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Assessment of genetic variability and correlation coefficient to improve some agronomic traits in rice

ABSTRACT

This study was carried out 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) crosses. The results indicated that 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 /plantin comparison with its corresponding evaluates of additive genetic variance. 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 of days number to heading, plant height, number of panicles / plant, panicle length and fertility percentage.

Keywords: *Heritability, Correlation, Genetic parameters, Yield, Rice.*

1. INTRODUCTION

Rice (Oryza sativa L.) is central to the lives of billions of people around the world.Rice provides 27% of dietary energy and 20% of dietary protein in the developing world. Rice is cultivated in at least 114, mostly developing countries and is the primary source of income and employment for more than 100 million households in Asia and Africa (FAO, 2004).Rice crop 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 (RRTC, 2013).

Genetic parameters such as genotypic coefficient of variation and phenotypic coefficient of variation are useful in detecting the amount of variability present in the germplasm. Heritability coupled with high genetic advance helps in determining the influence environment on the expression the genotypic and reliability of characters (Nirmalaet al.,2015). Yield traits breeding for grain yield increasing would be most effective, if the traits involved are highly heritable and genetically independent or positively correlated with grain yield. However, it is very difficult to judge whether observed variability is highly heritable or not (Osman et al., 2012). Moreover, knowledge of heritability is important for selection based improvement as it indicates the extent of transmissibility of a character into future generations (Sabesan et al., 2009).The utilization of heritability and genetic advance of yield traits and inferences from significant genotypic correlation between yield and its components should permit selection of predictable rice genotypes for upland ecosystem (Osman et al., 2012).

Productivity improvement for rice has become of immense necessary to feed nearly half of the world's population. Genetic resource of rice is the primary material for improving in rice(Perera et al., 2014).Over dominance pseudo-over dominance is the most important contributor to heterosis of yield, number of grains /panicleand grain weight. Dominance x dominance interaction is important for heterosis of tillers / plant and grain weight and has roles in yield and grain number. Cumulative effects of these components may adequately explain the genetic basis of heterosis in the hybrid (Zhou Gang et al., 2012).With the above background informationthisstudy aimed to study the magnitude of the genetic variance components i.e. additive genetic variance (σ2A), dominance genetic variance (σ2D) and broad and narrow sense heritability for agronomic characteristics and yield as well as to estimate the correlation between studied traits.

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2. MATERIAL 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, at 2010 and 2011 successive seasons. The research involving four rice genotypes, i.e. three commercial varieties (Giza178, Sakha103 and Sakha106), one promising line (Gz 9057-6-1-3-2) as well as six bold grain lines (SKC 23819-189-1-1-1-3-1-2-4-2, SKC 23819-192-2-1-2-2-4-2-1-2, SKC 23819-192-2-1-2-3-1-1-1-2, SKC 23819-192-2-1-2-4-5-3-2-1, SKC 23819-192-2-2-1-1-2-1-2-2 and SKC 23819-192-2-2-1-1-2-2-1-2). The parental genotypes have a wide range of variations for all studied traits. Origin and parentage of the ten parents were illustrated in (Table 1).

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-	America/Egypt	(L 204/Giza177)
6	SKC 23819-192-2-1-2-2-4-2-1-	Egypt /America	(L 204/Giza177)
7	SKC 23819-192-2-1-2-3-1-1-1-	Egypt /America	(L 204/Giza177)
8	SKC 23819-192-2-1-2-4-5-3-2-	Egypt/America	(L 204/Giza177)
9	SKC 23819-192-2-2-1-1-2-1-2-	Egypt/America	(L 204/Giza177)
10	SKC 23819-192-2-2-1-1-2-2-1-	Egypt/America	(L 204/Giza177)

The ten parental genotypes in this study were sown in the growing season of 2010 in three sowing dates with 15 days intervals to overcome the difference of heading date among the parental varieties. After 30 days from the sowing, the seedling of ten parents were transplanted to the experimental field in three rows, each row was five meters long 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) crosses. The hybridization technique of Jodon (1938) and modified by Butany (1961) was used and the hot water method of emasculation was utilized. 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. The studied traits were number of days to heading (day), plant height (cm), number of panicles/ plant, number of filled grains/ panicle, panicle length, panicle weight (g), spikelets fertility percentage, grain weight (g), and grain yield / plant(g).

Genotypes means were used for the analysis of variance Singh and Chaudhary (1985). The correlation coefficients were tested using the formula according to Gomez and Gomez (1983). The data were subjected to analysis of variance as suggested by Panse and Sukhatme (1957) and the analysis of variance for line x tester crossing followed the design of Kempthorne (1957).

3. RESULTS AND DISCUSSION

3.1 Analysis of variance

The results on analysis of variance revealed that highly significant differences were observed 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 heterosis was highly significant for all traits. Obtained result agreement with Singh*et al.* (2011) and Abdelkhalik*et al.* (2013).

