Genetic Behavior and Cluster Analysis of Some Floral Traits Affecting Cross Breeding in The Production of Hybrid Rice Seed

Abd El-Hadi, A. H.* ; H. F. El-Mowafi** and O.A. El-Badawy**
*Genetics Department, Faculty of Agriculture, Mansoura University, Egypt.
**Rice Research and Training Center (RRTC), Field Crop Research Institute, ARC, Egypt.

ABSTRACT

Genetic development of improved genotypes with good floral charactaristics is the an important approach in the production of hybrid rice seed. Ten rice parental lines where four of them have cytoplasmic male sterility while the other six use restorer. These ling were crossed to obtain 24 hybrid combinations, through a factorial mating design. The parental lines and their 24 F_1 hybrids were grown in randomized complete blocks design with three replications at Rice Research and Training Center Farm, Sakha Kafr El-Sheikh, Egypt during the two seasons of 2011 and 2012. Data were recorded on six floral traits viz., anther length, anther breadth, number of pollen grains anther^{-1}, stigma length, stigma breadth and glume opening angle. The analysis of variance of all genotypes revealed highly significant mean squares for all studied traits, suggesting the presence of genetic differences among the genotypes used in this study. The magnitude of genetic parameters indicated that the additive variance (σ^2 A) for anther length, number of pollen grains anther^{-1}, glume opening angle traits were higher than the corresponding non-additive variance including dominant (σ^2 D). These results indicated that these traits were largely governed by additive gene action. Thus, the estimated values of heritability in broad sense were higher than heritability in narrow sense for all the studied floral traits. A major part of the total phenotypic variance was due to non-additive including dominance genetic variances for all floral traits. The maternal effects were affective in stigma breadth (37.25%) and glume opening angle (70.15%). The contribution of maternal and paternal interactions (Line x Tester) were found to be vital for anther breadth (57.86%) and stigma breadth (37.43%). The ten parental lines were distinctly classified into two major clusters (below 1200 Euclidean distance) according to the similarity diagram.

Keywords: *Hybrid rice, floral traits, line x tester, genetic parameters*

INTRODUCTION

Rice (*Oryza sativa* L.) is the major food for more than half of the world's population. In Egypt, rice is one of the major cereal crop, with annual cultivated area of about 600.000 hectares, with the production of about 6 million tons of paddy rice. The average yields 9.88 t/ha., which is considered among the highest average yield per hectare in the world (RRTC, 2012). Hybrid rice offers an opportunity to increase the yield potentiality. It has a yield advantage of 15 to 20% over conventional high yielding variety. In self-pollinated crops like rice, hybrid seed production is difficult, as the floral traits are unfavorable for outcrossing (Raghavendra and Hittalmani, 2015). Use of male sterility system has immensely helped in hybrid breeding. Though the three line system involving cytoplasmic male sterility-fertility restoration system is effective for the development of commercial rice hybrids. This system is cumbersome and tedious as it involves three lines (A, B and R) and has negative effects on cytoplasm. The breeding of yield rice and quantitatively better rice varieties is not possible without prior knowledge of their genetic properties. Therefore, the breeders use suitable quantitatively genetic method to combine the desired properties of different varieties. The magnitudes of genetic parameters also is useful to breeders for genetic improvement of the existing genotypes on the basis of their performances in different hybrid combinations (Rahaman, 2016). One of the major problems of low seed set in hybrid seed production plot is "very low out crossing" of CMS lines in rice. A cyto-sterile line with high out crossing potential will certainly economize the cost of hybrid seed production. The most important floral traits influencing out crossing is male sterility in rice. Male fertile plant shows very little, if any out crossing due to self-pollinating nature of rice flower. Floral morphology and flowering behaviour of CMS lines is important (Ali *et al.,* 2013; Ghadi *et al.,* 2013). However, in male sterile plants, extent of out crossing is further influenced by its floral traits such as anther length, anther width, number of pollen grains anther^{-1}, stigma length, stigma breadth and glume opening angle as reported by (Mahalingam *et al*., 2013). Hence, assessing and understanding the genetic variability and the inheritance pattern of floral traits is essential for proper choice of CMS lines (Sheeba *et al.,* 2006).This study aimed to investigate the nature of inheritance of some floral traits during outcrossing four cytoplasmic male sterile lines and by restorer lines.

