

**GENETIC VARIABILITY AND CHARACTER ASSOCIATIONS IN
IRRIGATED RICE (*Oryza sativa* L)**

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ABSTRACT

Eighteen advanced breeding lines were evaluated for yield and yield contributing characters to observe their variability, associations and direct and indirect effect on yield during Boro season, 2009. All the tested characters showed significant variation. Effective tillers/m² and spikelet sterility (%) had high genotypic variance, high heritability, high genetic advance and high genotypic coefficient of variation. Effective tillers/m², panicle length (cm), thousand grain weight (g) and growth duration (days) showed significant positive association with grain yield. Path coefficient analysis also revealed that effective tillers/m², thousand grain weight (g) and growth duration (days) had higher direct effects on yield (t/ha). All together with the genetic variability, correlation and path analysis revealed that effective tillers/m², thousand grain weight (g) and growth duration (days) are the most important yield components in rice. Therefore, from the present study it could be suggested that emphasize should be given on these characters for the selection of genotypes for higher grain yield in irrigated rice.

Keywords: Rice (*Oryza sativa* L.), GCV, PCV, heritability, genetic advance, correlation

INTRODUCTION

Rice yield is dependent on many yield contributing characters as well as on the environmental influence. Association of different characters is essential to determine their contribution towards yield. Yield component analysis is of fundamental importance to determine the direct and indirect contributions towards yield. As the yield is polygenically controlled and also influenced by its component characters, direct selection for yield is often misleading. Knowledge about genetic variability of yield contributing characters, interrelationship among them and their relation with yield are necessary for a successful breeding program. As the yield potential of modern varieties (MV) has reached to a certain level, selection based on related characters to yield can help to get progenies having high yield potential. Therefore, the present study was conducted to explore the characters highly responsible for high yield potential.

MATERIALS AND METHODS

Eighteen advanced breeding lines were evaluated at the BRRI regional station, Comilla during the year 2008-09 under irrigated rice ecosystem using RCB design with three replications. Forty two days old seedlings were transplanted 16.2m² area using single seedling per hill. Fertilizer doses were 80:60:40 kg N P K and 70 kg Gypsum per

hectare. Except N all other fertilizers were used as basal dose and N fertilizer was top dressed in three equal splits at 15, 30 and 45 days after transplanting. Standard crop management practices were done as and when necessary. Data on plant height (cm) effective tillers per m², panicle length (cm), spikelet sterility %, 1000 grain weight (g) and growth duration (days) were taken from randomly selected ten plants from each plot. Yields were taken from whole plot crop cutting and converted it to ton per hectare. Genotypic variance (σ^2_g), phenotypic variance (σ^2_p), genotypic coefficient of variation (GCV %), phenotypic coefficient of variation (PCV %), heritability (h^2_b %), genetic advance (GA) and genetic advance in percent mean (GAPM) were estimated by the formula suggested by Singh and Choudhary (1985). Genotypic and phenotypic correlation coefficient and path coefficient analysis were done through Basic stat. The estimate of GCV and PCV were classified as low, medium and high (Sivasubramanian and Madhavamenon, 1973). The heritability was categorized as suggested by Robinson *et al.* (1949). Again, genetic advance was classified by adopting the method of Johnson *et al.* (1955).

RESULTS AND DISCUSSION

Genetic Variability

Mean sum of square, mean, range, variance components, coefficient of genotypic and phenotypic variations, heritability estimates, genetic advance and genetic advance in percent of mean (GAPM) are presented in Table 1. Mean sum of square for all the characters were highly significant due to genotypes indicated wide range of variability among the genotypes for these traits. The Genotypic variance (σ^2_g), phenotypic variance (σ^2_p), genotypic coefficient of variation (GCV %), phenotypic coefficient of variation (PCV %) were close to each other for the traits plant height (cm), panicle length (cm), 1000 grain weight (g), growth duration (days) and yield (t/ha) which indicated less environmental influence and additive gene action for these traits.

