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# QUANTITATIVE ANALYSIS OF RICE (ORYZA SATIVA L.)

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### Abstract

Analysis of variance of forty upland genotypes indicated that all the genotypes were significantly different, with respect to the characters. Number of tillers per plant, Number of panicles per plant, kernel L/B ratio and Grain Yield per plant exhibited high PCV and GCV which in turn indicated the existence of non-additive gene effects whereas for other traits environmental influence was very less. High heritability coupled with high genetic advance as per cent of mean was observed in all the eleven characters studied. Hence all those traits were said to be controlled by additive gene action. The genetic correlation revealed that grain yield per plant had strong negative and significant association with days to first flower at both genotypic and phenotypic levels. So it could be inferred that grain yield and days to first flower could be used as selection criteria for the improvement of grain yield per plant. Path analysis indicated that maximum direct effect on grain yield was exhibited through number of tillers per plant which should be taken in account while developing new high yielding rice varieties.

Key words : PCV, GCV, Heritability, Path analysis, Genotypic, Phenotypic.

#### Introduction

A population with more diverse genotypes is of considerable value as the success of any breeding programme relies on the genetic variability present in the base population for effective selection and recombination breeding. Information on the nature and degree divergence would help the plant breeder in choosing the right type of parents for breeding programme. Hence, estimates of genetic diversity for grain yield and quality parameters among genotypes are important for planning the future crossing programme. In the present study, an attempt was made to classify and understand the nature and magnitude of genetic advance.

# Materials and Methods

The experimental material for the study comprised of 40 genotypes laid in Randomized Block Design (RBD) with three replication at experimental farm of plant breeding (11°24 N latitude and 79°44 E longitude, + 5.79MSL), Annamalai University, Tamil Nadu, India. In each genotype, one seedling per hill was transplanted in the main field after 25 days with spacing of 20cm\*20cm.

Standard agronomic practices and plant protection measures were taken as per schedule observations were recorded on fire randomly selected plants per replication for days to first flower, (days) plant height (cm), number of tillers per plant, number of panicles per plant, number of grains per panicle, panicle length (cm), hundred grain weight (g), kernel length (mm), kernel breadth (mm), kernel L/B ratio and grain yield per plant. The analysis of genetic divergence was done using Mahalanobis (1936)  $D^2$  statistics. The genotypes were grouped into different clusters, inter and intra clusters distances and mean performances for characters were also computed.

# **Results and Discussion**

Analysis of variance (Table 1) revealed that all the treatments were significantly different. The relative values of genotypic and phenotypic coefficient of variation provide important information on the magnitude of variation (Table 2). Genotypic coefficient of variation measures the variability of any character. The extent of the environmental influence of any character in indicated by the magnitude of the differences between the genotypic and phenotypic coefficients of variation. Large differences reveal high genetic influence.

High phenotypic variations composed of high genotypic variations and less of environmental variations, indicates the presence of high genetic variability for different traits and less influence of environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits. Similar results were observed by Kumar *et al.* (1994), Chaudhary and Singh (1994), Pathak and Sharma (1996), Sarvanan and Senthil (1997), Rother *et al.* (1998), Satya *et al.* (1999), Shivani and Reddy (2000), Iftekharudduala *et al.* (2001) and Sao (2002).

Coefficients of variations studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for all the traits studied indicating that the characters were less influenced by the environment. Therefore, selection on the basis of phenotype along can be effective for the improvement of these traits.

High PCV and GCV were recorded for kernel L/B ratio, kernel breadth, number of panicles per plant. The high magnitude of GCV and PCV for the above traits suggested the presence of high degree of variability and so better scope for the improvement through simple selection

Moderate GCV and PCV were recorded for grain yield per plant, panicle length, number of grains per panicle, hundred grain weight and plant height. This indicates the existence of comparatively moderate variability for these traits, which could be exploited for improvement through selection in advanced generations. Narrow differences between PCV and GCV were observed for plant height, kernel length, days to first flower which suggested that these traits were less influenced by environmental factors. Hence they could be improved through simple selection.

Knowledge of heritability of a character to a breeder is an important as it indicates the possibility and extent to which improvement is possible through selection. Heritability in broad sense includes both fixable (additive) and non-fixable (dominant and epistatic) variances and also provides a good indication about the repeatability of the traits. All the characters recorded high estimates of heritability, hence indicated that expression of these traits is less influenced by the environment and could be improved through mere selection.

Although, the presence of high heritability values indicates the effectiveness of selection on the basis of phenotypic performance, it does not show any indication to the amount of genetic progress. High heritability does not always indicate high genetic gain. Burton (1952) pointed out the heritability in combination with intensity of selection and amount of variability present in the population influences gains to be obtained from selection. Therefore, heritability and genetic advance should be considered together in selection process for obtaining the best segregants.

