



Assessment of Genetic Variability and Correlation Coefficient to Improve Some Agronomic Traits in Rice

A. G. Hefena¹, M. S. Sultan², M. A. Abdel-Moneam², S. A. Hammoud¹,
C. Barutçular³ and A. EL-Sabagh⁴*

¹Rice Research Section, Field Crops Research Institute, ARC, Giza, Egypt.

²Department of Agronomy, Faculty of Agriculture, Mansoura University, Egypt.

³Department of Field Crops, Faculty of Agriculture, Cukurova University, Turkey.

⁴Department of Agronomy, Faculty of Agriculture, Kafrelsheikh University, Egypt.

Authors' contributions

This work was carried out in collaboration between all authors. Authors AGH, MSS, MAAM and SAH designed the study, wrote the protocol, data collection and wrote the first draft of the manuscript. Authors AGH, MAAM, AES and CB performed the manuscript preparation and proofreading. All authors read and approved the final manuscript.

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ABSTRACT

This study was conducted to evaluate genetic components, heritability and correlation coefficient effects of the parents and their F1 for some agronomic as well as yield and yield traits. A line x tester cross was conducted among the ten parents (four lines and six testers) in 2010 to produce (24) F1 crosses evaluated during 2011. The results indicated that both GCA showed highly significant for all studied traits. The mean squares of lines x testers interaction (SCA) exhibited highly significant differences for all studied traits. Higher estimates for non-additive or dominance genetic variance was computed for number of panicles / plant, number of filled grains / panicle and grain yield / plant in comparison with its corresponding evaluates of additive genetic variance.

*Corresponding author: E-mail: ayman.elsabagh@agr.kfs.edu.eg;

Concerning to heritability estimates, high values were observed in broad sense heritability. Meanwhile, evaluate of narrow-sense heritability were low to moderate for number of panicles / plant, number of filled grains / panicle, 1000-grain weight and grain yield / plant. Heritability estimates in narrow sense were relatively low for panicle weight and spikelet fertility percentage. As for correlation for grain yield / plant the results recorded highly positive correlation coefficient with each number of days to heading, plant height, number of panicles / plant, panicle length, panicle weight, fertility percentage and 1000-grain weight.

Keywords: Agronomic traits; heritability; correlation; genetic parameters; *Oryza sativa*.

1. INTRODUCTION

Rice (*Oryza sativa* L.) is central to the lives of billions of people around the world. It is a staple food crop for more than half of the world's human population. Rice grain contains 75 to 80% starch, 12% water and 7% protein [1]. It also plays a significant role in Egypt, as strategic crop for sustaining the food self-sufficiency and for increasing the export the total rice production in Egypt reached 7.1 million tons with a national average of 9.9 tons/ha in 2012 growing season. This average ranked the first among the rice producing countries in the world [2].

Productivity improvement of rice crop has become of immense important to feed nearly half of the world's population. The breeders of rice are working to assess the genetic variability by digging out desirable characters and evaluation them up to which extent they are heritable, so various morphological characters have been identified that play pivotal role for high rice production [3]. Knowledge of heritability is important for selection based improvement as it indicates the extent of transmissibility of a character into future generations [4]. Heritability and genetic advance utilization of yield traits and inferences from significant correlation between yield and its attributes should permit selection of predictable rice genotypes [5]. It is important to know heritability and genetic variability of important agronomic traits for improving high yielding varieties [6].

Genetic variability for agronomic traits is the key component of breeding programs for broadening the gene pool of rice. Plant breeders commonly select for yield attributes which indirectly increasing yield. Genetic characters such as genotypic coefficient of variation and phenotypic coefficient of variation are useful in detecting the amount of variability present in the germplasm [7]. Genetic resource of rice is the primary material for improving in rice [8]. The new genotypes development requires some

knowledge about the genetic variability presents in the germplasm of the crop to build efficient breeding programme and The knowledge about genetic variability can help to know if these variations are heritable or non-heritable [9]. The nature and extent of genetic variation governing the inheritance of characters and association will facilitate effective genetic improvement [10]. Therefore, with the above background information this study aimed to study the magnitude of the genetic variance components i.e. additive genetic variance (σ^2A), dominance genetic variance (σ^2D) and broad and narrow sense heritability for agronomic characteristics and yield as well as to estimate the correlation between studied traits.

