

RESEARCH ARTICLE

Studies on Variability, Association and Path Analysis in Rice Landraces of Tamil Nadu

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ABSTRACT

The present study aimed analyze the variability, correlation, and path analysis in 97 rice landraces of Tamil Nadu for ten quantitative characters. The Phenotypic Coefficient of Variation and Genotypic Coefficient of Variation of the traits, namely total number of tillers, productive tillers per plant, and yield per plant, were high, indicating that these traits were not affected by the environment. Moderate Phenotypic coefficient of variation and Genotypic Coefficient of Variation was observed for the traits days to 50% flowering, plant height, days to maturity, and test weight, indicating that selection based on the heritable nature of the trait would be effective. High heritability coupled with high genetic advance as a percentage of mean was recorded for days to 50% flowering, plant height, the total number of tillers, productive tillers per plant, days to maturity, test weight, and plant yield. This shows that direct selection of these traits in crop improvement will be very effective because additive effects control these traits. In the association analysis, the plant height at the genotypic and phenotypic levels and test weight at the genotypic level showed a highly significant and significant positive correlation with plant yield. Path coefficient analysis shows that the total number of tillers, panicle length, decorticated grain length, and decorticated grain width had a strong positive effect on the performance of a single plant. Direct selection of characteristics such as plant height, test weight, the total number of tillers, panicle length, decorticated grain length, and decorticated grain width can increase single plant yield. Therefore, selection based on these traits for improving rice yield would be desirable.

Received : 10th December, 2021

Revised : 23rd December, 2021

Revised: 11th January, 2022

Accepted : 21st January, 2022

Keywords: Variability; PCV; GCV; Correlation; Path analysis; Rice landraces

INTRODUCTION

Rice referred to as “Global grain” (Shalini and Tulsi, 2008) is cultivated in an area of 163.2 million hectares worldwide with a production of 751.9 million tons (FAO, 2020), feeding half of the world’s population and 70% of the population in India. Compared to other crop varieties and cultivars, the genetic variability of rice germplasm in the world, including local varieties, is quite large. According to N.I.Vavilov, India, is the main centre of origin and diversity of rice. India has got wide variability in the rice germplasm collections for various qualitative and quantitative traits and sources of resistance to different biotic and abiotic stresses. In the long domestication process, through the selection process, agricultural groups have made significant contributions to the origin, evolution, and

accumulation of the remarkable variability in several of our local varieties (Pandravada et al., 2017). The existence of genetic variability is the basic requirement for any crop improvement programmes. Therefore, the genetic variability available in the local rice germplasm may be exploited for rice improvement programmes aimed widening the genetic base and breaking the yield barrier in rice to ensure food security. Estimation of genotypic variation and heritability and genetic advance in the germplasm would be helpful for genetic improvement of yield. As the inheritance of foremost trait yield is controlled by polygenes and highly influenced by component traits, direct selection for yield is always a paradox in crop improvement. Correlation is an index that measures the degree of association between

two features that work simultaneously (Hays et al., 1995). Hence, the knowledge on character association will be useful in the identification of the relative contribution of component traits for yield improvement. Phenotypic correlation gives only the simple relationship between two characters. As the expression of a character is a result of the interaction of genotype with the environment, estimation of genotypic and phenotypic association among traits will be valuable for breeding programs besides phenotypic variation (Johnson et al., 1955). The inter-relationship among yield components and components associated with yield can be determined using path analysis (Dewey and Lu, 1959) to choose traits that contribute indirectly to yield. Keeping this in view, the present investigation was undertaken to study the variability, correlation, and path analysis in a set of rice landraces for various quantitative traits.

