A Breeding Study of Some Grain Quality Characters in Rice (*Oryza sativa* L.)

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Abstract

The present study was conducted at the farm of The Rice Research and Training Center, (RRTC), Sakha, Kafr El-Sheikh, Egypt, during the 2016, 2017 and 2018 seasons. Six rice cultivars (Oryza sativa L.) that differed in their grain quality characters were used as parents to produce six generations of three crosses of rice namely 'Giza178'×'Egyptian Yasmine', 'Giza177'×'UPR82-1-7' and 'IET1444'×'Pusa Basmati1'. Generation mean analysis was used to estimate types of gene actions, heterosis, inbreeding depression, heritability and genetic advances for milling%, grain dimensions and cooking and eating characters. The results indicated that the scaling test was significant for one scale in all the crosses for all the traits, indicating an inadequacy of the simple additive dominance model. Segregation analysis indicated partial dominance for grain quality characters for almost crosses except gel consistency and amylose content percentage. This suggested over dominance for most traits in most crosses. Moreover, evaluation of genetic parameters indicated the importance of additive gene effects. That were significant and positive in the inheritance of grain quality characters for the three crosses. Exceptions were grain length and grain shape which were significant and negative. Different types of gene action were detected, varying by the characters and the crosses under study. Epistasis was observed among the crosses. Heritability estimates for milling and eating and cooking quality were low to moderate indicating that selection exercised in late generations may be effective. Heritability estimates for grain dimensions were high, suggesting that selection in early generation will be effective in future.

Keywords: *Oryza sativa*, Back Cross, Grain Quality.

Introduction

Rice (*Oryza sativa* L.) is an important staple food crop in many parts of the world. (Manful 2010). It feeds more than 50% of Earth's inhabitants especially in developing countries Yield is the most noticeable characteristic to farmers while the crop is in the ground, but when the product of the crop, the milled rice, reaches the market, quality becomes the key determinant of its sale-ability .Thus Rice breeders presently pay great attention to rice quality improvement (Gnanamalar and Vivekanandan, 2013). Grain quality is one of the most important quantitative traits in rice. It is a multi-faceted trait involving physical and biochemical aspects relating to milling, appearance, cooking and eating quality and nutrition (Fitzgerald et al., 2009; Bao, 2014). The grain and cooking characters which are influenced by physico-chemical properties of starch play an important role in determining the texture and consumer acceptance of cooked rice. Many of the physico-chemical quality characters follow a complex polygenic mode of inheritance. The characters gel consistency and head rice recovery percentage contributed maximum towards genetic divergence (Chamundeswar, 2010). The generation mean analysis has been considered to be one of the best methods for estimating the different components of genetic variance and presence or absence of epistasis. The concept of generation mean analysis was developed for the estimation of genetic components of variation. Additive and non-additive gene action were found for amylose content Swain and (Nagaraju, 2004). Additive and non-additive gene action for grain shape (Kumar et al., 2006; Nayak et al., 2007) while studying genetics of quality characters in three crosses found that kernel length was controlled by both additive and dominance effects, kernel length/breadth ratio was controlled by additive, dominance and epistatic effects in all crosses. For alkali spreading value, additive, dominance and all three interactions were important.

Cooked kernel length was controlled by additive (d), and additive x additive (i), additive, dominance (h) and additive and additive (i) were significant. Additive, dominance and epistatic gene actions of additive x additive and dominance x dominance and duplicate type of interaction controlled the elongation ratio. Amylose content was under the control of duplicate epistasis. Lakshmi (2009) studied generation mean analysis in two crosses and found that both additive ([d]and [i]) and dominant type ([h] and [l] components were significant for hulling percent, gelatinization temperature for both the crosses. Additive variance was available for selection for head rice recovery and kernel elongation . Before launching any breeding program, surveys of genetic variability are absolutely necessary to start an efficient breeding program. Heritability and genetic variability are prerequisites for carrying out selection based improvements. The information about these help breeding programmes by broadening the gene pool of rice and gives an indication about the efficiency of transformation of characters into future generations (Selvaraj et al., 2011). The detection and estimation of epistasis would also enable the breeders to understand the genetic cause of heterosis with greater reliability. Lacking information about these breeding parameters, the present study was planned to investigate the genetics of some grain quality characters by using six-generations of the three crosses under normal conditions.

Materials and Methods

The present study was conducted at the farm of The Rice Research and Training Center, (RRTC), Sakha, Kafr El-Sheikh, Egypt, during 2016, 2017 and 2018 seasons to study the genetic behavior of some grain quality characters of rice cultivars . Six rice cultivars that differed in their grain quality characters 'Giza 178' and 'Giza 177' (both short grain) and 'Egyptian Yasmine, 'IET1444', 'UPR82-1-7' and 'Pusa Basmati' (all long grain) were used as parents to produce six generations of three crosses of rice. Namely Giza 178×Egyptian Yasmine, Giza 177×UPR82-1-7 and IET1444 × Pusa Basmati 1 were used to apply generation mean analysis. Reciprocal crosses were carried out following the technique proposed by Jodon (1938) and modified by Botany (1961) in the 2016 season. Hybrid seeds along with the parents were grown in the next season (2017). Some of the F1s were left for self-fertilization to produce seeds of F2 plants and some were back crossed with the parents to produce of BC1 (F1xP1) and BC2 (F1xP2). In 2018, parents, F1, F2 and backcross (BC1 & BC2) generations were raised in the field. Experiments were laid out in a randomized complete block design with three replications. Each replicate contained a single row for parental lines, and F1's, with eight rows for each of the backcrosses and 15 for the F2 generation. The length of each row was one meter. Row to row and plant to plant distance was 20 cm. Normal agronomic practices were followed for growing the crop. At maturity five plants per replication for F1 and each parent, 50 for each of the backcrosses and 100 for the F2 generation were selected to harvest grain rice on individual plant basis. About 150 grams (three replication) of rough rice for all samples were taken and well mixed and cleaned.

