

ESTIMATION OF GENETIC COMPONENTS, HERITABILITY AND CLUSTER ANALYSIS FOR SOME AGRONOMIC CHARACTERS IN RICE.

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ABSTRACT

Nine parents of rice were crossed to obtain 36 F₁ hybrids, through half diallel cross. These parents included one exotic variety, four commercial varieties and four promising lines. Hayman's 1954 method was employed for this purpose. The nine parents and their F₁s were grown in randomized complete block design with three replications at the Rice Research and Training Center Farm, Sakha, Kafr El-Sheikh, Egypt. Results revealed highly significant mean squares for all characters, suggesting the presence of genetic differences among genotypes for all studied traits. Significant or highly significant and positive of additive component (D) for all characters except for panicle weight and number of panicles plant⁻¹ were found. The dominance components H₁ and H₂ were highly significant for all characters studied. The environmental component (E) was insignificant for all characters except spikelet fertility% and grain yield plant⁻¹. Heritability estimates in broad sense were high for all studied characters. The nine parents were distinctly classified into five clusters (below 25 Euclidean distance) according to the similarity.

INTRODUCTION

Rice is one of most important grains in the world. It is not only a stable food, but also contributes major economic activity and a key source of income and employment for the rural population. Also, rice is considered the main food for all human ages because its grains are rich in protein, minerals, vitamins and fiber (Alam *et al*, 1998). The total rice production in Egypt reached 6.6 million tons with a national average of 10.00 ton/ha. This average ranked the first among the rice producing countries in the world. Rice production should be increased by about 60% by the year 2025 to feed the additional rice consumers (Duwayri *et al*, 1999)

MATERIALS AND METHODS

These studies were conducted at Rice research and training center (RRTC), Sakha, Kafr El-Sheikh, Egypt during the two successive rice seasons 2010 and 2011 to estimate the genetic components, heritability and cluster analysis for agronomic characters in rice. The experimental materials were one exotic variety (HR5824-B-3-2-3), four commercial varieties (Giza 177, Sakha 101, Sakha 104 and Giza 171) and four promising lines (GZ 6910-28-1-3-1, GZ 7685-8-1-3-2, GZ 6522-15-1-1-3 and GZ 6903-1-2-2-1). A half diallel cross was conducted among the nine parents in 2010 season to produce 36 crosses in 2011 season. The parental varieties and the resulting 36 crosses were evaluated in a Randomized Complete Block Design (RCBD)

experiment with three replications. Each replication contained 25 individual plants with spaced at 20 cm among rows and 20 cm among plants. All agronomic practices such as land preparation, fertilizer application, weeding and pest control were done as recommended with rice crop during both seasons of the study. The nine parents were evaluated for following agronomic traits; days to maturing, plant height (cm), chlorophyll content, number of panicles plant⁻¹, panicle length (cm), panicle weight (g), 1000-grain weight (g), spikelet fertility (%) and grain yield plant⁻¹.

Statistical analysis:

The genetic components of variation were calculated, by using Hayman's procedure (1954) and presented by Singh and Chaudhary (1977):

D = Components of variation due to additive gene effects.

F = Mean of covariance of additive and dominance effects over the arrays

H₁ = Component of variation due to dominant gene effects.

H₂ = Dominance indicated asymmetry of positive and negative effects;

Where :

$$H_2 = H_1 \{1 - (U - V)^2\}$$

U = Proportion of positive genes in the parents.

V = Proportion of negative genes in the parent { or of the genes with positive (negative) effects } and where **U+V = 1**.

h² = Dominance effects (as the algebraic sum over all loci in heterozygous phase in all crosses).

E = Component of variation due to environmental effects.

The estimate of three components of genetic variation were determined using the following equations :

$$D = V_{oLo} - E$$

$$F = 2V_{oLo} - 4W_{oLo} - 2(n-2) E/n,$$

$$H_1 = V_{oLo} - 4W_{oLo} + 4V_{iLi} - (3n-2) E/n,$$

$$H_2 = 4 V_{iLi} - 4V_{oLi} - 2E,$$

$$h^2 = 4(M_{Li} - M_{Lo})^2 - 4(n-1) E/n^2.$$

Where:

$$E = \text{Environmental effect} = \left[\frac{\text{Error SS} + \text{Re p SS}}{\text{Error df} + \text{Re p df}} \right] / \text{No. of replications}$$

V_{oLo} = Variance among parents.

