

**STUDIES ON GENETIC VARIABILITY,
HERITABILITY AND GENETIC ADVANCE FOR
GRAIN YIELD AND GRAIN QUALITY TRAITS IN
SOME PROMISING GENOTYPES
OF RICE (*Oryza sativa* L.).**

**El-Abd, A. B., S. E. M. Sedeek, S. A. A. Hammoud
and A. A. Abd Allah.**

Rice Research Section, Field Crops Research Institute, ARC, Giza, Egypt.

ABSTRACT

The nature and magnitude of genetic variability, phenotypic and genotypic coefficients of variation, broad-sense heritability and expected genetic advance were studied for fifteen grain yield and grain quality traits in ten promising genotypes of rice (*Oryza sativa* L.) and their two parental lines; namely, Giza 178 and GZ 6296-12-1-2-2-1, during 2006 and 2007 summer seasons at the Research Farm of the Rice Research and Training Center, Sakha, Kafr El-Sheikh, Egypt.

The data revealed highly significant mean squares for all traits, suggesting the presence of genetic differences among the rice genotypes for all studied traits. The phenotypic coefficient of variability (PCV) was, generally, higher than the genotypic coefficient of variability (GCV) for number of panicles/plant, brown grain length, brown grain shape, grain elongation, gelatinization temperature, gel consistency and amylose content (%) traits, which indicated that environmental effect constituted a major portion of the total phenotypic variation. On the other hand, plant height, number of filled grains/panicle, 1000-grain weight, hulling (%), milling (%), head rice (%), protein content (%) and grain yield/plant exhibited low variations between phenotypic and genotypic coefficients of variations, indicating that these traits should be emphasized in selection programs. High broad-sense heritability, coupled with high genetic advance, were observed for plant height, number of panicles/plant, number of filled grains/panicle, brown grain length, brown grain

shape, grain elongation, gelatinization temperature, gel consistency, protein content (%) and grain yield/plant, indicating the role of additive genetic variance in the expression of these traits and direct selection might be highly effective.

Correlation analysis revealed that grain yield was strongly and positively correlated with each of number of panicles/plant, number of filled grains/panicle and 1000-grain weight. Moreover, highly significant and positive estimates of phenotypic correlation coefficients were recorded between brown grain length and each of hulling (%), milling (%) and gelatinization temperature. Furthermore, gelatinization temperature was significantly and positively associated with hulling (%) and milling (%). Otherwise, amylose content (%) was significantly and negatively associated with brown grain length and protein content (%).

Key words: Rice - Genetic variability, Heritability, Genetic advance, Correlation coefficient.

INTRODUCTION

Rice is the most important staple food for about one-half of the human race. Efforts have been made at Rice Research Section for encouraging and boosting local rice production in Egypt, and this has led to a tremendous increase in area planted, approximately one millions hectares. Output and productivity in paddy rice production, in the last two decades, were increased more than two times comparing with the latest productivity. Since 1980, Egypt has been the largest rice producing country in Africa, (Warda, 1996). Improving rice productivity and quality traits is of crucial importance. To accomplish this, rice breeding programs should aim at broadening the genetic base of the breeding stock, (Vanaja and Babu, 2004). 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 cultivars requires a thorough knowledge of the existing genetic variation for grain 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 a quantitative trait in nature and is polygenically controlled. Selection on the basis of grain yield character alone, usually, is not very effective and efficient. However, selection, based on grain yield components characters, could be more efficient and reliable. Knowledge of the association between grain yield and its components characters, and among the component characters themselves and between grain quality traits, can improve the efficiency of selection in plant breeding. Owing to a complex situation, selection for an optimum advance on grain yield should be on the basis of judiciously computed index. The correlation studies, taken alone, are often misleading and the actual dependence of grain yield on the correlated yield component characters needs confirmation, which can easily be untangled.

In the present study, therefore, an attempt has been made to partition the variance components, especially phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability (h^2) and expected genetic advance (GA) for grain yield and yield components and some grain quality traits in some promising genotypes of rice. Also, the phenotypic correlation coefficients have been done among all possible pairs of the studied traits. These estimates could be useful in developing reliable selection indices.

MATERIALS AND METHODS

The present experiment was carried out at Research Farm of the Rice Research and Training Center, Sakha, Kafr El-Sheikh, Egypt, during 2006 and 2007 summer planting seasons. Twelve promising genotypes of rice (*Oryza sativa* L.), sourced from Rice Breeding Program, were used in this study to estimate the genetic variability, heritability, expected genetic advance and phenotypic correlation coefficients among all possible pairs of the studied traits. The genotypes used were Giza 178 and GZ 6296-

12-1-2-2-1 and their ten promising lines progeny derived from F₇ generation.

The genotypes were grown in a randomized complete block design, with three replications. Thirty-day old seedlings of each genotype were individually transplanted in 10-row/replicate with spacing of 20 cm among rows and 20 cm among plants. All pre- and post-stand establishment management, such as land preparation, fertilizer application, weeding, pest control and other cultural practices were done as required.

