INHERITANCE OF SOME YIELD COMPONENTS AND GRAIN QUALITY TRAITS IN RICE (*Oryza sativa* L)

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ABSTRACT

The investigation was laid out at the Experimental Farm of Rice Research and Training Center (RRTC), Sakha, Kafer EL-Sheikh, Egypt, during three successive rice growing seasons, 2010, 2011 and 2012.The study aimed to fin the effect of gene action in the inheritance of grain yield, its components and some rice grain quality traits under normal conditions. The materials for this study consisted of six rice genotypes namely; Sakha101, Sakha102, Egyptian Yasmin, GZ1368s-5-4, IET1444 and IR78875-176-B2-B, These genotypes have a wide range of variation due to their different genetic background. The six rice parents were crossed to produce F1 hybrid seeds of three crosses, namely, Sakha101 x GZ1368s-5-4, Sakha102 x IET1444 and Egyptian Yasmin x IR78875-176-2B. The six populations, P1, P2, F1, F2, BC1 and BC2 for each cross were utilized to determine the genetic parameter of the studied characters.

The results revealed that mid parent values (m) were highly significant in positive direction for all traits in all crosses, Moreover, additive effect was highly significant in negative direction for grain yield/plant trait in cross I, as well as, grain length, grain shape and amylose content % in cross II. In addition, dominance effect was played an important role in the inheritance of grain shape, and amylose % in negative direction and grain yield in positive direction in cross III. These results also indicated that all types of gene interaction were played an important role in the inheritance of all traits, according to the cross itself.

The broad sense heritability was high for all traits, it was ranged between (85.51 and 98.73%) for 1000 grain weight in cross I and grain yield/plant in cross I, respectively. Moreover, low to moderate estimated values of narrow sense heritability were observed for all traits in all crosses, the highest value (32.5%) was recorded for grain shape trait in cross III. However, the great discrepancy between the estimates of heritability in broad and narrow sense for 1000-grain

weight character was reflected in low estimates of dominance variance or high estimates of additive variance for this trait. In addition, low estimates of expected genetic advance (9.03 and 9.04) were observed for amylose %, and 1000-grain weight in cross I, respectively. Low to moderate expected genetic advance with low narrow sense heritability for amylose content % and 1000-grain weight could be expected because this trait is under polygenic control. Moreover, additive and dominance components of variation were significant in the inheritance of these traits, but additive component was higher than the dominance one.

__Conclusively,__ the results suggested that early generation selection may be effective in improving of these traits in cross I. On the other hand, the results also indicated that the selection in late generations will be improving grain shape in cross II and 1000 grain weight in cross III.

Key words: Rice, Inheritance, Gene action, Yield components and Grain quality traits.

INTRODUCTION

Rice is one of the most important food crops in the world. It is estimated that 40 per cent of the world's population take rice as their major source of food. The advent of higher yielding semi dwarf varieties has been instrumental in achieving consistent progress in rice production in the past three decades and attaining self-sufficiency.

Rice is a highly self-fertilized plant, which means that pollen from the same flower or from another flower on the same plant will pollinate itself. Pollen is shed from the stamens and lands on the pistil of either the same flower or another flower of the same plant over 95% of the time.

In Egypt, rice is considered as one of the most important field crops, since it contributes about 20% of the total cereal consumption. Annually, more than one and half million feddans is cultivated with rice (one feddan = 4200 m2) producing about 6.5 million tons of rice, with an average of 4.6 ton/fed. (10.9 ton/ha) (RRTC, 2013).