MATERIALS AND METHODS

This study was carried out at the experimental farm of Rice Research and Training Center (RRTC ,(Sakha , Kafer El-Sheikh, Egypt, during the two successive growing seasons of 201 1and 201 .2The genetic materials used in this investigation involved ten genotypes. A line x Tester mating design was used, where four cytoplasmic male sterile lines ;i .e ,.IR69625A, IR58025A, Pusa6A and G46A were used as" Female Lines" and the six restorer lines ;i.e ,.Giza178R, Giza182R, GZ5121, GZ6296, PR2 and PR78 ,were used as" Male Testers ."Thus, the obtained 24 F $_1$hybrids along with their ten parents were evaluated in a randomized complete blocks design (RCBD) with three replications during 201 2rice growing season .Seedlings were transplanted into 20 x 20 cm spacing. All agronomic practices were done as recommended for rice plantation 15 .plants from each replication were randomly selected to measure the following traits :anther length) mm ,(anther breadth (mm ,(number of pollen grains anther ,$^{1-}$ stigma length) mm ,(stigma breadth) mm (and glume opening angle) ^{o} .(Data were subjected to statistical analysis using Line x Tester analysis and genetic components of each parameter as outline by) Kemptherne .(1957 ,Cluster analysis among

the ten studied rice parental lines were computed using *NTSYSpc version 2.1* statistical package.

Table 1: Cytoplasmic male sterile lines and tester lines used for the study.

Genotypes	Cytoplasm source	Origin
CMS lines (female)		
1 IR69625A	CMS line (WA)	IRRI
2 IR58025A	CMS line (WA)	IRRI
3 Pusa 6A	CMS line (WA)	IRRI
4 G46A	CMS line (Gambiaca)	IRRI
Restorer lines (male)		
5 Giza178R	Egypt (Indica-Japonica type)	Egypt
6 Giza182R	Egypt (Indica type)	Egypt
7 GZ5121-5-2R	Egypt (Indica type)	Egypt
8 GZ 6296-12-1-2-1-1	Egypt	Egypt
9 PR2	Egypt-India (Indica type)	Egypt
10 PR78	Egypt-India (Indica type)	Egypt

RESULTS AND DISCUSSION

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 the data presented in Table 2 revealed the presence of highly significant differences among genotypes, parents, parents vs crosses, crosses, lines, testers and line x tester interactions most floral traits. The significant differences among the genotypes, parents, parent's vs crosses, crosses, lines, testers and line x tester interactions indicated that the genotypes had wide genetic diversity among themselves. The significance of the means of sum of squares due to lines and testers indicated a prevalence of additive variance. However, means 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 variance. The mean square of SCA was higher than those of the GCA variances for these traits, indicated the non-additive gene action is playing its role in the inheritance of these traits. Nadali Bagheri and Nadali Babaeian-Jelodar (2011), and Elbadawy (2009) reported the predominance of dominant and additive gene action variances. The ratio of GCA to SCA was less than unity for the three male parent's floral traits. It suggested greater importance of non-additive gene action in its expression and indicated very good prospect in the exploitation of hybrid breeding. On the other side, the female parent's floral traits viz., stigma length, stigma breadth and glume opening angle which appears in Table 2. revealed the presence of highly significant differences among the genotypes, parents, parents vs crosses, crosses, lines, testers and line x tester interactions indicating the presence of differences among genotypes and a wide genetic variation Mahalingam *et al.* (2013). The mean sum of squares due to parents versus crosses was insignificant for stigma breadth trait. However, means of sum of squares due to line x tester were also highly significant for stigma length, breadth and glume opening angle, indicating the importance of both additive and non-additive variance. So, the breeding method will be selection in early generations. Data showed that the values of SCA were greater than GCA variances for these traits, indicated the importance of non-additive gene action in the inheritance of these traits. In the same trend the ratio of GCA to SCA was less than unity indicating the dominance gene action had a major role in inheritance of this traits, here the suitable breeding method is hybridization. Elbadawy (2009).

Table 2: Analysis of variance and mean square values of line x tester analysis for the six floral traits.

