



GENETIC VARIABILITY AND INTERRELATIONSHIP ANALYSIS OF QUANTITATIVE TRAITS IN RICE (*Oryza sativa* L.) GERMPLASM

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ABSTRACT

The present investigation was carried out to assess the genetic variability parameters, correlation and path analysis in 95 elite rice germplasm collections for 12 yield and its contributing traits during *kharif*, 2018 in a randomized block design, replicated twice. The analysis of variance for mean sum of squares due to genotypes showed significant differences for all the quantitative characters studied at 1 and 5% level of significance. PCV and GCV were high for traits like days to 50% flowering, tillers plant⁻¹, productive tillers plant⁻¹, length/breadth ratio and grain yield plant⁻¹. High heritability (> 60%) coupled with high genetic advance as percentage of mean (> 30%) was recorded for days to 50% flowering, leaf length, tillers plant⁻¹, productive tillers plant⁻¹, L/B ratio, grain width, 100 grain weight and grain yield plant⁻¹ indicating the preponderance of additive gene action. The grain yield plant⁻¹ had highly significant and positive correlation both at genotypic and phenotypic levels with tillers hill⁻¹, productive tillers plant⁻¹, panicle length and days to 50% flowering. High direct effects of these characters appeared to be the main reason for their strong association with grain yield except for number of productive tillers plant⁻¹ which had strong association with yield through indirect effect (*i.e.* through tillers plant⁻¹). Hence, direct selection for these characters would be very effective for further improvement of grain yield in rice and for the selection of elite genotypes.

Keywords: Correlation, germplasm, path analysis, quantitative traits, rice, variability

INTRODUCTION

Rice is the staple food of about three-fourth population of India and is a source of livelihood for 120-150 million rural households (Mohanthy and Yamano, 2017). India is the 2nd largest producer of rice in the world and achieved self-sufficiency in rice production due to green revolution. But as per the conservative estimates of the Population Foundation of India, the country's population will be 1546 million by the end of 2030 and 1824 million by the end of 2050 for which India shall need to produce 137 million tonnes of rice on 37 million ha land in 2050 as compared to the current production of 105 million tonnes of rice on 43 million ha (CRRI, 2013). This means that the yield has to be increase by 50% in next three decades to keep India food secure (Pathak *et al.*, 2018). However, the yield level in rice has reached a plateau and improving its productivity has become a crucial task. Crop improvement programmes, therefore, should aim at broadening the genetic base of breeding stock by introgressing genes from diverse sources. Thus, there is a need to evaluate the untapped germplasm

collections for exploitation. Direct selection based on crop yields is often a paradox in breeding programmes because yield is a complex polygenically inherited character, influenced by its component traits. Breeding programmes should, therefore, take into consideration the character association of various component traits with yield and among themselves. Partitioning the total variation present in germplasm into phenotypic, genotypic and environmental components and determining the magnitude of these components for various traits along with heritability and genetic advance shall be a measure of the type of gene action thus helps in deciding a breeding procedure for genetic improvement of a trait. The relative contribution of individual traits may be accomplished by correlation studies. Significant positive correlation between yield and its component traits viz., number of productive tillers plant⁻¹, number of grains panicle⁻¹ and 1000 grain weight in rice was reported by Saha *et al.* (2019) and Thorat *et al.* (2019). In rice, yield is determined by indirect traits like plant height, growth period, tillering ability, panicle length, seed length, seed setting rate and grains panicle as well as direct traits like panicle number unit⁻¹ area/plant, filled grains panicle⁻¹ and 1000-grain-weight (Huang *et al.*, 2013; Li *et al.*, 2019). The technique of path coefficient analysis is used to have an idea of direct and indirect contribution of a trait towards yield which enables breeders to rank genetic attributes according to their contribution (Dewey and Lu, 1959). In present study, an attempt was made to characterize a set of rice germplasm accessions for quantitative traits and to identify the variability available in rice germplasm collection.

