Plant Archives Vol. 19 No. 2, 2019 pp. 2522-2526 **e-ISSN:2581-6063 (online), ISSN:0972-5210**

GENETIC VARIABILITY, ASSOCIATION AND PATH ANALYSIS FOR GRAIN YIELD AND QUALITY TRAITS IN RICE (*ORYZA SATIVA* L.)

Thippannagari Radha, P. Satheesh Kumar*, K. Saravanan And S. Suganthi

Depart. of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai Univ., Annamalainagar-608002 (T.N.)

Abstract

Forty two rice genotypes were evaluated for genetic parameters. High heritability estimates combined with genetic advance were observed for days to 50 per cent flowering, plant height, hundred grain weight, grain length, grain L/B ratio, kernel length, kernel L/B ratio and grain yield per plant indicating that these characters are governed by additive genes. The genetic advance as per cent of mean for panicle length was low. The genotypic correlation coefficients were larger than phenotypic correlation coefficients. Grain yield per plant was positively significant correlated with hundred grain weight. Path coefficient analysis revealed the maximum direct of kernel L/B ratio followed by grain L/B ratio, grain breadth, days to 50% flowering, number of productive tillers per plant, hundred grain weight and panicle length.

Key words : Rice, Variability, Correlation, Path analysis.

Introduction

The rice-wheat cropping system is the world's largest agricultural production system occupying 24 million ha throughout India and China alone and around 85% of this area falls in the Indo-Gangetic plain (IGP) (Shukla *et al.,* 2005). Rice is the primary food source for more than one third of world's population (Prasad *et al.,* 2010) and provides 21% of energy and 15% of protein requirements of human populations globally (Maclean *et al.,* 2002; Depar *et al.,* 2011). In Asia, India has the largest area under rice cultivation (44.3 milion ha) accounting for 29.4 per cent of the global rice area (Mahata *et al.,* 2012).

Rice is one of the staple food and feed crop not only in India but also in the world. Most of the characters of interest to breeders are complex and they are result of the interaction of a number of components (Paul *et al.,* 2018). The information on certain genetic parameters of variability for different characters of economic significance is important for plant breeders before releasing any variety.

The presence and magnitude of genetic variability in a gene pool is the per-requisite of a breeding programme. Heritability estimates provide the information on the proportion of variation that is transmissible to the progenies in subsequent generations. Genetic advance provides information on expected genetic gain resulting from selection of superior individuals. The grain yield is a complex characters, quantitative in nature and an integrated function of a number of component traits. Therefore, selection for yield *per se* may not be much rewarding unless other yield attributing traits are taken into consideration. Correlation study provides a measure of association between characters and helps to identify important characters to be considered while making elucidates selection. The present study implication in deciding desirable traits for development of high yielding variability.

Materials and Methods

The experiment comprised of 42 genotypes of rice grown during Samba, 2014 at the Plant Breeding Farm (11°24' N latitude, 79°44' E longitude and ± 5.79 m MSL), Faculty of Agriculture, Annamalai University, Annamalainagar, Tamil Nadu, India in a randomized block design with three replications. Twenty five days old seedlings were transplanted in 3 M rows at a spacing of 20 ×15 cm between and within rows respectively. All the recommended package of practices were followed to raise a good crop. For this study, correlation and path coefficient of grain yield and quality traits *viz.,* days to

****Author for correspondence :*** E-mail : psnsathishkumar@gmail.com

Table 1: Analysis of variance for twelve characters in rice.

Source	df	MSS											
		DFF	PH	NPT	PL	HGW	GL	GB	GLBR	KL	KB	KLBR	GYD
Replication	2	3.094	0.765	2.869	1.801	0.024	0.009	0.033	0.007	0.004	0.006	0.027	1.083
Genotype	41	392.290**	897.104**	15.337**	55.264*	0.533**	0.036**	0.008**	2.319**	0.022**	0.22**	0.468**	96.32**
Error	82	1.067	10.923	1.793	36.020	0.008	0.004	0.002	0.004	0.002	0.003	0.009	0.05

*Significant at 5 Per cent level.

**Significant at 1 Per cent level.

50 per cent flowering, plant height (cm), number of productive tillers per plant, panicle length (cm), hundred grain weight (g), grain length (mm), grain breadth (mm), grain L/B ratio, kernel length, kernel breadth, kernel L/B ratio and grain yield per plant (g) were recorded. Correlation coefficient at the genotypes and phenotypic levels was computed from the variance and co-variance components as suggested by Panse and Shukhatme (1967). Path analysis was done as suggested by Dewy and Lu (1959).

