

## Multivariate analysis and character association for agromorphological traits in elite rice germplasm

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### Abstract

The investigation was carried out in fifty elite rice genotypes to understand the association among the yield and yield related components, their direct and indirect effects on the grain yield using correlation and path analysis and the genetic divergence was assessed using multivariate analysis. Significant differences were observed among all the genotypes for the traits studied. High amount of heritability and genetic advance were observed for plant height, number of tillers per plant, number of productive tillers per plant, panicle weight and number of filled grains per panicle. Character association at both genotypic and phenotypic level revealed significant positive association of grain yield per plant with test weight. Path coefficient analysis revealed that number of productive tillers had highest direct positive effect on grain yield per plant followed by plant height and panicle length. Principal component analysis showed that a cumulative variance of 45% from PC1 attributed by number of tillers per plant, number of productive tillers per plant and days to fifty percent flowering would be beneficial in contributing to the total morphological diversity. The cluster analysis based on euclidean distance and neighbor joining method grouped the genotypes into six clusters. Cluster II constituted maximum number of genotypes (n=15) followed by cluster VI with ten genotypes. Thus the traits which contribute to maximum divergence can be focused in selection and divergent genotypes present in the different clusters can be utilized for further improvement in future breeding programmes.

**Key words:** Rice, Correlation, Path analysis, PCA, Cluster analysis

## 1. Introduction

Rice (*Oryza sativa* L.) is one of the important major staple cereal crops, feeding more than half of the world population (Shivani *et al.*, 2021). In view of the rapidly growing global population, the basic objective of the plant breeders has been yield improvement in the staple food crops like rice. It has been estimated that rice production in India needs to be increased to 121.2 million tonnes by the year 2030 (Kumar *et al.*, 2014), from the present level of 112.76 million tonnes (2017-18) to withstand self-sufficiency

in rice (DoE&S, 2019). Therefore, increase in production of rice plays an important role in food security and poverty alleviation. Breeding of high yielding varieties with wide adaptability is the ultimate aim of the plant breeders, and the knowledge on genetic variability for the trait under improvement is of great significance for the success of any plant breeding programme.

The heritability and genetic advance are the most important selection parameters as heritability estimates



along with genetic advance are more helpful in predicting the gain under selection. Heritability along with the genetic advance should be used in predicting the ultimate effect for selecting superior varieties (Ali *et al.*, 2002). The correlation and path analysis determines the association between yield and its components and also brings out the relative importance of their direct and indirect effects with grain yield. Essentially, this method of analysis could benefit the breeder to choose appropriate selection strategies to improve grain yield.

Multivariate analytical tools are widely used in describing the inherent variation among crop genotypes. These tools includes principal component analysis and cluster analysis. Principal component analysis has employed for identifying the importance and contribution of each component to the total variance (Noirot *et al.*, 1996) and it has been successfully used in the evaluation of crop germplasm for understanding the relationship and correlation among the variables studied (Zafar *et al.*, 2008). Cluster analysis has been employed to classify the available genotypes

into distinct groups on the basis of their genetic diversity. Based on these points, the present study was carried out with the objective of studying the genetic variability, trait relationship associations and genetic diversity among fifty elite rice genotypes.

## 2. Material and methods

The material for the present study consisted of 50 elite genotypes (released varieties) of rice maintained at ICAR-Indian Institute of Rice Research, Rajendranagar, Hyderabad, Telangana, India (Table 1). The experiment was laid out in randomized block design with two replications during *Kharif*, 2019. All the cultural practices were followed as per the package of practices adopted for rice. Observations were recorded on five randomly selected plants in each replication for days to 50 per cent flowering, plant height, panicle length, number of tillers per plant, number of productive tillers per plant, panicle weight, number of filled grains per panicle, number of unfilled grains per panicle, test weight and grain yield per plant.