V_r = The variance of one array (rth array).

V_{iLi} = Mean variance of the arrays.

W_r = The covariance between the parents and their off-spring in one array (rth array).

W_{oLo} = Mean covariance between the parents and arrays.

V_{oLi} = Variance of the mean of arrays.

(M_{Li} - M_{Lo}) = difference between mean of the parents and mean of their n² progeny.

Test of significance among parameter estimates were made using the standard error estimation technique suggested by Hayman (1954). The above estimates were then used in computing other parameters following Hayman (1958):

$(H_1/D)^{1/2}$ = The mean degree of dominance at each locus.

$H_2/4H_1$ = The ratio of genes with positive and negative effects in the parents.

$K_D/K_R = \{(4DH_1)^{1/2} + F\} / \{(4DH_1)^{1/2} - F\}$

= The ratio of dominance and recessive genes in the parents.

The estimates of heritability:

The heritability estimates were computed following the formula of Mathers and Jinks (1982).

1- Broad sense heritability (H_{bs}) :

$$H_{bs} = \frac{1/2D + 1/2H_1 - 1/4H_2 - 1/2F}{1/2D + 1/2H_1 - 1/4H_2 - 1/2F + E}$$

2- Narrow sense heritability (H_{ns}) :

$$H_{ns} = \frac{1/2D + 1/2H_1 - 1/2H_2 - 1/2F}{1/2D + 1/2H_1 - 1/4H_2 - 1/2F + E}$$

RESULTS AND DISCUSSION

Mean performance:

Mean performance of the nine parents and their F₁ of the diallel cross for the nine studied characters are presented in Table (1).

As revealed in the Table (1), the mean performance for the a forenamed characters, varied from cross to cross combination. For No. of days to maturity, the F₁ mean values of most of crosses (27 crosses) were intermediate between the two parents involving indicating partial or no dominance effect. It was noticed that four of the F₁ mean values were in direction of earlier parents. This in turn suggested that earliness was dominant over lateness for these crosses. On the other hand, five crosses were towards the lateness. Complete to over dominance was observed in most of the crosses towards taller parents for plant height (21 crosses), put only two crosses exhibited dominance effect towards the shorter parents. However, plant height character of the rest 13 crosses was show intermediate between the two parents involved. Regarding the chlorophyll content character, different results were obtained. The F₁ mean values of 20 crosses were towards higher parents, while three only were tended towards lower parents. However, 11 crosses were intermediate between the two parents involved.

Regarding the panicle length results in Table (10), clearly showed that out of 36 crosses, 23 have their mean values intermediate to the their respective parents. However, the F₁ means of nine different crosses tended towards higher parents, while four crosses tended to the lower parents. For the spikelet fertility % (Table 10), results indicated that the three parents, Gz6522-15-1-1-3 (96%), Giza 177 (94%) and Gz6910-28-1-3-1 (92%) and the crosses, Giza 177 x Gz7685-8-1-3-2 (96%), HR5824-B-3-2-3 x Gz6522-15-1-1-3 (96%) and Gz7685-8-1-3-2 x Gz6903-1-2-2-1 (96%) showed the highest mean values in this respect.

Table 1 : Mean performance of parental varieties and their F₁ crosses for all characters under study.

