Inheritance Studies of Amylose Content, Yield and Grain Quality Characters in Different Rice Genotypes (*Oryza sativa* L.)

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ABSTRACT

Breeding for produced new rice varieties with good grain quality especially for low amylose content has become one of the most important goals in plant breeding programmes. In this experiment, three rice genotypes(Giza178, Giza175 and IR64) were used as a perants to study the inheritance amylose content, heritabilityand genetic parameters for grain yield per plant, 1000-grains weight, grain length, grain shape, hulling%, milling%, head rice% and gelatinization temperature characters. A randomized complete block design (RCBD) was used with three replications for six generations viz., P_1, P_2, F_1, F_2, BCP_1 and BCP_2 of a cross between Giza 178 (low amylose content) x Giza 175 (high amylose content) (cross I) and Giza178 (low amylose content) x IR64 (intermediate amylose content) (cross II) were used for the study. The results showed that the F_1 plants of cross I gave intermediate amylose content in the endosperm 22.58%, while, the amylose content of F_2 plants varied from 13.10 to 35%. and classified into two categories, i.e. 13.10-19 % and 20.50 -35 %.. These results indicated that high amylose content was incompletely dominant over low amylose. Cross II (Giza 178/IR64) low amylose content parent (Giza178) and intermediate amylose parent (IR64) gave 19.84% amylose content in F_1 plants, while in F_2 grains amylose values ranged from9.5 to 24.1. The plants could be classified into 3 categories. Category 1 with 9.5% - 11% a, category 2 (14.5-19.05%) and Category 3 (21.1-24.1%). Selection for intermediary segregates would be ineffective because the dosage effects would dissipate in further generations.

Keywords: Rice, Amylose, additive, gene action, heritability

INTRODUCTION

Rice is staple food crop for a big portion of the world's population, also is a source of dietary energy and has a high protein and mineral content (Mukamuhirwa 2016). Rice grain quality has become the most important factor in rice production because it is directly related to its market value and thus has an effect on farmer income (Zhang, 2007).

Rice grain quality enhancement is a high-priority research objectives in rice breeding programmes. High yielding rice varieties with good quality is extremely important for breeding quality in rice (Lang and Buu., 2004). Milling recovery, physical appearance, cooking and eating features and nutritional value are rice quality traits (Cheng *et al.*, 2005). The definition the quality of various rice products, such as eating, cooking, and processing qualities, is determined by starch properties such as gelatinization temperature (GT), apparent amylose content (AAC), and other physicochemical properties (Kottearachchi *et al.*, 2014). Amylose content is one of the most important characteristics of rice grain quality. The amylose-to-total-starch ratio, expressed as amylose content, varies from cultivar to cultivar; it means 18-32% in indica rice and10-22% in japonica. The high amylose levels are usually associated with dry, fluffy, and separate cooked rice grain (Lang and Buu., 2004). Gelatinization temperature is another characteristic linked to grain quality(Kottearachchi *et al.*, 2014). For example, low-GT rice has a softer texture than high-GT rice among freshly cooked waxy and low-AAC rice; and among intermediate- and high-AAC rice, intermediate-GT rice is softer than low-GT rice when freshly cooked, but they have equal hardness values on accelerated staling (Perez

et al. 1993). Knowing the relationship between physicochemical properties and end-use qualities will help breeders selected rice with desirable characteristics. However, a lack of knowledge about the genetic basis and associated selection techniques retards breeding development. Indica rice endosperm starch contains more amylose than japonica rice endosperm starch (Lang and Buu., 2004). In plant breeding programme, evaluation of genetic variability available in crop species is the first step to select better performing lines. Breeders can use knowledge of heritability and genetic advance to decide and select superior plants with high heritability and genetic advance so that they can perform better for the traits of interest in subsequent generations. Grain yield and yield component traits are complicated traits that are affected not only by their associated characters but also by the environment. Early generation selection becomes less successful as genotype and environment interact more (Rahman *et al.*, 1986). To improve the quantitative and qualitative characteristics, it is essential to estimate the different forms of gene action (Sathya and Jebaraj,2013).

