

HERITABILITY, GENETIC ADVANCE AND CORRELATION STUDIES OF SOME IMPORTANT TRAITS IN RICE

H.R. Bughio, M.A. Asad, I. A. Odhano, M.A. Arain, and M. S. Bughio

Plant Breeding and Genetics Division, Nuclear Institute of Agriculture, Tando Jam-Pakistan

ABSTRACT

Genetic variability, estimates of broad sense heritability, genetic advance as percent of mean and genotypic and phenotypic correlation coefficients were observed in eight rice genotypes at Nuclear Institute of Agriculture, Tando Jam in 2005. High heritability coupled with high genetic advance was exhibited for number of fertile grains per panicle, number of productive tillers per plant and grain yield per plant, indicating additive gene action and possibility of improving these traits by simple selection. High heritability with moderate genetic advance was exhibited for plant height, 1000-grain weight and panicle length indicating the involvement of additive and non-additive type of gene action and postponement of selection programs for the improvement of these traits. The characters productive tillers per plant, panicle length, number of fertile grains per panicle, panicle fertility percentage and 1000-grain weight showed significant positive correlation with grain yield per plant. While plant height and days to 50% flowering were observed non-significant and negatively correlated with grain yield per plant. Fertile grain had significant and positive correlation with panicle fertility percentage.

Key Words: *Oryza sativa* L., heritability, genetic advance, genotypic and phenotypic correlation.

INTRODUCTION

Among the cereals, rice is a leading food crop and a primary food source for nearly one half of the world's population. It has unique importance for its industrial usage viz, in making foods for infants, snacks, breakfast cereals, fermented products and rice bran oil. Rice straw is also used in paper making and still serves as an important cattle feed throughout Asia. In Pakistan, rice has an important place in national economy for fetching the foreign exchange. Pakistan earned a foreign exchange of Rs.55.39 billion by exporting a quantity of 2.891 million tons of rice in 2005 (Anonymous, 2005-06). Yield per hectare is the most important consideration in rice breeding programmes, and is considered as a complex character in inheritance as it involves several related components. The most important components of yield being the number of panicles per plant, number of spikelets per panicle, percentage of filled grains and weight of 1000 grains (Ashvani *et al.*, 1997a and Surek and Beser, 2003). It is therefore important to know the factors or traits that influence the grain yield directly or indirectly or both and to determine the heritability and genetic advance under selection of those traits so that response to selection can be predicted.

Knowledge of correlation that exists between important characters facilitates the planning of a more efficient breeding programme. Breeding for high yield would be more effective, if components involved are highly heritable and positively correlated (Kumari *et al.* 2003). Fortunately, some breeders have identified yield components that contribute indirectly for increase in yield (Saravanan and Senthil 1997). The present study was therefore undertaken to determine phenotypic and genotypic correlation coefficients among various agronomic traits in rice and to analyze their interrelationship. In addition, estimates on broad sense heritability and genetic advance for the selected traits were also computed.

MATERIALS AND METHODS

The plant material used in the investigation comprised of five mutants (IR6-15-1, IR6-15A, IR6-15B, IR6-25A, and IR6-25B) along with three commercial rice varieties (IR6, Shua-92 and Shadab) at Nuclear Institute of Agriculture, Tando Jam in 2005. One month old seedlings of these genotypes were transplanted in the field, laid out in a randomized complete block design with three replications of plot size 4.5m² per replication per treatment. Plant to plant and row-to-row distance was maintained at 20cm. During growth and development of plants, the recommended production practices were applied. At maturity, the middle ten plants were consecutively taken for collecting data from each row in each replication, while two plants on either end of each row were treated as non-experimental. Data on days to 50% flowering from seedling, plant height (cm), number of panicles per plant, panicle length (cm), number of fertile grains per panicle, 1000 grain weight (g) and grain yield per plant were taken. Data were subjected to analysis of variance (Steel and Torrie, 1980). Estimates of broad sense heritability, genetic advance at 5% selection intensity and genetic advance as percent of mean were also calculated. Phenotypic and

genotypic correlations among different characters were obtained by analyzing the data following the technique given by Kwon and Torrie (1964).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among genotypes for all the plant characters studied (Table I). Genetic variability for grain yield and yield components in rice genotypes have also been found by Bhandarkar *et al.*, (2002) and Kumari *et al.*, (2003). All the studied characters were found highly heritable with values ranging from 0.998 for fertile grains per panicle, 0.992 for grain yield per plant and plant height, 0.965 for days to 50% flowering, 0.921 for productive tillers per plant, 0.896 for panicle fertility percentage, 0.809 for panicle length and 0.591 for 1000 grain weight (Table II). The presence of high heritability estimates is directly helpful in making selection of superior genotypes on the basis of phenotypic performance. Johnson *et al.*, (1955) suggested that heritability estimates along with genetic advance (as percent of mean) are more useful in predicting the effect of selection for the best individual. High heritability combined with high genetic advance is the indication of additive gene effect and suggests the positive role of these characters in genetic improvement (Dhananjaya *et al.*, 2003; Ashvani *et al.*, 1997a; Saravanan and Senthil (1997) and Datke *et al.*, 1997). In our studies number of fertile grains per panicle, number of productive tillers per plant and grain yield per plant showed better combination of heritability and genetic advance as percent of mean. The characters with high value of heritability accompanied by high genetic advance indicate that they might have been transmitted to their progenies and therefore phenotypic selection based on these characters could be effective. In general, genotypic correlation coefficients were higher than their corresponding phenotypic correlation coefficients indicating a fairly strong inherent relationship among the traits. The lower estimates of phenotypic correlation coefficients indicated that the relationships were affected by environment at phenotypic level. Such environmental influences in reducing the correlation coefficients in rice were also reported by Chaubey and Singh (1994).

