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Research Article

Studies on genetic diversity, correlation and path analysis in rice germplasm

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Abstract
The present investigation was carried out to explore the extent of divergence, correlation and path analysis in 77 rice genotypes for twelve characters during *Rabi*, 2021. Ten clusters were formed by Mahalanobis' D^2 analysis of which cluster I was the largest with 28 genotypes. Cluster IV and IX were the smallest with one genotype each. The maximum intra-cluster distance was observed between cluster X and the maximum inter-cluster distance was between clusters VIII and X. The days to 50 % flowering contributed to the maximum divergence. Superior mean performance for grain yield per plant was recorded in cluster IX. The grain yield per plant was found to be positively correlated with the days to 50 % flowering, the total number of tillers, the total number of productive tillers, panicle length, leaf width, the total grains per panicle, filled grains per panicle and spikelet fertility. Path analysis results revealed that the total number of productive tillers, leaf width, filled grains per panicle, days to 50% flowering, the total grains per panicle and spikelet fertility had a positive direct effect with grain yield. The selection should be done for these traits for yield improvement.

Keywords: Rice, germplasm, genetic diversity, correlation, path analysis.

INTRODUCTION

Rice (*Oryza sativa* L.) is the staple food crop globally consumed by more than half of the world population. Asia alone produces 705.39 million tonnes of rice, accounting for more than 90 % of global rice output of 782 million tonnes**.** In India, rice is grown over a total area of 43.66 million hectares with a production of 118.87 million tonnes and a yield of 2.7 tonnes per hectare (India stat, 2020). Tamil Nadu is one of the major rice producing states in India with an area of 19.00 lakh hectares and production and productivity of 68.66 lakh metric tonnes and 3.61 tonnes/hectare, respectively. Rice is a vital source of food security accounting for more than 40% of food grain production in India. Rice also plays a pivotal role in nutrition, employment, economy, culture and history besides being a staple food crop in India. The current rice production scenario is threatened by population growth, which is expected to reach 1824 million by 2050. This has to be achieved with production constraints such as an increase in temperature, erratic rainfall due to climate, shortage of human labour, urbanization of farm lands, plateauing trend observed in rice varieties due to narrow genetic base.

India offers a wide range of diversity and variability that can be used to expand rice's genetic base. Tamil Nadu has long been known as a rice-growing region with a complex ecosystem and diverse genetic pool. Landraces are important germplasm because they contain a diversified set of adaptation genes, and their incorporation could assure a broad genetic base (Mondal *et al*., 2016).

Plant genetic diversity has been measured using morphological and quantitative characteristics. The Mahalanobis' D^2 statistics is a useful tool for finding clustering patterns, establishing a link between genetic and geographical divergence, and studying the roles of various quantitative features in determining maximum divergence (Murthy and Arunachalam, 1966).

Knowledge of the relationship between yield and its attributing qualities is essential for the selection process, which may be explained using correlation and path coefficient analysis, in order to generate high yielding varieties with broad adaptability. The correlation coefficient-based character association aids in evaluating the relative effect of various component traits on grain yield, whereas path analysis explains whether the association of dependent character with the independent variables is due to their direct or indirect effects via other traits. Correlation just assesses the relationship between two variables whereas path coefficient analysis evaluates the direct and indirect causes of association (Dewey and Lu, 1959).

Therefore, the present study was aimed at assessing the genetic diversity, correlation and the direct and indirect effects of various component traits on grain yield in the traditional landraces of rice to provide a basis for selection and yield improvement.

MATERIALS AND METHODS
The experimental material used in the present study comprised of 72 traditional landraces of rice, two advanced cultures and three checks (**Table 1**) collected from the Department of Rice, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore for evaluation. The genetic material was raised at the Department of Rice during *Rabi,* 2021 in Randomized Block Design (RBD) in two replications for assessing the genetic diversity. Each germplasm was grown in a plot size of 3 m² with a spacing of 20 x 20 cm. Single seedling per hill was maintained. Recommended package of practices was followed for the successful establishment of the crop. Data on the quantitative traits *viz*., plant height (cm), the total number of tillers per plant, the total number of productive tillers per plant, panicle length (cm), leaf length (cm), leaf width (cm), the total number of grains per panicle, filled grains per panicle, spikelet fertility (%), thousand grain weight (g) and single plant yield (g) were recorded in five randomly tagged plants in each genotype in each replication.

