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# Genetic variability, correlation and path analysis for quantitative traits in rainfed upland rice (*Oryza sativa* L.)

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### Abstract

An experiment was carried out during *Kharif* 2018 to estimate the genetic parameters of variation, correlation and direct and indirect effects of yield components on grain yield in rice. The experimental material consists of 32 genotypes. Genotypes were planted in Randomized Block Design with three replications. The analysis of variance revealed that highly significant differences among the genotypes for all the characters. It indicated the presence of sufficient amount of genetic variability in the studied material for all the traits. High values of GCV and PCV was observed for grain yield per plant. High heritability coupled with high genetic advance as percentage of mean were recorded for grain yield per plant, number of grains per panicle, harvest index, test weight, biological yield per plant, plant height, flag leaf angle and number of tillers per plant. These characters showed substantial contribution of genotypic variance for their phenotypic expression. They can be further improved by direct selection for these characters. Based on correlation studies, grain yield per plant depicted significant positive correlation with harvest index, biological yield per plant and panicle length. Path coefficient analysis revealed that, eight characters had high direct positive effect on grain yield per plant like, harvest index, biological yield per plant, days to 50% flowering, number of productive tillers per plant, flag leaf angle, test weight, number of grains per panicle and panicle length. It showed that these characters may be included in selection criteria to enhance the grain yield in rice. During formulating of selection criteria in rice improvement programme following characters like, Harvest index, biological yield per plant, and panicle length should be included.

**Keywords:** Genetic variability, heritability, genetic advance, correlation and Path coefficient analysis

### Introduction

Rice (*Oryza sativa* L.) is one of the most important cereal crop related to genus *Oryza* of family *Poaceae* and ranking first among the three major cereals followed by wheat and maize. Rice provides 21% and 15% of global human per capita and protein. The area, production and productivity of rice in India were 43.19 m ha, 110.15 mt, and 2550 kg/ha, respectively. Similarly, the area, production and productivity of rice in Madhya Pradesh were 17.03 m ha, 32.98 mt and 1937 kg/ha, respectively in 2016-17 (Anonymous 2017-18).

The achievement of breeding programme depends upon the magnitude of genetic variability present in the population and the range to which the desirable characters are heritable. Phenotypic correlation is the correlation of observed values of variable and subjected to the variation in the environment. Knowledge of association between different characters is highly important for planning a sound breeding programme. Selection would be more emphatic based on the trait, which has got higher genetic advance and correlation with grain yield.

The path coefficient analysis splits the correlation coefficient into the measure of direct and indirect effects of various traits towards dependent variable and helps in estimating the relationship as well as to formulate selection criteria for improvement of grain yield.

### Material and Methods

The experiment was carried out at experimental area of rice in Instructional Farm, College of Agriculture, Rewa (M.P.) during *Kharif* 2018. The experimental material consists of 32 genotypes. Genotypes were planted in Randomized Block Design with three replications. The nursery was sown on 4/07/2018 and 20 days old seedlings were transplanted with spacing of 25 x 15 cm with a row length of 2.0 m for each genotype. All the recommended package and practices were adopted.

Ten randomly plants were selected from each genotype in each replication and observations were recorded on these plants for the characters *like*, Plant height (cm), number of tillers per plant, number of productive tillers per plant, panicle length (cm), number of grains per panicle, flag leaf angle ( $^{\circ}$ ), test weight (g), biological yield per plant (g), harvest index (%) and grain yield per plant (g), while days to 50% flowering and days to maturity were recorded on plot basis.

