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Genetic Variability Study for Yield and Yield Components in Rice (*Oryza sativa* L.)

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ABSTRACT

Sixty five rice germplasms were evaluated for variability, heritability, genetic advance, correlation coefficient and path correlation in different yield and yield contributing traits. The data was recorded on five randomly selected plants for eleven quantitative characters. The analysis of variance revealed significant differences for the characters under study, indicating the presence of high genetic variability among the genotypes. The estimates of GCV were lower than the respective PCV, indicating the influence of environmental factors on the expression of the traits studied. Characters like days to maturity, days to 50% flowering and panicle weight showed high heritability coupled with moderate genetic advance as percent of mean, suggesting that selection for the improvement of these characters may be rewarding. Grain yield had high positive and significant association with panicle weight, filled grains per panicle, total grains per panicle and panicle length. Path coefficient analysis showed maximum direct contribution towards grain yield per plant with panicle weight followed by numbers of effective tillers per plant.

Highlights

* The panicle weights, filled grains per panicle, total grains per panicle showed high heritability along with moderate genetic advance.
* The genotypes RP 5330-63-5-2-1-B, LC-5 and GK 5022 can be used effectively as donor parent for hybridization programme.

Keywords: Heritability, genetic advance, correlation, path-coefficient, GCV, PCV

The knowledge of genetic variability for the characters of economic importance and their heritability and genetic advance is of utmost importance in designing future breeding programme. The germplasm serves as a valuable source of base population and provides scope for wide variability. The knowledge about genetic variability of yield contributing traits, interrelationship among them and their relation with yield are necessary for successful breeding programme. Though a wide range of genetic variability has been reported for yield traits in the past, but still there exists untapped genetic variability in germplasms which is of paramount importance in selecting the potential parents so as to get maximum heterosis and

superior recombinants. Genetic parameters such as genotypic coefficient of variation and phenotypic coefficient of variation are useful in detecting the amount of variability present in the germplasm. Heritability is a good index of the transmission of character from parents to their offspring (Falconer, 1981). The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic populations.

However, it is not necessary that a character showing high heritability will also exhibit high genetic advance (Johnson, *et. al.,* 1955). Genetic advance is the measure of genetic gain under selection. Heritability coupled with high genetic advance helps in determining the influence of environment

on the expression of the genotype and reliability of characters. Genotypic correlation among yield trait and its components provide the information about their performance and association with one another. With the above background information, the present investigation was undertaken to estimate genetic variability for yield characteristic and unravel the correlation of different grain yield traits among a set of sixty five rice germplasms.

MATERIALS AND METHODS

The present investigation was carried out at the Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi during the *kharif* season 2016. Experimental materials consisted of 65 rice germplasms presented in table 1 received from DBT Networking Project, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. Each genotype was grown in 5 m² plot in three replications. Recommended management practices were followed. Observations on yield and yield attributing traits were recorded on ten randomly selected plants of each germplasm in every replication. The observations were recorded on eleven quantitative characters viz., days to 50% flowering, days to maturity, effective tillers per plant, plant height(cm), panicle length(cm), panicle weight(g), filled grains per panicle, total grains per panicle, spikelet fertility percent, test weight(g) and grain yield per plant(g).

The data was analyzed by the Analysis of Variance (ANOVA) and interrelationships among traits values were estimated using SAS software version 9.1 (SAS Institute, 1998). 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). The correlation coefficient among pairs of characters was calculated according to the formula suggested by Searle (1961). To test the significance of correlation coefficients, the estimated values were compared with the table value (statistical table by Fisher and

