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SUMMARY

The present investigation was carried out at the Farm of Rice Research and Training Center (RRTC), Sakha, Kafr El-Sheikh, Egypt, during the three successive growing seasons of 2011, 2012 and 2013. The genetic materials used in this investigation involved four CMS lines of rice obtained from different sterile sources of Wild Abortive and Gambiaca. These lines were; IR69625A, IR58025A, Pusa6A and G46A. In addition, six tester lines, i.e, Giza178R, Giza182R, GZ5121-5-2, GZ6296-12-1-2-1-1, PR2 and PR78 were used as "Testers".

Data were recorded on morphological traits i.e., plant height (cm), number of tillers per plant, days to heading. Floral traits i.e., anther length (mm), anther breadth (mm), stigma length (mm) stigma breadth and glume opening angle (^{o}). yield and its component traits i.e., panicle length, panicle weight, number of filled grains per panicle, number of spikelets per panicle, spikelets fertility, 1000-grain weight, yield (t/fed.). As recommended by standard evaluation of **IRRI (2014).**

The obtained results can be summarized as follows:

I. Morphological traits:

A) Analysis of variances:

1. The analysis of variances for all studied morphological traits cleared highly significant mean squares for genotypes, parents, crosses, parents *vs.* crosses and lines x testers indicating that non additive (dominance or epitasis) genetic variance were of great importance in the inheritance of these characters. The pedigree method can be used to improve all traits under study and develop the new hybrid rice verities. Therefore, the analysis of all sources of variation

demonstrated the presence of genetic variability within the genotypes for these traits.

2. GCA/SCA ratios were found to be less than unity for morphological, It suggested greater importance of non-additive gene action in their expression and indicated very good prospect for the exploitation of non-additive genetic variation for these traits through hybrid rice breeding.

B) Mean performance:

1- Plant height, G46A, GZ6296 and IR69625A X GZ6296-12-1-2-1-1, Pusa 6A X GZ5121-5-2R and IR69625A X Giza178R gave the lowest values for plant height.

2- Number of tillers per plant: the genotypes G46 A, GZ5121-5-2R, Giza 182R and the hybrid combination; G46A x PR78 gave the highest mean values for this trait.

3- Days to heading: the genotypes G46A was the ideal female parent for earliness. The tester GZ6296-12-1-2-1-1 was the best male parent for early days to flowering. Hybrid combination G46 A / Giza 178R was the earliness with high differences compared with all others, line, testers and hybrids, respectively.

C) Combining abilities:

I. General combining ability effects (GCA):

1- Among the four cytoplasmic male sterile lines (CMS), IR69625A and Pusa6A were the best general combiners for plant height. But, the restorers, Giza178R, Giza182R, GZ5121-5-12 and GZ6296-12-1-2-1-1 were the best general combiners among the testers for plant hieght.

2- For number of tillers plant^{-1}, the best general combiners from the CMS lines was G46A. The restorer line PR78 was the best general combiners among the testers.

3- One line namely, G46A displayed favorable significant negative GCA with values of -6.825 these cultivar could be considered as good combiners for earliness for days to heading. Highly significant positive values of GCA effects would be interest in most traits under study, except for heading date and plant height whereas the highly significant negative values would be useful from the breeder's point of view for these two traits.

II. Specific combing ability (SCA):

Morphological traits: from estimates of specific combining ability effects (SCA) of the hybrid combinations, it could be concluded that for plant height, the crosses combinations IR69625A/GZ6296, Pusa6A/GZ5121 and G46A/PR78 were the best specific combination for plant height. For number of tillers, the best specific combiners were IR69625A/PR2 and G46A/PR78. For no. days to heading, the cross combinations IR69625A/GZ6296 and Pusa6A/Giza182R were the best specific combination for earliness.

D) Genetic parameters and heritability:

Genetic parameters, as well as, heritability values were estimated for all studied morphological traits. The estimates of the non-additive (σ^2 D) for all the three vegetative traits was higher those additive variance (σ^2 A), indicated that the former characters were largely governed by non-additive gene action and could be

utilize by these genotype in hybrid breeding program. The heritability values were higher for the three vegetative characters. However, heritability estimates in the narrow sense (h^2n) were low for the same traits.These results indicated that the non-additive play important role in genetic controlling for these traits. These traits were not influenced by environmental effect.