**Table 1:** List of genotypes

S.N.	Name of genotype	S.N.	Name of genotype
1	Rewa 1326-3-15	17	Rewa 1326-7-77
2	Rewa 1326-3-56	18	Rewa 1326-7-5
3	Rewa 1326-3-5-2	19	Rewa 1326-11-12-4
4	Rewa 1326-3-34-4	20	Rewa 1326-11-67-2
5	Rewa 1326-3-53	21	Rewa 1326-16-1
6	Rewa 1326-3-55-11	22	Rewa 1328-18-16
7	Rewa 1326-3-32-2	23	Rewa 1328-18-9
8	Rewa 1326-3-15-7	24	Rewa 1328-18-105
9	Rewa 1327-2-66-2	25	Rewa 1328-18-102
10	Rewa 1327-2-96-4	26	Rewa 1328-18-16-3
11	Rewa 1327-2-57	27	Rewa 1329-19-210-2
12	Rewa 1329-4-123-11	28	Rewa 1329-19-208
13	Rewa 1329-4-26-1	29	Rewa 1329-24-16
14	Rewa 1329-4-21-3	30	Rewa 1329-24-223
15	Rewa 1329-4-182-1	31	Rewa 1330-25-25-3
16	Rewa 1326-7-338	32	Rewa 1330-25-25-11

### Statistical analysis

Different genetic parameters such as genotypic and phenotypic variance, GCV and PCV, heritability, genetic advance, genetic advance as percent of mean were estimated by using following formula

### Analysis of variance

The analysis of variance for twelve studied characters were estimated as per the model proposed by Panse and Sukhatme (1961) [16].

The genotypic and phenotypic variance was calculated as per the formulae (Burton and Devane1952) [4, 5].

$$\text{Genotypic variance } (\sigma^2g) = \frac{(\text{Mean sum of squares due to treatments} - \text{Mean sum of squares due to error})}{\text{Number of replications}}$$

$$\text{Phenotypic variance } (\sigma^2p) = (\sigma^2g) + (\sigma^2e)$$

Where, ( $\sigma^2e$ ) = Error variance

### Genotypic and phenotypic coefficients of variance:

The genotypic and phenotypic coefficient of variance was calculated by the formulae given by Burton (1952) [4, 5].

$$\text{Genotypic coefficient of variation (GCV \%)} = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV \%)} = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100$$

Categorization of the range of variation was affected as proposed by Siva subramanian and Madhavamenon (1973) as low (<10%), moderate (10-20%) and high (>20%).

### Heritability (Broad sense) $h^2$

Heritability in broad sense  $h^2_{(b)}$  was calculated by the formula given by Lush (1940).

$$\text{Broad sense Heritability} = \frac{\sigma^2g}{\sigma^2p} \times 100$$

Where,  $\sigma^2g$  = Genotypic variance and  $\sigma^2p$  = Phenotypic variance

As proposed by Johnson *et al.* (1955) [9], heritability was categorized as: low (<30%), moderate (30 – 60%) and high (>60%)

### Genetic advance

The genetic advance was calculated by the following formula given by Johnson *et al.* (1955) [9].

$$GA = k \sigma_p H$$

Where, GA = Genetic advance, k = Selection differential at 5% selection intensity

$\sigma_p$  = Phenotypic standard deviation and H= Heritability

### Genetic advance as percent of mean (GA as percent mean)

Genetic advance as percent of mean was calculated as per the formula.

$$GA \text{ as percentage of mean} = \frac{\text{Genetic advance}}{\text{General mean}} \times 100$$

The degree of genetic advance as percent of mean was classified as suggested by Johnson *et al.* (1955) [9] as low (<10%), moderate (10-20%) and high (>20%).

### Correlation coefficient analysis

Genotypic and phenotypic correlation coefficients were calculated using the method given by Johnson *et al.* (1955) [9]. The significance of correlation coefficients was tested by comparing the genotypic and phenotypic correlation coefficients with table value [Fisher and Yates (1967)] at (n-2) degrees of freedom at 5% and 1% level where, 'n' denotes the number of treatments used in the calculations.

### Path coefficient analysis

Path coefficient analysis was carried out by the procedure originally proposed by Sewall Wright (1921) which was subsequently elaborated by Dewey and Lu (1959) to estimate the direct and indirect effects of the individual characters on yield.