Since high heritability along with high genetic advance was observed for all the characters taken under study, it conveyed the predominance of additive gene affects in controlling the traits and hence strong selection factors could improve these traits (Table 2). Similar findings were reported by Tuhina – Khatun *et al.* (2015) for days to first flowering, plant height, number of tillers per plant, number of panicles per plant and grain yield per plant, Santhosh Kumar *et al.* (2015) for number of tillers per plant and number of grains per

panicle, Singh *et al.* (2013) for number of panicles per plant, number of grains per panicle and grain yield per plant, Chandramohan *et al.* (2016) for number of grains per panicle, panicle length and thousand grain weight, Chanbeni *et al.* (2012) for number of grains per panicle and Nirmaladevi *et al.* (2015) for hundred grain weight. The genotypic and phenotypic correlation coefficient was studied for different trails along with grain yield to understand interrelationship among them. Estimates pf correlation in rice genotypes are presented in Table 2.

A positive value of correlations 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 the other and vice-versa. 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 showed similar trend but genotypic correlation coefficients were of higher in magnitude than the correlation phenotypic correlation coefficients which might be due to marking or modifying effect of environment (Singh, 1980).

In present investigation, there was strong negative and significant correlation between grain yield per plant and days to first flower at both genotypic and phenotypic levels (Table 3). Thus negative correlation between grain yield and days to first flower indicated that grain yield per plant would be reduced when the genotypes had late flowering nature. Contrary findings were reported by Mohan *et al.* (2015) and Thippeswamy *et al.* (2016) in which they reported positive significant correlation between grain yield per plant and days to first flower at both levels .Similar findings reported by C.A Sowmiya and M. Venkatesan(2017)

Also, days to first flower had positive significant correlation with plant height and negative significant correlation with grain yield per plant at genotypic and phenotypic levels. The results clearly indicated that long duration genotypes would be tall yet contribute less grain yield.

Number of tillers per plant had the maximum correlations among all the characters studied for correlation coefficients. It had positive and significant correlation with the number of panicles per plant, number of grains per panicle, panicle length, hundred grain weight, kernel length, kernel L/B ratio and grain yield per plant.

From the investigation, plant height showed significant positive correlation with kernel length at both genotypic and phenotypic levels.

Panicle length showed significant positive correlation with hundred grain weight, kernel length, grain yield per plant at both phenotypic and genotypic level, kernel L/B ratio at genotypic level. From the above discussion, it may be seen that selection of these characters would ultimately help in identifying genotypes with high yield potential.

Path coefficient analysis allows separating the direct and indirect effects through other contributes by apportioning the correlations (Wright, 1921) for better interpretation of cause and effect relationship. The results clearly showed significant difference in genotypic and phenotypic direct and indirect effects, indicating the predominance of environmental influence in expression of the traits.

In the present investigation, the residual effect was 0.1620 (Table 4). Perusal of results obtained in path analysis revealed that high direct effect on grain yield was exhibited by number of panicles per plant. Contrary reports were given by Thippeswamy *et al.* (2016), Mohan *et al.* (2015), Yadav *et al.* (2011) and Akhtar *et al.* (2011).

Panicle length recorded low positive direct effect on grain yield per plant.

The trait, number of panicles per plant and kernel breadth had high negative direct effect on grain yield per plant. In addition to the direct effect, indirect effect of number of tillers per plant via hundred grain weight was high and positive on grain yield per plant was observed.

High positive indirect effect was observed by plant height through number of panicle per plant on grain yield per plant. But Ravindra Babu *et al.* (2012) and Yadav *et al.* (2011) reported positive low indirect effect on grain yield by the same.

Plant height also had high and positive indirect effect on grain yield through number of tillers per plant.

Also, panicle length was detected to have very high negative indirect effect through number of panicles per plant on grain yield. Kernel L/B ratio has also observed very high positive indirect effect through number of tillers per plant on grain yield.

From the above discussion, it was inferred that the pattern of path coefficient observed in the present study was in agreement with the correlation attained. In general, the character days to first flower recorded negative grain yield per plant. Hence it could be used as selection criteria in breeding programme to develop high yielding new plant type rice varieties.

S. No.	Source	df	Days to first flower	Plant Height	No of tillers per plant	No. of Productive tillers per plant	No. of Grains per Panicle	Panicle length	100 seed weight	Kernel length	Kernel Breadth	Kernel L/B ratio	Grain yield per plant
1	Replication	2	4.98	34.72	0.91	0.81	246.81	0.28	0.02	0.01	0.02	0.08	4.66
2	Genotype	39	191.10	653.10	28.70	24.66	804.04	55.53	0.31	1.28	1.82	3.59	55.44
3	Error	78	7.31	19.20	1.95	1.69	127.34	1.78	0.02	0.08	0.08	0.30	6.69