MATERIAL AND METHODS

A set of 97 rice landraces (Table 1.) of Tamil Nadu maintained at the Department of Rice, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, were raised at the paddy breeding station, during Kharif 2019 season for characterization. The experiment was laid out in a Randomized Block Design with two replications. Each landrace was raised in 3 rows of 8.0 m in length at a spacing of 20 x 20cm. All the recommended packages of practices were followed for the successful establishment and crop growth. Data on ten quantitative characters, namely plant height, number of tillers per plant, productive tillers per plant, panicle length, days to maturity, test weight, decorticated grain length, decorticated grain width, and single plant yield were recorded in five randomly tagged plants for each genotype in each replication except for days to 50 % flowering which is recorded on a plot basis. The data were analyzed as per the standard statistical procedures. For each character, the Phenotypic coefficient of variation (PCV) and the Genotypic coefficient of variation (GCV) was computed based on the methods given by Burton (1952). Heritability (h²) in the broad sense was estimated according to Lush (1949) and explained by Allard (1960). Genetic advance and genetic advance as percentage of mean were derived according to the method of Johnson et al (1955) for each character under study. Phenotypic, genotypic, environmental coefficients of correlation and path analysis of important component traits and quality traits with grain yield were worked out

following the procedure of Dewey and Lu (1959).

Figures and Structures

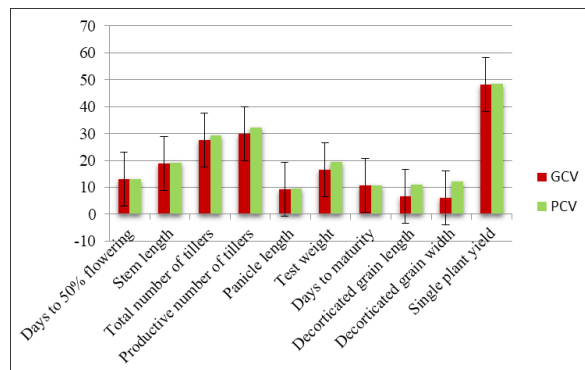


Figure.1. Genotypic coefficient of variation and Phenotypic coefficient of variation for ten quantitative traits of 97 rice landraces

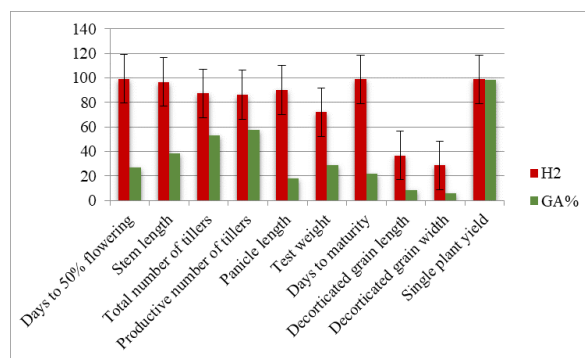


Figure.2 Heritability and Genetic advance as per cent of mean for ten quantitative traits of 97 rice landraces

Table 1. List of landraces utilized for the study

S.No	Name of land races
1	Sornavari
2	Periya samba
3	Sarapilli samba
4	Manaparai
5	Manavari
6	Arupathamkuruvai
7	Panamara samba
8	Vellai samba
9	Thooyala
10	Arupatham samba
11	Mattaikar
12	Kallurundaikar
13	Senthooram



14	Purple puttu	58	White paddy
15	Chennangi	59	Thattan samba
16	Vellaigundu samba	60	Anaikomban
17	Godumarai samba	61	Koolavalai
18	Ayyan samba	62	Valasamudon
19	Arupatham vellai	63	Gandhasala
20	Puthupatty samba	64	Manimenikki
21	Mangam samba	65	Salem – 9
22	Poongar	66	Chinnaadukku nel
23	Shenmolagi	67	Periyasandigar
24	Sadai samba	68	Kattuyanam
25	Vellaikuruvai	69	Varakkal
26	Rangoon samba	70	Kaviya samba
27	Nellore samba	71	Thillainayagam
28	Vadakkathikar	72	Norungan
29	Muthuvellai	73	Kavuni
30	Sembalai	74	Senkar
31	Seevan samba	75	Murugankar
32	Moshanam	76	Kudaivazhai
33	Kappikar	77	Kuruvaikalanjiyam
34	Salem – 3	78	Palkachaka
35	Chinthamani	79	Sornakuruvai
36	Varigarudan samba	80	Thogai samba
37	Arasamba	81	Malayalathan samba
38	Ariyan red	82	Kattikar
39	Pamani samba	83	Kaatuponni
40	Jeeraga Samba	84	Kalarkar
41	Vaanginathan	85	Rama kuruvaikar
42	Salem	86	Aarkadukichili
43	Vellaichithiraikar	87	Matta kuruvai
44	Ponkambi samba	88	Karuthakar
45	Kaar	89	Katta samba
46	Varigamban samba	90	Red sirumani
47	Korangu samba	91	Ponmani samba
48	Uppumolagi	92	Kaliyan samba
49	Chetty samba	93	Kalli madaiyan
50	Chittan samba	94	Karungan
51	Puluthiperattaikar	95	Mikuruvai
52	Karthigai samba	96	Vellaikudaivazhai
53	Alther samba	97	Vadakkathi samba
54	Val samba		
55	Sembilipiriyam		
56	Senthinayagam		
57	Mapillai samba		



