



Correlation Studies of F_5 Families in Rice (*Oryza sativa* L.)

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ABSTRACT

One hundred and fourteen F_5 families of rice belonging to six crosses along with seven parents were evaluated during *kharif*, 2015 at Andhra Pradesh Rice Research Institute and Regional Agricultural Research Station, Maruteru to study variability, heritability, genetic advance as per cent of mean and nature and direction of association among themselves and with grain yield. Data was recorded on ten characters which showed significant differences among themselves. High PCV and GCV were observed for grain yield per plant and test weight. High heritability coupled with high genetic advance as per cent of mean was observed for number of grains per panicle, grain yield per plant and test weight indicating the presence of additive gene action in governing the inheritance of these traits. Hence, direct phenotypic selection is useful with respect to these traits. The study of character association revealed that panicle length showed significant positive association with grain yield per plant indicating that direct selection can be practiced for this character.

Key words: *Correlation, Genetic advance, Heritability, Variability.*

Globally, rice is planted on about 158 million hectares with an annual production of 478 million tons. India ranks first in area (43.85 million hectares) and second in the production (104.78 million tonnes) with a productivity of 2185 kg ha⁻¹. Andhra Pradesh occupies an area of 3.80 million hectares with a production of 11.56 million tones and productivity of 3244 kg ha⁻¹ (www.indiaagristat.com, 2014-15). Demand for rice is increasing day by day and keeping in view of the future demand of rice as a food for human, there is a continuous need to evolve new varieties, which should exceed the yields of existing ones. Variation present in the population is an important prerequisite for improvement of any crop species. Estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) gives information on nature and magnitude of variation present in a population. Broad sense heritability is the relative magnitude of genotypic and phenotypic variances for the traits and is used as a predictive role in selection procedures (Allard, 1960). The estimate of heritability alone is not very much useful because it includes the effect of both additive and non additive gene. Heritability estimates along with genetic advance are more helpful in predicting gain under selection than heritability estimate alone (Sinha *et al.*, 2004 and Johnson *et al.*, 1955).

To know how the improvement of one character will bring simultaneous improvement in other characters, study of correlations is essential for a plant breeder. Information on the correlation coefficient between grain yield and yield contributing traits is a prerequisite for improving yield. The present study was therefore undertaken to study variability, heritability, genetic advance as percent of mean and nature and direction of association among themselves and with grain yield that helps in selection of superior genotypes.

MATERIAL AND METHODS

The experimental material consisted of one hundred and fourteen F_5 families belonging to six crosses of rice with seven parents obtained from Andhra Pradesh Rice Research Institute and Regional Agricultural Research Station, Maruteru and were sown in randomized block design with two replications during *kharif*, 2015. Thirty days old seedlings were transplanted with a spacing of 20 cm and 15 cm between rows and plants, respectively. Observations were recorded on five randomly selected plants for eight characters *viz.*, plant height, number of panicles per plant, panicle length, grain yield per plant, test weight, kernel length, kernel breadth and L/B ratio while for other two characters *viz.*, days to 50 per cent flowering, days to maturity, observations were recorded on

Table 1. Analysis of variance (mean sum of squares) for 10 characters for 121 genotypes of rice (*Oryza sativa* L.) during *kharif*, 2015.

Source of variations	d. f.	Days to 50% flowering	Days to maturity	Plant height	Number of panicles per plant	Panicle length	Grain yield per plant	Test weight	Kernel length	Kernel breadth	Kernel L/B ratio
		Mean sum of squares									
Replications	1	0.04	0.264	0.051	0.810	3.499	3.380	0.001	0.013	0.000	0.051
Genotypes	120	65.833**	66.903**	122.849**	4.795**	8.045**	52.314**	52.299**	0.336**	0.098**	0.216**
Error	120	2.071	0.981	4.117	0.510	1.250	1.706	1.160	0.025	0.196	0.038

Table 2. Estimates of genetic variability parameters of yield and yield component attributes in rice (*Oryza sativa* L.) during *kharif*, 2015.

S.No	Character	Range		Mean	Variability parameters		h ² (bs)	GAM
		Min.	Max.		PCV	GCV		
1	Days to 50% flowering	89	126	116	5.03	4.87	94.00	9.73
2	Days to maturity	117	151	142	4.10	4.04	97.00	8.20
3	Plant height (cm)	95.3	136.9	110.73	7.20	6.96	94.00	13.86
4	Number of panicles per plant	7	16	11	15.03	13.51	81.00	25.01
5	Panicle length (cm)	17.4	29.2	24.02	8.98	7.68	73.00	13.52
6	Grain yield per plant (cm)	10	43.75	19.59	26.53	25.68	94.00	51.20
7	Test weight (g)	11.5	41.4	21.36	24.20	23.67	96.00	47.69
8	Kernel length (mm)	5.3	6.95	6.2	6.85	6.36	86.00	12.16
9	Kernel breadth (mm)	1.75	2.8	2.33	10.39	8.48	67.00	14.24
10	L/B ratio	2.15	3.95	2.71	13.17	11.04	70.00	19.06

plot basis. The mean values over two replications were used for statistical analysis and analysis was done as per Panse and Sukhatme (1985), Burton and Devane (1953), Johnson *et al.* (1955) and Falconer (1964).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the genotypes for all the characters indicating the presence of sufficient genetic variability in the studied material (Table 1).

