THE UTILIZATION OF CYTOPLASMIC MALE STERILE (CMS) AND RESTORER LINES IN THE DEVELOPING OF HYBRID RICE.

Abd El-Hadi, A. H.*; Kawser S. Kash*; H. F. El-Mowafi** and G. B. Anis**
*Genetics Department, Fac. Agric., Mansoura University, Egypt.
**Rice Res. and Training Center (RRTC),Field Crops Res. Inst., ARC, Egypt.

ABSTRACT

The present investigation was conducted to determine the magnitudes of combining ability and heterosis obtained from hybrids three produced by utilization of CMS, maintainer and restorer lines in rice. The experiment was carried out during the two growing seasons of 2010 and 2011 at Rice Research and Training Center (RRTC) Farm, Sakha, Kafr El-Sheikh, Egypt. Twelve F_1 hybrids were obtained from crossing three CMS lines as female parent with four restorer lines. These hybrids were evaluated along with their parents for genotypic variances. The analysis of variance revealed highly significant differences among genotypes, parents, parents vs. crosses for days to heading (day); plant height (cm); panicles plant^{-1}; panicle length (cm); filled grains panicle^{-1}; spikelets fertility% and grain yield plant^{-1} except parents vs. crosses for panicle length (cm). The variance among males (testers) were either significant of highly significant for all studied traits. The variances among crosses due to males and females (lines x testers) interactions, showed highly significant SCA effects for all the studied traits except for plant height (cm). The estimated values for variance of general combining ability (σ^2GCA) were less than specific combining ability variance (σ^2SCA) for all studied traits except plant height (cm). This result indicated the preponderance of non-additive gene action. It was supported by the ratio of (σ^2GCA/ σ^2SCA) which was less than one for all studied traits except for plant height (cm), indicating that the non-additive type of gene action played a major role in the inheritance of these traits. Heritability estimates in broad sense (h^2_b%) were high for all studied traits. However, heritability estimates in the narrow sense (h^2_n%) were moderate for days to heading (day) (44.58%), plant height (cm) (45.81%) and filled grains panicle^{-1} (53.80%) and low for the other traits. Three parental lines viz.; IR69625A; G46A and GZ9057-6-1-3-2 were identified as good general combiners for grain yield plant^{-1}(g). Hybrid combinations as G46A x Giza178; IR69625A x GZ6296-12-1-2-1-1 and Large stigma A x GZ9057-6-1-3-2 showed high mean performances due to the presence of SCA effects.

INTRODUCTION

Rice (*Oryza sativa,* L.) is a major staple food that feeds more than one-half of the human population worldwide. The three-line hybrid rice breeding technology takes advantage of heterosis (hybrid vigor) and have been successfully applied in many countries, leading to more than 20% yield increase over their inbred varieties (Lin and Yuan 1980 and Nuruzzaman *et al.,* 2002). The three-line hybrid rice breeding system was developed in the 1970s after the revolutionary discovery of the wild abortive cytoplasmic male sterile line (CMS-WA) for the breeding of CMS lines, which solved the

problem of self-pollination in the varieties which were used for hybrid rice production. In this technology, a restorer line that contains the restorer gene is used as the pollen parent to recover male fertility in the F_1 plants (hybrid rice) after its cross with the CMS line Sri and Sharma (2012). The present investigation aimed to study the nature of combining ability; heterosis over standard check variety and genetic parameters for three diverse CMS lines; four restorer lines and their 12 hybrid combinations for yield and its components traits in the developed hybrids of rice.

MATERIALS AND METHODS

The parental material comprised three CMS lines viz; IR69625A; G46A and Large stigma A, were used as female lines and crossed with four diverse genotypes used as male (testers) in a line x tester mating design system in 2010 rice growing season. Thus, the resultant twelve hybrids along with their seven parents, three maintainers lines IR69625B; G46B and Large stigma B; four restorer lines, Giza 178; GZ6296-12-1-2-1-1; PR78 and GZ9057-6-1-3-2 and the standard check (Giza178) were evaluated in a Randomized Complete Blocks Design (RCBD) with three replications at Rice Research and Training Center (RRTC) Farm, Sakha, Kafr El-Sheikh, Egypt during 2011 growing season. Seedlings were transplanted into 20 x 20 cm spacing. All agronomic practices such as fertilization, irrigation, weed and pest control were done as recommended with rice crop during both seasons of this study. The data were recorded on five randomly selected plants from each replication to investigate all quantitative traits. The studied traits were i.e., days to heading (day); plant height(cm); panicles plant^{-1}; panicle length (cm); filled grains panicle^{-1}; spikelets fertility% and grain yield plant^{-1} (g). All genotypic means were utilized in an analysis of variance as described by (Singh and Chaudhary, 1985) for combining ability. The percent increase or decrease of F_1 hybrids over standard check variety was calculated to estimate heterosis.