MATERIALS AND METHODS

The experimental material for the present study comprised of 95 rice germplasm collections maintained as 'T' numbers at Department of Rice, Centre for Plant Breeding & Genetics, TNAU, Coimbatore (India). These germplasm collections were raised in a randomized block design with two replications at Department of Rice, Centre for Plant Breeding & Genetics, TNAU, Coimbatore during *kharif*, 2018. Each genotype was raised in two rows of 3 m row length. A plant spacing of 20 x 20 cm was adopted. The genotypes were raised in two blocks per replication. All the recommended agronomic practices were followed (DOA/TNAU, 2020). Five competitive plants were selected at random for each genotype in each replication to record the data on all yield and yield attributing characters (except days to flowering) viz., leaf length, leaf width, panicle length, plant height, number of tillers plant⁻¹, number of productive tillers plant⁻¹ and grain traits, viz., grain length, grain width, L/B ratio, 100 grain weight and grain yield plant⁻¹. Days to 50 flowering was recorded on plot basis. The data recorded were subjected to statistical analysis of variance technique as proposed by Panse and Sukhatme (1961). Phenotypic and genotypic coefficients of variation were calculated as per the formula suggested by Burton and Devane (1953). Heritability, genetic advance and correlation coefficient for all possible combination of characters were worked out as per Johnson *et al.* (1955). Path analysis was carried out using the method suggested by Dewey and Lu (1959).

RESULTS AND DISCUSSION

The analysis of variance showed significant differences for all the characters studied among the genotypes (Table 1). This suggested that the genotypes tested were genetically diverse and considerable amount of variability existed among them. In general, the magnitude of PCV was higher than the corresponding GCV for all the characters suggesting the influence of environment on the expression of the traits. However, the differences between PCV and GCV were very small for most

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

Source of variation	df	DFF (days)	LL (cm)	LW (cm)	PL (cm)	PH (cm)	TILL (No)	PT (No)	GL (mm)	GW (mm)	L/B ratio	100-GW (g)	SPY (g)
MSS													
Replication	1	1.67	2.01	0.005	1.06	1.24	1.54	1.01	0.0005	0.0003	0.100	0.03	1.05
Genotype	94	751.38**	82.99**	0.05**	10.18**	205.89**	24.06**	21.6**	0.005**	0.003**	0.96**	0.324**	101.36**
Error	94	83.46	9.20	0.005	1.11	22.86	2.65	2.39	0.0005	0.0004	0.105	0.035	11.25

DFF - Days to 50% flowering; LL - Leaf length; LW - Leaf width; PL - Panicle length; PH - Plant height; TILL - Number of tillers plant⁻¹; PT - Number of productive tillers plant⁻¹; GL - Grain length; GW - Grain width; L/B ratio - Length/breadth ratio; 100GW - 100 grain weight; SPY - Grain yield plant⁻¹; ** Significant at 1% level of probability

of the characters indicating the lesser contribution of environmental variation towards the expression of these traits.

The estimates of PCV and GCV were found high (> 20) for days to 50% flowering, number of tillers plant⁻¹, number of productive tillers plant⁻¹, length/breadth ratio and grain yield plant⁻¹ (Table 2) suggesting that these traits are under the influence of genetic control. Also, there was less effect of environment on characters. Hence, these traits can be relied upon, and simple selection can be practiced for further improvement. Similar results were reported by Setty *et al.* (2019) for number of tillers plant⁻¹, number of productive tillers plant⁻¹ and grain yield plant⁻¹. Moderate PCV and GCV were recorded for leaf length, leaf width, plant height, grain width and 100 grain weight and low PCV and GCV were recorded for panicle length and grain length. These results were found similar with Devi *et al.* (2017) and Kalpana *et al.* (2018) and for leaf length, leaf width and 100 grain weight; Siddi (2020) for panicle length and Aditya and Anuradha (2013) for grain length. Low PCV and GCV indicates narrow genetic base for these traits and improvement in these traits could be brought about by hybridization or induced mutation to widen the genetic base followed by pedigree selection in advance generation (Gangashetty *et al.*, 2013). In general, high coefficient of variability shows scope of selection in favour of traits of interest and low coefficient of variability indicates the need for creation of variability and selection. Heritability in broad sense was found to be high (> 60%) for all the characters studied. High heritability (> 60%) coupled with high genetic advance as percent mean (> 30%) was recorded for days to 50% flowering, leaf length, number of tillers plant⁻¹, number of productive tillers plant⁻¹, L/B ratio, grain width, 100 grain weight and grain yield plant⁻¹. Therefore, indicating a predominance of additive gene effects and the possibilities of effective selection based on these traits for crop improvement program. Similar findings were reported by Pragnya *et al.* (2018) for days to 50% flowering and number of tillers plant⁻¹; Shivani *et al.* (2018) for days to 50%