The present work was undertaken to study the pattern of inheritance of low amylose content in crosses with intermediate and high amylose parents and estimate the heritability for some yield and grain quality characters in rice to establish the quality status and offer suggestions for future rice breeding for grain quality.

MATERIALS AND METHODS

The study was carried out at the experimental farm of Rice Research and Training Center (RRTC), Agriculture

Research Center, Sakha, Kafr El-Sheikh, Egypt during the three successful seasons (2018- 2020) in order to investigate inheritance pattern of low amylose content in crosses with intermediate- and high amylose parents in three rice cultivars represented in Table 1 and estimate the heritability for yield and grain quality characters. Six generations P_1, P_2, F_4, F_2, BCP_1 and BCP_2 of a cross between Giza 178 (low amylose content) x Giza 175(high amylose content) and Giza 178 (low amylose content) x IR64(intermediate amylose content)and were practiced to apply generation mean analysis. Crosses were made in 2018 season. Hybrid seeds along with the parents were grown in next season (2019). Some of the F_{1s} were left to self-fertilize, resulting in seeds of F_2 plants, while others were backcrossed with the parents, resulting in BC_1 (F_1xP_1) and BC_2 plants (F_1xP_2). Next season, parents, F_1, F_2 and backcross (BC_1 and BC_2) generations were raised in field during the season 2020. Experiment was set up in randomized complete block design with three replications. A single row for parental lines and F_{1s}, eight rows for each of the backcrosses, and 15 rows for the F_2 generation were found in each replicate. The length of each row was one meter. The distance between rows and plants was 20 x 20cm. Normal recommendations of agronomic practices were followed for growing the crop. At maturity twenty plants per replication for F_1 and each parent, 120 for each of the backcrosses and 250 for the F_2 generation were selected to harvest grain rice on individual plant basis.

Table 1. Cultivars, percentage, origin, grain length and amylose content and pedigree of the parents used under study.

cultivars	Pedigree	Origin	Grain length	Amylose content
Giza 178	Giza 175/Milyang 49	Egypt	Short	Low
Giza 175	IR28/IR1541-76//G.180/Giza 14	Egypt	Short	High
IR64	IR5657-33-2-1/IR2061-465-1-5-5	IRRI	Long	Intermediate

Grain yield per plant and 1000- grains weight after harvesting were determined. For all samples,150 grammars of rough rice (three replications) were taken and well mixed and cleaned. All samples were analyzed for the following grain quality characters: Amylose content was estimated for milled rice samples following the methods of Juliano (1971). Grain length and shape were measured for paddy rice grain according to Khush *et al*., (1979). Hulling%, milling% and head rice% were determine according to Adair (1952) by using Satake testing machines. Gelatinization temperature (G.T.) was estimated for milled rice samples following the methods of Little *et al*., (1958).

Data analysis: The content effects were assessed from the difference in amylose content. Thesegregating grains were classified in different categories by the frequency distribution of segregant for amylose content. Scaling test for additive and dominance models' adequacy. Genetic parameters as broad

and narrow senses heritability's were estimated according to Powers *et al*.,(1950) and Warner,(1952).

RESULTS AND DISCUSSION

The cross I (Giza178/Giza 175):