All samples were analyzed for the following grain quality characters:

1. Milling Characters: Hulling%, Milling% and Head rice% were determined according to Adair (1952) by using Satake testing machines.

2. Physical characters: Grain length, width and shape were measured for milled rice grain according to Khush et al. (1979).

3. Cooking and eating quality characters: Gelatinization temperature (G.T.), amylose content and gel consistency test (G.C.) were estimated for milled rice samples following the methods of Little et al., (1958). Juliano (1971) and Cagampang et al. (1973) respectively. Elongation ratios were calculated according to Azeez and Shafi (1966).

Genetic parameters as broad and narrow sense heritability's were estimated according to Powers et al. (1950) and Warner, (1952), respectively. Genetic advance in percent of mean and phenotypic and genotypic coefficients of variations were estimated using the procedure suggested by Burton, (1952). The following genetic parameters were estimated for the studied characters, heterosis and degree of dominance followed Mather and Jinks, (1971), scaling test for adequacy of additive and dominance model and genetic components followed Mather, (1949) and expected genetic advance (Gs %) after Johnson et al. (1955).

Results and Discussion

1. Scaling Tests

Table 1 showed scaling test for adequacy of additive and dominance model of milling characters, grain physical characters, cooking and eating characters in the three studied crosses. The scaling test was significant for one scale in all the crosses for all the quality traits studied, indicating inadequacy of simple additive dominance model.

2. Genetic Parameters

2.1. Degree of Dominance

Milling characters and grain dimensions (Table 2) showed partial dominance in all crosses except cross 1 for hulling % and cross2 for head rice % were over dominance. According to Sivasubramanian and Mahadevamenon (1973), hulling percentage was independent of grain size and shape and all these traits showed partial dominance. Kernel elongation and gelatinization temperature indicated partial dominance in all crosses except cross 3 for kernel elongation and cross 2 for gelatinization temperature were over dominance. While gel consistency and amylose content % indicated over dominance except cross 3 for amylose content% was partial dominance.

It was remarkable that partial to complete and/or over dominance were both detected for all crosses for the studied characters depending on the crosses as well as the character.

Table 1. Scaling test for adequacy of additive and dominance model of all tested characters in the three studied crosses.

Characters	Crosses	A	B	C
Hulling%	CR1	66.312±3.361**	60.162±0.511**	49.932±0.723**
	CR2	63.932±4.71**	63.177±461**	51.872±0.872**
	CR3	59.702±4.66**	60.272±0.611**	32.733±0.549**
Milling %	CR1	73.182±1.336**	70.364±0.812**	65.983±0.783**
	CR2	71.251±0.983**	71.453±o.793**	71.974±0.830**
	CR3	68.311±o.888**	68.433±0.731**	71.991±0.772**
Head rice %	CR1	12.831±0.361**	11.543±1.361**	9.875±0.655**
	CR2	14.546±0.451**	13.612±2.666**	10.812±0.763**
	CR3	13.477±0.989**	14.876±1.782**	9.755±0.876**
Grain length	CR1	0.923±0.012**	0.936±0.213**	0.765±0.0231**
	CR2	0.836±0.23 **	0.886±0.179**	0.807±0.119**
	CR3	1.341±0.046**	0.995±0.119**	0.931±0.291**
Grain width	CR1	0.069±0.078**	0.106±0.057**	0.244±0.065**
	CR2	0.076±0.034**	0.093±0.049**	0.497±0.031**
	CR3	0.076±0.091**	0.087±0.032**	0.466±0.072**
Grain shape	CR1	0.735±0.041**	0.981±0.041**	0.874±0.034**
	CR2	0.899±0.038**	0.889±0.061**	0.763±0.044**
	CR3	0.754±0.056**	0.0902±0.522**	0.7755±0.066**
Grain Elongation	CR1	28.119±0.836**	22.736±1.036**	17.851±0.833**
	CR2	21.816±0.903**	18.546±0.921**	22.789±0.729**
	CR3	15.940±0.776**	7.833±0.711**	8.134±0.727**
Gelatinization temp	CR1	2.664±0.236**	1.352±0.254**	2.493±0.336**
	CR2	2.912±0.117**	2.667±0.254**	2.576±0.256**
	CR3	3.092±0.269**	1.445±0.336**	3.122±0.364**
Gel Consistency	CR1	15.723±0.859**	16.345±1.514**	21.333±1.23**
	CR2	7.441±0.913**	8.711±1.362**	17.879±2.06**
	CR3	18.762±1.25**	20.933±0.561**	8.65±0,994**
Amylose content%	CR1	4.933±0.298**	3.091±0.664**	1.696±0.664**
	CR2	5.664±0.342**	1.283±0.451**	0.997±0.367**
	CR3	0.339±0.369**	4.237±0.955**	2.367±0.489**

*Significant at 5% level **Significant at 1% level, respectively. Where(CR1), Giza 178xEgyptian yasmine; CR2 ,Giza 177xUpr 82-1-7 and CR3.IET1444 x Pusa Basmati 1.