The mean data recorded for various biometrical traits were subjected to statistical analysis using Mahalanobis D·statistic (Mahalanobis, 1936) and Tocher's method for determining group constellation. The D·statistics, correlation and path analysis were computed using the GENRES software.

RESULTS AND DISCUSSION
The analysis of variance (ANOVA) revealed that the genotypes differed significantly for all the characters under investigation indicating the existence of variation among the genotypes. Based on Tocher's cut off value, the Mahalanobis D^2 analysis divided 77 genotypes into ten clusters (**Table 2**). Cluster I was the largest, populated by 28 genotypes, followed by cluster II with 24 genotypes. There were 10 genotypes in cluster III. Cluster V had four genotypes followed by cluster VI which had three genotypes. The clusters VII, VIII and X had two genotypes each. The smallest and solitary clusters were IV and IX. The divergent nature of the genotypes used in the present study is indicated by the distribution of 77 genotypes into 10 clusters. The existence of genetic divergence in the rice germplasm was earlier reported by Sri Lakshmi *et al.* (2021) and Rukmini Devi *et al.* (2020). Grouping of genotypes into various clusters was random and this randomness in a grouping may be attributed towards the interchange of genetic material across locations which by natural as well as human selection have consequently increased the genetic diversity.

The genotypes grouped within the same cluster showed a narrow genetic divergence and would be almost genetically similar, and the genotypes in different clusters exhibited a wider range of genetic variability. The typical intra and inter cluster distances are shown in **Table 3**. The intra cluster distance ranged from 257.798 (cluster X) to 112.840 (cluster V). Hence, the genotypes in cluster X were more dissimilar among them or in other words had maximum divergence among the genotypes within that cluster followed by cluster VII (232.802), cluster VIII (228.322), cluster VI (156.333), cluster I (155.533), cluster II (144.588), cluster III (128.625) and finally cluster V (112.840).

The highest inter-cluster distance was found between clusters VIII and X (2417.340) followed by clusters VII and VIII (2237.628). The genotypes present in these two clusters exhibited maximum genetic distance. The minimum inter cluster distance was observed between clusters II and IV (244.891) followed by clusters I and III (262.094) indicating the close proximity and hence, the lower values of genetic distances indicate the similarities of the genotypes falling between the clusters. The maximum amount of heterosis may be harnessed by selecting parents from genetically divergent clusters. In the recombination breeding programme, highly heterotic F_1 and a broad spectrum of transgressive segregants

Table 1. List of 77 rice genotypes used in this study

Code	Landraces	Code	Landraces	Code	Landraces
L1	Sarapillisamba	L27	Sadai Samba	L53	Karunkuruvai
L2	Manavari	L28	KaruppuKavuni	L54	Burma Black
L3	ArupathamKuruvai	L29	Mysore Malli	L55	SornaKuruvai
L4	Panamara Samba	L30	Atthurkichali Samba	L56	Thogai Samba
L5	Arupatham Samba	L31	Seeraga Samba	L57	Malayalathan Samba
L6	Senthooram	L32	Thooyamalli	L58	Kattikar
L7	Channangi	L33	Mapillai Samba	L59	Mattakuruvai
L8	Poongar	L34	Arcotkitchali	L60	Red Sirumani
L9	Poongar selection	L35	Illupam poo samba	L61	Senkar
L10	Sembarai	L36	Basumathi	L62	Kalvalai
L11	Sembarai	L37	NalanNamak	L63	Rasagadam
L12	Varigarudam Samba	L38	Milagu samba	L64	Godavari samba
L13	Varigarudam Samba Selection	L39	VasanaiSeeraga Samba	L65	Kalarkar
L14	Pamani Samba	L40	Ghandasali	L66	Kadaikuluthan
L15	Uppumolagi	L41	Kuzhiyadichan	L67	Vadivel
L16	Katta Samba	L42	ThulasiVasanai samba	L68	Kaliyan Samba
L17	Karthigai Samba	L43	Thengai Poo samba	L69	Kallimadayan
L18	Karthigai Samba II	L44	ChinnaAdukku nell	L70	Karungan
L19	Purple puttu	L45	Kaviya Samba	L71	Sembala
L20	Rangoon Samba	L46	Norungan	L72	Vellaikudaivazhai
L21	Muthuvellai	L47	Kavuni	L73	CO51
L22	Chetty Samba	L48	KuruvaiKalanjiam	L74	CO52
L23	Chittan Samba	L49	Kothamalli Samba	L75	CR1009 Sub 1
L24	Gandhasala	L50	Nootripathu	L76	CB 12132
L25	Murugankar	L51	Mattaikar	L77	CB 12122
L26	Karuthakar	L52	Kallukar		