The hybridization between low amylose parent Giza178 (16.69%) and the high amylose parent Giza175 (26.73%) gave the F_1 plants intermediate amylase content in the endosperm and the ratio was 22.58% this ratio belonged in category intermediate amylose content. While, the amylose content in F_2 plants varied from 13.10 to 35%. These results indicted that the F_2 plants could essentially be classified into two categories, i.e. 13.10-19% and 20.50 -35%, and the number in (Table 2) were devided into to 59 seeds in the first category and 191 in the second category. These results indicated that high amylose content was incompletely dominant over low amylose Manzhong(1998).The grains, selected from the crosses particularly for higher amylose content, need to be tested in further generations as dosage effects in later generations disappear Kumar and Khush(1988). ($X^2 = 54.03$) in (Table2). The data also, among the second category (from 20.50 - 35%) seeds could be grouped into two category (20.50 - 24.0) intermediate amylose (25.50 - 35.0%) 1: 2:1 in F_2 (X^2=26.19). The results in BC_1 (Table3) seeds also clearly segregated into 2 classes, one class with lowamylose had 50 plants and the second classe were found in 70 plants (intermediate and high amylose content showing a segregation of 1:1 ($X^2 = 1.78$). In fact, every seed of F_2 is genetically different from the other and bulk seed analysis would gain biased information

Table 2 . Frequency distribution of the amylose content in cross Giza178/Giza 175.

Population	Amylose content% Cross I		
	Mean	Range	
Giza 178 (P_1) (L)	16.69	16.00 - 17.59	
Giza 175 (P_2) (H)	26.73	25.30 - 28.60	
(IR64x Giza 175) F_1	22.58	20.65 – 25.6	

Populations	Amylose content%	Observed frequently	X^2 1:3	1:2:1	1:1
F$_2$	13.10 – 19.2	59	54.03	—	—
	20.50 – 24.0	116	—	26.19	—
	25.50 – 35.0	75	—	—	—
BCP$_1$	8.49 – 17.49	50	—	—	1.78
	20.49 – 28.49	70			
BCP$_2$	15.79 –19.59	53	—	—	1.28
	20.79 – 28.70	67			

The results in BCP_2 analyses showed that the frequency of seeds were ranged from 15.79 –19.59%, which belonged to low amylase content and 20.79 - 28.70% belonged to intermediate and high amylose categories showed pattern in Fig(1) and the number of seeds were 53 seeds were found in category one, while 67 in category two.
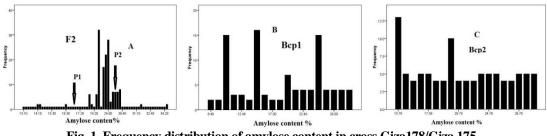

Fig. 1. Frequency distribution of amylose content in cross Giza178/Giza 175.

- Cross II (Giza 178/IR64):

This cross produced from hybridization between Giza178 variety, which low amylase content and IR64 variety, belonged to intermediate amylase content. The results showed that the amylose content in F_1 plants was 19.84% this ratioin the F_1 in endosperm was lower than intermediate amylose parent. While, the analyses of F_2 grains were ranged from 9.5 to 24.1%(Table3). The plants were classified into 3 categories (Table 3). Category 1 was 9.5% - 11% amylose 53 plants, while category 2 was ranged from 14.5-19.05% and included 126 plants. On the other hand, category 3 ranged from 21.1 - 24.1%, which included 71 plants. This results suggests a segregation ratio were 1:2:1 (X^2= 60.02), which indicated that the 53 plants were belonged to very low amylose 126 plants were belonged to low amylose and 71 plants intermediate amylose (Table 3). If it consider two categories, low and intermediate amylose containing plants, the segregation pattern was plants having very low amylose and 187 having plants intermediate and high amylose in a 1:3 ratio (X^2 = 27).

In BCP$_1$ plants segregated ratio were 1:1 (X^2 = 1.96) the first one included 43 plants were ranged from 13.67-19.78% amylose content. While the seconde one included 57 plant and ratio ranged from (0.27-24.46% (Table 3). Also, in

BCP$_2$ plants segregated ratio were 1:1, the first one included 45 seeds gave (12-19.0%)amylose category included 55 seeds (20.13-24.7% amylase content). These results recommended that, the parental lines it could be similar range for the amylose content and selection for intermediary segregants would be ineffective because the dosage effects would dissipate in further generations. Manzhong(1998).

Table 3. Frequency distribution of the amylose content in cross Giza178/IR64.