Genotypes	DM	PH (cm)	CC	No. pp	PL (cm)	PW (g)	SF (%)	1000- GW (g)	GYP (g)
1 Giza 177	120	100	44.37	19	20	3.70	94	28.00	47.14
2 Sakha 101	141	92	48.97	20	24	4.13	89	27.30	42.16
3 Sakha 104	130	108	46.63	24	22	3.93	91	27.10	46.07
4 Giza 171	102	136	30.73	28	23	4.13	90	20.00	09.70
5 HR 5824-B-3-2-3	109	83	37.43	22	20	3.17	90	20.07	34.44
6 GZ 6910-28-1-3-1	136	100	40.60	26	20	3.90	92	29.27	60.00
7 GZ 7685-8-1-3-2	120	99	40.80	20	20	3.47	86	30.07	07.93
8 GZ 6522-15-1-1-3	120	104	40.80	21	26	3.70	96	27.67	64.09
9 GZ 6903-1-2-2-1	131	99	42.07	28	24	4.00	86	27.67	64.07
F₁ hybrid									
1 X 2	139	116	42.47	28	24	0.90	93	29.67	48.77
1 X 3	124	111	42.63	24	22	4.20	93	27.27	40.47
1 X 4	138	134	41.23	37	20	4.20	91	27.40	66.03
1 X 5	120	106	44.77	29	21	3.00	94	20.87	02.07
1 X 6	130	107	46.93	32	23	0.77	94	29.07	09.03
1 X 7	120	111	42.00	38	21	4.37	96	29.70	60.00
1 X 8	122	100	43.03	44	21	4.40	93	29.17	40.90
1 X 9	133	90	44.90	37	24	6.00	94	30.43	41.47
2 X 3	130	107	46.23	28	22	0.03	88	28.67	42.93
2 X 4	143	137	40.27	30	20	0.13	89	24.47	44.70
2 X 5	130	111	42.43	26	23	4.43	87	29.97	63.40
2 X 6	140	101	46.63	33	24	4.70	90	29.00	04.03
2 X 7	120	108	42.80	38	20	0.23	93	27.17	49.17
2 X 8	136	111	48.80	39	20	4.00	93	28.03	42.07
2 X 9	134	111	43.47	34	23	0.27	92	28.30	41.30
3 X 4	141	140	40.13	40	26	6.00	94	27.77	42.43
3 X 5	120	103	44.20	37	21	3.63	90	29.87	62.63
3 X 6	136	100	40.13	38	23	3.90	89	31.30	68.03
3 X 7	122	107	43.23	37	24	0.10	94	28.27	40.87
3 X 8	124	109	48.77	44	23	4.70	92	30.20	41.40
3 X 9	137	111	43.00	39	23	4.23	87	27.77	43.87
4 X 5	136	110	39.13	31	23	3.17	84	24.80	61.90
4 X 6	146	129	43.77	34	24	0.47	92	27.40	40.23
4 X 7	124	122	44.70	42	21	4.90	95	24.23	64.00
4 X 8	137	139	40.27	40	20	4.90	93	27.07	42.17
4 X 9	140	136	44.70	36	20	0.00	92	27.60	68.33
5 X 6	130	97	40.97	33	23	3.37	90	27.00	44.33
5 X 7	120	97	41.37	30	21	3.60	90	27.37	00.90
5 X 8	118	106	43.80	31	21	4.20	96	29.03	49.47
5 X 9	124	100	43.73	39	21	4.67	94	27.30	48.13
6 X 7	128	100	42.00	30	23	4.73	91	30.40	43.40
6 X 8	130	101	49.67	38	20	4.00	90	28.23	47.00
6 X 9	138	100	46.13	37	20	4.93	90	29.90	80.70
7 X 8	120	107	40.13	36	24	4.60	87	28.00	42.43
7 X 9	121	106	40.93	27	24	4.93	96	29.40	69.10
8 X 9	126	113	47.10	39	24	4.03	94	29.10	63.67

Abbreviations: DM₁ days to maturing; PH₁(cm)₁ plant height; CC₁ chlorophyll content; No. PP, No-of panicles per plant; PL(cm), Panicle length; PW(g), Panicle weight; SF%, spikelet fertility%; 1000-GW(g), 1000-grain weight and GYP(g) grain yield per plant.