S. O. V	d.f	A. L. (mm)	A. B. (mm)	N. P. g. / A	S. L. (mm)	S. B. (mm)	G. O. A. (°)
Replications	2	0.000	0.000	88.675	0.00003	0.003	0.014
Genotypes	33	**0.309	**0.014	**504301	**0.07578	**0.010	**20.13
Parents	9	**0.569	**0.027	**928017	**0.16451	**0.029	**27.69
Parents vs. crosses	1	**0.148	**0.035	**241455	**0.00475	0.001	**10.04
Crosses	23	**0.215	**0.009	**349927	**0.04415	**0.003	**17.62
Females (Lines)	3	**0.027	**0.003	**43475	**0.00301	**0.010	**91.72
Males (Testers)	5	**0.908	**0.016	**1480158	**0.14682	**0.004	**12.04
Females × Males (L × T)	15	**0.021	**0.008	**.34474	**0.01816	**0.002	**4.660
Error	66	0.0003	0.0002	539.116	0.00053	0.000117	0.149
GCA		0.005	0.000028	7955.51	0.00066	0.000025	0.327
SCA		0.007	0.002434	11311.7	0.00587	0.001403	1.504
GCA/SCA		0.703	0.0116	0.70330	0.11161	0.01784	0.217

* And ** Significant at 0.05 and 0.01 levels, respectively. A. L.= anther length, A.B.= anther breadth, N.P.g./A= number of pollen grains anther^{-1}, S. L.= stigma length, S. B.= anther breadth and G. O. A.= glume opening angle

The mean of squares due to parents versus crosses were insignificant for the three female parents for floral traits. However, the mean squares due to line x tester were significant for stigma length and breadth, indicating the importance of both additive and non-additive genetic variance. Thus, selection in the early generations would be effective. The values of SCA were greater than GCA variances for these traits, which indicated the importance of non-additive gene action in the inheritance of these traits. In the same trend, the ratio of GCA to SCA was less than unity indicating that dominance gene action would have a major role in the inheritance of these traits, here the suitable breeding method would bethe hybridization. The predominance of dominant and additive gene action

variances was reported by El-badawy (2009) and Mahalingam *et al.*, (2013).

Mean performance: Regarding the anther length, in table 3 out of the 24 crosses, only the mean values of eight crosses were more the longest anther of their corresponding parents. Among the crosses five showed intermediate mean values between their parents, indicating partial or no dominance effects. The mean values of anther length of the parents ranged from 1.80 to 1.95 mm for the CMS lines G46A and IR58025A, respectively. While it ranged for the restorer lines of Giza178R and PR78 from 1.49 to 2.82 mm, respectively. The aromatic restorer lines PR2 and PR78 besides the four crosses, IR69625A x PR2, IR58025A x PR2, Pusa6A x PR2 and

G46A x PR2 gave the highest mean values of 2.747 and 2.818 mm for parents and 2.42, 2.47, 2.44 and 2.45 mm, respectively. For anther width, the F_1 means of some crosses tended towards the widest anther width parent. However, the F_1 means of the other crosses were intermediate between their two parents while the rest of crosses (six crosses) exhibited dominance effect towards the lower anther width parent. The results showed that, the two restorer parents PR2 and PR78 gave the highest mean values (more than 0.5 mm). Among the crosses, the hybrid combinations, Pusa6 A x GZ6296 and Pusa6 A x PR2 gave the highest mean values of anther width being 0.449 and 0.450 mm, respectively. The mean performance of four male sterile lines viz., IR69625 A, IR58025 A, Pusa 6A and G46 A for six floral traits revealed that certain genotypes exhibited superiority over others as seen in Table 3. In evaluating the suitability of Cytoplasmic Male Sterile (CMS) lines to local conditions, high out crossing rate is one of the most important character required for getting good seed yield in hybrid seed production plot. The line G46A showed higher mean values for stigma length of 1.458mm and breadth of 0.67 mm. The other genotypes of IR69625 A, IR58025 A, Pusa 6A had values for stigma length ranged from 1.04 to 1.29 mm. While, for stigma breadth, the values ranged from 0.32 to 0.44 mm compared with the CMS line G46 A. All the CMS lines had above 99.50% pollen sterility. Similar findings were observed by Behla *et al.,* (2007), Ansari *et al.,* (2010). Mahalingam *et al.,* (2013) and Hasan *et al.,* (2014).

Table 3: Mean performances of lines, testers and their crosses for anther length, anther breadth and number of pollen grains anther[-1] traits.