RESULTS AND DISCUSSION

The results presented in Table 1 showed that the mean squares of the genotypes were highly significant for all studied traits. These findings indicated that there were significant differences among genotypes. The same trend is found for parents and crosses. However, parents versus crosses (heterosis measurements) were significant for all studied traits except for plant height (cm) indicating the presence of heterosis effects for these traits. Analysis of variance revealed significant and highly significant differences among lines (females) for various traits under study i.e., days to heading (day); plant height (cm); panicles plant^{-1}; panicle length (cm); filled grains panicle^{-1}; spikelets fertility% and grain yield plant^{-1} (g) while, variance among males (testers) were significant and highly significant for all traits. The variances among crosses due to males and females (lines x testers) interactions, indicated that SCA effects were highly significant for all traits

except for plant height (cm). The predominance of SCA effects suggested that dominance and epistatic gene interactions were important for controlling these traits. These results confirmed the earlier findings by Janardhanam *et al.,* (2000); Satyanarayana *et al.,* (2000); Panwar (2005); Kumar *et al.,* (2006) and Ammar *et al.*, (2012).

The values of the variance of general combining ability (σ²GCA) were less than the variance of specific combining ability (σ²SCA) for all studied traits except plant height (cm) showing the preponderance of non-additive gene action. It was supported by σ²GCA/ σ²SCA ratio which was less than one for all studied traits except plant height (cm), indicating that the non-additive type of gene action played a major role in the inheritance of these traits. The degree of dominance i.e., ratio of dominance variance (σ² D) to additive variance (σ² A) being greater than unity for days to heading (day); plant height (cm) and filled grains panicle[-1] (Table 1) while, it was less than unity for the rest of traits under study. Several workers have reported the preponderance of non-additive gene action for panicles plant[-1]; filled grains panicle[-1] and spikelet fertility% among them, (Vaithiyalingan and Nadarajan, 2005), panicle length (Punitha *et al.,* 2004) and yield plant[-1] (Sharma, 2006 and Ammar *et al.*, 2012).

Table 1 : Mean squares for the analysis of variance, estimates of genetic components and contribution of lines, testers and line x tester to the total variance for rice genotypes.

S. O. V.	d.f.	Days to heading (day)	Plant height (cm)	Panicles plant[-1]	Panicle length (cm)	Filled grains panlce[-1]	Spikelets fertility %	Grain yield plant[-1] (g)
Replications	2	1.11	1.00	1.63	0.04	9.63	1.16	2.97
Genotypes	18	158.53**	270.42**	51.68**	5.48**	6865.77**	112.41**	111.42**
Parents	6	276.96**	525.20**	54.56**	8.77**	6522.27**	17.10**	14.77**
Crosses	11	49.93**	74.05**	24.57**	4.16**	6396.57**	79.75**	68.45**
P. vs Cross.	1	642.55*	901.86*	332.11*	0.23	14088.01*	1043.57*	1163.92*
Lines	2	122.69**	276.69*	48.44*	8.66**	23463.03**	170.00**	149.13*
Testers	3	85.67**	70.93*	34.99**	3.79*	6171.44**	89.01**	49.52**
L x T	6	7.81**	8.06	11.41**	2.84**	820.32**	45.03**	51.02**
Error	36	0.77	3.02	1.02	0.19	20.45	1.37	1.84
σ²GCA	-	1.25	1.99	0.34	0.02	167.15	0.82	0.25
σ² SCA	-	2.34	1.68	3.46	0.88	266.62	14.55	16.39
σ²GCA/ σ²SCA	-	0.53	1.18	0.10	0.02	0.63	0.06	0.01
σ² A	-	2.51	3.97	0.68	0.05	334.30	1.63	0.50
σ² D	-	2.34	1.68	3.46	0.88	266.62	14.55	16.39
σ² A/ σ² D	-	1.10	2.36	0.19	0.06	1.25	0.11	0.03
h²bs %	-	86.27	65.20	80.24	83.33	96.70	92.21	90.15
h²ns %	-	44.58	45.81	13.22	4.39	53.80	9.31	2.67
Contribution (%) of Lines	-	44.68	67.94	35.84	37.86	66.70	38.76	39.61
Contribution (%) of Testers	-	46.80	26.12	38.83	24.87	26.30	30.44	19.73
Contribution (%) of Line x Tester	-	8.52	5.94	25.33	37.27	7.00	30.80	40.66

*, ** Significant and highly significant at 0.05 and 0.01 levels of probability, respectively.

Concerning heritability estimates in broad sense ($h^2_b\%$), the results indicated that the $h^2_b\%$ were high for the all studied traits. However, heritability estimates in the narrow sense ($h^2_n\%$) were moderate for days to heading (day) (44.58%); plant height (cm) (45.81%) and filled grains panicle^{-1} (53.80%) and low for the rest of traits under study. These results indicated that a major part of the total genotypic variance was additive for days to heading (day); plant height (cm) and filled grains panicle^{-1} and non-additive in nature for panicles plant^{-1}; panicle length (cm); spikelets fertility% and grain yield plant^{-1} (g) traits (Table 1). These results were in close agreement with those reported by El-Mowafi (1994); El-Mowafi and Abou Shousha (2003); El-Mowafi *et al.,* (2005); Akinwale *et al.,* (2011) and Ammar *et al.*, (2012).

