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Genetic variability and character association study for yield and its component traits in rice (*Oryza sativa* L.)

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Abstract
The present investigation was carried out with thirty two genotypes of rice to study nature and magnitude of variability, degree of association between yield and its component traits and to assess direct and indirect effects of different characters on the grain yield. The analysis of variance revealed significant differences for the characters under study, indicating the presence of high genetic variability among the genotypes. The value of PCV was relatively higher than GCV values with small differences which indicate less environmental influence on the expression of all the traits. High heritability was recorded for all the traits studied. Filled grains per panicle and total grain per panicle exhibited highest heritability followed by plant height and unfilled grains per panicle. Positive and significant correlation was observed between unfilled grains per panicle and yield. In path coefficient analysis the traits like days to maturity, effective tillers, plant height, filled grain per panicle, unfilled grain per panicle and test weight show positive direct effect whereas traits like days to 50% flowering, panicle length, total grains per panicle and spikelet fertility % showed negative direct effect with grain yield per plant.

Keywords: PCV, GCV, heritability, genetic advance, correlation and path coefficient analysis

Introduction
Rice, *Oryza sativa* L. (2n=24) belongs to family Poaceae (Graminae) and the genus *Oryza* has two cultivated species namely: *Oryza sativa* (Asian rice) and *Oryza glaberrima* (African rice). Rice is a short day self-pollinated crop, needs a hot humid climate with an average temperature $21\ ^0C$ to $37\ ^0C$ throughout the life cycle of crop. About 90% of the world's rice is grown and consumed by Asians. Asian cultivated rice is the world's most important food crop and is primary food source for more than one third of the world's population. Rice accounts for about 35 to 60% of the calories consumed by 3 billion Asians (Khush, 2005) [8]. The execution of any breeding programmes depends largely on the presence of significant genetic variability to permit effective selection. To increase the production, a critical analysis of genetic variability, heritability and genetic advance for quantitative traits components is essential for effective genetic improvement along with the estimation of nature of character associations of yield and yield attributing traits by means of correlation coefficients and assessment of the direct and indirect contribution of yield components on grain yield through path-coefficient analysis is a pre-requisite for initiating any crop improvement programme and for adoption of appropriate selection techniques (Pallavi *et al.,* 2017) [13]. Heritability is a good index of the transmission of character from parents to their offspring. The estimates of heritability provide authentic information about a particular genetic attribute which will be transmitted to the successive generations and constitute an efficient guide for breeders in the choice of parents for crop improvement in selection of elite genotypes from diverse genetic populations (Rashmi *et al.*, 2017) [18]. Therefore, the objective of this study was to assess the genetic variability, heritability and genetic advance of yield and yield related traits in rice genotypes to assist the future breeding programme for yield improvement and to identify the elite genotypes.

Materials and Methods
The present experiment on genetic variability, correlation, and path coefficient study was conducted at the Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, in a randomized block design (RBD) with three replications following a recommended spacing of (15×20) cm between plants and rows respectively. The study consists of thirty two rice genotypes obtained from the Department of Genetics and Plant

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Breeding, Banaras Hindu University, Varanasi. Observations were recorded on eleven yield and yield contributing quantitative traits on five randomly selected plants from each entry in each replication and their mean were used for the statistical analyses. The quantitative characters that were evaluated include days to 50 flowering %, days to maturity, effective tillers per plant, plant height (cm), panicle length (cm), filled grains per panicle, unfilled grains per panicle, total grains per panicle, spikelet fertility percent (%), test weight (g) and grain yield per plant (g). The thirty two rice genotypes were tabulated in (Table 1).

Table 1: List of rice genotypes used in the present study

S. No.	Genotypes	S. No.	Genotypes	S. No.	Genotypes	S. No.	Genotypes
1	PB01	11	IC256528	21	IC256621	31	IC260964
2	IC256514	12	IC256530	22	TETAP	32	IC264136
3	IC256515	13	IC256534	23	IC256629		
4	IC256516	14	IC256535	24	IC256754		
5	IC256518	15	IC256537	25	IC256807		
6	IC256520	16	IC256538	26	IC260891		
7	IC256521	17	IC256589	27	IC260917		
8	IC256523	18	IC256613	28	IC260924		
9	IC256525	19	IC256616	29	IC260937		
10	IC256527	20	IC256617	30	IC260961		

