

Original Research Article

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Genetic Variability and Interrelationship Analyses for Quantitative Traits in Elite Germplasm of Rice (*Oryza sativa* L.)

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ABSTRACT

The present investigation was carried out to assess the genetic variability parameters, correlation and path analysis in 32 rice elite germplasm for 13 yield and its contributing traits during kharif 2018 at Field Experimentation Centre, Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom of Agriculture, Technology and Sciences, Uttar Pradesh in Randomized Block Design, replicated thrice. The analysis of variance for mean sum of squares due to genotypes showed significant differences for all the quantitative characters studied at 1% level and 5% level of significance. PCV and GCV was found high for traits like number of tillers per hill, number of panicle per hill, biological yield, harvest index and grain yield per hill. The difference between Phenotypic Coefficient of Variation and Genotypic Coefficient of Variation was low for days to 50% flowering, plant height, number of spikelet's per panicle and days to maturity traits indicating less influenced by the environment. The characters like number of tillers per hill, number of panicle per hill, biological yield and grain yield per hill showed high heritability coupled with high genetic advance as percentage of mean indicating the preponderance of additive gene action. The grain yield per plant had highly significant and positive correlation both at genotypic and phenotypic levels with number of tillers per hill, number of spikelet's per hill and harvest index, high direct effects of these characters appeared to be the main reason for their strong association with grain yield. Hence, direct selection for these characters would be very effective for further improvement of grain yield in rice and for development of hybrids in crop improvement programmes.

Keywords

Variability parameters, Correlation coefficient, Path analysis, Rice (*Oryza sativa* L.)

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Introduction

Rice (*Oryza sativa*, $2n = 24$) is world's important staple cereal food crop growing in at least 114 countries under diverse conditions (Pandey *et al.*, 2010). The rice plant belongs to the genus *Oryza*, sub tribe Oryzineae of the

family Gramineae. This genus has 24 species, of which 22 are wild and two, viz. *O. sativa* and *O. glaberrima*, are cultivated. Rice is the longest continuously grown cereal crop in the world according to International Rice Research Institute (IRRI). Rice is known as the "Grain of life" and synonymous with food

for Asians as it supplies starch, protein and micronutrients. The average percent of protein in rice grain is 8 percent, iron 1.2mg and zinc 0.5mg. The amino acid profile shows that rich it is rich in glutamic acid and aspartic acid, highest quality cereal protein rich in lysine (3.8%) FAO - 2013.

Globally rice is cultivated now 154 million hectares with annual production of around 600 million tonnes and average productivity of 3.9 tonnes per hectare. More than 90% of this produced and consumed in Asian countries shares the world is 21.6% rice production.

India stands first in area (43.97 m.ha) and world's second largest producer (109.32 Mt) of rice after china with the productivity of 2.55 tons per hectare.

The year 2016-17 recorded the highest rice production (109.32) still now. It is estimated that in India, the demand for rice will be 129.6 million tons by 2040 and 137.3 million tons by 2050 for internal consumption. (Directorate of Economics and Statistics, 2016 -17).

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 Singh *et al.*, (2018). Therefore, the objective of this study was to assess the genetic variability, heritability and genetic advance of yield and yield associated traits in some promising rice genotypes to assist the future breeding programs for better yield improvement.

Materials and Methods

The present investigation was carried out at Field Experimentation Centre of Department of Genetics and Plant Breeding, SHUATS, Prayagraj (U.P.) during *Kharif*-2018. This comprised of 32 rice genotypes which were obtained from Department of Genetics and Plant Breeding, SHUATS, Prayagraj (U.P.) and raised in Randomized Block Design with three replications. The recommended packages of practices were followed to ensure a good crop stand. The observations for all traits were recorded on five randomly selected plants for each entry in each replication for 13 quantitative traits *viz.*, days to 50% flowering, plant height, flag leaf length, flag leaf width, number of tillers per hill, number of panicle per hill, panicle length, number of spikelet's per panicle, days to maturity, biological yield, harvest index, test weight and grain yield per hill were recorded per plot through judgmental sampling.

The data was analyzed and interrelationships among traits values were estimated using software INDOSTAT. 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 Johnson *et al.*, (1955). 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 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 and was calculated by the formula suggested by Dewey and Lu (1959).