Success in crop improvement generally depends on the magnitude of genetic variability and the extent to which the desirable characters are heritable. Development of high-yielding varieties requires a thorough knowledge of the existing genetic variation for yield and its components and grain quality traits. The observed variability is a combined estimate of genetic and environmental causes, of which only the former one is heritable. However, estimates of heritability alone do not provide an idea about the

expected gain in the next generation, but have to be considered in conjunction with estimates of genetic advance. Grain yield character in rice is quantitative trait in nature and is polygenically controlled. Selection on the basis of grain yield character alone is usually not very effective and efficient. However, selection based on its component characters could be more efficient and reliable. Quality is defined as a major factor which decides market values of agricultural products and foods in each phase from production through consumption. Rice grain quality has always been an important consideration in rice variety selection and development, it is second only to yield as a major breeding and thus relates to a number of factors, while the cooking and eating quality is a part of the factors in assessing the grain quality of rice. In the future, grain quality will be even more important once, the very poor-many of whom depend largely on rice for their staple food become better off and begin to demand higher quality rice**.**

Estimation of the types of gene action involved in the expression of traits, the level of additive effects, and the degree of dominance are very important in developing a breeding method for the trait of interest**,** Hallauer and Miranda (1988). Alleles with dominance or additive phenotypic effects influence heritability differently, depending on whether they are in homozygous or heterozygous conditions. Knowledge of the way genes act and interact will determine which breeding system can optimize gene action more efficiently, and will elucidate the role of breeding systems in the evolution of crop plants.

This investigation aimed to determine mode of inheritance and type of gene action and genetic effects of genes and to estimates of genetic variance, broad and narrow sense heritability and genetic advance for yield and grain quality traits.

MATERIALS AND METHODS

The present study was laid out at the Experimental Farm of Rice Research and Training Center (RRTC), Sakha, Kafer EL-Sheikh, Egypt, during three successive rice growing seasons, 2010, 2011 and 2012 to study the effect of gene action in the inheritance of grain yield, its components and some rice grain quality traits. The materials for this study consisted of six rice genotypes namely; Sakha101, Sakha102, Egyptian Yasmin, GZ1368s-5-4, IET1444 and IR78875-176-2B, These genotypes have a wide range of variation due to their different genetic background.

The six rice parents were crossed to produce F_1 hybrid seeds of three crosses. These three crosses were Sakha101 x GZ1368s-5-4, Sakha102 x IET1444 and Egyptian Yasmin x IR78875-176-2B. The six populations, P_1,

P_2, F_1, F_2, BC_1 and BC_2 for each cross were utilized to determine the genetic parameter of the studied characters.

In 2010 season, the parental genotypes were grown at RRTC farm in three planting dates with ten days interval in order to overcome the differences in flowering time between parents. Thirty days old seedling of each parent was individually transplanted in the field in 10 rows. Each row was 5m long and included 25 hills. At flowering time, hybridization between parents was carried out following the technique proposed by Jodon (1938) and modified by Botany (1961) and the aforementioned three crosses were produced.

In 2011 season, parents and F_1 hybrid seeds of the three crosses together with their parental lines were planted under normal conditions. At heading, parents were crossed again to produce the F_1 hybrid seeds of three crosses following the same technique. Moreover, some of F_1 plants were left to be self-pollinated in order to produce F_2 seeds, while some other plants were crossed with their own parents as a male to produce BC_1 and BC_2 seeds. At harvest, seeds of different generations were individually harvested to be grown in the next season.

Subsequently, in 2012, summer season, seeds of the P_1, P_2, F_1, BC_1, BC_2 and F_2 of each cross were sown in normal conditions to estimate the genetic parameter of the seven rice agronomic characters and seven rice quality characters. Eighteen entries belongs to different generations (6 parents, 3F1's, 3F2's, 3BC1, 3BC2) were cultivated in a randomized complete block design experiment with four replication. Each replicate contained 10 rows of each P_1, P_2, 5 rows of each of F_1, BC_1 and BC_2 and 15 rows of F_2 generations. In all growing seasons of the study, all cultural practices such as field preparation, sowing method, transplanting and fertilizers, weed control were applied as recommended. Eight yield and quality rice characteristics, number of panicles/plant, 1000-grain yield, grain yield/plant, grain length, grain shape, gelatinization temperature and amylose content were measured following the standard evaluation system for rice (IRRI 1996).

