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COMBINING ABILITY AND GENETIC ANALYSIS OF SOME QUANTITATIVE CHARACTERS IN RICE

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ABSTRACT

General combining ability (GCA), specific combining ability, (SCA) and genetic analysis were used in this study for F_1 generation obtained from half diall cross among six rice parents namely; Giza159, Giza176, Giza171 (old Egyptian varieties), Toride1, Fukuishiki (Japan differential varieties) and Sakha102 (released Egyptian varieties). Two field experiments were conducted at the Experimental Farm of Rice Research & Training Center, Sakha, Kafr El-Sheikh, Egypt, during 2004 and 2005 seasons. The results showed that both (GCA) and (SCA) variances were found to be highly significant for all nine characters studied in F_1 generations. This would indicate the importance of both additive and non-additive genetic variance in determining the performance of these nine characters.

Analysis by components of variation showed that additive (D) genetic variances were significant for all characters in F_1 generation except number of panicle/plant, grain yield/plant and 1000-grain weight. The two dominance components H1 and H2 were found to be highly significant for all traits studied in the F_1 generations. Also, the magnitudes of these components were found to be larger than those of the additive genetic variance. These results indicated that the dominance genetic variation had greater role in the inheritance of these traits

F value was positive in F_1 for all traits except number of panicles/plant and grain yield/plant. This indicates more dominant alleles present in the parental lines than recessive alleles in the F_1 generation. Dominance variance over all heterozygous loci (h^2) was significant in the 1000-grain weight and panicle weight in the F_1 generation.
The estimates of average degree of dominance $(H1/D)^{1/2}$ were found to be greater than unity for all traits under investigation in the F_1, indicating the presence of overdominance for these traits at F_1 generations.

Clustering analysis based on similarity of quantitative characters, produced two large groups: the first one included Giza171, while the second group was divided into two sub-groups: the first sub-group included Giza159, and Giza176. While, the second sub-group included Fukuishiki alone in branch. On the other hand, the second branch included Sakha102 and Toride1, which were similar in plant height and grain yield/plant.

Key words: *Combining ability Additive variance, Genetic analysis, Quantitative characters, Cluster analysis, Rice ,Oryza sativa*

INTRODUCTION

Rice (*Oryza sativa* L.) is the main staple food and a main source for calories for more than one-half of the world population (Alam *et al* 1998). In Egypt, rice is the second major field crop after wheat. The annual rice production is about 5-6 million tons and the present national average yield is 3.98 t/fadden (9.4 t/ha) (Badawi 2005). Increasing the yield is the main target for plant breeding programs via selecting the superior genotypes, which will transfer their desirable characteristics to next generations.

Combining ability implies the capacity of a parent to produce progenies when crossed with other parents (Fahmi *et al* 2005). In breeding programs, information on combining ability assess to know the nature of gene action, desirable parents and important quantitative traits may be found (Borgohain and Sharma 1998).

Consequently, the main objective of this research is to study combining ability (general and specific) and study of the inheritance of some quantitative characters in F_1 generations in rice.

MATERIALS AND METHODS

Six rice varieties viz, Giza159, Giza176, Giza171, Toride1, Fuknishiki, and Sakha102 were crossed in all possible combinations excluding reciprocals in 2004 season. The hybridization technique using the hot water method for emasculation was utilized (**Jodon (1938)** and **Butany 1961)**. The six parents and 15 F_1 were evaluated at the Experimental Farm of Rice Research & Training Center, Sakha, Kafr El-Sheikh Governorate, Egypt, during the rice growing season of 2005. Parents and hybrids were grown in a RCBD with three replication. Each plot contained three rows and each rows contained 25 plants growing spacing 20x20cm. Seeds were sowing at 30 days and transplanted to the permanent field. Parentage and country released under investigation are given in Table (1).

Table 1. Parentage, country of release and main characters of six parental lines.