Results and Discussion

The mean sum of square due to the treatments showed significant difference among all the genotypes at 5% level of significance and 1% level of significance for all the characters. Indicating that these genotypes were genetically variant from each other and similar findings were reported by Rahman (2012) and Paikhomba *et al.*, (2014), Rashmi *et al.*, (2017).

The estimates of PCV and GCV in (Table 1) were found high (>20) for number of tillers per hill, number of panicles per hill, biological index, harvest index and grain yield per hill, these were found similar with results of Padmaja *et al.*, (2008) and ubarhande *et al.*, (2009). Moderate PCV and GCV were recorded for flag leaf length, flag leaf width, panicle length and test weight and low PCV and GCV were recorded for days to 50% flowering, plant height, number of spikelet's per panicle and days to maturity, these results were found similar with Islam *et al.*, (2015), kalpana *et al.*, (2018), Devi *et al.*, (2017) and Idris *et al.*, (2013).

Heritability in broad sense was found to be high (>60%) for all the characters except for harvest index. High heritability (>60%) coupled with high genetic advance as percent mean (>30%) was recorded for number of tillers per hill (60.62, 43.44), number of panicles per hill (84.99, 57.92), biological yield (83.16, 56.73) and grain yield per hill (73.75, 50.87). Therefore indicating a predominance of additive gene effects and the possibilities of effective selection can be conducted based on these traits for crop improvement program. Similar findings were

reported by Sharma and Sharma (2007), sinha *et al.*, (2004), Rai *et al.*, (2014) and Nuruzzaman *et al.*, (2017). Thus these characters offer the best possibility of improvement through selection procedures.

For achieving rational improvement in yield and its related parameters, knowledge on mechanism of correlation, cause and effect relationship provides a basis for formulating suitable selection methods for the yield

In this present investigation in (Table 2) plant height (rp=0.044**,rg=0.096*), flag leaf length (rp=0.063**, rg=0.003*), flag leaf width (rp=0.155**, rg=0.082*), number of tillers per hill (rp=0.341**, rg=0.289**), number of spikelet's per panicle (rp=0.274**, rg=0.229*), biological yield (rp=0.584**, rg=0.567**) and harvest index (rp=0.461**, rg=0.512**) show significant positive correlation with grain yield per plant at both phenotypic (rp) and genotypic (rg) levels, as yield is a dependent character, the performance of these quantitative characters will also affect the grain yield per plant.

While the above selective characters will indicate that an improvement in these traits will increase the grain yield in rice. Therefore any perspective changes in these characters would also affect the yield in the desirable direction of the objective. These observations are in conformity with the findings of Sharma and Sharma (2009), Subudhi and Dikshit (2009), Rajendra *et al.*, (2017) and Rashid *et al.*, (2014).

Path analysis provides statistical technique for formulating efficient selection strategy. Which helps in determining the characters identified as direct and indirect yield contributing traits and should be given due consideration while devising selection strategy for developing better varieties (Table 3).

Table.1 Estimates of range, mean, coefficient of variation, heritability, genetic advance, genetic advance as % of mean

Characters	Range	Mean	Coefficient of Variation		Heritability (bs) %	Genetic advance (GA)	Genetic advance as % of mean
			GCV	PCV			
Days to 50% flowering	82.00-101.00	89.16	5.78	5.93	94.84	10.33	11.59
Plant height	98.81-142.05	113.90	8.35	8.95	87.00	18.27	16.04
Flag leaf length	30.09-49.40	39.22	13.66	15.22	80.56	9.91	25.26
Flag leaf width	1.27-2.23	1.61	13.65	14.86	84.31	0.41	25.82
Number of tillers per hill	6.60-19.40	11.33	27.09	34.79	60.62	4.92	43.44
Number of panicle per hill	5.00-15.33	8.38	30.50	33.09	84.99	4.86	57.92
Panicle length	19.10-33.00	27.38	12.11	14.01	74.77	5.91	21.58
Number of spikelet's per panicle	104.33-160.67	124.79	9.47	10.58	80.14	21.80	17.47
Days to maturity	116.00-134.00	125.33	5.04	5.12	96.70	12.79	10.20
Biological yield	16.80-91.40	59.66	30.20	33.12	83.16	33.85	56.73
Harvest index	16.02-55.45	40.53	20.32	26.57	58.45	12.97	32.00
Test weight	20.08-38.26	29.26	13.40	13.44	99.39	8.05	27.51
Grain yield per hill	11.07-36.20	23.88	28.75	33.48	73.75	12.15	50.87

