



Correlation and path analysis in rice (*Oryza sativa* L.) CMS lines

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ABSTRACT

Forty rice genotypes were assessed to determine yield attributing traits. Correlations have found that choosing plants with high hulling percentage, stigma exertion percentage, rice head recovery percentage, milled grain percentage, panicle number per plant, full grain number per panicle, and shorter days to 50% heading results in higher yields. Path coefficient findings indicate that test weight had the strongest positive direct effect on single plant yield, preceded by full grain number per panicle, hulling %, and stigma exertion percentage, demonstrating that selecting for these traits was likely to result in a direct enhancement in single plant yield. Regression analysis found that the days to 50% heading, full grain number per panicle, stigma exertion percentage, hulling percentage, milled grain percentage and rice head recovery percentage had a significant and positive relationship with single plant yield. As a result, accessions with a greater panicle number per plant, higher full grain number per panicle, higher proportion of stigma exertion, early flowering, and rice head recovery would be most suited for a yield advancement strategy.

Keywords: Correlogram, direct effects, genotypic correlation coefficient, indirect effects, phenotypic correlation coefficient, and regression coefficient.

In Indian agriculture, rice (*Oryza sativa* L.) plays a key role. The efficiency of plant breeding depends on available evolutionary divergence, understanding of desired traits and effective selection procedures that enable current genetic resources to be exploited. Rice genotypes are gradually being improved by crossbreeding better lines. Hybrid rice has been shown to break the yield barrier of inbred rice types. Hybrid rice outperforms promising varieties, making it a vital technology for fulfilling the world's rising rice consumption. There are various variables that contribute to the effectiveness of hybrid seed production such as days to 50% heading, pollen load, pollen longevity and morphological features of florets, including stigma and style size, stigma exertion, glume opening angle and duration of spikes opening (Virmani, 1994). Among them, stigma exertion and glume opening angle are recognized as essential component in enhancing pollination and seed set (Sheeba *et al.*, 2006). Successful parent selection necessitates knowledge of the kind and degree of population diversity, character conglomeration with yield and among themselves, and the extent of environmental effect on the manifestation of these traits (Acquaah, 2012).

Considering the importance of interdependence of characteristics with grain yield, an investigation was conducted on rice maintainer lines with the aim to assess

yield and inter dependent characteristics related to quality. This morphological study will help to detect any interaction between these characteristics that eventually contributes to the construction of an appropriate plant type that combines the desirable expression of different characteristics.

MATERIALS AND METHODS

The assay with three replications was conducted in RBD and each plot was placed in 2 rows of 4 m in length. Seeds were sown on elevated nursery beds of all 38 maintainer lines and 2 standard checks, and seedlings that were thirty-one days were transplanted in the main field. Data on plant height, panicle number per plant, panicle length, full grain number per panicle, single plant yield was recorded from each replication to the five random plant, however, the measurement of the kernel length, kernel breadth, L/B ratio, thousand seed weight, hulling (%), rice head recovery (%) per plot was done using random samples from each plant. In the replication, data was obtained from 10 random plants of each genotype on the angle of glume opening and the stigma exertion. The mean data for each individual character have been exposed to ANOVA following Panse and Sukhatme (1985) method, correlations with formulas from Singh and Chaudhary (1985), Dewey and Lu (1959) for path analysis, and regression analysis was carried out using INDOSTAT software ver 9.2.