Table 1. List of elite rice cultivars used in the study

S.No	Designation	S.No	Designation
G1	Improved Samba Mahsuri (RP Bio 226)	G26	ORJ 1338
G2	RP 6113-Patho BB-12 (GSY-BB-IPB-2-12)	G27	RP 6224-GSR IR1-5-S10-D3-Y2
G3	JGL 24423	G28	Gontra Bidhan 3
G4	IR 95797-CR3847-2-1-1-1-1	G29	CRR 484-2-1-1-1-1
G5	JGL 21078	G30	JR 206
G6	TRC-2015-7	G31	RP 6264-HHZ 10-DT7-Y1
G7	RP 5865-300-4-1-1-1-2-3	G32	RNR 11718
G8	NDRK 50065	G33	RP 6265-GSR IR 1-5-S12-D3-Y2
G9	RP 5208-3 (IR87707-445-B-B-B)	G34	RP 6189-HHZ 17-Y16-Y3-SAL1
G10	CSR 49 (CSR 2K 242)	G35	CSR RIL-01-IR 165
G11	OR(T)-35	G36	RP 6112-MS-T193-5-22-55-33-1-3
G12	CR 2459-26-2-1-1-S-B1-2B-1	G37	TRC 2015-5
G13	RP 5955-15-1-1-1-1	G38	RCPR 22-IR84899-B-183-20-1-1-1
G14	CR 3997-8-IR 91648-B-89-B-5-1	G39	CR 3996-11-240-3-1
G15	Rewa 1121-475-15-1-1	G40	RP 5943-421-16-1-1-B
G16	AAGP 9412	G41	MTU 1212 (MTU2223-5-2-2-1-1)
G17	RP 5898-101-3-2-1-1	G42	RCPR 17-IR 83929-B-B-291-3-1-1
G18	RP 5950-24-6-2-1-1-B	G43	AD 13116
G19	CB 12 186	G44	KJT 20-1-7-14-9
G20	CB 13 168	G45	RP 5977-MS-M-42-1-9-4-2-35-8-6
G21	YNP 7060	G46	MTU 1263
G22	CN 1222-11-8-7	G47	RP 6221-HHZ 8-SAL9-DT2-Y2
G23	Improved Dokra-Dokri	G48	KMP 222
G24	Telangana Sona (RNR 15048)	G49	R-RHZ-MI-81
G25	MTU 1010	G50	OR(CZ)-9-1



Data of the above traits were subjected to statistical analysis viz, Analysis of variance (ANOVA), genetic variability components such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability ( $h^2$ ) and genetic advance as percent mean (GAM). Correlation coefficients were calculated using the formulae suggested by Falconer (1964) and path analysis by Dewey and Lu (1959). The genotypes were grouped into different clusters by applying euclidean distance and neighbor joining method. Principal component analysis (PCA) and principal component score were derived using the software SAS version 9.3 to reveal the best relationships among traits.

### 3. Results and Discussion

In any crop the genetic variability is a pre-requisite for selection of superior genotypes. In the present study, variance analysis for all the characters studied revealed

significant variation among the genotypes (Table 2). High GCV was observed for the traits, number of tillers per plant, number of productive tillers per plant, panicle weight, number of filled grains, test weight and single plant yield. Similar results were reported by Lakshmi *et al.*, (2017) for number of tillers per plant, by Nandeshwar *et al.*, (2015) for panicle weight and by Sameera *et al.*, (2015) for single plant yield. For all the characters under the study, phenotypic coefficient of variation (PCV) in general was higher than genotypic coefficient of variation (GCV) indicating the influence of environment on the manifestation of these characters. However, the difference between the PCV and GCV was less for the characters, days to 50 per cent flowering, plant height, number of tillers, number of filled grains per panicle, test weight and single plant yield indicating low environmental influence and predominance of genetic factors controlling variability in these traits (Table 3).