Statistical Analysis

The experimental data were compiled by taking mean value over randomly selected plants for all the three replications and subjected to the following statistical analysis. The analysis of variance was carried out by following the procedure of randomized block design (RBD) analysis (Panse and Sukhatme, 1967). Differences were declared statistically significant at $P < 0.05$. In this study, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated by the formula given by Burton and Devane (1953). Heritability in broad sense (h^2) and genetic advance as percent of mean were estimated by the formula as suggested by Allard (1960) [2]. The simple phenotypic correlation coefficients among pairs of characters were calculated according to the formula suggested by Searle (1961) [21]. To test the significance of correlation coefficients, the estimated values were compared with the table value at n-2 degrees of freedom (where n denotes the number of genotypes tested) at 5% and 1% levels of significance. Path-coefficient analysis was done to partition the total correlation into direct and indirect effects due to the dependent variable. Wright (1934) suggested this analysis and it was further elaborated by Dewey and Lu (1959) [7].

Results and Discussion

The analysis of eleven quantitative traits was carried out to partition the total variation into genotypic variation and variation due to other sources. The results of ANOVA revealed significant differences among the genotypes in respect to all the characters under study (Table 2). The analysis of variance exhibited the presence of highly significant differences at ($P < 0.01$) among the genotypes for all the characters studied. The results are in accordance to those found by (Loitongbam *et al.,* 2019) [11].

Estimation of Genetic parameters

Estimation of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), broad sense heritability (h^2), genetic advance (GA) and genetic advance as percentage of the mean (GAM) are shown in Table 3. In this study, the value of PCV were relatively higher than GCV values with small differences which indicate less environmental influence on the expression of all the traits. These findings were similar to the findings of Babu *et al.* (2012) [3] Prasad *et al.* (2014), and Rashid *et al.* (2017) [17].

The highest PCV and GCV were recorded for unfilled grains per panicle followed by grain yield per plant, effective tillers per plant, total grain per panicle and filled grain per panicle indicating that these traits were under the major influence of genetic control and less variable due to environmental factors. Therefore, such traits are important for further improvement. These findings are in close agreement with the researchers Shrivastava *et al.* (2015) [22], Limbani *et al.* (2017) [10], Prasad *et al.* (2017), Rashid *et al.* (2017) [17] for unfilled grains per panicle, grain yield per plant, effective tillers per plant, total grain per panicle and filled grain per panicle. High heritability was recorded for all the traits studied. The highest heritability was found in filled grains per panicle (98.44%) followed by total grains per panicle (98.22%) and plant height (96.60%), unfilled grains per panicle (96.07%), test weight (94.76%), days to 50% flowering (93.24%), days to maturity (92.96%), effective tillers per plant (92.75%) and grain yield per plant (89.63%). High heritability was observed in panicle length (81.50%) followed by spikelet fertility % (79.61%). Similar reports were also made by Rashid *et al.* (2017) [17], Prasad *et al.* (2017). This indicated that selection of these traits would be more effective as compared to others. High heritability coupled with high genetic advance as percent was recorded for unfilled grains per panicle, filled grains per panicle, total grains per panicle and effective tillers per plant indicating effectiveness of selection for the improvement of these traits, while high heritability coupled with moderate genetic advance as percent of mean were observed for panicle length, days to maturity, days to 50% flowering and spikelet fertility % which is indicative of non-additive gene action. These results of high heritability and high genetic advance by percent mean are in conformity with the findings of Bisne *et al.* (2009) and Rashid *et al.* (2017) [17]. Genetic advance as percent of mean (5%) was realized highest for unfilled grains per panicle (155.95) followed by effective tillers per plant (94.47) and grain yield per plant (92.40). Lowest value was observed in spikelet fertility % (20.49) followed by days to maturity (21.45). All the characters studied had high to moderate genetic advance as percent of mean.