The relative role of lines; testers and line x tester interaction in the expression of various traits indicated dominant influence of paternal effects shown by testers for days to heading (46.80%) and panicles plant^{-1} (38.83%). Maternal effect were shown by lines appeared to be important for plant height (cm) (67.94%); panicle length (cm) (37.86%); filled grains panicle^{-1} (66.70%); spikelet fertility % (38.76%) and grain yield plant^{-1} (39.61%). The contribution of maternal x paternal effects in crosses was important for yield plant^{-1} (40.66%) only. These findings were similar with those obtained by Thirumeni *et al.,* (2000) and Saleem *et al.,* (2010).

Identification of the best parents based on mean performance and general combining ability effects:-

The mean performance of parents and hybrids is thought to be one of the important criterion for their evaluation. However, the parents with high mean value may or may not transmit their high performance to their F_1 hybrids. This parental ability is estimated in terms of GCA effects. Assessment of parents on the basis of mean performance and GCA effects separately results in the classification of different sets of parents as better ones. However assessing the parents using both these criteria would be more pertinent. Harer and Bapat (1982) stated that mean performance of the parents with nature of combining ability provides the criteria to select the parents for hybridization. On this basis, those parents who perform better for both mean performance and GCA effects would be treated as desirable good parents. In the present study, based on significantly better mean performance and GCA effects, the best parents could be identified from (Table 2).

Significant positive estimates of GCA effects are preferable for all traits under study except for days to heading (day) and plant height (cm). Days to heading varied from 77.00 to 105 days among lines and 91.67 to 101.33 days among testers. One line IR69625A gave highly significant negative (desirable) estimate of GCA effects with (-3.64 ± 0.25) among lines and two testers also gave highly significant and negative values (desirable) of GCA effects GZ6296-12-1-2-1-1 (-2.50 ± 0.36) and GZ9057-6-1-3-2 (-2.50 ± 0.36). The mean performance for plant height (cm) varied from 86.67 to 101.00 (cm) among lines and 98.00 to 130.00 (cm) among testers (Table 2). On the other hand, the two lines of IR69625A and Large stigma A and the two testers GZ6296-12-1-2-1-1 and GZ9057-6-1-3-2 showed highly significant negative (desirable) estimates of GCA effects for plant height (cm) with values of (-2.39 ± 0.50); (-3.14 ± 0.50); (-2.28 ± 0.71) and (-2.06 ± 0.71),

respectively (Table 2). Range of panicles plant[-1] varied from 13.33 to 23.00 panicles plant[-1] among lines and 16.67 to 25.67 panicles plant[-1] among testers. Only one line of IR69625A as CMS line and PR78 as a tester gave highly significant positive estimates GCA effects with values of (1.89 $\pm$0.29) and (2.69$\pm$0.41), respectively. Among lines, panicle length (cm) varied from 22.63 to 26.03 (cm) and among testers, it varied from 23.97 to 28.03 (cm). Three parents showed highly significant positive estimates of GCA effects desirable for panicle length (cm), G46A (0.92$\pm$0.12) among lines and Giza178 (0.24$\pm$0.18) and PR78 (0.81$\pm$0.18) among testers. These parents appeared to be as good general combiner for panicle length. The mean performance for filled grains panicle[-1] ranged from 110.33 to 235.33 among lines and 137.00 to 223.67 among testers. The estimates of GCA effects showed that the line G46A and the testers Giza178; PR78 and GZ9057-6-1-3-2 gave highly significant positive (desirable) for filled grains panciel[-1] with (51.03$\pm$1.30); (10.81$\pm$1.85); (16.69$\pm$1.85) and (11.58$\pm$1.85), respectively. Range of spikelet fertility % varied from 92.58 to 96.59 % among lines and 88.79 to 94.45 % among testers. Five parents expressed highly significant positive (desirable) values of GCA effects for the same trait. The attractive general combiners were IR69625A (2.08$\pm$0.34) and G46A (2.27$\pm$0.34) among lines whereas, Giza178 (1.19$\pm$0.48); PR78 (2.36$\pm$0.48) and GZ9057-6-1-3-2 (1.08$\pm$0.48) among testers (Table 2). Swamy *et al.,* (2003) identified two good combiner lines for high spikelets fertility % in rice. Yield being an ultimate product of all traits is very important. Mean grain yield plant[-1] varied from 47.26 to 51.56 (g) among CMS lines and 44.72 to 49.70 (g) among testers. Three parents showed desirable GCA effects for this trait. However, IR69625A (2.26$\pm$0.39) followed by G46A (1.81$\pm$0.39) among females and GZ9057-6-1-3-2 (3.43$\pm$0.55) among males were found to be the best general combiners for yield plant[-1]. The results are in coincide with those of Petchiammal and Kumar (2007) and Saleem *et al.,* (2010) who identified several good combiner lines on the basis of mean performance and GCA effects for yield plant[-1].