## Results and Discussion

### Analysis of variance

The results on analysis of variance (ANOVA) for yield and yield component characters studied are presented in table-2. The analysis of variance revealed highly significant differences among the genotypes for all the characters. It indicated the presence of ample amount of genetic variability in the studied material for all the traits. Similar findings were also reported by Sarawgi *et al.* (2014) [22], Badri *et al.* (2015) [3], Sameera *et al.* (2016) and Abebe *et al.* (2017) [1].

### The mean performance of genotypes

The genotypes Rewa 1326-7-338 (28.16 g), Rewa 1330-25-34-3 (26.76 g) and Rewa 1326-16-1 (26.10 g) are identified as higher yielders. The yield potential of these genotypes are due to early days to maturity, long panicle length, high number of grains per panicle, high flag leaf angle, very high test weight and high harvest index. Similar kinds of Result's were also

reported by Subdhu *et al.* (2012), Tariku *et al.* (2013)<sup>[25]</sup> and Rolando *et al.* (2016)<sup>[20]</sup>. These genotypes are best performing rice genotypes for grain yield and suggesting that these genotypes could be used as donors for grain yield improvement in rice.

### Genetic parameters of variation

The extent of genotypic and phenotypic coefficient of variation, heritability and genetic advance as percentage of mean were recorded for all studied characters are presented in table-3.

High values of GCV and PCV were recorded for grain yield per plant and harvest index. It indicated that these characters have quantitative inheritance and considerably influenced by environmental factors. The above result's are agreement with findings of Devi *et al.* (2016)<sup>[6]</sup> for grain yield per plant and Badri *et al.* (2015)<sup>[3]</sup> for harvest index.

High heritability coupled with high genetic advance were recorded for plant height, flag leaf angle, grain yield per plant, biological yield per plant, harvest index, number of grains per panicle, test weight and number of tillers per plant. These characters showed substantial contribution of additive gene action for their phenotypic expression. They can be further improved by direct selection for these characters. Similar Result's were also reported by Abebe *et al.* (2017)<sup>[1]</sup> for plant height, Sameera *et al.* (2016) for flag leaf angle, Devi *et al.* (2016)<sup>[6]</sup> for grain yield per plant and test weight, Rahman *et al.* (2015)<sup>[17]</sup> for biological yield per plant, Yadav *et al.* (2011) for harvest index, Sameera *et al.* (2015)<sup>[11, 21]</sup> for number of grains per panicle and number of tillers per plant.

### Character association

The correlation coefficient was partitioned into phenotypic and genotypic correlation coefficient. Genotypic correlation coefficients provide a measure of genetic association between characters and were generally used in selection of one character as a means of improving another. The magnitude of

genotypic correlation was higher than phenotypic correlation. The phenotypic correlation coefficient of studied characters are presented in table-4. Correlation coefficient depicted the nature of association among the characters. The study of correlation coefficient helps the breeder to formulate the selection criteria with desired combination of characters.

At phenotypic level, grain yield per plant had significant positive correlation with harvest index, number of grains per panicle, biological yield per plant, test weight and panicle length. The following scientists are agreement with the present findings of Kumar *et al.* (2018)<sup>[12]</sup> for harvest index and biological yield per plant, Naseer *et al.* (2015)<sup>[15]</sup> for number of grains per panicle and test weight, Sameera *et al.* (2015)<sup>[11, 21]</sup> for panicle length. Hence, it can be conclude from this study that harvest index, biological yield per plant, test weight, number of grains per panicle and panicle length should be considered as the selection criteria for improvement of grain yield per plant in rice.

### Path coefficient analysis

The direct effect of studied traits towards grain yield per plant and its indirect effect through other characters were computed and presented in table-5.