2.2. Additive Genetic Variance and Dominance Genetic Variance

Table 2 indicated that additive genetic variance (½D) were higher than that of the dominance genetic variance (¼H) in three cross under study for milling characters, grain dimensions and all cooking and eating quality, but the dominance variance was the highest value in cross 1 and cross 3 for the milling %. The results suggested that early generation selection may be effective in improving of milling % in these crosses cross 1 and cross 3. These results were observed indicated that additive that variance played an important role in the inheritance of milling characters in these crosses. The same results for grain length, grain width and grain shape characters in the three crosses. Similar results were obtained by Kishore et al. (2008).

In cross 2 both additive and dominance variance in milling % hulling % and cross 1 for head rice were the biggest value. Both additive and non-additive gene effects were important for amylose content with predominance of additive effects (Chamundeswari, 2010).

2.3. Broad and Narrow Sense Heritability

It is clear from Table 2 that hulling percentage in cross 2 recorded the highest broad sense heritability (78.92%) and narrow sense (63.85%) (medium) compared to the other crosses studied (Table 2). Broad sense heritability and narrow sense heritability estimates were lowest for milling % in cross1.The highest broad sense heritability was observed for cross 3 and the same cross gave 38.07 for narrow sense. Heritability, the broad sense value, was high. While , heritability estimates in the narrow sense was moderate values in all study crosses for head rice %. Moreover, the results in Table 2 indicated that heritability broad sense values were high for grain dimensions. On the other hand, heritability estimate in the narrow sense was moderate. These results were in agreement with those obtained by partitioning of the genetic variance. These results also were in 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).

Table 2. Estimation of genetic parameters for all tested characters in the three crosses.

characters	Crosses	Degree of Domains	Genetics variance		Heritability		G.S%
			½D	¼H	Broad sense	Narrow sense	
Hulling%	CR1	-5.5131	0.0642	0.0175	67.49	53.01	0.487
	CR2	-0.6329	0.1982	0.0368	78.92	63.85	0.920
	CR3	0.7617	0.0827	0.0217	78.37	62.09	0.591
Milling %	CR1	0.4020	0.2077	0.2246	65.92	31.66	0.741
	CR2	0.5271	0.3794	0.1923	71.16	47.22	1.195
	CR3	0.6089	0.1861	0.3132	82.87	38.07	0.922
Head rice %	CR1	0.5665	0.5912	0.2117	81.01	59.52	1.8284
	CR2	1.7864	0.4930	0.1317	68.70	54.22	1.6268
	CR3	0.9952	0.3486	0.1259	76.79	56.79	1,6882
Grain length	CR1	-0.2602	0.0534	0.0183	71.04	52.87	4.745
	CR2	0.2916	0.0336	0.0094	70.84	55.35	6.235
	CR3	0.0480	0.0657	0.0266	81.42	57.97	6.235
Grain width	CR1	-0.3529	0.0471	0.0303	92,46	56.27	14.27
	CR2	-0.1340	0.0282	0.0127	83.81	57.79	9.358
	CR3	0.1612	0.0609	0.0510	93.50	50.88	15.629
Grain shape	CR1	-0.1895	0.0429	0.0213	88.05	58.89	13.767
	CR2	0.1736	0.0106	0.0054	76.36	50,66	7.177
	CR3	-0.1865	0.0427	0.0334	85.31	47.45	10.449
Kernel Elongation	CR1	0.2014	4.7975	1.4820	51.85	39.61	4.299
	CR2	-0.9706	4.7411	4.7240	52.56	26.33	3.905
	CR3	-1.2577	4.2547	2.1841	60.52	39.99	5.04
Gelatinization T temp	CR1	0.1594	0.3546	0.2244	74.81	45.81	18.128
	CR2	1.5900	0.4286	0.1794	70.34	49.58	22.503
	CR3	-8.660	0.3524	0.6874	98.45	33.37	14.939
Gel consistency	CR1	1.3406	1.5908	5.7855	79.28	17.10	1.310
	CR2	2.2727	5.6670	17.441	82.54	20.24	2.658
	CR3	5.2350	6.3623	5.2121	75.39	41.44	4.252
Amylose content%	CR1	1.5593	0.2938	0.1331	45.07	31.01	3.267
	CR2	-1.1343	0.3040	0.1433	50.46	34.30	3.368
	CR3	-.05726	2.3020	1.0400	51.22	35.29	7.014

(CR1), Giza 178xEgyptian yasmine; CR2, Giza 177xUpr 82-1-7 and CR3.IET 1444 x Pusa Basmati 1.