Cate.	Genotypes	A. L. (mm)	A. B. (mm)	N. P. g. / A	S. L. (mm)	S. B. (mm)	G. O. A. (°)
CMS Lines	IR69625 A	1.83	0.34	1158.4 S[1]	1.04	0.44	31.3
	IR58025 A	1.95	0.30	1323.4 S	1.29	0.32	26.0
	Pusa 6 A	1.85	0.37	1192.2 S	1.21	0.34	24.5
	G 46A	1.80	0.30	1130.1 S	1.46	0.67	29.8
Restorer lines (Testers)	Giza 178	1.49	0.39	731.08 F[2]	0.71	0.38	29.7
	Giza 182	2.10	0.47	1511.5 F	0.95	0.38	23.8
	GZ 5121	1.79	0.45	1107.1 F	0.88	0.39	27.8
	GZ 6296-12-1-2-1-1	1.85	0.46	1195.8 F	0.83	0.35	25.7
	PR 2	2.75	0.52	2336.2 F	1.17	0.42	26.2
	PR 78	2.81	0.55	2426.7 F	1.18	0.37	23.5
Hybrid combinations	IR69625A / Giza 178 R	1.86	0.37	1204.6 F	0.86	0.45	30.0
	/ Giza 182 R	2.05	0.37	1440.5 F	1.15	0.48	29.7
	/ GZ 5121	2.11	0.35	1527.4 F	1.13	0.37	26.3
	/ GZ 6296	1.90	0.42	1252.5 F	0.96	0.42	29.0
	/ PR 2	2.42	0.37	1917.6 F	1.08	0.41	28.3
	/ PR 78	2.34	0.39	1820.1 F	1.07	0.42	28.0
	IR58025A / Giza 178 R	1.84	0.39	1174.5 F	0.93	0.42	27.3
	/ Giza 182 R	2.02	0.36	1410.4 F	1.00	0.38	26.8
	/ GZ 5121	2.04	0.38	1426.3 F	0.92	0.36	26.3
	/ GZ 6296	1.96	0.38	1334.1 F	1.01	0.36	27.1
	/ PR 2	2.47	0.54	1983.3 F	1.21	0.43	24.3
	/ PR 78	2.43	0.39	1928.3 F	1.13	0.35	24.3
	Pusa 6 A / Giza 178 R	1.80	0.35	1130.1 F	1.00	0.43	27.7
	/ Giza 182 R	2.06	0.35	1460.0 F	1.09	0.39	24.5
	/ GZ 5121	1.94	0.40	1300.4 F	1.00	0.40	25.3
	/ GZ 6296	1.92	0.45	1277.4 F	1.00	0.39	24.7
	/ PR 2	2.44	0.45	1947.8 F	1.15	0.42	22.7
	/ PR 78	2.41	0.38	1908.8 F	1.21	0.38	24.3
	G 46 A / Giza 178 R	1.90	0.40	1254.3 F	0.97	0.43	30.2
	/ Giza 182 R	1.99	0.38	1371.4 F	1.04	0.46	29.0
	/ GZ 5121	1.87	0.43	1215.3 F	0.98	0.43	28.5
	/ GZ 6296	1.91	0.38	1264.9 F	1.03	0.43	29.0
	/ PR 2	2.45	0.40	1960.2 F	1.15	0.42	29.3
	/ PR 78	2.39	0.41	1885.7 F	1.11	0.43	29.7
LSD	0.05%	0.12	0.07	176.8	0.12	0.06	1.94
	0.01%	0.18	0.10	235.2	0.16	0.08	2.58

[1]: Sterile and [2]: Fertile. A. L.= anther length, A.B.= anther breadth, N.P.g./A= number of pollen grains anther[-1],
S. L.= stigma length, S. B.= anther breadth and G. O. A.= glume opening angle.

Number of pollen grains anther[-1] is a desirable trait for pollination as it enhances the chance of anther shedding. It significantly varied among the tested CMS lines from 1130.1 to 1192.2 per anther but they were completely sterile. While in restorer lines number of pollen grains anther[-1] ranged from 731.08 for Giza 178R to 2426.7 for PR78 depending on anther size and length. Indicating that fertility restoration in these pollinators i. e. Giza178R, Giza182R, GZ5121-5-2R, GZ6296-12-1-2-1-1, PR2 and PR78 was under dominant gene. The cytoplasmic genetic sterility system of IR69625A, IR58025A, Pusa 6 A and G46A were sporophytic in nature. In general, the results are in agreement with those reported by Majumder *et al.,* (2014). In this study six restorer lines i. e. Giza 178R, Giza 182R, GZ 5121-5-2R, GZ 6296-12-1-2-1-1, PR2 and PR78 were evaluated for stigma length, stigma breadth and glume opening angle as presented in Table 3. Stigma length and stigma breadth showed significant variation, where the highest stigma length was 1.183 mm in pollen parent PR78 and PR2 1.167 mm. Stigma breadth was nearest between all restorers. In general, the restorer lines were found to have smaller stigmas than the CMS lines. Behla *et al.,* (2007) observed variation for stigma length which ranged from 1.13 to 2.09 mm, whereas glume

opening angle was ranging from 23.43^o to 30.20^o. In this study angle of floret opening for the testers varied from 23.50^o to 29.67^o. In the present study maximum angle was observed in Giza178R which was at par with PR2 and GZ5121, and minimum in case of PR78.