Results and Discussion

Analysis of variance indicated the existence of highly significant differences among the genotypes for all the characters studied. This suggested that there is an inherent genetic difference among the genotypes table 1. The mean, range, phenotypic coefficient of variation, genotypic coefficient of variation, heritability and genetic advance as per cent of mean selection intensity for different characters are given in table 2. A close examination of experimental results revealed a high estimate of phenotypic coefficient of variation for panicle length, grain breadth, grain L/B ratio, kernel breadth and grain yield per plant and higher phenotypic and genotypic coefficients of variation for kernel breadth, grain yield per plant and grain L/B ratio.

A moderate value of phenotypic coefficient of variation was observed for days to 50 per cent flowering, plant height, number of productive tillers per plant, hundred grain weight, grain length, kernel length and kernel L/B ratio. Moderate value of genotypic coefficient of variation was observed for days to 50 per cent flowering, plant height, panicle length, hundred grain

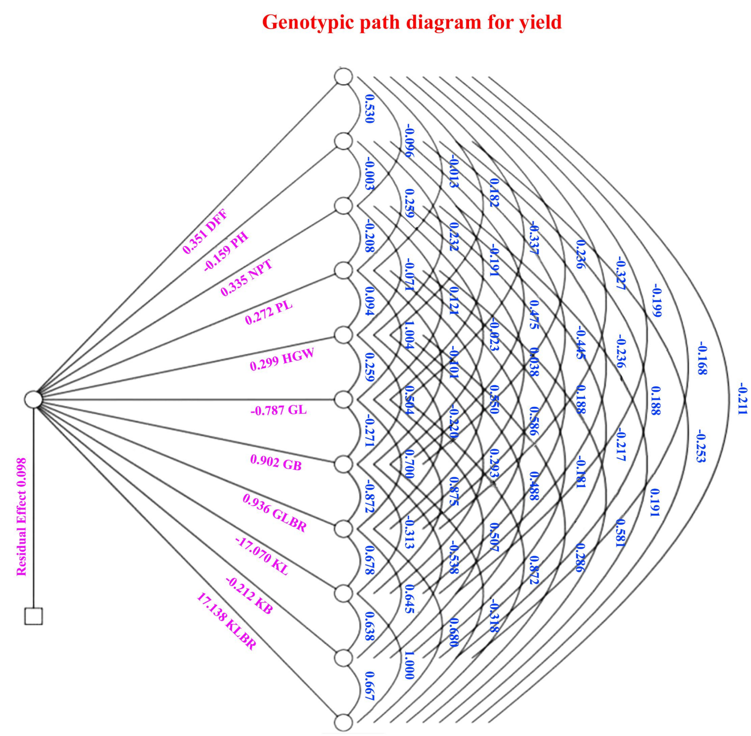

Fig. 1: Diagram of factors influencing yield at genotypic level

Table 2: Mean, range, PCV, GCV, heritability and genetic advance as per cent of mean for twelve characters in rice.

	Mean±SE	Range	PCV (%)	GCV (%)	h^2 (%)	GA as % Mean
DFF (Days)	83.88 0.59	62.00-105.00	13.67	13.61	99.19	27.93
PH (cm)	100.57 1.91	74.13-152.00	17.40	17.09	96.43	34.57
NPT	21.97 0.77	14.73-28.47	11.43	9.67	71.58	16.86
PL (cm)	21.95±3.47	15.98-42.80	29.68	11.54	15.12	9.24
HGW (g)	2.27±0.04	1.47-3.07	18.59	18.59	99.98	38.29
GL (mm)	0.85 0.04	0.61-1.21	14.26	12.10	72.01	21.15
GB (mm)	0.26 0.03	0.21-0.33	24.33	17.20	50.00	25.05
GLBR	3.40 0.02	1.96-5.68	25.86	25.85	99.91	53.23
KL (mm)	0.63 0.01	0.41-0.91	14.78	12.96	76.92	23.42
KB (mm)	0.22 0.02	0.21-0.23	35.37	25.12	50.44	36.75
KLBR	2.95±0.02	1.94-4.25	13.64	13.26	94.44	26.54
GYD (g)	27.35±0.82	23.29-32.18	20.73	20.71	99.84	42.63

DFF – Days to 50 per cent flowering
PH – Plant height
PL – Panicle length
HGW – Hundred grain weight
GB – Grain breadth
GLBR – Grain L/B ratio
KB – Kernel breadth
KLBR – Kernel L/B ratio
NPT – Number of productive tillers per plant
GL – Grain length
KL – Kernel length
GYD – Grain yield per Plant

weight, grain length, grain breadth, kernel length and kernel L/B ratio. However, Ganeshan *et al.,* (1995) differed with these observations and reported high genotypic coefficients of variation for these characters.

