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## Genetic Architecture, Inter-relationship and Selection Criteria for Yield Improvement in Rice (*Oryza sativa* L.)

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**Abstract:** This study has been conducted to determine the extent of genetic association between yield of Rice (*Oryza sativa* L.) and its components. The present experiment was carried out with 40 Rice (*Oryza sativa* L.) genotypes which were evaluated in a randomized block design with 3 replications during wet season of 2007 and 2008. Results showed that sufficient amount of variability was found in the entire gene pool for all traits studied. Higher magnitude of genotypic and phenotypic coefficients of variation was recorded for seed yield, harvest index, biological yield, number of spikelets per panicle, flag leaf length, plant height and number of tillers indicates that these characters are least influence by environment. High heritability coupled with high genetic advance as percent of mean was registered for seed yield, harvest index, number of spikelets per panicle, biological yield and flag leaf length, suggesting preponderance of additive gene action in the expression of these characters. Grain yield was significantly and positively associated with harvest index, number of tillers per hill, number of panicle per plant, panicle length, number of spikelet's per panicle and test weight at both genotypic and phenotypic levels. Path coefficient analysis revealed that harvest index, biological yield, number of tillers per hill, panicle length, number of spikelets per panicle, plant height and test weight had direct positive effect on seed yield, indicating these are the main contributors to yield. From this study it may be concluded that harvest index, number of tillers per hill, panicle length and number of spikelet per panicle and test weight are the most important characters that contributed directly to yield. Thus, these characters may serve selection criteria for improving genetic potential of rice.

**Key words:** Rice, direct and indirect effects, correlation, polygenic traits, yield

### INTRODUCTION

“Rice is life” was the theme of International Year of Rice 2004 signifies its devastating importance on global food system (FAO, 2004). It is the most important cereal crop providing energy, protein and vitamins for half of the world's population (Nguyen, 2010; Tiwari *et al.*, 2011). Grain yield is a complex polygenic character (Mustafa and Elsheikh, 2007; Atta *et al.*, 2008; Majumder *et al.*, 2008; Selvaraj *et al.*, 2011) which depends on its main components *viz*; number of spikes per plant, spike length, number of grains per spike and 1000 grain weight. Therefore, selection based on *per se* performance is not effective thus; consideration of other yield components at the same time more proficient. Resourceful crop improvement scheme refers to the collection of superior alleles into a single targeted genotype (Wang and Wolfgang, 2007; Tripathi *et al.*, 2011). The nature and extent of genetic variation governing the inheritance of characters and association will facilitate effective genetic improvement (Ismail *et al.*, 2001). It is apparent that

information of morphological and physiological aspects of crop is also key feature to plan a resourceful breeding program. Thus, the genetic reconstruction of plant architecture is required for developing high yielding crop varieties.

Correlation coefficient is a statistical measure which determines the degree (strength) and direction of relationship between two or more variable. The better way of exploiting genetic correlation and path coefficient with several traits having high heritability is to construct a selection index that combines information on all the characters associated with the dependent variable. Wide difference between genotypic and phenotypic correlations between two characters is due to dual nature of phenotypic correlation which is determined by genotypic and environmental correlations and heritability of the characters (Falconer, 1981). Keeping in view the above perspectives, the present research work was taken up to assess associations between various components of grain yield to provide basis for selection and yield improvement in rice.

**MATERIALS AND METHODS**

**Experimental design:** The experimental material comprising forty rice genotypes were evaluated in randomized block design with 3 replications during wet season of 2007-2008 in two consecutive cropping seasons at field experimentation center of Department of Genetics and Plant Breeding, Sam Higginbottom Institute of Agriculture, Technology and Sciences, Allahabad. This experimental site is situated at 25.87°N latitude and 81.5°E latitude and 98 meter above the sea level. It has a sub-tropical climate with extremes of summer and winter. Each genotype was grown in a plot of 2 m<sup>2</sup> keeping 20×15 cm spacing. Standard agronomic practices compatible to this ago-ecological zone were adopted to ensure good crop growth.

**Data collection:** The observations were recorded on 10 randomly selected plants from each replication for various characters *viz.*, days to 50% flowering, plant height, number of tillers per hill, panicle length, number of panicles per hill, number of spikelets per panicle, flag leaf length, flag leaf width, grain yield per hill, biological yield per hill, harvest index and test weight. The general reference for data collection was standard evaluation system for rice (Anonymous, 2002).