Table 2: Genetic parameters for yield & yield contributing traits in some rice germplasm accessions

Characters	Mean	Min	Max	Coefficient of variation		h ² (%) (broad sense)	GA in % of mean
				PCV (%)	GCV (%)		
Days to 50% flowering	91.65	61.00	124.50	21.91	21.87	80.00	44.95
Leaf length (cm)	28.18	18.50	38.17	19.12	17.96	79.00	34.76
Leaf width (cm)	1.11	0.65	1.47	13.25	9.74	85.00	14.74
Panicle length (cm)	20.48	16.67	24.33	8.50	7.13	70.31	12.31
Plant height (cm)	82.26	51.50	96.83	10.82	9.89	83.59	18.63
Tillers plant ⁻¹ (No.)	12.21	7.17	22.17	23.07	19.79	73.55	34.96
Productive tillers plant ⁻¹ (No.)	11.37	6.67	21.67	23.00	20.43	78.95	37.40
Grain length (mm)	5.40	4.00	6.50	8.41	8.20	95.11	16.48
Grain width (mm)	2.00	1.00	2.90	17.56	16.86	92.16	33.33
Length/breadth ratio	2.75	1.55	3.50	25.50	22.76	79.69	41.86
100 grain weight (g)	2.15	1.01	2.85	18.97	18.39	93.96	36.72
Grain yield plant ⁻¹ (g)	19.25	4.33	39.00	34.30	31.23	82.91	58.58

Table 3: Phenotypic (rp) and genotypic (gp) correlation coefficient between yield and its component traits of rice genotypes

Characters		Days to 50% flowering	Leaf length (cm)	Leaf width (cm)	Panicle length (cm)	Plant height (cm)	Tillers plant ⁻¹ (No.)	Productive tillers plant ⁻¹ (No.)	Grain length (mm)	Grain width (mm)	Length/breadth ratio	100-grain weight (g)	Grain yield plant ⁻¹ (g)
Days to 50% flowering	rg	1.000	0.002	-0.047	0.256**	0.227**	0.221**	0.056	-0.085	0.048	-0.082	-0.276	0.232**
	rp	1.000	0.001	-0.014	0.232**	0.201**	0.201**	0.044	-0.052	0.030	-0.050	-0.268	0.212**
Leaf length	rg		1.000	-0.163*	0.272**	0.218**	0.060	0.112	-0.002	-0.158	0.046	-0.18**	0.129
	rp		1.000	-0.175**	0.265**	0.210**	0.012	0.051	0.036	-0.135	0.059	-0.157*	0.120
Leaf width	rg			1.000	-0.030	0.088	-0.024	-0.022	-0.275**	0.495**	-0.526**	0.266**	0.051
	rp			1.000	-0.064	0.060	-0.019	-0.016	-0.287**	0.428**	-0.218**	0.246**	0.041
Panicle length	rg				1.000	0.313**	0.074	0.080	-0.116	0.030	-0.521**	-0.016	0.225**
	rp				1.000	0.301**	0.050	0.001	-0.013	-0.094	0.071	-0.011	0.201**
Plant height	rg					1.000	0.211**	0.175**	-0.046	-0.143*	-0.158*	0.090	0.168*
	rp					1.000	0.19**	0.165*	-0.003	-0.157*	-0.178**	0.058	0.148*
Tillers plant ⁻¹ (No.)	rg						1.000	0.911**	0.169*	-0.150*	0.334**	-0.060	0.482**
	rp						1.000	0.895**	0.170**	-0.105	0.320**	-0.067	0.462**
Productive tillers plant ⁻¹ (No.)	rg							1.000	0.130*	-0.270**	0.350**	-0.128	0.406**
	rp							1.000	0.120	-0.290**	0.310**	-0.110	0.385**
Grain length	rg								1.000	-0.272**	0.707**	-0.092	-0.50**
	rp								1.000	-0.293**	0.657**	-0.086	-0.45**
Grain width	rg									1.000	-0.851**	0.141*	-0.19**
	rp									1.000	-0.822**	0.121	-0.18**
Length/breadth ratio	rg										1.000	-0.180	-0.104
	rp										1.000	-0.124	0.024
100 grain weight	rg											1.000	0.049
	rp											1.000	0.035
Grain yield plant ⁻¹ (g)	rg												1.000
	rp												1.000