Regarding panicle weight results showed that, the three parents Sakha 101, Giza 171 and Gz6903-1-2-2-1 gave the highest mean values

(more than 4 g). The crosses, Giza 177 x Gz6903-1-2-2-1, Sakha 104 x Giza 171, Giza 177 x Sakha 101, Giza 177 x Gz6903-1-2-2-1, and Giza 171 x Gz6903-1-2-2-1 gave highest mean values of more than (5.50 g).

Concerning 1000-grain weight, the parents Gz7685-8-1-3-2, Gz6910-28-1-3-1 and Giza 177 showed the results clearly indicated that highest mean values of 30.07, 29.27 and 28.00 g, respectively, while the crosses, Sakha 104 x Gz6910-28-1-3-1, Giza 177 x Gz6903-1-2-2-1, Gz6910-28-1-3-1 x Gz7685-8-1-3-2 and Sakha 104 x Gz6522-15-1-1-3 gave heaviest weight of 1000-grain and ranged from 30.20 to 31.30 g and were superior in this respect. The highest grain yield per plant was obtained from the crosses, Sakha 101 x Giza 171 (84.70 g), Sakha 104 x Gz6903-1-2-2-1 (83.87 g), Sakha 101 x Sakha 104 (82.93g), Sakha 101 x Gz6522-15-1-1-3 (82.57 g), Sakha 104 x Gz6522-15-1-1-3 (81.40 g) and Gz6910-28-1-3-1 x Gz6903-1-2-2-1 (80.70 g). However, the lowest were estimated for the crosses, HR5824-B-3-2-3 x Gz6910-28-1-3-1, HR5824-B-3-2-3 x Gz6903-1-2-2-1 and HR5824-B-3-2-3 x Gz6522-15-1-1-3 with values of 44.33, 48.13 and 49.47 g per plant. The parental lines Sakha 101 and Sakha 104 manifested highest mean performance of 72.16 and 66.57 g, respectively, for the grain yield.

Analysis of variances:

The analysis of variance for the studied characters calculated and the results presented in Table (2) showed that the genotypes mean square were found to be larger than their corresponding mean square for the error. Moreover, the results of F-test values. These findings indicated the presence of large variations among them. Similarly, the results indicated that the mean square of parents and crosses showed highly significant for all characters. These findings indicated overall wide differences among these populations. Parents Vs crosses mean squares indicated that the average heterosis could be highly significant in all crosses for all agronomic characters except days to maturing and panicle length.

Table 2 : The estimates of mean square of ordinary analysis for all characters under study.

s.o.v	d.f	Days to maturing (days)	Plant height	Chlorophyll content (SPAD)	No. of panicles /plant	Panicle length
Replication	2	1.49	14.29	4.51	11.65	0.19
Genotypes	44	241.77**	504.07**	24.43**	138.85**	14.41**
parents	8	473.73**	626.04**	37.73**	35.01*	48.35**
crosses	35	195.65**	441.19**	17.19**	87.02**	6.97**
P vs F ₁	1	0.03	1729.35**	171.25**	2783.47**	3.42
Error	88	1.40	12.58	1.73	14.68	1.00

*, ** significant at 0.05 and 0.01 level of probability, respectively.

Table 2 : Continued.

s.o.v	d.f	Panicle weight	Spikelet fertility (%)	1000-grain weight	Grain yield/plant
Replication	2	0.02	821.34	0.52	120.25
Genotypes	44	1.77**	3612.00**	9.42**	400.04**
parents	8	0.31**	3961.68**	7.93**	386.83**
crosses	35	1.69**	2794.21**	9.58**	352.27**
P vs F ₁	1	16.19**	29437.35**	15.64**	2177.39**
Error	88	0.02	268.54	0.18	51.21

*, ** significant at 0.05 and 0.01 level of probability, respectively.