**Statistical analysis:** The mean performance of individual genotype over two years was pooled and employed for statistical analysis. PCV and GCV were calculated by the formula given by Burton (1952), heritability in broad sense (h<sup>2</sup>) by Burton and deVane (1953) and genetic advance *i.e.*, the expected genetic gain were calculated by using the procedure given by Johnson *et al.* (1955). Correlation coefficient and path coefficient was worked out as method suggested by Al-Jibouri *et al.* (1958) and Dewey and Lu (1959), respectively. The estimated values were

compared with table values of correlation coefficient to test the significance of correlation coefficient prescribed by Fisher and Yates (1967).

**RESULTS AND DISCUSSION**

The variability parameters (Table 1) revealed that a wide range of genotypic (Vg) and phenotypic variance (Vp) was observed for all the characters studied. The higher magnitude of Genotypic (GCV) and Phenotypic Coefficients of Variation (PCV) was recorded for traits like seed yield per hill, harvest index, biological yield, number of spikelets per panicle, flag leaf length, number of tiller per hill and plant height. However, moderate estimates were observed for panicle length and test weight rest of the character showed low estimates of GCV and PCV. The studies on genotypic and phenotypic coefficient of variation indicated that the presence of high amount of variance and role of the environment on the expression of these traits. The magnitude of phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters which may be due to higher degree of interaction of genotypes with the environment. Similar findings were also observed by Chaubey and Singh (1994), Sharma and Richharia (1995), Bhandarkar *et al.* (2002), Das *et al.* (2005), Dutt *et al.* (2007) and Pandey *et al.* (2010).

The proportion of genetic variability which is transmitted from parents to offspring is reflected by heritability (Lush, 1949). Heritability and genetic advance when calculated together would prove more useful in predicting the resultant effect of selection on phenotypic expression (Johnson *et al.*, 1955). Based on this consideration high heritability coupled with high genetic advance as percent of mean was registered for seed yield per hill, harvest index, number of spikelets per panicle, biological yield and flag leaf length, suggesting

Table 1: Genetic variability parameters for different quantitative traits in rice

Characters	Variance		GCV %	PCV %	H (bs) %	GA	GG
	Vg	Vp					
Days to 50% flowering	37.26	42.52	6.23	6.65	87.6	11.77	12.01
Plant height	153.88	155.73	12.89	12.96	98.8	25.40	26.39
No. of tillers/hill	3.54	5.09	12.58	15.07	69.7	3.23	21.64
No. of panicles/hill	2.32	4.21	11.42	15.39	55.1	2.33	17.47
Flag leaf length	16.37	17.70	16.17	16.81	92.5	8.01	32.04
Flag leaf width	0.002	0.006	3.20	6.21	26.6	0.04	3.40
Panicle length	3.33	3.73	8.01	8.48	89.4	3.55	15.61
No. of spikelets/panicles	337.43	359.12	14.95	15.42	94.4	36.68	29.85
Biological yield(g)	79.28	81.65	13.39	13.59	97.1	28.07	27.19
Seed yield/hill	38.06	39.19	15.05	15.27	97.1	12.52	30.56
Harvest index	99.39	103.74	16.03	16.37	95.8	20.10	32.32
Test weight	4.04	4.28	8.89	9.14	94.6	24.03	17.81

Vg: Genotypic variance, Vp: Phenotypic variance, GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, H (bs): Heritability broad sense, GA: Genetic advance, GG: Genetic gain

preponderance of additive gene action in the expression of these characters. Therefore, selection may be effective through these characters. High heritability associated with moderate genetic advance as percent of mean was observed for test weight and panicle length. Whereas, days to 50% flowering recorded high heritability and low genetic advance which revealed the non-additive gene action in the expression of these characters in their inheritance, hence in this case selection may not be effective. These findings were in agreement with the findings of earlier researcher (Singh *et al.*, 2002; Mohanumad and Ahmed, 2002; Vivek *et al.*, 2000; Vaithiyalingan and Nadarajan, 2006; Manickavelu *et al.*, 2006; Bagheri *et al.*, 2008; Pandey *et al.*, 2009; Pandey and Anurag, 2010).

Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield. While selecting the suitable plant type, correlation studies would provide reliable information in nature, extent and the direction of the selection, especially when the breeder needs to combine high yield potentials with desirable agronomic traits and grain quality characters. A positive value of correlation shows that the changes of two variables are in the same direction, i.e., high value of one variable are associated with high values of other and vice-versa. When correlation is negative the movements are in opposite directions, i.e., high values of one variable are associated with low values of other. The breeder is always concerned for the selection of superior genotypes on the basis of phenotypic expression. However, for the

quantitative characters, genotypes are influenced by environment, thereby affecting the phenotypic expression. Information regarding the nature and extent of association of morphological characters would be helpful in developing suitable plant type, in addition to the improvement of yield a complex character for which, direct selection is not effective.