The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficients of variation but the difference is very less indicating that low environmental influence (Table 2). High PCV and GCV was observed for grain yield per plant and test weight indicating the presence of high variability among the lines studied while number of panicles

per plant and L/B ratio exhibited moderate PCV and GCV indicating the presence of moderate amount of variability among these genotypes. Days to 50% flowering, days to maturity, plant height and panicle length exhibited low PCV and GCV where as kernel breadth reported low GCV indicating the presence of low amount of variation in these genotypes pertaining to these traits. These results were in conformity with the findings of Sameera *et al.* (2015), Shrivastava *et al.* (2014), Patel *et al.* (2014), Paikhomba *et al.* (2014), Khare *et al.* (2014), Gangashetty *et al.* (2013) and Aditya and Bhartiya (2013).

High heritability coupled with high genetic advance as per cent of mean was observed for number of panicles per plant, grain yield per plant and test weight, which indicated the predominance of additive gene action in the inheritance of these traits and simple selection can be practiced for these

Table 3. Phenotypic and genotypic correlation coefficient of 121 lines (114 families and 7 parents) of rice (*Oryza sativa* L.) during *kharif*, 2015.

S.No	Characters		Days to 50% flowering	Days to maturity	Plant height	Number of panicles per plant	Panicle length	Test weight	Kernel length	Kernel breadth	L/B ratio
1.	Days to 50% flowering	r_p	1.0000								
		r_g	1.0000								
2.	Days to maturity	r_p	0.9294**	1.0000							
		r_g	0.9602**	1.0000							
3.	Plant height	r_p	0.1920**	0.2161**	1.0000						
		r_g	0.2139**	0.2309**	1.0000						
4.	Number of panicles per plant	r_p	0.3248**	0.3565**	0.4577**	1.0000					
		r_g	0.3811**	0.3956**	0.4890**	1.0000					
5.	Panicle length	r_p	-0.0293	-0.0708	0.3670**	0.1449*	1.0000				
		r_g	-0.0641	-0.0902	0.4296**	0.1642*	1.0000				
6.	Test weight	r_p	0.2425**	0.2301**	0.0031	0.0657	-0.2633**	1.0000			
		r_g	0.2519**	0.2382**	-0.0045	0.0769	-0.3254**	1.0000			
7.	Kernel length	r_p	0.1655**	0.1890**	0.1743**	0.1822**	0.0085	0.2252**	1.0000		
		r_g	0.2002**	0.2147**	0.1916**	0.2170**	-0.0117	0.2383**	1.0000		
8.	Kernel breadth	r_p	0.0891	0.1018	0.0069	-0.0871	-0.2794**	0.4000**	-0.0360	1.0000	
		r_g	0.0929	0.1116	0.0170	-0.1380	-0.3990**	0.5120**	-0.0414	1.0000	
9.	L/B ratio	r_p	-0.0355	-0.0486	0.0824	0.1631*	0.2648**	-0.2066**	0.5326**	-0.8083**	1.0000
		r_g	-0.0320	-0.0443	0.0841	0.2003**	0.3281**	-0.2653**	0.5847**	-0.8287**	1.0000
10.	Grain yield per plant	r_p	0.0830	0.0380	0.0523	-0.0193	0.3157**	-0.1071	-0.0152	-0.0204	0.0234
		r_g	0.0794	0.0499	0.0475	-0.0286	0.3543**	-0.1138	-0.0176	-0.0280	0.0297

traits. The high estimates of heritability coupled with moderate genetic advance as per cent of mean for plant height, panicle length, kernel length, kernel breadth and L/B ratio indicating the presence of both additive and non additive gene actions and heterosis breeding for such traits will be effective. High heritability coupled with low genetic advance was reported for days to 50% flowering and days to maturity indicating the presence of non additive gene action and hence simple selection for these traits would not be effective. Similar results were reported by Sameera *et al.* (2015), Patel *et al.* (2014), Paikhomba *et al.* (2014) and Aditya and Bhartiya (2013).

The study of character association (Table 3) revealed that the character panicle length showed significant positive association with grain yield per plant indicating that direct selection can be practiced for this character. Other traits *viz.*, days to 50% flowering, days to maturity, plant height and L/B ratio recorded positive non significant correlation with grain yield while number of panicles per plant, test weight, kernel length and kernel breadth

reported negative non significant correlation with grain yield indicating that these traits have little influence on yield.

Days to 50% flowering showed positive significant association with days to maturity (0.9294**/0.9602), plant height (0.1920**/0.2139**), number of panicles per plant (0.3248**/0.3811), test weight (0.2425**/0.2519) and kernel length (0.1655**/0.2002**) while days to maturity with plant height (0.2161**/0.2309**), number of panicles per plant (0.3565**/0.3956**), test weight (0.2301**/0.2382**), kernel length (0.1890**/0.2147**) at both the levels.

Plant height reported positive significant correlation with number of panicles per plant (0.4577**/0.4890**), panicle length (0.3670**/0.4296**) and kernel length (0.1743**/0.1916**) where as number of panicles with panicle length (0.1449*/0.1642*), kernel length (0.1822**/0.2170**) and L/B ratio (0.1631*/0.2003**) at both genotypic and phenotypic levels.

Panicle length showed significant positive association with grain yield per plant (0.3157**/

0.3543**) and L/B ratio (0.2648**/0.3281**) while test weight reported positive significant correlation with kernel length (0.2252**/0.2383**) and kernel breadth (0.4**/0.5120**) where as kernel length showed positive significant association with L/B ratio (0.5326**/0.5847**) at both the levels. Strong positive association among the traits indicated that simultaneous selection for these characters would result in improvement of high yielding varieties.

These results are in agreement with the findings of Jambhulkar and Bose (2014), Khare *et al.* (2014) and Patel *et al.* (2014).

Thus the trait, panicle length, can be exploited as an important criterion in the selection programmes for the yield improvement.

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