Table 2. Analysis of variance (ANOVA) for yield and yield components in elite rice genotypes

Sl. No.	Character	Mean sum of square
1	Days to 50 % flowering	112.46**
2	Plant height	360.28**
3	Panicle length	8.24**
4	Number of tillers	9.89**
5	Number of productive tillers	6.43**
6	Panicle weight	0.47**
7	Number of filled grains	1068.33**
8	Number of unfilled grains	1655.44**
9	Test weight	53.99**
10	Single plant yield	31.08**

\*\* Significant at 1 % level of probability

Table 3. Genetic variability parameters for ten yield components in 50 elite rice genotypes

Characters	Mean	Range		GCV %	PCV %	Heritability ( $h^2$ )	GAM
		Min	Max				
DFF	93.99	82	115	7.94	8.02	97.96	16.20
PH	93.99	66	135.1	14.03	14.51	93.43	27.94
PL	21.98	16.1	29	7.54	10.66	50.12	11.01
NT	11.46	7	18	19.22	19.59	96.21	38.84
NPT	10.53	7	15	16.67	17.39	91.93	32.94
PW	2.249	1.11	3.81	20.42	22.76	80.54	37.76
NFG	95.17	51	163	24.15	24.41	97.80	49.20
NUFG	33.81	2	180	78.93	91.31	74.73	140.57
TW	21.59	12.68	42.27	24.05	24.06	99.92	49.54
SPY	18.19	10.51	26.03	21.57	21.74	98.46	44.11

DFF: Days to 50% flowering; PH: Plant height; PL: Panicle Length; NT: Total number of tillers per plant; NPT: Number of productive tillers per plant; PW: Panicle weight; NFG: Number of filled grains per panicle; NUGF: Number of unfilled grains per panicle. TW: Test weight; SPY: Single plant yield; PCV: Phenotypic coefficient of variation; GCV: Genotypic coefficient of variation;  $h^2$ : Heritability; GAM: Genetic advance as percent mean.



The information of genetic variability alone will not be of much use to the breeder unless it is supplemented with the information on heritability, which gives a measure of the heritable portion of the total variation (Fiyaz *et al.*, 2011). Genetic advance is dependent on phenotypic variability and heritability in addition to selection intensity, so the heritability estimates in conjunction with genetic advance will be more effective and reliable in predicting the response to selection (Johnson *et al.*, 1955). Heritability in broad sense includes both additive and non-additive gene effects (Hanson *et al.*, 1956). While, narrow sense heritability includes only additive components (Johnson *et al.*, 1955). In the present study, heritability in broad sense was estimated. Highest broad sense heritability was reported in the case of days to fifty percent flowering, plant height, number of tillers, number of productive tillers, panicle weight, number of filled grains per panicle, test weight and single plant yield. However, medium heritability estimates were observed in panicle length. The expected genetic advance over mean of the characters was found to be highest for plant height, number of tillers, number of productive tillers, panicle weight, number of

filled grains per panicle, test weight and single plant yield. These results are in conformity with Devi *et al.*, (2016), Lakshmi *et al.*, (2017) for plant height, number of filled grains per panicle and 1000 seed weight, Satish *et al.*, (2017) for panicle weight, Karande *et al.*, (2015), Lakshmi *et al.*, (2017) for single plant yield. This study clearly showed that there is ample scope to improve these traits through selection.

### 3.1 Correlation between characters

Selection based on the direction and magnitude of association between yield and its attributes is very important in identifying the key characters, as this information can be exploited for crop improvement through designing suitable breeding programmes. Phenotypic and genotypic correlations between yield and yield components *viz.*, days to 50 per cent flowering, plant height, panicle length, number of tillers per plant, number of productive tillers per plant, panicle weight, number of filled grains per panicle, number of unfilled grains per panicle, test weight and single plant yield were computed separately for the rice genotypes considering in this study. The results are presented in table 4.

Table 4. Genotypic and phenotypic correlation coefficients among ten yield components in 50 elite rice genotypes. Upper diagonal correlations are genotypic correlations and lower diagonal correlations are phenotypic correlation.