A narrow magnitude of difference between phenotypic and genotypic coefficients of variation for characters, namely days to 50 per cent flowering, plant height, hundred grain weight, grain L/B ratio, kernel L/B ratio and grain yield per plant. Suggested a limited role of environmental variation in the expression of these characters. Thus selection based on genotypic performance of the characters would be effective to bring about considerable improvement in these characters.

The estimates of heritability were observed to be high in magnitude for all the characters, except panicle length, grain breadth and kernel breadth. The percentage of heritability is ranged from 15.12 per cent (panicle length) and 99.98 (hundred grain weight) table 2. Similar results were reported by Hossain *et al.,* (2003).

High estimates of heritability coupled with high genetic advance were observed for the characters *viz.,* days to 50 per cent flowering, plant height, hundred grain weight, grain length, grain breadth, grain L/B ratio, kernel length, kernel breadth, kernel L/B ratio and grain yield per plant. It indicates that most likely the heritability is due to additive gene effects and selection may be effective. Moderate genetic advances were observed for number of productive tillers per plant. Low genetic advances were observed for panicle length Table 2. Similar results were also reported by Sarkar *et al.,* (2007), Anbanandan *et al.* (2009) and Satheeshkumar and Saravanan (2012).

Genotypic correlations were observed to be greater than the corresponding phenotyic correlation coefficients for all the characters indicating the superiority of

Table 3: Phenotypic and genotypic correlation for twelve quantitative characters in rice.

Characters		DFF (Days)	PH (cm)	NPT	PL (cm)	HGW (g)	GL (mm)	GB (mm)	GLBR	KL (mm)	KB (mm)	KLBR	GYD (g)
Days to 50% flowering	P	1.000	0.519**	-0.082	0.006	0.181	-0.283	0.233	-0.325**	-0.199	-0.038	-0.208	0.157
	G	1.000	0.530**	-0.096	-0.013	0.182	-0.337*	0.236	-0.327**	-0.199	-0.168	-0.211	0.217
Plant height	P		1.000	-0.007	0.006	0.228	-0.152	0.466**	-0.438**	-0.232	0.021	-0.249	0.034
	G		1.000	-0.003	0.259	0.232	-0.191	0.475**	-0.445**	-0.236	0.188	-0.253	0.061
Number of productive tillers per plant	P			1.000	-0.040	-0.061	0.050	-0.021	0.033	0.159	-0.082	0.157	0.013
	G			1.000	-0.208	-0.071	0.121	-0.023	0.038	0.188	-0.217	0.191	0.149
Panicle length	P				1.000	0.035	0.348*	-0.040	0.215	0.230	0.011	0.227	-0.013
	G				1.000	0.094	1.004	-0.101	0.550**	0.586**	-0.181	0.581**	-0.262
Hundred grain weight	P					1.000	0.219	0.501**	-0.220	0.293	0.081	0.285	0.265
	G					1.000	0.259	0.504**	-0.220	0.293	0.488**	0.286	0.376*
Grain length	P						1.000	-0.229	0.596**	0.743**	0.043	0.744**	-0.005
	G						1.000	-0.271	0.700**	0.875**	0.507**	0.872**	0.046
Grain breadth	P							1.000	-0.866**	-0.310*	-0.095	-0.314**	0.127
	G							1.000	-0.872**	-0.313*	-0.538**	-0.318**	0.202
Grain L/B ratio	P								1.000	0.677**	0.097	0.678**	-0.091
	G								1.000	0.678**	0.645**	0.680**	-0.132
Kernel length	P									1.000	0.103	0.997**	0.106
	G									1.000	0.638**	1.000**	0.152
Kernel breadth	P										1.000	0.081	0.050
	G										1.000	0.667**	-0.016
Kernel L/B ratio	P											1.000	0.097
	G											1.000	0.143
Grain yield per plant	P												1.000
	G												1.000

*Significant 5% level, **Significant 1% level.

Table 4: Genotypic path co-efficient for twelve components in rice.