The collected data were subjected to the proper statistical analysis of variance of Randomized Complete Block Design as described by Snedecor and Cochran (1967). The present data were predicted to biometrical model suggested by Mather (1949) and Hayman (1958) in order to estimate the gene actions and to separate the genetic components of variations controlling the studied characters. The scaling test of inquest is important because in most of the cases, estimation of additive and dominance components of variances are made immoderation of the gene interaction. Individual scaling test was applied to the six populations data of each cross as outlined by Mather (1949) and Hayman and Mather (1955). Expected genetic variance of VBC_1, VBC_2

and VF_2 in terms of additive (½D) and dominance (¼H) are derived by Mather (1949) as follows:

Additive genetic variance **(½D)** = 2VF2 - (VBC1 + VBC2)

                         (D) = 4VF2 - 2(VBC1+ VBC2)

Dominance genetic variance **(¼H)** = VBC1 + VBC2 - VF2 – VE

                        (H) = 4(VBC1 + VBC2 - VF2 – VE)

    The heritability in both broad and narrow sense was determined by Powers *et al* (1950) and Warner (1952), respectively, as follows:

$$\text{Heritability in broad sense (h}^2 \text{ bs)} = \frac{\text{Genetic variance (VG)}}{\text{Phenotypic variance (Vph)}}$$

$$\text{Heritability in narrow sense (h}^2 \text{ ns)} = \frac{\text{Additive genetic variance (VA)}}{\text{Phenotypic variance (Vph)}}$$

    Predicted and expected values of genetic advance (GS and GS %) were calculated according to Johnson *et al*. (1955).

$$GS = K. \, h^2 \text{ ns}. \, \sigma ph$$

$$GS \% = GS / \, \bar{x} \times 100$$

Where: **K** =Selection differential and equals 2.06 upon selecting the highest 5% of population, Hanson *et al* (1956), **h² ns** = Heritability in narrow sense and **σph** = Phenotypic standard deviation.

RESULTS AND DISCUSSION

    The present data were subjected to biometrical model in order to estimate the gene action and to separate the genetic components of variations governing the studied characters besides other genetic parameters to give a complete description and full information about the inheritance of the traits under study. Gene action and genetic effects of genes, estimates of genetic variance, broad and narrow sense heritability and genetic advance were discussed as follow:

1-Estimates of gene action and genetic effects of genes

1000 grain weight

    Data in Table (1) showed that the values of A, B and Cof the scaling test for 1000 grain weight were highly significant in all studied crosses, indicating the important of interaction components, i.e. additive x additive (i) additive x dominance (j) and dominance x dominance (L) in the inheritance of 1000 grain weight.

    It is clear in Table (2) that the mid parent value (m) was positively significant in the three studied crosses. On the other hand, additive effect (d)

Table (1): Scaling test for adequacy of additive and dominance model in the three studied crosses characters.

Character	Cross	A	B	C
1000 grain weight (gm)	I	-0.33±0.07**	0.42±0.11**	-13.95±1.9**
	II	3.35±0.13**	3.34±0.13**	24.6±3.35**
	III	57±0.26**	17.34±0.27**	24.72±8.34**
Grain yield/plant\ (gm)	I	15.3±2.32**	20.03±2.33 **	33.09±97.
	II	-7.39±3.3*	-46.±3.82**	64.7±91.09
	III	16.3±3.12**	15.07±2.12**	12.14±74.89
Grain length (mm)	I	-1.16±0.019 **	0.027±0.02	-3.17±0.45**
	II	-3.26±0.007 **	-17.45±0.05 **	-8.87±0.3**
	III	-6.86±0.14 **	-14.7±0.08 **	-10.24±0.53**
Grain shape	I	0.15±0.018**	5.07±0.013**	1.49±0.07 **
	II	0.887±0.027**	-4.22±0.021**	-0.33±0.128 **
	III	-1.9±0.038**	--5.65±0.025**	-1.22±0.16 **
Amylose content %	I	-2.48±0.27**	-43.77±0.2**	4.87±1.04**
	II	-17.28±0.014**	-19.68±0.012**	-36.96±0.025**
	III	-8.08±0.076**	-41.48±0.064**	-10.73±0.46**