The desirable general combiners identified in the present studies for yield and its components are recommended to be used in multiple hybrid rice breeding programs to identify superior genotypes for development of high yielding cultivars. The GCA variance is primarily due to function of the additive genetic variance and represents a fixable portion of genetic variation. If epistasis is present, GCA also includes additive x additive type of non-allelic interaction (Singh and Narayanan, 2004).

Identification of hybrids based on mean performance, specific combining ability effects and standard heterosis:

Marilia *et al.,* (2001) stated that specific combining ability (SCA) effects of hybrids alone had limited value for parental choice in breeding programme, and must be used in combination with other parameters such as hybrid means and GCA of the respective parents. The hybrid combinations with high mean performance, desirable SCA estimates and involving at least one of the parents with high GCA would likely to enhance the concentration of favorable alleles (Kenga *et al.,* 2004) and this is what a breeder desires to improve a trait. Similar views have been expressed by various researchers

(Thirumeni *et al.,* 2000; Manivannan and Ganesan, 2001; Gnanasekaran *et al.,* 2006; Saleem *et al.,* 2010 and Tiwari *et al.,* 2011) in rice. The identification of good specific combiners (hybrids) has been adjudged on the basis of mean performance; SCA effects and standard heterosis estimates (Table 3) in the present investigation.

Mean performances and negative (desirable) and significant estimates of standard heterosis for hybrids ranged from 95.00 to 108.33 day and -2.28 to -6.86 %, respectively for days to heading (day). Three hybrid combinations gave highly significant negative estimates (desirable) of SCA effects and seven hybrids had significant and negative estimates over standard heterosis for this trait. The best three crosses for SCA and standard heterosis were IR69625A x PR78; G46A x GZ9057-6-1-3-2 and Large stigma A x GZ6296-12-1-2-1-1. Semi-dwarf plant height (80-100 cm) is desirable for recording high yield in rice variety as vigor in plant height may lead to unfavorable grain/straw ratios and below optimum yield due to lodging. The mean performance values for plant height (cm) varied from 106.33 for the cross Large Stigma A x GZ6296-12-1-2-1-1 to 122.67 (cm) for the cross G46A x PR78. Three good specific combiners had highly signifaicnt negative (desirable) values of SCA effects viz., IR69625A x PR78 (-1.06$\pm$1.00); Large stigma A x Giza178 (-1.19$\pm$1.00) and G46A x GZ9057-6-1-3-2 (-2.19$\pm$1.00) were identified among all hybrids (Table 3). Nine hybrid combinations gave significant and highly significant positive heterosis over standard parent (undesirable) and ranged from 3.77 to 15.75 %. More panicles plant[-1] is believed to be closely associated with high grain yield per plant resulting high productivity. Therefore, the cross combinations which had more panicles plant[-1] were to be identified. The mean performance for panicles plant[-1] ranged from 21.67 to 30.67 for the crosses G46A x GZ6296-12-1-2-1-1 and G46A x PR78, respectively. The estimates of SCA effects for the same trait showed that, five hybrids Large stigma A x GZ9057-6-1-3-2; Large Stigma A x GZ6296-12-1-2-1-1; G46A x Giza178; IR69625A x GZ6296-12-1-2-1-1 and G46A x PR78 gave highly significant and positive values with the values of 0.67 $\pm$ 0.58; 1.00 $\pm$ 0.58; 1.11 $\pm$ 0.58; 1.67 $\pm$ 0.58 and 2.22 $\pm$ 0.58, respectively. The observed standard heterosis values (desirable) ranged between 10.68 % (IR69625A x GZ9057-6-1-3-2) to 22.68 % (G46A x PR78). Regarding panicle length (cm), larger panicle is associated with high filled grains panicle[-1] resulting into higher productivity. Therefore, hybrids with positive SCA effects and standard heterosis for panicle length (cm) are desirable. The present study revealed that the mean performance for panicle length (cm) ranged between 23.00 cm (IR69625A x GZ6296-12-1-2-1-1) to 27.43 cm (G46A x Giza178). Five hybrid combinations were good specific combiners for this trait and ranging from (0.33 $\pm$ 0.25) for the cross Large stigma A x GZ6296-12-1-2-1-1 to (0.94 $\pm$ 0.25) for the cross IR69625A x GZ9057-6-1-3-2. Gnanasekaran *et al.,* (2006) isolated best specific combiners in rice for increased panicle length. Out of the fifteen crosses four crosses possessed significant and highly significant positive estimates for standard heterosis for panicle length. The filled grains panicle[-1] directly contributes to the seed yield hence positive heterotic effect would be highly significant and desirable.