These results agreed with those obtained by Umadevi *et al.*, (2010). Mean performance of line x tester combinations for stigma length, stigma breadth and glume opening angle are shown in Table 3.

The mean values of the 24 F_1 crosses, were intermediate with respect to their parents. However, the F_1 mean values of the different crosses for stigma length varied from 0.86 to 1.208mm in the two hybrid combinations IR69625A x Giza178R and IR58025A x PR2, respectively. While, stigma breadth ranged from 0.35mm for IR58025A x PR78 to 0.48mm for IR69625A x Giza182R. Whereas glume opening angle varied from 22.67^o for Pusa 6A x PR2 to 30.17^o for G 46A x Giza 178R. In general, these findings suggested the presence of either partial or no dominance effects. With respect to angle of floret opening, complete or over dominance effects was observed in most of the crosses for largest angle of floret opening. As revealed in Table 3, some crosses showed intermediate mean values between the parents of each cross for this trait indicating partial or no dominance effects. These findings are in close agreement with those obtained by El Badawy (2009) and Mahalingam *et al.*, (2013).

Genetic components for floral traits: The estimates of genetic parameters for studied floral traits are shown in Fig. 1. The results indicated that the value of non-additive variance (σ^2 D) for anther breadth, stigma length, stigma breadth and glume opening angle traits were higher than those for additive variance (σ^2 A). These results indicated that these traits were largely governed by dominance gene action. On the other hand, results indicated that the additive variance (σ^2 A) of anther length and number of pollen grains anther-1, traits were higher than those non-additive variance (σ^2 D). These results indicated that these traits were largely governed by additive gene action and would be improved through select in early generations. Similar results were obtained by Abd Allah (2008) and El Badawy (2009).

Concerning heritability, the results cleared that the estimated values of heritability in broad sense were high for all studied floral traits as shown in Figure 2, indicating that these traits were under genetic control and the environmental effect was insignificant. On the other hand, heritability values in narrow sense were relatively low for these traits except anther length and number of pollen grains per anther. The results also illustrated that a major part of the total phenotypic variance was due to non-additive and additive genetic for all floral traits. Accordingly, it was expected to obtain an effective heterosis yielding high hybrids for these traits. Similar results were obtained by Abd Allah (2008) and El badawy (2009). Singh R. and B. Singh (2011). Singh *et al.*, (2014).

Fig. 1. The additive, dominance and environmental variances for the six studied traits.

Fig. 2. The broad sense and narrow sense heritability for the six studied traits.

The proportional of contribution for lines, testers and their interaction to the total variance are presented in Figure 3. It is clear that, the testers played an important role in the genetic control of anther length, number of pollen grains/anther and stigma length traits due to the predominant of paternal influence for inheritance of these traits.

On the contrary, maternal lines effects contributed about 67.90% for glume opening angle. The stigma breadth was also highly affected by maternal effect which would be used as a donor for improving the process of hybrid rice breeding program by increasing the outcrossing. The contribution of maternal and paternal interactions (line x tester) were found vital for anther breadth (56.80%) and stigma breadth (53.05%). These results indicated that there were wide variation between the parental lines for these traits and could be used as genetic materials to develop new hybrid combinations in hybrid breeding program.Similar results were obtained by Abd Allah (2008) and El badawy (2009).

Fig. 3. The contributions of lines, testers and their interaction for the six studied traits.

Clustering analysis of rice genotypes based on similarity of floral traits:

Cluster analysis used six floral traits which were namely; anther length, anther breadth, number of pollen grains anther^{-1}, stigma length, stigma breadth and glume opening angle. All traits, were checked for normality where they had good approximations of normal distributions. The generated cluster divided the ten rice genotypes into two main groups based on some floral traits.

Table 4: Similarity matrix for ten rice varieties based on the six floral studied tarits.