Table 1. Estimation of statistical and genetic parameters of yield and its contributing traits of 18 rice genotypes

Parameters	Mean sum of square	Grand mean	Range	σ^2_g	σ^2_e	σ^2_p	h^2_b	GA	GAPM	GCV	PCV
Plant height(cm)	86.11**	96.38	78-101.8	28.49	0.75	29.2	97.5	10.9	11	5.5	5.6
Effective tillers/m ²	4241.43**	296.02	213-375	1225.34	565.4	1790.8	68.4	59.7	20	11.8	14.3
Panicle length(cm)	7.72**	21.70	18.9-26.8	2.47	0.31	2.8	88.8	3.1	14	7.2	7.7
Spikelets sterility (%)	81.98**	21.16	9.2-36.2	25.31	6.06	31.4	80.7	9.3	44	23.8	26.5
1000 grain weight (g)	13.62**	22.94	20-28.1	4.32	0.66	5	86.7	4.0	17	9.1	9.7
Growth duration (Days)	90.72**	153.35	143-160	29.70	1.62	31.3	94.8	11	7	3.6	3.7
Yield (t/ha)	3.27**	5.89	3.9-7.4	1.06	0.09	1.2	92.1	2.1	35	17.5	18.2

** = Significant at 1% level

σ^2_g = Genotypic variance, σ^2_e = Environmental variance, σ^2_p = Phenotypic variance, h^2_b = Heritability in broad sense, GA = Genetic advance, GAPM = Genetic advance in percent mean, GCV = Genotypic coefficients of variations and PCV = Phenotypic coefficients of variations

But some differences were found for effective tillers per m² and spikelet sterility (%) indicating that environment had more influence on the expression of these characters. The highest GCV was found in spikelets sterility % (23.80, effective tillers per m² (11.8) and yield (17.5 t/ha) indicated wide range of variability for these traits. Very little GCV was found in growth duration (3.6 days) followed by plant height (5.5

cm), panicle length (7.2 cm) and 1000 grain weight (9.1 g) indicating lack of inherent variability and limited scope for improvement through selection for these traits among the tested genotypes. High h^2_b values were observed in all the characters except effective tillers/ m^2 . Sinha (1980) stated that h^2_b indicates the effectiveness of selection is not always accompanied by high GA. High h^2_b estimate with high GAMP for yield (t/ha), 1000 grain weight (g), panicle length (cm), spikelets sterility % and plant height (cm) suggested that they were simply inherited traits governed by a few major genes or additive gene effects. While high h^2_b estimates with low GAMP for growth duration (days) indicated non additive type of gene action and genotype x environment (g x e) interaction plays a significant role in the expression of the trait. The grain yield (t/ha) showed high GCV and h^2_b together with high GAPM suggesting better scope for selection. Akanda *et al.* (1997) opined that the characters with high values of GCV and heritability accompanied by high genetic advance in percentage of mean indicating that they might transmit to their progenies and therefore, phenotypic selection based on these characters would be effective.

Character Associations

Character association analysis among grain yield and yield contributing characters (Table 2) revealed that in most of the cases the genotypic correlation coefficient were higher than the respective phenotypic correlation coefficients. This indicated that the suppressive effect of the environment modified the phenotypic expression of these characters by reducing phenotypic correlation values. Plant height (cm) showed positive correlation with panicle length (cm) and growth duration (days) and negative correlation with spikelets sterility (%). Effective tillers per m^2 showed significant r_g and r_p for panicle length (cm), growth duration (days) and yield (t/ha). Singh (1980) also reported the similar result. Panicle length showed negative correlation between spikelets sterility (%) and positive correlation with yield. The correlation with spikelets sterility (%) and growth duration (days) were positively significant. The correlation among 1000 grain weight (g), growth duration (days) and yield (t/ha) were significantly positive both at the genotypic and phenotypic levels. Similar results have been reported by Shaha *et al.* (1989) in rice. Significantly positive r_g and r_p were also found between growth duration (days) and yield (t/ha).