E) Heterosis effects:

Morphological traits: for plant height the most pronounced useful hetrotic effects relative to the better and mid parents under study were detected for the F_1 hybrids IR69625A x GZ6296 and relative to standard check variety (Giza178R) was IR58025A x PR78 for shortness. For number of tillers the best hybrid was G46A x PR78, relative to better parent. Either mid-parent or standard check variety (Giza178R) the best hybrid was G46A x PR78. For earliness relative to better parent the best hybrid combinations were Pusa6A x Giza178R, IR58025A x PR78 and Pusa 6A x PR78. Relative to mid-parent the best hybrid was Pusa6A x PR78. However, the standard heterosis was highly significant and negative in the crosses G46A x Giza 178R and G46A x PR78.

II. Floral traits:

A) Analysis of variances:

1- Analysis of variance of floral traits viz., for anther length, anther breadth, number of pollen grains anther^{-1}, stigma length, stigma breadth and glume opening angle. Highly significant differences among genotypes, parents, parents *vs* crosses, crosses, lines, testers and line x tester interactions in the three male parent for floral traits. Indicating that the genotypes had a wide genetic diversity among themselves. Mean of

sum of squares due to line x tester were also significant for anther length, anther breadth, number of pollen grains anther^{-1}, indicating the importance of both additive and non-additive genetic variance.

2- The ratio of GCA to SCA was less than unity indicating greater importance of non-additive gene action in its expression and indicated very good prospect for the exploitation of non-additive genetic variation in these traits.

B) Mean performance:

1- Anther length, IR58025A, restorer lines PR2 and PR78 besides the crosses IR69625A x PR2, IR58025A x PR2, Pusa6A x PR2 and G46A x PR2 gave the highest mean values for this trait.

2- Anther width: the two restorer parents PR2 and PR78 gave the highest mean values (more than 0.5mm). Among the crosses, the combinations, Pusa6 A x GZ6296 and Pusa6 A x PR2 gave the highest mean values of anther width being 0.449 and 0.450mm.

3- Number of pollen grains anther^{-1}: the CMS lines ranged from 1130.1 to 1192.2 per anther but it is completely sterile. In restorer lines ranged from 731.08 for Giza 178R to 2426.7 for PR78 depending on anther size. Fertility restoration in these pollinators (Giza178R, Giza182R, GZ5121-5-2R, GZ6296-12-1-2-1-1, PR2 and PR78) were under dominant gene control.

4- Stigma length: The line G46A registered higher mean values for stigma length (1.458mm) and breadth (0.667mm). The other genotypes IR69625 A, IR58025 A, Pusa 6A had a values for stigma length ranged from (1.042mm to 1.292mm). While, for stigma breadth the values ranged from (0.317 to 0.442mm) compared with the CMS line G46A.

5- Glume opening angle: the two genotypes IR69625A and G46A had desirable stigma traits, and desirable glume opening angle with the mean value of 31.33^{o} and 29.83^{o}, respectively which is highly associated with higher out crossing rate.

C) Combining abilities:

I. General combining ability effects (GCA):

1- Among the female parents, the estimates recorded one significant positive estimates of GCA for IR69625A with value of 0.040. Indicated that this line was a good combiner for anther length in hybridization to produce the commercial F_1. The testers PR2 and PR78 had significant and positive GCA effects with values of 0.394 and 0.294. This finding indicated that these lines were good combiners for this trait.

2- For anther breadth, the best general combiners from the CMS lines were IR58025A and G46A. The male parents PR2 and PR78 were scored as the top most favorable parents of GCA effects with values of 0.044 and 0.023.

3- One male sterile line IR69625A showed highly significant GCA effects for number of pollen grains/anther but this pollen grains is sterile. The testers PR2 and PR78 had preferable significant positive GCA effects of 502.7 and 375.1, respectively.

4- Stigma length: One CMS line (IR69625A) had significant positive GCA effects of 0.016 for this trait. Among testers, PR2 and PR78 manifested significantly positive GCA effects. Indicating the aromatic testers PR2 and PR78 are good combiners for this trait in hybrid rice program.

5- Stigma breadth: Among lines; IR69625A and G46A had positive GCA effects with values of 0.005 and 0.013. Among testers four testers Giza178R, Giza182R, PR2 and PR78 expressed significantly positive GCA estimates for stigma breadth.