Fifteen equidistance plants, from each genotype in each replication, were taken at maturity and data on grain yield traits; i.e., plant height (cm), number of panicles per plant, number of filled grains per panicle, 1000-grain weight (g) and grain yield (t/ha) were recorded, according to the standard evaluation system for rice, IRRI (1996).

In addition, the laboratory analysis was conducted for grain quality traits. The samples were milled raw and analyzed for physicochemical properties. Milled rice out turn was determined by dehulling 200 g rough rice in Satake Rice Mill. Head rice out turn was determined by separating broken parts from milled rice by hand. Milled rice and head rice out turns were expressed as percentages of rough rice and milled rice, respectively. Brown grain length and breadth were measured by slide calipers. In determining the brown grain shape, brown rice was first classified into three classes based on length; viz., extra long (more than 7.5 mm in length), long (6.61 to 7.5 mm in length), medium (5.51 to 6.6 mm in length) and short (5.5 mm or less in length). The grains were again classified into three classes considering length to breadth ratio; i.e., slender (ratio over 3.0), medium (ratio 2.1 to 3.0), bold (ratio 1.1 to 2.0) and round (ratio less than 1.1). Amylose content was determined by the procedure of Juliano (1971). For measurement of grain elongation ratio, ten measured (length and width) grains were taken into 20 ml. glass test tube and soaked for 20 minutes with 5 ml. of tap water. After soaking, the test tubes were put into boiling water for around 30 minutes. When the grains were cooked properly, test tubes were taken out and the water was removed inside the test tubes.

Thereafter, cooked grains were kept on a glass sheet for few minutes to evaporate extra moisture and, then, the length and width of the cooked grains were measured. Grain elongation ratio means the proportionate change of rice grain after cooking, but different research groups define it in different ways, such as Sood and Siddiq (1980), who considered both length and width wise expansion of grain after cooking and proposed the following formula to measure grain elongation:

$$PC = \frac{L_F / W_F - L_O / W_O}{L_O / W_O}$$

Where, L_F , W_F = length and width of the grain after cooking; L_O , W_O = length and width of the grain before cooking, respectively, and PC is the proportionate change. The following criterion was adapted for classifying genotypes, with respect to grain elongation:

<u>Degree of elongation</u>	<u>Proportionate change (PC)</u>
Very high	> 1.00
High	0.70 – 1.00
Medium	0.40 – 0.69
Low	0.10 – 0.39
Poor	< 0.10

Alkali spreading value was determined, according to procedure of Little *et al.* (1958) and was classified as Alkali spreading value of 1.0 - 3.0 corresponds to high, 4.0 - 5.0 corresponds to intermediate and 6.0 to 7.0 corresponds to low desirable gelatinization temperature. Moreover, gel consistency was measured, as described by Cagampang *et al.* (1973), the rice grain gel was classified, according to the following scale:

<u>Scale (mm)</u>	<u>Gel consistency type</u>
81-100	Very soft
61-80	Soft
41-60	Medium
36-40	Hard
Less than 35	Very hard

Based on amylose content, milled rice was classified as waxy (1-2% amylose), very low (>2-9% amylose), low (>9-20% amylose), intermediate (>20-25% amylose) and high (25-33% amylose), Juliano (1972). Protein content was determined by micro Kjeldahl method, AOAC (1970). Analysis of variance was computed for each season assuming that the cultivars under study are random. As the error variances of the experiments were statistically homogeneous, the two experiments were statistically combined over the two seasons, according to Le Clerg *et al.* (1962), then, it was subjected to analysis of variance, which was used to partition the gross phenotypic variability into the components due to genetic (hereditary) and non-genetic (environmental) factors and to estimate the magnitude of them. Genotypic variance is the part of the phenotypic variance, which can be attributed to genotypic differences among the phenotypes. Similarly, phenotypic variance is the total variance among phenotypes, when grown over the range of environments of interest, Dudley and Moll (1969). Hence, variance components, genotypic (V_g), phenotypic (V_p) and error (V_e) variances were estimated using the formula of Wricke and Weber (1986) and Prasad *et al.* (1981), as follows:

$$\begin{aligned} V_g &= [\text{MSG} - \text{MSE} / r] \\ V_{ph} &= [\text{MSG} / r] \\ V_e &= [\text{MSE} / r] \end{aligned}$$

Where, MSG, MSE and r are the mean squares of genotypes, mean squares of error and number of replications, respectively. Phenotypic (PCV) and genotypic (GCV) coefficients of variation were evaluated, according to the methods of Burton (1952), Johnson *et al.* (1955) and Kumar *et al.* (1985), as follows:

$$\begin{aligned} \text{PCV} &= [\sqrt{V_p} / X] \times 100 \\ \text{GCV} &= [\sqrt{V_g} / X] \times 100 \end{aligned}$$

Where, V_p , V_g and X are the phenotypic variances, genotypic variances and grand mean per season, respectively, for the traits under consideration. Broad-sense heritability (h_2B), expressed as the percentage of the ratio of the genotypic variance (V_g) to the phenotypic variance (V_{ph}) was estimated on genotypic

mean basis, as described by Allard (1999). Genetic advance (GA) expected and GA as percent of the mean, assuming selection of the superior 5% of the genotypes were estimated in accordance with the methods, illustrated by Fehr (1987), as follows:

$$GA = K (S_{ph}) h_2 b$$

$$GA \text{ (as \% of the mean)} = (GA / x) \times 100$$

Where, *k* is a constant (which varies depending upon the selection intensity and, if the latter is 5%, it stands at 2.06). (*S_{ph}*) is the phenotypic standard deviation ($\sqrt{V_{ph}}$), *h₂B* is the heritability ratio and *x* refers to the season mean of the trait. The phenotypic correlation coefficients were computed, according to the method of Dewey and Lu (1959).