RESULTS AND DISCUSSION

Correlation analysis

There was a substantial and positive interaction of days to 50 percent heading with the full grain number per panicle (0.47**), rice head recovery % (0.44**), stigma exertion % (0.42**), single plant yield (0.38**), and milled grain percentage (0.36**), which were in accordance with Patel *et al.* (2017) findings (Table 1 and Fig.1). Positive and significant interaction was shown by kernel length (0.47**) with angle of flower opening. Single plant yield (0.47**) and full grain number per panicle (0.34*) had a positive significant phenotypic association with stigma exertion (%) (0.39**), kernel length (0.50**), Gel consistency (0.49**), cooked kernel length (0.39**), and 1000-seed weight (0.36*) all had a substantial and favorable phenotypic interaction with the panicle number per plant. Kumar *et al.* (2018) reported similar results. The association of panicle length (0.81**), kernel length (0.50*), 1000-seed weight (0.42**) and cooked kernel length (0.39*) with plant height was significant and positive. These results are akin with findings of Vanisree *et al.* (2013). Full grain number per panicle revealed a significant and negative phenotypic interrelation with kernel length (-0.79**), cooked kernel length (-0.78**), kernel breadth (-0.48*). The conglomeration of hulling (%) was positive and significant with milled grain percentage (0.71**), single plant yield (0.51**), and rice head recovery percentage (0.46**), similar findings reported by Choudary *et al.* (2013). The correlation between milling (%) with rice head recovery percentage (0.79**) and single plant yield (0.41**) was positive and significant. Significant positive phenotypic correlation was showed by rice head recovery percentage with amylose content (0.56**) and single plant yield (0.43**). Positive and substantial correlation of kernel length was displayed with cooked kernel length (0.85**) and kernel breadth (0.31*). Negative and significant association of cooked kernel length with single plant yield (-0.23**) was found.

Positive and significant conglomeration of single plant yield with hulling (%) (0.51**), stigma exertion percentage (0.47**), rice head recovery percentage (0.43**), milled grain percentage (0.41**), panicle number per plant (0.40**), full grain number per panicle (0.40**), and Days to 50% heading (0.38**), indicating that each of these characteristics were essential for improvement of yield. It did, however, show a significant and negative association with cooked kernel length (0.33**). Similar findings were found by Atsedemariam (2018) for Days to 50% heading and Rukmini Devi *et al.* (2014) for full grain number per panicle.

Path coefficient analysis

The days to 50% blooming showed a direct phenotypic positive effect (0.179) on grain yield (Table 2 and Fig. 2). The proportion of stigma exertion had a greater phenotypic favorable direct influence on single plant yield (0.201). Archana *et al.* (2018) reported similar findings. Thousand seed weight (0.804) showed a greater direct phenotypic positive effect on single plant yield. The full grain number per panicle had a direct significant phenotypic effect on single plant yield (0.349). Similar results were reported by Patel *et al.* (2017) for the significant direct effect of the full grain number per panicle on single plant yield. Hulling (%) (0.336) had a substantial direct phenotypic effect on single plant yield. Other traits that had a direct phenotypic negative effect on single plant yield were kernel length (-0.271), kernel breadth (-0.324), and cooked kernel length (-0.252).

Panicle number per plant had less direct positive phenotypic effect on single plant yield (0.118), Ekka *et al.* (2011) found similar results for positive direct effect of panicle number per plant on single plant yield. High direct positive phenotypic effect on single plant yield (0.1701) was recorded by Amylose content. Gel consistency had direct negligible negative phenotypic effect on single plant yield (-0.107). Angle of flower opening (0.040), panicle length (0.071) and plant height (0.075) had direct positive phenotypic negligible effect on single plant yield

Regression analysis

Multiple linear regressions

Table 3 shows the regression coefficients and probability of the estimated factors predicting single plant yield. The following model equations for calculating grain yield/plant (Y) were created based on these observations.

$$Y = 0.42 + 0.29 \text{ DFF} + 0.27 \text{ AFO} + 0.58 \text{ SEP} + 0.38 \text{ NET} + 0.08 \text{ PH} - 0.14 \text{ PL} + 0.020 \text{ NGP} - 0.12 \text{ TW} - 0.63 \text{ HP} - 0.62 \text{ MP} + 0.39 \text{ RHR} - 1.45 \text{ KL} + 0.66 \text{ KB} + 0.43 \text{ AC} - 0.10 \text{ GC} - 1.43 \text{ KLAC}$$

The t-test for the parameters found that the days to 50% heading, full grain number per panicle, stigma exertion percentage, hulling percentage, milled grain percentage and rice head recovery (%) each contributed significantly to single plant yield.

Stepwise regression

Table 4 shows the features that were included or deleted from the model generated using stepwise regression. Days to 50% heading, effective tillers per plant, grains per panicle, 1000-seed weight, head rice recovery, kernel length and gel consistency were all incorporated into the model with none being eliminated. The partial

Table 1: Phenotypic correlation coefficients of outcross, quality and yield traits in maintainer lines of rice

	DH	AFO	SEP	PNP	PH	PL	FGNP	TSW	HP	MP	HRR	KL	KB	AC	GC	CKL	GYP
DH	1.00																
AFO	0.23	1.00															
SEP	0.42**	0.25	1.00														
PNP	-0.42**	0.19	-0.18	1.00													
PH	0.35*	0.22	0.08	-0.02	1.00												
PL	0.02	0.08	-0.06	0.81**	1.00												
FGNP	0.47**	-0.26	0.34*	-0.10	0.02	1.00											
TSW	-0.34*	0.30	-0.10	0.42**	1.00	-0.78**	1.00										
HP	0.18	0.01	0.06	-0.20	0.07	0.29	1.00										
MP	0.36*	-0.08	0.32*	-0.18	0.08	0.29	0.71**	1.00									
HRR	0.44**	-0.12	0.40**	-0.15	0.48**	0.42**	0.46**	1.00									
KL	-0.30	0.47**	-0.07	0.50***	0.83**	0.83**	0.79***	1.00									
KB	-0.03	0.10	-0.06	0.06	0.71***	0.71***	0.71***	0.33*	1.00								
AC	0.20	-0.30	0.12	0.20	-0.00	-0.24	0.21	1.00	1.00								
GC	-0.16	0.36*	-0.15	0.49**	0.14	-0.37*	-0.06	-0.85**	0.25	1.00							
CKL	-0.38*	0.30	0.39*	0.38*	0.74**	0.56**	0.33*	1.00	1.00	1.00							
GYP	0.38**	0.10	0.47**	-0.11	0.04	0.43**	-0.23*	-0.31**	-0.19	0.28*							

* Significant at 5 per cent level; ** Significant at 1 per cent level

DH: Days to 50% heading, AFO: Angle of Flower opening, SEP: Stigma Exertion Percentage, PNP: Panicle number per plant, PH: Plant height (cm), PL: Panicle length (cm), FGNP: Full grain number per panicle, TSW: 1000-seed weight, HP: Hulling (%), MGP: Milled grain percentage, HRR: Rice head recovery%, KL: Kernel length (mm), KB: Kernel breadth (mm), AC: Amylose content, GC: Gel consistency, CKL: cooked kernel length, SPY: Single plant yield (g).

Table 2: Phenotypic path coefficients of outcross, quality and yield traits in maintainer lines of rice

	DH	AOF	SEP	PH	PNP	PL	TSW	FGNP	HP	MP	HRR	KL	KB	AC	GC	CKL	GYP
DH	1.00																
AOF	0.179*	1.00															
SEP	0.009	0.040	1.00														
PH	0.067	0.039	0.201*	1.00													
PNP	0.054	0.058	0.055	0.075	1.00												
PL	-0.047	0.018	-0.024	0.038	0.119	1.00											
TSW	-0.002	-0.014	0.013	-0.082	0.005	-0.072	1.00										
FGNP	-0.275**	0.216*	0.018	0.369**	0.266**	0.225*	0.804**	1.00									
HP	0.146	-0.074	0.081	0.027	-0.171	-0.015	-0.256**	0.349**	1.00								
MGP	0.059	0.006	0.055	0.255**	0.019	-0.093	0.025	0.027	0.337**	0.208*	1.00						
HRR	-0.025	0.004	-0.015	0.056	0.013	0.022	0.017	-0.020	-0.054	-0.087	0.059	1.00					
KL	0.024	-0.005	0.016	0.021	-0.020	-0.011	-0.019	0.024	0.026	0.043	-0.028	-0.272**	1.00				
KB	0.081	-0.107	0.001	-0.188*	-0.130	-0.093	-0.218**	0.197	0.053	0.095	0.130	0.130	0.130	1.00			
AC	0.016	-0.028	-0.007	-0.170	-0.004	0.002	-0.228**	0.143	-0.040	-0.011	0.001	-0.097	-0.324**	0.068	1.00		
GC	-0.007	0.010	-0.008	-0.014	0.020	0.001	0.000	-0.007	-0.012	-0.015	-0.019	0.010	-0.009	-0.076	0.024	1.00	
CKL	0.017	-0.035	0.028	-0.016	-0.050	-0.003	-0.016	0.031	0.039	0.049	0.050**	-0.033	0.008	-0.108	0.031	0.007	1.00
GYP	0.094	-0.064	0.016	-0.159	-0.095	-0.043	-0.184*	0.183*	0.048	0.075	0.114	-0.212**	-0.078	0.048	-0.061	-0.252*	-0.319**

Phenotypic Residual effect = 0.6674 Bold values are direct effects

Table 3: Multiple linear regression in predicting rice grain yield

	Beta Wt.	Simple R ²	Reg.Coeff.	Std.Err.	t-value	t Prob.	Partial R ²
INTERCEPT a		0	-47.7038	34.354	1.389	0.178	0.077
DH	0.206	0.083	0.14931	0.1385	2.7139	0.0099 **	0.048
AFO	0.1108	0.014	0.24271	0.3673	0.7829	0.4386	0.019
SEP	0.0812	0.0407	0.09397	0.1786	3.5744	0.0010 **	0.012
PNP	0.2814	-0.0349	0.54101	0.389	0.7715	0.4452	0.078
PH	0.2816	0.0501	0.14078	0.1354	1.1142	0.2722	0.045
PL	-0.108	-0.0059	-0.29381	0.6167	0.3370	0.7379	0.01
FGNP	0.6291	0.2781	0.04049	0.0203	3.0379	0.0043 **	0.147
TSW	0.8443	-0.0953	0.91927	0.5689	0.7004	0.4879	0.102
HP	0.456	0.2553	0.51437	0.2064	4.1657	0.0002 **	*0.213
MGP	-0.0782	-0.0404	-0.09456	0.3654	3.7195	0.0006 **	0.003
RHR	0.0585	0.0296	0.04616	0.2207	3.6181	0.0009 **	0.002
KL	-0.4653	0.115	-2.744	2.7974	1.5725	0.1241	0.04
KB	-0.2193	-0.0064	-5.02214	6.8072	0.1797	0.8583	0.023
AC	0.1061	0.0306	0.16087	0.4867	1.8560	0.0712	0.005
GC	0.0366	-0.0112	0.01198	0.0973	1.9838	0.0545	0.001
CKL	-0.0376	0.0125	-0.16199	1.1719	2.1798	0.0355 *	0.001

Table 4: Stepwise regression in predicting rice grain yield

Variables entered	Variables removed	Beta	R square	Regression coefficient	Standard error	T- value	Probability
DH	-	0.13	0.055	0.09	0.11	0.85	0.40
PNP	-	0.43	-0.053	0.83	0.31	2.61	0.01 *
FGNP	-	0.75	0.332	0.04	0.01	3.00	0.005 **
TSW	-	0.14	0.072	0.16	0.17	0.95	0.34
AFO	-	0.22	0.028	0.50	0.35	1.41	0.16
SEP	-	0.67	-0.076	0.73	0.27	2.70	0.01*
RHR	-	0.15	0.078	0.12	0.14	0.85	0.39
KL	-	-0.31	0.079	-1.89	1.76	1.06	0.29
GC	-	-0.25	0.077	-0.08	0.05	1.59	0.12

and cumulative determination coefficients (R²), the probability value of parameters added to or removed from models, and the standard error of the variables all were included. The chosen factors explained 99.75 percent and 99.91 per cent of the overall variances in grain yields, respectively, according to the findings. Due to their small relative proportions, the additional parameters were not included in models.

According to stepwise regression analysis yield exhibited a significant positive association with the number of effective tillers, thousand seed weight, and percentage of stigma exertion, but a negative link with kernel length and gel consistency. The coefficient of determination (R²) reveals how much variation in the dependent variable was caused by the independent variable, with R² = 0.29 indicating that independent characteristics were responsible for 29% of the variation in the yield parameter.

CONCLUSION

According to phenotypic correlations, single plant yield had a significant and positive association with hulling (%) (0.51**), stigma exertion percentage (0.47**), rice head recovery(%) (0.43**), milled grain percentage (0.41**), panicle number per plant (0.40**), full grain number per panicle (0.40**), and days to 50% heading (0.38**), According to the path coefficient study, 1000-seed weight had the maximum positive direct effect on seed yield per plant, accompanied by the full grain number per panicle, hulling (%), and stigma exertion (%), indicating that each of these characters were essential for yield potential. However, it had a negative relationship with kernel breadth (-0.32), kernel length (-0.272), and cooked kernel length (-0.252). Selecting these traits would very certainly result in a direct increase in single plant yield. Regression analysis revealed a substantial and positive conglomeration of single plant yield with Days to 50% heading, full grain number per

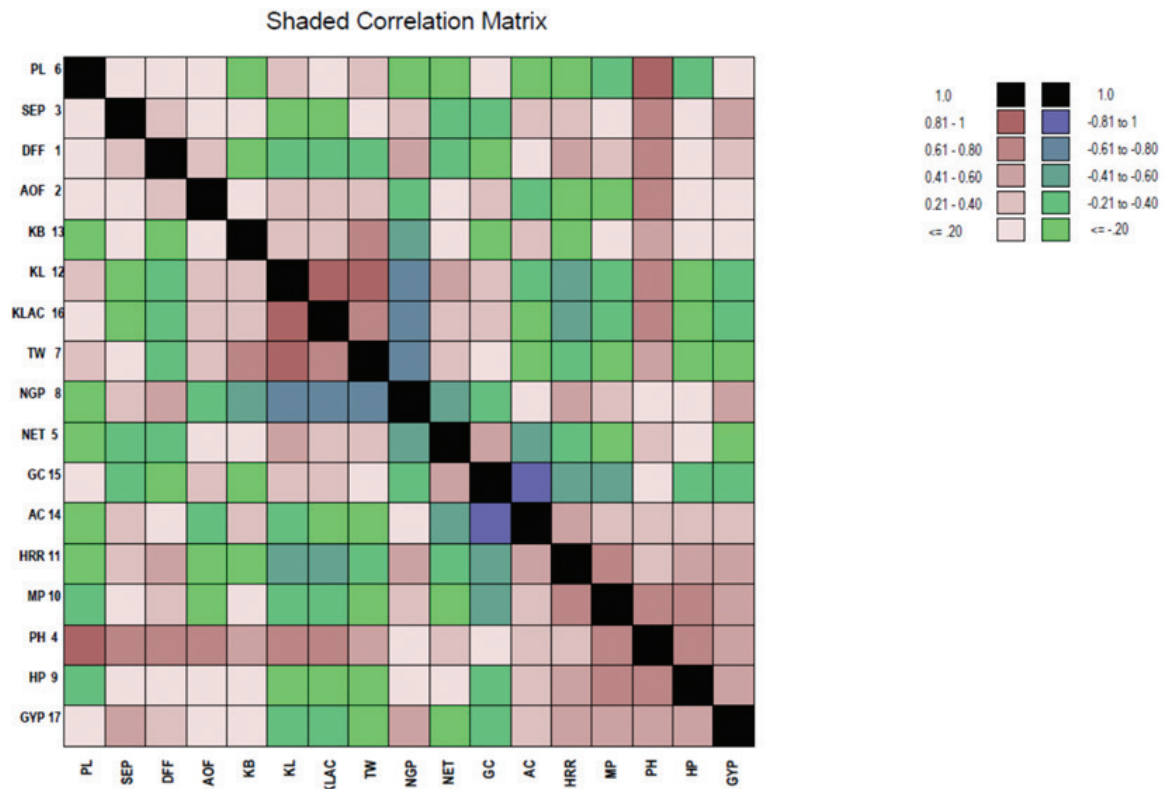


Fig. 1: Correlogram visualizing the correlation in yield and yield component traits of maintainer lines of rice

