

Genetic Variability, Heritability and Character Association Studies for Yield and Yield Related Traits in Rice (*Oryza sativa* L.)

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ABSTRACT

The nineteen genotypes of rice (*Oryza sativa* L.) were evaluated for genetic variability, heritability, genetic advance, correlation and path coefficient analysis considering eleven quantitative and qualitative traits. The analysis of variance showed that genotypes differed significantly for all the eleven traits studied. The highest PCV and GCV were recorded for grain yield per plant whereas it was moderate for number of productive tillers per plant, number of panicle/m², panicle length and number of grains per panicle. High heritability coupled with high genetic advance as per cent of mean were observed for number of

productive tillers per plant, number of panicle/m², panicle length and number of grains per panicle and grain yield per plant which indicated that these traits are under the influence of additive gene action. Grain yield per plant had significant positive correlation with number of productive tillers per plant, number of panicles/m², number of grains/panicle, test weight and protein content. Path analysis revealed that the test weight was the major contributor of grain yield per plant followed by number of productive tillers per plant, number of panicles/m², number of grains/panicle and protein content. For maximizing the grain yield per plant emphasis should be given in selection of characters such as number of productive tillers per plant, number of panicles/m², number of grains/panicle, test weight and protein content.

Keywords Genetic variability, Heritability, Genetic advance, Correlation, Path coefficient.

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the pivotal staple cereal crops feeding more than half of the world population. Globally rice is planted in an area of about 162 million ha and 755 million tonnes of paddy is harvested annually (FAO 2020). Rice is the most important food crop of India. It is the backbone of livelihood for millions of rural families and plays an essential role in the country's food security, so the term "rice is life" is most suitable in case of India

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(Mahajan *et al.* 2017). In India the area under rice crop was 43.78 million hectares. However, the rice production has registered to 118.43 million tones. The milled rice yield has recorded 2705 kg/ha during 2020-21 (Anonymous 2020-21). It is estimated that by 2035, global demand for rice will increase to 852 million tons, however, records have shown that annual growth in yield was close to 1% only in the past decade (Khush 2013). But there is dire need to increase production to meet the growing population (Kumar *et al.* 2014). In view of the growing population, the basic objective of the plant breeders would always be towards yield improvement in staple food crops. It has been estimated that the world will have to produce 60% more rice by 2030 than what it produced in 1995 (Babu *et al.* 2012). For framing the efficient breeding methodology applicable to the genetic improvement of the population, the kind of variation present in the breeding population is of great importance. Biometrical estimates like genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) provides the estimates of the contribution of environment and genotype towards total variation and hence assist in framing proper breeding program. The systematic breeding program involves the steps like creating genetic variability practicing selection and utilization of selected genotypes to evolve promising varieties. Direct selection based on crop yields is often a paradox in breeding programs because yield is a complex polygenically inherited character, influenced by its component traits. 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. While selecting the suitable plant type, correlation studies would provide reliable information in nature, extent and the direction of the selection, especially when the breeder needs to combine high yield potentials with desirable agronomic traits and grain quality characters. The better way of exploiting genetic correlation and path coefficient with several traits having high heritability is to construct a selection index that combines information on all the characters associated with the dependent variable. Efforts are to be taken with a systematic research approach to exploit the yield potential by direct and indirect selection. The nature and extent of genetic variation governing the

inheritance of characters and association will facilitate effective genetic improvement. Keeping in view the above perspectives, the present research work was taken up to assessing genetic variability, phenotypic and genotypic associations between various components of grain yield to provide basis for selection and yield improvement in rice.

MATERIALS AND METHODS

The present experiment was carried out during *kharif* 2020 at Agricultural Research Station, Ummedganj, Agriculture University Kota, Rajasthan. The experimental material consisted of 19 rice genotypes. Source of the genotypes are given in Table 1. Each genotype was transplanted in fifteen rows of 5 meter length with a spacing of 20 cm between rows and 15 cm between plants in a Randomized Block Design replicated thrice. Crop management practices and plant protection methods for raising a healthy crop were followed as per recommendations. Observations on five randomly selected plants from each replication were recorded for nine characters viz., plant height, number of productive tillers per plant, number of panicles/ m², panicle length, number of grains/ panicles, test weight, amylose content, protein content and grain yield/plant while two characters namely days to 50% flowering and days to maturity were recorded on whole plant basis. The plants were

Table 1. Details of rice genotypes used in the study.