RESULTS AND DISCUSSION

Mean performance of genotypes:

Analysis of variance showed highly significant differences among the studied genotypes for all traits, suggesting a substantial to moderate genetic variability in all parameters evaluated, Tables (1) and (2). It is clear from Table (3) that plant height mean values ranged between 85.85 and 108.46 cm. The most desirable plant height, which ranged between 90 and 100 cm, as a goal of rice plant breeder, was recorded in SK 28-115-20-5-7-1, SK 28-79-2-5-8-4, SK 28-61-1-2-5-3, SK 28-34-5-4-2-3, SK 28-23-6-7-2-4, SK 28-15-3-2-1-1, SK 28-8-5-4-1-2 and the parental line, Giza 178, which exhibited short stature plants, resistant to lodging and easily mechanically harvested. On the contrary, the genotypes, SK28-56-5-2-2-1 and SK28-40-8-6-2-2 were the tallest plants, with 103.61 and 108.46 cm plant height, respectively.

In addition, number of panicles/plant varied from 22.31 to 34.60. The largest numbers of panicles/plant (34.60, 32.36, 30.27, 28.42 and 28.37) were observed in SK 28-79-2-5-8-4, SK 28-34-5-4-2-3, SK 28-115-20-5-7-1, SK 28-61-1-2-5-3 and SK 28-15-3-2-1-1, rice genotypes respectively, comparing with their parental lines, Giza 178 and Gz 6296-12-1-2-2-1; and the genotypes grand mean values (26.35, 22.40 and 27.32, respectively). On the other hand, the lowest numbers of panicles /plant were recorded in Gz

6296-12-1-2-2-1, SK 28-23-6-7-2-4, SK 28-40-8-6-2-2 and SK28-56-5-2-2-1 rice genotypes, ranged from 22.40 to 24.63. More filled grains / panicle were displayed by SK 28-79-2-5-8-4 followed by SK 28-61-1-2-5-3, SK 28-45-5-6-1-1, SK 28-115-20-5-7-1 and SK28-56-5-2-2-1, their estimated values (156.67, 155.00, 152.33 and 149.00 grains/panicle) were higher than their parental lines values, Giza 178 (135.00 grains/panicle) and Gz 6296-12-1-2-2-1 (118.00 grains/panicle).

Moreover, heavy 1000-grain weights were detected in SK 28-79-2-5-8-4, SK 28-115-20-5-7-1, SK 28-45-5-6-1-1, SK 28-61-1-2-5-3 and SK 28-34-5-4-2-3, while, Giza 178 and Gz 6296-12-1-2-2-1 had light 1000-grain weights, comparing with other studied genotypes. However, the superiority of grain yield was achieved in SK 28-79-2-5-8-4 (11.96 t. / ha.), followed by SK 28-115-20-5-7-1 (11.84 t. / ha.), SK 28-34-5-4-2-3 (11.61 t. /ha) and SK 28-45-5-6-1-1 (11.48 t. /ha.). Otherwise, the parental line, Gz 6296-12-1-2-2-1 was the lowest yielding potentiality rice genotype (9.90 t/ha).

Manifestly, the results in Table (4) illustrated that the estimated mean values of hulling (%) varied from heavy husks (77.56 %) in Gz 6296-12-1-2-2-1 to light husks (81.57 %) in SK 28-34-5-4-2-3. while, high milling return was recorded in SK 28-34-5-4-2-3, SK 28-23-6-7-2-4, SK 28-61-1-2-5-3 and SK 28-79-2-5-8-4, all estimated values exceeded 72 %.

However, Giza 178 rice cultivar had the highest head rice percentage (64.59 %), followed by SK 28-23-6-7-2-4 (64.41 %), SK 28-79-2-5-8-4 (63.93 %) and SK 28-61-1-2-5-3 (63.65 %), while, low estimates were observed in SK 28-45-5-6-1-1 (59.50 %), SK 28-40-8-6-2-2 (61.04 %) and SK28-56-5-2-2-1 (61.35 %). Their values were lower than the grand mean value (62.67 %). Length of brown grains varied from short (4.60 mm) in SK 28-15-3-2-1-1 to medium (6.05 mm) in SK 28-8-5-4-1-2. In addition, brown grain shape varied from bold (1.55) in SK 28-56-5-2-2-1 to medium (2.80) in SK 28-79-2-5-8-4. The short brown grain length and bold grain shape are preferred to Egyptian consumers.