Where: Crosses I, II and III were Sakha 101 x GZ1368s-5-4, Sakha 102 x IET 1444 and Egyptian Yasmin x IR78875-176-B2-B, respectively.
*and **: Significant at 0.05, 0.01 probability levels, respectively.

was either positively (2.21) or negatively (-5.2) highly significant in crosses II and III, respectively. The genetic parameters, dominance effect (h) and additive x additive type of gene interaction (i) for 1000 grain weight were positive and high significant in cross I, while it was negative and highly significant in cross II. Moreover, additive x dominance (j) type of gene interaction was highly significant in negative direction in cross III. In addition, dominance x dominance (L) type of gene interaction was highly significant in negative direction in crosses, I and III, while, it was in positive direction in cross, II. The results indicated that the selection in late generations will be improving 1000 grain weight in cross III. Similar results were obtained previously by El-Hissewy (2004), Akram *et al.* (2007), Shehata *et al.* (2009) and Onyia (2011).

Grain yield per plant

      Data in Table (1) showed that values of A and B in the scaling test for grain yield per plant were highly significant in all studied crosses, except, value of A in cross, II, which showed to be significant only. However, the calculated value of

Table (2). Components of generation mean in the three studied crosses characters.

Character	Cross	Genetic components of generation means					
		m	d	h	I	j	l
1000 grain weight (gm)	I	27.05**	-0.07	20.33**	14.03**	-0.37	-14.13**
	II	31.39**	2.21**	-19.08**	-17.9**	-0.007	11.21**
	III	32.32**	-5.2**	-2.78	-1.68	-5.82**	-21.36**
Grain yield / plant (gm)	I	56.48**	3.03*	16.44	-2.24	-2.37	-37.58 *
	II	70.03**	20.7**	-92.44**	-118.1**	19.3**	171.5**
	III	51.35**	5.31**	39.24**	19.23	0.61	-50.6**
Grain length (mm)	I	5.86**	-0.111	1.22	2.03*	-0.59**	-0.9
	II	7.85**	-0.035**	-5.57**	-7.94**	0.088	18.13**
	III	7.59**	-0.039	-10.97**	-7.49**	0.118	20**
Grain shape	I	2.43**	0.24**	1.85**	1.64**	0.68**	-2.88 **
	II	2.07**	-0.67**	1.28	1.72*	-0.54**	-2.27 *
	III	2.85**	0.67**	-3.45**	-2.72**	-0.15	6.74 **
Amylose content %	I	24.39**	0.23	-15.77**	-12.96**	0.17	11.84**
	II	20.54**	-2.4**	-5.97*	-5.96**	-1.6**	16.9**
	III	21.38**	0.084	-10.7**	-8.05**	2.82**	16.33**

Where: Crosses I, II and III were Sakha 101 x GZ1368s-5-4, Sakha 102 x
        IET1444 and Egyptian Yasmin x IR78875-176-B2-B, respectively.
*and **: Significant at 0.05, 0.01 probability levels, respectively.

C of scaling test was insignificant in all crosses, indicating the important of interaction components, i.e. additive x additive (i), additive x dominance (j) and dominance x dominance (L) in the inheritance of grain yield per plant.

Table (2) illustrated that the mid parent value (m) and additive effect (d) was positively significant in the three studied crosses. The dominance (h) gene effect was either highly significant negative or positive in crosses, II and III, their estimated values were (-92.44 and 39.24), respectively. Highly significant and negative estimates of additive x additive (i) type of gene interaction (-118.1) was recorded for grain yield per plant in the second cross, Sakha 102 x IET1444, in addition, it was controlled also by highly significant positive estimates (19.3) of additive x dominance type of gene interaction. Moreover, dominance x dominance (L) was highly significant in negative directions in crosses I and III, while it was positive in cross II, (Table 2). The results indicated that selection inlate generation will be very important to improve grain yield per plant. Similar results were reported by Abd El-Lattef *et al*. (2012) and Hassan *et al.* (2013).