Sl. No.	Name of the genotypes	Source
1	RSK-1155-3-3-1	ARS, Kota
2	RSK-1155-6-1-2	ARS, Kota
3	RSK-1157-5-4-1	ARS, Kota
4	RSK-1164-11-1	ARS, Kota
5	RSK-1165-4-2	ARS, Kota
6	RSK-1156-6-3-1	ARS, Kota
7	RSK-1157-4-5-1	ARS, Kota
8	RSK-1157-9-2-2	ARS, Kota
9	RSK-1165-4-2	ARS, Kota
10	RSK-1167-11-1	ARS, Kota
11	RNSK-1168-2-1	ARS, Kota
12	RSK-1171-1-1	ARS, Kota
13	RSK-1173-1-1	ARS, Kota
14	RNSK-1165-3-2	ARS, Kota
15	P-1121	IARI, New Delhi
16	P-1592	IARI, New Delhi
17	P-2511	IARI, New Delhi
18	P-1612	IARI, New Delhi
19	P-1460	IARI, New Delhi

selected from the middle rows to minimize the border effect. Analysis of variance is used for testing whether there is significant difference between the treatment or not. It was carried out by following the procedure of Randomized Block Design (RBD) analysis (Panse and Sukhatme 1985) for each of the thirty genotypes. Analysis of variance was computed based on RBD as per standard procedure given by Panse and Sukhatme (1985). Correlation coefficient were calculated at genotypic and phenotypic level using the formulae suggested by Singh and Chaudhary (1979). The direct and indirect effects at both the level were estimated by using grain yield as dependent variable using path coefficient suggested by Wright (1921) and elaborated by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Variability parameters

Variability in the population is a prerequisite especially for characters where improvement is required. Success of plant breeding programs largely depends on the amount of genetic variability present in a given crop species for the character under improvement. Analysis of variance revealed significant differences among the genotypes for all the characters. A wide range of variability was exhibited by most of the traits under (Table 2). The genotypic coefficient of variation measures the range of variability available in the crop and also enables a breeder to compare the amount of variability present among different characters. The phenotypic expression of the character is the result of interaction between genotype and environment. Hence, the total variance should be partitioned into heritable and non- heritable components to assess the true breeding nature of the particular trait under study. In present investigation, the estimates of PCV

were higher than their corresponding GCV for all the traits studied (Table 3). But almost all the character considered has the small difference between PCV and GCV values specifying less effect of environment in expression of these characters suggesting phenotypic differences may be considered as genotypic difference among the genotypes for selection. The higher magnitude of genotypic (GCV) and phenotypic coefficients of variation (PCV) was recorded for grain yield per plant (g), However, moderate estimates were observed for productive tillers per plant, number of panicles/ m², panicle length, number of grains/ panicle whereas rest of the character showed low estimates of GCV and PCV. The studies on genotypic and phenotypic coefficient of variation indicated that the presence of varying amount of variance and role of the environment on the expression of these traits. These findings were in accordance with the findings of Dhakal *et al.* (2020), Keerthiraj and Biju (2020), Singh *et al.* (2020), Islam *et al.* (2020), Jadhav *et al.* (2020), Kumar *et al.* (2019), Lingaiah (2015), Mishu *et al.* (2016). Heritability estimates indicate the relative degree at which a character is transmitted from parents to off-spring. High heritability values indicated that the characters under study were less influenced by environment in their expression. The traits exhibiting high heritability could be improved by adopting simple selection methods. Further, the information on genetic variation, heritability and genetic advance helps to predict the genetic gain that could be obtained in later generations, if selection is made for improving the particular trait under study. In the present study high heritability was observed for traits like; number of panicle/m² (95.8%), grain yield per plant (93.58%), panicle length (92.22%), test weight (92.12%), plant height (89.96%), number of grains per panicle (88.58%), days to maturity (84.03%) whereas, characters like; Number of pro-

Table 2. Analysis of variance (ANOVA) for 11 quantitative and qualitative traits in nineteen rice genotypes.