Estimates of genetic components and heritability:

Table (3) and (4) present the genetic components and heritability of nine agronomic characters under investigation. Significant or highly significant and positive values of additive component (D) for all characters except panicle weight and number of panicles plant⁻¹. Moreover, the dominance component H₁ and H₂ were highly significant for all characters studied and ranged between (1.70±0.38) for panicle weight and (2053.43±311.85) for spikelet fertility % of H₁ and ranged between (1.47±0.33) and (1858.53±268.08) of H₂ for the former characters, respectively. These results indicated that both additive and dominance components were observed to contribute in the expression of all studied characters except for number of panicles per plant and panicle weight. The magnitude of H₁ was more than H₂ in all characters indicating that at most loci the positive and negative alleles were in equal proportion. However, these results were in general agreement with those reported by El-Mowafi (1994), Hammoud (1996), El-Refaee (2002) and Hammoud (2004).

Dominance variance over all heterozygous loci (h₂) was highly significant for all characters except days to maturing and panicle length indicating that dominance was unidirectional, while was not unidirectional for days to maturing and panicle length El-Refaee (2002). The estimates of (F) were insignificant and negative for plant height, panicle weight and grain yield plant⁻¹ and not significant and positive for number of panicles plant⁻¹ spikelet fertility % and 1000-grain weight suggested that dominant and recessive genes were in equal proportion. On the contrary, (F) value was significant and highly significant for days to maturing, chlorophyll content and panicle length, revealing that there was asymmetric gene distribution with an excess of dominant alleles as compared with recessive ones in the parents. The environmental component (E) was insignificant for all characters except spikelet fertility% and grain yield plant⁻¹ and differed in its magnitude indicating that these characters are affected by environmental components with different degrees.

Estimates of the mean degree of dominance (H₁/D)^{1/2} were over one for all characters studied except days to maturing, plant height and panicle length. This finding indicating that over dominance and epistatic gene effects played a major role in the inheritance of this traits. The estimates of (H₂/4H₁) ratio did not reach the ratio 0.25 in case of all the characters and ranged between 0.14 to 0.23 for panicle length and grain yield per plant, respectively, indicating that genes having positive and negative effects were equally distributed in the parents.

The ratio of the total number of dominant to recessive alleles in the parents (K_D/K_R) was less than unity for plant height (0.868), panicle weight (0.571) and grain yield plant⁻¹ (0.658) indicating an excess of dominant alleles as compared with recessive ones in the parents, while it was more than one for all other characters indicating that proportion of dominant alleles was greater.

Heritability estimates (Table 4) in broad sense were high for all studied characters while, heritability estimates in narrow sense was relatively high for days to maturing (85.69 %), plant height ((76.74 %) and grain yield plant⁻¹ (60.22%). This further suggested that a major part of the total phenotypic variance for these characters was due to additive genetic variance. Accordingly, it is expected that an effective phenotypic selection for these characters can be achieved with satisfactory degree of accuracy. In case of chlorophyll content and number of panicles plant⁻¹, the estimates of such parameter were low and gave the values of 31.70 and 20.54, respectively. This further suggested that a major part of the total phenotypic variance for these characters was due to dominance genetic variance and environmental effects. These finding led to conclusions the selection for such characters must be done in the late generations. These results in general agreement with those reported by El-Mowafi (1988), El-Mowafi (1994), Kumar *et al.* (1994), El-Refaei (2002), Hammoud (2004), Awad Allah (2006) and Abd Allah (2008).

Table 4 : The estimates of heritability in both broad and narrow sense for all agronomic characters studied.

Agronomic characters	Broad sense heritability (Hbs)	Narrow sense heritability (Hns)
Days to maturing (days)	99.42	85.69
Plant height (cm)	97.62	76.74
Chlorophyll content (SPAD)	92.59	31.70
No. of panicles per plant	89.34	20.54
Panicle length (cm)	92.23	54.63
Panicle weight (g)	99.03	41.93
Spikelet fertility(%)	92.45	54.98
1000-grain weight (g)	98.20	52.82
Grain yield per plant (g)	88.00	60.22

Similarity matrix :

The similarity matrix based on the nine agronomic characters was used to establish the level of relatedness between the nine varieties. Pair-wise estimates of similarity ranged from (1.10) to (9.25) table (5). Two varieties (Sakha 101) and (Giza 171) were the closest genotypes with the highest similarity index of (9.25). this was followed by (9.10) similarity between a pair of varieties (HR5824-B-3-2-3) and (GZ6903-1-2-2-1). The lowest level of similarity (1.10) was obtained between Giza 177 and Giza 171.