Grain length (mm)

Data in Table (1) showed that values of A, B and C in the scaling test for grain length were highly significant in all studied crosses, except value of B in cross I, indicating the important of interaction components, i.e. additive x additive (i), additive x dominance (j) and dominance x dominance (L) in the inheritance of grain length.

Table (2) indicated that mid parent value (m) was highly significant in positive direction in all crosses. The highest estimated value was recorded in cross II (7.85) followed by cross III (7.59) and cross I (5.86). Moreover, additive effect was highly significant in negative direction in cross II. In addition, the genetic parameters, dominance effect, additive x additive type of gene interaction were highly significant in negative direction in crosses, II and III. On the other hand, additive x dominance type of gene interaction was found to be highly significant in negative direction in cross I, while, dominance x dominance type of gene interaction was found to be highly significant in positive direction in crosses II and III. These results indicated that all types of gene interaction were played an important role in the inheritance of grain length according to the cross itself. These results were in agreement with El-Abd *et al.* (2009), Sultan *et al.* (2010), Abd El-Lattef *et al.* (2012) and Hassan *et al.* (2013).

Grain shape:

Data in Table (1) showed that the values of A, B and C of the scaling test for grain shape were highly significant in all studied crosses, indicating the important of interaction components, i.e. additive x additive (i), additive x dominance (j) and dominance x dominance (L) in the inheritance of grain shape.

Table (2) showed that the mid parent value (m) was positively significant in the three studied crosses. On the other hand, additive effect (d) was either negative (-0.67) or positive (0.24 and 0.67) and highly significant in crosses I, II and III, respectively, The genetic parameters, dominance effect (h) and additive x additive type of gene interaction (i) for grain shape were either positive or negative and high significant in crosses I and III, respectively. Moreover, additive x dominance (j) type of gene interaction was either highly significant in positive direction in cross I or in negative direction in cross II. In addition, dominance x dominance (L) type of gene interaction was significantly in negative direction in crosses, I and II, while, it was highly significant in positive direction in cross III. The results indicated that the selection in late generations will be improving grain shape in cross II. Similar results were obtained previously by El-Abd *et al.* (2001), El-Abd *et al.* (2009) and Hassan *et al.* (2013).

Amylose content (%):

Data in Table (1) showed that values of A, B and C of the scaling test for amylose content % were highly significant in all studied crosses, indicating the important of interaction components, i.e. additive x additive (i), additive x dominance (j) and dominance x dominance (L) in the inheritance of amylose content (%).

Obviously, Table (2) shows that the mid parent value (m) and dominance x dominance type of gene interaction were positively significant in the three studied crosses. The additive (d) gene effect was highly significant in negative direction in cross II, while it was insignificant positive in other two crosses. Highly significant and negative estimates of both dominance gene effect and additive x additive (i) type of gene interaction were recorded for amylose content % in all the studied crosses. In addition, the rice crosses, Sakha 102 x IET1444 and Egyptian Yasmin x IR78875-176-B2-B were controlled by highly significant negative (-1.6) and positive (2.82) estimates of additive x dominance type of gene interaction, respectively. The results indicated that selection in late generation will be very important to improving amylose content %. Similar results were reported by El-Abd *et al.* (2001), El-Hissewy (2004) and El-Abd *et al.* (2008).

Estimates of genetic Variance, Heritability, and expected genetic advance:.
1000 Grain weight (gm):

Table (3) further showed that the estimates of additive genetic variance (D) were higher than that of the dominance genetic variance (H) in crosses II and III,. These findings indicated that the additive genetic variance in cross II and III played major role than that of dominance genetic variance in the inheritance of 1000 grain weight character in the majority of these rice crosses, these results indicated also that additive variance played an important role in the inheritance of this character in these crosses. Similar results were obtained by El-Abd (2003), Mohan Lai and Chauhan (2011) and Basavaraja *et al.* (2013).