Source of variation	Degree of freedom	Days to 50% flowering	Mean sum of square			
			Days to maturity	Plant height (cm)	Number of productive tillers per plant	Number of panicle/m ²
Replication	2	3.18	5.28	6.69	0.86	117.54
Genotypes	18	10.96**	37.97**	80.35**	7.85**	5780.90**
Error	36	1.40	2.26	2.88	0.93	83.25

Table 2. Continued.

Source of variation	Degree of freedom	Mean sum of square					
		Panicle length (cm)	Number of grains per panicle	Test weight (g)	Amylose content (%)	Protein content (%)	Grain yield per plant (g)
Replication	2	0.04	35.81	0.32	1.59	0.19	0.75
Genotypes	18	29.55**	986.54**	17.05**	3.04**	1.25**	41.78**
Error	36	0.81	40.66	0.47	0.43	0.22	0.93

*, ** = Significant at 5 and 1 % level, respectively.

ductive tillers per plant (71.18%), Amylose content (67.19%) depicted moderate estimate of heritability. Remaining characters showed low estimates of heritability (Table 3). Comparable reports were also made by Singh *et al.* (2013) Mishu *et al.* (2016) Islam *et al.* (2016). Heritability estimates indicates both additive and non-additive gene action. So, high heritability does not always indicate high genetic gain. Heritability along with genetic advance can be used as efficient selection parameters instead of heritability alone as both together indicates that most likely the heritability is due to additive gene effects. This indicated that effective selection can be done for these traits compared to others. The high heritability coupled with high genetic advance as percent of mean of was recorded for grain yield per plant, number of productive tillers per/plant, number of panicle/m², panicle length, number of 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 detected for plant height which is indicative of non-additive gene

action. These results are in line with the findings of Jadhav *et al.* (2020), Singh *et al.* (2020), Chuchert *et al.* (2018), Srujana *et al.* (2017), Islam *et al.* (2016), Hossain *et al.* (2015), Tiwari (2015) and Singh *et al.* (2013).

Correlation and path coefficient analysis

A thorough understanding of the association of plant characters among themselves and with yield is essential for successful crop improvement programs. It enables the breeders to manipulate the expression of these traits in crop improvement. The efficiency of selection for yield mainly depends on the direction and magnitude of association between yield and its components and among themselves. Correlation analysis provides information on the nature and magnitude of the association of different component characters with grain yield, which is regarded as a complex trait which the breeder is ultimately interested in. It also helps us to understand the nature of inter-relationship among the component traits themselves. Therefore

Table 3. Genetic variability parameters for yield and its attributing traits in rice genotypes.

Sl. No.	Characters	Range	Mean	GCV(%)	PCV(%)	Heritability % (bs)	Genetic advance	Gen adv as % of mean
1	Days to 50% flowering	96-104	99.70	1.79	2.15	69.52	3.07	3.08
2	Days to maturity	126-142	132.28	2.61	2.85	84.03	6.52	4.93
3	Plant height (cm)	102.67-123	111.98	4.54	4.78	89.96	9.93	8.87
4	Number of productive tillers per plant	6.0-11.33	8.33	18.22	21.60	71.18	2.64	31.67
5	Number of panicle/m ²	172-307.67	239.87	18.17	18.56	95.80	87.87	36.63
6	Panicle length (cm)	18.50-29.10	24.93	12.41	12.93	92.22	6.12	24.55
7	Number of grains per panicle	122.33-175	145.35	12.22	12.98	88.58	34.43	23.68
8	Test weight (g)	21.83-28.87	24.93	9.43	9.82	92.12	4.65	18.64
9	Amylose content (%)	22.07-26.23	23.72	3.94	4.80	67.19	1.58	6.65
10	Protein content (%)	6.83-9.09	7.67	7.49	9.55	61.50	0.95	12.10
11	Grain yield per plant (g)	9.67-22.10	15.57	23.97	24.77	93.58	7.35	47.76

Table 4. Estimation of phenotypic and genotypic correlation coefficients between yield and yield attributing characters.