Table 2. Distribution of rice genotypes in to ten clusters

Cluster Number	Number of genotypes	Landraces
I	28	L3, L49, L47, L5, L20, L22, L43, L13, L26, L58 L32, L16, L37, L14, L40, L12, L10, L53, L23, L63, L11, L59, L27, L18, L55, L36, L39, L19
II	24	L64, L66, L52, L31, L57, L3, L56, L65, L60, L7, L68, L1, L69, L51, L67, L2, L34, L29, L50, L24, L8, L62, L71, L61
III	10	L72, L70, L15, L21, L25, L48, L28, L54, L4, L17
IV	1	L9
V	4	L74, L76, L30, L77
VI	3	L42, L45, L41
VII	2	L46, L35
VIII	2	L44, L38
IX	1	L75
X	2	L6, L73

can be obtained in the segregating generations by attempting crosses between genotypes in clusters VIII and X followed by clusters VII and VIII. On the contrary, effecting crosses between genotypes of genetically homogeneous clusters will narrow down the genetic base. Similar findings were reported by Rukmini Devi *et al.* (2020) and Lahari *et al.* (2017).

Table 3. Intra (bold) and inter cluster distance of seventy-seven rice germplasm for 12 traits

Cluster number	I	II	III	IV	V	VI	VII	VIII	IX	X
I	**155.533**	307.739	262.094	285.058	369.110	411.074	633.385	814.079	819.607	913.854
II		**144.588**	270.862	244.891	633.020	879.281	369.069	1604.834	1469.450	748.074
III			**128.625**	321.581	740.690	601.979	841.399	1146.570	1377.160	1178.792
IV				**0**	701.410	493.428	482.889	1246.238	1161.630	1273.100
V					**112.840**	663.419	689.150	854.380	419.138	596.271
VI						**156.333**	1396.927	324.938	499.466	1945.795
VII							**232.802**	2237.628	1647.640	542.089
VIII								**228.322**	414.322	2417.340
IX									**0**	1712.847
X										**257.798**

Table 4. Cluster mean for different quantitative traits

CLUSTER	PH	DFF	TNT	TNPT	PL	LL	LW	TGP	FGP	SF	TGW	SPY	PH
I	120.66	91.87	15.62	12.89	22.76	37.88	1.25	115.54	70.70	59.69	22.06	16.57	120.66
II	130.97	81.77	16.63	14.57	22.73	31.67	1.23	110.10	65.44	58.04	21.71	18.58	130.97
III	127.27	87.25	16.13	13.42	22.96	35.51	1.22	109.08	64.93	58.25	27.03	19.18	127.27
IV	160.84	87.50	12.80	10.00	30.52	36.54	1.27	141.20	89.3	60.47	20.96	18.56	160.84
V	96.50	97.50	22.16	15.72	23.11	27.98	1.38	107.46	65.33	59.27	16.36	30.47	96.50
VI	141.85	104.66	15.71	12.46	23.39	38.91	1.16	124.10	77.13	56.95	23.86	21.05	141.85
VII	129.82	78.25	15.80	13.75	24.09	34.37	1.08	92.10	46.90	51.59	13.92	19.39	129.82
VIII	111.64	114.50	18.67	15.55	26.46	37.17	1.27	131.50	84.05	60.33	24.47	19.02	111.64
IX	113.55	114.50	17.15	12.45	20.95	24.70	1.67	92.13	44.05	48.05	16.16	36.23	113.55
X	74.475	80.75	20.95	17.62	20.05	26.20	1.74	80.98	50.93	64.09	13.68	26.21	74.47