Variety	Parentage	Country of release
Giza 159	Giza 14/Agami M1.	Egypt
Giza 176	Calrose 76/Giza 172//Gz 242	Egypt
Giza 171	Nahda / Calady 40	Egypt
Toride1	TKM1/NORIN 8*5	Japan
Fuknishiki	KINKIUS45/KINKIUS11//ZENTH/3/KINKIUS45/ KINKIUS11/4HATSUNISHIKI	Japan
Sakha 102	Gz 4098-7-1/ Giza 177	Egypt

Also, averages of two years of nine quantitative characters under study were used for constructing genetic relationships among rice varieties (Table 2).

Table 2. Six Parental rice cultivars and mean of different traits (Average of two years)

Parents	Heading date (days)	Plant height (cm)	No. of tillers /plant	No. of panicles /plant	Grain yield /plant (g)	1000-grain weight (g)	Panicle weight (g)	No. of filled grains /panicle	Panicle length (cm)
Giza 159	146.29	133.73	23.00	20.02	56.44	24.06	3.13	141.66	20.66
Giza 176	144.61	103.47	27.00	23.20	58.39	23.06	2.51	126.33	21.33
Giza 171	144.61	135.82	22.33	21.66	55.43	23.13	3.39	187.66	22.13
Toride1	133.55	113.20	20.66	19.75	53.52	23.73	2.26	159.00	22.90
Fukuishiki	121.77	138.80	21.33	20.20	44.33	23.96	2.20	166.00	22.93
Sakha 102	124.95	109.43	22.00	20.69	52.47	22.46	2.43	161.66	25.40

Analysis of field experiments data

Combining ability effects for F_1 were analyzed according to Griffing (1956) using Method 2 and Model one fixed model. The data obtained were also subjected to analysis described by Hayman (1954) to obtain more information about the genetic behavior of the traits under study. All statistical parameters and analysis of *variance* were computed by IRRISTAT and MSTAT-Cpc software. Genetic relationships among individuals and populations were measured by similarity of number of quantitative characters as reported by Zhang *et al* (1995), Dingkhuhn and Asch (1999) and El-Malky (2004). Clustering analysis was conducted using the Numerical Taxonomy and Multivariate Analysis system, Version 2.1 (NTSYSpc, Rolhf 2000). The output was analyzed using an agglomerative hierarchical clustering method with complete linkage strategy. Firstly, a matrix of dissimilaritv values was produced and the phenotypic distance between each pair of lines was estimated as Euclidean distance. Secondly, cluster analysis was then conducted on the Euclidean distance matrix with un-weighed pair-group method based on arithmetic average (UPGMA) to develop a dendogram.

RESULTS AND DISCUSSION

Analysis of variance

Table (3) presents the mean square values among F_1 and F_2 generations. The data showed that both general combining ability (GCA) and specific combining ability (SCA) variance were highly significant for all nine characters studied in F_1 generation. This would indicate the importance of both additive and non-additive genetic variance in determining the performance of these nine characters. The GCA/SCA ratio in F_1 were found to be greater than unity for heading date, plant height, number of tillers/plant, number of panicles/plant, grain yield/plant and number of field grains/panicle. Indicating that, additive and additive x additive types of gene action were of greater importance in the inheritance of these characters. The results concluded that selection procedures based on the accumulation of additive effects would be successful in improving these traits. Theses results were in agreements with those obtained by Anandakunar and Rangasamy (1984), Aidy *et al* (1986) Abd El-Aty (2001), El-Refaee (2002) and Hammoud (2004).

Table 3. Mean squares of general and specific combining ability and GCA/SCA for nine characters.

S.O.V.	d.f	Heading date (days)	Plant height (cm)	No. of tillers/plant	No. of panicles/plant
Replication	2	1.63	1.28	1.97	0.55
Genotypes	20	395.73**	474.30**	22.13**	13.24**
Error	40	0.63	4.77	1.53	0.73
GCA	5	341.23**	358.56**	14.41**	5.36**
SCA	15	62.14**	91.28**	5.03**	4.10**
Error	40	0.21	1.59	0.51	0.25
GCA/SCA		5.49	3.93	2.86	1.31

Table 3. Continued.