Table 1: Name of the rice germplasms used under study

Sl. No.	Genotype	Sl. No.	Genotype	Sl. No.	Genotype
1	OR 1946-2-1	2	IR 83142-76	3	Vandana
4	IR 82635-B-B-47-1	5	IR 82589-B-B-7-2	6	IR 82635-B-B-23-1
7	CRR 660-2	8	CRR 428-237-1-3-1	9	Rewa 1208-15
10	IR 83399-B-B-52-1	11	PAU 3832-79-4-3-1	12	IR 83182-6-4
13	IR 78755-190-B-1-3	14	IR 82635-B-B-25-4	15	RP 5345-9-6-3
16	RRF-48	17	IR 55423-01	18	CB 10-504
19	GK 5022	20	Anjali	21	IR 10L-105
22	B 11576F-MR-18-2	23	CR 3631-1-3	24	BAU 411-05
25	IR 82921-B-B-1	26	BD 104	27	IR 77298-14-1-2-13
28	CR 422-63-51-B-2-1-1-1-B	29	IR 1718-59-1-2-3	30	IR 82635-B-B-145-1
31	NDR 1140	32	CR 3633-1-2	33	IR 368B-TB-25-MP-2
34	UPLRI – 7	35	IR 87694-28-7-2-1	36	RP 5330-63-5-2-1-B
37	MGD 1206	38	IR83867-B-B-250-CRA-1-1	39	IR 83926-B-B-71-4
40	IR 60080-46A	41	BD 108	42	BVS 1
43	BVD 111	44	BVD 203	45	BAU 389-02
46	BAU/IRRI 497	47	LC -1	48	LC -2
49	LC -3	50	LC -4	51	LC -5
52	LC – 6	53	LC – 7	54	LC – 8
55	LC – 9	56	LC – 10	57	LC – 11
58	LC – 12	59	LC – 13	60	LC – 14
61	LC – 15	62	LC – 16	63	LC – 17
64	LC – 18	65	LC – 19		

Table 2: Analysis of variance (ANOVA) for eleven quantitative traits in sixty five rice germplasms

Source of variation	df	Mean Sum of Squares										
		DF	DM	ET	PH	PL	PW	FGP	TGP	SF%	TW	GYP
Replication	2	1.00	10.23	7.45	114.74	0.51	0.07	5.17	15.32	25.18	7.34	1.65
Treatment	64	994.01**	960.59**	12.90**	2060.52**	23.77**	2.48	3692.41**	4949.83**	181.33**	44.57**	95.23**
Error	128	4.99	4.19	2.55	88.75	0.72	0.11	244.88	157.38	40.46	3.01	8.36

**Significant at $p < 0.01$.*

Table 3: Variability parameters for eleven quantitative characters in 65 rice germplasms

Trait		DF	DM	ET	PH	PL	PW	FGP	TGP	SF%	TW	GYP
Range	**Min.**	82.33	111.67	6.27	63.42	15.79	0.91	43.93	52	60	10.02	5.22
	Max.	155.34	180.34	15.00	188.54	33.38	5.77	210.07	251.33	93.63	32.30	33.90
Grand Mean		106.11	138.84	9.72	119.72	25.46	3.03	127.52	156.09	81.32	21.92	22.38
SE (±)		1.29	1.18	0.92	5.44	0.49	0.19	9.03	7.24	3.67	1.00	1.67
PCV (%)		17.24	12.94	25.21	22.81	11.39	31.38	29.28	26.84	11.50	18.73	27.30
GCV (%)		17.11	12.86	19.12	21.41	10.89	29.36	26.58	25.61	8.43	16.98	24.04
h^2 % (broad sense)		98.51	98.70	57.48	88.10	91.40	87.51	82.43	91.03	53.42	82.18	77.59
GA as % of mean (5%)		34.98	26.32	29.85	41.40	21.44	56.57	49.72	50.33	12.72	31.71	43.63
GA as % of mean (1%)		44.83	33.73	38.26	53.06	27.47	72.50	63.72	64.50	16.31	40.64	55.91

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

Yates, 1963) at n-2 degrees of freedom (where n denotes the number of genotypes tested) at 5% and 1% level 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).

RESULTS AND DISCUSSION

ANOVA

The analysis of variance revealed highly significant differences among the germplasms for all the eleven quantitative characters indicating the existence of significant amount of variability among the characters studied (Table 2). These findings are in accordance with the findings of Paikhomba *et al.* (2014).

Per se performance

Genotype RP 5330-63-5-2-1-B (33.90 g) recorded highest mean performance for grain yield per plant followed by LC-5 (33.09 g) and GK 5022 (32.36

g) indicating that these genotypes can be used in hybridization programme in order to achieve desirable increment in yield. Genotype MGD 1206 was earliest in flowering and maturity suggesting that this genotype can be used as a donor parent in hybridization programme for evolving early maturity or short duration rice. Germplasm LC-10 had highest mean performance for panicle length followed by Anjali and BAU/IRRI 497. Germplasm IR 83926-B-B-71-4 was the shortest and IR 83142-76 was the tallest.