PH-plant height (cm), DFF-Days to 50 % flowering, TNT-Total number of tillers, TNPT-Total number of productive tillers, PL-Panicle length (cm), LL-Leaf length (cm), LW-Leaf width (cm), TGP-Total grains per panicle, FGP-Filled grains per panicle, SF-Spikelet fertility (%), TGW-Thousand grain weight (g), SPY-Single plant yield (g).

Based on the cluster mean value (**Table 4**), it was observed that genotype in cluster IV exhibited the highest plant height (160.84 cm), the total number of grains per panicle (141.20), the total number of filled grains per panicle (89.30) and panicle length (30.52 cm). The genotypes in cluster X had the highest total number of productive tillers (17.62), leaf width (1.74) and spikelet fertility (64.09%). Cluster VII had the earliest flowering genotypes (78.25 days) followed by cluster X (80.75 days). Cluster V had the maximum total number of tillers (22.16) followed by cluster X (20.95). Cluster VI had the highest leaf length (38.91 cm) followed by cluster I (37.88 cm). The cluster IX recorded the maximum single plant yield (36.23 g) followed by cluster V (30.47 g) and cluster III recorded the highest thousand grain weight (27.03 g) followed by cluster VIII (24.47 g). None of the clusters possessed genotypes with all the desirable traits for direct selection and utilization in the crop improvement programmes. This is in conformity with the reports of Ranjith *et al.* (2018) and Kavurikalpana *et al*. (2018). It is always preferable to look for genotypes belonging to different clusters with many desired traits.

The contrasting genotypes for plant height were found in the IV and X, for days to 50% flowering in VII and VIII and IX, for the total number of tillers in V and IV, for the total number of productive tillers in X and IV, for panicle length in IV and X, for leaf length in VI and IX, for leaf width in X and VII, for total grains per panicle in IV and X, for filled grains per panicle in IV and IX, for spikelet fertility in X and IX, for 1000 grain weight in III and X and for single plant yield in IX and I. Thus, the lowest and highest cluster mean values for different traits were present in different clusters. Hence, lines with specific traits can be selected from different clusters for trait-based crop improvement programmes.

Based on the percentage contribution of different quantitative traits to the genetic divergence presented in **Table 5**, it was noticed that the maximum contribution was recorded by days to 50 % flowering (43.57 %) followed by thousand grain weight (34.27 %) and plant height (17.70 %). These observations were in agreement with the report of Kumari *et al.* (2018) and Rashmi *et al.* (2017) for days to 50% flowering; Sowmiya and Venkatesan

Table 5. Contribution of different quantitative characters towards genetic divergence among 77 germplasm of rice

S.NO.	CHARACTER	CONTRIBUTION (%)
1	Plant height	17.70
2	Days to 50 % flowering	43.57
3	Total number of tillers	0.11
4	Total number of productive tillers	1.11
5	Panicle length	0.06
6	Leaf length	2.11
7	Leaf width	0.10
8	Total grains per panicle	0.10
9	Filled grains per panicle	0.06
10	Spikelet fertility SF	0.10
11	Thousand grain weight	34.27
12	Single plant yield	0.71

(2017) for hundred grain weight. Hence, these traits may be given importance during the selection of parents for hybridization and selection in segregating generations.