Furthermore, it is customary to use liner expansion as the measure of grain elongation, but this seems to be a poor

Table (1): Mean squares of twelve rice genotypes for grain yield component traits.

Source of variation	df	Plant height (cm)	No. of panicles /plant	No. of filled grains/panicle	1000- grain weight (g)	Grain yield (t/ha)
Rep.	2	6.704	0.052	2.080	0.110	0.006
Genotypes	11	128.764**	40.742**	363.098**	4.704**	1.465**
Error	22	5.274	1.834	3.386	0.099	0.032

(**), highly significant at 0.01 level of probability, respectively.

Table (2): Mean squares of twelve rice genotypes for grain quality traits.

Source of variation	df	Hull. (%)	Mill. (%)	Head rice (%)	Brown grain length (cm)	Brown grain shape	Grain elongation	Gelat. temp. (GT)	Gel consist. (GC)	Amy. cont. (AC)	Prot. cont. (PC)
Rep.	2	0.138	0.061	0.072	0.033	0.001	0.037	0.008	76.411	0.707	0.002
Genotypes	11	5.1**	6.2**	6.7**	0.6**	0.5**	0.2**	2.3**	1045.4**	2.7**	1.2**
Error	22	0.408	0.120	0.079	0.027	0.030	0.014	0.120	102.283	0.583	0.013

(**), highly significant at 0.01 level of probability, respectively.

Table (3): Range and mean performance for grain yield and some yield components traits of twelve promising genotypes of rice in, 2006 and 2007 seasons (combined data).

Genotypes	Plant height (cm)	No. of panicles /plant	No. of filled grains/panicle	1000-grain weight (g)	Grain yield (t/ha)
Giza 178	98.15 f	26.35 cde	135 bc	22.57 a	11.34 c
GZ 6296-12-1-2-2-1	86.89 ab	22.4 a	118 a	23.51 b	9.90 a
SK 28-8-5-4-1-2	95.41 ef	25.31 bcd	137 c	24.85 d	10.16 a
SK 28-15-3-2-1-1	97.72 f	28.37 ef	145 e	25.57 e	10.74 b
SK 28-23-6-7-2-4	90.90 bcd	23.27 ab	140.67 d	23.98 bc	10.17 a
SK 28-34-5-4-2-3	92.89 cde	32.36 gh	145 e	25.32 dc	11.61 cb
SK 28-40-8-6-2-2	103.61 g	24.66 abc	132 b	23.66 b	10.60 b
SK 28-45-5-6-1-1	85.85 a	27.19 de	152.33 g	25.76 ef	11.48 c
SK 28-56-5-2-2-1	108.46 h	24.63 abc	147.33 ef	24.23 c	10.79 b
SK 28-61-1-2-5-3	92.55 cde	28.42 ef	155 gh	25.56 e	11.40 c
SK 28-79-2-5-8-4	94.71 def	34.60 h	156.67 h	26.78 g	11.96 e
SK 28-115-20-5-7-1	90.19 bc	30.27 fg	149 f	26.23 f	11.84 de
Grand mean	94.78	27.32	142.75	24.84	11.00
Range	85.85- 108.46	22.31- 34.60	118.00- 156.67	22.57- 26.78	9.90- 11.96
LSD 5%	3.889	2.293	3.116	0.535	0.301
LSD 1%	5.286	3.117	4.235	0.727	0.409

Means followed by the same letter (s) are not significantly different at 0.05 level.

Table (4): Range and mean performance for grain quality traits of twelve promising genotypes of rice in, 2006 and 2007 seasons (combined data).