Table 2. Mean variability, heritability (broad sense) and genetic advance as per cent of mean in rice landraces

S. NO.	Characters	Mean	GV	PV	EV	GCV (%)	PCV (%)	ECV (%)	H ² (%)	GA%
1	Days to 50% flowering (days)	94.05	147.91	148.87	0.96	12.96	13.00	1.04	99.35	26.61
2	Plant height (cm)	153.00	815.83	843.24	27.42	18.83	19.14	3.45	96.74	38.15
3	Total number of tillers	15.59	17.97	20.59	2.62	27.45	29.38	10.47	87.27	52.83
4	Productive number of tillers	14.24	15.53	18.02	2.50	29.98	32.30	12.02	86.18	57.31
5	Panicle length (cm)	24.59	5.10	5.67	0.57	9.18	9.68	3.07	89.94	17.94
6	Days to maturity (days)	123.87	175.84	178.05	2.21	10.68	10.74	1.20	98.75	21.86
7	Test weight (g)	25.75	17.91	24.89	6.98	16.43	19.37	10.26	71.95	28.72
8	Decorticated grain length (mm)	4.96	0.11	0.30	0.19	6.68	11.09	8.85	36.67	8.30
9	Decorticated grain width (mm)	2.06	0.02	0.07	0.05	6.02	12.31	10.74	28.57	6.06
10	Single plant yield (g)	35.16	287.07	290.69	3.62	48.18	48.48	5.41	98.75	98.63

GCV: Genotypic Coefficient of Variation

H²: Heritability

PCV: Phenotypic Coefficient of Variation

GA%: Genetic Advance as per cent of mean

ECV: Environmental Coefficient of Variation

Table 3. Genotypic and phenotypic correlation coefficients for various quantitative characters in rice land races

Correlation		DFF	PH	TNT	PNT	PL	TW	DM	DGL	DGW	SPY
DFF	G	1	0.386**	0.062	0.014	0.382**	-0.018	0.931**	-0.260**	0.260**	0.158
	P	1	0.378**	0.060	0.013	0.364**	-0.02	0.922**	-0.145	0.124	0.157
PH	G		1	0.042	0.056	0.289**	0.233*	0.333**	-0.281**	0.260**	0.262**
	P		1	0.047	0.059	0.277**	0.187*	0.326**	-0.133	0.148	0.256**
TNT	G			1	0.971**	0.158	0.115	0.051	-0.071	0.153	0.145
	P			1	0.913**	0.134	0.075	0.047	-0.026	0.078	0.139
PNT	G				1	0.141	0.055	-0.002	-0.029	0.224*	0.087
	P				1	0.126	0.06	0.001	0.001	0.069	0.081
PL	G					1	-0.027	0.329**	-0.416**	-0.325**	0.156
	P					1	-0.007	0.305**	-0.225*	-0.205*	0.153
TW	G						1	0.010	0.218*	0.535**	0.182*
	P						1	0.015	0.118	0.223*	0.153
DM	G							1	-0.245**	0.274**	0.155
	P							1	-0.120	0.135	0.153
DGL	G								1	-0.021	-0.420**
	P								1	0.150	-0.241*
DGW	G									1	0.059
	P									1	0.030
SPY	G										1
	P										1

DFF: Days to fifty percent flowering

PL : Panicle length in cm

DGW : Decorticated grain width

PH : Plant height in cm

TW: Test weight

SPY : Single plant yield

TNT : Total number of tillers

DM : Days to maturity

**Significant at 1% level of probability

PNT : Productive number of tillers

DGL : Decorticated grain length

*Significant at 5% level of probability

P= Phenotypic correlation coefficient

G= Genotypic correlation coefficient



Table 3. Genotypic and phenotypic correlation coefficients for various quantitative characters in rice land races