6- Glume opening angle: Among lines, IR69625A and G46A had preferable significant positive GCA effects. The testers, Giza178R and GZ6296 expressed significant positive GCA effects with value of 1.511 and 0.804, respectively.

II. Specific combing ability (SCA):

Floral traits: from estimates of specific combining ability effects (SCA) of the hybrid combinations, it could be concluded that for anther length, the cross combinations IR69625AxGZ5121, IR58025AxPR78, Pusa6AxGZ6296, G46AxGiza178R, G46Ax PR2 and G46AxPR78 were the best specific combinations for anther length and number of pollen grains per anther. For anther breadth, the best specific combiners were IR 58025AxPR2, IR69625AxPR78, Pusa6AxGZ6296, G46AxGiza178R and G46AxGZ5121. For female floral traits, the cross combinations IR69625AxGiza182R, IR58025AxPR78 and Pusa6AxGiza178R were the best specific combination for these traits.

D) Genetic parameters and heritability:

Genetic parameters, as well as, heritability values were estimated for all studied floral traits. The estimates of the non-additive (σ^2 D) for all floral traits was higher those additive genetic variance (σ^2 A), indicated that these traits were largely governed by non-additive gene action and could be utilize by these genotypes in

hybrid breeding program. The heritability values were higher for the floral traits. However, heritability estimates in the narrow sense (h^2n) were low for the same traits. These results indicated that non-additive genetic variance play an important role in genetic controlling for these traits.

E) Heterosis effects:

Floral traits: for anther length the most pronounced useful hetrotic effects relative to the better and mid-parents was the F_1 hybrid IR69625A x GZ5121 and relative to standard check variety (Giza178R) was the F_1 hybrid IR69625A x PR2 for tallness of anther. For anther breadth the best hybrid was IR58025A x PR2, relative to better parent, mid-parent and standard check variety (Giza178R). For number of pollen grains per anther heterosis relative to better parent and mid-parent the best hybrid combination, IR69625A x GZ5121 was the best combinor. However, the standard heterosis was highly significant in the crosses IR69625A x PR2 and G46A x PR2. For stigma length the best hybrid combination which showed hetrotic effects relative to the better, mid parents and standard check variety (Giza178R) was the F_1 hybrid IR69625A x GZ5121. For stigma breadth the best hybrid was Pusa6AxGiza178R, relative to better parent and mid-parent. While, in standard check variety (Giza178R) the best hybrid was IR69625AxGiza182R. For glume opening angle heterosis relative to better parent the best hybrid combinations, IR58025A x GZ6296. Relative to mid-parent the best hybrid was G46A x PR78. However, the standard heterosis was highly significant in the cross G46A x Giza178R.

II. Yield and its component traits:

A) Analysis of variances:

1- Analysis of variance of yield and its component traits. Highly significant differences among genotypes, parents, parents *vs* crosses, crosses, lines, testers and line x tester interactions in all traits. Indicating that the genotypes had wide genetic diversity among themselves. Means of sum of squares due to line x tester were also significant indicating the importance of both additive and non-additive variance.

2- The ratio of GCA to SCA was less than unity indicating greater importance of non-additive gene action in its expression and indicated very good prospect for the exploitation of non-additive genetic variation in yield and its component traits.

B) Mean performance:

1- **Panicle length**, Pusa6A, restorer lines PR2 and PR78 besides the crosses IR69625A x PR2, G46A x PR2 and G46A x PR78 gave the highest mean values.

2- **Panicle weight**: the CMS line Pusa 6A, testers PR78 and PR2 gave the highest mean values. Among the crosses, the combinations, IR58025A x PR2, G46A x PR2 and G46A x Giza PR78 gave the highest mean values.

3- **Filled grains panicle^{-1}**: the parental lines PR78 and PR2 showed the highest mean values. The hybrid combinations G46A/PR78, G46A/PR2, IR58025A/PR2 and IR58025A/Giza178R gave the highest mean values.

4- **Number of spikelet's panicle^{-1}**: The line Pusa6A registered higher mean values. The testers PR2 and the crosses IR58025 A x PR2, IR58025 A x PR78, Pusa 6A x GZ6296, and G46A x Giza 182R, G46A x PR2 and G46A x PR78 recorded the highest number of spikelets panicle^{-1}.