Genotypes	Hulling (%)	Milling (%)	Head rice (%)	Brown grain length (cm)	Brown grain shape	Grain elongation	Gelat. temp. (GT)	Gel consist. (GC)	Amy. cont. (AC)	Prot. cont. (PC)
Giza 178	77.94 abc	70.30 cd	64.59 g	5.31 b	2.35 c	1.26 e	4.46 a	70.39 cd	19.57 c	6.75 cd
GZ 6296-12-1-2-2-1	77.56 ab	69.59 b	62.54 c	5.53 bc	2.45 c	0.9 cd	5.35 bc	58.97 abc	18.83 bc	6.02 a
SK 28-8-5-4-1-2	79.57 def	71.72 e	63.10 d	6.05 d	2.53 cd	0.84 a-d	6.43 de	45.50 a	18.34 bc	7.02 e
SK 28-15-3-2-1-1	79.86 ef	70.66 d	63.25 de	4.60 a	1.94 d	0.89 bcd	5.51 c	95.26 f	19.07 bc	6.12 a
SK 28-23-6-7-2-4	80.57 fg	72.38 f	64.41 g	5.45 b	2.48 cd	1.44 e	4.89 ab	73.01 cde	18.44 bc	6.49 b
SK 28-34-5-4-2-3	81.57 g	72.66 f	62.23 c	5.80 cd	2.92 e	0.77 abc	6.67 de	98.74 f	16.62 a	7.55 f
SK 28-40-8-6-2-2	78.65 bcd	69.44 b	61.04 b	5.27 b	1.75 ab	0.65 a	4.57 a	51.40 ab	17.91 ab	8.10 g
SK 28-45-5-6-1-1	77.34 a	68.17 a	59.50 a	5.46 b	2.66 cde	0.84 a-d	6.27 d	90.77 ef	18.37 bc	6.64 bc
SK 28-56-5-2-2-1	78.94 cde	70.02 bc	61.35 b	4.49 a	1.55 a	1.05 d	5.63 c	65.27 bcd	16.85 a	7.65 f
SK 28-61-1-2-5-3	80.05 ef	72.37 f	63.65 ef	5.50 bc	2.59 cd	0.96 cd	7.00 e	82.47 def	19.62 c	6.73 c
SK 28-79-2-5-8-4	80.55 fg	72.36 f	63.93 f	5.49 b	2.8 de	0.83 a-d	6.78 de	98.42 f	18.53 bc	6.94 de
SK 28-115-20-5-7-1	78.93 cde	70.92 d	62.50 c	5.23 b	2.53 cd	0.72 ab	5.56 c	90.41 ef	17.69 ab	7.03 e
Grand mean	79.29	70.88	62.67	5.35	2.38	0.94	5.76	76.72	18.32	6.92
Range	77.56-81.57	69.44-72.66	59.50-64.59	4.60-6.05	1.55-2.80	0.65-1.44	4.46-7.00	45.50-98.74	16.62-19.57	6.02-8.10
LSD 5%	1.082	0.587	0.476	0.278	0.293	0.202	0.586	17.126	1.293	0.199
LSD 1%	1.471	0.798	0.647	0.378	0.398	0.275	0.797	23.578	1.757	0.270

Means followed by the same letter (s) are not significantly different at 0.05 level.

measurement, as it fails to take into account the widthwise swelling, which is independent of lengthwise swelling. Hence, proportionate change in the L/W ratio of grain on cooking, as detailed under materials and methods was taken as the measure of elongation in the genotypes studied. The results indicated wide variation for this trait, out of twelve genotypes studied, three were in the range of 0.70 to 1.00 (very high grain elongation), eight were recorded more than unity (high grain elongation) and only one rice genotype namely, SK 28-40-8-6-2-2, that had medium grain elongation (lower than 0.70).

Gelatinization temperature, as measured by alkali digestion scores, was found to vary from intermediate in three rice genotypes; namely, Giza 178, SK 28-23-6-7-2-4 and SK 28-40-8-6-2-2, to low in other remaining genotypes, indicating that the rice genotypes under study needed a short time when cooked, that saved energy. Gel consistency largely varied from medium (length of gel, 41 to 60 mm) in flaky rices; i.e., Gz 6296-12-1-2-2-1, SK 28-8-5-4-1-2 and SK 28-40-8-6-2-2; to soft gel (length of gel, 61-80) in Giza 178, SK 28-23-6-7-2-4 and SK 28-56-5-2-2-1 to very soft gel consistency (length of gel 81-100 mm) in other remaining genotypes, which subsisted a soft grain for a long time after cooking. Low amylose content was detected for all studied genotypes, their estimated values ranged between 16.62 and 19.57 %. Genotypes with low amylose content are moist, sticky and glossy when cooked, and readily split and disintegrate when over cooked. On the other hand, a wide range of protein content (6.02 to 8.10 %) was investigated among the genotypes studied. The grains of SK 28-40-8-6-2-2 genotypes studied. The grains of SK 28-40-8-6-2-2 had the highest protein content (%) followed by SK 28-56-5-2-2-1, SK 28-34-5-4-2-3 and SK 28-115-20-5-7-1. On the contrary, the genotypes, Gz 6296-12-1-2-2-1 and SK 28-15-3-2-1-1 had the lowest protein content (%) in their grains.

Estimates of genetic parameters:

A comparison of the data in Table (5) indicated that the magnitude of genetic variance (σ^2_g) was greater than that of environmental variance (σ^2_e) for various grain yield components

traits. However, high estimates of phenotypic (σ^2_p) and genotypic (σ^2_g) variances were recorded for number of filled grains/panicle, plant height and number of panicles/plant, indicating a better scope for the genetic improvement, and showing that the environment did not have a major impact on the variability pattern of these traits. High phenotypic and genotypic variances, also, were observed for number of filled grains/panicle by Bidhan, *et al.* (2001).

It is difficult to compare the variance among the range of various characters because they are not of unit free, thus, estimates of phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV), broad-sense heritability and genetic advance, as a percentage of mean for grain yield and its components, were evaluated and compared in Table (5). The difference between the values of phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) was low, and the phenotypic coefficient of variability (PCV) was comparatively higher than the corresponding genotypic coefficients of variability (GCV) for all grain yield components traits. This suggests that environmental effects constitute a major portion of the total phenotypic variation in these traits. Thus, the selection of superior genotypes, based on such traits, would not be effective. The magnitude of PCV and GCV was highest for number of panicle/plant, number of filled grains/panicle and plant height, while, the lowest estimated values of (PCV) and (GCV) were recorded for 1000-grain weight. The results are in accordance with findings previously reported by Durai *et al.* (2001), Nayak *et al.* (2002), Mohammad, Tahir *et al.* (2002), Hasib *et al.* (2004), Sarma and Bhuyan (2004) and Devi *et al.* (2006).