S.O.V.	d.f	Grain yield/plant	1000-grain weight	Panicle weight	No. of filled grains/panicle	Panicle length
Replication	2	14.21	1.55	0.10	9.38	0.0850
Genotypes	20	136.43**	8.57**	0.6904**	1409.08**	5.735**
Error	40	7.00	1.10	0.04	17.83	0.2354
GCA	5	100.98**	1.22**	0.09**	612.01**	1.4352**
SCA	15	26.98**	3.4021**	0.28**	422.25**	2.0751**
Error	40	2.33	0.37	0.01	5.94	0.08
GCA/SCA		3.74	0.36	0.31	1.45	0.69

General combining ability effects

Estimates of general combining ability effects for F_1 generation are presented in Table (4). Highly significant negative values of GCA for heading date and plant height would be of interest from the plant breeder point of view. However, the positive value of GCA effects would be useful for the other traits and could be used as a good donor for transferring these characters to their offspring.

Table 4. Estimate of GCA effects for the parental lines at F_1 generation for nine characters in rice

Parents	Heading date (days)	Plant height (cm)	No. of tillers/plant	No. of panicles/plant
Giza 159	5.27**	3.88**	1.18**	0.16
Giza 176	6.62**	-7.20**	2.01**	1.32**
Giza 171	4.35**	9.60**	-0.82**	0.32**
Toridel	-2.64**	-3.66**	0.01	-0.16
Fuknishiki	-9.674**	3.60**	-1.07**	-1.07**
Sakha 102	-4.29**	-6.22**	-1.32**	-0.56**
L.S.D. at 0.05	0.148	0.407	0.318	0.160
at 0.01	0.229	0.631	0.492	0.247

Table 4. continued.

Parents	Grain yield/plant	1000-grain weight	Panicle weight	No. of filled grains/panicle	Panicle length
Giza 159	2.70*	0.15	-0.04*	-10.56**	-0.15**
Giza 176	3.21**	-0.60**	0.08**	-5.51**	-0.53**
Giza 171	-2.14**	-0.31**	0.17**	12.19**	-0.42**
Toridel	3.16**	0.42**	-0.07**	-2.72**	0.28**
Fuknishiki	-5.32**	0.31**	-0.09**	-2.31**	0.46**
Sakha 102	-1.61**	0.03	-0.06**	8.90**	0.35**
L.S.D. at 0.05	0.493	0.195	0.036	0.787	0.090
at 0.01	0.764	0.302	0.057	1.219	0.140

As for heading date, the three rice varieties Toridel, Fuknishiki and Sakha102 showed highly significant negative estimates of GCA effects in F_1 generation proving to be good general combiners for developing early genotypes. The rice varieties Giza176, Toridel and Sakha102 exhibited highly significant desirable negative estimates of GCA effects for plant height in F_1 generation proving to be good general combiners for developing short stiff genotypes. Concerning number of tillers per plant and number of panicles per plant, Giza176 proved to be good general combiners in both the F_1 generation. Desirable highly significant GCA effects were detected by Giza159 and Giza176 for grain yield per plant, by Fuknishiki for 1000-grain weight, by Giza171 for panicle weight, by Giza171 and Sakha102 for number of filled grains per panicle and Sakha102 for panicle length in F_1 and proving to be good general combiners in this respect.

Specific combining ability effects

Estimates of specific combining ability effects from F_1 generation are shown in Table (5). SCA for heading date was negative and highly

Table 5. Specific combining ability (SCA) of 15 crosses for nine agronomic characters.