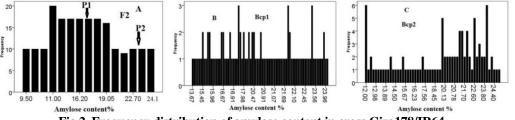| Populations	Amylose content%				
	Cross II				
	Mean		Range		
Giza 178 (P$_2$) (L)	16.69		16.00 - 17.59		
IR64 (P$_1$) (M)	23.35		22.50 - 24.2		
(Giza 178 x IR64) F$_1$	19.84		17.56 - 22.20		
Populations	Amylose content	Observed frequently	X^2		
			1:3	1:2:1	1:1
F$_2$	9.5-11	53	27	60.02	—
	14.7-19.05	126			
	21.1-24.1	71			
BCP$_1$	13.67-19.78	43	—	—	1.96
	20.27-24.46	57			
BCP$_2$	12- 19.0	45	—	—	1.00
	20.13- 24.7	55			

Fig.2. Frequency distribution of amylose content in cross Giza178/IR64.

Mean performance:

The mean of the basic generations, i.e., P$_1$, P$_2$, F$_1$, F$_2$, BC$_1$ and BC$_2$, which are shown in (Table 4). The results revealed that in most of the studied characteristics, the two parents were a wide variety of means, which is consistent with the results of (Feng *et al.*, 2017). This is an important quality trait that needs to be improved in rice. In both crosses, the mean values in F$_1$ were higher than the highest

parent for grain yield per plant, 1000- weight, grain length, hulling%, milling% and head rice%. Also, the mean values in F$_1$ for grain length and gelatinization temperature were higher than the highest parent. On the other hand, the F$_2$ mean values were intermediate between the two parents for all characters under study for the two crosses except 1000-weight and grain shape were higher than the highest parent in the cross I.

Table 4. Means and standard error of the six populations for rice yield and some grain quality characters for two crosses under study.

Generation	Grain yield /plant (g)		1000- grain weight (g)		Grain length (m)		Grain shape	
	CRI*	CRII**	CRI	CRII	CRI	CRII	CRI	CRII
P$_1$	50.53±0.02	50.53±0.04	20.40±0.04	20.40±0.04	7.42±0.01	7.42±0.01	2.40±0.01	2.40±0.01
P$_2$	45.35±0.03	57.26±0.15	20.00±0.01	22.61±0.01	7.17±0.02	8.62±0.01	2.39±0.02	3.20±0.01
F$_1$	60.13±0.06	71.47±0.10	25.70±0.02	23.17±0.07	7.69±0.03	8.78±0.01	2.51±0.01	2.73±0.02
F$_2$	48.94±0.31	56.94±.61	21.30±0.12	22.50±0.14	7.39±0.06	8.39±0.08	2.44±0.20	2.77±0.05
BCP$_1$	52.24±0.22	64.67±0.34	22.70±0.09	23.12±0.11	7.45±0.06	8.12±0.06	2.24±0.04	2.58±0.04
BCP$_2$	48.88±0.27	67.49±0.64	24.90±0.08	23.64±0.11	7.51±0.04	8.45±0.04	2.10±.003	2.81±0.12
Generation	Hulling %		Milling %		Head rice%		Gelatinization temp	
	CRI	CRII	CRI	CRII	CRI	CRII	CRI	CRII
P$_1$	80.38±0.04	80.38±0.04	70.05±0.02	70.05±0.03	65.53±0.23	65.53±0.02	6.39±0.01	6.39±0.01
P$_2$	81.08±0.05	79.19±0.01	71.10±0.02	68.50±0.06	63.33±0.02	63.30±0.01	6.02±.0.01	5.11±0.01
F$_1$	82.14±0.04	81.54±0.04	71.40±0.03	71.89±.015	66.77±0.22	65.80±0.02	6.67±0.05	5.17±0.03
F$_2$	80.90±0.12	80.34±21	71.06±0.10	69.99±0.23	64.79±0.14	63.32±0.25	6.09±.0.10	5.15±0.12
BCP$_1$	80.74±0.09	80.44±013	70.49±0.07	69.98±0.16	65.42±0.09	64.00±0.14	6.00±0.07	5.10±0.10
BCP$_2$	81.23±0.10	79.53±0.20	71.36±0.07	68.61±0.18	63.56±0.12	58.78±0.21	5.03±0.07	4.40±0.09

*= Cross I (Giza178/Giza 175) and **= Cross II (Giza 178/IR64).