Moreover, high broad-sense heritability was recorded for all grain yield components traits, where it ranged between 91 and 98 % for number of panicles/plant and number of filled grains/panicle, respectively. Convenient estimates of GCV, coupled with high broad-sense heritability and high expected genetic advance were exhibited for plant height, number of panicles/plant, number of filled grains/panicle and grain yield, meanwhile, there was not a big difference between PCV and

GCV. Thus, these two mentioned traits resulted to be highly heritable, points to the predominance of additive gene effect, easily fixable and can be taken as unit traits for effective selection. On the contrary, the lowest estimated value of expected genetic advance was observed for 1000-grain weight. The results are in confirmatory with those of Agrawal (2003), Patil *et al.* (2003), Kuldeep, Tyagi *et al.* (2004), Sinha *et al.* (2004), Vivek, Shukla *et al.* (2004), Bose *et al.* (2005), Elayaraja *et al.* (2005), Mall *et al.* (2005), Singh *et al.* (2005), Suman *et al.* (2005) and Suresh and Anbuselvam (2005).

Conspicuously, the results in Table (6) revealed that the genotypic variance (σ^2_g) was more prominent than that of the environmental variance (σ^2_e) for all grain quality traits under study, indicating the influence of genetic components of variation on the expression of grain quality traits. Moreover, the phenotypic coefficients of variability (PCV) were relatively larger than the genotypic coefficients of variability (GCV) for various grain quality traits. The highest estimated values of both (PCV) and (GCV) were found in gel consistency, followed by grain elongation, brown grain shape and gelatinization temperature, otherwise, the lowest estimates were recorded in hulling (%), milling (%) and head rice (%). Mishra and Verma (2002) reported that the phenotypic coefficient of variation was higher than the genotypic coefficient of variation (GCV) for various grain quality traits. Grain elongation and gel consistency recorded the highest magnitude of GCV. Moreover, high heritability, coupled with high genetic advance, were exhibited for grain elongation trait, indicating the role of additive genetic variance in the expression of this trait.

In addition, all quality characters exhibited high estimates of broad-sense heritability that averaged from 64 %, for amylose content, and 98 % for protein content, which revealed that these characters were less influenced to by environment and there could be a greater correspondence between phenotypic and breeding values.

Likewise, high expected genetic advance for gel consistency, grain elongation, brown grain shape, gelatinization

Table (5): Estimates of variance components; genotypic (GCV) and phenotypic (PCV) coefficients of variability; broad-sense heritability (h^2b) and the expected genetic advance (G.S. %) for grain yield and its component traits of rice.

Traits	Grand mean	Variance components			Genetic variability		h^2b (%)	Genetic advance	
		σ^2g	σ^2e	σ^2p	GCV	PCV		G.S.	G.S. (%)
Plant height (cm)	94.78	41.16	1.76	42.92	6.77	6.91	92	12.43	13.12
No. of panicles/plant	27.32	12.97	0.61	13.58	13.18	13.49	91	6.94	25.39
No. of filled grains/panicle	142.75	119.90	1.13	121.03	7.67	7.71	98	22.24	15.58
1000-grain weight(g)	24.84	1.54	0.03	1.57	4.99	5.04	96	2.47	9.96
Grain yield (t/ha.)	11.00	0.48	0.01	0.49	6.28	6.35	96	1.38	12.53

Table (6): Estimates of variance components; genotypic (GCV) and phenotypic (PCV) coefficients of variability; broad-sense heritability (h^2b) and the expected genetic advance (G.S. %) for grain quality traits of rice.

Traits	Grand mean	Variance components			Genetic variability		h^2b (%)	Genetic advance	
		σ^2g	σ^2e	σ^2p	GCV	PCV		G.S.	G.S. (%)
Hulling (%)	79.29	1.57	0.14	1.70	1.58	1.65	85	2.29	2.89
Milling (%)	70.88	2.03	0.04	2.07	2.01	2.03	96	2.85	4.02
Head rice (%)	62.67	2.20	0.03	2.23	2.37	2.38	97	3.00	4.79
Brown grain length (cm)	5.35	0.19	0.01	0.20	8.10	8.29	91	0.83	15.58
Brown grain shape	2.38	0.17	0.01	0.18	17.10	17.61	89	0.77	32.37
Grain elongation	0.94	0.05	0.01	0.05	22.73	23.87	83	0.38	40.82
Gelatinization. temp.	5.76	0.71	0.04	0.75	14.64	15.05	90	1.6	27.86
Gel consistency	76.72	314.4	34.09	348.48	23.11	24.33	82	31.60	41.19
Amylose Content (%)	18.32	0.692	0.194	0.886	4.541	5.139	64	1.242	6.779
Protein content (%)	6.92	0.371	0.004	0.375	8.798	8.849	98	1.233	17.813

temperature, protein content (%) and brown grain length signified that considerable improvement could be achieved in these traits by selection from segregating populations. The high broad-sense heritability and high expected genetic advance, coupled with high GCV exhibited by the abovementioned traits, implied that these traits are under additive gene effects and could be relied upon for further selection, based on phenotypic performance. Kumar *et al.* (2006) reported that high heritability along with low genetic advance was exhibited only for amylose content, indicating that this trait was under the influence of environment, while, brown grain length, brown grain shape and protein content traits exhibited high heritability along with high to moderate genetic advance, suggesting that these characters could be of high importance for selecting better genotypes in rice improvement programmes. Similar results were observed by Yadav *et al.* (2002), El-Abd (2003), Chaudhary *et al.* (2004), and Vanaja and Luckins, (2006).