Genetic variability

The magnitude of genetic variability decides the effectiveness of selection. It is an established fact that greater the variability among the genotypes better is the chance for further improvement in the crop. In this study, the estimates of PCV were higher than their corresponding GCV for all the traits studied (Table 3). These findings were similar to the findings of Singh *et al.* (2013) Paikhomba *et al.* (2014) and Anis *et al.* (2016). A high estimate of phenotypic and genotypic coefficients of variation were recorded for
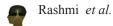
Table 4: Estimate of phenotypic correlation between yield and its related characters from 65 rice germplasms

Character	DM	ET	PH	PL	PW	FGP	TGP	SF%	TW	GYP
DF	0.9763***	-0.0840	0.5526***	0.0995	0.1200	0.2833***	0.3262***	-0.0194	-0.2852***	0.0160
DM		-0.1016	0.5646***	0.1437*	0.1404	0.2842***	0.3320***	-0.0374	-0.2411***	0.0342
ET			0.0210	-0.1880**	-0.2762***	-0.2036**	-0.2624***	0.1091	-0.1380	0.1450*
PH				0.3251***	0.4053***	0.3754***	0.3860***	0.0988	0.0680	0.3474***
PL					0.5255***	0.4156***	0.4568***	0.0122	0.2902***	0.4382***
PW						0.7462***	0.6816***	0.2752***	0.4627***	0.7144***
FGP							0.9047***	0.3632***	-0.0922	0.5401***
TGP								0.0382	-0.1698*	0.4718***
SF%									0.1281	0.2560***
TW										0.3585***

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

*Significant at $p<0.05$; **Significant at $p<0.01$; ***Significant at $p<0.001$

Table 5: Phenotypic path matrix of eleven quantitative traits on grain yield per plant in a diverse collection of 65 rice germplasms

Character	DF	DM	ET	PH	PL	PW	FGP	TGP	SF%	TW	GYP
DF	**-0.1098**	-0.1072	0.0092	-0.0607	-0.0109	-0.0132	-0.0311	-0.0358	0.0021	0.0313	0.0160
DM	0.0340	**0.0349**	-0.0035	0.0197	0.0050	0.0049	0.0099	0.0116	-0.0013	-0.0084	0.0342
ET	-0.0311	-0.0376	**0.3705**	0.0078	-0.0697	-0.1023	-0.0754	-0.0972	0.0404	-0.0511	0.1450*
PH	0.0229	0.0234	0.0009	**0.0414**	0.0135	0.0168	0.0156	0.0160	0.0041	0.0028	0.3474***
PL	0.0089	0.0129	-0.0169	0.0292	**0.0897**	0.0472	0.0373	0.0410	0.0011	0.0260	0.4382***
PW	0.0771	0.0902	-0.1775	0.2604	0.3376	**0.6425**	0.4794	0.4379	0.1768	0.2973	0.7144***
FGP	0.0180	0.0180	-0.0129	0.0238	0.0264	0.0473	**0.0634**	0.0574	0.0230	-0.0058	0.5401***
TGP	0.0176	0.0179	-0.0141	0.0208	0.0246	0.0367	0.0488	**0.0539**	0.0021	-0.0092	0.4718***
SF%	0.0000	0.0001	-0.0002	-0.0002	0.0000	-0.0006	-0.0008	-0.0001	**-0.0021**	-0.0003	0.2560***
TW	-0.0216	-0.0183	-0.0105	0.0052	0.0220	0.0351	-0.0070	-0.0129	0.0097	**0.0758**	0.3585***

$R^2 = 0.6522$ and Residual effect = 0.5898; values in bold characters are direct effects and rest are indirect effects.

*Significant at $p<0.05$; **Significant at $p<0.01$; ***Significant at $p<0.001$.*

panicle weight followed by filled grains per panicle indicating that these traits were under the major influence of genetic control and less variable due to environmental factors. PCV was recorded highest for panicle weight (31.38) followed by filled grains per panicle (29.28) and grain yield per plant (27.30). Low magnitude of PCV was exhibited by panicle length (11.39) followed by spikelet fertility percent (11.50) and days to maturity (12.94). Similarly, GCV was also high for panicle weight (29.36) followed by filled grains per panicle (26.58) and total grains per panicle (25.61). Therefore, traits like panicle weight and filled grains per panicle are important for further improvement. These findings are in close

agreement with the researchers Tuhina Khatun *et al.* (2015) and Sawarkar and Senapati (2014).