Crosses	Heading date (days)	Plant height (cm)	No. of tillers /plant	No. of panicles /plant	Grain yield /plant (g)	1000-grain weight (g)	Panicle weight (g)	No.of filled grains /panicle	Panicle length (cm)
Giza 159x Giza 176	-3.83**	-14.76**	-12.40**	1.89**	2.66**	1.32**	0.19**	-8.71**	.87**
Giza 159x Giza 171	2.28**	5.64**	5.14**	0.30	-0.72	-1.24**	-0.03	-16.08**	1.86**
Giza 159x Toridel	8.21**	-0.77	-3.07**	-0.88**	5.85**	-0.87**	-0.11*	-19.17**	-0.68**
Giza 159x Fuknishiki	-12.24**	11.62**	12.47**	1.05**	-4.44**	2.14**	-0.36**	5.42**	2.15**
Giza 159x Sakha 102	7.32**	-7.97**	4.59**	1.14**	1.89**	0.12	-0.16**	7.88**	-0.25
Giza 176x Giza 171	8.00**	13.58**	-6.07**	1.58**	3.68**	-1.45**	-0.47**	-11.21**	0.98**
Giza 176x Toridel	-1.10**	12.28**	1.42	0.38	-0.26	2.09**	0.49**	37.79**	-0.52**
Giza 176x Fuknishiki	2.478**	-6.56**	10.33**	-1.34**	3.15**	-2.87**	0.49**	-11.29**	0.37**
Giza 176x Sakha 102	4.42**	5.40**	5.95**	-0.73**	-5.85**	1.35**	0.53**	-8.83**	-0.63**
Giza 171x Toridel	-10.93**	-8.07**	1.06	1.68**	-2.77**	0.69**	-0.53**	-13.25**	0.90**
Giza 171x Fuknishiki	-6.47**	-6.70**	0.91	1.51**	-10.09**	0.36	0.70**	-31.33**	-0.88**
Giza 171x Sakha 102	-13.25**	7.10**	2.66**	-4.18**	-2.23**	3.15**	0.17**	17.79**	-2.91**
Toridelx Fuknishiki	-0.97**	-5.58**	-1.74	-2.24**	8.37**	2.20**	0.67**	-19.42**	0.72**
Toridelx Sakha 102	-0.33	6.80**	1.11	3.83**	1.73**	-0.91**	0.61**	-19.96**	0.79**
Fuknishiki x Sakha 102	6.59**	-10.29**	-5.51**	-0.75**	0.38	0.49	-0.33**	10.29**	-0.52**
L.S.D. at 0.05	0.407	1.118	1.986	0.439	1.354	0.536	0.100	2.16.	0.248
at 0.01	0.459	1.261	2.240	0.495	1.528	0.604	0.113	2.438	0.279

significant in seven crosses in F_1 generation. The best cross combinations for earliness were (Giza171 x Sakha102), (Giza159 x Fuknishiki), (Giza171 x Toridel) and (Giza171 x Fuknishiki), which indicated that one of these combinations could be useful for selecting early maturing lines. Concerning plant height, seven crosses were highly significant and negative in F_1 and the best crosses were (Giza159 x Giza176) and (Fuknishiki x Sakha102) in F_1 generation. While, for number of tillers per plant the best cross was (Giza176 x Toridel), which gave highly significant positive estimates of SCA effects.

As for grain yield per plant, six crosses showed highly significant positive SCA effects in F_1 and ranged between 1.887 and 8.369, and the best cross was (Giza176 x Fuknishiki).

As for 1000-grain weight, the crosses (Giza171 x Sakha102) and (Giza159 x Giza176) showed highly significant positive SCA effects.

Concerning panicle weight, the best hybrids were (Giza176 x Toridel), (Giza176 x Fuknishiki), (Giza176 x Sakha102) and (Giza171 x Fuknishiki) where highly significant positive SCA effects were detected, while in number of filled grains per panicle, the best crosses were (Giza159 x Fuknishiki), (Giza159 x Sakha102) and (Giza176 x Toridel) which gave highly significant positive SCA effects. While, in panicle length the best hybrids was (Giza159 x Fuknishiki), (Giza176 x Fuknishiki) and (Giza171 x Toridel).

From the previous data it observed that the best genotypes which showed desirable SCA effects could be obtained from crossing good by good, good by low and low by low general combiners. Similar conclusion was drawn by Rao *et al* (1980); Ramalingam *et al* (1993), Abd El-Aty (2001), El-Refaee (2002) El-Malky (2004) and Hammoud (2004).