Traits	DFF	PH	PL	NT	NPT	PW	NFG	NUFG	TW	SPY
DFF	1	0.04	-0.111	0.067	0.106	-0.006	0.045	0.573**	-0.415**	-0.475**
PH	0.032	1	0.228*	0.012	0.038	0.153	-0.119	-0.054	0.281**	0.081
PL	-0.066	0.227*	1	-0.041	0.01	0.235*	-0.231*	0.02	0.488**	0.183
NT	0.069	0.011	0.003	1	0.95**	-0.108	-0.091	0.132	-0.207*	-0.073
NPT	0.1	0.038	-0.014	0.884**	1	-0.071	-0.047	0.053	-0.146	-0.049
PW	0.005	0.158	0.215*	-0.103	-0.049	1	0.397**	0.427**	0.095	-0.102
NFG	0.045	-0.115	-0.156	-0.085	-0.052	0.37**	1	0.092	-0.562**	-0.256*
NUFG	0.497**	-0.032	-0.032	0.082	0.071	0.343**	0.059	1	-0.315**	-0.319**
TW	-0.409**	0.272**	0.347**	-0.203*	-0.139	0.087	-0.556**	-0.271**	1	0.274**
SPY	-0.465**	0.073	0.142	-0.069	-0.05	-0.093	-0.249*	-0.295**	0.271**	1

\* and \*\* Indicate significance at 5% and 1% levels respectively; DFF: Days to 50% flowering; PH: Plant height; PL: Panicle Length; NT: Total number of tillers per plant; NPT: Number of productive tillers per plant; PW: Panicle weight; NFG: Number of filled grains per panicle; NUGF: Number of unfilled grains per panicle. TW: Test weight; SPY: Single plant yield.

Grain yield per plant was significant positively correlated with test weight at genotypic (0.274) and phenotypic (0.271) level. Test weight showed significant and positively correlation with panicle length and plant height. Similar findings were reported by Ashok *et al.*, (2016); Kalyan *et al.*, (2017); Lakshmi *et al.*, (2017) and Priya *et al.*, (2017). Significant positive association also observed for panicle weight with panicle length and number of filled grains

both at phenotypic and genotypic levels. Other yield components *viz.*, plant height (0.081) and panicle length (0.183) showed non-significant positive association with grain yield at genotypic level. Similar findings were earlier reported by Madhavalatha *et al.*, 2005, Tejaswini *et al.*, 2016 for plant height and Madhavalatha *et al.*, 2005, Krishna *et al.*, 2008 and Seyoum *et al.*, 2012 for panicle length. While a negative association was found with days to fifty percent



flowering, number of tillers, number of productive tillers, panicle weight, number of filled grains and number of unfilled grains per panicle.

### 3.2 Path coefficient analysis

The simple correlation does not provide the true contribution of the characters towards the grain yield. The genotypic correlations were partitioned into direct and indirect effects through path coefficient analysis, which allows separation of the direct effect and their indirect effects through other attributes by apportioning the correlations (Wright, 1921) for better interpretation of cause and effect relationship. The estimates of path coefficient analysis are furnished for yield and yield

component characters in table 5. Among the characters studied at the genotypic level, number of productive tillers (0.904) had highest direct positive effect on grain yield per plant followed by plant height (0.130) and panicle length (0.128). At the phenotypic level, with respect to positive direct effect, the contribution to grain yield per plant by number of productive tillers per plant (0.218) was the highest followed by panicle length (0.116), plant height (0.077) and panicle weight (0.044). On the other hand, direct negative effect to grain yield was recorded by test weight, number of tillers per plant, number of filled grains per panicle, number of unfilled grains per panicle and days to fifty percent flowering.

Table 5. Genotypic and phenotypic path analysis of direct (diagonal) and indirect effects of various traits on plot