Correlation coefficient analysis

Correlation coefficient analysis measures the mutual relationship of various traits of plant that determines the component characters on which selection can be based for genetic improvement in yield. The phenotypic and genotypic

correlation coefficient between yield and its component traits were computed for all possible combinations and presented in Table 4 and Table 5. The results on correlation analysis showed that the characters like days to maturity ($r_g = 0.6617$ $r_p = 0.6246$), days to 50% flowering ($r_g = 0.6564$ $r_p = 0.6202$), effective tillers per plant ($r_g = 0.5557$ $r_p = 0.5534$), filled grain per panicle ($r_g = 0.5061$ $r_p = 0.4923$), total grain per panicle ($r_g = 0.4675$ $r_p = 0.4533$) and plant height ($r_g = 0.3258$ $r_p = 0.3100$) found highly significant and positive correlation with yield at both genotypic and phenotypic level which indicated strong association of these traits with the yield. Similar results were also reported by Rajeshwari *et al.* (2004) for plant height and total grains per panicle. Positive and significant correlation was also observed between yield and number of unfilled grains per panicle ($r_g = 0.2600$ $r_p = 0.2504$) whereas, characters like panicle length ($r_g = 0.1120$ $r_p = 0.0814$) and test weight ($r_g = 0.1952$ $r_p = 0.1997$) showed the positive but non-significant correlation. Panicle length had positive and significant association with test weight. This was in accordance with the findings of Allam *et al.* (2015) [1]. Grain yield per plant was found to be positive and significantly correlated with traits like days to 50% flowering, days to maturity, plant height, effective tillers per plant, filled grains per panicle, unfilled grain per panicle and total grains per panicle at both genotypic and phenotypic levels indicating the relative utility of these traits for selection with respect to grain yield. Similar findings were observed by Allam *et al.* (2015) [1], Sudeepthi *et al.* (2018).

Path coefficient analysis
Path coefficient analysis developed by Sewall Wright (1918) determines the significance of correlations between yield components and assigns relative importance to yield relations (Table 6; Table 7). Traits like days to maturity, effective tillers per plant, plant height, filled grains per panicle, unfilled grains per panicle and test weight exhibit positive direct effect while days to 50% flowering, panicle length, total grain per panicle and spikelet fertility % had negative direct effect on grain yield per plant. These findings are in accordance with Kishore *et al.* (2015) [9], Sudeepthi *et al.* (2018). The strong positive association of days to maturity with grain yield per plant was mainly through its direct effect at phenotypic level. However, it was also due to the indirect effect through days to 50% flowering, plant height, filled grains per panicle, unfilled grains per panicle, total grains per panicle and test weight resulting into a considerable positive and significant association of it with grain yield per plant. The strong and positive association of filled grain per panicle with grain yield per plant was mainly through its direct effect at genotypic level and it was also due to the indirect effect through days to 50% flowering, days to maturity, plant height, panicle length, unfilled grains per panicle and total grains per panicle resulting into a considerable positive and significant association of it with grain yield per plant. Hence, selection for these characters could bring improvement in yield and yield components. This was also observed by Maurya *et al.* (2019) [12], Bagheri *et al.* (2011) [4], Sarker *et al.* (2014) [20], Ratna *et al.* (2015) [19].

Table 2: Analysis of variance (ANOVA) for eleven quantitative traits in thirty two rice genotypes

Source of variation	df	Mean sum of squares										
		DF	DM	ET	PH	PL	FGPP	UFGPP	TGPP	SF (%)	TW	GYP
Replication	2	6.14	6.13	1.38	59.68	0.71	30.95	11.23	90.79	6.62	0.57	30.92
Treatment	32	514.79**	493.45**	59.39**	1861.29**	29.28**	6198.68**	1414.51**	11149.81**	271.80**	54.85**	277.71**
Error	64	12.15	12.14	1.51	21.56	2.06	32.63	19.02	66.85	21.38	0.99	10.31

Days to 50% flowering(DF), days to Maturity(DM), no. of effective tillers per plant(ET), plant height(PH), panicle length(PL), filled grains per panicle(FGPP), unfilled grains per panicle(UFGPP), total grains per panicle(TGPP), spikelet fertility percent(SF%), test weight(TW), grain yield per plant(GYP).
*Significant at $p < 0.05$; **Significant at $p < 0.01$

Table 3: Variability parameters for eleven quantitative characters in thirty two rice genotypes