Heritability

The heritable portion of the overall observed variation can be ascertained by studying the heritability in broad sense. The estimates of heritability were observed to be high in magnitude for all the characters, except effective tillers and spikelet fertility. The percentage of heritability (broad sense) is ranged from 53.72% (spikelet fertility) to 98.70% (Days to Maturity) (Table 3). The highest heritability was found in days to maturity (98.70%) followed by days to 50%

flowering (98.51%) and panicle length (91.40%). Lowest heritability was observed in spikelet fertility percent (53.72%) followed by number of effective tillers (57.48%). Days to maturity and days to 50% flowering exhibited highest heritability followed by panicle length and total grains per panicle. Similar reports were also made by Singh *et al.* (2015) and Mahto *et al.* (2003). This indicated that selection of these traits would be more effective as compared to others.

Genetic advance

High heritability does not always indicate high genetic gain. Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. In the present set of materials, high heritability coupled with high genetic advance as percent was recorded for panicle weight, total grains per panicle and filled grains per panicle indicating effectiveness of selection for the improvement of these traits while high heritability coupled with low genetic advance as percent of mean were observed for panicle length, days to maturity and days to 50 percent flowering which is indicative of non-additive gene action (Table 3). These results are in conformity with the findings of Krishna *et al.* (2010), Singh *et al.* (2012) and Sawarkar and Senapati (2014). Genetic advance as percent of mean (5%) was realized highest for panicle weight (56.57) followed by total grains per panicle (50.33) and filled grains per panicle (49.72). Lowest value was observed in spikelet fertility percent (12.72) followed by panicle length (21.44) and days to maturity (26.32).

Correlation coefficient analysis

Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield. Correlation among traits is generally due to the presence of linkage and pleiotropic effect of different genes. The results on correlation analysis showed that grain yield has positive and significant association with panicle weight, filled grains per panicle, total grains per panicle, panicle length, test weight, plant height and spikelet fertility percent
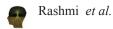
(Table 3). Similar results were also reported by Akhter *et al.* (2004), Singh *et al.* (2013) and Sawarkar and Senapati (2014). Mutual association between different yield components is shown in table 4.

Path coefficient analysis

It is a reliable statistical technique, devised by Wright (1921), which helps in determining yield contributing characters and thus is useful in indirect selection. It measures the direct and indirect contribution of independent variables on dependent variable and helps breeder in determining the yield components. Findings of path analysis indicated that panicle weight had the maximum direct contribution along with highly significant correlation with the grain yield per plant followed by numbers of effective tillers per plant. Panicle length, test weight (and filled grains per panicle were the next positive contributor to the grain yield per plant. Traits like days to maturity, number of effective tillers, plant height, panicle length, panicle weight, filled grains per panicle, total grains per panicle and test weight exhibit positive direct effect while days to 50% flowering and spikelet fertility per cent had negative direct effect on grain yield per plant (Table 5). Panwar *et al.* (2007) and Babu *et al.* (2012) have also reported similar type of finding. The magnitude of residual effect (0.5898) indicated that there may be few more characters which could have been included for estimation of direct and indirect contributors towards their relationship with grain yield per plant.

CONCLUSION

From this study, 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 from present set of germplasms for yield improvement. On the basis of *per se* performance, genotypes *viz.,* RP 5330-63-5-2-1-B, LC-5 and GK 5022 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. Genotype MGD 1206 was earliest in flowering and maturity suggesting that this genotype can be used as a donor in hybridization programme for evolving early maturing rice variety. Characters like panicle

weight, total grains per panicle and filled grains per panicle showed high heritability coupled with high genetic advance indicating they are less influenced by environment and phenotypic estimates of such traits would be very close to their actual genetic potential which can be further improved by means of simple selection and therefore, need top priority during selection. Based on correlation result panicle weight, filled grains per panicle, total grains per panicle, panicle length, test weight, plant height and spikelet fertility percent can be used as selection indices for improving yield.

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