2

3

The successful utilization of CMS in development of hybrids is not possible unless the effective restorer lines are identified. In the present study, more number of filled grains panicle[-1] is closely associated with high yield plant[-1] resulting in high productivity. Data in Table 3 cont. showed that mean performance varied from 151.0 to 295.0. Four hybrid combinations were recorded highly significant positive estimates of SCA effects (desirable) for this trait. In this study, all hybrid combinations were recorded significant and highly significant positive estimates of heterosis over the standard variety for this trait. The range of heterosis was 10.21 to 115.56% for the crosses Large stigma A x GZ6296-12-1-2-1-1 and G46A x GZ9057-6-1-3-2, respectively. Spikelet fertility percent is very important in hybrid rice breeding programe. Mean performance for this trait raged from 79.10 to 90.97 %. Five good specific combiners viz.; IR69625A x PR78 (1.13$\pm$0.67), G46A x PR78 (1.94$\pm$0.67), G46A x GZ9057-6-1-3-2 (3.47$\pm$0.67), IR69625A x Giza178 (3.49$\pm$0.67) and Large stigma A x GZ6296-12-1-2-1-1 (4.90$\pm$0.67) were identified among all hybrids. Since this trait has a direct bearing on the yield, hence manifestation of heterosis in positive direction is desirable for this trait. Out of 12 crosses, only one expressed positive and highly significant heterosis over standard variety. On the contrary, eight hybrid combinations recorded highly significant negative estimates of heterosis over check variety Giza 178 ranging from -4.29 to -11.12%   for the crosses IR69625A x GZ9057-6-1-3-2 and Large stigma A x PR 78, respectively (Table 3 cont.). These results were in conformity with the results obtained by Singh (2000) and Tiwari *et al.,* (2011). The grain yield plant[-1] (g) is very complex trait. It is multiplicative end product of several basic components of yield (Grafius, 1959). In the present investigation results showed that the mean performance ranged between 49.07 to 64.04 (g). Three crosses scored highly significant positive estimates of SCA effects for this trait. All hybrid combinations scored highly significant and positive heterosis (desirable) effects over standard variety Giza178. The highest values were recorded for the crosses, G46A x Giza178; IR69625A x GZ9057-6-1-3-2 and IR69625A x GZ6296-12-1-2-1-1 with heterosis values over the standard variety of 43.20; 41.18 and 38.61%, respectively. The minimum values recorded for the crosses Large stigma A x GZ6296-12-1-2-1-1 (9.72%); Large stigma A x Giza178 (15.38%) and Large stigma A x PR78 (17.64%) (Table 3 cont.). These findings were in close agreement with Faiz *et al.,* (2006), Saleem *et al.,* (2008), Rahimi *et al.,* (2010) and Tiwari *et al.,* (2011).

REFERENCES

Akinwale, M.G.; G. Gregorio; F. Nwilene; B.O. Akinyele; S.A. Ogunbayo and A.C. Odiyi (2011). Hertiability and correlation coefficient analysis for yield and its components in rice (*Oryza sativa,* L.). Afric. J. of Plant Sci., 5(3): 207-212.

Ammar, G.G.; G. Nematzadeh ;   N. Bagheri; A. Ebrahimi and M. Oladi (2012). Evaluation of general and specific combining ability in parental lines of hybrid rice. Inter. J. of Agric.: Res. and Review. Vol., 2 (4), 455-460.

El-Mowafi, H.F. (1994). Studies on rice breeding. Ph.D. Thesis, Fac. of Agric., Kafr El-Sheikh, Tanta Univ., Egypt.

El-Mowafi, H.F. and A.A. Abou-Shousha (2003). Combining ability and heterosis analysis of diverse CMS lines in hybrid rice. J. Agric. Res. Tanta Univ., 29(1): 106-127.

El-Mowafi, H.F.; A.O. Bastawisi; M.I. Abo-Youssef and F.U. Zaman (2005). Exploitation of rice heterosis under Egyptian conditions. Egypt. J. Agric. Res., 389 (5A): 143-166.

Faiz, F. A.; M. Sabar; T. H. Awan; M. Ijaz and Z. Manzoor (2006). Heterosis and combining ability analysis in Basmati rice hybrids. JAPS, J. Animal and Plant Sci., 16(1/2): 56-59.

Gnanasekaran, M.; P. Vivekanandan and S. Muthuramu (2006). Combining ability and heterosis for yield and grain quality in two line rice (*Oryza sativa,* L.) hybrids. Ind. J. Genet., 66(1): 6-9.

Grafius, J. E. (1959). Heterosis in barley. Agron. J., 51(3): 551-554.

Harer, P. N. and D. R. Bapat (1982). Line × tester analysis of combining ability in grain sorghum. J. Maharashtra Agric. Uni., 7(2): 230-232.

Janardhanam, V.; N. Nadarajan and S. Jebaraj (2000). Studies on heterosis in rice (*Oryza sativa,* L.). Madras Agric. J., 88(10-12): 721-723.

Kenga, R.; S. O. Albani and S. C. Gupta (2004). Combining ability studies in tropical sorghum [*Sorghum bicolor*, L. (Meonch)]. Field Crop. Res., 88: 251-260.

Kumar, S. T.; R. Narasimman; P. Thangavelu; R. Eswaran and C. P. S. Kumar (2006). Combining ability analysis for yield and its component characters in rice (*Oryza sativa,* L.). Int. J. Plant Sci., 2(1): 151-155.