Estimates of phenotypic correlation coefficients:

The phenotypic correlation coefficients among all possible pairs of grain yield components traits are presented in Table (7). Obviously, grain yield was positively and strongly correlated with each of number of panicles/plant (0.850), number of filled grains/panicle (0.731) and 1000-grain weight (0.640). This result indicated that these traits were found to be the principal grain yield components. Hence, any selection based on these traits might bring the desired improvement in grain yield. Plant height showed a non-significant either positive correlation with grain yield (t/ha.) (0.051) or negative with each of number of panicles/plant (-0.137) and 1000-grain weight (-0.088). Among grain yield components traits, number of filled grains/panicle was significantly and positively associated with plant height (0.300) and highly significantly with number of panicles/plant (0.702) and 1000-grain weight (0.786). However, a highly significant and positive estimate of phenotypic correlation coefficient (0.747) was recorded between number of panicles/plant and 1000-grain weight. Present findings coincided with the results of Bhandarkar

et al. (2002), Chaudhary and Motiramani (2003), Mahto et al. (2003), Chand et al. (2004), Sinha et al. (2004), Deng, et al. (2005), Patil and Sarawgi (2005) and Satyanarayana et al. (2005). However, the current results did not coincide with the findings of *Islam et al. (2002)*, who reported that grain yield per plant was positively correlated with plant height. The difference in these results might be attributed to the difference in genetic materials and environmental condition of the experiment.

The data in Table (8) revealed that highly significant positive estimates of phenotypic correlation coefficients were recorded between hulling (%) and each of milling (%) (0.848), head rice (%) (0.492), brown grain length (0.432), gelatinization temperature (0.527) and gel consistency (0.430), while either positive or negative insignificant estimates were recorded between hulling (%) and the other remaining quality traits. Moreover, milling (%) was highly significantly and positively associated with head rice (%) (0.719), brown grain length (0.479), gelatinization temperature (0.520) and gel consistency (0.335), while, it was highly significantly and negatively correlated with brown grain shape (-0.434). In addition, it was insignificantly either positive or negative with the other remaining traits.

Furthermore, either highly significant positive (0.498 and 0.503) or highly significant negative (-0.498) estimates of phenotypic correlation coefficients were found between head rice (%) and each of grain elongation, amylose content (%) and brown grain shape respectively. Brown grain length was highly significantly either positively associated with gelatinization temperature (0.482) or negatively correlated with amylose content (%) (-0.362). However, brown grain shape was highly significantly and negatively correlated with grain elongation (-0.457). Highly significant and positive estimate of phenotypic correlation coefficient (0.497) was detected between grain elongation and amylose content (%), while, such estimate was in negative direction (-0.394) between grain elongation and gelatinization temperature.

Besides, the phenotypic correlation coefficient was highly significantly positive (0.505) between gel consistency and

Table (7): Estimates of phenotypic correlation coefficients among all possible pairs of grain yield and its component traits over two seasons (2006 and 2007).

Traits	1	2	3	4
1- Plant height (cm)	1			
2- No. of panicles/plant	-0.137	1		
3- No. of filled grains/panicle	0.300*	0.702**	1	
4- 1000-grain weight (g)	-0.088	0.747**	0.786**	1
5- Grain yield (t/ha.)	0.051	0.850**	0.731**	0.640**

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

Table (8): Estimates of phenotypic correlation coefficients among all possible pairs of grain quality traits over two seasons (2006 and 2007).

Trait	1	2	3	4	5	6	7	8	9
1- Hulling (%)	1								
2- Milling (%)	0.848**	1							
3- Head rice (%)	0.492**	0.719**	1						
4- brown grain length (cm)	0.432**	0.479**	0.111	1					
5- brown grain shape	-0.223	-0.434**	-0.498**	-0.124	1				
6- Grain elongation	0.055	0.120	0.498**	0.115	-0.457**	1			
7- Gelati. temp.	0.527**	0.520**	-0.009	0.482**	0.128	-0.394**	1		
8- Gel consistency	0.430**	0.335*	0.164	-0.041	-0.249	-0.043	0.505**	1	
9- Amylose Content (%)	-0.094	-0.012	0.503**	-0.362**	-0.226	0.497**	-0.249	0.269	1
10- Protein content (%)	0.217	0.088	-0.294	-0.086	0.201	-0.449	0.123	-0.270	-0.664**

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

gelatinization temperature. On the contrary, it was highly significantly negative (-0.664) between amylose content (%) and protein content (%). In addition, insignificant either positive or negative correlations were noted among the other traits. These findings are in harmony with those reported earlier by *El-Abd (2003) and Kang, et al. (2006)*. The present study indicated that there was a genetic variability for the different traits under consideration, but it was unlikely that these accessions encompassed the full range of diversity to be found in Egypt. Thus, collection, conservation and further evaluation for the selection of better germplasm for superior grain yield and grain quality traits were essential.

