75.2**	2.8**	7.8**	81.4**	2.3**	1.1**	5.7**
TNAU6464	1.7**	-7.8**	0.5 ^{ns}	-1.1**	-51.0**	-10.1**	-13**	-65.6**	-1.4**	0.4*	-13.9**
TNAU831358	-0.8**	-1.5**	1.6**	0.3 ^{ns}	-19.9**	-5.5**	-9.0**	-37.5**	-0.4**	0.1 ^{ns}	-9.7**
TNAU831399	2.2**	-9.5**	-4.9**	0.5*	-27.6**	-7.4**	-9.8**	-45.9**	-1.1**	-1.5**	-14.9**
MTU-1010	-7.8**	-9.4**	2.3**	-1.4**	-58.9**	5.3**	10.3**	-40.1**	-0.9**	-0.8**	13.8**
IR62164-32-2-2-2-1	16.2**	36.9**	3.5**	-0.4 ^{ns}	42.7**	6.7**	11.8**	59.3**	-0.01 ^{ns}	-1.8**	9.8**
CT6510-24-1-2	-1.8**	-1.1*	3.1**	0.02 ^{ns}	19.5**	-3.1**	0.5 ^{ns}	15.2**	-0.9**	-1.4**	12.7**
L.S.D 5%	0.31	1.02	0.6	0.4	3.0	0.8	3.5	3.2	0.14	0.27	1.5
L.S.D 1%	0.44	1.44	0.9	0.6	4.2	1.2	4.9	4.5	0.19	0.39	2.1

** : Highly significant at 1% * : significant at 5% ns : Non significant

Specific combining ability (SCA) effects:

Specific combining ability effects for the grain yield and contributing traits of the crosses are shown in Table 6. For days to heading, data in the same Table revealed that 11 hybrid combinations recorded highly significant and significant negative (desirable) values of specific combining ability effects. The highest significant negative values were shown in the hybrid combinations; IR69625A X Giza179 (-9.5), G46A X CT6510-24-1-2 (-5.5) and IR69625A X MTU-1010 (-4.5), these findings were in agreement with other results obtained by Saidaiah *et al.*, (2010), Awad-Allah (2011) and Latha *et al.*, (2013). Concerning plant height, results are shown in Table 6 showed that eight hybrid combinations recorded highly significant and significant negative (desirable) values of specific combining ability effects. The highest significant negative values were shown in the hybrid combinations; IR69625A X Giza179 (-14.4), G46A X CT6510-24-1-2 (-11.1) and IR69625A X TNAU6464 (-4.8), these results were in agreement with the results obtained by Saidaiah *et al.*, (2010) Awad-Allah (2011) and Sanghera and Hussain (2012). The negative values of SCA effects means decreased plant height and could be useful to breed short stature rice hybrids and rice cultivars. While, the positive values of SCA effects means increased plant height and could be useful to breed restorer lines. Regarding number of panicles/plant data in Table 6 showed that seven hybrid combinations recorded highly significant positive and desirable values. The highest significant positive values were shown in the hybrid combinations; IR69625A X MTU-1010 (3.9), G46A X GZ5121 (2.6) and G46A X MTU-1010 (2.6). These results were in agreement with those reported by Saidaiah *et al.*, (2010), Awad-Allah (2011) and Sanghera and Hussain (2012). For panicle length, data in Table 6 showed that six hybrid combinations recorded highly significant positive values of SCA effects. The highest significant positive values were shown in the cross combinations; G46A X TNAU831399 (2.6), G46A X GZ5121 (2.3) and IR69625A X Giza178 (1.5), these findings were in agreement with those obtained by Saidaiah *et al.*, (2010), Sanghera and Hussain (2012) and Ali *et al.*, (2014). For number of spikelets/panicle, 11 hybrid combinations showed highly significant and significant (desirable) positive values of SCA effects. The highest values were shown in the hybrid combinations; G46A X TNAU831399 (77.4), G46A X GZ5121 (72.3) and G46A X IR62164-32-2-2-2-1 (37.8) and G46A X Giza178 (37), these results were similar to with others recorded by Sanghera and Hussain (2012) and Ali *et al.*, (2014). For pollen fertility percentage data showed that nine hybrid combinations recorded desirable, highly significant and significant positive value of specific combining ability effects. The highest significant positive values were shown in the cross combinations; IR69625A X GZ5121 (12.2), G46A X TNAU831399 (9.7) and IR69625A X Millie (6.8), these results were in agreement with those obtained by many researchers among them Awad-Allah (2011), Sanghera and Hussain (2012) and Latha *et al.*, (2013). Concerning spikelets