At phenotypic level positive and direct effect on grain yield per plant were exhibited by harvest index, biological yield per plant, test weight, panicle length, number of productive tillers per plant, number of grains per panicle, days to maturity and flag leaf angle. Similar findings were also reported by previous scientist's like, Nandan *et al.* (2010)<sup>[14]</sup> for harvest index, Kumar *et al.* (2018)<sup>[12]</sup> for biological yield per plant, Kishore *et al.* (2015)<sup>[11]</sup> for test weight, Rajamadhan *et al.* (2011)<sup>[18]</sup> for panicle length, Rashid *et al.* (2017)<sup>[19]</sup> for number of productive tillers per plant, Khare *et al.* (2014)<sup>[10]</sup> for number of grains per panicle. These characters may be including in selection criteria for simultaneously increased the grain yield per plant in rice.

**Table 2:** Analysis of variance for twelve yield and yield component characters in 32 Rice (*Oryza sativa* L.)

Source of variation	Mean sum of squares												
	df	DTF	DM	PH	NTPP	NPTPP	PL	NGPP	FLA	TW	BYPP	HI	GYPP
Replication	2	71.84	71.44	64.67	7.49	10.56	2.105104	222.01	97.69	0.10	9.36	51.52	7.39
Genotype	32	90.10**	114.95**	880.62**	7.56**	6.38**	13.77**	2488.81**	454.26**	27.67**	75.76**	742.85**	85.41**
Error	64	4.14	4.38	14.50	0.88	1.71	0.97	18.79	18.02	0.28	0.98	8.49	0.80

\*\* significant at 5% and 1% level of probability, respectively. DTF= Days to 50% flowering, DM=Days to maturity, PH= Plant height, NTPP= Number of tillers per plant, NPTPP=Number of productive tillers per plant, PL= Panicle length, NGPP= Number of grains per panicle, FLA= Flag leaf angle, TW= Test weight, BYPP= Biological yield per plant, HI= Harvest index, GYPP= Grain yield per plant

**Table 3:** Estimates of variability and genetic parameters for twelve yield and yield component characters in 32 Rice (*Oryza sativa* L.)

Character	GCV (%)	PCV (%)	h <sup>2</sup> (bs) %	GA as % of mean
Days to 50% flowering	7.38	7.89	87.4	14.21
Days to maturity	5.43	5.75	89.4	10.59
Plant height	18.29	18.75	95.2	36.78
Number of tillers per plant	15.48	18.30	71.5	26.97
Number of productive tillers per plant	14.38	20.84	47.6	20.45
Panicle length	8.30	9.20	81.4	15.44
Number of grains per panicle	17.81	18.01	97.8	36.28
Flag leaf angle	19.04	20.18	89.0	36.99
Test weight	16.24	16.49	97.0	32.96
Biological yield per plant	16.11	16.42	96.2	32.54
Harvest index	26.00	26.45	96.6	52.67
Grain yield per plant	28.55	28.95	97.2	57.99

**Table 4:** Phenotypic and genotypic correlation coefficient analysis for twelve yield and yield component characters in 32 Rice (*Oryza sativa* L.)

Character	DTF	DM	PH	NTPP	NPTPP	PL	NGPP	FLA	TW	BYPP	HI	GYPP	
DTF	P	1	0.871**	-0.111	-0.167	-0.193	-0.249 *	-0.100	0.098	-0.191	-0.318 *	0.151	-0.005
	G	1	0.863	-0.118	-0.215	-0.301	-0.280	-0.100	0.136	-0.211	-0.340	0.166	0.004
DM	P		1	-0.276*	-0.057	-0.091	-0.200 *	-0.224 *	-0.032	-0.134	-0.302 *	0.090	-0.049
	G		1	-0.297	-0.065	-0.114	-0.222	-0.226	-0.030	-0.146	-0.317	0.100	-0.042
PH	P			1	0.013	0.024	0.074	0.075	-0.236 *	0.016	0.381**	-0.055	-0.111
	G			1	-0.007	0.018	0.067	0.083	-0.264	0.014	0.397	-0.060	0.129
NTPP	P				1	0.927	0.375 **	-0.199	-0.178	0.087	0.428**	-0.020	0.178
	G				1	0.995	0.385	-0.275	-0.187	0.105	0.501	-0.089	0.141
NPTPP	P					1	0.361**	-0.103	-0.168	0.202 *	0.442 **	0.108	0.306
	G					1	0.410	-0.223	-0.162	0.278	0.624	0.054	0.329
PL	P						1	0.111	0.095	0.156	0.180	0.222 *	0.306 *
	G						1	0.112	0.110	0.174	0.180	0.250	0.329
NGPP	P							1	0.162	-0.079	0.292 *	0.412**	0.512**
	G							1	0.182	-0.081	0.294	0.419	0.516
FLA	P								1	0.276*	-0.255 *	0.326 *	0.177
	G								1	0.300	-0.258	0.355	0.205
TW	P									1	0.152	0.422 **	0.476**
	G									1	0.156	0.440	0.493
BYPP	P										1	-0.052	0.448**
	G										1	-0.038	0.451
HI	P											1	0.857 **
	G											1	0.862