Heritability estimates in broad sense for all cooking and eating characters 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). The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic population, hence prior knowledge about the heritability of the traits is a prerequisite for any selection program (Singh et al., 2011). Broad sense heritability explains both fixable (additive) and non-fixable (dominant and epistatic) variances which helps in estimating the inheritance of a character (Nirmaladevi et al., 2015). On the basis of heritability the traits are classified into 3 categories: highly heritable (>70%), medium heritable (50 - 70%) and low (< 50%), (Robinson, 1966).

2.4. Genetic Advances

Genetic advance as percent mean was categorized as low (0-10%) in all crosses for milling characters, grain length, kernel elongation, gel consistency and amylose content%. Low genetic advance values were gotten in studied crosses with low narrow sense heritability for all milling character could be expected because this trait is under polygenic control. Genetic advance for grain width, grain shape and gelatinization temp was medium for all crosses under study except cross 2. Grain width and grain shape Ga was low except in cross 2 where high genetic advances were seen.

3. Genetic Component of Generation Means

3.1. Milling characters:

3.1.1. Hulling Percent

The estimated values of the parameters m, d, h, i, j and l of six parameter model are shown in (Table 3). The mean values for this trait ranged from 77.985% to 79.690, cross 2 recorded highest hulling recovery of 79.690% while cross 1 recorded

the lowest one (77.985) for hulling percentage, additive[d] gene effects were significant and positive in all crosses (Table 3). Highly significant and positive dominance [h] gene effects and were observed in cross3 and highly significant and negative dominance [h] gene effects were observed in cross 1 and cross 2. Additive x additive [i] interaction effects were significant and negative in crosses 1 and 2. The magnitude of additive x additive [i] effects were highest in the cross 1. Dominance x dominance [l] effects were positive and significant in crosses 1, 2 and 3 of was found to be significant and negative. Two crosses (1and 2) recorded significant and positive additive x dominance [j]epistatic effects whereas anther cross expressed negative significant effects. In three crosses dominant effect and dominant x dominant effects were displayed with opposite signs and then indicated the presence of duplicate epistasis (non-allelic gene interactions).

3.1.2. Milling Percent

Data in Table 3 showed that the mean of cross 2 was superior in milling % comparing with the other two crosses. Two crosses (cross 1 and cross 2) recorded positive and significant, while cross 3 recorded negative and significant additive, [d] gene effects. The role of dominance [h] effects were observed for cross 3, it exhibited highest positive and significant effects (Table 3).

Additive x additive [i]interaction effects were significant and positive in cross 3 whereas cross 1 and cross 2 recorded negative and significant effect. Additive x dominance [j] was positive and non-significant in case of cross 2, while it was negative and significant in cross 1 and cross 3. Negative and significant dominance x dominance [l] effects were observed in cross 3, whereas cross 1 and cross 2 exhibited positive and significant effects for milling percentage. In two crosses 1and 2 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 genetic variance (Hayman, 1957). When epistasis is of major importance, it is impossible to obtain unbiased estimates of additive or dominance genetic effects. Therefore epistatic components cannot be ignored in formulating breeding programs to develop varieties. (Paul et al., 2003).

3.1.3. Head Rice Recovery

Data indicated also that mean of cross1 was superior in head rice % comparing with the other cross. Additive [d] gene effects, dominance [h] gene effects and effects additive x additive [i] gene effects were significant and positive for all crosses under study (Table 3). Additive x dominance [j] effects were positive and significant in cross 1 and cross 2, while negative and significant in cross 3. All the three crosses exhibited negative and significant dominance x dominance [l] effects (Venkanna, 2014).

4. Physical Characters

Data in Table 3 indicated that mid parent value for grain length, (m) was highly significant in all crosses. The highest estimated value was recorded in cross 3 (6.45) followed by cross 2 (5.920) then cross 1 (5.590). Moreover, additive effect was highly significant in negative direction in all crosses but cross 1 had the highest value. In addition, the genetic parameters, dominance effect, additive x additive type of gene interaction were highly significant in negative direction in cross 2, but the same parameters were highly significant in positive direction in crosses 1 and cross 3. In contrast, the additive x dominance type of gene interaction was found to be highly significant in cross 3. Whereas, dominance x dominance type of gene interaction was found to be highly significant in positive direction in crosses 2. 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) and Hassan et al. (2013).

The classification of epistatis largely depends on the parameters dominant effect (h) and dominant X dominant (I). According to Mather and Jinks (1971), if dominance effect and dominant X dominant are significantly different from zero and have opposite signs, then duplicate epistasis is indicated. The same two parameters here, were significant, had same sign and, thus, indicated the presence of complementary epistatis.

The estimates of mean (m) were highly significant for all the crosses for grain width (Table3). Additive effects were found significant in cross 2 only, but Additive effects were observed as non-significant in cross 1 and cross 3. Non-significant in those cases may be ascribed to large error variances (Edwards et al.,1975).Whereas dominance effect was significant for all cross. Additive x additive (i) interaction was significant for all crosses, additive x dominance (j) interaction was significant for cross1 and cross 2, whereas dominance x dominance (1) interaction was also significant for cross 1 and cross 2.