fertility percentage data showed that three hybrid combinations recorded highly significant and significant positive (desirable) value of specific combining ability effects. The highest significant positive value were shown in the cross combinations IR69625A X GZ5121 (11.3) and IR69625A X TNAU831358 (7.8). These genotypes appeared to be good combiners to improve rice cultivars and hybrids for grain yield/plant, these findings were in agreement with other results obtained by Saidaiah *et al.*, (2010), Awad-Allah (2011), Sanghera and Hussain (2012) and Latha *et al.*, (2013). For number of filled grains/panicle, data in Table 6 showed that ten hybrid combinations recorded highly significant positive and desirable values of SCA effects. The highest significant positive values were shown in the crosses; G46A X TNAU831399 (81.5), G46A X GZ5121 (69.8) and IR69625A X MTU-1010 (31.6). These positive values indicated that desirable types of non-additive effects could be present in these cross combinations for number of filled grains/panicle, these findings were in agreement with those reported by Saidaiah *et al.*, (2010), Sanghera and Hussain (2012) and Ali *et al.*, (2014). Concerning panicle weight, 11 hybrid combinations recorded highly significant and significant positive and desirable values of SCA effects. The highest significant positive values were shown in the cross combinations; G46A X GZ5121 (1.8), IR69625A X Giza178 (1.6), G46A X TNAU831399 (1.4) and G46A X Giza178 (1.3), these results were in agreement with those recorded by Saidaiah *et al.*, (2010) and Hasan *et al.*, (2015). For 1000-grain weight data revealed that ten hybrid combinations had highly significant positive (desirable) values of SCA effects. The highest significant positive values were shown in the cross combinations; G46A X CT6510-24-1-2 (2.7), IR69625A X TNAU831358 (2.6), G46A X Millie (2.4) and IR69625A X Giza 179 (2.0), these findings were in agreement with other results obtained by Ali *et al.*, (2014) and Hasan *et al.*, (2015). So, it could be suggested that one or more of the former hybrid combinations may be used in improving 1000-grain weight in rice hybrids or rice cultivars. Concerning grain yield/plant, eight hybrid combinations gave highly significant positive values of SCA effects. The highest significant positive values were shown in the hybrid combinations; G46A X TNAU 831399 (24.2), IR69625A X Giza 178 (11), IR69625A X Millie (5.2), G46A X Giza 178 (5.1) and IR69625A X TNAU 831358 (5), these results were in agreement with many others among them Saidaiah *et al.*, (2010), Awad-Allah (2011), Sanghera and Hussain (2012), Ali *et al.*, (2014) and Hasan *et al.*, (2015). These results indicated that the non-additive gene effects were predominant in these particular rice hybrid combinations for grain yield/plant and could be contributed to the wide differences in grain yield/plant between the involved parents in these hybrid combinations. Accordingly, it could be suggested that one or more of these hybrid combinations could be used as a new hybrid or used in improving grain yield in hybrid rice breeding programme. The hybrids showing high SCA effects involving low/low general combiners indicate the non-additive genetic effects and these

crosses could be exploited for heterosis breeding programme, Singh *et al.*, (2007), Saidaiah *et al.*, (2010) and Shanthi *et al.*, (2011). It is concluded from the present results, that there is the possibility to breed good hybrids and rice cultivars with desirable traits and high yielding rice lines than the existing lines either through heterosis breeding or through recombinant breeding with selection in later generations to develop traits adaptable high yielding parental lines of hybrid.

The proportional contribution of lines, testers and line × tester interaction for the expression of traits is presented in Table 7. It is evident that testers was more important for days to heading (63.88%), plant height (76.56%), no. of panicles/plant (43.75%), no. of spikelets/ panicle (45.38%), pollen fertility percentage (56.3%), spikelets fertility percentage (77.58%), no. of

filled grains/ panicle (53.15%), panicle weight (54.64%) and grain yield/plant (58.16%). These results are similar to those obtained by Awad-Allah *et al.*, (2015), Waza *et al.*, (2015) for days to heading and plant height, Sanghera and Hussain (2012) for no. of panicles/plant, Hasan *et al.*, (2015) for no. of spikelets/ panicle. It revealed preponderance testers influence for these traits. The contribution of maternal and paternal interaction (line x tester) was more important for panicle length (67.25%) and 1000-grain weight (70.11%). These results are agreed with the results obtained by Aditya and Bhartiya (2015) for 1000-grain weight, Waza *et al.*, (2015) and Rahaman (2016) they found the contribution of maternal and paternal interaction (line x tester) was more important for grain yield/plant.

Table 6 : Specific combining ability effects for the morphological and yield traits of the crosses during 2014 rice growing season.