Analysis by components of variation

The estimated genetic components of variation for all characters studied in F_1 generations are shown in Table (6). Additive (D) genetic variances were significant for all characters in F_1 generation except number of panicle/plant, grain yield/plant and 1000-grain weight. The two dominance components H1 and H2 were found to be highly significant for all traits studied. Also, the magnitudes of these components were found to be larger than those of the additive genetic variance. These results indicated that the dominance genetic variation had greater role in the inheritance of these traits. Similar results for different traits were reported by Roy and Panuwar (1997), Surek and Korkut (1998), Chauhan *et al* (1994), Abd-Aty *et al* (2002), El-Refaee (2002) and Hammoud (2004).

Table 6. Estimate of genetic parameters in F_1 for nine characters in rice

Source of variance	Heading date (days)	Plant height (cm)	No. of tillers/plant	No. of panicles/plant
(D) Additive effect	169.10 ± 22.47**	236.15 ± 33.64**	4.52 ± 1.94*	1.45 ± 2.02
H_1	271.37 ± 57.04**	388.40 ± 85.41**	20.88 ± 4.92**	16.39 ± 5.13**
H_2	218.88 ± 50.95**	334.32 ± 76.30**	16.06 ± 4.40**	14.72 ± 4.59**
h_2	16.74 ± 34.29	0.171 ± 51.35	2.30 ± 2.96	1.45 ± 3.08
(F) Gene distribution	37.46 ± 54.89	117.17 ± 82.19	0.30 ± 4.74	-0.26 ± 4.94
(E) Environmental effects	0.226 ± 8.493	1.535 ± 12.716	0.518 ± 0.733	0.241 ± 0.765
$(H1/D)^{1/2}$	1.266	1.282	2.149	3.356
$H2/4H_1$	0.2016	0.2151	0.1922	0.2245
KD/KR	1.191	1.479	1.0314	0.947
r	0.776**	0.348	0.355	0.156
H.ns	62.62	50.41	49.93	30.12
H.bs	99.84	99.10	94.27	95.69

Table 6. Continued

Source of variance	Grain yield/plant	1000-grain weight	Panicle weight	No.of filled grains/panicle	Panicle length
(D) Additive effect	21.82 ± 14.09	1.35 ± 0.94	0.22 ± 0.11*	1198.0±415.79**	2.642±1.20**
H_1	118.01 ± 35.77*	11.90 ± 2.38**	1.11 ± 0.28**	3825.62±1055.54**	9.30±3.04**
H_2	86.28 ± 31.96*	11.34 ± 2.13**	0.87 ± 0.25**	3268.18±942.94**	6.63±2.72**
h_2	-1.09 ± 21.51	6.29 ± 1.43**	0.51 ± 0.17**	2191.55±634.66**	0.73±1.83
(F) Gene distribution	-13.20 ± 34.43	-0.18 ± 2.29	0.42 ± 0.27	548.95±1015.79	4.60±2.93
(E) Environmental effects	2.447 ± 5.326	0.372 ± -0.355	1.368 ± 4.237	65.937±157.157	7.558±0.454
$(H1/D)^{1/2}$	2.325	29.676	2.223	1.786	1.876
$H2/4H_1$	0.1827	0.2382	0.1959	0.2370	0.1782
KD/KR	0.769	0.623	2.492	1.294	2.735
r	0.342	0.0184	0.398	0.349	0.388
H.ns	58.15	10.58	71.11	30.31	16.84
H.bs	95.73	89.61	94.54	95.27	96.37

A positive F value indicates an excess of dominant genes, while negative value indicates an excess of recessive genes. In this study F value was positive in F_1 for all traits except number of panicles/plant and grain yield/plant. This indicates that more dominant alleles are present in the parental lines than recessive alleles in the F_1 generation.