Lin, S. C. and L. P. Yuan (1980). Hybrid rice breeding in China. In Innovative approaches to rice breeding International Rice Research Institute, Manila, Philippines, 35-51.

Manivannan, N. and J. Ganesan (2001). Line × tester analysis over environments in sesame. Ind. J. Agric. Res., 35(4): 225-258.

Marilia, C. F.; T. C. Servio; O. R Vatter; V. Clibas and T. M Siu (2001). Combining ability for nodulation in common bean (*Phaseolus vulgaris,* L.) genotype from Indean and middle American gene pools. Euphytica, 118: 265-270.

Nuruzzaman, M.; M.F. Alam; M.G. Ahmed; A. M. Shohael; M. K. Biswas; M. R. Amin and M. M. Hossain (2002). Studies on parental variability and heterosis in rice. Pakistan J. of Biolo. Sci., 5(10): 1006-1009.

Panwar, L. L. (2005). Line × tester of combining ability in rice (*Oryza sativa*, L.). Ind. J. Genet, 65(1): 51-52.

Petchiammal, K. I. and C. R. A. Kumar (2007). Combining ability studies for yield and yield associated traits in rice (*Oryza sativa,* L.) involving Assam rice cultivars. Int. J. Agric. Sci., 3(2): 234-236.

Punitha, D.; A. J. Joel; S. Manomani and K. Thiyagarajan (2004). Combining ability for yield and its components. Advances in Plant Sci., 17(1): 345-348.

Rahimi, M.; B. Rabiei; H. Samizadeh and A. Kafi Ghasemi (2010). Combining ability and heterosis in rice (*Oryza sativa,* L.) cultivars. J. Agr. Sci. Tech., 12(1): 223-231.

Saleem, M. Y.; J. I. Mirza and M. A. Haq (2008). Heritability, genetic advance and heterosis in line x tester crosses of basmati rice. J. of Agric. Res., 4(3): 18-23.

Saleem, M.Y.; J.I. Mirza and M.A. Haq (2010). Combining ability analysis for yield and related traits in basmati rice (*Oryza sativa,* L.). Pak. J. Bot., 42(1): 627-637.

Satyanarayana, P. V.; I. Kumar and M. S .S. Reddy (2000). Studies on combining ability and heterosis in rice. IRRN, 23(3): 10.

Sharma, R. K. (2006). Studies on gene action and combining ability for yield and its component traits in rice (*Oryza sativa,* L.). Ind. J. Genet., 66(3): 227-228.

Singh, P. and S.S. Narayanan (2004). Biometrical Techniques in Plant Breeding. Kalyani Pub. New Delhi, India.

Singh, R. S. (2000). Heterosis studies in rice using WA based CMS system for developing hybrids for Eastern Uttar Pradesh. Annals Agric. Res., 21(2): 79-83.

Sri K. and D. Sharma (2012). Identification of maintainers and restorers for WA and Kalinga sources of CMS lines in rice (Oryza sativa L.). Electronic Journal of Plant Breeding,3 (4): 949-951.

Swamy, M. H.; M. R. G. Rao and B. Vidhachandra (2003). Studies on combining ability in rice hybrids involving new CMS lines. Karnataka J. Agric. Sci., 16(2): 228-230.

Thirumeni, S.; M. Subramanian and K. Paramasivam (2000). Combining ability and gene action in rice. Trop. Agric. Res., 12: 375-385.

Tiwari, D.K.; P. Pandey; S.P. Giri and J.L. Dwivedi (2011). Heterosis studies for yield and its components in rice hybrids using CMS system. Asian J. of Plant Sci., 10 (1): 29-42.

Vaithiyalingan, M. and N. Nadarajan (2005). Combining ability studies in inter racial crosses of rice (*Oryza sativa,* L.). Res. Crops, 6(2): 281-286.

استخدام السلالات العقيمة الذكر سيتوبلازميا والمعيده للخصوبة فى انتاج الآرز الهجين .

أشــرف حســين عبــدالهادي¹ ، كــوثر ســعد قــش¹ ، حمــدى فتــوح المــوافى² و جلال بكر أنيس²

(١) قسم الوراثة كلية الزراعة- جامعة المنصورة ، مصر.

(٢) مركز البحوث والتدريب فى الآرز ، معهد بحوث المحاصيل الحقلية ، مركز البحوث الزراعية، مصر.