**Significant at 1% level of probability P= Phenotypic correlation coefficient

*Significant at 5% level of probability G= Genotypic correlation coefficient

flowering and plot yield; Rukmini *et al.* (2017) for productive tillers plant⁻¹ and 100 grain weight and Akter *et al.* (2018) for grain width. Thus, these characters offer the best possibility of improvement through selection procedures.

For achieving rational improvement in yield and its related parameters, knowledge on mechanism of correlation, cause and effect relationship provides a basis for formulating suitable selection methods for the yield. In the present study correlation analysis was carried out both at phenotypic and genotypic levels. In general, the estimation of genotypic correlation was higher than that of phenotypic correlation (Table 3), which indicated the low influence of environmental factors and relative stability of the genotypes. Genotypic correlation may be either due to pleiotropic action of genes or due to linkage or more likely both. The main genetic cause of such correlation is pleiotropy, which refers to manifold effects of a gene (Falconer, 1960).

In present study, days to 50% flowering (rp = 0.212**, rg = 0.232**), panicle length (rp = 0.201**, rg = 0.225**), plant height (rp = 0.148*, rg = 0.168*), number of tillers plant⁻¹ (rp = 0.462**, rg = 0.482**) and number of productive tillers plant⁻¹ (rp = 0.406**, rg = 0.385**), showed highly significant positive correlation with grain yield plant⁻¹ at both phenotypic (rp) and genotypic (rg) levels (Table 2). As yield is a dependent character, the performance of these quantitative characters will also affect the grain yield plant⁻¹. Improvement in the above selective characters shall increase grain yield in rice. Therefore, any perspective changes in these characters would also affect the yield in the desirable direction. These observations are in conformity with those of Gour *et al.* (2017) and Setty *et al.* (2019) for number of tillers plant⁻¹; Hossain *et al.* (2018) and Acharya *et al.* (2019) for productive tillers plant⁻¹, panicle length and plant height and Tiwari *et al.* (2019) for days to 50%

Table 4: Direct (diagonal) and indirect (off diagonal) effect of various traits on yield of rice genotypes