These results indicated the excess of dominant genes controlling these traits. Dominance variance over all heterozygous loci (h^2) was significant in the 1000-grain weight and panicle weight in the F_1 generation. In conclusion, significant values of (h^2) indicating the prevalent of dominance effect over all loci in all crosses, while insignificant values indicating the absence of the dominance effect over all loci in the heterozygote's and that could be due to the presence of a considerable amount of canceling dominance effects in the parental varieties. The results agreed with El-Abd (1999), El-Refaee (2002) and Hammoud (2004).

The estimates of average degree of dominance $(H1/D)^{1/2}$ were found to be greater than unity for all traits under investigation in the F_1, indicating the presence of over dominance in the inheritance of these traits at F_1.

The estimates of H2/4H1 ratio did not reach the ratio 0.25 for all characters and ranged between 0.17 to 0.23 in F_1, indicating that genes having positive and negative effects were not equally distributed in the parents.

The proportion of dominant and recessive alleles in the parents (KD/KR) was greater than unity in all characters except number of tillers/plant, grain yield/plant and 1000-grain weight, indicating that the proportions of dominant alleles were greater for these characters in F_1 generation. El-Abd (1999), El-Refaee (2002) and Hammoud (2004) found similar results.

The environmental component (E) was insignificant indicating that these characters were affected by the environmental components with different degrees.

The correlation coefficients (r) between the parental lines (Yr) and the parental order of dominance (Wr+Vr) for all the characters studied according to Hayman (1954) are given in Table (6). The results showed that correlation coefficients were highly significant and positive for heading date and number of filled grains/panicle in F_1, indicating that the decreaser genes were dominant over the increaser ones. On the other hand, number of panicle/plant was highly significant and negative; this means that the dominance genes were associated with high mean expression. According to Hayman (1954), if the correlation between parental mean values and Wr+Vr is small, it means that the genes with positive and negative effects in the parental lines could be in equal proportions.

Heritability in narrow sense value is an indicator of the efficiency of selection in identifying the best genotypes. Heritability in both broad and narrow senses in F_1 generation are shown in Table (6). Heritability estimates in broad sense were found to be high for all characters. While, heritability in narrow sense were found to be lower than those of broad sense, indicating the importance of non-additive genetic variance in the inheritance of these characters. Therefore, it could be concluded from Hayman (1954) analysis and combining ability analysis that selection procedures which are known to be effective in shifting gene frequency when both additive and non-additive genetic variation are involved would be successful in improving the most traits under examination. These results agreed with those obtained by Kumar *et al* (1994), El-Hissewy and El-Kady (1992), Main *et al* (1997), Rather *et al* (1998), El-Refaee (2002), Hammoud (2004) and Sedeek (2006).

Clustering of the varieties based on agronomic characters

The characters used for this purpose in the present study were the same agronomical quantitative characters, which were studied in the previous two analyses. Normality was checked for all traits, which indicated that all traits had good approximations of normal distributions (Fahmi *et al* 2005).

Clustering varieties, based on similarity of quantitative characters, produced two large groups (Fig.1). The first one included Giza171, while the second group was divided into two sub-groups, the first sub-group included Giza159, and Giza176, which were similar in heading date and grain yield/plant. While, the second sub-group included Fuknishiki, which was in lonely due to its tallest in plant height, highest one in number of filled grains/panicle and lowest one in the grain yield/plant. On the other hand, the second branch included Sakha102 and Toride1, which were similar in plant height and grain yield/plant