Correlation		DFF	PH	TNT	PNT	PL	TW	DM	DGL	DGW	SPY
DFF	G	1	0.386**	0.062	0.014	0.382**	-0.018	0.931**	-0.260**	0.260**	0.158
	P	1	0.378**	0.060	0.013	0.364**	-0.02	0.922**	-0.145	0.124	0.157
PH	G		1	0.042	0.056	0.289**	0.233*	0.333**	-0.281**	0.260**	0.262**
	P		1	0.047	0.059	0.277**	0.187*	0.326**	-0.133	0.148	0.256**
TNT	G			1	0.971**	0.158	0.115	0.051	-0.071	0.153	0.145
	P			1	0.913**	0.134	0.075	0.047	-0.026	0.078	0.139
PNT	G				1	0.141	0.055	-0.002	-0.029	0.224*	0.087
	P				1	0.126	0.06	0.001	0.001	0.069	0.081
PL	G					1	-0.027	0.329**	-0.416**	-0.325**	0.156
	P					1	-0.007	0.305**	-0.225*	-0.205*	0.153
TW	G						1	0.010	0.218*	0.535**	0.182*
	P						1	0.015	0.118	0.223*	0.153
DM	G							1	-0.245**	0.274**	0.155
	P							1	-0.120	0.135	0.153
DGL	G								1	-0.021	-0.420**
	P								1	0.150	-0.241*
DGW	G									1	0.059
	P									1	0.030
SPY	G										1
	P										1

DFF: Days to fifty percent flowering

PH : Plant height in cm

TNT : Total number of tillers

PNT : Productive number of tillers

P= Phenotypic correlation coefficient

PL : Panicle length in cm

TW: Test weight

DM : Days to maturity

DGL : Decorticated grain length

G= Genotypic correlation coefficient

DGW : Decorticated grain width

SPY : Single plant yield

**Significant at 1% level of probability

*Significant at 5% level of probability

RESULTS AND DISCUSSION

GCV and PCV

The analysis of variance showed significant differences for all the characters studied among the genotypes suggesting that the genotypes tested were genetically diverse with the existence of a considerable amount of variability among them. PCV was higher than GCV (Figure.1 and Table. 2) for all the traits studied. Similar results were reported by Augustina et al. (2013) and Abebe et al. (2017). The traits, namely productive tillers per plant (32.30, 29.98%), number of tillers per plant (29.38, 27.45%), and single plant yield (48.48, 48.18%), recorded high PCV and GCV, indicating that these traits are under genetic control and simple selection can be practiced for its improvement. Similar findings were reported by Chouhan et al. (2020) and Nithya et al. (2020). Moderate PCV and GCV were observed for the traits viz., plant height (19.14, 18.83%), days to 50% flowering (13.00, 12.96%), test weight (19.37, 16.43%), and days to maturity (10.74, 10.68%) which shows that these traits have a narrow genetic base and it can be improved upon by hybridization

and pedigree selection in subsequent generations. Comparable results were reported earlier by Abebe et al. (2017) and Nithya et al. (2020). Low GCV and moderate PCV were observed in decorticated grain length (6.68, 11.09%) and decorticated grain width (6.02, 12.31%). Low PCV and GCV were observed for panicle length (9.68, 9.18%) which is in accordance with the report of Rajpoot et al. (2017). Therefore, improvement for these traits needs the creation of variation by either mutation or hybridization followed by selection.

Heritability and GA

High heritability and high genetic advance as per cent of the mean (Figure.2 and Table. 2) were recorded for the traits, namely plant height (96.74, 38.15%), productive tillers per plant (86.18, 57.31%), the total number of tillers (87.27, 52.83%), days to 50% flowering (99.35, 26.61%), test weight (71.95, 28.72%), single plant yield (98.75, 28.63%) and days to maturity (98.75, 21.86%) showing the preponderance of additive gene effects and the possibilities of effective selection based on these traits for the crop improvement program.