أجرى هذا البحث لدراسة امكانيه الاستفاده من القدرة على الائتلاف وقوة الهجين باستخدام نظـام الثلاث سلالات فى الآرز (سـلاله العقم الـذكرى السيتوبلازمى الـوراثى CMS والسـلاله المحافظه على خصوبتها B والسلاله المعيده للخصوبه R) وذلك لانتاج الآرز الهجين. أجريت هذه الدراسة خلال موسمين زراعيين هما ٢٠١٠ و ٢٠١١ بمزرعة مركز البحوث والتدريب فى الارز بسخا – كفر الشيخ – مصر وذلك باستخدام نظام تحليل السلاله x الكشاف لثلاث سلالات عقيمه ذكريا وراثيا هجنت مع الآصناف المعيده للخصوبه لانتاج تقاوى هجن الدراسة. أظهر تحليل التباين وجود تباينات معنويه للتراكيب الوراثيه والاباء والهجن وتفاعلات متوسط الهجين المعبرة عن قوة الهجين وذلك لكل الصفات المدروسة (عدد الأيـام اللازمـه للتزهير – طـول النبـات – عدد السنابل للنبات – طول السنبله – عدد الحبوب الممتلئه فى السنبله – النسبه المئويه للخصوبة – محصول الحبوب لكل نبات) ما عدا تفاعلات متوسط الهجين المعبرة عن قوة الهجين لصفة طول السنبله. كان التباين الوراثى الراجع إلى القدرة العامة على الائتلاف أقل من التبـاين الوراثى الراجع إلى القدرة الخاصة على الائتلاف لكل الصفات المدروسة ماعدا صفة طول النبات. وكانت النسبة بين تبايني القدرتين العامة والخاصة على الائتلاف اقل من الوحدة لجميع الصفات المدروسة ما عدا صفة طول البنات مما يشير إلى أهميـة التباين الوراثى الغير مضيف لهذه الصفات. أوضحت البيانـات أن قيم درجة التوريث بمعناها الواسع كانت عاليـة لجميع الصفات المدروسة فى حين كانت قيم درجة التوريث بمعناها الضيق متوسطه الى منخفضة لتلك الصفات. كانت أفضل الآباء فى قدرتها العامة على الائتلاف للصفات المدروسة هـى IR69625A وG46A وG46A و 2-3-1-6-Gz9057 وكانـت افضل الجهن من حيث قدرتها الخاصة على الآئتلاف هى 178 G46A x Giza و IR69625A 1-1-2-1-12-Gz6296 x2-3-1-6-Gz9057و Large stigma A x Gz9057-6-1-3-2 وكذلك من حيث قوة الهجين ومتوسط القيم.

قام بتحكيم البحث

كلية الزراعة – جامعة المنصورة	أ.د / على ماهر العدل
مركز البحوث الزراعية	أ.د / عبد السلام عبيد دراز

Table 2 : Mean performances and general combining ability effects of lines and testers of rice genotypes.

Parents	Days to heading (day)		Plant height (cm)		Panicles plant[-1]		Panicle length (cm)		Filled grains panlce[-1]		Spikelets fertility %		Grain yield plant[-1] (g)	
	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA
CMS lines														
IR69625A	105	-3.64**	99.00	-2.39**	19.67	1.89**	25.20	-0.76**	193.67	-23.97**	93.11	2.08**	47.26	2.26**
G46A	88.3	2.36**	101.00	5.53**	23.00	0.22	26.03	0.92**	235.33	51.03**	92.58	2.27**	51.56	1.81**
Large stigma A	77.00	1.28**	86.67	-3.14**	13.33	-2.11**	22.63	-0.16**	110.33	-27.06**	96.59	-4.34**	48.36	-4.06**
G.M.	90.11	--	95.56	--	18.67	--	24.62	--	179.78	--	94.09	--	49.06	--
S.E.	--	0.25	--	0.50	--	0.29	--	0.12	--	1.30	--	0.34	--	0.39
Restorer lines														
Giza178	101.00	1.17**	106.33	0.61	25.67	-1.53**	26.10	0.24**	137.00	10.81**	88.79	1.19**	44.72	-0.73**
GZ6296-12-1-2-1-1	91.67	-2.50**	98.00	-2.28**	23.00	-1.42**	23.97	-0.55**	142.33	-39.08**	92.05	-4.63**	46.44	-1.90**
PR78	101.33	3.83**	130.00	3.72**	16.67	2.69**	28.03	0.81**	223.67	16.69**	93.59	2.36**	48.37	-0.80**
GZ9057-6-1-3-2	92.00	-2.50**	103.33	-2.06**	22.33	0.25	25.23	-0.50**	176.00	11.58**	94.45	1.08**	49.70	3.43**
G.M.	96.50	--	109.41	--	21.91	--	25.83	--	169.75	--	92.22	--	47.31	--
S.E.	--	0.36	--	0.71	--	0.41	--	0.18	--	1.85	--	0.48	--	0.55

** = highly significant at 0.01 level of probability.

Table 3 : Mean performances, specific combining ability effects and standard heterosis for rice hybrids.