The data in Table 3 indicated that the estimates of mean (m) were highly significant for all the crosses for grain shape. The additive effect was negative significant in cross 2 and cross 3, While the dominance effect was positive significant for crosses 2 and 3. Additive x additive (i) interaction was significant for crosses1 and 2, additive x dominance (j) interaction was significant for cross 2 and cross 3, whereas dominance x dominance (1) interaction was also negative significant for cross 3. The components were opposite in direction indicating duplicate epistasis for this trait for which bi-parental mating was suggested. Duplicate types of epistasis was also reported by Nayak et. al. (2007). Kernel length, kernel width, length/width ratio, elongation ratio, were controlled by additive gene action. Vivekanandan and Giridharan (1995).

5. Cooking and Eating Characters

5.1. Elongation

Table 3 indicated the highest mean value of elongation was found with cross 1. Results obtained from regression analysis

Table 3. Genetic component of generations mean all tested characters in the three rice crosses.

Characters	Crosses	m	d	h	i	j	l
Hulling%	CR1	77.985**	0.996**	-3.692**	-2.848**	0.843**	7.401**
	CR2	79.690**	2.507**	-2.547**	-1.202**	0.382**	4.494**
	CR3	78.961**	1.112*	4.174**	0.044	-4.311**	-9.241**
Milling %	CR1	71.270**	1.224**	-3.619**	-4.356**	-0.611**	4.797**
	CR2	72.944**	2.686**	0.779	-0.576	0.121	3.220**
	CR3	71.089**	-2.415**	11.748**	7.814**	-8.875**	-23.516**
Head rice %	CR1	66.833**	4.317**	4.167**	3.034**	2.317**	-1.134
	CR2	65.473**	4.659**	18.303**	15.418**	3.044**	-9.297**
	CR3	54.114**	02.312**	27.077**	20.408**	-9.013**	-4.458**
Grain length	CR1	5.590**	-0.960**	0.835**	1.092**	0.030	-1.045**
	CR2	5.920**	-0.578**	-1.504**	-1.664**	-.028	2.031**
	CR3	6.450**	-0.507**	0.984**	0.934**	0.533**	-0.936**
Grain width	CR1	2.350**	0.053	0.316*	0.360**	-.032	-0.420*
	CR2	2.810**	0.280**	-0.582**	-0.560**	0.120**	0.667**
	CR3	2.32**	0.097	0.348*	-.0394**	-0.192**	0.255
Grain shape	CR1	2.379**	-0.446	0.027	0.120	0.048	-.005
	CR2	2.107**	-0.434**	-0.080**	-0.136*	-0.109**	0.183
	CR3	2.805**	-0.365**	0.695**	0.866**	0.552**	-0.450*
Grain Elongation	CR1	66.047**	7.592**	21.967**	19.615**	-4.089**	-89.278**
	CR2	58.922**	9.281**	50.748**	58.340**	1.460	120.944**
	CR3	53.263**	9.834**	-38.365**	-27.900**	1.514*	36.376**
Gelatinization temp	CR1	4.580**	-0.050	0.115	0.060	0.295	2.250**
	CR2	4.220**	0.006	1.153**	0.420	0.467**	3.110**
	CR3	4.729**	0.057	2.737**	3.170**	0.107	1.610*
Gel consistency	CR1	82.00**	-5.837**	41.260**	36.993**	-2.654**-	-13.521**
	CR2	83.00**	-7.666**	-14.418**	-20.668**	10.416**	8.836*
	CR3	78.667**	12.667**	6.832**	-8.002**	9.836**	19.669**
Amylose content%	CR1	19.030**	-0.849**	0.243	-0.198	-0.567**	1.647*
	CR2	19.750**	0.865**	-6.530**	5.558**	1.722**	11.879**
	CR3	26.443**	2.992**	-0.483	0.144	1.897**	3.366

* significant at 5% level **Significant at 1% level, respectively. Where(CR1),Giza 178xEgyptian yasmine; CR2 ,Giza 177xUpr 82-1-7 and CR3.IET1444 x Pusa Basmati 1. And m, mean of F2 ;d ,additive effect ; h, dominance effect ; i , additive x additive ; j , additive x dominance ; l, dominance x dominance.

showed that additive gene effect (d). Dominance gene effect (h) and epistasis (i), (j) as well (I) were significant for grain elongation for all crosses under study except additive x dominance gene effect (j) for cross 2 (Table 3). The duplicate type of epistasis can be effectively utilized in pedigree breeding by delaying the selection and it is easier to exploit duplicate type than the complementary type of epistasis. Nayak et.al. (2007) reported predominant role of additive gene effect.

5.2. Gelatinization Temperature

The analysis of gene effects in six-parameter model showed that dominance gene effect (h) was significant and positive in crosses 2 and 3and additive x dominance gene effect (j) for cross 2 while additive x additive was significant and positive in cross 3 ,whereas dominance x dominance were significant for three crosses for this character. As shown in Table 3, some of the additive effects were negative. The negative or positive signs for additive effects depend on which parent is chosen as P1 (Cukadar-Olmedo and Miller, 1997). Tomar and Nanda (1985) reported duplicate epistasis for gelatinization temperature.

5.3. Gel Consistency

The mean value for all characters were soft . The results obtained from regression analysis showed that additive gene effect as well as dominance gene effects and epistasis were significant for three crosses of gel consistency (Table 3). In the role of the inheritance of gel consistency, direct selection may not be useful. The corresponding fixable gene effects (additive gene effects) were greater than the magnitude of non-fixable gene effects (additive x dominance gene effects, Kamara et al., 2017).