The broad sense heritabilities for the present trait were high, (85.51, 91.96 and 94.09) in the three studied crosses, I, II and III respectively. While, low values (25.03, 23.38 and 19.86) were estimated in narrow sense heritability for the same crosses, alternatively, Table (5). However, the great discrepancy between the estimates of heritability in broad and narrow sense for 1000 grain weight character was reflected in low estimates of dominance variance or high estimates of additive variance for this trait. These finding were in close agreement with those reported earlier by Sreeparvathy *et al.* (2010), El-Gamal (2013) and Sathya and Jebaraj (2013).

Table(3) Estimates of additive genetic variance (½D), dominance genetic variance(¼H), broad and narrow-sense heritability and genetic advance (GS%) for rice for the three studied crosses Characters.

Character	Cross	Genetic variance		Heritability		GS %
		D	H	Broad sense	Narrow sense	
1000 grain weight (gm)	I	0.78	-0.8	85.51	25.03	9.04
	II	1.44	-1.4	91.96	23.38	97.91
	III	3.68	-3.52	94.09	19.86	12.777
Grain yield / plant\(gm)	I	43.9	-40.24	98.73	17.74	22.45
	II	38.46	-34.44	95.91	26.34	25.784
	III	32.88	-34.32	87.25	17.49	21.047
Grain length (mm)	I	0.188	-0.18	90.71	26.58	21.735
	II	0.34	-0.328	91.70	22.31	18.109
	III	0.52	-0.44	96.06	35.37	38.167
Grain shape	I	0.088	-0.044	90.83	19.73	26.027
	II	0.136	-0.128	92.96	24.88	48.612
	III	0.154	-0.132	95.12	32.5	50.544
Amylose content %	I	1.4	-1.32	96.6	17.28	9.036
	II	1.88	-1.84	96.96	10.42	7.363
	III	0.4	-0.384	88.71	29.43	9.729

Where: Crosses I, II and III were Sakha 101 x GZ1368s-5-4, Sakha 102 x
IET1444 and Egyptian Yasmin x IR78875-176-B2-B, respectively.

Low estimates of expected genetic advance (9.04, 97.91 and 12.77) were observed in crosses, I, II and III, respectively. Low expected genetic advance with low narrow sense heritability for 1000 grain weight character could be expected because this trait is under polygenic control. Moreover, additive and dominance components of variation were significant in the inheritance of this trait, but additive component was higher than the dominance one. The results suggested that early generation selection may not be effective in improving of 1000 grain weight character in all crosses. Similar results were obtained earlier by El-Abd *et al.* (2007) and Ahmadikhah (2010).

Grain yield per plant (gm):
    Data in Table (3) showed that additive genetic variance was higher than that of dominance genetic variance in the majority of the crosses I and II for grain yield per plant. The relative magnitude of the additive variance to dominance variance was dependent on the cross itself, it was 1.09 times than

that of dominance variance in the cross I, namely, (Sakha 101 X GZ1368s-5-4), while it was reached 1.12 times than that of dominance variance in the cross II, namely, (Sakha 102 X IET1444), while, it less than that of dominance variance in the cross III, namely, (Egyptian Yasmin X IR78875-176-B2-B). This could lead to the conclusion that some breeding programs would be more effective and faster with certain crosses than with other crosses.

Heritability estimates in broad sense for this trait were high (98.73, 95.91 and 87.25) in the three studied crosses. Moreover, narrow sense heritability was low (17.74, 26.34 and 17.49) in the all studied crosses respectively. The results were in harmony with that presented by El-Abd *et al.* (2007), Sreeparvathy *et al.* (2010) and Basavaraja *et al.* (2013).

The expected genetic advance under top 5% of selection were moderate (22.45, 25.78 and 21.04) in crosses I, II and cross III, respectively. These results indicated that the selection in early generation may be effective in improving of grain yield per plant character in all crosses. Similar results were exhibited by El-Abd *et al.* (2007), Karim *et al.* (2007) and Sathya and Jebaraj (2013).