**Table 2 :** Analysis of variance for eleven characters in rice genotypes

S. No	Characters	Genotypic (%)	Phenotypic (%)	Heritability (%)	Genetic advance as per cent of mean	
1	Days to first flower	8.04	8.50	89.34	15.65	
2	Plant Height	12.78	13.35	91.66	25.20	
3	No of tillers per plant	22.78	25.15	82.05	42.51	
4	No. of Productive tillers per plant	23.73	26.22	81.93	44.26	
5	No. of Grains per Panicle	12.04	15.07	63.92	19.84	
6	Panicle length	16.20	16.99	90.97	31.84	
7	100 seed weight	12.08	13.42	81.00	22.40	
8	Grain yield per plant	16.61	19.74	84.00	17.95	
9	Kernel length	9.51	10.37	88.44	64.23	
10	Kernel Breadth	33.16	35.26	78.57	59.68	
11	Kernel L/B ratio	32.68	36.87	70.84	28.80	

Table 2 : Magnitude of variability for eleven characters in rice genotype

			Days		No of	No. of	No. of		100			Kernel	Grain
S.	Characters		to Plant		tillers	Productive	Grains	Panicle	seed	Kernel	Kernel	L/B	yield
No			first Height		per	thers per	per	length	weight	length	Breadth	ratio	per
			flower	0.041	plant	plant	Panicle	0.10.11	0.011	0.051	0.15	0.01.4	plant
1	Days to first flower		1.00	-0.34*	-0.33*	-0.35*	-0.28	-0.43**	-0.31*	-0.3/*	0.15	-0.31*	-0.28
		G	1.00	-0.39**	-0.41**	-0.43**	-0.35*	-0.48**	-0.38**	-0.44**	0.19	-0.41**	-0.36*
2	Plant Height	Р		1.00	0.27	0.26	0.04	0.10	0.13	0.31*	0.01	0.21	0.10
		G		1.00	0.30	0.29	0.04	0.12	0.17	0.34*	0.03	0.21	0.12
3	No of tillers per plant	Р			1.00	0.97**	0.43**	0.42**	0.34	0.75**	-0.31*	0.67**	0.32*
5	rio or uners per plane	G			1.00	1.00**	0.61**	0.47**	0.45**	0.90**	-0.37*	0.87**	0.43**
4	No. of Productive tillers per plant					1.00	0.46**	0.43**	0.36	0.74**	-0.31*	0.41**	0.34*
-						1.00	0.63**	0.48**	0.48**	0.91**	-0.37*	0.86**	0.47**
5	No. of Grains per Panicle						1.00	0.50**	0.61**	0.40**	-0.37*	0.36*	0.31*
5							1.00	0.69**	0.50**	0.55**	-0.49**	0.59**	0.44**
6	Doniala langth							1.00	1.00**	0.37*	-0.24	0.26	0.54**
0	Panicie lengui	G						1.00	0.71**	0.43**	-0.26	0.41**	0.68**
7	100 seed weight								1.00	0.35*	-0.00	0.32*	0.75**
/									1.00	0.46**	-0.03	0.37*	0.91**
0	Kernel length									1.00	-0.48**	-0.75	0.37*
0										1.00	-0.47**	0.90**	0.44**
0	17 1 D 14	Р									1.00	1.00**	-0.08
9	Kernel Breadth										1.00	-0.72**	-0.12
10		Р										1.00	0.87**
10	Kernel L/B ratio											1.00	0.42**
	a · · · · ·	Р											1.00
11	Grain yield												1.00

Table 3 : Phenotypic and genotypic correlation coefficients among yield attributing characters in rice genotypes

 Table 4 : Path coefficient analysis showing direct and indirect effects of yield attributing characters on grain yield per plant in rice genotypes

S. No	Characters	Days to first flower	Plant Height	No of tillers per plant	No. of Productive tillers per plant	No. of Grains per Panicle	Panicle length	100 seed weight	Kernel length	Kernel Breadth	Kernel L/B ratio	Grain yield per plant
1	Days to first flower	-0.12	0.03	-1.27	1.24	0.04	0.09	-0.46	0.02	-0.06	0.13	-0.36
2	Plant Height	0.046	-0.09	0.93	-0.85	-0.00	-0.02	0.20	-0.02	-0.01	-0.07	0.12
3	No of tillers per plant	0.048	-0.03	3.09	-2.88	-0.06	-0.08	0.53	-0.04	0.12	-0.27	0.43
4	No. of Productive tillers perplant	0.05	-0.03	3.09	-2.88	-0.06	-0.08	0.57	-0.04	0.12	-0.27	0.47
5	No. of Grains per Panicle	0.04	-0.00	1.88	-1.81	-0.10	-0.12	0.60	-0.02	0.16	-0.18	0.44
6	Panicle length	0.06	-0.01	1.44	-1.36	-0.07	-0.17	0.86	-0.02	0.08	-0.13	0.68
7	100 seed weight	0.04	-0.1	1.38	-1.39	-0.05	-0.13	1.20	-0.02	0.00	-0.11	0.91
8	Kernel length	0.05	-0.03	2.79	-2.62	-0.05	-0.08	0.55	-0.04	0.16	-0.28	0.44
9	Kernel Breadth	-0.02	-0.00	-1.15	1.07	0.05	0.05	-0.03	0.02	-0.33	0.23	-0.12
10	Kernel L/B ratio	0.05	-0.02	2.67	-2.47	-0.06	-0.07	0.44	-0.04	0.24	-0.31	0.42

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