Table.2 Phenotypic (rp) and Genotypic (gp) correlation coefficient between yield and its component traits of rice genotypes

Characters		Days to 50% flowering	Plant height	Flag leaf length	Flag leaf width	Number of tillers per hill	Number of panicle per hill	Panicle length	Number of spikelet's per panicle	Days to maturity	Biological yield	Harvest index	Test weight	Grain yield per plant
Days to 50% flowering	rg	1.00	0.262**	0.309**	0.210*	0.158	0.023	-0.212*	0.08	0.249*	0.372**	-0.462**	-0.216*	0.057
	rp	1.00	0.244*	0.273**	0.197	0.122	0.025	-0.162	0.066	0.224*	0.329**	-0.363**	-0.211*	0.067
Plant height	rg		1.00	0.385**	0.529**	0.013	0.079	0.222*	0.142	-0.203*	0.326**	-0.262**	0.023	0.044**
	rp		1.00	0.329**	0.481**	0.006	0.089	0.184	0.087	-0.185	0.310**	-0.157	0.017	0.096*
Flag leaf length	rg			1.00	0.653**	-0.561**	-0.463**	0.188	-0.13	-0.086	0.194	-0.138	-0.148	0.063**
	rp			1.00	0.536**	-0.410**	-0.411**	0.149	-0.124	-0.067	0.146	-0.146	-0.13	0.003*
Flag leaf width	rg				1.00	-0.456**	-0.428**	0.252*	-0.268**	-0.158	0.028	-0.184	-0.155	0.155**
	rp				1.00	-0.294**	-0.360**	0.237*	-0.219*	-0.161	0.072	-0.145	-0.147	0.082*
Number of tillers per hill	rg					1.00	0.880**	-0.261*	0.527**	0.274**	0.370**	-0.024	-0.034	0.341**
	rp					1.00	0.679**	-0.181	0.444**	0.206*	0.302**	0.021	-0.025	0.289**
Number of panicle per hill	rg						1.00	-0.251*	0.473**	-0.127	0.331**	0.229*	-0.107	0.497
	rp						1.00	-0.231*	0.444**	-0.108	0.333**	0.106	-0.098	0.398
Panicle length	rg							1.00	-0.123	-0.02	0.086	0.12	0.475**	-0.127
	rp							1.00	-0.105	-0.037	0.062	0.115	0.414**	0.112
Number of spikelet's per panicle	rg								1.00	-0.011	0.305**	-0.025	0.083	0.274**
	rp								1.00	-0.02	0.279**	-0.029	0.078	0.229*
Days to maturity	rg									1.00	0.047	-0.13	-0.045	0.087
	rp									1.00	0.042	-0.11	-0.046	0.084
Biological yield	rg										1.00	-0.437**	0.061	0.584**
	rp										1.00	-0.363**	0.053	0.567**
Harvest index	rg											1.00	-0.018	0.461**
	rp											1.00	-0.01	0.512**
Test weight	rg												1.00	-0.05
	rp												1.00	-0.043
Grain yield per plant	rg													1.00
	rp													1.00

** Significance at 1% and * Significance at 5% level

Table.3 Direct (diagonal) and indirect (off diagonal) effect of different traits on yield of rice genotypes