5- **spikelets fertility %**: the crosses IR69625A x PR2, IR69625A x Giza178R, Pusa 6A x GZ5121-5-2R, IR58025A x Giza178R , IR58025A x GZ6296 and G46A x GZ5121-5-2R gave the highest mean values for spikelets fertility.

6- **1000- grain weight (g):** the testers GZ5121-5-2R, PR2 and PR78 recorded the highest mean values. The crosses IR69625A x PR2, IR69625A x PR78, IR58025A x PR2, Pusa 6A x PR2 and G46A x PR78 gave desirable mean values for this trait.

7- **Yield (t/fed.):** the male parents Giza182R showed the highest mean values for yield (t/fed). Among the lines the maintainer line IR58025B recorded the best value for this trait. The most desirable mean values were detected by the hybrid combinations, G46A x PR78 (6.016 t/fed), IR58025A x PR78 (5.822 t/fed), Pusa 6A x PR78 (5.652 t/fed) and IR69625A x PR78 (5.528).

C) Combining abilities:

I. General combining ability effects (GCA):

1- Among the female parents, the CMS line G46A was a good general combiner for all yield traits. Among the testers PR2 and PR78 were the best combiner for yield and its component traits.

II. Specific combing ability (SCA):

Yield characters: the two cross combinations IR58025A/ Giza178R and G46A/PR78 were the best specific combinations for panicle length, panicle weight and number of filled grains panicle^{-1}. Also, the two cross combinations IR58025A/ PR2 and G46A/PR78 were the best specific combinations for number of spikelets

panicle^{-1}, spikelets fertility (%), 1000- grain weight (g) and yield (t/fed).

D) Genetic parameters and heritability:

Genetic parameters, as well as, heritability in the broad sense (h^2b) values were estimated for yield and its component traits. The estimates of the non-additive (σ^2 D) for all yield and its component traits was higher those additive variance (σ^2 A), indicated that these traits were largely governed by non-additive gene action. The h^2b values were higher for the yield and its component traits. However, heritability estimates in the narrow sense (h^2n) were low for the same traits. These results indicated that non-additive play important role in genetic controlling for these traits.

E) Heterosis effects:

Yield and its component traits: for panicle length the most useful hetrotic effects relative to better parent was founed in the F_1 hybrid G46A x Giza182R and to mid parents was IR69625A x GZ5121 and relative to standard check variety Giza178R was G46A x PR2 for tallness of panicle. For panicle weight the best hetrotic effects relative to the better was G46A x PR2 and to mid-parent was G46A x PR78 and relative to the standard check variety (Giza178R) was G46A x PR78. For number of filled grains panicle^{-1} the two hybrid combinations G46A x PR2 and G46A x PR78, verified outperformed in all models of heterosis. For number of spikelets panicle^{-1} the best heterotic effects relative to all the models of heterosis were G46A x Giza 182R, G46A x PR78 and IR58025A x Giza178R. For spikelets fertility %, the best heterotic effects relative to the better was IR69625A x PR2 and to mid-parent was IR69625A x PR2. For 1000-

grain weight the best heterotic effects relative to all the models of heterosis was IR69625A x PR2, IR69625A x PR78, IR58025A x PR2, Pusa 6A x PR2 and G46A x PR78. For yield (t/fed.), the best hetrotic effects relative to better and mid parents was IR69625A x PR2. While, relative to standard check variety (Giza178R) was G46A x PR78.

F) Molecular genetic analyses:

From 10 primers only six primers recorded the polymorphic bands of the materials under study which may be related to *Rf* genes and could be using as added marker selection in early generations of hybrid rice programe to decrease the costly, labors, timing and accelerate the breeding method for development new promising homozygote lines using as a parental lines to develop new hybrid combinations with desirable traits and tolerant to biotic and a biotic stress.

In conclusion, it could be concluded that:

The parental lines Giza178R, PR2 and PR78 had good restoration ability for CMS lines to produce new hybrid combinations depending on cytoplasmic male sterile source. Also, they had favorable male floral traits that influencing on the ability of restoration.

The female line IR69625A, IR58025A and G46A were found to be a good combiners for floral traits under study.

These female lines had desirable floral traits that could be utilize in increasing the outcrossing rate to get high seed set in hybrid rice seed production.

The restoring ability does not depend only on the restorer genes and number or expression of *Rf* genes, but also depend on the genetic background of the CMS lines.