2. MATERIALS AND METHODS

The present study was carried out at the Experimental Farm of the Rice Research and Training Center (RRTC), Sakha, Kafr EL-Sheikh, Egypt, in 2010 and 2011 successive seasons. The research involved four rice genotypes (three commercial varieties (Giza178, Sakha103 and Sakha106 and and one promising line (Gz 9057-6-1-3-2) as well as six bold grain lines (Table 1).

The ten parental genotypes in this study were sown during 2010 in three sowing dates with 15 days intervals to overcome the difference of heading date among the parental varieties. 30 days old seedlings were transplanted in three rows of five meters length and (20 cm x 20 cm) spacing between plants and rows. A line x tester cross was conducted among the ten parents (four lines and six testers) in 2010 to produce (24) cross combinations. The hybridization technique of Jodon [11] and modified by Butany [12] was used and the hot water method of emasculation was utilized. In 2011 the parental varieties and their resulting 24 crosses were arranged in a randomized complete block design (RCBD) with three replications. Each replication contained 34 rows and each row contains 25 individual plants for each genotype.

Table 1. Names, origin and parentage of the parents utilized in this study

No.	Entry	Origin	Parentage
1	Giza 178	Egyptian	(Giza175/Milyang49)
2	Sakha 103	Egyptian	(Giza 177/Suweon 349)
3	Sakha 106	Egyptian	(Giza 177/Hexi 30)
4	GZ9057-6-1-3-2 (Giza 179)	Egyptian	(Gz 6296/Gz 1368-S-5-4)
5	SKC 23819-189-1-1-1-3-1-2-4-2	America/Egypt	(L 204/Giza177)
6	SKC 23819-192-2-1-2-2-4-2-1-2	Egypt /America	(L 204/Giza177)
7	SKC 23819-192-2-1-2-3-1-1-1-2	Egypt /America	(L 204/Giza177)
8	SKC 23819-192-2-1-2-4-5-3-2-1	Egypt/America	(L 204/Giza177)
9	SKC 23819-192-2-2-1-1-2-1-2-2	Egypt/America	(L 204/Giza177)
10	SKC 23819-192-2-2-1-1-2-2-1-2	Egypt/America	(L 204/Giza177)

The studied traits were number of days to heading, plant height (cm), number of panicles/plant, number of filled grains/ panicle, panicle length (cm), panicle weight (g), spikelets fertility (%), 1000 grain weight (g), and grain yield / plant (g).

The data were subjected to analysis of variance as suggested by Panse and Sukhatme [13] and the analysis of variance for line x tester crossing followed the design of Kempthorne [14]. The correlation coefficients were tested using the formula according to Gomez and Gomez [15].

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance

The results on analysis of variance revealed highly significant differences among genotypes for all studied traits (Table 2). The parental lines and the crosses showed highly significant differences for all studied characters. Parents vs. crosses mean squares indicated that average was highly significant for all traits. Obtained result agreement with Singh et al. [16]. The results also illustrated that the general combining ability variance of lines (female parents) was highly significant for all studied characters. The general combining ability variances of testers (male parents) were also highly significant for all characters. The mean squares of lines x testers interaction (SCA) exhibited highly significant differences for all characters, this might be due to the wide genetic diversity of lines and testers. These results were agreement with [17].