crosses	Traits	Days to heading	Plant height	No. of Panicles/plant	Panicle length	No. of spikelets/panicle	Pollen fertility (%)	Spikelets fertility (%)	No. of filled grains / panicle	Panicle weight	1000-grain weight	Grain yield /plant
G46A X Giza178		-1.4**	4.8**	1.8**	0.8**	37.0**	-2.1**	-4.3 ^{ns}	28.3**	1.3**	0.04 ^{ns}	5.1**
IR69625A X Giza178		2.5**	0.3 ^{ns}	0.9 ^{ns}	1.5**	25.2**	-0.3 ^{ns}	-1.6 ^{ns}	21.8**	1.6**	1.9**	11**
G46A X Giza179		-4.3**	-4.4**	0.3 ^{ns}	-0.1 ^{ns}	4.7*	-4.8**	-7.8**	-8.6**	-1.2**	-2.56**	-5.0**
IR69625A X Giza179		-9.5**	-14.4**	-0.003 ^{ns}	-2.6**	-77.4**	-9.7**	2.6 ^{ns}	-81.5**	-1.4**	2.0**	-24.2**
G46A X GZ5121		-1.6**	1.0 ^{ns}	2.6**	2.3**	72.3**	1.5*	-0.02 ^{ns}	69.8**	1.8**	-1.5**	4.3**
IR69625A X GZ5121		1.0**	1.6*	-2.6**	0.5 ^{ns}	-16.7**	12.2**	11.3**	0.3 ^{ns}	0.3**	0.8**	1.5 ^{ns}
G46A X Millie		4.5**	-3.0**	-3.9**	-0.7*	-28.8**	-3.4**	-4.3 ^{ns}	-31.6**	-0.4**	2.4**	-4.8**
IR69625A X Millie		1.5**	-0.1 ^{ns}	2.2**	-0.1 ^{ns}	-37.8**	6.8**	6.3*	-20.2**	-0.5**	-0.8**	5.2**
G46A X IR25571-31		-0.5*	1.4*	0.4 ^{ns}	-0.1 ^{ns}	-21.2**	-2.5**	-3.5 ^{ns}	-23.7**	-0.3*	-0.6**	4.1**
IR69625A X IR25571-31		5.5**	11.1**	-2.0**	-0.4 ^{ns}	18.0**	-0.8 ^{ns}	-1.9 ^{ns}	16.7**	-1.1**	-2.7**	1.5 ^{ns}
G46A X TNAU6464		2.5**	1.5*	0.3 ^{ns}	-1.1**	24.7**	3.3**	3.3 ^{ns}	28.7**	-0.2*	0.94**	1.3 ^{ns}
IR69625A X TNAU6464		1.4**	-4.8**	-1.8**	-0.8**	-37.0**	2.1**	4.3 ^{ns}	-28.3**	-1.3**	-0.04 ^{ns}	-5.1**
G46A X TNAU831358		-2.5**	-0.3 ^{ns}	-0.9 ^{ns}	-1.5**	-25.2**	0.3 ^{ns}	1.6 ^{ns}	-21.8**	-1.6**	-1.9**	-11**
IR69625A X TNAU831358		4.3**	4.4**	-0.3 ^{ns}	0.1 ^{ns}	-4.7*	4.8**	7.8**	8.6**	1.2**	2.6**	5.0**
G46A X TNAU831399		9.5**	14.4**	0.003 ^{ns}	2.6**	77.4**	9.7**	-2.6 ^{ns}	81.5**	1.4**	-2.0**	24.2**
IR69625A X TNAU831399		1.6**	-1.0 ^{ns}	-2.6**	-2.3**	-72.3**	-1.5*	0.02 ^{ns}	-69.8**	-1.77**	1.5**	-4.3**
G46A X MTU-1010		-1.0**	-1.6*	2.6**	-0.5 ^{ns}	16.7**	-12.2**	-11.3**	-0.3 ^{ns}	-0.3**	-0.8**	-1.5 ^{ns}
IR69625A X MTU-1010		-4.5**	3.0**	3.9**	0.7*	28.8**	3.4**	4.3 ^{ns}	31.6**	0.4**	-2.4**	4.8**
G46A X IR62164-32-2-2-1		-1.5**	0.1 ^{ns}	-2.2**	0.1 ^{ns}	37.8**	-6.8**	-6.3*	20.2**	0.5**	0.8**	-5.2**
IR69625A X IR62164-32-2-2-1		0.5*	-1.4*	-0.4 ^{ns}	0.1 ^{ns}	21.2**	2.5**	3.5 ^{ns}	23.7**	0.3*	0.6**	-4.1**
G46A X CT6510-24-1-2		-5.5**	-11.1**	2.0**	0.4 ^{ns}	-18**	0.8 ^{ns}	1.9 ^{ns}	-16.7**	1.1**	2.7**	-1.5 ^{ns}
IR69625A X CT6510-24-1-2		-2.5**	-1.5*	-0.3 ^{ns}	1.1**	-24.7**	-3.3**	-3.3 ^{ns}	-28.7**	0.2*	-0.9**	-1.3 ^{ns}
L.S.D 5%		0.4	1.4	0.9	0.6	4.2	1.2	4.9	4.5	0.19	0.39	2.1
L.S.D 1%		0.6	2.0	1.3	0.8	6.0	1.7	6.9	6.3	0.27	0.55	2.9

** : Highly significant at 1% * : significant at 5% ns : Non significant

Table 7 : Percent contribution of different components (lines, testers and lines x testers) towards the crosses sum of squares for various traits in rice

Traits	Contribution of line %	Contribution of tester %	Contribution of line x tester %
Days to heading	7.24	63.88	28.88
Plant height (cm)	6.16	76.56	17.28
No. of panicles/plant	32.82	43.75	23.43
Panicle length (cm)	0.05	32.7	67.25
No. of spikelets/ panicle	14.18	45.38	40.43
Pollen fertility (%)	3.72	56.3	39.98
Spikelets fertility (%)	4.67	77.58	17.75
No. of filled grains/ panicle	13.89	53.15	32.95
Panicle weight (g)	4.38	54.64	40.98
1000-grain weight (g)	0.1	29.8	70.11
Grain yield/plant (g)	0.0	58.16	41.84

Estimation of heterosis effects:

Better-parent heterosis (BP), mid-parent (MP) heterosis and standard heterosis (SH) for grain yield and its components are shown in Tables 8, 9 and 10. For Days to heading, the data revealed that the three hybrids IR69625A X MTU-1010 (-6.1%), IR69625A X TNAU831358 (-5.4%) and IR69625A X CT6510-24-1-2 (-4.4%) showed highly significant negative and desirable values of better parent heterosis. Regarding data emphasized that the heterosis as deviation of mid-parent (MP), were highly significant negative for the six hybrids, the two hybrids IR69625A X TNAU831358 (-9.2%) and IR69625A X MTU-1010 (-6.8%) recorded highest negative values. Moreover, the data revealed that the standard heterosis, were negative highly significant and significant for 12 hybrids. The three hybrids IR69625A X MTU-1010 (-9.2%), IR69625A X Giza179 (7.3) and IR69625A X TNAU831358 (-7.3%) recorded the highest values. Significant desirable heterosis for this trait, also, was found by many others among them Sanghera and Hussain (2012), Latha *et al.*, (2013) and Elixon *et al.*, (2015). Concerning the plant height, the better-parent heterosis (BP) were not showed highly significant or significant negative values. However, for MP the three hybrids IR69625A X TNAU831399 (-6.1%), IR69625A X MTU-1010 (-5.3%) and IR69625A X TNAU6464 (-3.6%) showed highly significant and negative desirable heterosis for this trait. For standard heterosis data revealed that five hybrids showed highly significant and significant negative heterosis. The highest desirable values were observed in the three hybrids IR69625A X MTU-1010 (-8.8%), IR69625A X TNAU6464 (-7.4) and IR69625A X TNAU831399 (-7.4%), respectively. On the other hand 18, 17 and 7 hybrids out of the 22 hybrids were highly significant and significant positive in BP, MP and SH heterosis respectively. These hybrids may be to useful to breed good restorer lines. The hybrids showed negative values may be good rice hybrids or may be useful to breed good rice cultivars. Similar results were found by many authors among them Awad-Allah (2011), Sanghera and Hussain (2012), Latha *et al.*, (2013) and Elixon *et al.*, (2015). Obviously more number of productive tillers give high grain yield. Evidently, data presented in Tables 8, 9 and 10 showed highly significant and significant positive values in BP heterosis for the ten and one hybrids. Moreover, for mid-parent heterosis, 19 F₁ hybrids showed highly significant and significant positive values. While, for SH heterosis nine and two hybrids showed highly significant and significant positive heterosis. The highest values were recorded in the hybrids IR69625A X TNAU831358 showed the highest significant values (60.2; 71.5 and 61.6%) for BP, MP and SH heterosis, respectively. The number of panicle bearing tillers/plant is believed to be closely associated with high grain yield/plant so, the hybrids with more number of panicle bearing tillers/plant may be identified. The variety or hybrid with low tillering capacity is not wanted in transplanted rice culture Bhuiyan *et al.*, (2014). Similar results were reported by Sanghera and Hussain (2012), Ali *et al.*, (2014) and Bhuiyan *et al.*, (2014). A hybrid

with longer panicle length is desirable, since the lengthy panicles are generally associated with higher number of spikelets per panicle resulting in higher productivity. Data in Tables 8, 9 and 10 revealed that highly significant and significant positive heterosis over BP in six and three hybrids. However, for MP heterosis 13 and one hybrids showed highly significant and significant positive values. While, for SH two and one hybrids showed highly significant and significant positive heterosis values. The hybrids IR69625A X Millie (24.6%), G46A X Giza179 (24.1%) and G46A X Giza178 (15.2%) showed the highest values for BP heterosis. While, for MP heterosis, the two hybrids IR69625A X Millie (32%) and G46A X Giza179 (25.1%) showed the highest values. However, for SH heterosis the hybrids G46A X IR25571-31 (13.5%) and IR69625A X Millie (12.8%) showed highly significant positive values. While, the hybrid G46A X Giza 178 (6.8%) showed significant positive value. This data suggested that the panicle length is one of the most important traits contributing to heterosis and breeders can exploit it to best advantage in hybrid rice varieties and its parental lines. These results were in agreement with those reported by Awad-Allah (2011), Latha *et al.*, (2013) and Elixon *et al.*, (2015). For spikelets/panicle, heterosis over better parent (BP), mid-parent heterosis (MP) and standard heterosis (SH) shown in Tables 8, 9 and 10 revealed that 10, 14 and 6 hybrids showed highly significant and significant positive values in BP, MP and SH heterosis, respectively. The highest values 89.5, 96.1 and 91.3% were recorded in the hybrids G46A X Giza 178, G46A X IR25571-31 and G46A X IR25571-31 for BP heterosis, MP heterosis and SH heterosis. The previous data agreed with the data reported by Awad-Allah (2011), Sanghera and Hussain (2012), Ali *et al.*, (2014) and Awad-Allah *et al.*, (2015). For pollen fertility the data revealed that the better parent heterosis (BP), the hybrids G46A X IR62164-32-2-2-2-1 (7.1%) and G46A X IR25571-31 (5.3%) showed highly significant positive values. However, for mid-parent heterosis and standard heterosis (SH) were G46A X IR62164-32-2-2-2-1 (8.5%), G46A X Giza178 (6.4%) and G46A X IR25571-31 (5.7%) while, the hybrid IR69625A X Giza 178 (3.4%) showed significant positive value. Concerning standard heterosis (SH) were not showed highly significant or significant positive values. Similar results were reported by Awad-Allah (2011) and Hussain and Sanghera (2012). Spikelets fertility is one of the most important characters which directly influences grain yield potentiality in rice varieties and hybrids, as well as based on pollen and spikelets fertility the rice breeders can identified restorer lines, wide compatible lines, maintainer lines and hybrids. Better parent heterosis (BP), mid-parent heterosis (MP) and standard heterosis (SH) for spikelets fertility are presented in Tables 8, 9 and 10. The data revealed that the data revealed that the Better parent heterosis (BP), mid-parent heterosis and standard heterosis (SH) were not showed highly significant and significant positive values. Similar results were reported by many authors among them Soni and Sharma (2011), Tiwari *et al.*,