Overview, the results on various traits of the studied genotypes helped not only to have basic information of the extent of natural variation for the various traits and their selection-reliability, but also to identify the best donors that combined most of desirable grain yield and grain quality characteristics. These promising genotypes would be of considerable value of breeders engaged in the development of high yielding cultivars. Hence, breeders could choose donor parents for the hybridization programme, as well as for making selection for high yielding and superior grain quality lines in segregating population.

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الملخص العربي

دراسات على التباين الوراثي ودرجة التوريث والتحسين الوراثي المتوقع بالانتخاب لمحصول الحبوب وصفات جودة الحبوب في بعض التراكيب الوراثية المباشرة للأرز

عبدالمعطي بسيوني العبد - صابر السيد محمد صديق -

سعيد على على حمود - عبدالله عبدالنبي عبدالله

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

تمت دراسة طبيعة وحجم التباين الوراثي، وكل من معامل الاختلاف المظهري ومعامل الاختلاف الوراثي ودرجة التوريث بالمعنى الواسع والتحسين الوراثي المتوقع بالانتخاب وذلك لخمس عشرة صنف متضمنة محصول الحبوب وصفات جودة الحبوب باستخدام عشرة تراكيب وراثية من الأرز ناتجة من التهجين بين الصنف جيزة ١٧٨ والسلالة جيزة زد ٢٢٩٦-١٢-١-٢-٢-١ أثناء موسمي صيف زراعة الأرز ٢٠٠٦ و٢٠٠٧ وذلك بالمزرعة البحثية لمركز البحوث والتدريب في الأرز سخا - كفرالشيخ - مصر.

أوضحت النتائج أن مجموع مربع متوسطات قيم جميع الصفات المدروسة كانت عالية المعنوية مشيرة إلى وجود اختلافات وراثية كبيرة بين التراكيب الوراثية في جميع الصفات المدروسة. كما كانت قيم معامل الاختلاف المظهري عامة أعلى من قيم معامل الاختلاف الوراثي لصفات عدد الداليات بالنبات وطول الحبة البنية وشكل الحبة البنية ودرجة استطالة الحبة بعد الطهي ودرجة حرارة الجلتنة ودرجة سيولة الجيل والنسبة المئوية لمحتوى الحبوب من الاميلوز مشيرا إلى أن التأثير البيئي يشكل قسما كبيرا من إجمالي الاختلافات المظهرية. ومن ناحية أخرى، كان الفرق بين كل من معامل الاختلاف المظهري ومعامل الاختلاف الوراثي منخفضا لصفات ارتفاع النبات وعدد الحبوب الممتلئة بالنورة ووزن الألف حبة والنسبة المئوية لتصافى التقشير والنسبة المئوية لتصافى التبييض والنسبة المئوية للأرز الأبيض السليم والنسبة المئوية لمحتوى الحبوب من البروتين و محصول النبات الفردي مما يدل على ان هذه الصفات ينبغي التشديد عليها في برامج الانتخاب.

كما أظهرت النتائج ان درجة التوريث بالمعنى الواسع كانت عالية ومقرونة بنسب عالية لقيم التحسين المتوقع بالانتخاب لصفات ارتفاع النبات وعدد الداليات بالنبات وعدد الحبوب الممتلئة بالنورة وطول الحبة البنية وشكل الحبة البنية ودرجة استطالة الحبة بعد الطهي ودرجة حرارة الجلتنة ودرجة سيولة الجيل والنسبة المئوية لمحتوى الحبوب من البروتين و محصول النبات الفردي مبينة أهمية التباين الوراثي المضيف في سلوك هذه الصفات وان تأثير الانتخاب المباشر لها يكون عاليا.

أشارت نتائج تحليل التلازم، أن محصول النبات الفردي يتلازم تلازما موجبا وقويا مع كل من عدد الداليات بالنبات وعدد الحبوب الممتلئة بالنورة ووزن الألف حبة. إضافة إلى ذلك سجلت النتائج ان قيم معامل التلازم المظهري كانت عالية المعنوية وموجبة بين طول الحبة البنية وكل من النسبة المئوية لتصافى التقشير والنسبة المئوية لتصافى التبييض و درجة حرارة الجلتنة، كما تلازمت درجة حرارة الجلتنة تلازما مغنويا موجبا مع النسبة المئوية لتصافى التقشير والنسبة المئوية لتصافى التبييض. وعلى النقيض من ذلك، تلازمت النسبة المئوية لمحتوى الحبوب من الاميلوز تلازما مغنويا سالبا مع طول الحبة البنية و النسبة المئوية لمحتوى الحبوب من البروتين.