Characters	DFF	PH (Days)	NPT (cm)	PL	HGW (cm)	GL (g)	GB (mm)	GLBR (mm)	KL	KB (mm)	KLBR (mm)	GYD (g)
Days to 50% flowering	0.351	-0.084	-0.032	-0.004	0.054	0.266	0.213	-0.306	3.403	-0.036	-3.608	0.217
Plant height	0.186	-0.159	-0.001	0.071	0.069	0.151	0.428	-0.417	4.033	0.040	-4.340	0.061
Number of productive tillers per plant	-0.034	0.001	0.335	-0.057	-0.021	-0.096	-0.021	0.035	-3.217	-0.044	3.268	0.149
Panicle length	-0.005	-0.041	-0.070	0.272	0.028	-0.790	-0.091	0.515	-10.005	-0.039	9.964	-0.262
Hundred grain weight	0.064	-0.037	-0.024	0.026	0.299	-0.204	0.455	-0.205	-4.998	0.103	4.897	0.376*
Grain length	-0.119	0.030	0.041	0.273	0.078	-0.787	-0.244	0.655	-14.939	0.107	14.951	0.046
Grain breadth	0.083	-0.075	-0.008	-0.028	0.151	0.213	0.902	-0.816	5.339	-0.113	-5.446	0.202
Grail L/B ratio	-0.115	0.071	0.013	0.150	-0.066	-0.551	-0.787	0.936	-11.573	0.136	11.654	-0.132
Kernel length	-0.070	0.038	0.063	0.160	0.088	-0.689	-0.282	0.635	-17.070	0.135	17.144	0.152
Kernel breadth	-0.059	-0.030	-0.073	-0.049	0.146	-0.399	-0.485	0.604	-10.892	-0.212	11.433	-0.016
Kernel L/B ratio	-0.074	0.040	0.064	0.158	0.086	-0.687	-0.287	0.636	-17.072	0.141	17.138	0.143

Residual effect = 0.098 *Significant 5% level **Significant 1% level

phenotypic expression under the influence of environmental factors table 3. Kernel L/B ratio showed maximum positive and significant correlation with kernel length at both phenotypic (0.99) and genotypic (1.00) levels. Grain yield per plant recorded positive and significant correlation with hundred grain weight (0.37) at genotypic level only. This corroborates with the findings of Satheeshkumar and Saravanan (2012) for hundred grain weight. It suggests that priority should be given to these traits while making selection for yield improvement. Days to 50 per cent flowering recorded significant positive correlation with plant height (0.51 and 0.53) at both levels.

Plant height had significant positive correlation with grain breadth (0.46 and 0.47) at both phenotypic and genotypic levels. Panicle length had significant positive correlation with grain length (0.34) at phenotypic level only and significant positive correlation with grain L/B ratio (0.55), kernel length (0.58) and kernel L/B ratio (0.58) at genotypic level only. Hundred grain weight showed significant positive correlation with grain breadth (0.50 and 0.50) at both phenotypic and genotypic levels and kernel breadth (0.48) at genotypic level only. Grain length had significant positive correlation with grain L/B ratio (0.59 and 0.70), kernel length (0.74 and 0.87) and kernel L/B ratio (0.74 and 0.87) at both phenotypic and genotypic levels and significant positive correlation with kernel breadth (0.50) at genotypic level only. Grain L/B ratio had significant positive correlation with kernel length (0.67 and 0.67) and kernel L/B ratio (0.67 and 0.68) at both phenotypic and genotypic levels and significant positive correlation with kernel breadth (0.64) at genotypic level only. Kernel length had significant positive correlation with kernel breadth (0.63) at genotypic level only. Kernel breadth had significant positive correlation with kernel L/B ratio (0.66) at genotypic level only.

Genotypic path analysis studies revealed that all the characters were showed positive direct effects except plant height, grain length, kernel length and kernel breadth table 4. The maximum positive direct effects were observed for kernel L/B ratio, grain L/B ratio, grain breadth, days to 50 per cent flowering, number of productive tillers per plant, hundred grain weight and panicle length, positive direct effect as well as correlation coefficients indicated that selection may be exercised for these traits for yield improvement. Similar results were reported by Janardhanam *et al.,* (2001), Sabesan *et al.,* (2009), Makwana *et al.,* (2010), Satheeshkumar and Saravanan (2012) and Satheeshkumar *et al.,* (2018).