(2011), Hussain and Sanghera (2012) and Ali *et al.*, (2014). Number of filled grains/panicle is one of the most important characters which directly influences grain yield potentiality in rice varieties and hybrids. With respect to the BP, MP and SH heterosis of the hybrids were studied for number of filled grains/panicle are presented in Tables 8, 9 and 10. The data revealed highly significant and significant positive values in BP, MP and SH heterosis for nine, six and ten hybrids, respectively. The hybrid G46A X Giza178 showed the highest values (86.3% for BP heterosis. While, the hybrid G46A X IR25571-31 showed highest values 111.3 and 86.7% MP and SH heterosis. Similar results were reported by Awad-Allah (2011), Rahman *et al.* (2013), Awad-Allah *et al.*, (2015) and Elixon *et al.*, (2015). Better parent heterosis, mid-parent heterosis and standard heterosis for panicle weight are shown in Tables 8, 9 and 10. Data revealed that, seven, eight and three hybrids showed highly significant and significant positive values in BP, MP and SH heterosis, respectively. The highest values were showed in the three hybrids G46A X Giza179 (105.6%) for BP, G46A X Giza178 for MP (118.4%) and G46A X IR25571-31 (118.4%) for SH heterosis. The previous data agreed with the data reported by Awad-Allah (2011) and Awad-Allah *et al.*, (2015). Tables 8, 9 and 10 revealed the better parent heterosis, mid-parent heterosis and standard heterosis for 1000-grain weight. Data revealed that five, nine and five hybrids exhibited highly significant and significant positive values in BP, MP and SH heterosis, respectively. The highest values were

detected in hybrid IR69625A X Gz 5121 (16%, 17.2% and 12.9 %) for BP, MP and SH heterosis, respectively. Moreover, 1000-grain weight is one of the most important characters which directly influences grain yield potentiality in rice varieties and hybrids. These results agreed with the results reported by Awad-Allah (2011), Rahman *et al.* (2013), Ali *et al.*, (2014) and Awad-Allah *et al.*, (2015). Heterosis over better parent (BP), mid-parent heterosis (MP) and standard heterosis (SH) for grain yield are cited in Tables 8, 9 and 10. Data indicated that 13, 13 and ten hybrids showed highly significant and significant positive values in BP, MP and SH heterosis, respectively. The highest value was detected in hybrid G46A X Giza178 (89.2%) for BP heterosis. While, the hybrid IR69625A X Millie (132.2 and 47.1%) showed highest values for MP and SH heterosis, respectively. Moreover, the eight hybrids showed values for SH heterosis more than 15% over the check variety Egyptian hybrid rice one, these hybrids were G46A X MTU-1010 (36.7%, G46A X Giza179 (30%), G46A X CT6510-24-1-2 (28.3%), IR69625A X CT6510-24-1-2 (22.8%), G46A X IR62164-32-2-2-1 (22.4%), G46A X Giza178 (22%), G46A X IR25571-31 (19.7%), IR69625A X MTU-1010 (19.2%) and IR69625A X IR62164-32-2-2-1 (16%). The previous data agreed with the data reported by Awad-Allah (2011), Hussain and Sanghera (2012), Sanghera and Hussain (2012), Latha *et al.*, (2013), Ali *et al.*, (2014), Venkanna *et al.*, (2014), Awad-Allah *et al.*, (2015) and Elixon *et al.*, (2015).

Table 8 : Estimates of percentage of heterosis over better-parent (BP) for all studied traits and crosses.