Moreover, BCP$_1$ were higher than the highest parent for grain yield, 1000-grains weight traits in both crosses, grain length in cross I and hulling% in cross II. While, BCP$_2$

mean values were higher than the highest parent for grain yield in cross II, 1000-grain weight in both cross, grain length, hulling%, milling %,head rice% in cross I.

Scaling tests: Data in (Table5) showed that scaling test for adequacy of additive and dominance model of grain yield, 1000-grain weight, grain physical character, milling characters cooking and gelatinization temp in the two crosses under study. The scaling test was significant for one scale in both the crosses for all the traits under study.

Heritability in broad and narrow sense: Data in(Table 5) showed that head rice percentage followed by milling percentage in crossII recorded the highest broad sense heritability (99.62 and 99.60%, respectively) and narrow sense were (98.04 and 97.16%, respectively) compared to anther cross under study (Table 5). While, were lowest for Hulling% in cross1(85.59 and 59.54, respectively). Heritability, the broad sense values, was high for all studied characters in two crosses. While, heritability estimates in the narrow sense were moderate to high values for all characters in all study crosses. These results were in agreement with those obtained by partitioning of the genetic variance and also agreement with those reported by Bharadwaj *et al.*, (2007). High heritability values were expected, because most likely such traits are controlled by additive gene effects (Bagati *et al.*, 2016).

Heritability estimates in broad sense for all characters under study was higher than narrow sense heritability indicating that the selection in early generation may be not effective in improving such characters (Salem *et al.*, 2015). Its also will helping plant breeders in selecting elite genotypes from a diverse genetic population, so prior knowledge of trait heritability is needed for any selection programme (Singh *et al.*, 2011). Broad sense heritability explains aadditive, dominant and epistatic variances which helps in estimating the inheritance of a characters (Nirmaladevi *et al.*, 2015).

Table5. Scaling test for adequacy of additive and dominance model of all studied characters in the two studied crosses.

Characters	Crosses	A	B	C	HBs	HNs
Grain yield /plant	CRI	-6.17±0.44**	-7.74±0.55**	-20.40±1.23**	98.53	69.79
(g)	CRII	7.34±0.68**	6.26±1.28**	-22.95±2.47**	98.88	63.29
1000-grainweight	CRI	-0.70±0.18	4.07±0.17**	-6.06±0.48**	94.32	94.21
(g)	CRII	2.67±0.24**	1.49±0.23**	0.62±0.59**	89.45	77.07
Grain length	CRI	-0.21±0.12**	0.15±0.18**	-0.42±0.24**	87.83	61.93
(m)	CRII	0.05±0.12**	-0.49±0.09**	2.01±0.28**	97.44	79.68
Grain	CRI	-0.44±0.07**	-68±0.07**	-0.03±0.18**	93.58	79.59
shape	CRII	0.03±0.08**	0.33±0.09**	0.51±23**	90.24	90.16
Hulling	CRI	-1.04±0.20**	-0.75±0.22**	-2.12±0.47**	85.59	59.54
%	CRII	-1.03±0.27**	-1.67±0.40**	**-1.30**±0.86	97.49	76.08
Milling	CRI	-3.14±0.15**	1-.46±0.15**	0.80±0.39*	95.59	85.80
%	CRII	-1.97±0.32	-3.34±0.32**	2.38±0.83**	99.60	97.16
Head rice	CRI	-8.26±18**	-12.40±24**	4.19±57**	98.38	90.80
%	CRII	-3.34±0.29**	-11.53±.43**	-7.14±0.98**	99.62	98.04
Gelatinization	CRI	-1.05±0.16**	-2.63±0.15**	-1.37±.41**	91.93	88.83
temp	CRII	-1.19±0.19**	-1.48±0.18**	-1.25±0.50**	97.70	87.60

*Significant at 5% level **Significant at 1% level, respectively. Where(CR1) Giza178/Giza 175and CRII((Giza 178/IR64).HBs (broad sense heritability) and HNs (narrow sense heritability).