3.2 Genetic Components of Variance and Heritability

Results in (Table 3) showed that the additive genetic variance as a portion of the total genetic variance was smaller than the non-additive or

dominance genetic variance for all studied traits except for number of panicles / plant, number of filled grains / panicle and panicle length. This result indicated that additive genetic variance played the major role compared to the dominance variance in the inheritance of previous traits and phenotypic variance for these traits was due to additive genetic variance and environmental effects. These findings led to conclusions the selection for such traits must be done in the early segregating generations. This result agreed with [18-20].

Both additive and dominance genetic variances (σ^2A and σ^2D) were positive for all traits. These results indicate that the two genetic variance components might be important in the inheritance of these traits. These results were in general agreement with those reported by [19].

Concerning to heritability estimates in broad sense ($h^2_b\%$), the results indicated that the heritability values were more than 85% for all studied traits (Table 3). On the other hand, heritability estimates in the narrow sense ($h^2_n\%$) were low to moderate for the same traits. These results indicated that a major part of the total genotypic variance was non-additive in nature for these traits. These results were in general agreement with those reported by [21-26].

Heritability in narrow sense is an indicator of the efficiency of selection procedure in identifying the superior genotypes. In (Table 3) it was observed that heritability estimates in broad sense were high for all traits, while heritability estimates in narrow sense were relatively low for days to heading, plant height, number of filled grains / panicle, panicle weight, spikelets fertility percentage, and grain yield / plant and moderate for panicle length and 1000-grain weight. These results are in full agreement with previous results obtained by [27,28].

Table 2. Analysis of variance and mean square from line x testers' analysis for rice studied traits

S.V	D.F	Days to heading(days)	Plant height (cm)	No. of panicles / plant	No .of filled grains / panicle	Panicle length (cm)
Reps.	2	0.992	0.381	0.191	26.90	0.123
Genotypes	33	74.09**	303.7**	96.02**	2600**	9.753**
Parents	9	121.6**	379.3**	24.01**	515.3**	9.769**
Parents Vs.	1	706.6**	2839.2**	481.6**	0.308**	0.470**
Crosses						
Crosses	23	644.0**	163.9**	107.4**	3530**	10.15**
Lines (gca,L)	3	320.1**	806.4**	721.7**	6216**	64.22**
Testers(gca,T)	5	90.52**	60.68**	5.840**	4459**	2.040**
Line x testers(sca)	15	233.4**	69.93**	18.45**	2682**	2.041**
Error	66	21.74	0.268	0.496	15.99	0.215

*,** Significant at 5% and 1% levels of probability, respectively

Table 2. Continue

S. V	D.F	Panicle weight (g)	Spikelets fertility (%)	1000-grain weight (g)	Grain yield plant ⁻¹ (g)
Reps.	2	0.024	0.281	0.003	1.569
Genotypes	33	0.503**	610.1**	43.41**	272.0**
Parents	9	0.312**	25.25**	125.3**	174.2**
Parent Vs. Crosses	1	0.425**	936.0**	37.83**	2478**
Crosses	23	0.581**	824.8**	11.59**	214.3**
Lines (gca, L)	3	1.434**	3033**	49.97**	376.0**
Testers (gca, T)	5	0.275**	815.6**	13.62**	234.3**
Line x testers (sca)	15	0.513**	386.2**	3.249**	175.3**
Error	66	0.019	0.964	0.032	10.45

*,** Significant at 5% and 1% levels of probability, respectively

Table 3. Estimation of additive genetic variance (σ^2A), dominance genetic variance (σ^2D), environmental variance (σ^2E) and heritability in broad and narrow senses for studied characters

Traits	σ^2A	σ^2D	σ^2E	Heritability (%)	
				h^2_{bs}	h^2_{ns}
Days to heading (day)	1.167	5.076	0.329	94.98	17.76
Plant height (cm)	8.324	23.22	0.268	99.15	26.16
No. of panicles plant ⁻¹	7.374	5.983	0.496	96.42	53.22
No .of filled grains panicle ⁻¹	96.58	88.9	15.99	98.40	9.643
Panicle length (cm)	0.675	0.608	0.215	85.64	45.06
Panicle weight (g)	0.010	0.164	0.019	90.12	5.607
Spikelets fertility (%)	39.45	128.4	0.964	99.42	23.37
1000-grain weight (g)	0.707	1.072	0.963	98.23	39.06
Grain yield plant ⁻¹ (g)	4.992	54.95	10.45	85.15	7.090