Characters		Days to 50% flowering	Plant height	Flag leaf length	Flag leaf width	Number of tillers per hill	Number of panicle per hill	Panicle length	Number of spikelet's per panicle	Days to maturity	Biological yield	Harvest index	Test weight	Grain yield per plant
Days to 50% flowering	G	-0.057	0.134	0.438	-0.264	1.386	-0.188	0.023	-0.081	-0.809	0.535	-1.304	0.129	0.057
	P	-0.064	-0.012	0.010	0.002	0.002	0.001	0.007	0.000	-0.006	0.290	-0.293	-0.004	0.067
Plant height	G	-0.015	-0.511	0.547	-0.665	0.115	-0.657	-0.024	-0.144	0.660	0.469	-0.739	-0.014	0.044**
	P	-0.016	-0.051	0.012	0.004	0.000	0.002	-0.008	0.000	0.005	0.274	-0.127	0.000	0.096*
Flag leaf length	G	-0.018	0.197	-1.418	-0.820	-4.919	3.834	-0.020	0.132	0.280	0.279	-0.388	0.089	0.063**
	P	-0.017	-0.017	-0.038	0.005	-0.007	-0.009	-0.007	0.000	0.002	0.129	-0.118	-0.002	0.003*
Flag leaf width	G	-0.012	0.271	0.926	-1.256	-3.996	3.542	-0.027	0.270	0.511	0.041	-0.518	0.093	0.155**
	P	-0.013	-0.025	0.020	-0.009	-0.005	-0.008	-0.011	0.000	0.004	0.064	-0.117	-0.003	0.082*
Number of tillers per hill	G	-0.009	0.007	-0.796	0.573	8.763	-7.289	0.028	-0.532	-0.890	0.532	-0.067	0.020	0.341**
	P	-0.008	0.000	-0.016	-0.003	0.016	0.015	0.008	-0.001	-0.005	0.266	0.017	0.000	0.289**
Number of panicle per hill	G	-0.001	0.041	-0.656	0.537	7.711	8.283	0.027	-0.477	0.412	0.476	0.647	0.064	0.497
	P	-0.002	-0.005	-0.016	-0.003	0.011	0.021	0.010	-0.001	0.003	0.294	0.086	-0.002	0.398
Panicle length	G	0.012	0.114	0.266	-0.316	-2.283	2.076	0.107	0.124	0.064	0.124	0.338	-0.285	-0.127
	P	0.010	-0.009	0.006	0.002	-0.003	-0.005	-0.045	0.000	0.001	0.054	0.093	0.008	0.112
Number of spikelet's per panicle	G	-0.005	0.073	-0.185	0.337	4.615	-3.919	0.013	1.009	0.034	0.438	-0.070	-0.050	0.274**
	P	-0.004	-0.004	-0.005	-0.002	0.007	0.010	0.005	0.002	0.001	0.246	-0.024	0.001	0.229*
Days to maturity	G	-0.014	-0.104	-0.123	0.198	2.404	1.053	0.002	0.011	-3.243	0.068	-0.366	0.027	0.087
	P	-0.014	0.009	-0.003	-0.001	0.003	-0.002	0.002	0.000	-0.026	0.037	-0.089	-0.001	0.084
Biological yield	G	-0.021	0.167	0.275	-0.036	3.244	-2.743	-0.009	-0.308	-0.154	-1.438	-1.232	-0.037	0.584**
	P	-0.021	-0.016	0.006	0.001	0.005	0.007	-0.003	0.000	-0.001	-0.882	-0.293	0.001	0.567**
Harvest index	G	0.026	-0.134	-0.195	0.230	-0.207	-1.898	-0.012	0.025	0.420	-0.627	2.822	0.010	0.461**
	P	0.023	0.007	-0.005	-0.001	0.003	0.002	-0.005	0.005	0.002	-0.320	0.807	-0.018	0.512**
Test weight	G	0.012	0.011	-0.209	0.194	-0.294	0.885	-0.050	-0.083	0.146	0.087	-0.051	0.599	-0.050
	P	0.013	-0.008	-0.004	-0.001	-0.004	-0.002	-0.018	-0.014	0.001	0.046	-0.008	0.018	-0.043

P=Phenotypic level and G= Genotypic level, Genotypic path (Residual effect=0.27689) and Phenotypic path (Residual effect=0.07708)

Characters like number of number of tillers per hill (G=8.763, P=0.016), number of spikelets per panicle (G=0.274**, P=0.229*) and harvest index (G=2.822, P=0.807) show direct positive significant association with grain yield per plant at the both phenotypic (P) and genotypic (G) levels indicating that these characters would be more effective in selection criteria for developing better varieties. These results were similar with the findings of Srikanth *et al.*, (2017), Rohit *et al.*, (2017), Tefera *et al.*, (2017), Vinoth *et al.*, (2016) and Roy *et al.*, (2015).

From this study, we conclude that the germplasms exhibited a wide range of variability for most of the traits. This ensures the ample scope for selection of promising genotypes from present set of germplasms for yield improvement.

Characters like number of tillers per panicle, number of panicles per hill, biological yield and grain yield per hill showed high heritability coupled with high genetic advance indicating they are less influenced by environment and phenotypic estimates of such traits would be very closely relates to their actual genetic potential which can be further enhanced by means of simple selection and therefore, need top priority during selection.

Based on correlation coefficient and path analysis results number of tillers per hill, number of spikelet's per panicle and harvest index show direct positive significant association with grain yield of the plant and these traits can be used as selection indices for improving yield or for developing better varieties.

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