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Research Note

Correlation and path coefficient analysis among grain yield and kernel characters in rice (O*ryza sativa L.*)

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Abstract
An investigation was carried out using 43 rice genotypes including 30 hybrids and 13 parents for grain yield and kernel characters to understand the association among yield components and their direct and indirect influence on the grain yield. Analysis of variance revealed considerable variability among the genotypes for all the characters. The correlation analysis indicated that grain yield was significantly associated with number of productive tillers per plant, kernel breadth, hundred grain weight and number of filled grains per panicle. Results of path-coefficient analysis revealed that days to 50% flowering had the highest positive direct effect on grain yield followed by panicle length, kernel L/B ratio, hulling percentage and number of productive tillers per plant. Hence, selection based on these traits could help to bring simultaneous improvement of yield, yield attributes and kernel characters.

Keywords Rice, correlation, pathcoefficient, kernel, yield

Rice is the principal staple cereal food and source of calories for more than half of the world's population. According to UN estimates, the world population will grow from 6.3 billion in 2003 to 8.5 billion in 2030. Out of this five billion people will be rice consumers and there is a need of 38 per cent more rice by 2030. Hence, we must produce 40 per cent more rice by 2025 to satisfy the growing demand without adversely affecting the resource base (Khush, 2006). The grain yield and grain quality trait of rice is a complex character which is directly (or) indirectly related with other. Knowledge on the association between grain yield with yield contributing and grain quality traits is important for selection of desirable genotypes in a breeding programme. Correlation coefficient measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield and quality. Path analysis that permits the partitioning of the correlation coefficient into its components. Correlation in combination with path analysis would give a better insight into cause and effect relationship between different pairs of characters.

The experimental material comprised 43 genotypes of rice including 13 parents and their 30 hybrids. The set of hybrids were generated during *kharif*, 2011 in line x tester pattern for the purpose and evaluated along with parents in Randomized Complete Block Design with two replications during January, 2012 at research farm of Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai, Tamil Nadu. Twenty five days old seedlings of 30 hybrids and 13 parents were transplanted in the field. Single row of each parent and hybrid was 3 m measured with 20 x 15 cm, row to row and plant to plant spacing, respectively. Single seedling was planted in each hill. Recommended package of practices and plant protection measures were followed to obtain a good harvest.

Observations were recorded on randomly selected ten plants excluding border plants in each entry in each replication for plant height (cm), number of productive tillers per plant and grain yield per plant. Days to 50% flowering was recorded on plot basis. For panicle traits like panicle length (cm) and number of filled grains panicle, observations were recorded from ten randomly selected panicles. Required quantities (100 g) of harvested seeds were used to record the hulling percentage, milling percentage and head rice recovery. Observations on grain characteristics *viz.*, kernel length, kernel breadth, kernel L/B ratio were recorded from 10 randomly selected kernels. Correlation coefficient was computed as per the procedure outlined by Karl Pearson (1932) and path coefficient analysis was carried out as suggested by Dewey and Lu (1959).

Analysis of variance was significant for all the traits among the entries, indicting the presence of considerable genetic variation in the experimental material (Table 1). In the present study, the grain yield per plant showed positive and significant association with number of productive tillers per plant, kernel breadth, hundred grain weight and number of filled grains per panicle at genotypic level (Table 2). These results were in agreement with the earlier findings of Malarvizhi *et al.* (2010) and Immanuel Selvaraj *et al.* (2011) for all the traits and Sarkar *et al*. (2007) and

Sabesan *et al.* (2009) for kernel breadth. A significant negative association was observed between kernel L/B ratio and single plant yield and this was in accordance with the findings of Nandan *et al.* (2010) and Malini *et al.* (2011). The highest degrees of associations were observed among kernel breadth, number of productive tillers per plant and hundred grain weight.

Knowledge on interrelationship between yield attributing characters and grain quality traits revealed the intensity and direction of association with each other. This could facilitate effective selection for simultaneous improvement of one (or) more yield contributing traits and grain quality characters. Plant height exhibited significant and positive inter correlation with panicle length. Immanuel Selvaraj *et al.* (2011) and Nagendra Rao *et al*. (2010) were also reported the same result for plant height with panicle length. Hundred grain weight exhibited positive and significant association with kernel length and kernel breadth. The results were supported by the earlier findings of Nandan *et al.* (2010).

Hulling percentage recorded a significant and positive inter correlation with milling percentage and head rice recovery which is in consonance withManonmani *et al.* (2010). Kernel length expressed a positive and significant inter correlation with kernel L/B ratio. This was in agreement with results of Sarika Mathure *et al.* (2011). Kernel breadth showed significant and negative association with kernel L/B ratio. This was in agreement with the findings of Jyothula and Nitu Singh (2010) and Rajeswari *et al*. (2010).

Path analysis partitions the genotypic correlation coefficient into direct and indirect effects, indicates the relative significance for each component character to the dependent trait. It forms the best method to evaluate the cause and effect relationship in order to get the developmental relationship between them.

Path coefficient analysis using single plant yield as a dependent variable and other yield contributing and grain quality traits were considered as independent variable. Three yield contributing characters *viz.*, days to 50% flowering, number of productive tillers per plant and panicle length exhibited high and positive direct effects on single plant yield (Table 3). Similar results were also reported by Satish Chandra *et al*. (2009) for days to 50% flowering and number of productive tillers per plant, Nagendra Rao *et al*. (2010) for panicle length. The grain quality traits *viz.*, hulling percentage and kernel L/B ratio showed high and positive direct effects on single plant yield. Nandan *et al*. (2010) and Mohana Krishna *et al*. (2009) were also expressed high positive direct effect this trait on single plant yield.

Hulling percentage and milling percentage exerted a high positive indirect effect through kernel breadth. Head rice recovery showed high indirect positive effects through kernel length and kernel breadth. Kernel length had high and positive indirect effects through kernel L/B ratio, whereas kernel breadth showed negative and moderate indirect effect on kernel L/B ratio. From the present study, it can be concluded that the characters *viz.*, days to 50% flowering, number of productive tillers per plant, panicle length, hulling percentage and kernel L/B ratio could be used as selection indices for the improvement of grain yield and kernel characters in rice.

References

Dewey, D.R. and Lu, K.H. 1959. A correlation and path coefficient analysis components of crested wheat grass seed production. *Agron, J*., **51**: 575-81.

Grafius, J.E. 1960. Does over dominance exist for yield in corn. *Agron. J*., **52**: 361.

Immanuel Selvaraj, C., Pothiraj Nagarajan, Thiyagarajan, K., Bharathi, M. and Rabindran. 2011. Genetic parameters of variability, correlation and path coefficient studies for grain yield and other yield attributes among rice blast disease resistant genotypes of rice (*Oryza sativa* L**.)**. *Afr. J. Biotech*., **10** (17): 3322-3334.

Jyothula and Nitu Singh. 2010. Correlation of quantitative and qualitative charecters with yield in rice mutant lines. *The Andhra Agric. J*., **57** (3): 301-305.

Karl Pearson. 1932. Tables for statisticians and biometricians, *part II, Nature*,130.

Khush, K. 2006. Rice Research challenge for the 21st century. *J. Rice Res*., **1** (1): 12-18.

Krishna Veni, B. and Shobha Rani, N. 2007. Heterosis and combining ability for yield and yield components in rice. *J. Res. ANGRAU*., **31** (3): 44-51.

Malarvizhi, D., Thiyagarajan, K., Vijayalakshmi, C. and Manonmani, S. 2010. Genetic analysis to assess the physiological efficiency of parental lines in rice. *Electron. J. Plant Breed*., **1** (2): 100-113.

Malini, N., Sundaram, T. and Hari Ramakrishnan, S. 2011. Interrelations among grain quality characters in rice. *Electron. J. Plant Breed*., **2** (3): 397-399.

Manonmani, S., Malarvizhi, D., Robin S., Umadevi, M., Ameenal, M., Pushpam, R., Mohana Sundaram, K. and Thiyagarajan, K. 2010. Breeding three line rice hybrids with good grain quality. *Electron. J. Plant Breed*., **1** (4): 1265-1269.

Mohana Krishna, D., Reddy, D.M., Reddy, K.H.P. and Sudhakar, P. 2009. Character association and interrelationship of yield and quality attributes in rice (*Oryza sativa* L.). *The Andhra Agric. J.*, **56** (3): 298-301.

Nagendra Rao, K., Bayyapa Reddy, K. and Krishna Naik. 2010. Studies on genetic variability, correlation and path coefficient analysis in rice under saline soil conditions. *The Andhra Agric. J*., **57** (4): 335-338.

Nandan, R., Sweta and Singh, S.K. 2010. Character association and path analysis in rice (*Oryza sativa* L.) Genotypes. *World J. Agric. Sci*., **6** (2): 201-206.

Rajeswari, S., Robin, S., Chandirakala, R., Premalatha, N and Muthuramu, S. 2010. Genetic analysis and character association of quality in rice. *Oryza*, **47** (2): 86-90.

Sabesan, T., Suresh, R. and Saravanan, K. 2009. Genetic variability and correlation for yield and grain quality characters of rice grown in coastal saline low land of Tamilnadu. *Electron. J. Plant Breed*., **1**: 56-59.

Sarika Mathure, Asif Shaikh, N., Renuka, Kantilal Wakte, Narendra Jawali, Ratnakar Thengane and Altafhusain Nadaf. 2011. Characterisation of aromatic rice (*Oryza sativa* L.) germplasm and correlation between their agronomic and quality traits. *Euphytica*, **179**: 237-246.

Sarkar, K.K., Bhutia, K.S., Senapati, B.K. and Roy, S.K. 2007. Genetic variability and character association of quality traits in rice *(Oryza sativa* L.). *Oryza*, **44** (1): 64-67.

Satish Chandra, B., Dayakar Reddy, T., Ansari, N.A and Sudheer Kumar S. 2009. Correlation and path analysis for yield and yield components in rice (*Oryza sativa* L.). *Agric. Sci. Digest*., **29** (1): 45-47.

Table 1 Analysis of Variance (ANOVA) for grain yield and kernel characters in rice

Source of variation	df	DFF	PH	NPT	PL	NFG	HGW	HP	MP	HRR	KL	KB	KLBR	SPY
Replication	1	32.66	13.87	0.06	0.05	1.38	0.01	0.06	0.01	0.14	0.02	0.01	0.01	0.39
Genotypes	42	288.51**	83.94**	2.27**	3.10**	711.70**	0.06**	5.31**	5.62**	3.08**	0.35**	0.10**	0.20**	20.90**
Error	42	0.78	2.02	0.06	0.05	2.93	0.01	0.09	0.18	0.14	0.01	0.01	0.01	0.42

DFF- Days to 50% flowering, PH- Plant height, NPT- Number of productive tillers per plant , PL- Panicle length, NFG- Number of filled grains per panicle, HGW- Hundred grain weight, HP- Hulling percentage, MP- Milling percentage, HRR- Head rice recovery, KL- Kernel length, KB- Kernel breadth, KLBR- Kernel L/B ratio and SPY- Single plant yield., * & ** Significant at 5% and 1% level, respectively

Table 2. Genotypic correlation coefficients of different traits on single plant yield

Characters	DFF	PH	NPT	PL	NFG	HGW	HP	MP	HRR	KL	KB	KLBR	SPY
DFF	1.000	0.473*	-0.281*	-0.018	0.077	-0.141	-0.082	-0.143	0.031	0.003	-0.213	0.147	-0.016
PH		1.000	0.060	0.422*	0.083	-0.100	0.126	0.231	0.143	-0.050	-0.053	0.022	-0.025
NPT			1.000	0.151	0.063	-0.135	0.050	0.191	0.151	0.007	-0.055	0.012	0.532*
PL				1.000	0.019	0.057	0.219	0.138	0.086	-0.053	0.197	-0.252	-0.006
NFG					1.000	-0.314*	0.032	0.144	-0.171	-0.447*	0.074	-0.309*	0.293*
HGW						1.000	0.078	0.103	0.028	0.356*	0.555*	-0.228	0.398*
HP							1.000	0.729*	0.434*	-0.152	0.316*	-0.331*	-0.018
MP								1.000	0.434*	0.045	0.182	-0.077	0.009
HRR									1.000	-0.112	0.312*	-0.289*	-0.011
KL										1.000	0.012	0.543*	-0.008
KB											1.000	-0.815*	0.587*
KLBR												1.000	-0.497*

* - Significant at 5% level

Table 3. Direct (diagonal) and indirect effects of different traits on single plant yield

Characters	DFF	PH	NPT	PL	NFG	HGW	HP	MP	HRR	KL	KB	KLBR	SPY
DFF	**0.963**	0.014	-0.648	-0.013	-0.038	0.042	-0.044	0.133	-0.005	-0.010	-0.822	0.814	-0.016
PH	0.455	**0.029**	0.137	0.318	-0.040	0.030	0.068	-0.216	-0.022	0.197	-0.280	0.120	-0.025
NPT	-0.271	0.002	**0.421**	0.114	-0.031	0.040	0.027	-0.178	-0.023	-0.027	-0.293	0.065	0.532*
PL	-0.017	0.012	0.347	**0.753**	-0.009	-0.017	0.118	-0.129	-0.013	0.209	0.411	-0.960	-0.006
NFG	0.074	0.002	0.145	0.015	**-0.487**	0.093	0.018	-0.135	0.026	0.903	0.392	-0.515	0.293*
HGW	-0.136	-0.003	-0.311	0.043	0.153	**-0.296**	0.042	-0.096	-0.004	-0.741	0.570	-0.635	0.398*
HP	-0.079	0.004	0.116	0.165	-0.016	-0.023	**0.539**	-0.681	-0.066	0.598	0.712	-0.142	-0.018
MP	-0.138	0.007	0.439	0.104	-0.070	-0.031	0.393	**-0.934**	-0.066	-0.176	0.913	-0.428	0.009
HRR	0.030	0.004	0.347	0.065	0.083	-0.008	0.234	-0.405	**-0.152**	0.442	0.463	-0.256	-0.011
KL	0.002	-0.001	0.016	-0.040	0.218	-0.105	-0.082	-0.042	0.017	**-0.564**	0.063	0.744	-0.008
KB	-0.205	-0.002	-0.127	0.148	-0.036	-0.164	0.171	-0.170	-0.047	-0.046	**0.085**	-0.220	0.587*
KLBR	0.141	0.001	0.027	-0.190	0.150	0.068	-0.178	0.072	0.044	-0.966	-0.344	**0.658**	-0.497*

* - Significant at 5% level