Traits	Genotypic/ Phenotypic	DFF	PH	PL	NT	NPT	PW	NFG	NUFG	TW
DFF	Genotypic	-0.702	-0.028	0.078	-0.047	-0.074	0.004	-0.032	-0.402	0.291
	Phenotypic	-0.506	-0.016	0.033	-0.035	-0.051	-0.003	-0.023	-0.251	0.207
PH	Genotypic	0.005	0.130	0.030	0.002	0.005	0.020	-0.015	-0.007	0.037
	Phenotypic	0.002	0.077	0.017	0.001	0.003	0.012	-0.009	-0.002	0.021
PL	Genotypic	-0.014	0.029	0.128	-0.005	0.001	0.030	-0.030	0.003	0.062
	Phenotypic	-0.008	0.026	0.116	0.000	-0.002	0.025	-0.018	-0.004	0.040
NT	Genotypic	-0.069	-0.012	0.042	-1.028	-0.977	0.111	0.094	-0.136	0.213
	Phenotypic	-0.021	-0.003	-0.001	-0.301	-0.266	0.031	0.026	-0.025	0.061
NPT	Genotypic	0.096	0.034	0.009	0.859	0.904	-0.064	-0.042	0.048	-0.132
	Phenotypic	0.022	0.008	-0.003	0.193	0.218	-0.011	-0.011	0.015	-0.030
PW	Genotypic	0.000	0.000	0.000	0.000	0.000	-0.001	0.000	0.000	0.000
	Phenotypic	0.000	0.007	0.009	-0.005	-0.002	0.044	0.016	0.015	0.004
NFG	Genotypic	-0.022	0.058	0.113	0.044	0.023	-0.194	-0.488	-0.045	0.274
	Phenotypic	-0.017	0.043	0.058	0.031	0.019	-0.137	-0.370	-0.022	0.206
NUFG	Genotypic	0.046	-0.004	0.002	0.011	0.004	0.035	0.007	0.081	-0.026
	Phenotypic	-0.046	0.003	0.003	-0.008	-0.007	-0.032	-0.005	-0.093	0.025
TW	Genotypic	0.185	-0.125	-0.218	0.092	0.065	-0.042	0.251	0.140	-0.446
	Phenotypic	0.107	-0.071	-0.091	0.053	0.036	-0.023	0.146	0.071	-0.262

Residual: 0.79 (genotypic path); Residual: 0.83 (Phenotypic path); DFF: Days to 50% flowering; PH: Plant height; PL: Panicle Length; NT: Total number of tillers per plant; NPT: Number of productive tillers per plant; PW: Panicle weight; NFG: Number of filled grains per panicle; NUGF: Number of unfilled grains per panicle. TW: Test weight.

Thus, it is understood that number of productive tillers per plant was highest at both genotypic and phenotypic level and hence can be considered as the major contributor to yield. These results are in accordance with the previous studies by Kalyan *et al.*, 2017, Lakshmi *et al.*, 2017, Priya *et al.*, 2017. It is also understood that the increased grain

yield through the direct effect of number of productive tillers per plant is through the indirect effect of days to fifty percent flowering, plant height, panicle length and number of tillers per plant followed by moderate to low indirect effects of number of filled grains per panicle, panicle weight and test weight. These findings are in concurrence



with earlier reports (Padmaja *et al.*, 2011, Lakshmi *et al.*, 2017, Priya *et al.*, 2017 for days to fifty percent flowering and by Kalyan *et al.*, 2017, Priya *et al.*, 2017 for plant height). Thus, the trait number of productive tillers per plant appears to be important trait on which emphasis can be laid as a selection criterion for yield.

### 3.3 Principal component analysis

PCA was performed for all the ten traits among the 50 elite rice genotypes as indicated in table 6. On the basis of

scree plot, four principal components (PC) having eigen values more than 1 were chosen which accounted for 73% variability among all the traits studied. Breakdown of this cumulative variance revealed contribution of 26%, 19%, 16% and 12% for PC1, PC2, PC3 and PC4, respectively. PC1, PC2, PC3 and PC4 had eigen values of 2.56, 1.93, 1.61 and 1.21 respectively.

Table 6. Eigen values, proportion of total variance, cumulative per cent variance represented by first four principal components and factor loadings of different characters in rice

Particulars	PC 1	PC 2	PC 3	PC 4
Eigenvalue	2.56	1.93	1.61	1.21
Variability (%)	26	19	16	12
Cumulative (%)	26	45	61	73
Characters	Factor loadings			
Days to 50 % flowering	0.42	-0.05	0.19	-0.50
Plant height	-0.15	0.07	0.44	-0.03
Panicle length	-0.24	0.06	0.50	0.04
Number of tillers	0.23	0.63	0.07	0.17
Number of productive tillers	0.22	0.63	0.09	0.20
Panicle weight	0.09	-0.26	0.52	0.46
Number of filled grains	0.31	-0.30	-0.08	0.60
Number of unfilled grains	0.38	-0.11	0.38	-0.20
Test weight	-0.49	0.06	0.28	-0.13
Single plant yield	-0.39	0.12	-0.10	0.22