Parental varieties	IR69625A	IR58025A	Pusa6A	G46A	Giza178R	Giza182R	GZ5121	GZ6296	PR2	PR78
IR69625A	0.00									
IR58025A	1.65.0	0.00								
Pusa6A	34.5	131.2	0.00							
G46A	28.3	193.3	62.3	0.00						
Giza178R	427.3	592.3	461.1	399.0	0.00					
Giza182R	353.2	188.1	319.3	381.4	780.4	0.00				
GZ5121	51.4	216.3	85.2	23.1	376.0	404.4	0.00			
GZ6296	37.8	127.6	3.8	65.8	464.7	315.7	88.7	0.00		
PR2	1177.8	612.8	1144.0	1206.1	1605.1	824.7	1229.1	1140.4	0.00	
PR78	1268.3	1103.3	1234.5	1296.6	1695.6	915.2	1319.6	1230.9	90.5	0.00
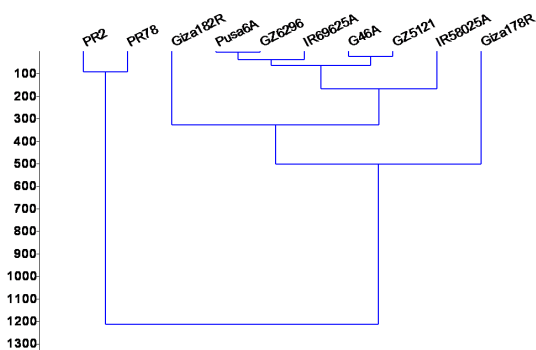
Figure 4: Cluster diagram for ten rice varieties classified by six floral studied traits.

The first group included PR2 and PR78, which gave the best results for all floral studied traits. The second group was divided into two sub groups based on all floral traits except glume opening angle. The first sub group, which was higher in these floral traits, included seven rice parental varieties IR69625A, IR58025A, Pusa6A, G46A, Giza182R, GZ5121 and GZ6296. The CMS line G46A and promising line GZ5121 of branch one were similar in all floral traits except stigma breadth. The three rice varieties IR69625A, Pusa6A and GZ6296 of branch one were similar in all floral traits except stigma length and glume opening angle. Giza182R as restorer variety was separated alone into on branch because it has larger anther length and no. of pollen grains anther-1. The

CMS line IR58025A was separated from the seven rice varieties in one branch based on no. of pollen grains anther-1. The second sub group included Giza 178R based on the lower in most of floral studied traits. These results are in agreement with similar results obtained by Anis (2009) and Abd El-Hadi *et al.,* (2013).

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السلوك الـوراثي والتحليل الشـجري العنقودي لبعض الصفات الزهريـة التي تؤثر على التلقيح الخلطي فى انتـاج تقاوي الأرز الهجين

أشرف حسين عبدالهادي[1] ، حمدى فتوح الموافى[2] و أسامة عبدالله البدوى[2]

1- قسم الوراثة كلية الزراعة- جامعة المنصورة ، مصر.

2- مركز البحوث والتدريب فى الأرز ، معهد بحوث المحاصيل الحقلية ، مركز البحوث الزراعية، مصر.

يعتبر تحسين التراكيب الوراثية الجيدة لصفات الزهرة في الأرز عامل هام ومؤثر فى عملية انتاج تقاوي الأرز الهجين. ولقد تم تهجين أربع سلالات عقيمة الذكر سيتوبلازمياً مع ستة تركيب وراثيه معيده للخصوبة ودلك للحصول على 24 هجيناً وذلك من خلال طريقة تزاوج عاملي السلالة فى الكشاف. وتم زراعة السلالات الأبوية والهجن الناتجة منها فى تصميم قطاعات كاملة العشوائية ذو ثلاث مكررات بالمزرعة البحثية لمركز البحوث والتدريب فى الأرز – سخا – كفر الشيخ خلال موسمين زراعيين هما 2011 و 2012. وتم تسجيل البيانات على ستة صفات زهرية مختلفة. وأظهرت النتائج وجود إختلافات عالية المعنوية بين التراكيب الوراثية المختلفة وتبين أن الفعل الوراثى المضيف كان أعلى من الفعل الوراثى السيادى (غير التجميعي) لصفة طول المتك وعدد حبوب اللقاح فى المتك وزاوية تفتح الزهرة مما يدل على أن الفعل الوراثى التجميعي هو الذى يتحكم فى وراثة تلك الصفات. وأوضحت النتائج ان المكافىء الوراثى فى المدى الواسع كان أعلى من المكافىء الوراثى فى المدى الضيق لكل الصفات المدروسة. كانت نسبة مساهمة تفاعل السلالات مع الكشافات لصفة عرض المتك (57.86%) ولصفة عرض الميسم (34.43%). وبتحليل الشجرة العنقودية للسلالات العشر تم تقسيمهم الى مجموعتين رئيسيتين وذلك حسب درجة التشابه بينهم.