In general, the genotypic and the phenotypic correlation coefficients (Table 2) showed similar trend but genotypic correlation coefficients were of higher in magnitude than the corresponding phenotypic correlation coefficients which might be due to masking or modifying effect of environment (Singh, 1980). These findings are corroborating the observations of Meenakshi *et al.* (1999), Chaubey and Singh (1994) and Bhattacharyya *et al.* (2007). Very close values of genotypic and phenotypic correlations were also observed between days to 50% flowering with flag leaf length and biological yield, harvest index with test weight and seed yield, plant height with number of spikelets per panicle and test weight, number of spikelets with biological yield, test weight with flag leaf length; which might be due to shrinking environmental variance to minor proportions as reported by Dewey and Lu (1959).

Seed yield was significantly and positively associated with number of tillers per hill (0.356\*\*, 0.311\*\*), number of panicle per plant (0.465\*\*, 0.366\*\*), panicle length (0.305\*\*, 0.283\*\*), number of spikelet's per panicle (0.320\*\*, 0.301\*\*), test weight (0.207\*\*, 0.197\*) and harvest index (0.625\*\*, 0.626\*\*) at both genotypic and phenotypic levels (Table 2). Similar findings were also reported by Rao *et al.* (1997), Prasad *et al.* (2001),

Table 2: Estimates of genotypic (rg) and phenotypic (rp) correlation coefficients among different quantitative characters in rice

Characters	r	Plant height	No. of tillers /hill	No. of panicle /plant	Flag leaf length	Flag leaf width	Panicle length	No. of spikelets /panicle	Biological yield	Harvest index	Test weight	Seed yield/hill
Days to 50% flowering	rg	0.082	-0.113	-0.214*	0.099	-0.178	-0.120	0.086	-0.133	-0.045	-0.079	-0.161
	rp	0.077	-0.098	-0.146	0.093	-0.128	-0.107	0.076	-0.133	-0.032	-0.059	-0.142
Plant height	rg		0.098	0.115	0.305**	-0.189*	0.295**	0.156	-0.063	0.174	-0.013	-0.114
	rp		0.090	0.090	0.293**	-0.105	0.275**	0.152	-0.059	0.165	-0.013	-0.112
No. of tillers/hill	rg			0.985**	0.182	0.328**	-0.218*	-0.151	0.109	0.221*	-0.202*	0.356**
	rp			0.873**	0.132	0.171	-0.211*	-0.126	0.084	0.204*	-0.166	0.311**
No. of panicle/plant	rg				0.182*	0.387**	-0.283**	-0.140	0.232*	0.222*	-0.228*	0.465**
	rp				0.117	0.144	-0.222*	-0.086	0.157	0.197*	-0.178	0.366**
Flag leaf length	rg					0.171	0.143	0.223*	-0.197*	0.182*	-0.139	0.015
	rp					0.088	0.139	0.216*	-0.185*	0.166	-0.135	0.012
Flag leaf width	rg						-0.608**	-0.156	0.123	-0.245**	-0.075	-0.143
	rp						-0.281**	-0.038	0.054	-0.133	-0.038	0.113
Panicle length	rg							-0.035	-0.061	-0.228*	-0.039	0.305**
	rp							0.006	-0.053	-0.209*	-0.045	0.283**
No. of spikelets/panicle	rg								-0.065	0.339**	-0.223*	0.319**
	rp								-0.062	0.319**	-0.217*	0.301**
Biological yield	rg									-0.475**	0.065	-0.378**
	rp									-0.480**	0.059	-0.367**
Harvest index	rg										0.138	0.625**
	rp										0.136	0.626**
Test weight	rg											0.207*
	rp											0.199**

\*Significant at 5% level and \*\* significant at 1% level, rg: Genotypic correlation and rp-: Phenotypic correlation

Table 3: Direct (diagonal values) and indirect effects of different characters on seed yield/hill at genotypic level