This conforms with Augustina et al. (2013) and Abebe et al. (2017). Low heritability and low genetic advance as per cent of mean were observed in decorticated grain width (28.57, 6.06%). Similar results were obtained by Sabesan et al. (2009) and Gokulakrishnan et al., (2014). Panicle length (89.94, 17.94%) recorded high heritability and moderate genetic advance as per cent of the mean. This is in line with Abebe et al. (2017). The decorticated grain length (36.67, 8.30%) recorded moderate heritability and low genetic advance as per cent of the mean. The result was contradictory to Sahu et al. (2017) and Tiwari et al. (2019).

Association analysis

The influence of various yield components in the expression of yield can be understood from character association studies. Association between two different traits is the result of linkage and pleiotropic effect of genes. Therefore, to see suitable selection strategies for improvement in yield, it is essential to know about the correlation between yield and yield component traits (Table 3.). The traits viz., plant height (0.262, 0.256) at both genotypic and phenotypic levels and test weight (0.182, 0.153) at genotypic level exhibited a highly significant and significant positive correlation with single plant yield, respectively. Decorticated grain length (-0.420, -0.241) had shown a highly significant and significant negative correlation with single plant yield at both levels. Other components such as days to 50% flowering (0.158, 0.157), total number of tillers (0.145, 0.139), number of productive tillers per plant (0.087, 0.081), panicle length (0.156, 0.153), days to maturity (0.155, 0.153) and decorticated grain width (0.059, 0.030) exhibited non-significant association with single plant yield at genotypic and phenotypic levels. Similar results were obtained by Madhukar et al., (2017) and Kalyan et al., (2017).

Path analysis

Direct and indirect effects of characters on single plant yield were given in Table 4. Among all the characters studied, the total number of tillers (38.811), panicle length (9.254), decorticated grain length (6.188), and decorticated grain width (14.220) had a high positive direct effect on single plant yield. Days to 50% flowering (-7.052), number of productive tillers per plant (-41.329), and test weight (-11.316) exhibited a highly negative direct effect on single plant yield. The moderate positive direct effect was shown by plant height (2.136) and

low negative effect by days to maturity (-1.383). Days to 50% flowering possessed highly positive indirect effect through the total number of tillers (2.416), panicle length (3.536) and decorticated grain width (3.698), whereas highly negative indirect effect through days to maturity (-1.288) and decorticated grain length (-1.605). It showed highly positive effect through plant height (0.824) and high negative effect through the productive number of tillers (-0.569). It had a low positive indirect effect through test weight (0.198).

Plant height had highly positive indirect effect (1.619, 2.677, 3.702) through the total number of tillers, panicle length, decorticated grain width, and negative indirect effect (-2.720, -2.314, -2.640, -1.737) through days to 50% flowering, the productive number of tillers, test weight, decorticated grain length respectively. Total number of tillers per plant showed highly positive indirect effect through panicle length (0.089) and decorticated grain width (2.180).

A very high and positive indirect effect on single plant yield was exhibited by the total number of tillers per plant (37.704), panicle length (1.304), and decorticated grain width (3.187) through the number of productive tillers per plant. A low and positive indirect effect was shown through plant height (0.119) and decorticated grain length (-0.180). The indirect effect of the number of productive tillers per plant through days to 50% flowering (-0.097) and days to maturity (0.003) were negligible. Panicle length possessed highly positive indirect effect through the total number of tillers (6.149), and highly negative indirect effect through days to 50% flowering (-2.695), productive number of tillers (-5.826), and decorticated grain width (-4.620) It exhibited highly positive indirect effect through plant height (0.618) and 1000 grain weight (0.307).

Test weight had highly positive indirect effect through the total number tillers (4.464), decorticated grain length (1.350) and decorticated grain width (7.610). It recorded highly negative indirect effect through productive number of tillers (-2.283) and highly positive indirect effect through plant height (0.498). A very high and positive indirect effect on yield was observed through total number of tillers (1.963), panicle length (3.049) and decorticated grain width (3.902). It showed a very high negative indirect effect through days to 50% flowering (-6.564) and decorticated grain length (-1.514).