Hybrids	Days to heading (day)			Plant height (cm)			Panicles plant[-1]			Panicle length (cm)		
	Mean	SCA	SH %	Mean	SCA	SH %	Mean	SCA	SH %	Mean	SCA	SH %
IR69625A/ Giza178	98.33	0.08	-3.59**	110.00	0.06	3.77*	24.67	-1.22**	-1.32	24.67	-0.27**	-5.11**
IR69625A/ GZ6296-12-1-2-1-1	95.00	0.42	-6.86**	107.67	0.61	15.75**	27.67	1.67**	10.68**	23.00	-1.14**	-11.53**
IR69625A/ PR78	98.67	-2.25**	-3.26**	112.00	-1.06**	5.66**	29.67	-0.44	18.68**	25.97	0.47**	-0.11
IR69625A/ GZ9057-6-1-3-2	96.33	1.75**	-5.55**	107.67	0.39	15.75**	27.67	0.00	10.68**	25.13	0.94**	-3.34**
G46A/ Giza178	104.33	0.08	2.28*	119.00	1.14**	12.26**	25.33	1.11**	1.32	27.43	0.83**	5.50**
G46A/ GZ6296-12-1-2-1-1	101.00	0.42	-٠.٩٨	114.33	-0.64	7.85**	21.67	-2.67**	-13.32**	26.63	0.81**	2.42**
G46A/ PR78	108.33	1.42**	٦.٠٩**	122.67	1.69**	15.72**	30.67	2.22**	22.68**	26.50	-0.67**	1.92**
G46A/ GZ9057-6-1-3-2	98.67	-1.92**	-3.26**	113.00	-2.19**	6.60**	25.33	-0.67**	1.32	24.90	-0.96**	-4.23**
Large stigma A/ Giza178	103.00	-0.17	0.98	108.00	-1.19**	1.88	22.00	0.11	-12.00**	24.97	-0.56**	-3.96**
Large stigma A/ GZ6296-12-1-2-1-1	98.67	-0.83**	-٣.٢٦**	106.33	0.03	0.31	23.00	1.00**	-8.00**	25.07	0.33**	-3.57**
Large stigma A/ PR78	106.67	0.83**	٣.٩٢**	111.67	-0.64	5.34*	24.33	-1.78**	-2.68*	26.30	0.21	1.15*
Large stigma A/ GZ9057-6-1-3-2	99.67	0.17	-٢.٢٨*	108.33	1.81**	2.19	24.33	0.67**	-2.68*	24.80	0.02	-4.61**
G.M.	100.72	--	--	111.72	--	--	25.53	--	--	25.45	--	--
S.E. (SCA)	--	0.51	--	--	1.00	--	--	0.58	--	--	0.25	--
L.S.D. at 0.05 % (SH) at 0.01 %	--	--	1.81 2.76	--	--	3.58 5.47	--	--	2.08 3.18	--	--	0.90 1.37

*, ** Significant and highly significant at 0.05 and 0.01 levels of probability, respectively.

Table 3 : Cont.

Hybrids	Filled grains panlce[-1]			Spikelets fertility %			Grain yield plant[-1] (g)		
	Mean	SCA	SH %	Mean	SCA	SH %	Mean	SCA	SH %
IR69625A/ Giza178	200.67	7.19**	46.47**	٩٠.٩١	3.49**	4.61**	54.45	-4.50**	21.75**
IR69625A/ GZ6296-12-1-2-1-1	151.33	7.75**	10.45*	٧٩.٢٠	-2.47**	-11.01**	61.99	4.21**	38.61**
IR69625A/ PR78	200.33	0.97	46.22**	٨٩.٧١	1.13**	0.79	59.15	0.26	32.26**
IR69625A/ GZ9057-6-1-3-2	178.33	-15.92**	30.16**	٨٥.١٨	-2.14**	-4.29**	63.14	0.03	41.18**
G46A/ Giza178	261.67	-6.81**	91.00**	84.63	-2.99**	-4.91**	64.04	5.53**	43.20**
G46A/ GZ6296-12-1-2-1-1	200.33	-18.25**	46.22**	٧٩.٣٦	-2.42**	-10.83**	55.53	-1.81**	24.17**
G46A/ PR78	273.33	-1.03	99.51**	٩٠.٧٢	1.94**	1.93	58.13	-0.31	29.98**
G46A/ GZ9057-6-1-3-2	295.33	26.08**	115.56**	٩٠.٩٧	3.47**	2.21	59.24	-3.42**	32.46**
Large stigma A/ Giza178	190.00	-0.39	38.68**	٨٠.٥٠	-0.50	-9.55**	51.60	-1.03**	15.38**
Large stigma A/ GZ6296-12-1-2-1-1	151.00	10.50**	10.21*	٨٠.٠٧	4.90**	-10.03**	49.07	-2.40**	9.72**
Large stigma A/ PR78	196.33	0.06	43.30**	٧٩.١٠	-3.07**	-11.12**	52.61	0.04	17.64**
Large stigma A/ GZ9057-6-1-3-2	181.00	-10.17**	32.11**	٧٩.٥٧	-1.33**	-10.59**	60.18	3.39**	34.57**
G.M.	206.63	--	--	84.16	--	--	57.42	--	--
S.E. (SCA)	--	2.61	--	--	0.67	--	--	0.78	--
L.S.D. at 0.05 % (SH) at 0.01 %	--	--	9.34 14.25	--	--	2.41 3.68	--	--	2.80 4.27

*, ** Significant and highly significant at 0.05 and 0.01 levels of probability, respectively.