3.3 Correlation Coefficient

The study of correlation coefficients among various agronomic traits is of great importance, since correlation can enable researchers to predict the performance of complex and quantitative traits that is difficult to measure

by using linked simple measured traits. Thus, enhancing significantly the selection efficiency since the influence of environment will be minimal in case of the simple traits [29]. The estimates of correlation coefficients among all studied characters are presented in Table 4.

Table 4. Estimates of phenotypic correlation coefficients among each pair of studied traits

Traits	Days to heading	Plant height	No. of panicles / plant	No. of filled grains / Panicle	Panicle length	Panicle weight	Spikelets fertility	1000-grain weight	Grain yield /plant
Days to heading	0.00								
Plant height	0.142	0.00							
No. of panicles / plant	0.479**	0.580**	0.00						
No. of filled grains / Panicle	0.002	0.215	0.401**	0.00					
Panicle length	-0.007	0.492**	0.278	0.169	0.00				
Panicle weight	0.027	-0.338*	-0.236	0.253	-0.022	0.00			
Spikelets fertility%	-0.234**	-0.369*	-0.179	0.497**	-0.476**	0.356*	0.00		
1000-grain weight	0.436**	-0.535**	0.015	-0.103	-0.319	0.417**	0.201	0.00	
Grain yield / plant	0.253**	0.206**	0.181**	0.080**	0.020**	0.230**	0.151**	0.193**	0.00

Concerning to number of days to heading, data showed highly significant positive correlation with number of panicles / plant, 1000-grain weight (g) and grain yield / plant, (0.479, 0.436 and 0.253), respectively and highly significant negative correlation with spikelets fertility percentage (-0.234). These results are in similar to those of [30].

As for plant height gave highly significant positive correlation coefficient with each of number of panicles / plant (0.580), panicle length (0.492) and grain yield/ plant (0.206). Also it was found highly significant negative correlation between plant height and 1000-grain weight (-0.535) while found significant negative correlation with panicle weight (-0.338) and fertility percentage (-0.369). This result is in accordance with to those of [31].

With regard to number of panicles / plant highly significant positive correlation coefficient was showed with number of filled grains / panicle (0.401) and grain yield / plant (0.181). The obtained results are in harmony with those reported by [32].

Regarding number of filled grains / panicle, data cleared highly significant positive correlation coefficient with fertility percentage the value was (0.497) and grain yield / plant (0.080) similar results were previously obtained by [20].

Significant and positive correlation coefficient was recorded between panicle length and grain yield / plant with value of 0.020, and highly significant negative correlation with spikelet fertility percentage with value of -0.476. The obtained results are in harmony with those reported by [27,20,17].

On the other hand, panicle weight showed positive highly significant correlation coefficient with 1000- grain weight and the value was (0.417) and grain yield / plant (0.230), while significant positive correlation coefficient with spikelet fertility percentage with value (0.356). The result is in agreement with [32,31].

Highly significant positive correlation coefficient for fertility percentage was observed with grain yield / plant (0.151). Similar results were previously obtained in different crops by [33,34].

On the other hand, 1000- grain weight showed positive highly significant correlation coefficient with grain yield / plant (0.193). The obtained

results are in harmony with those reported by [20,17].

4. CONCLUSION

The results of the present study suggested that, the overall results indicated that there is adequate genetic variability present in the material studied. The broad sense heritability and correlation analysis of the study revealed that the number of panicles / plant, the number of grains / panicle, spikelets fertility % and 1000 grain weight were the most important yield components, these characters also showed moderate to high heritability in percentage of mean and selection based on these traits would be most effective.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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