A high and positive indirect effect on yield was exhibited by days to maturity through plant height (0.711). Decorticated grain length exhibited high positive indirect effect through days to 50% flowering (1.830) and the number of productive tillers per plant (1.203). It showed high positive and high negative indirect effects through days to maturity (0.338) and plant height (-0.600), respectively

A very high and positive indirect effect on single plant yield by decorticated grain width was recorded through the total number of tillers per plant (5.949). Highly positive effect was observed through plant height (0.556) and high negative indirect effect through days to maturity (-0.379). Similar results were obtained by Madhukar et al., (2017) and Maurya et al. (2018).

Therefore, the test weight exhibited a significant positive correlation from association studies, and test weight from path analysis exhibited a highly negative direct effect on single plant yield, it concluded that the decreasing of single plant yield when the test weight is increasing. Decorticated grain length showed a highly significant negative correlation and a highly positive direct effect on single plant yield. It depicts that the increase in decorticated grain length leads to an increase in single plant yield.

Formulae and equations

1. For each character, PCV and GCV were computed based on the methods given by Burton (1952).

a) Phenotypic coefficient of variation (%)

$$PCV = \frac{\sqrt{\text{Phenotypic variance}}}{\text{Grandmean}} \times 100$$

b) Genotypic coefficient of variation (%)

$$GCV = \frac{\sqrt{\text{Genotypic variance}}}{\text{Grandmean}} \times 100$$

2. Heritability (h²) in the broad sense was estimated according to Lush (1940).

$$h^2 \text{ (B.S.)} = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

3. Genetic advance was derived according to the method of Johnson et al., (1955) for each character under study.

$$\text{Genetic Advance (GA)} = k \times h^2 \times \sigma_p$$

4. Genetic advance was expressed as percentage of mean and classified by using the formula suggested by Johnson et al., (1955).

Genetic Advance as percentage of mean
 (GAM) = $\frac{\text{Genetic advance}}{\text{Grand mean}} \times 100$

5. Genotypic correlation coefficient:

$$r_{g(xy)} = \frac{COV g(xy)}{\sqrt{\sigma^2 g_x \times \sigma^2 g_y}}$$

6. Phenotypic correlation coefficient:

$$r_{p(xy)} = \frac{COV p(xy)}{\sqrt{\sigma^2 p_x \times \sigma^2 p_y}}$$

7. Path coefficient analysis:

The relative influence of yield components on yield by themselves (direct effects) and through other traits (indirect effects) was evaluated by the method of path coefficient analysis as suggested by Dewey and Lu (1959). The direct and indirect effects derived from path analysis were classified based on the scale given below (Lenka and Misra 1973).

Path coefficients range	Category
More than 1.00	Very high
0.30 to 0.99	High
0.20 to 0.29	Moderate
0.10 to 0.19	Low
0.0 to 0.09	Negligible

CONCLUSION

Based on the results of the present study it may be concluded that wide variation existed among the genotypes for the characters studied. So, there is enormous scope for the selection of genotypes with desirable traits for yield improvement. High to moderate PCV and GCV, high heritability with high genetic advance as percentage of mean were recorded for days to 50% flowering, plant height, total number of tillers, productive tillers per plant, days to maturity, test weight and single plant yield indicating

that these traits were controlled by the additive type of gene action. Correlation and path analysis showed that direct selection for characteristics such as plant height, test weight, total number of tillers, panicle length, decorticated grain length and decorticated grain width could increase single plant yield. Therefore, these traits may be focused on improving grain yield in rice.

Funding and Acknowledgment

The research work submitted for publication does not involve any external funding.

Ethics statement

Not applicable.

Originality and plagiarism

We (authors) ensure that the article was written and submitted using the results from of our original work, and the words of others that have been used were appropriately cited.

Consent for publication

All the authors agreed to publish the content.

Competing interests

There was no conflict of interest in the publication of this content.

Data availability

All the data of this manuscript are included in the MS. No separate external data source is required. If anything is required from the MS, certainly, this will be extended by communicating with the corresponding author through corresponding official mail: priyangars565@gmail.com

Author contributions

Idea conceptualization-DK,SG, Experiments- RSP, Guidance -DK,KA,SG, Writing original draft – RSP, Writing- reviewing & editing -RSP,DK,KA.

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