crosses	Traits Days to heading	Plant height	No. of Panicles/plant	Panicle length	No. of spikelets/panicle	Pollen fertility (%)	Spikelet fertility (%)	No. of filled grains / panicle	Panicle weight	1000 grain weight	Grain yield /plant
G46A X Giza178	29.3**	42.5**	16.1 ^{ns}	15.2**	89.5**	0.5 ^{ns}	-1.8 ^{ns}	86.3**	103.2**	6.8**	89.2**
IR69625A X Giza178	2.0**	6.7**	14.3 ^{ns}	7.8*	16.4**	1.4 ^{ns}	1.7 ^{ns}	18.4**	21.5**	2.7 ^{ns}	14.6*
G46A X Giza179	29.8**	23.9**	14.4 ^{ns}	24.1**	51.7**	-0.4 ^{ns}	-0.6 ^{ns}	68.8**	105.6**	1.0 ^{ns}	78.9**
IR69625A X Giza179	-1.1 ^{ns}	13.6**	33.3**	0.7 ^{ns}	8.2 ^{ns}	-6.9**	-2.9 ^{ns}	6.2 ^{ns}	-0.4 ^{ns}	-13.1**	-5.4 ^{ns}
G46A X GZ5121	19.8**	27.9**	6.9 ^{ns}	2.7 ^{ns}	19.0**	-10.6**	-13.2 ^{ns}	12.0**	-17.9*	-2.8 ^{ns}	-28.7**
IR69625A X GZ5121	1.7*	12.4**	30.4**	3.3 ^{ns}	-8.6*	-5.9**	-2.5 ^{ns}	-11.0*	27.9**	16.0**	-4.5 ^{ns}
G46A X Millie	21.0**	20.0**	21.4 ^{ns}	12.6**	-13.2**	-23.2**	-23.6**	-29.6**	-14.9*	-1.8 ^{ns}	-33.8**
IR69625A X Millie	11.7**	25.4**	25.6**	24.6**	81.6**	-6.1**	-5.2 ^{ns}	69.1**	42.2**	-17.1**	68.6**
G46A X IR25571-31	21.0**	27.5**	28.6**	10.6**	72.2**	5.3**	4.2 ^{ns}	79.3**	72.7**	2.4 ^{ns}	36**
IR69625AX IR25571-31	8.2**	3.0 ^{ns}	24.7**	-7.6*	-17.5**	-9.6**	-1.7 ^{ns}	-18.9**	-9.9 ^{ns}	11.5**	14.9*
G46A X TNAU6464	33.6**	26.0**	-8.4 ^{ns}	7.1 ^{ns}	-5.5 ^{ns}	-6.9**	-8.8 ^{ns}	-4.1 ^{ns}	5.9 ^{ns}	9.5**	2.1 ^{ns}
IR69625AXTNAU6464	0.7 ^{ns}	-1.2 ^{ns}	50.6**	2.1 ^{ns}	1.9 ^{ns}	-36.1**	-38.9**	-37.5**	-33.1**	-1.3 ^{ns}	-25.6**
G46A X TNAU831358	34.8**	27.9**	-12.1 ^{ns}	3.4 ^{ns}	6.2 ^{ns}	-20.6**	-23.8**	-6.9 ^{ns}	16.1*	14.1**	-1.7 ^{ns}
IR69625A X TNAU831358	-5.4**	9.6**	60.2**	8.6*	33.5**	-17.1**	-20.4**	12.9*	12.8 ^{ns}	-8.7**	0.2 ^{ns}
G46A X TNAU831399	34.8**	22.1**	10.6 ^{ns}	8.7*	-4.1 ^{ns}	-11.4**	-12.2 ^{ns}	-4.7 ^{ns}	-6.6 ^{ns}	-7.4**	19.9*
IR69625AXTNAU831399	0.7 ^{ns}	-1.2 ^{ns}	0.02 ^{ns}	9.2**	34.3**	-28.9**	-31.2**	-3.3 ^{ns}	-4.2 ^{ns}	-2.2 ^{ns}	-37.3**
G46A X MTU-1010	19.7**	23.9**	15.4*	-9.9**	-21.2**	0.6 ^{ns}	0.1 ^{ns}	-21.1**	-13.3*	-1.8 ^{ns}	42.9**
IR69625A X MTU-1010	-6.1**	-2.6 ^{ns}	37.5**	-9.2**	-23.7**	-2.5 ^{ns}	1.8 ^{ns}	-22.3**	-17.2*	-0.03 ^{ns}	24.6**
G46A X IR62164-32-2-2-2-1	57.5**	88.2**	0.9 ^{ns}	3.6 ^{ns}	13.9**	7.1**	9.8 ^{ns}	25.0**	-46.5**	-25.5**	24.0**
IR69625AXIR62164-32-2-2-2-1	10.8**	33.8**	46.4**	6.8 ^{ns}	-19.7**	-3.0 ^{ns}	5.0 ^{ns}	-13.4**	-25.8**	-6.2**	17.5**
G46A X CT6510-24-1-2	31.0**	33.5**	12.7 ^{ns}	-9.9**	50**	-6.4**	-6.8 ^{ns}	39.8**	-11.9 ^{ns}	2.4 ^{ns}	26.8**
IR69625A X CT6510-24-1-2	-4.4**	5.5**	34.5**	-1.8 ^{ns}	-4.6 ^{ns}	-17.8**	-19.1**	-22.9**	-18.3**	-8.8**	21.4**
L.S.D 5%	1.2	4.1	2.6	1.6	11.9	3.3	13.8	12.6	0.5	1.1	5.8
L.S.D 1%	1.7	5.4	3.4	2.1	15.8	4.4	18.3	16.8	0.7	1.4	7.7

** : Highly significant at 1% * : Significant at 5% ns : Non significant

Table 9 : Estimates of percentage of heterosis over mid-parents (MP) for all studied traits and crosses.