Table 1. **Mean squares for eight quantitative plant characters in rice genotypes.**

Source of variation	Degree of freedom	Days to 50% flowering	Plant height	Productive tillers per plant	Panicle length	Fertile grains per panicle	Panicle fertility percentage	1000 grain weight	Grain yield per plant
Genotypes	7	5.867**	7.956**	0.809**	2.458**	47.249**	6.149**	1.759**	16.480**
Repeats	2	16.534	44.469	9.512	4.33	2810.68	13.375	9.234	134.63
Error	14	0.581	0.351	0.756	0.82	5.643	1.394	3.781	1.081

** Significant at 1 % level of probability

Table 2. **Estimates of broad sense heritability and genetic advance for certain quantitative plant characters in rice.**

Parameters	Days to 50% flowering	Plant height	Productive tillers per plant	Panicle length	Fertile grains per panicle	Panicle fertility percentage	1000 grain weight	Grain yield per plant
Heritability (B.S.)	0.965	0.992	0.921	0.809	0.998	0.896	0.591	0.992
G. A. (% of mean)	3.985	8.238	18.765	7.958	42.122	4.397	8.414	18.711

Results of correlation coefficients at genotypic and phenotypic level (Table 3) showed that grain yield was significantly and positively correlated with number of productive tillers per plant, panicle length, number of fertile grains per panicle, panicle fertility percentage and 1000-grain weight as have been found by Selvarani and Rangasamy, (1998). Grain yield exhibited weak correlation with plant height and days to 50% flowering. Contrarily significant negative correlation between grain yield and plant height has been found by Chandra and Das (2000) in some rice genotypes. Number of productive tillers per plant showed the highest positive correlation with panicle fertility percentage (0.996) followed by panicle length (0.773), and 1000-grain weight (0.710), Mishra and Verma, (2003) also found similar results. Panicle length was significantly and positively associated with fertile grains per panicle (0.851) and non-significantly with panicle fertility percentage. Fertile grains per panicle were strongly and positively correlated with panicle fertility percentage (0.928) while panicle fertility percentage in turn was strongly associated with 1000 grain weight (0.978) as found by Ashvani *et al.*, (1997b) and Ananthi *et al.*, (2006).

CONCLUSION AND RECOMMENDATIONS

This study revealed that shorter plant, higher number of productive tillers per plant, adequate number of fertile grains per panicle are the important characters which should be considered while selection to be made for higher yield in rice genotypes.

Table 3. Genotypic and phenotypic correlation coefficients among various plant traits in rice.

Parameters	r-values	Plant height	Productive tillers per plant	Panicle length	Fertile grains per panicle	Panicle fertility percentage	1000 grain weight	Grain yield per plant
Days to 50% flowering	r_p	0.08 ^{NS}	-0.25 ^{NS}	0.056 ^{NS}	-0.2434 ^{NS}	-0.1211 ^{NS}	0.3989 ^{NS}	-0.3421 ^{NS}
	r_g	0.08 ^{NS}	0.20 ^{NS}	0.061 ^{NS}	-0.250 ^{NS}	-0.103 ^{NS}	0.509 ^{NS}	-0.352 ^{NS}
Plant height	r_p		-0.0329 ^{NS}	-0.218 ^{NS}	0.1249 ^{NS}	0.3002 ^{NS}	0.3159 ^{NS}	0.2637 ^{NS}
	r_g		-0.038 ^{NS}	-0.236 ^{NS}	0.125 ^{NS}	0.135 ^{NS}	0.149 ^{NS}	0.267 ^{NS}
Productive tillers per plant	r_p			0.705**	0.6774**	0.9265**	0.5262**	0.6719**
	r_g			0.773*	0.707*	0.996*	0.710*	0.708*
Panicle length	r_p				0.766**	0.632**	0.108 ^{NS}	0.385**
	r_g				0.851*	0.664 ^{NS}	0.109 ^{NS}	0.430*
Fertile grains per panicle	r_p					0.8795**	0.2052 ^{NS}	0.8283**
	r_g					0.928*	0.271 ^{NS}	0.832*
Panicle fertility percentage	r_p						0.7272**	0.9559**
	r_g						0.978*	1.032*
1000 grain weight	r_p							0.4972**
	r_g							0.649*

*, ** = Significant at 5% and 1 % level of probability respectively, NS = Non significant ; r_p = Phenotypic correlation coefficient
 r_g = Genotypic correlation coefficient

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