Path analysis partitions correlation coefficient into direct and indirect effect which probes the cause and effect relationship (Fig. 1). Maximum direct effect on yield was exhibited by kernel L/B ratio (17.13) observed *via.,* grain L/B ratio, panicle length, kernel breadth, hundred grain weight, number of productive tiller per plant and plant height followed by grain L/B ratio (0.93), grain breadth (0.90), days to 50 per cent flowering (0.35), number of productive tillers per plant (0.33), hundred grain weight (0.29) and panicle length (0.27) table 4.

The results revealed high estimates of genotypic and phenotypic coefficient of variation for grain L/B ratio, kernel breadth and grain yield per plant. Estimates of heritability in broad sense coupled with high genetic advance as per cent of mean were observed for all the traits except panicle length. Grain yield per plant exhibited high significant and positive genotypic correlation with hundred grain weight. Hence, the selection based on these traits could be more effective in rice.

References

Anbanandan, V., K. Saravanan and T. Sabesan (2009). Variability, heritability and genetic advance in rice (*Oryza sativa* L.). *Int. J. Plant Sci.,* **3(2):** 61-63.

Depar, N., I. Rajpar, M.Y. Memom, M. Imtiaz and Zia-ul-Hassan (2011). Mineral nutrient densities in some domestic and exotic rice genotypes. *Pak. J. Agric. Agrl. Eng. Vet. Sci.,* **27:** 134-142.

Dewey, D.H. and K.H. Lu (1959). A correlation and path analysis of crested wheat grass seed production. *Agron. J.,* **51:** 515-518.

Ganeshan, K., W. Manuel and T. Sundaram (1995). Analysis of hybrid components and yield in rice. *Oryza,* **32:** 111-112.

Hossain, M.A. and M.E. Haqque (2003). Genetic variability and path analysis in rice genotypes. *Bang. J. Plant Breed. Genet.,* **16(1):** 33-37.

Janardhanm, V., N. Nadarajan and S. Jebaraj (2001). Correlation and path analysis in rice (*Oryza sativa* L.). *Madras Agric. J.,* **88(10-12):** 719-720.

Maclean, J.L., D.C. Dawe, B. Hardy and C.P. Hettel (2002). Rice almanac, 3rd Edn., CABI Publishing, Wallingford, pp. 25-33.

Mahata, M.K., P. Debnath and S.K. Ghosh (2012). Critical limits of zinc in soil and rice plant grown in alluvial soils of West Bengal, India. *SAARC, J. Agric.,* **10(2):** 137-146.

Makwana, B.P., G.C. Jadeja, C.G. Patel, R.M. Patel and R.A. Gami (2010). Path analysis of qualitative and quantitative characters in slender grain rice (*Oryza sativa* L.). *Int. J. Plant Sci.,* **5(1):** 294-296.

Panse, V.G. and P.V. Shukhatme (1967). Statistical methods for agricultural workers 2nd Ed. ICAR, New Delhi, 152-157.

Paul, A., E. Ahmad, D.N. Singh and M.K. Singh (2018). Identification of selection parameters for evaluating superior rice hybrids. *Oryza,* **55(1):** 230-233.

Prasad, R., L.C. Praad and R.K. Agarwal (2010). Genetic diversity in Indian germplasm of aromatic rice. *Oryza,* **46:** 197-201.

Sabesan, T., R. Suresh and K. Saravanan (2009). Genetic variability and correlation for yield and grain quality characters of rice grown in coastal saline low land of Tamil Nadu. *Elec. J. Plant Breeding,* **1:** 56-59.

Sarkar, K.K., K.S. Bhutia, B.K. Senapathi and S.K. Roy (2007). Genetic variability and character association of quality traits in rice (*Oryza sativa* L.). *Oryza,* **44(1):** 64-67.

Satheeshkumar, P. and K. Saravanan (2012). Genetic variability, correlation and path analysis in rice (*Oryza sativa* L.). *Int. J. Curr. Res.,* **4(9):** 82-85.

Satheeshkumar, P., K. Saravanan and T. Sabesan (2018). Genetic parameters correlation and path analysis for grain yield and yield component characters of rice (*Oryza sativa* L.) grown under coastal saline low land of Tamil Nadu. *Res. J. Agric. Sci.,* **9(1):** 50-53.

Shukla, A.K., S.K. Sharma, R. Tiwari and K.N. Tiwari (2005). Nutrient depletion in the rice-wheat cropping system of the Indo-genetic plains. *Better Crops.,* **89(2):** 28-31.