PCA loadings for component 1 (PC1) indicated that days to fifty percent flowering (0.42) and number of filled grains per panicle (0.31) had relatively higher contributions to the total morphological variability whereas it is negatively correlated with plant height, single plant yield, test weight and panicle length. The highly positive correlated variables with PC2 were number of tillers (0.63), and number of productive tillers per plant (0.63) whereas panicle weight and number of filled grains per panicle were observed to be negatively correlated. Component 3 (PC3) was positively correlated with panicle weight (0.52), panicle length (0.50), plant height (0.44) and negatively correlated with number of filled grains per panicle and single plant yield. The variables which are positive and strongly correlated with PC4 were number of filled grains per panicle (0.60) and panicle weight (0.46) contributing 12% variability and negatively correlated with days to fifty percent flowering, test weight and plant height. On the basis of PCA analysis, the first two principal components

accounted for 45% of the genetic variance. Similar results were reported by Worede *et al.*, (2014) for 61.2% of the total variability using the first and second PCs for 24 rice genotypes. Selection of traits via number of tillers per plant, number of productive tillers per plant and days to fifty percent flowering lying in these two principal components would be beneficial in contributing to the total morphological diversity.

### 3.4 Cluster analysis

The dendrogram was constructed based on euclidean distance and neighbor joining method clustered the 50 genotypes into six clusters (Figure 1, Table 7). Cluster I comprised of six genotypes. On the other hand, cluster II had 15 rice genotypes; cluster III comprised 6 genotypes; cluster IV with 8; cluster V with 5 and cluster VI with 10 genotypes. The mean value of all the clusters for different traits is given in table 8. The mean values of traits days to fifty percent flowering (98 days), plant height (99.8 cm) and panicle length (22.6 cm) was highest for cluster I. Number



of tillers per plant(14) and number of productive tillers per plant (12) showed highest mean values in cluster III and lowest in case of cluster V. The highest mean value for panicle weight (2.42 gram) observed in cluster VI and lowest for cluster III. Number of filled grains per panicle shown highest (108) mean value for cluster V and lowest (87) for cluster I and vice versa for number of unfilled grains per panicle. Cluster II showed highest mean value for test weight (22.52 grams) and lowest (19.48 grams) by cluster III. The trait single plant yield showed highest mean value by cluster III and lowest by cluster I. The genotypes clustered into six different clusters indicate high degree of heterogeneity which may be directly utilized for selecting genotypes as parents belonging to different groups to combine desirable characters for future hybridization programs. Similar result of grouping of the

accessions into six clusters was reported by Chouhan *et al.*, (2015).

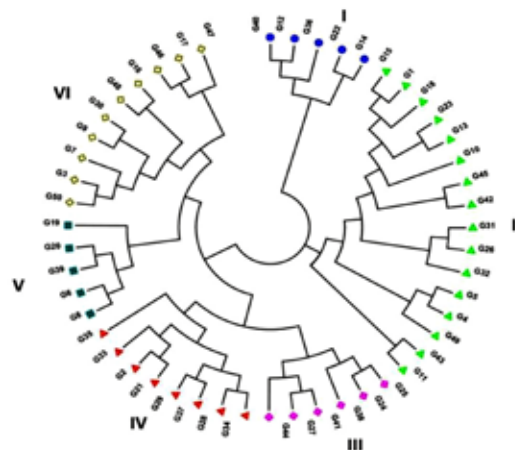


Figure 1. Dendrogram of fifty elite rice genotypes based on euclidean distance and neighbor joining method.

Table 7. Grouping of 50 elite rice genotypes into different clusters based on PCA

S. No.	Clusters	No. of genotypes	List of genotypes
1	Cluster I	6	G40, G12, G36, G22, G14, G15
2	Cluster II	15	G1, G18, G23, G13, G10, G45, G42, G31, G26, G32, G5, G4, G49, G43, G11
3	Cluster III	6	G25, G24, G38, G41, G27, G44
4	Cluster IV	8	G34, G28, G37, G29, G21, G2, G33, G35
5	Cluster V	5	G8, G6, G39, G20, G19
6	Cluster VI	10	G50, G3, G7, G9, G30, G48, G16, G46, G17, G47

Table 8. Cluster wise mean phenotypic value of ten traits.