Table 2. Genotypic (r_g) and phenotypic (r_p) correlation coefficient among yield and its contributing traits of 18 rice genotypes

Parameters		Effective tillers/ m^2	Panicle length	Spikelets sterility (%)	1000 grain weight (g)	Growth duration (days)	Yield (t/ha)
Plant height(cm)	r_g	0.239	0.310*	-0.339*	0.158	0.356**	0.108
	r_p	0.207	0.279*	-0.279*	0.143	0.325*	0.116
Effective tillers/ m^2	r_g		0.331*	-0.038	0.222	0.544**	0.853**
	r_p		0.293*	-0.013	0.114	0.416**	0.641**
Panicle length(cm)	r_g			-0.423**	0.252	0.204	0.319*
	r_p			-0.372**	0.239	0.187	0.274*
Spikelets sterility (%)	r_g				-0.150	0.339*	0.154
	r_p				0.125	0.309*	0.127
1000 grain weight (g)	r_g					0.429**	0.532**
	r_p					0.384**	0.476**
Growth duration (Days)	r_g						0.716**
	r_p						0.664**

* and** indicates significant at 5% and 1% level of significance, r_g and r_p indicates genotypic and phenotypic correlation coefficient.

Path Analysis

In correlation studies, with the increasing number of variables, the indirect association becomes complex and important. In such situation, path coefficient analysis is useful to find out direct and indirect causes of associations. Path coefficient analysis permits a critical examination to specific factors acting to produce a given correlation and measures the relative importance of each factor. From the results of path analysis (Table 3) it was evident that direct effects contributed by effective tillers per m² (0.5818), growth duration (days) (0.3140) and 1000 grain weight (g) (0.2984) were high indicating that among the component traits, these three characters contributed maximum for grain yield in rice. These three characters also showed significantly positive genotypic correlation with yield which indicates that selection based on these characters would to be effective. Panicle length (cm) showed negligible direct effect (0.0607) but indirect positive effect via effective/m² made positively significant genotypic correlation with yield (0.3190*). On the other hand spikelet sterility had also positive (negligible) direct effect but its indirect effect through other characters was mostly negative. Plant height (cm) showed negative direct effect (-0.1719) and insignificant positive genotypic correlation with yield which indicated that indirect causal factors are to be considered.

Table 3. Partitioning of genotypic correlation with grain yield into direct (bold) and indirect effect of yield contributing traits in 18 rice genotypes

Parameters	Plant height (cm)	Effective tillers/m ²	Panicle length (cm)	Spikelets sterility (%)	1000 grain weight (g)	Growth duration (Days)	Genotypic correlation with yield
Plant height(cm)	-0.1719	0.1287	0.0181	-0.0207	0.0454	0.1086	0.1082
Effective tillers/m ²	-0.0389	0.5818	0.0729	-0.0014	0.0834	0.1548	0.8525**
Panicle length(cm)	-0.0514	0.1839	0.0607	-0.0263	0.0899	0.0622	0.3190*
Spikelets sterility (%)	0.0644	-0.0122	-0.0245	0.0651	-0.0421	0.1030	0.1537
1000 grain weight (g)	-0.0261	0.1041	0.0354	-0.0092	0.2984	0.1297	0.5323**
Growth duration (Days)	-0.0595	0.2868	0.0305	0.0214	0.1233	0.3140	0.7165**

*and**indicates significant at 5% and 1% level of significance

Residual effect, R= 0.41

The residual effect of the present study was 0.41, indicating that 59 percent of the variability in grain yield was contributed by the six component characters studied in this path analysis. This gave an impression that a few other characters than those involved in the present study might also contributed to yield. The genetic variability, correlation and path analysis showed that effective tillers/ m², growth duration (days) and thousand grain weight (g) are the most important yield components in rice. Therefore, emphasis should be given on these characters for the selection of genotypes for higher grain yield in rice.

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