Genetic Component of Generation Means:

Grain yield /plant: The results obtained from (Table 6) revealed that additive gene effect (d) was highly significant and positive in cross I, in contrast the same parameter was significant and negative in cross II .While, dominance gene effect (h) gene effect and additive x dominance interaction were significant and positive in two crosses. Additive x additive and dominance x dominance were positive and significant in cross I (Table 6)**.**

According for1000-grain weight, the results shwed that additive gene effect (d) was highly significant and negative in two crosses under study, while dominance gene effect (h) and additive x additive gene effects were significant and positive in both crosses. Additive x dominance gene effect was significant and negative in cross I but the same parameters was significant and positive in cross II. However, the negative significant (I) in two crosses under study (Table 6). For grain length,which is important quantitative traits closely related to the exterior quality of rice. Grain length is considered to be the fast stable characters compared to other traits (Juliano 1993). However, data in (Table 6) indicated that the highest grain length was recorded in cross II (8.39), while the lowest one was recorded in cross I (7.39). Also, additive effect was highly significant and negative in both crosses. The dominance effect was highly significant in positive direction in crosses I and II. While, additive x additive gene interaction was highly significant and negative direction in cross II, In contrast the same parameters were highly significant in positive direction in crossI. The additive x dominance and dominance x dominance gene effects were significant and positive in cross II but the same parameters were significant and negative in cross I. 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 Abd El-Lattef *et al*. (2012).

As for grain shape, The data in (Table 5) indicated that the means were highly significant for both crosses for grain shape and the additive effect was positive significant in cross I, while the additive effect and additive x additive (i) interaction were negative significant in two crosses. Additive x dominance (j) and dominance x dominance (1) interaction were positive negative significant for cross I. The components were oriented in the opposite direction, suggesting duplicate epistasis for this trait, for which bi-parental mating was proposed. Duplicate types of epistasis were also reported by Nayak *et al*., (2007). Grain shape is simultaneously controlled by triploid endosperm, cytoplasmic as well as maternal genes (Rafii *et,al*., 2014).

In hulling % trait: The estimated values of the six parameter model's parameters m, d, h, I j, and l are shown in (Table 6) and the results showed that the cross I recorded highest hulling recovery (80.90%), while cross II recorded the lowest one (80.84). Additive (d) gene effect was significant and positive in cross II only, while additive (d) gene effect was highly

significant and negative in cross I (Table 6). Highly significant and positive dominance (h) gene effect was found in cross I. Additive x additive (i) interaction effect was non-significant crosses I and II. Dominance x dominance [l] effect was positive and significant in cross II and cross I was found to be significant and negative. Two crosses (I and II) recorded significant and positive additive x dominance [j] epistatic effects. In cross I dominant effect and dominant x dominant effect were displayed with opposite signs and then indicated the presence of duplicate epistasis (non-allelic gene interactions).

Milling%: Data in (Table 6) showed that the mean of cross I gave the highest value of milling% comparing anther cross. In cross II the data gave positive and significant, while cross I gave negative and significant additive, [d] gene effect. The dominance [h] effect was no significant for both crosses (Table 6). Additive x additive [i] interaction effect was significant and negative for both crosses under study. Additive x dominance [j] was positive and significant in cross II, while it was negative and significant in cross I. Cross I and cross II exhibited positive and significant dominant X dominant effects for milling percentage. In cross II dominance effects and dominant X dominant effects were displayed with opposite signs that indicated the presence of duplicate epistasis. The presence of epistatic gene effects causes an upward bias in the estimates of both additive and dominance geneticvariance (Hayman, 1957).