5.4. Amylose Content

The mean values for cross 1 and cross 2 were low for amylose content while cross 3 had high amylose content % (Table 3). From results it was clear that the additive effects were greater than the dominance effects for this characters. The contribution of the parents to dominance effects varied according to trait. The sign for dominance effect is a function of the F1 mean value in relation to the mid-parental value and indicates which parent is contributing to the dominance effect Cukadar-Olmedo

Table 4. Mean estimates of parents , F1 generation and heterosis as deviation from $\bar{M}$p and $\bar{B}$p for rice of all tested characters in three studied crosses.

Characters	Crosses			Mean performance		Heterosis %
		$\bar{P}$1	$\bar{P}$2	$\bar{F}$1	$\bar{M}$p	$\bar{B}$p
Hulling%	CR1	78.986	77.680	77.990	-1.070*	-1.262*
	CR2	83.010	78.760	79.540	-1.663**	-4.180**
	CR3	80.030	69.185	78.738	5.536**	-1.614**
L.S.D 5%	-	-	-	-	-0.946	1.092
1%	-	-	-	-	1.272	1.469
Milling %	CR1	71.757	68.088	70.660	1.055*	-1.528**
	CR2	75.350	70.220	74.137	1.858**	-1.610**
	CR3	73.610	60.690	72.084	5.859**	-3.432**
L.S.D 5%	-	-	-	-	0.895	1.o33
1%	-	-	-	-	1.204	1.390
Head rice %	CR1	69.500	65.500	68.633	1.679**	-1.247**
	CR2	71.030	67.800	72.300	4.156**	1.788**
	CR3	66.570	53.168	66.538	11.139**	-0.048
L.S.D 5%	-	-	-	-	0.580	0.670
1%	-	-	-	-	0.780	0.901
Grain length	CR1	5.014	6.993	5.746	-4.289**	14.599**
	CR2	4.965	5,676	5.676	2.910**	14.320**
	CR3	5,618	7.698	6.708	0.751**	19.402**
L.S.D 5%	-	-	-	-	0.346	0.503
1%	-	-	-	-	0.586	0.676
Grain width	CR1	2.518	2.348	2.403	-1.233**	-4.567**
	CR2	2.868	2.547	2.686	-0.794**	-6.346**
	CR3	2.452	1.875	2.210	2.149**	-0.869**
L.S.D 5%	-	-	-	-	0.046	0.053
1%	-	-	-	-	0.062	0.072
Grain shape	CR1	1.991	2.978	1.991	-3.763**	-19.711**
	CR2	1.731	2.382	1.731	2.747**	-11.293**
	CR3	2.294	4.128	2.294	-5.325**	-26.357**
L.S.D 5%	-	-	-	-	0.057	0.065
1%	-	-	-	-	0.076	0.088
Grain elongation	CR1	64.039	40.679	54.711	4.492**	-14.566**
	CR2	69.473	53.830	54.060	12.314**	-22.186**
	CR3	61.959	45.319	43.175	19.509**	30.317**
L.S.D 5%	-	-	-	-	3.340	3.857
1%	-	-	-	-	4.492	5.187
Gelatinization temp	CR1	4.800	5.490	5.200	1.069**	-5.282**
	CR2	4.360	5.302	5.571	15.142**	5.130**
	CR3	6.883	6.302	6.500	-6.245**	-6.917**
L.S.D 5%	-	-	-	-	0.464	0.536
1%	-	-	-	-	0.624	0.721
Gel consistency	CR1	91.800	98.166	99.250	4.192**	1.104
	CR2	71.500	69.000	78.000	8.711**	4.698**
	CR3	75.000	69.333	87.000	20.555**	16.000**
L.S.D 5%	-	-	-	-	2.619	3.025
1%	-	-	-	-	3.523	4.068
Amylose content%	CR1	18.840	19.405	19.563	2.304*	3.838
	CR2	19.570	21.283	19.455	4,756**	-.588
	CR3	28.795	26.605	27.073	2.264*	1.759
L.S.D 5%	-	-	-	-	2.241	2.588
1%	-	-	-	-	3.015	3.481

* significant at 5% level **Significant at 1% level, respectively. Where(CR1),Giza 178xEgyptian yasmine; CR2 ,Giza 177xUpr 82-1-7 and CR3.IET1444 x Pusa Basmati 1. And m, mean of F2 ;d ,additive effect ; h, dominance effect ; i , additive x additive ; j , additive x dominance ; l, dominance x dominance.

and Miller, (1997) preponderance of additive gene action in the inheritance of the trait amylose content. Estimates of genetic components showed both additive and non-additive gene effects to be important. Swain and Nagaraju (2004).

6. Heterosis

6.1. Milling Characters

Data presented in Table 4 indicated that highly significant positive values of heterosis were recorded for milling and head rice % characters as a deviation from mid-parent in three cross Paramasivam et. al. (1996) and cross 3 in hulling %. Also data in (Table4) showed that the heterosis values for head rice % of cross 2 only was positive highly significant as deviation from the better parent (1.788) , while the remaining crosses recorded negative significant mean heterotic for this traits. These results agreed with Surender (2002).