crosses	Traits Days to heading	Plant height	No. of Panicles/plant	Panicle length	No. of spikelets/panicle	Pollen fertility (%)	Spikelets fertility (%)	No. of filled grains / panicle	Panicle weight	1000-grain weight	Grain yield /plant
G46A X Giza178	13.9**	29.7**	27.6**	22.3**	91.6**	6.4**	4.6 ^{ns}	100.3**	118.4**	13.3**	99.2**
IR69625A X Giza178	1.3*	4.8**	18.9*	9.1**	27.4**	3.4*	4.3 ^{ns}	32.5**	28.2**	10.6**	37.7**
G46A X Giza179	18.1**	23.1**	31.0**	25.1**	65.2**	1.68 ^{ns}	5.0 ^{ns}	74.3**	113.3**	9.3**	89.6**
IR69625A X Giza179	-3.3**	6.2**	34.2**	4.9 ^{ns}	8.8*	-5.2**	-1.2 ^{ns}	7.4 ^{ns}	1.3 ^{ns}	-7.3**	3.2 ^{ns}
G46A X GZ5121	7.2**	10.5**	28.8**	9.4**	23.9**	-8.1**	-7.6 ^{ns}	14.6**	-16.5*	-2.3 ^{ns}	-18.2*
IR69625A X GZ5121	1.0 ^{ns}	5.1**	39.4**	4.9 ^{ns}	-4.7 ^{ns}	-4.8**	-0.1 ^{ns}	-4.9 ^{ns}	28.2**	17.2**	-4.2 ^{ns}
G46A X Millie	5.9**	6.2**	23.2*	13.8**	-0.8 ^{ns}	-20.2**	-21.3**	-21.5**	-11.8 ^{ns}	6.0**	-17.8 ^{ns}
IR69625A X Millie	10.3**	20**	41.2**	32.0**	92.7**	-6.1**	-4.2 ^{ns}	81.3**	44.3**	-11.7**	132.2**
G46A X IR25571-31	14.7**	19.3**	52.5**	23.0**	96.1**	5.7**	8.5 ^{ns}	111.3**	106.4**	3.4 ^{ns}	57.0**
IR69625AXIR25571-31	1.6**	2.2 ^{ns}	30.8**	-1.8 ^{ns}	0.7 ^{ns}	-5.7**	-1.6 ^{ns}	-1.0 ^{ns}	5.9 ^{ns}	14.1**	15.3*
G46A X TNAU6464	14.0**	13.9**	9.4 ^{ns}	12.2**	2.5 ^{ns}	-2.4 ^{ns}	-3.9 ^{ns}	-1.0 ^{ns}	10.0 ^{ns}	10.9**	6.3 ^{ns}
IR69625A X TNAU6464	-2.9**	-3.6*	59.2**	2.3 ^{ns}	2.0 ^{ns}	-35.5**	-38**	-36.7**	-29.2**	1.5 ^{ns}	-17.3*
G46A X TNAU831358	14.4**	15.8**	6.1 ^{ns}	10.8**	19.7**	-15.7**	-18.5**	-1.6 ^{ns}	21.8**	14.6**	1.0 ^{ns}
IR69625AXTNAU831358	-9.2**	7.1**	71.5**	11.1**	39.4**	-15.2**	-17.9**	14.4**	20.7**	-7.8**	12.5 ^{ns}
G46A X TNAU831399	15.7**	7.4**	19.7*	15.4**	16.9**	-6.2**	-6.8 ^{ns}	8.0 ^{ns}	-5.0 ^{ns}	-6.5**	23.3**
IR69625A X TNAU831399	-2.4**	-6.1**	5.7 ^{ns}	10.5**	53**	-27.5**	-29.6**	5.4 ^{ns}	-0.6 ^{ns}	-1.8 ^{ns}	-26.1**
G46A X MTU-1010	7.1**	11.6**	40.2**	0.4 ^{ns}	-17.4**	2.0 ^{ns}	5.6 ^{ns}	-13.0**	-5.5 ^{ns}	2.0 ^{ns}	70.7**
IR69625A X MTU-1010	-6.8**	-5.3**	48.3**	-3.3 ^{ns}	-13.7**	-0.1 ^{ns}	3.4 ^{ns}	-10.9**	-11.4 ^{ns}	5.3*	30.3**
G46A X IR62164-32-2-2-2-1	32.7**	34.9**	26.1**	9.9**	37.6**	8.5**	12.6 ^{ns}	54.1**	-28.5**	-20.4**	50.0**
IR69625A XIR62164-32-2-2-2-1	5.6**	4.9**	63.3**	8.0*	3.4 ^{ns}	2.1 ^{ns}	6.4 ^{ns}	10.4**	-2.3 ^{ns}	-1.2 ^{ns}	24.7**
G46A X CT6510-24-1-2	15.3**	13.2**	40**	1.3 ^{ns}	56.6**	-3.1 ^{ns}	0.2 ^{ns}	56.3**	-3.2 ^{ns}	3.4 ^{ns}	54.9**
IR69625A X CT6510-24-1-2	-5.2**	-3.0 ^{ns}	48.9**	5.6 ^{ns}	7.5*	-17.5**	-16.3*	-10.5**	-11.9 ^{ns}	-6.6**	30.3**
L.S.D 5%	1.1	3.5	2.2	1.4	10.3	2.9	11.9	10.9	0.5	0.9	5.0
L.S.D 1%	1.4	4.7	3.0	1.8	13.7	3.8	15.9	14.5	0.6	1.3	6.7

** : Highly significant at 1% * : Significant at 5% ns : Non significant

Table 10 : Estimates of percentage of heterosis over standard heterosis (SH) for all studied traits and crosses.