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

S.O.V	D.F	Days to heading(days)	Plant height (cm)	No. of panicles plant^{-1}	No .of filled grains panicle^{-1}	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**
P.Vs.C	1	706.6**	2839.2**	481.6**	0.308**	0.470**
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

*and** significant at 5% and 1% levels of probability, respectively.

Table 2: continue.

S.O.V	D.F	Panicle weight	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**
P.Vs.C	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

*and** significant at 5% and 1% levels of probability, respectively.

The results also illustrated that the general combining ability variance of lines (female parents) showed highly significant for all studied characters. The general combining ability variances of testers (male parents) were 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 Singh*et al.* (2011), Abdelkhalik*et al.* (2013) and Anis *et al.* (2016b).

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 characteristics except for number of panicles/ plant, number of filled grains / panicleand panicle length characters. This result indicated that dominance genetic variance played the major role compared to the additive variance in the inheritance of these traits and phenotypic variance for these traits was due to dominance genetic variance and environmental effects (Pazza *et al.* 2016). These findings led to conclusions the selection for such traits must be done in the late segregating generations. This result agreed with Zhou Gang *et al.* (2012), Anis (2013) Perera*et al.* (2013).

Both additive and dominance genetic variances (σ^2A and σ^2D) were positive for all traits. Their respective values for σ^2A and σ^2D were (1.167 and 5.076) for days to heading, (8.324 and 23.22) for plant height, (7.374 and 5.983) for number of panicles plant^{-1}, (96.58 and 88.9) for number of filled grains panicle^{-1}, (0.675 and 0.608) for panicle length,(0.01 and 0.164) for panicle weight, (39.45 and 128.4) for spiklets fertility percentage, (0.707 and 1.072) for 1000-grain weight at last (4.992 and 54.95) for grain yield / plant, respectively. These results indicate that the two genetic variance components might be

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important in the inheritance of these traits. These results were in general agreement with those reported byAnis (2013) and Perera*et al.* (2013).

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 %	
				$h^2_{b\,\%}$	$h^2_{n\,\%}$
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	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

Concerning to heritability estimates in broad sense (h^2_b%), the results indicated that the heritability values were more than 90% for all studied traits except for panicle length and grain yield plant^{-1}the values were 85.64% and 85.15% , respectively (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 Anil and Mani (2010), Fahliani*et al.* (2010), Kayande and Debaje (2010), and Mohan and Chauhan (2011) and Anis *et al.,* (2016 a).

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^{-1}, panicle weight, spiklets fertility percentage, and grain yield plant^{-1}, and moderate for panicle length and 1000-grain weight. These results are in full agreement with previous results obtained by Chakraborty and Chakraborty (2010) and Adilakshmi and Rani (2012).

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(Anis *et al.* 2016a). 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	Heading date	Plant height	No. of panicles plant^{-1}	No. of filled grains Panicle^{-}	Panicle length	Panicle weight	Spikelets fertility%	1000-grain weight	Grain yield plant^{-1}
Heading date	0.00								
Plant height	0.142	0.00							
No. of panicles plant^{-1}	0.479**	0.580**	0.00						
No. of filled grains Panicle^{-1}	0.002	0.215	0.401**	0.00					

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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^{-1}	0.253**	0.206**	.181**	0.080	0.020**	0.230	0.151**	-0.133	0.00

Concerning to heading date, data showed that highly significant positive correlation with each of 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 Anis (2009) and Minnie *et al.* (2013).

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 El-Sherif (2011) and Essa (2012).

With regard to number of panicles/ plant highly significant positive correlation coefficient was showed with number of filled grains panicle^{-1} (0.401), and grain yield plant^{-1} (0.181). The obtained results are in harmony with those reported by El-Sherif (2011). Regarding number of filled grains /panicle, data cleared highly significant positive correlation coefficient with fertility percentage the value was (0.497) similar results were previously obtained byNandeshwar*et al.* (2010) and Fazza et al. (2016a,b).

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 Chakraborty and Chakraborty (2010) ;Fazaa et al., (2016a, b) and Anis*et al.,* (2016 b). On the other hand, panicle weight showed positive highly significant correlation coefficient with 1000- grain weight and the value was (0.417) and significant positive correlation coefficient with spikelet fertility percentage with value (0.356). The result is in agreement with Nandeshwar*et al.* (2010) and Essa (2012). Highly significant positive correlation coefficient for fertility percentage was observed with grain yield plant^{-1} (0.151). Similar results were previously obtained in different crops by Sedeek*et al.* (2007); Abd el-wahed et al., (2015) and Barutçular et al., (2016).

4. CONCLUSION

The results of the present study suggested that the hybrid combinations viz., Giza 177 x Chinese2 followed by the hybrid, Giza 177 x Sakha 106, Chinese2 x Gz8479-6-2-3-1 and Sakha 101 x IR67701B were existing rice hybrids due to good heterosis values for grain yield trait. Thus these genotypes with higher magnitude of this trait could be either evolved by breeding program for genetic improvement of yield in rice.

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