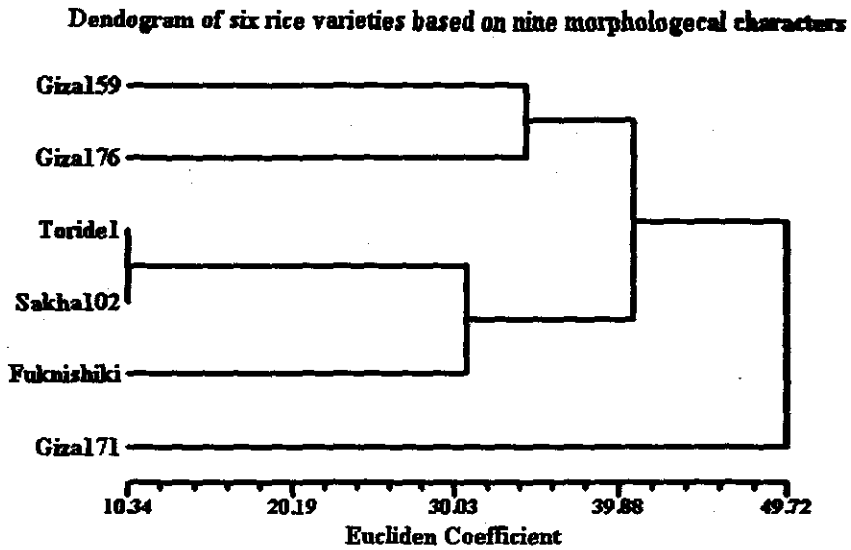

Figure 1. Cluster diagram for six varieties classified by nine morphological quantitative characters.

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القدرة على الائتلاف والتحليل الوراثي لبعض الصفات الكمية في الأرز

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مركز البحوث والتدريب في الأرز – معهد بحوث المحاصيل الحقلية – مركز البحوث الزراعية

أستخدم في هذا البحث أصناف الأرز الست وهم جيزة 159 وجيزة 171 وجيزة 176 وتوريدي واحد وفيوكونيشكي وسخا 102 وتم الحصول على 15 هجين منها فى الجيل الاول.

واستخدمت القدرة العامة والخاصة والتحليل الوراثي للجيل الأول وقد أجريت هذه الدراسة في مركز البحوث والتدريب في الأرز – سخا – كفر الشيخ – مصر وذلك خلال موسمي 2004، 2005 وقد وجد من نتائج تحليل التباين أن كلا من القدرة العامة والخاصة على الائتلاف كانت عالية المعنوية وهذا يشير إلى أهمية الفعل الوراثي المضيف والغير مضيف للصفات التسع المدروسة.

وقد أظهرت نتائج تحليل مكونات التباين أن التباين الوراثي المضيف كان معنويا لكل الصفات في الجيل الأول ما عدا صفة عدد السنابل بالنبات الفردي ، ومحصول النبات الفردي ، ووزن الألف حبة. كما كانت تأثيرات السيادة (H1&H2) عالية المعنوية لكل الصفات المدروسة في الجيل الأول. كما وجدت أهمية هذه المكونات أكثر من التباين الوراثي المضيف. وهذه النتائج تشير إلى أهمية دور الفعل السيادي في توارث هذه الصفات.

كما كانت قيمة F موجبة في الجيل الأول لكل الصفات ما عدا صفة عدد السنابل بالنبات الواحد ومحصول النبات الفردي. وهذا يشير إلى أن الاليلات السائدة كانت أكثر من الاليلات المتنحية للآباء في الجيل الأول.

كما وجد أن التباين السيادي عالي المعنوية في وزن الألف حبة ، ووزن السنبلة في الجيل الأول.

كما كانت درجات السيادة اكبر من الواحد الصحيح لكل الصفات المدروسة في الجيل الأول مما يشير إلى وجود السيادة الفائقة في هذه الصفات في الجيل الأول.

وقد أظهرت الشجرة الناتجة عن درجة التشابه في الصفات الكمية انقسامها إلى مجموعتين كبيرتين.

المجموعة الأولى شملت الصنف جيزة 171 فقط ، بينما المجموعة الثانية انقسمت إلى تحت مجموعتين حيث احتوت تحت المجموعة الأولى الصنفين جيزة 159 وجيزة 176. بينما تحت المجموعة الثانية انقسمت إلى فرعين الأول شمل الصنف فيكو نشكى فقط ، وعلى الجانب الأخر وجد الصنفين سخا 102 والصنف توريدى1 معا بدرجة تشابه عالية وهذا يرجع إلى التشابه بينهما في صفة طول النبات ومحصول النبات الفردي.

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