The single plant yield showed a positive and significant correlation with the days to 50% flowering (0.209), the total number of tiller (0.183), the total number of productive tillers (0.334), panicle length (0.263), leaf width (0.436), total grains per panicle (0.312), filled grains per panicle (0.224) and spikelet fertility (0.576) (**Table 6**). These observations were supported by the earlier findings of Priya *et al*. (2017) for plant height along and Seneega *et al*. (2019) for the number of productive tillers per plant. Seneega *et al*. (2019) reported the characters plant height, the number of productive tillers, panicle length and grains per panicle exhibited significant and positive association with plant yield. In contrast, there was a negative and significant correlation of single plant yield with plant height

(-0.210), leaf length (-0.250) and thousand grain weight (-0.240). Plant height exhibited a highly significant positive correlation with panicle length (0.242), total grains per panicle (0.240), filled grains per panicle (0.215) and thousand grain weight (0.268). Similar findings were supported by Sreedhar and Reddy (2019) and Priyanka *et al*. (2016) for panicle length. It is also highly significant and negatively correlated to the total number of tillers (-0.279). Days to 50 % flowering was displaying a significant positive association with the number of grains per panicle (0.182), filled grains per panicle (0.160*) and panicle length (0.200) indicating that the increase in the duration of the genotypes would enhance the length of the panicles as well as the number of grains and filled grains per panicle. Similar results were reported by Sahanabnath and Kole (2021) and Sreedhar and Reddy (2019) for the total number of grains per panicle and Umarani *et al.* (2019) for panicle length.

Table 6. Correlation analysis among yield and yield component traits in rice

Characters	PH	DFF	TNT	TNPT	PL	LL	LW	TGP	FGP	SF	TGW	SPY
PH	1											
DFF	-0.059	1										
TNT	-0.279 **	0.045	1									
TNPT	-0.151	-0.076	0.808 **	1								
PL	0.242 **	0.2 *	0.070	-0.029	1							
LL	0.109	0.133	-0.059	-0.040	-0.004	1						
LW	-0.133	0.157	0.165 *	0.117	0.135	-0.113	1					
TGP	0.240 **	0.182 *	-0.056	0.006	0.342**	0.046	0.066	1				
FGP	0.215 **	0.160 *	-0.029	0.037	0.172 *	-0.003	0.104	0.889 **	1			
SF	0.066	0.048	0.017	0.063	0.237**	-0.093	0.127	0.441 **	0.775 **	1		
TGW	0.268 **	0.052	-0.251 **	-0.195 *	-0.028	0.377 **	-0.188 *	0.047	0.042	0.005	1	
SPY	-0.210 **	0.209 **	0.183*	0.344**	0.263**	-0.250 **	0.436**	0.312**	0.224**	0.576**	-0.240**	1

*and ** indicates significant at 5% and 1% level respectively, PH-plant height, DFF-Days to 50 % flowering, TNT-Total number of tillers, TNPT-Total number of productive tillers, PL-Panicle length, LL-Leaf length, LW-Leaf width, TGP-Total grains per panicle, FGP-Filled grains per panicle, SF-Spikelet fertility, TGW-Thousand grain weight, SPY-Single plant yield.

Table 7. Partitioning of correlation into direct and indirect effects by path analysis

Characters	PH	DFF	TNPT	TNT	PL	LL	LW	TGP	FGP	SF	TGW	Correlation for SPY
PH	**-0.0194**	-0.0097	-0.1133	0.0284	-0.0035	-0.0220	-0.0453	0.0167	-0.0359	0.0035	-0.0097	-0.210 **
DFF	0.0011	**0.1642**	0.0185	0.0144	-0.0029	-0.0266	0.0539	0.0126	-0.0267	0.0025	-0.0019	0.209 **
TNPT	0.0054	0.0075	**0.4050**	-0.1523	-0.0010	0.0119	0.0565	-0.0039	0.0049	0.0009	0.0090	0.183*
TNT	0.0028	-0.0124	0.3224	**-0.1854**	0.0004	0.0079	0.0398	0.0004	-0.0030	0.0032	0.0069	0.344**
PL	0.0947	0.0528	0.0285	0.0056	**-0.0146**	0.0508	0.0463	0.0106	-0.0287	0.0140	0.0010	0.263**
LL	-0.0021	0.0219	-0.0242	0.0076	0.0006	**-0.2001**	-0.0386	0.0032	0.0005	-0.0049	-0.0136	-0.250 **
LW	0.0025	0.0260	0.0672	-0.0223	-0.0020	0.0227	**0.3425**	0.0046	-0.0185	0.0067	0.0068	0.436**
TGP	-0.0046	0.0299	0.0750	0.0980	0.1577	-0.0092	0.0225	**0.0695**	-0.1483	0.0232	-0.0017	0.312**
FGP	-0.0041	0.0263	-0.0120	-0.0880	-0.0025	0.0006	0.0357	0.0619	**0.1667**	0.0409	-0.0015	0.224**
SF	-0.0013	0.0080	0.2370	0.3180	-0.0019	0.0188	0.0436	0.0306	-0.1293	**0.0527**	-0.0002	0.576**
TGW	-0.0052	0.0086	-0.1017	0.0367	0.0004	-0.0755	-0.0645	0.0033	-0.0071	0.0002	**-0.0361**	-0.240**