Table 5 : Similarity matrix for nine varieties based on nine agronomic characters.

Entries	١	٢	٣	٤	٥	٦	٧	٨	٩
Giza 177	0.00								
Sakha 101	3.92	0.00							
Sakha 104	3.70	3.44	٠,٠٠						
Giza 171	1.10	9.25	٨,٩٣	٠,٠٠					
HR5824-B-3-2-3	5.55	8.52	٨,٢٨	١,٦٠	٠,٠٠				
GZ6910-28-1-3-1	3.66	3.21	١,٨٦	٨,١٥	٨,٣٩	٠,٠٠			
GZ7685-8-1-3-2	1.80	3.80	٣,٥٨	١,١١	٥,٤٦	٣,٧٠	٠,٠٠		
GZ6522-15-1-1-3	3.92	3.66	٢,٩٢	٨,٦١	٨,٤٢	١,٩٦	٣,٩٠	٠,٠٠	
GZ6903-1-2-2-1	4.44	3.01	٢,٤٧	٧,٨٥	٩,١٠	١,٩٩	٤,٢٠	٢,٨٣	٠,٠٠

Cluster analysis:

The genetic divergence can provide a visual idea about variabilities presented in nine genotypes, in addition to assure the continued genetic improvement. The genetic divergences based on Euclidean distance using morphological characters (quantitative traits) among nine parents, were graphically illustrated as a dendrogram in (Figure 1).

The standardized Euclidean distance ranged from 16 to 78.12 in the nine parents, where the minimum distance was observed between Giza 177 and GZ 7685-8-1-3-2, while the maximum Euclidean distance was observed between Giza 171 and Sakha 101. The nine parents were distinctly classified into five clusters (below 25 Euclidean distance).

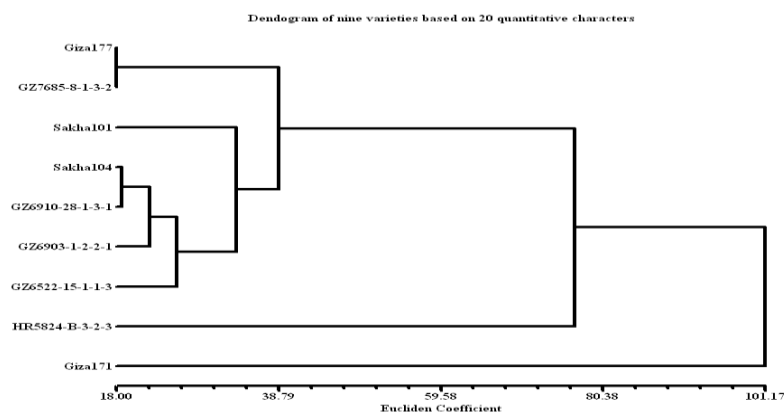


Figure (1): Cluster diagram for nine varieties classified by nine agronomic characters studied.

The first group included all varieties except Giza 171, which was long duration. The first group was divided into two sub groups based on maturing, plant height, spikelet fertility percentage and grain yield per plant. The first sub group, which was higher in these four characters, included seven varieties (Giza 177, GZ7685-8-1-3-2, Sakha 101, Sakha 104, GZ6910-28-1-

3-1, GZ6903-1-2-2-1 and GZ6522-15-1-1-3) except for HR5824-B-3-2-3, which was lower in these characters. The two varieties Giza 177 and GZ7685-8-1-3-2 of branch one were similar in all characters except grain yield per plant. Sakha 101 variety was separated alone into one branch because it has long maturing and highest grain yield per plant when compared with the rest five varieties. GZ6522-15-1-1-3 was separated from four varieties in one branch based on maturing, plant height and number of panicles per plant. GZ6903-1-2-2-1 genotype was separated from these three varieties based on maturing, plant height and spikelet fertility percentage. On the other hand, the remaining two varieties Sakha 104 and GZ6910-28-1-3-1 were similar in all characters except in grain yield per plant.