Grain length (mm):

Table (3) shows that the estimates of additive genetic variance were higher than that of dominance genetic variance in the three studied crosses. The relative magnitude of the additive genetic variance was approximately ten times (or more than ten) that of dominance genetic variance in cross I while it was reached 1.037 times than that of dominance variance in the cross II and 1.2 in the cross III. This finding indicated that the additive variance played an important role than the dominance variance in the inheritance of grain length character in the majority of the rice crosse I. Similar results were obtained by El-Abd (2003) and Kishore *et al.* (2008).

High estimates of heritability in broad sense (90.71, 91.70 and 96.06) were observed in the three studied crosses, respectively, Table (3). However, the same crosses gave moderate estimates of heritability in narrow sense, their estimated values were (26.58, 22.31 and 35.37), respectively. These results were in agreement with those obtained by the partitioning of the genetic variance. These results also were in agreement with those reported by Singh *et al.* (2006) and Bharadwaj *et al.* (2007).

Moderate estimates of expected genetic advance were observed in the three studied crosses, (21.735, 18.109 and 38.176), respectively. High heritability coupled with moderate genetic advance indicated that additive type of gene action was played a significant role in the expression of this character. It was suggested that selection may be effective in improving this

trait in early segregation. On the contrary, high expected genetic advance were estimated by El-Abd (2003) and Asfaliza *et al.* (2012).

Grain shape:

Table (3) reveals that high estimates of additive genetic variance (D) were computed for each of the three studied crosses in comparison with their corresponding estimates of dominance genetic variance (H). The relative magnitude of the additive genetic variance was 2.0, 1.06 and 1.17 times more than dominance genetic variance in all crosses. This finding illustrated that additive variance played a major role than the dominance variance in the inheritance of grain shape character. This in turn, suggested that rice breeding programs could be effective for improving such trait. Similar results were detected previously by El-Abd (2003), Singh *et al.* (2006) and Bharadwaj *et al.* (2007).

High broad sense heritability were recorded in the three studied crosses, it was varied from (90.83, in cross, I) to (95.12 in cross, III). On the other hand, moderate estimates of narrow sense heritability (19.73, 24.88 and 32.5) were observed for all the studied crosses, respectively. These findings indicate that selection for this trait could be effective in early generation. These results were in harmony with those of Bharadwaj *et al.* (2007), El-Abd *et al.* (2008) and Veerabadhiran *et al*. (2009).

Moreover, the expected genetic advance were ranged between moderate and high (26.027, 48.612 and 50.544) in crosses, I, II and cross III, respectively. Furthermore, the estimates of high heritability coupled with high expected genetic advance, could be indicated that selection for grain shape in early generation would be effective for improving grain shape character in all crosses. These results were similar to those obtained by Sarawgi *et al.* (2000), Mohan Lai and Chauhan (2011) and Asfaliza *et al.* (2012).

Amylose content %:

From the data presented in Table (3) it appeared that the relative magnitude of the additive genetic variance was higher than that of dominance genetic variance in the majority of the three studied crosses for amylose content %. The estimates of additive genetic variance were reached 1.06, 1.42 aand 1.05 times than that of dominance genetic variance in all the studied crosses, respectively. Heritability estimates in broad sense for this trait was high (96.60, 96.96 and 88.71) in the three studied crosses, respectively. Meanwhile, narrow sense heritability was low (17.28, 10.42 and 29.43) in all the studied crosses, respectively.

The excepted gain from selection was low (9.036, 7.363 and 9.729) in crosses, I, II and III, respectively, indicating that the selection in early generation may be not effective in improving amylose content % character.

These findings were contradicted with those obtained previously by El-Abd (2003), Veerabadhiran *et al*. (2009) and Karladee *et al.* (2012).

Conclusively, the results suggested that early generation selection may be effective in improving of these traits in cross I. On the other hand, the results also indicated that the selection in late generations will be improving grain shape in cross II and 1000 grain weight in cross III.

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توارث بعض صفات المحصول وصفات جودة الحبوب
فى الأرز

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** قسم بحوث الأرز- معهد بحوث المحاصيل الحقلية-مركز البحوث الزراعية- الجيزة مصر.