6.2. Physical Characters

In Table 4 for grain length, the heterosis as a deviation from mid-parent and better parent were significant and positive in three cross but only in cross 1recorded significant and negative heterosis as a deviation from mid-parent. Both positive and negative significant heterosis for grain length were reported (Singh and Singh, 1985). For grain width and grain shape, three crosses showed significant and negative relative heterosis and heterobeltiosis. The exceptions were heterosis as division in mid parent that was significant and positive in cross 3 for grain width and cross 2 for grain shape. The same trends for grain shape were previously observed (Gnanamalar and Vivekanandan 2013).

6.3. Cooking and Eating Characters

6.3.1. Elongation Percent

Data presented in Table 4 indicated that highly significant positive values of heterosis were recorded as a deviation from mid-parent in cross 1. Also data in Table 4 showed that the heterosis values for elongation % of cross 3 was positive and highly significant as deviation from the better parent (30.317), while the remaining crosses recorded negative significant mean heterosis for this trait. Linear elongation without breadthwise expansion is considered a highly desirable trait in rice quality (Gnanamalar and Vivekanandan, 2013).

6.3.2. Gelatinization Temperature

Cross 2 showed positive and significant heterosis as a deviation from mid-parent and better parent ,whereas cross 1 gave the same as a deviation from mid-parent .

6.3.3. Gel Consistency

Three crosses recorded significant and positive heterosis and

heterobeltiosis for gel consistency except cross 1 heterosis as deviation better parent was not significant . The maximum heterosis is was recorded by cross 3 (20.555 and 16.000 per cent respectively) and the minimum of 4.192 per cent was found in cross 1 as deviation mid-parent standard heterosis this trait (Gnanamalar and Vivekanandan, 2013).

6.3.4. Amylose Content

Data presented in Table 4 indicated that highly significant positive values of heterosis were recorded for this character a deviation from mid-parent in the three cross. These values of heterosis were ranged between 2.264% for the cross 2 and 4,756% for cross 3. Also data in Table 4 showed that the heterosis for values amylose content % of three crosses were no significant as deviation from the better parent.

Conclusion

Finally, it can be concluded that broad sense heritability estimates were high for milling, grain dimensions, gel consistency and gelatinization temperature in three crosses under study. Low to moderate narrow sense heritability estimates were evident for grain quality characters. Both additive (d) and dominance (h) gene effects were important for all the results, that indicated that epistasis is determined to some extent by the genotypes used for the study for grain quality characters.

References

Abd El-Lattef AS, AAB Abo-Khalifa, and AAA El-Gohary (2012) Inheritance of some quantitative characters under drought conditions in rice (*Oryza sativa* L.) IJBPAS 1 (5): 620-635.

Adair CR (1952) The McGill miller method for determining the milled quality of small samples of rice .Rice J. 55 (2): 21-23.

Azeez MH and M Shafi (1966) Quality in rice. Tech. Bull. No.13 Dept. Agric.Govt West Pakistan, P.S.O.

Bagati S, AK Singh, RK Salgotra, R Bhardwaj, M Sharma, SK Rai and A Bhat (2016) Genetic variability, heritability and correlation coefficients of yield and its component traits in Basmati rice (*Oryza sativa* L.) Sabrao J. Breed. Genet. 48 (4): 445-452.

Bao JS (2014) Genes and QTLs for rice grain quality improvement in Rice - Germplasm Genetics and Improvement, ed. W. Yan (Rijeka: In Tech), 239–278.

Bharadwaj C, R Mishra, CT Satyavathi S K Rao and KS Kumar (2007) Genetic variability, heritability and genetic advance in some new plant type based crosses of rice (*Oryza sativa* L.). Indian J. Agric. Res. 41 (3): 189-194.

Botany WT (1961) Mass emasculation in rice. Inster. Rice Comm. Newsletter 9: 9-13.

Burton GW (1952) Mass emasculation in rice. Inster. Rice Comm. Newsletter 9: 9–13.

Cagampang GB, CM Perez and BO Juliano (1973) A gel consistency test for eating quality of rice .J. Sci. Food Agric. 24: 1589-1594.

Chamundeswari N (2010) Genetic studies on quality traits in rice (*Oryza sativa* l.) Doctor Of Philosophy. Ranga Agricultural University. Srivenkateswara, India.

Cukadar-Olmedo B and JF Miller (1997) Inheritance of the stay green trait in sunflower. Crop. Sci. 37: 150-153.

Edwards LH, H Ketata, and EL Smith (1975). Gene action of heading date, plant height, and other characters in two winter wheat crosses. Crop Sci. 16: 275-277.

Fitzgerald MA, SR McCouch, and RD Hall (2009) Not just a grain of rice: the quest of quality. Trends Plant Sci. 14: 133–139.

Gnanamalar RP and P Vivekanandan (2013) Heterosis for grain yield and grain quality traits in rice (*Oryza sativa* L.) Asian J. Plant Sci. Res. 3 (3): 100-106.

Hassan HM, AB El-Abd, G Lamo and NM El Baghdady (2013) Inheritance of grain quality and yield traits in rice using triple test cross analysis. Egypt. J. Plant Breed. 17 (2): 147-161.

Hayman BI (1957) The description of genetic interaction in continuous variation. Biometrics 11: 69-82.