REFERENCES

- Abd Allah, R. M. (2008). Genetical and morphological studies on environmental genetic and cytoplasmic male sterility lines in rice. M.Sc. Thesis, Fac. of Agric. Mansoura Univ. Egypt.
- Alam, M. F.; M. R. Khan.; M. Nuruzzaman.; S. Parvez.; A .M. Swaraz.; I Alam and N. Ahsan (2004). Genetic basis of heterosis and inbreeding depression in rice (*Oryza sativa* L.). J Zhejiang Univ. Sci. 5(4): 406-411.
- Awd-Allah, M. M. A. I.(2006). Application of genetic engineering tools on rice genome. M.Sc. thesis, genetic Department, Fac. of Agric., Al-Azhar University, Egypt.
- Duwayri, M.; D. V. Tran and V. N. Nguyen (1999). Reflection on yield gaps in rice production. Intr. Rice Commission Newsletter.FAO, Rome (48): 13-25.
- El-Mowafi, H.F. (1988). Breeding studies on some traits of crosses and cultivated and induced rice lines. M.Sc. Thesis, Fac. of Agric., Tanta University, Kafr El-Sheikh, Egypt.
- El-Mowafi, H. F. (1994). Studies on rice breeding. Ph. D. Thesis, Fac. Agric., Kafer El-Shiekh Tanta Univ., Egypt.
- El-Refae, Y. Z. E. (2002). Genetical and biochemical studies on heterosis and combining ability in rice . M. Sc. Thesis, Fac. Agric., Tanta Univ., Kafr El-Sheikh, Egypt.
- Hammoud, S. A. M. (2004). Inheritance of some quantitative characters in rice (*Oryza sativa* L.). Ph. D. Thesis, Fac. Agric. Minofiya Univ., Shibin El-Kom, Egypt.
- Hammoud, S.A.M. (1996). Breeding studies on some rice characters. M.Sc. Thesis. Fac. Agric., Menoufiya Univ., Egypt.
- Hayman, B. I. (1954). The analysis of variance of diallel table. Biometrics. 10: 235-244.
- Hayman, B. I. (1958). The separation of epistatic from additive and dominance variation in generation means. Heredity. 12: 371-390.
- Kumar, R.; Krishnapal; S. K. Mondal; Rai; Ramashankar; S. C. Prasad and R. Rai (1994). Genetic study of major characters in upland rice. Environment and Ecology, 12:2, 363-365; 7 ref.

- Mather, K. and J. L. Jinks (1982). Biometrical genetics. 3rd ed. Cambridge Univ. press, London, N.Y.
- Singh, R. K. and B. D. Chaudary (1977). Biometrical methods in quantitative genetic analysis. Kalyani Publishers, Ludhiana, India, pp. 300.

**تقدير المكونات الوراثية ودرجه التوريث وتحليل الشجرة الوراثية لبعض الصفات
المحصولية في الأرز**
**عمرو فاروق عبد الخالق، وائل حمدي محرم الكلاوى ، اشرف صلاح مصطفى عبداللطيف
و جلال بكر أنيس**
مركز بحوث الأرز – معهد المحاصيل الحقلية – مركز البحوث الزراعية