crosses	Traits Days to heading	Plant height	No. of Panicles/plant	Panicle length	No. of spikelets/panicle	Pollen fertility (%)	Spikelets fertility (%)	No. of filled grains / panicle	Panicle weight	1000-grain weight	Grain yield /plant
G46A X Giza178	1.2 ^{ns}	15.6**	-6.3 ^{ns}	6.8*	62.85**	-0.9 ^{ns}	-3.4 ^{ns}	57.3**	67.1**	0.9 ^{ns}	22.0**
IR69625A X Giza178	0.0 ^{ns}	0.0 ^{ns}	0.0 ^{ns}	0.0 ^{ns}	0.0 ^{ns}	0.0 ^{ns}	0.0 ^{ns}	0.0 ^{ns}	0.0 ^{ns}	0.0 ^{ns}	0.0 ^{ns}
G46A X Giza179	1.6*	0.6 ^{ns}	1.5 ^{ns}	3.3 ^{ns}	27.5**	-8.9**	-3.8 ^{ns}	22.6**	56.9**	12.5**	30.0**
IR69625A X Giza179	-7.3**	-6.6**	18.2*	-8.9**	-23.1**	-11.7**	-6.0 ^{ns}	-27.7**	-24.0**	-3.2 ^{ns}	-17.4**
G46A X GZ5121	-6.2**	3.8*	7.4 ^{ns}	-4.1 ^{ns}	0.02 ^{ns}	-17.1**	-14.7*	-14.7**	-39.8**	-7.2**	-38.2**
IR69625A X GZ5121	-1.7**	5.4**	31.0**	-3.5 ^{ns}	-29.2**	-10.8**	-4.1 ^{ns}	-32.2**	-5.7 ^{ns}	12.9**	-16.6**
G46A X Millie	-5.3**	-2.6 ^{ns}	-17.2*	-7.7*	-27.1**	-27.2**	-30**	-48.9**	-35.3**	8.9**	-57.3**
IR69625A X Millie	9.5**	17.5**	10.0 ^{ns}	12.8**	29.1**	-11.0**	-11.3 ^{ns}	12.5**	8.0 ^{ns}	-8.0**	47.1**
G46A X IR25571-31	-5.3**	3.5 ^{ns}	24.1**	13.5**	91.3**	-7.7**	-2.4 ^{ns}	86.7**	81.5**	-3.2 ^{ns}	19.7**
IR69625A X IR25571-31	-6.1**	-4.9*	20.4**	-5.2 ^{ns}	-8.3**	-14.3**	-7.9 ^{ns}	-15.5**	-5.3 ^{ns}	8.5**	1.1 ^{ns}
G46A X TNAU6464	4.6**	2.2 ^{ns}	-10.1 ^{ns}	-3.5 ^{ns}	-20.6**	-10.0**	-12.3 ^{ns}	-30.3**	-25.1**	3.4 ^{ns}	-28.6**
IR69625AXTNAU6464	-1.3*	-7.4**	47.8**	-7.6*	-27.6**	-38.2**	-41.2**	-57.4**	-50.7**	-3.9 ^{ns}	-35.0**
G46A X TNAU831358	5.6**	3.8 ^{ns}	-11.3 ^{ns}	-2.2 ^{ns}	-10.8**	-21.2**	-24.3**	-32.4**	-17.9**	8.8**	-33.0**
IR69625A X TNAU831358	-7.3**	2.7 ^{ns}	61.6**	2.8 ^{ns}	-5.1 ^{ns}	-17.7**	-20.8**	-24.9**	-16.8**	-11.1**	-12.6*
G46A X TNAU831399	5.6**	-0.9 ^{ns}	-13.7 ^{ns}	0.8 ^{ns}	-19.5**	-12.7**	-14.1 ^{ns}	-30.8**	-33.9**	-10.7**	-22.7**
IR69625A X TNAU831399	-1.3*	-7.4**	-12.5 ^{ns}	1.3 ^{ns}	-4.5 ^{ns}	-30.0**	-32.7**	-35.7**	-29.4**	-4.8*	-45.2**
G46A X MTU-1010	-6.3**	0.6 ^{ns}	18.2*	-7.2*	-27.1**	-9.2**	-3.4 ^{ns}	-29.5**	-26.5**	-7.2**	36.7**
IR69625A X MTU-1010	-9.2**	-8.8**	40.9**	-6.4 ^{ns}	-29.4**	-7.6**	-1.7 ^{ns}	-30.6**	-29.8**	-2.7 ^{ns}	19.2**
G46A X IR62164-32-2-2-2-1	23.3**	52.7**	11.3 ^{ns}	-4.1 ^{ns}	46.2**	-6.1**	-0.1 ^{ns}	46.1**	-24.0**	-19.3**	22.4**
IR69625A XIR62164-32-2-2-2-1	8.5**	25.4**	61.6**	-1.1 ^{ns}	3.1 ^{ns}	-8.0**	-1.8 ^{ns}	1.3 ^{ns}	5.3 ^{ns}	1.5 ^{ns}	16.0*
G46A X CT6510-24-1-2	2.6**	8.3**	22.2**	-5.2 ^{ns}	37.6**	-11.9**	-6.5 ^{ns}	28.7**	-24.0**	-3.2 ^{ns}	28.3**
IR69625A X CT6510-24-1-2	-6.3**	-1.1 ^{ns}	45.8**	3.3 ^{ns}	-12.5**	-22.0**	-18.9*	-29.0**	-29.6**	-11.3**	22.8**
L.S.D 5%	1.2	4.1	2.6	1.6	11.9	3.3	13.8	12.6	0.5	1.1	5.8
L.S.D 1%	1.7	5.4	3.4	2.1	15.8	4.4	18.3	16.8	0.7	1.4	7.7

** : Highly significant at 1% * : Significant at 5% ns : Non significant (Ck) : Egyptian Hybrid 1 (check cultivar)

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