Hayman BI (1958). The Separation of Epistatic from Additive and Dominance Variation in Generation Means. Heredity 12: 371-390.

Jodon NE (1938) Experiments on artificial hybridization of rice. J. Amer. Soc. 30: 249–305.

Johanson HW, HF Robinson and RE Comstock (1955) Estimates of genetic and environment variability in soybean. Agron. J. 47: 214 – 222.

Juliano BO (1971) A simplified assay for milled rice amylose Cereal. Sci. Today 16: 334-338.

Kamara N, MD Asante, R Akromah and CS Kamara (2017) Genetic analysis of yield and yield components in *Oryza sativa* cross. African Crop Sci. J. 25 (4): 539– 550.

Khush GS, CM Paule, and NM Dela-Cruze (1979) Rice grain quality evaluation and improvement at IRRI. In Proceedings of the Workshop on Chemical Aspects of Rice Grain Quality (pp. 21–31). Los Baños: International Rice Research Institute.

Kishore NS, VR Babu, NA Ansari, and AR Prasad (2008) Genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.) genotypes of different eco-geographical regions. Res. Crops. 9 (1): 147-150.

Kumar N, PL Kulwal, A Gaur, P Khurana, JP Khurana, AK Tyagi, (2006) QTL analysis for grain weight in com-mon wheat. Euphytica, doi: 10.1007/s10681-006-9133-4.

Lakshmi AD (2009) Study of gene action for grain quality, physiological and yield traits in rice (*Oryza sativa* L.). Ph.D Theis submitted to Acharya N.G Ranga Agricultural University, Hyderabad.

Little R, G Hilder and EH Dawson (1958) Differential effect of dilute alkali on 25 varieties of milled white rice. Cereal Chem . 35: 111-126.

Manful J (2010) Strategies to add value to rice and rice-based products in Africa. a Presented at the 3rd International Rice Congress held in Hanoi, Vietnam. 8 –11 November.

Mather K (1949) Biometrical Genetics, Dover publications Inc., New York.

Mather K and JL Jinks (1971) Biometrical Genetics. 2nd edition. Chapman and Hall, London, UK.

Nayak AR, D Chaudhary, and JN Reddy (2007). Genetics of yield and yield components in scented rice. Oryza 44 (3): 227-230.

Nirmaladevi G, G Padmavathi, S Kota and VR Babu (2015) Genetic variability, heritability and correlation coefficients of grain quality characters in rice (*Oryza sativa* L.). Sabrao J. Breed. Genet. 47 (4): 424-433.

Paramasivam K, S Giridharan, APMK Soundaraj and P Parthasarathy (1996) Heterosis and combining ability for grain characters in rice. Madras Agric. J. 83 (2): 110-114.

Paul CP , NQ NG and TAO Ladeinde (2003) Mode of gene action of inheritance for resistance to rice yellow mottle virus. African Crop Sci. J. 11 (3): 143-150.

Powers LR, LF Locke and JC Garrett (1950) Partitioning method of genetic analysis applied to quantitative characters of tomato crosess. U. S. Tech. Bull. 998: 56.

Robinson HF, RE Comstock and PH Harvey (1966) Estimation of heritability and the degree of dominance in corn. Agron. J. 41: 353-359.

Salem KFM, YM Yaseen, AB El-Abd and A Ayoub (2015) Inheritance of some yield components and grain quality traits in rice (*Oryza sativa* L). J. Prod. Dev. 20 (2): 161–177.

Selvaraj CI, P Nagarajan, K Thiyagarajan, M Bharathi and R Rabindran (2011) Genetic parameters of variability, correlation and path coefficient studies for grain yield and other yield attributes among rice blast disease resistant genotypes of rice (*Oryza sativa* L.). African J Biotechnol. 10 (17): 3322–3334.

Singh NB and HG Singh.(1985) Heterosis and combining ability for kernel size in rice. Indian J. Genet. 45 (2): 181-185.

Singh SK, CM Singh and GM Lal (2011) Assessment of genetic variability for yield and its component characters in rice (*Oryza sativa* L.). Res. Plant Biol. 1(4): 73-76.

Sivasubramanian V and P Mahadevamenon (1973) Path analysis for yield and yield components of rice. Madras Agric. J. 60: 1217-1221.

Surender RCH (2002) Study of genetic divergence, variability, stability, gene action and character association for certain physiological quality and yield components in Rice (*Oryza sativa* L.) Ph.D. Thesis. Acharya N.G. Ranga Agricultural University, Hyderabad.

Swain B and M Nagaraju (2004) Diallel analysis for amylose content in rice. Oryza 41 (3): 125-127.

Tomar JB and JS Nanda (1985) Genetics and association studies of kernel shape in rice. India J .Genet. 45 (2): 278-283.

Venkanna V, N Lingaiah , CHS Raju and VT Rao (2014) Genetic studies foe quality traits of F2 population in rice (*Oryza sativa* L.). Internat. J. Appl. Biol. and Pharmaceutical Technol. 5 (2): 125-127.

Vivekanandan P and S Giridharan (1995) Genetic analysis of kernel quality traits in rice. Oryza 32: 74-78.

Warner JN (1952) A method for estimating heritability. Agron. J. 44: 427–430.