Traits	Cluster I (n=6)	Cluster II (n=15)	Cluster III (n=6)	Cluster IV (n=8)	Cluster V (n=5)	Cluster VI (n=10)
DFP	98	94	92	93	94	94
PH	99.8	93.2	95.2	91.7	95.3	92.3
PL	22.6	22.1	21.9	21.1	21.8	22.3
NT	12	11	14	12	8	12
NPT	11	10	12	11	8	11
PW	2.12	2.32	2.05	2.20	2.17	2.42
NFG	87	92	95	99	108	96
NUFG	47	35	35	26	24	35
TW	21.77	22.52	19.48	22.24	20.35	21.48
SPY	15.75	18.22	19.39	19.22	17.48	18.46

n: Number of genotypes per cluster; DFF: Days to 50% flowering; PH: Plant height; PL: Panicle Length; NT: Total number of tillers per plant; NPT: Number of productive tillers per plant; PW: Panicle weight; NFG: Number of filled grains per panicle; NUGF: Number of unfilled grains per panicle. TW: Test weight; SPY: Single plant yield.

#### 4. Conclusion

In the present study, both univariate and multivariate analysis of the agro-morphological traits clearly showed the existence of wide variability among the genotypes studied. Critical analysis of the character association and

path analysis indicated that the number of productive tillers per plant and panicle length possessed both positive association and high positive direct effects. Hence, selection for these traits could bring improvement in yield



and yield components. PCA identified number of tillers per plant, number of productive tillers per plant and days to fifty percent flowering in different principal components playing a prominent role in classifying the variation existing in the genotypes. Multivariate clustering pattern could also suggest the crop scientists about the suitability of different genotypes of rice for breeding program.

### Authors' contribution

Conceptualization of research (RAF, FJ, LVS); Designing of the experiments (RAF, RMS); Contribution of experimental materials (LVS, CM, RAF); Execution of field/lab experiments and data collection (MK, SD, CK); Analysis of data and interpretation (RAF, MK, SD); Preparation of manuscript (MK, SD, RAF); Revision of the manuscript (RAF, FJ, LVS, CM, RMS)

### Declaration

The authors declare no conflict of interest.

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### 5. References

1. Ali A, AS Khan and MA Asad. 2002. Drought tolerance in wheat: genetic variation and heritability for growth and ion relations. *Asian Journal of Plant Science* **1**: 420-422
2. Ashok S, DP Jyothula and R Babu . 2016. Character association and path analysis for yield components and grain quality parameters of rice (*Oryza sativa* L.). *International Journal of Agriculture Science Research* **6**: 253-258
3. Chouhan S, A Singh , A Singh , S Singh , N Singh and P Singh. 2015. Agro-morphological diversity in wild rice accessions of Eastern Indo-Gangetic region of India. *Bangladesh Journal of Botany* **43**: 337-344
4. Devi RK, K Parimala, V Venkanna, N Lingaiah, Y Hari and SB Chandra. 2016. Estimation of variability for grain yield and quality traits in rice (*Oryza sativa* L.). *International Journal of Pure & Applied Bioscience* **4**: 250-255.
5. Dewey JR and KH Lu. 1959. Correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal* **51**: 515-518
6. DoE&S. 2019. Directorate of Economics & Statistics, Department of Agriculture, Cooperation and Farmers welfare, Government of India.
7. Fiyaz RA, KT Ramya, Chikkalingaiah, BC Ajay, C Gireesh and RS Kulkarni. 2011. Genetic variability, correlation and path coefficient analysis studies in rice (*Oryza sativa* L.) under alkaline soil condition. *Electronic Journal of Plant Breeding* **2**:531-537
8. Hanson CH, HF Robinson and RK Comstock. 1956. Biometrical studies on yield in segregating population of Korean Lasphadezia. *Agronomy Journal* **48**:314-318
9. Johnson HW, HF Robinson and RE Comstock. 1955. Estimates of genetic and environmental variability in soybeans. *Agronomy Journal* **47**:314-318
10. Kalyan B, KV Radha Krishna and LVS Rao. 2017. Path coefficient analysis for yield and yield contributing traits in rice (*Oryza sativa* L.) genotypes. *International Journal of Current Microbiology and Applied Sciences* **6**: 2680-2687
11. Karande SS, BL Thaware, SG Bhave and MM Burondkar. 2015. Estimate of genetic variability and heritability in some exotic germplasm lines in Kharif rice (*Oryza sativa* L.). *International Journal of Applied Biology and Pharmaceutical Technology* **6**: 128-130
12. Karl Pearson. 1932. Tables for statisticians and biometricians, Stat. J. Biometrics
13. Khush GS. 2013. Strategies for increasing the yield potential of cereals: case of rice as an example. *Plant Breeding* **132**:433-436
14. Kumar A, P Dasgupta and R Kumar. 2014. Emerging Opportunities and Challenges in Rice Production, *Popular Kheti* **2**:6-11
15. Lakshmi L, BMN Rao, S Raju and NS Reddy. 2017. Variability, correlation and path analysis in advanced generation of aromatic rice. *International Journal of Current Microbiology and Applied Sciences* **6**:1798-1806
16. Madhavilatha L, MR Sekhar, Y Suneetha and T Srinivas. 2005. Genetic variability, correlation and path analysis for yield and quality traits in rice (*Oryza sativa* L.). *Research on Crops* **6**: 527-537
17. Nandeshwar BC, S Pal, BK Senapati and DK De. 2015. Genetic variability and character association among biometrical traits in F2 generation of some