أجريت هذه الدراسة في مزرعة مركزا لبحوث والتدريب في الأرز ـ سخا- كفر الشيخ- مصر، خلال ثلاث مواسم زراعية متتالية للأرز هي ٢٠١٠ و٢٠١١ و٢٠١٢ لدراسة تأثير الفعل الجيتى فى وراثة بعض صفات المحصول ومكوناته وبعض صفات جودة الحبوب في الأرز تحت الظروف الطبيعية، ومادة هذه الدراسة تتكون من ست تراكيب وراثية (genotype) وهى سخا ١٠١ و سخا ١٠٢ والياسمين المصرى و GZ1368s-5-4 و IET1444 و IR78875-176-B2-B وهذه التراكيب الوراثية الست ذات مدى واسع من التباينات الوراثية متوافق مع هذه الخلفية الوراثية وهذه الست تراكيب الوراثية من الأرز استخدمت لإنتاج ثلاث هجن وهى سخا ١٠١ X GZ1368s-5-4 وسخا ١٠٢ X IET1444 والياسمين المصرى X IR78875-176-B2-B حيث كانت الست عشائر هى الأب الأول (P1) الأب الثانى(P2) و الجيل الأول (F1) والجيل الثانى (F2) والهجين الرجعى الأول (BC1) والهجين الرجعى الثانى (BC2) لكل هجين حيث يفيد ذلك فى تحديد القياسات الوراثية للصفات المدروسة والنتائج توحى بأن قيم متوسط الآباء (m) ذات معنوية عالية فى الإتجاه الموجب لكل الصفات فى كل الهجن. زد على ذلك كان التأثير الإضافى معنوى جدا في السالب لصفات محصول النبات من الحبوب فى هجين ١ كذك فى طول الحبة وشكل الحبة ونسبة المحتوى من الأميلوز % فى هجين ٢ كما أن تأثير الإضافة والسيادة يلعب دورا هاما فى وراثة شكل الحبة ونسبة المحتوى من الأميلوز % فى الإتجاه السالب ومحصول النبات من الحبوب فى الإتجاه الموجب فى الهجين٣. وهذه النتائج تشير إلى أن كل أشكال الفعل الجينى تلعب دورا هاما فى توارث كل الصفات مع نفس الهجن.

درجة التوريث فى المدى الواسع كانت عالية حيث كانت مابين (٨٥,٥١ إلى ٩٨,٧٣%) لصفة وزن الألف حبة وصفة محصول الحبوب للنبات فى الهجين

١بالترتيب. زد على ذلك أنها كانت منخفضة إلى متوسطة القيم فى المدى الضيق يشاهد ذلك فى كل الصفات فى كل الهجن وأعلى قيمة كانت ٣٢,٥% في صفة شكل الحبة الهجين ٣. وعلى هذا يوجد تناقض كبير بين قيم درجة التوريث فى المدى الضيق والواسع لصفة وزن ١٠٠٠حبة يعكس التقدير المنخفض للتباين السيادى أو المرتفع للتباين الإضافى لهذه الصفة. بالإضافة إلى أن تقدير قيمة التحسين الوراثى المتوقع بالإنتخاب (٩,٠٣ و٩,٠٤) يشاهد فى محتوى الأميلوز % ووزن الألف حبة فى الهجين١.

التحسين الوراثى المتوقع بالإنتخاب المنخفض إلى المتوسط المشاهد مع درجة التوريث المنخفضة فى المدى الضيق لصفات محتوى الأميلوز % ووزن الألف حبة متوقع بسبب أن هذه الصفات محكومة بعديد من الجينات. زد على ذلك إختلاف مكونات السيادة والإضافة كان معنوى فى توارث هذه الصفات لكن مكونات الإضافة كان أعلى من مكونات السيادة. هذه النتائج توحى بأن الإنتخاب فى الأجيال المتقدمة سيكون غير مؤثرفى تحسين هذه الصفات فى الهجين١ ولذلك على المربى تأخير الإنتخاب إلى الأجيال المتأخرة حتى يحدث انعزال للعوامل الوراثية.

التوصية: