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Research Note

Genetic variability and yield analysis in rice

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Abstract
Twenty-six diverse genotypes were cultivated for two consecutive warm wet seasons of 2015 and 2016 to study genetic variation and the cause-effect relationship of different quantitative characters on seed yield in rice. The genotypes showed significant variation for all the characters. Genotypic and phenotypic coefficients of variation were high for the flag leaf area, spikelet number, grain number, test weight and grain yield, and moderate for plant height, days to flowering, the number of panicle and primary branches per panicle. Heritability was high for days to flowering, plant height and test weight. Genetic advance as per cent of mean was very high for test weight and grain yield, moderate for plant height, flag leaf area and the number of grains, and low for spikelet fertility (%). Genotypic and phenotypic correlations of seed yield with plant height, flag leaf area, days to flowering, the number of primary and secondary branches per panicle, the number of spikelets and filled grains per panicle, spikelet fertility (%) and test weight were significant and positive. Genotypic path analysis indicated that direct selection for test weight, the number of primary and secondary branches per panicle in a positive direction with restricted selection for panicle number and spikelet fertility would increase the grain yield of rice in the population.

Key words
Rice, variability, heritability, correlation and path coefficients

Rice (O*ryza sativa* L.) is one of the three leading cereals in the family Poaceae. It is cultivated during warm wet (*kharif*) and winter (*rabi*) seasons in the tropical and subtropical humid regions of the world. Rice is used in the daily diet by more than half of the total world population. Rice is the staple food for a majority of the people of Asia, providing 50-60 per cent of the total calorie and 30 per cent of the total protein (Mackill *et al*., 2012).

Rice is grown in 117 countries with a total area of about 167 m. ha and production of about 769 MT with an average yield of about 4,602 kg/ha (FAOSTAT, 2017). Among the continents, Asia ranks first with over 89.8 per cent of the world production, followed by Africa (4.9%), America (4.7%), Europe (0.5%) and Oceania (0.1%). The leading ricegrowing countries are China (214.4 MT), India (168.5 MT), Indonesia (81.3 MT), Bangladesh (48.9 MT) and Vietnam with 42.7 MT (FAOSTAT, 2017). India ranks second in the world, next to China. The existence

of genetic variability is essential for selection, which is the ultimate tool in plant breeding. Rice shows a bewildering array of genetic variability. However, the selection is challenging due to the masking effect of non-heritable variation. Therefore, partitioning of the total variation to understand the role of the heritable component is very important, which will help the breeder to formulate a sound breeding programme. Correlation is a very important factor for any selection program. Success in selection depends on the knowledge of the association of component traits with grain yield. However, partitioning the correlation coefficients through path analysis is very important to understand the cause-effect relationship. This helps in understanding the relative importance of component characters for improvement in seed yield of rice.

Twenty-six genotypes collected from different geographical regions of India were cultivated with three replications in

a randomized complete block design (RCBD). The field experiments were conducted during the two consecutive *kharif* (warm wet) seasons of 2015 and 2016 at Agriculture Farm of Institute of Agriculture, Visva-Bharati, Sriniketan. The geographical location of the Farm is in the sub-humid, sub-tropical, lateritic belt of West Bengal at 23°39' N latitude and 87°42' E longitude with an average altitude of 58.9 meters above mean sea level. Each plot consisted of five rows of three-meter length with a spacing of 20 × 15 cm. Good agronomic practices were adopted for growing a healthy crop. Five plants in each plot were selected randomly for recording observations for the following traits: plant height, flag leaf area, panicle number, panicle length, primary and secondary branches per panicle, the number of spikelet and grain per panicle, spikelet fertility (%), test weight and grain yield per plant. Data on days to flowering were recorded on the basis of the whole plot. Biometrical analyses were done following procedures of Burton (1952) for phenotypic and genotypic coefficients of variability, Johnson *et al*. (1955) for heritability and genetic advance and, Al-Jibouri *et al*. (1958) for correlation coefficients and Dewey and Lu (1959) for path coefficients.

The pooled analysis of variance of 26 genotypes over two-crop growing seasons for 12 quantitative characters showed that mean squares due to the seasons were highly significant indicating the influence of season for expression of all the characters, except the number of grains per panicle. Mean squares due to genotypes were highly significant for all the characters, indicating the presence of genetic variability among the genotypes.

Values of phenotypic and genotypic coefficients of variation (PCV and GCV) were high for the flag leaf area, the number of spikelets, the number of grains, test weight, and grain yield per plant (**Table 1**). Plant height, days to flowering, length of panicle and primary branches per panicle showed moderate values of PCV

and GCV. Moderate PCV and low GCV were observed for spikelet fertility. The number of panicle and secondary branches per panicle exhibited moderate GCV and high PCV. Similar results were reported for flag leaf area (Saha *et al*., 2019), the number of spikelets (Saha *et al*., 2019), the number of grain (Yadav *et al*., 2018), test weight (Chandramohan *et al*.,2016), grain yield (Bhati *et al*., 2015; Mamata *et al*., 2018; Keerthiraj and Biju, 2020), plant height (Manjunatha *et al*.,2017; Pragnya *et al*., 2018), days to flowering (Behera *et al*., 2018), length of panicle (Pragnya *et al*., 2018). The large difference between PCV and GCV values for the number of panicles, flag leaf area, the number of secondary branches per panicle, spikelet fertility and seed yield is due to the greater contribution of the environment in the expression of these characters. The very little difference for days to flowering and plant height indicated greater genetic control in the expression of these characters and hence, less affected by the environment. Estimates of high heritability for plant height, days to flowering, length of panicle and test weight is due to little environmental influence on these characters. Flag leaf area, spikelet number, primary branches, filled grain number, grain yield and secondary branches having a moderate level of heritability were moderately influenced by the environment; and the number of panicles and spikelet fertility per cent having a low level of heritability were largely influenced by the environment. Similar results have been observed for *plant height* (*Devi et al., 2017),* days to flowering (Hasan *et al*., 2011; Singh *et al*., 2018) *and test weight (*Adhikari *et al., 2018).*

Estimates of genetic advance calculated as per cent of mean were very high for test weight and grain yield, moderate for plant height, flag leaf area, spikelet number and grain number per panicle, and low for spikelet fertility. Similar results were obtained earlier for grain yield (Abebe *et al*., 2017; Adhikari *et al., 2018*), test weight (Singh *et al*., 2018), the number of grains

Table 1. Mean, range and genetic parameters for twelve quantitative traits in rice

Character	Grand mean	Range	Coefficient of variation (%)		Herita-bility (%)	Genetic advance	Genetic advance as % of mean
			GCV	PCV			
Days to flowering	111.76	86.67- 135.83	10.41	10.54	97.60	23.69	21.20
Plant height (cm)	138.11	81.57- 172.3	16.73	17.41	92.30	45.74	33.12
Flag leaf area (cm²)	34.85	18.63- 55.75	25.69	30.05	73.10	15.77	45.25
Number of panicle	7.28	5.1- 9.81	16.38	24.28	45.50	1.66	22.81
Length of panicle (cm)	24.65	18.32- 30.26	11.61	12.55	85.60	5.46	22.15
Primary branch	9.63	6.5- 12.79	15.12	17.85	71.80	2.54	26.37
Secondary branch	23.94	12.11-32.73	19.06	25.10	57.70	7.14	29.82
Number of spikelet	127.03	70.26- 173.34	20.01	23.19	74.40	45.18	35.57
Number of grain	100.69	48.05-150.62	24.97	29.76	70.40	43.46	43.16
Spikelet fertility (%)	78.48	47.61- 93.23	6.04	11.93	25.70	4.95	6.31
Test weight (g)	20.70	10.2- 32.68	26.32	27.68	90.40	10.67	51.56
Grain yield (g)	12.30	5.5- 20.07	34.10	41.40	67.80	7.12	57.88

(Ketan and Sarkar, 2014) and the number of spikelets (Sumanth *et al.*, 2017). Heritability along with genetic advance provides better information than heritability alone for selecting the best individual (Johnson *et al*., 1955; Lerner, 1958). Greater values of heritability and genetic advance for plant height and grain number and test weight indicated the expression of these characters is under the control of preponderant additive genetic

effects (Johnson *et al*., 1955; Panse, 1957). Therefore, a selection for these characters might be rewarding in this population.

The analyses of different genetic parameters of variability indicated that improvement through the selection of plant height, grain number and test weight might be effective in this population.

Table 2. Genotypic (r_g) and phenotypic (r_p) correlations for twelve quantitative traits in rice

Character		Plant height	Flag leaf area	Number of panicle	Length of panicle	Primary branch	Secondary branch	Number of spikelet	Number of grain	Spikelet fertility per cent	Test weight	Grain yield
Days to flowering	r_g	0.491*	0.428*	-0.115	0.010	0.597**	0.502**	0.644**	0.863**	1.692**	0.329	0.789**
	r_p	0.472*	0.355	-0.074	0.015	0.509**	0.395*	0.552**	0.715**	0.836**	0.309	0.646**
Plant height	r_g		0.692**	-0.618**	0.365	0.584**	0.314	0.428*	0.431*	0.609**	0.528**	0.521**
	r_p		0.633**	-0.370	0.367	0.476*	0.254	0.368	0.360	0.298	0.498**	0.445*
Flag leaf area	r_g			-0.762**	-0.077	0.890**	0.626**	0.672**	0.674**	0.764**	0.706**	0.814**
	r_p			-0.428*	-0.025	0.646**	0.401*	0.499**	0.486*	0.331	0.598**	0.591**
Number of panicle	r_g				0.010	0.619**	-0.277	-0.292	-0.184	0.070	-0.697**	-0.550**
	r_p				0.017	-0.333	-0.124	-0.183	-0.114	0.023	-0.453*	-0.111
Length of panicle	r_g					-0.086	-0.063	-0.064	-0.172	-0.298	0.184	-0.107
	r_p					-0.045	0.017	-0.016	-0.111	-0.151	0.164	-0.051
Primary branch	r_g						0.754**	0.928**	0.884**	0.813**	0.439*	0.835**
	r_p						0.588**	0.777**	0.728**	0.413*	0.357	0.658**
Secondary branch	r_g							0.935**	0.778**	0.354	-0.012	0.719**
	r_p							0.837**	0.684**	0.171	-0.042	0.553**
Number of spikelet	r_g								0.981**	0.967**	0.157	0.885**
	r_p								0.918**	0.450*	0.118	0.710**
Number of grain	r_g									1.022**	0.170	1.000**
	r_p									0.730**	0.143	0.846**
Spikelet fertility per cent	r_g										0.360	1.217**
	r_p										0.209	0.716**
Test weight	r_g											0.584**
	r_p											0.471*

*, **: Significant at 5% and 1%, respectively.

In general, genotypic and phenotypic correlations (**Table 2**) showed a similar trend, with the magnitude of genotypic correlations being greater than the corresponding phenotypic correlations in a majority of the cases. Seed yield exhibited significant and positive correlations at both levels with plant height, flag leaf area, days to flowering, primary and secondary branches per panicle, spikelet and filled grain number, spikelet fertility (%) and test weight. This indicated the contributions of these traits towards seed yield. A similar association of grain yield was reported for days to flowering (Adhikari *et al., 2018*), plant height and test weight (Devi *et al*., 2017; Tiwari *et al*., 2019), the number of grains per panicle

(Khare *et al*., 2014; Devi *et al*., 2017), primary branches (Hossain *et al*., 2018) and secondary branches (Islam *et al.,* 2019). The results of character association implied that plant height, flag leaf area, days to flowering, primary and secondary branches per panicle, spikelet and grain number, spikelet fertility (%) and test weight might be important for determining seed yield in this population of rice.

The genotypic path coefficient analysis (**Table 3**) was carried out to study the effects of 10 characters on grain yield. Grain number being the product spikelet number and its fertility coefficient was excluded. The use of

Table 3. Genotypic path analysis of ten quantitative traits on seed yield in rice

Characters	Days to flowering	Plant height	Flag leaf area	Number of panicle	Length of panicle	Primary branch	Secondary branch	Number of spikelet	Spikelet fertility per cent	Test weight	Correlation with seed yield
Days to flowering	**0.2080**	0.3840	-0.6720	-0.0720	-0.0080	0.3630	0.4600	0.1640	-0.5710	0.5330	0.7890**
Plant height	0.1020	**0.7820**	-1.0880	-0.3860	-0.2900	0.3550	0.2880	0.1090	-0.2050	0.8540	0.5210**
Flag leaf area	0.0890	0.5410	**-1.5710**	-0.4760	0.0610	0.5410	0.5740	0.1710	-0.2580	1.1420	0.8140**
Number of panicle	-0.0240	-0.4830	1.1970	**0.6250**	-0.0080	-0.3770	-0.2540	-0.0740	-0.0240	-1.1290	-0.5510**
Length of panicle	0.0020	0.2850	0.1210	0.0060	**-0.7930**	-0.0520	-0.0570	-0.0160	0.1000	0.2970	-0.1070
Primary branch	0.1240	0.4560	-1.3980	-0.3870	0.0680	**0.6090**	0.6910	0.2360	-0.2740	0.7100	0.8350**
Secondary branch	0.1040	0.2460	-0.9830	-0.1730	0.0500	0.4590	**0.9170**	0.2380	-0.1200	-0.0190	0.7190**
Number of spikelet	0.1340	0.3340	-1.0550	-0.1830	0.0510	0.5650	0.8570	**0.2540**	-0.3260	0.2540	0.8850**
Spikelet fertility per cent	0.3520	0.4760	-1.2010	0.0440	0.2360	0.4950	0.3250	0.2460	**-0.3370**	0.5820	1.2180**
Test weight	0.0680	0.4120	-1.1090	-0.4360	-0.1460	0.2670	-0.0110	0.0400	-0.1210	**1.6190**	0.5830**

Residaul effect= 0.0399; *, **: Significant at 5% and 1% levels, respectively; Bold figures indicate direct effects.

only direct yield components in path analysis has been suggested by Shrivastava and Sharma (1976). The results revealed that inflation due to multi-colinearity, which may vitiate the results, is minimal as the majority of values in path analysis are less than unity (Gravois and Helms, 1992). The direct positive effect of test weight (1.619) was highest, followed by secondary branches (0.917), plant height (0.782), panicle number (0.625) and primary branches (0.609). These characters had a highly significant and positive association with grain yield. Very low residual effect (0.0399) indicated that 96 per cent of the variation in grain yield in this population is contributed by the ten characters included in the path analysis. *Similar results have been recorded earlier* for the number of panicle (Kole *et al*., 2008; *Devi et al., 2017),* plant height (Jambhulkar and Bose, 2014; Li *et al*., 2019), *test weight (*Kole *et al*., 2008; Islam *et al.,* 2019)*, primary branches (Hossain et al., 2018) and secondary branches (*Islam *et al.,* 2019). The overall results indicated that the direct selection of primary and secondary branches per panicle and test weight in the positive direction with restricted selection for panicle number and spikelet fertility would increase the grain yield of rice in this particular population.

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