When epistasis is of major importance, it is impossible to obtain unbiased estimates of additiveor dominance genetic effects. As a result, epistatic components must be considered when developing breeding programmes for new varieties (Paul *et al.*, (2003)**.**

For head rice%, data in (Table 6) showed that mean of cross I was superior in head rice% comparing with another cross. Additive [d] gene effect was significant and positive for both crosses under study (Table 6). While, dominance [h] gene effect was significant and positive for cross I and it was significant and negative for cross II. Additive x additive [i] gene effectwas negative and significantin twocrosses under study.Additive x dominance effect [j] and dominance x dominance [l] effect were significant and positive for both crosses (Venkanna, 2014).

In gelatinization temperature trait: the analysis of gene effect in six-parameter model indicated that additive gene effect (d) was significant and positive in crosses I and II. While, dominance gene effect (h)and additive x additive (i)were significant and negative in both crosses. On the other hand, additive x dominance gene effect (j) and dominance x dominance(I) were significant and positive for two crosses under study in Table 6. The negative or positive signs for additive effects depend on which parent is chosen as P_1. These results were agreements with (Bassuony and Lightfoot 2019), while (Tomar and Nanda 1985) reported duplicate epistasis for gelatinization temperature.

Table 6. Genetic component of generations mean all characters in the two rice crosses under study.

Characters	Crosses	m	d	h	i	j	I
Grain yield /plant	CRI	48.94**	3.37**	18.68**	6.49**	0.78**	7.43**
(g)	CRII	56.94**	-2.83**	54.11**	36.54	0.54**	-50.13**
1000-grain weight	CRI	21.30**	-2.19**	15.47**	9.97**	-2.38**	-13.34**
(g)	CRII	22.50**	-0.52**	5.21**	3.54**	0.59**	-7.70**
Grain	CRI	7.39**	-0.06**	0.76**	0.35**	-0.18**	-0.29**
length	CRII	8.39**	-0.26**	0.20**	-0.56**	0.34**	1.14**
Grain	CRI	2.44**	0.14**	-0.99**	-1.10**	0.13**	2.23**
shape	CRII	2.77**	-0.22**	-0.36**	-0.29**	0.18	0.58
Hulling	CRI	80.90**	-0.50**	1.74**	0.33	-0.15**	1.45**
%	CRII	80.84**	0.91**	0.35	-1.40	4.11*	6.11**
Milling	CRI	71.06**	-0.87**	0.26	-0.56**	-0.34**	0.81**
%	CRII	69.99**	1.37**	-0.15	-2.76**	0.60**	7.91**
Head rice	CRI	64.79**	1.86**	1.13**	-1.21**	0.75**	5.64**
%	CRII	63.32**	5.22**	-6.34**	-7.72**	4.10**	22.59**
Gelatinization	CRI	6.09**	0.98**	-1.85**	-2.31**	0.79**	5.99**
temp	CRII	٥.١5**	0.78**	-2.00**	-1.42**	0.14**	4.08**

* Significant at 5% level **Significant at 1% level, respectively. Where (CR1)Giza178/Giza 175and CRII((Giza 178/IR64). And m, mean of F2,d,additive effect, h, dominance effect, i, additive x additive, J, additive x dominance , I, dominance x dominance.

CONCLUSION

From the results it can be concluded that cross I, which produced from Giza178 (low amylose) x Giza 175 (high amylase). The results indicated F_1 plants were intermediate amylase, indicated that high amylose content was incompletely dominant over low amylose. While, the cross II produce from Giza 178(low amylose) x IR64 (intermediate amylose) the results indicated that selection for intermediary segregants would be ineffective because the dosage effects would dissipate in further generations.