P = Phenotypic and G = Genotypic

\*,\*\* significant at 5% and 1% level of probability, respectively

**Table 5:** Phenotypic path analysis for twelve yield and yield component characters in 32 Rice (*Oryza sativa* L.)

Character	DTF	DM	PH	NTPP	NPTPP	PL	NGPP	FLA	TW	BYPP	HI	GYPP
DTF	0.0354	0.0308	-0.0039	-0.0059	-0.0068	-0.0088	-0.0035	0.0035	-0.0068	-0.0113	0.0054	-0.0057
DM	0.0099	0.0114	-0.0031	-0.0007	-0.0010	-0.0023	-0.0025	-0.0004	-0.0015	-0.0034	0.0010	-0.0499
PH	0.0014	0.0035	-0.0128	-0.0002	-0.0003	-0.0010	-0.0010	0.0030	-0.0002	-0.0049	0.0007	0.1295
NTPP	0.0103	0.0035	-0.0008	-0.0613	-0.0569	-0.0231	0.0122	0.0109	-0.0054	-0.0263	0.0013	0.1789
NPTPP	-0.0071	-0.0033	0.0009	0.0339	0.0365	0.0132	-0.0038	-0.0062	0.0074	0.0161	0.0040	0.3062
PL	-0.0107	-0.0086	0.0032	0.0161	0.0155	0.0429	0.0048	0.0041	0.0067	0.0077	0.0095	0.3067
NGPP	-0.0020	-0.0045	0.0015	-0.0040	-0.0021	0.0023	0.0202	0.0033	-0.0016	0.0059	0.0084	0.5123
FLA	0.0002	-0.0001	-0.0005	-0.0003	-0.0003	0.0002	0.0003	0.0019	0.0005	-0.0005	0.0006	0.1775
TW	-0.0094	-0.0066	0.0008	0.0043	0.0100	0.0077	-0.0039	0.0136	0.0492	0.0075	0.0208	0.4760
BYPP	-0.1595	-0.1513	0.1906	0.2142	0.2211	0.0903	0.1461	-0.1278	0.0761	0.5002	-0.0260	0.4480
HI	0.1259	0.0753	-0.0463	-0.0172	0.0906	0.1852	0.3433	0.2716	0.3515	-0.0432	0.8318	0.8574

R square = 0.9824, Residual effect = 0.1328

## Conclusion

High heritability coupled with high genetic advance as percentage of mean were recorded for grain yield per plant, number of grains per panicle, harvest index, test weight, biological yield per plant, plant height, flag leaf angle and number of tillers per plant in all three micro-environments. These characters showed substantial contribution of additive gene action for their phenotypic expression. They can be further improved by direct selection for these characters. Significant positive phenotypic correlation along with direct positive effect towards grain yield per plant showed by the characters like, harvest index, biological yield per plant, flag leaf angle, number of productive tillers per plant and number of grains per panicle. It indicated that improvement in these characters simultaneously increased the grain yield in rice. It showed that these characters may be included in selection criteria to enhance the grain yield in rice.

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