Residual effect =0.2659

PH-plant height, DFF-Days to 50 % flowering, TNT-Total number of tillers, TNPT-Total number of productive tillers, PL-Panicle length, LL-Leaf length, LW-Leaf width, TGP-Total grains per panicle, FGP-Filled grains per panicle, SF-Spikelet fertility, TGW-Thousand grain weight, SPY-Single plant yield

The total number of tillers was highly significant and positively correlated with the total number of productive tillers (0.808) and significantly correlated with leaf width (0.165). It was negatively correlated with thousand grain weight (-0.251). The total number of productive tillers exhibited a negative correlation with thousand grain weight (-0.195). The panicle length exhibited a highly significant and positive correlation with the total grains per panicle (0.342), spikelet fertility (0.237) and significantly correlated with filled grains per panicle (0.172). The leaf length was highly significant and positively correlated with thousand grain weight (0.377). The leaf width was significant and negatively correlated with thousand grain weight (-0188). The total grains per panicle was highly significant and positively correlated with filled grains per panicle (0.889) and spikelet fertility (0.441). Filled grains per panicle exhibited a highly significant and positive correlation with spikelet fertility (0.775). Significantly positive intercorrelation among the total grains per panicle, filled grain per panicle, spikelet fertility and with that yield shows that improvement in these traits will enhance the yield and hence these traits may be given due importance in the selection process.

Path coefficient analysis revealed a positive direct effect between single plant yield and the total number of productive tillers (0.4050), leaf width (0.3425), filled grains per panicle (0.1667), days to 50 % flowering (0.1642), total grains per panicle (0.0695) and spikelet fertility (0.0527**) (Table 7**). Similar findings were reported by Umarani *et al*. (2019); Patil *et al*. (2015), Ashok *et al*. (2016), Chuchert *et al*.(2018), Tejaswini *et al*.(2018), Pankaj Garg *et al*. (2010), Babu *et al*.(2012) and Umarani *et al*.(2019). A negative direct effect on grain yield per plant

was observed in leaf length (-0.2001), the total number of tillers (-0.1854), thousand grain weight (-0.0361), plant height (-0.0194) and panicle length (-0.0146) which is similar to results obtained by Prasad *et al*. (2001).

The total number of tillers had a positive indirect effect on plant yield *via* the total number of productive tillers (0.3224) followed by spikelet fertility *via* the total number of tillers (0.3180) and spikelet fertility *via* the total number of productive tillers (0.2370) and finally the total grains per panicle *via* panicle length (0.1577). Moreover, thousand grain weight had a negative indirect effect *via* the total number of productive tillers on the single plant yield (-0.1017).

Finally in conclusion, the cluster X had the highest intra-cluster distance and the genotypes have the maximum diversity within the cluster and the highest inter-cluster distance was found between clusters VIII and X which implies that these two clusters are more diverse and crossing programmes would be effective between the genotypes within these clusters. The total number of productive tillers had the positive direct effect on yield followed by filled grains per panicle and the total number of tillers had a positive indirect effect on plant yield *via* the total number of productive tillers and also spikelet fertility *via* the total number of tillers and productive tillers and thus selection for these traits would help increase the plant yield.

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