أقيمت تجرب حقلية بهدف إجراء التحليل الدوري لتسعه أباء والحصول على ٣٦ هجين وكان إحدى هذه الأباء صنف مستورد وباقي الأصناف تجاريه وسلالات مبشرة وذلك من خلال استخدام طريقه هايمان في عام (١٩٥٤). وتم زراعه الأباء والجيل الأول في تجربته قطاعات كاملة العشوائية في ثلاث مكررات عام ٢٠١١ بمزرعة مركز البحوث والتدريب في الأرز بسخا – كفر الشيخ. أخذت البيانات على ٩ صفات محصولية. وأوضحت النتائج أن مجموع مربع متوسطات قيم الصفات المدروسة كانت عالية المعنوية مشيرة إلى وجود اختلافات وراثية كبيرة بين التراكيب الوراثية في جميع الصفات المدروسة. وكان التباين الوراثي المضيف معنوي وعالي المعنوية لجميع الصفات المدروسة ما عدا صفه عدد السنابل للنبات ووزن السنبل. وكان التباين الوراثي السياتي عالي المعنوية لجميع الصفات كما كان التباين البيئي غير معنوي لمعظم الصفات ما عدا صفه النسبة المئوية للحبوب الخصبة في السنبله ومحصول النبات الفردي. وتبين من النتائج أن درجه التوريث بمعناها الواسع كانت عالية لجميع الصفات محل الدراسة وان تحليل الشجرة الوراثية قسم الأباء إلى خمس مجاميع رئيسيه وذلك طبقا لدرجه القرابة ما بين تلك الأباء. وتوصى هذه النتائج إلى إمكانية استخدام هذه الهجن في برامج التربية والحصول منها على تراكيب وراثية متباينة تمكن من إجراء عملية الانتخاب الفردي في الأجيال التالي

قام بتحكيم البحث

كلية الزراعة – جامعة المنصورة
كلية الزراعة – جامعة كفر الشيخ

أ.د / احمد ابو النجا قنديل
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Table 3 : The estimates of genetic components for all characters studied.

Genetic Parameters	Estimates \pm S.E.								
	Days to maturing (days)	Plant height (cm)	Chlorophyll content (SPAD)	No. of panicles /plant	Panicle length (cm)	Panicle weight (gm)	Spikelet fertility (%)	1000-grian weight (gm)	Grian yield/plant (gm)
D	** 157.44 \pm 6.90	** 204.47 \pm 17.54	** 11.98 \pm 2.17	ns 6.80 \pm 9.83	** 15.79 \pm 0.89	ns 0.01 \pm 0.17	** 1226.95 \pm 141.29	** 2.58 \pm 0.55	** 111.36 \pm 21.09
H1	** 66.37 \pm 15.23	** 186.72 \pm 38.71	** 28.70 \pm 4.78	** 141.04 \pm 21.70	** 10.99 \pm 1.96	** 1.70 \pm 0.38	** 2053.43 \pm 311.85	** 8.16 \pm 1.22	** 171.00 \pm 46.54
H2	ns 44.57 \pm 13.10	** 147.56 \pm 33.27	** 19.69 \pm 4.11	** 125.80 \pm 18.66	ns 6.31 \pm 1.69	** 1.47 \pm 0.33	** 1858.53 \pm 268.08	** 6.36 \pm 1.05	** 162.85 \pm 40.01
h2	* -0.18 \pm 8.77	ns 251.38 \pm 22.29	** 24.82 \pm 2.75	ns 405.35 \pm 12.50	** 0.37 \pm 1.13	ns 2.37 \pm 0.22	ns 4270.27 \pm 179.59	ns 2.26 \pm 0.70	ns 311.65 \pm 26.80
F	ns 40.20 \pm 16.10	ns -27.57 \pm 40.91	ns 15.87 \pm 5.06	ns 3.27 \pm 22.94	ns 15.90 \pm 2.07	ns -0.22 \pm 0.41	* 58.15 \pm 329.60	ns 0.68 \pm 1.29	** -56.96 \pm 49.19
E	0.47 \pm 2.18	4.20 \pm 5.55	0.60 \pm 0.69	4.87 \pm 3.11	0.33 \pm 0.28	0.01 \pm 0.06	93.61 \pm 44.68	0.06 \pm 0.18	17.58 \pm 6.67
(H ₁ /D) ^{1/2}	0.649	0.906	1.048	4.555	0.834	4.196	1.294	1.778	1.239
(H ₂ /4 H ₁)	0.168	0.198	0.171	0.223	0.143	0.217	0.226	0.195	0.238
(K _D /K _R)	1.489	1.868	2.496	1.111	4.040	0.571	1.037	1.160	0.658
(r)	0.911	0.991	0.909	0.449	0.913	0.769	0.847	0.902	0.351

*, ** significant at 0.05 and 0.01 level of probability, respectively. and ns : Not Significant.