Traits	DF	DM	ET	PH	PL	FGPP	UFGPP	TGPP	SF%	TW	GYP
Range Min. Max.	66.37	98.37	4.83	86.00	23.40	52.30	2.07	68.17	64.92	14.99	5.68
	118.37	146.37	21.93	206.43	40.03	214.20	78.17	292.37	98.22	34.56	47.49
Mean	86.55	117.30	9.22	14.80	28.48	116.00	27.92	143.65	81.96	24.75	19.93
PCV (%)	15.49	11.19	49.44	18.69	11.71	39.39	78.80	42.69	12.49	17.59	50.04
GCV (%)	14.96	10.79	47.62	18.37	10.57	39.08	77.24	42.31	11.15	17.12	47.38
h² % (broad sense)	93.24	92.96	92.75	96.60	81.50	98.44	96.07	98.22	79.61	94.76	89.63
GA as % of mean (5%)	29.75	21.45	94.47	37.19	19.67	79.88	155.95	86.39	20.49	34.33	92.40
GA as % of mean (1%)	38.12	27.49	121.07	47.67	25.20	102.37	199.86	110.71	26.25	43.99	118.42

Days to 50% flowering(DF), days to Maturity(DM), no. of effective tillers per plant(ET), plant height(PH), panicle length(PL), filled grains per panicle(FGPP),unfilled grains per panicle(UFGPP), total grains per panicle(TGPP), spikelet fertility percent(SF%), test weight(TW), grain yield per plant(GYP).

Table 4: Estimates of phenotypic correlation between yield and its related characters from thirty two rice genotypes

Characters	DM	ET	PH	PL	FGPP	UFGPP	TGPP	SF%	TW	GYP
DF	0.9953**	0.0150	0.6253**	0.2072*	0.6395**	0.2489*	0.5662**	0.0029	0.3048**	0.6202**
DM		0.0342	0.5867**	0.1706	0.6211**	0.2387*	0.5491**	0.0058	0.2796**	0.6246**
ET			-0.1808	-0.2359*	-0.1224	-0.0876	-0.1272	-0.0559	-0.1502	0.5534**
PH				0.4319**	04836**	0.0515	0.3788**	0.1996	0.3672**	0.3100**
PL					0.2243*	0.1685	0.2273*	0.0028	0.4387**	0.0814
FGPP						0.5783**	0.9558**	-0.0994	0.0001	0.4923**
UFGPP							0.7899**	-0.7601**	-0.2465*	0.2504*
TGPP								-0.3404**	-0.0881	0.4533**
SF%									0.3128**	-0.1245

										0.1997
TW										

Days to 50% flowering(DF), days to Maturity(DM), no. of effective tillers per plant(ET), plant height(PH), panicle length(PL), filled grains per panicle(FGPP),unfilled grains per panicle(UFGPP), total grains per panicle(TGPP), spikelet fertility percent(SF%), test weight(TW), grain yield per plant(GYP).
*Significant at $p < 0.05$; **Significant at $p < 0.01$

Table 5: Estimates of genotypic correlation between yield and its related characters from thirty two rice genotypes.

Characters	DM	ET	PH	PL	FGPP	UFGPP	TGPP	SF%	TW	GYP
DF	0.9949**	-0.0019	0.6488**	0.2755**	0.6636**	0.2470*	0.5831**	0.0253	0.3210**	0.6564**
DM		0.0185	0.6088**	0.2346*	0.6453**	0.2362*	0.5659**	0.0292	0.2946**	0.6617**
ET			-0.1878	-0.2783**	-0.1371	-0.0942	-0.1400	-0.0409	-0.1700	0.5557**
PH				0.5111**	0.4977**	0.0527	0.3901**	0.2564*	0.3965**	0.3285**
PL					0.2548*	0.2214*	0.2683	-0.0520	0.4988**	0.1120
FGPP						0.5915**	0.9589**	-0.1262	-0.0082	0.5061**
UFGPP							0.7960**	-0.8036**	-0.2651**	0.2600*
TGPP								-0.3704**	-0.0993	0.4675**
SF%									0.3750**	-0.1225
TW										0.1952

Days to 50% flowering(DF), days to Maturity(DM), no. of effective tillers per plant(ET), plant height(PH), panicle length(PL), filled grains per panicle(FGPP),unfilled grains per panicle(UFGPP), total grains per panicle(TGPP), spikelet fertility percent(SF%), test weight(TW), grain yield per plant(GYP).
*Significant at $p < 0.05$; **Significant at $p < 0.01$

Table 6: Phenotypic path matrix of eleven quantitative traits on grain yield per plant in a diverse collection of thirty two rice genotypes