- Rice crosses. *Electronic Journal of Plant Breeding* 1: 758-763
18. Noirot M, S Hamon and F Anthony. 1996. The principal component scoring: a new method of constituting a core collection using quantitative data. *Genetics Resource Crop Evolution* 43:1-6
  19. Padmaja D, K Radhika, LVS Rao and V Padma. 2011. Correlation and path analysis in rice germplasm. *Oryza* 48: 69-72
  20. Priya S, Y Suneetha, RD Babu and SV Rao. 2017. Inter-relationship and path analysis for yield and quality characters in rice (*Oryza sativa* L.). *International Journal of Science and Environment Technology* 6: 381-390
  21. Sameera SK, AP Rajesh, V Jayalakshmi, PJ Nirmala and T Srinivas. 2015. Genetic variability studies for yield and yield components in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding* 6: 269-273
  22. Sathish V and BK Senapati. 2017. Study of genetic diversity in some newly developed Rice genotypes. *International Journal of Current Microbiology and Applied Sciences* 6: 2693-2698
  23. Seyoum M, S Alamerew and K Bantte. 2012. Genetic variability, heritability, correlation coefficient and path analysis for yield and yield related traits in upland rice (*Oryza sativa* L.). *Journal of Plant Science* 7: 13-22
  24. Shivani D, F Jabeen, K Chaithanya, MBVN Koushik, GD Dileep, EP Koti, K Supriya, RM Sundaram, JA Kumar and R Abdul. 2021. Assessment of genetic diversity of rice germplasm using microsatellite markers. *The Pharma Innovation* 10(5): 1393-1397
  25. Tejaswini KLY, M Srinivas, BNVSR Kumar, LM Lal Ahamed, KS Raju and PVR Rao. 2016. Correlation and path analysis studies of yield and its component traits in F5 families of rice (*Oryza sativa* L.). *IOSR Journal of Agriculture and Veterinary Science* 9: 80-85
  26. Worede F, T Sreewongchai, C Phumichai and P Sripichitt. 2014. Multivariate analysis of genetic diversity among some rice genotypes using morpho-agronomic traits. *Journal of Plant Science* 9:14-24
  27. Wright S. 1923. The theory of path coefficients a reply to Niles's criticism. *Genetics* 8: 239
  28. Zafar I, M Arshad, M Ashraf, T Mahmood and W Abdul. 2008. Evaluation of soybean (*Glycine max* L.) Merrill germplasm for some important morphological traits using multivariate analysis. *Pakistan Journal of Botany* 40:2323-2328