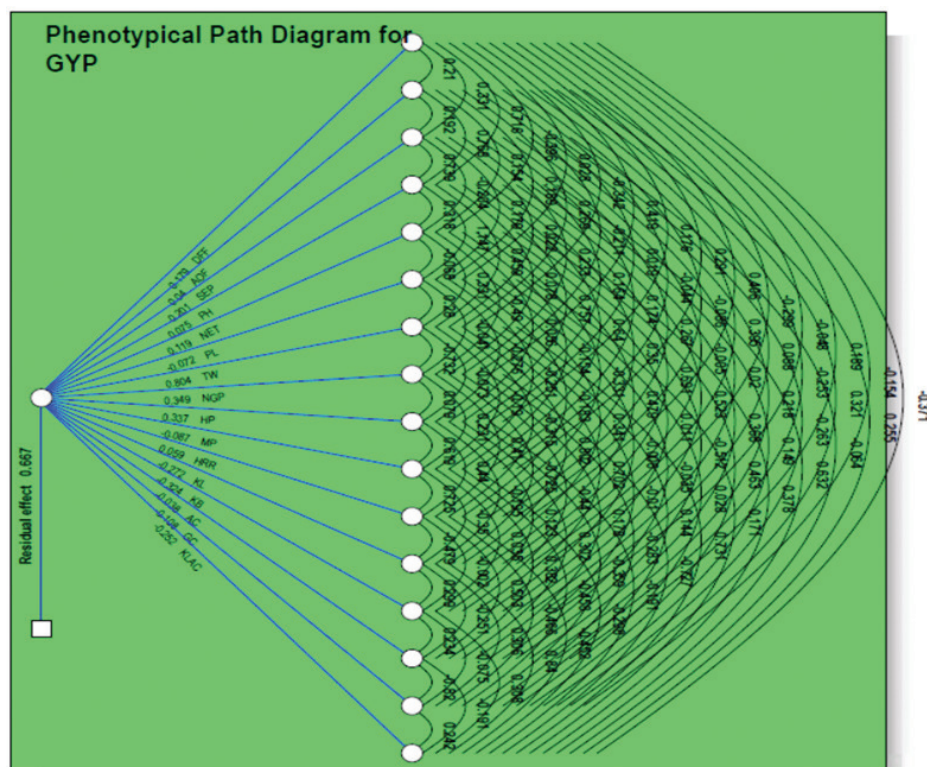


Fig. 2: Phenotypical path diagram indicating direct effect and indirect effect of different parameters on grain yield of rice maintainer lines

panicle, stigma exertion percentage, hulling percentage, milled grain percentage and rice head recovery percentage. Selection of accessions with a greater panicle number per plant would be effective for a yield improvement programme with higher percentages of stigma exertion, early maturity, higher full grain number per panicle and head rice recovery.

REFERENCES

- Acquaah G. 2012. Principles of plant genetics and breeding. Second edition. Wiley-Blackwell publications. 127129.
- Archana, R.S., Rani, M.S., Vardhan, K.V and Fareeda, G. 2018. Genetic diversity studies among rice (*Oryza sativa* L.) genotypes for grain yield, yield components and nutritional traits in rice. *Int. J. Commu. Syst.*, **6** (6): 134-137.
- Chaudary, P., Mishra, D.K and Koutu, G.K. 2013. Genetic variation, association and path coefficient analysis for grain yield and its components in RILs derived population of rice. *J. Progre. Agric.*, **4** (2): 54-56.
- Dewey, J.R. and Lu, K.H. 1959. Correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.*, **51**: 515-518.
- Ekka, R.E., Sarawgi, A.K and Kanwar, R.R. 2011. Correlation and path analysis in traditional rice accessions of Chhattisgarh. *J.Rice Res.*, **4** (1 and 2): 11-18.
- Kumar, S., Chauhan, M.P., Tomar, A., Kasana, R.K and Kumar, N. 2018. Correlation and path coefficient analysis in rice (*Oryza sativa* L.). *Pharma Innov. J.*, **7** (6): 20-26.
- Patel, J.R., Dixita, K., Patel, K.N., Prajapati, N.V., Soni and Ankit, P. 2017. Correlation and path coefficient analysis in rainfed upland rice (*Oryza sativa* L.). *Environ. Ecol.*, **35** (2): 789-794
- Rukmini Devi, K., Parimala, K., Venkanna, V and Cheralu, C. 2014. Genetic variability, heritability, correlation and path analysis for yield and quality traits in rice (*Oryza sativa* L.). *J. Res. PJTSAU.*, **42** (4): 7- 14.
- Singh, R.K. and Chaudhary, B.D. 1985. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi, Ludhiana, India. pp. 205-215.
- Vanisree, S., Swapna, K., DamodarRaju, C.H., SurenderRaju, C.H and Sreedhar, M. 2013. Genetic variability and selection criteria in rice. *J. Biol. Scientific Opinion*, **1**(4): 341-346.
- Virmani, S.S. 1994. Heterosis and hybrid rice breeding. Monograph TheorAppl Gent. 22. Springer-Verlag