Characters	Days to 50% flowering	Leaf length (cm)	Leaf width (cm)	Panicle length (cm)	Plant height (cm)	Tillers plant ⁻¹ (No.)	Productive tillers plant ⁻¹ (No.)	Grain length (mm)	Grain width (mm)	Length/ breadth ratio	100- grain weight (g)	Grain yield plant ⁻¹ (g)
Days to 50% flowering	0.231	0.000	0.002	0.019	0.005	0.026	-0.018	-0.030	-0.053	0.022	0.008	0.212
Leaf length	0.001	-0.025	-0.015	0.020	0.024	0.027	-0.021	0.000	0.081	-0.022	0.050	0.120
Leaf width	0.004	0.004	0.102	-0.058	0.002	0.046	-0.047	-0.002	-0.087	0.080	-0.003	0.041
Panicle length	0.051	-0.006	-0.006	0.131	0.009	0.023	-0.016	-0.001	0.006	0.010	0.000	0.201
Plant height	0.042	-0.054	0.009	0.046	0.026	0.136	-0.095	0.000	0.078	-0.039	-0.001	0.148
Tillers plant ⁻¹	0.029	-0.002	0.008	0.010	0.006	0.592	-0.184	0.002	0.032	-0.034	0.003	0.462
Productive tillers plant ⁻¹	0.009	-0.003	0.009	0.010	0.004	0.539	-0.202	0.001	0.044	-0.030	0.004	0.385
Grain length	-0.093	-0.091	-0.091	-0.008	0.001	0.090	-0.066	0.009	0.109	-0.313	0.003	-0.450
Grain width	0.015	0.004	0.027	-0.002	-0.004	-0.062	0.046	-0.004	-0.493	0.299	-0.004	-0.178
Length/breadth ratio	-0.015	-0.002	-0.024	-0.004	0.002	0.061	-0.018	0.006	0.350	-0.336	0.004	0.024
100 grain weight	-0.061	0.002	0.029	0.001	0.041	-0.029	0.051	-0.001	-0.020	0.051	-0.029	0.035
Grain yield plant ⁻¹	0.212	0.120	0.041	0.201	0.148	0.462	0.385	-0.450	-0.178	0.024	0.035	1.000

Note: Bold and diagonal figures indicate the direct effect, Residual effect: 0.3

flowering and number of tillers plant⁻¹. However, grain length and grain width exhibited highly significant negative correlation with grain yield plant⁻¹ at both phenotypic (rp) and genotypic (rg) levels. So, in the germplasm collections studied, the selection of genotypes possessing short and medium sized grains would enhance the yield rather than selecting long grained type.

As simple correlation does not provide any idea about the true contribution of the characters towards yield, these genotypic correlations were partitioned into direct and indirect effects through path coefficient analysis. In present study, the high degree of correlation between grain yield plant⁻¹ and number of tillers plant⁻¹ (0.462) and high direct effect of number of tillers plant⁻¹ (0.592) on grain yield plant⁻¹ followed by days to 50% flowering (0.212 & 0.231) and panicle length (0.201 & 0.131) [Table 4] revealed true relationship between them. The direct selection in above mentioned traits may be rewarding for yield improvement. The correlation coefficient was found positive and direct effect was negative for the number of productive tillers plant⁻¹ indicating that indirect effects seem to be the cause of correlation. It was found to influence yield through number of tillers plant⁻¹. Hence, prime emphasis should be given to number of tillers plant⁻¹ followed by days to 50% flowering, panicle length and number of productive tillers plant⁻¹ for realization of high and stable yields. These findings in relation to different component traits are in agreement with Hossain *et al.* (2018), Setty *et al.* (2019) and Acharya *et al.* (2019). The value of residual effect was low (0.30) indicating that major component traits contributing to yield has been included in this study.

The study showed that the germplasms exhibited a wide variability for most of the traits, thus revealing ample scope for selection of promising genotypes for yield improvement. Characters like tillers plant⁻¹, productive tillers plant⁻¹ and days to 50% flowering showed high GCV, PCV, high heritability and high genetic advance indicating that they are less influenced by environment; and the phenotypic estimates of these traits closely relate to their actual genetic potential which can be further enhanced by simple selection and need top priority during selection. Based on correlation coefficient and path analysis results the characters like tillers plant⁻¹, productive tillers plant⁻¹, panicle length and days to 50% flowering showed direct positive significant association with grain yield plant⁻¹ and these traits can be used as selection indices for improving yield or for developing better varieties.

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