Characters	Days to 50% flowering	Plant height	No. of tillers /hill	No. of panicle /plant	Flag leaf length	Flag leaf width	Panicle length	No. of spikelets /panicle	Biological yield	Harvest index	Test weight	Genotypic correlation with seed yield
Days to 50% flowering	-0.0723	-0.0059	0.0081	0.0155	-0.0072	0.0128	0.0087	-0.0062	0.0096	0.0033	0.0057	-0.161
Plant height		0.0146	0.0014	0.0017	0.0045	-0.0028	0.0043	0.0023	-0.0009	0.0025	-0.0002	-0.114
No. of tillers/hill			0.4628	0.4557	0.0844	0.1520	-0.1007	-0.0699	0.0503	0.1022	-0.0937	0.356**
No. of panicle/plant				-0.4336	-0.0788	-0.1676	0.1228	0.0608	-0.1007	-0.0963	0.0988	0.465**
Flag leaf length					0.0330	0.0057	0.0047	0.0074	-0.0065	0.0060	-0.0046	0.015
Flag leaf width						-0.0759	0.0461	0.0118	-0.0093	0.0186	0.0056	-0.143
Panicle length							0.1126	0.0039	0.0068	0.0257	0.0044	0.305**
No. of spikelets/panicle								0.0394	-0.0026	0.0134	-0.0088	0.319**
Biological yield									0.8943	-0.4256	0.0582	-0.378**
Harvest index										0.9744	0.1341	0.625**
Test weight											0.0076	0.207*

\*Significant at 5% level and \*\*Significant at 1% level, residual effect: 0.1291

Surek and Beser (2003), Yogamenakshi and Ambularmathi (2004) and Mustafa and Elsheikh (2007). Thus selection for higher yield on the basis of above characters would be reliable. Biological yield showed negative significant direct correlation with grain yield (0.378\*\*, 0.367\*\*) at both genotypic and phenotypic level. The genetic reasons for this type of negative association may be linkage or pleiotropy. Similar negative correlation was also reported by Chaudhury and Das (1998) and Shanthy and Singh (2001). According to Newell and Eberhart (1961), when two characters show negative phenotypic and genotypic correlation it would be difficult to exercise instant selection for these characters, hence, under such situations perceptive selection programme formulated for simultaneous improvement.

When characters having direct bearing on yield are selected, their associations with other characters are to be considered simultaneously as this will indirectly affect yield. Significant positive correlations at both the levels were recorded for plant height with flag leaf length and panicle length; harvest index with number of tillers per hill, number of spikelets per plant, number of panicles per plant and flag leaf length with number of spikelets per panicle. However, number panicle per plant with flag leaf length, flag leaf width, biological yield and harvest index with flag leaf length showed positive estimates but significant at genotypic level. Kole *et al.* (2008) also obtained the same association between plant height with panicle length and Ganesan *et al.* (1998) reported harvest index with panicles/plant, panicle length, grains/panicle and 100 grain weight. The overall results indicated that selection of higher panicle number, test weight with a reasonable balance for moderate spikelet number would particularly encourage the breeders to attain higher grain yield. These results are in conformity with Nayak *et al.* (2001), Hasib and Kole (2004) and Khedikar *et al.* (2004).

Information obtained from correlation study does not give comprehensive idea about the contributions of each component characters because, if relationship is due to multiple affect of gene (s) it is difficult to separate these

effects by selecting particular character. Therefore, it is important to establish the genetic basis of correlation. Path coefficient analysis is helpful to recognize direct and indirect causes of correlation and also enables us to compare the causal factors on the genetic basis of their relative contributions. Shrivastava and Sharma (1976) suggested that only direct yield components should be used for path analysis. Path coefficient at genotypic level (Table 3) showed that harvest index (0.974), biological yield (0.894), number of tillers per hill (0.462), panicle length (0.112), number of spikelet per panicle (0.039), plant height (0.014) and test weight (0.007) had direct positive effect on seed yield per hill, indicating these are the main contributors to yield. Parallel outcome of yield per plant with harvest index were also reported by Ganesan *et al.* (1998), Rasheed *et al.* (2002), Chaturvedi *et al.* (2008), Jayasudha and Sharma (2010) in rice and Singh and Chaudhary (2006) and Kotal *et al.* (2010) in wheat; with panicle length by Kishor *et al.* (2008); with number of tillers by Khan *et al.* (2005); with test weight by Luzikihupi (1998) and Chaturvedi *et al.* (2008) and with harvest index, panicle length and 100 grain weight by Chakraborty *et al.* (2010). However, days to 50% flowering (0.0723), number of panicle per plant (0.4336) and flag leaf width (0.0759) had direct negative effect. The dimensions of residual effect were very low which indicated the consideration of most of the yield contributing characters. Moreover, majority of values were less than unity which indicated that inflation due to multicollinearity was minimal (Gravois and Helms, 1992).

## CONCLUSION

Additive gene action governs on the expression of seed yield per hill, harvest index, number of spikelets per panicle, biological yield and flag leaf length indicates that these traits are least influence by environment hence; selection may be effective through these characters. Further, harvest index, number of tillers per hill, panicle length, test weight and number of spikelet per panicle

directly contributed to seed yield. Thus a genotype with higher magnitude of these traits could be either selected from existing genotypes or evolved by breeding program for genetic improvement of yield in rice.

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