Characters	DF	DM	ET	PH	PL	FGPP	UFGPP	TGPP	SF%	TW	GYP
DF	-0.8127	-0.8088	-0.0121	-0.5082	-0.1684	-0.5197	-0.2023	-0.4601	-0.0024	-0.2477	0.6202**
DM	1.0548	1.0598	0.0363	0.6218	0.1808	0.6582	0.2530	0.5819	0.0062	0.2963	0.6246**
ET	0.0091	0.0207	0.6059	-0.1096	-0.1429	-0.0742	-0.0531	-0.0771	-0.0339	-0.0910	0.5534**
PH	0.0240	0.0225	-0.0069	0.0383	0.0166	0.0185	0.0020	0.0145	0.0077	0.0141	0.3100**
PL	-0.0013	-0.0011	0.0015	-0.0027	-0.0064	-0.0014	-0.0011	-0.0014	0.0000	-0.0028	0.0814
FGPP	0.5285	0.5133	-0.1012	0.3997	0.1854	0.8265	0.4780	0.7899	-0.0821	0.0001	0.4923**
UFGPP	0.0125	0.0120	-0.0044	0.0026	0.0085	0.0290	0.0502	0.0396	-0.0381	-0.0124	0.2504*
TGPP	-0.2772	-0.2688	0.0623	-0.1855	-0.1113	-0.4679	-0.3867	-0.4896	0.1667	0.0431	0.4533**
SF%	- 0.0007	-0.0014	0.0131	-0.0467	-0.0007	0.0232	0.1778	0.0796	-0.2339	-0.0732	-0.1245
TW	0.0833	0.0764	-0.0410	0.1003	0.1198	0.0000	-0.0673	-0.0241	0.0854	0.2731	0.1997

$R^2 = 0.7858$ Residual effect = 0.4628(Phenotypic)
Values in bold characters are direct effects and rests are indirect effects.
*Significant at $p < 0.05$; **Significant at $p < 0.01$

Table 7: Genotypic path matrix of eleven quantitative traits on grain yield per plant in a diverse collection of thirty two rice genotypes

Characters	DF	DM	ET	PH	PL	FGPP	UFGPP	TGPP	SF%	TW	GYP
DF	-0.9767	-0.9718	0.0018	-0.6337	-0.2691	-0.6482	-0.2412	-0.5695	-0.0247	-0.3135	0.6564**
DM	1.2405	1.2468	0.0231	0.7591	0.2924	0.8045	0.2945	0.7056	0.0364	0.3673	0.6617**
ET	-0.0011	0.0112	0.6072	-0.1140	-0.1690	-0.0832	-0.0572	-0.0850	-0.0248	-0.1032	0.5557**
PH	0.0204	0.0191	-0.0059	0.0314	0.0160	0.0156	0.0017	0.0122	0.0080	0.0124	0.3285**
PL	-0.0056	-0.0048	0.0056	-0.0104	-0.0203	-0.0052	-0.0045	-0.0054	0.0011	-0.0101	0.1120
FGPP	2.8613	2.7822	-0.5910	2.1458	1.0986	4.3116	2.5502	4.1344	-0.5440	-0.0354	0.5061**
UFGPP	0.4268	0.4081	-0.1628	0.0911	0.3826	1.0219	1.7278	1.3753	-1.3885	-0.4581	0.2600*
TGPP	-3.0007	-2.9122	0.7206	-2.0076	-1.3805	-4.9345	-4.0963	-5.1461	1.9062	0.5111	0.4675**
SF%	-0.0052	-0.0060	0.0084	-0.0527	0.0107	0.0259	0.1651	0.0761	-0.2054	-0.0770	-0.1225
TW	0.0969	0.0889	-0.0513	0.1196	0.1505	-0.0025	-0.0800	-0.0300	0.1132	0.3018	0.1952

$R^2 = 0.8388$ Residual effect = 0.4015(Genotypic)
Values in bold characters are direct effects and rests are indirect effects.
*Significant at $p < 0.05$; **Significant at $p < 0.01$

Conclusion

In this experiment, we conclude that the germplasms exhibited a wide range of variability for most of the traits. This indicated that there is ample scope for selection of promising genotypes for yield improvement. Among the thirty two rice genotypes, on the basis of *per se* performance, genotypes PB01 and TETAP were found to be the best for yield and yield contributing traits. Therefore, these can be successfully utilized as parents in hybridization programme to obtain potential transgressive segregants in crop improvement programme.

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