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دراسات وراثية لمحتوى الأميلوز والمحصول وخصائص جودة الحبوب في أنماط وراثية مختلفة من الأرز (.Oryza sativa L)

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قسم بحوث الأرز بسخا ـ كفر الشيخ معهد بحوث المحاصيل الحقلية ـ مركز البحوث الزراعية

تعد التربية لانتاج أصناف الأرز الجديدة ذات صفات جودة عالية فى الحبوب وخاصة المحتوى المنخفض من الأميلوز أحد أهم الأهداف في برامج تربية النباتات. وقد أجريت الدراسة الحالية في مزرعة قسم بحوث الأرز والتدريب (RRTC) ، سخا ، كفر الشيخ ، مصر ، خلال ٢٠١٨-٢٠١٩ و ٢٠٢٠. كما تم استخدام ثلاثة طرز وراثية من الأرز مختلفة المحتوى من الاميلوز وهي (جيزة ١٧٨ ، وجيزة ١٧٥ ، و IR64) وذلك لدراسة محتوى الأميلوز وبعض الصفات المحصولية الاخرى. وتم عمل التهجينات بينهما من خلال التهجين بين الاباء المنخفضة المحتوى من الاميلوز والاباء المتوسطة والعالية المحتوي الأميلوز في الأرز (.Oryza sativa L) كما تم تقدير التوريث لبعض صفات المحصول وجودة الحبوب في الأرز من خلال دراسة ستة أجيال P1 وP2 و F1 و F2 و BCP1 و BCP2 الناتجة من التهجين بين جيزة ١٧٨ الهجين I (محتوى منخفض من الأميلوز) × جيزة ١٧٥ (محتوى مرتفع من الأميلوز) و هجين II جيزة ١٧٨ (محتوى منخفض من الأميلوز) × IR64 (محتوى أميلوز متوسط). تم استخدام تصميم القطاعات الكاملة (RCBD) بثلاثة مكررات.الهجين I (جيزة ١٧٨ / جيزة ١٧٥) . جيزة ١٧٨ منخفض الأميلوز (١٦,٦٩٪) جيزة ١٧٥ مرتفع الأميلوز (٢٦,٧٣٪) و محتوى الأميلوز للنباتات الجيل الاول الناتجة وسط بنسبة ٢٢,٥٨ ٪ .وتراوح محتوى الأميلوز في نباتات الجيل الثانى من ١٣,١٠ إلى ٣٥٪ ، ويمكن تصنيف نباتات الجيل الثانى أساسًا إلى فئتين : ١٣,١٠-١٩,٠ و ٢٠,٥٠- ٣٥٪.كانت نسبة الأميلوز العالية سائدة بشكل غير كامل على الأميلوز المنخفض.بينما أوضحت نتائج الهجين الثاني (جيزة IR64x١٧٨) (جيزة ١٧٨ منخفض محتوي الأميلوز) و (IR64 متوسط محتوي الأميلوز) فكانت نباتات الجيل الاول منخفض محتوي الأميلوز في هذا التهجين كان(١٩,٨٤٪) وتراوحت قيم الأميلوز في نباتات الجيل الثاني من ٩,٥ إلى ٢٤,١.يمكن تصنيف النباتات إلى ٣ فئات.الفئة ١(٩,٥ ٪ - ١١٪) ، الفئة ٢ (١٤,٥-١٩,٠٥٪) ولفئة ٣ (٢١,١-٢٤,١٪) سيكون اختيار نباتات متوسطة محتوي الأميلوز غير فعال لأن تأثيرات الجرعة ستتبدد في أجيال أخرى.كان اختيار القياس معنويا لمقياس واحد في كلا الهجينين لجميع صفات الجودة المدروسة.كانت تقديرات التوريث بالمعنى الضيق قيم متوسطة إلى عالية لجميع الصفات في جميع هجن الدراسة. كما كانت تقديرات التوريث بالمعنى الواسع لجميع الصفات قيد الدراسة أعلى من التوريث بالمعنى الضيق.