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of productive tillers per plant	Number of panicle/m ²	Panicle length (cm)	Number of grains per panicle	Test weight (g)	Amylose content (%)	Protein content (%)	Grain yield per plant (g)
Days to 50% flowering	1.000	0.940**	0.672**	-0.467**	-0.330**	0.470**	-0.325**	-0.436**	-0.367**	-0.209	-0.337**
	G	1.000	0.988**	0.703**	-0.547**	-0.364**	0.515**	-0.359**	-0.448**	-0.411**	-0.265*
Days to maturity	P	1.000	0.673**	-0.436**	-0.262*	0.484**	-0.253*	-0.384**	-0.286*	-0.155	-0.304*
	G	1.000	0.704**	-0.476**	-0.272*	0.508**	-0.267*	-0.399**	-0.336*	-0.160	-0.318*
Plant height (cm)	P		1.000	0.121	0.123	0.895**	0.101	0.081	-0.451**	0.267*	0.153
	G		1.000	0.141	0.134	0.929**	0.110	0.083	-0.475**	0.277*	0.155
Number of effective tillers per plant	P			1.000	0.837**	0.206	0.816**	0.842**	-0.049	0.695**	0.864**
	G			1.000	0.880**	0.205	0.896**	0.898**	-0.033	0.846**	0.942**
Number of panicle/m ²	P				1.000	0.239	0.953**	0.888**	-0.199	0.707**	0.892**
	G				1.000	0.240	0.978**	0.909**	-0.218	0.776**	0.914**
Panicle length (cm)	P					1.000	0.231	0.193	-0.537**	0.266*	0.225
	G					1.000	0.244	0.198	-0.588**	0.298*	0.240
Number of grains/panicle	P						1.000	0.931**	-0.201	0.770**	0.871**
	G						1.000	0.975**	-0.250	0.848**	0.896**
Test weight (g)	P							1.000	-0.223	0.804**	0.928**
	G							1.000	-0.216	0.904**	0.956**
Amylose content (%)	P								1.000	-0.152	-0.267*
	G								1.000	-0.150	-0.303*
Protein content (%)	P									1.000	0.720**
	G									1.000	0.815**
Grain yield per plant (g)	P										1.000
	G										1.000

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

this kind of analysis could be helpful to the breeder to design selection strategies to improve the grain yield. Genotypic correlations in general are high as compared to their phenotypic correlations and indicated strong inherent association between the characters which might be due to masking or modifying effects of environment. The grain yield is the complex trait controlled by minor genes and depends on many factors for its expression; selection for yield *per-se* is not always fruitful. Therefore it is highly desirable to include the yield attributing traits which show positive and significant association with grain yield for the yield improvement. The estimates of correlation coefficients (Table 4) revealed that, in general, the genotypic and the phenotypic correlation coefficients showed similar trend but genotypic correlation co-

efficients were of higher in magnitude than the corresponding phenotypic correlation coefficients. The correlation coefficient between grain yield per plant and other quantitative attributing to yield showed that seed yield was significantly and positively associated with number of productive tillers per plant, number of panicles/ m², panicle length, number of grains/panicle, test weight at both genotypic and phenotypic levels. Hence, selection of these characters would be the correct approach for improving the grain yield. This finding was in accordance with earlier reports of Meena *et al.* (2021), Lakshmi *et al.* (2017), Nanda *et al.* (2019), Saha *et al.* (2019), Umarani *et al.* (2019), Kumar *et al.* (2016) and Ramanjaneyulu *et al.* (2014).

Path coefficient analysis partition the correlation coefficient into direct and indirect effect and hence

Table 5. Estimation of genotypic and phenotypic direct and indirect effects between yield and yield attributing characters

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of productive tillers per plant	Number of panicles/ m ²	Panicle length (cm)	Number of grains/ panicle	Test weight (g)	Amylose content (%)	Protein content (%)	Correlation with grain yield per plant	
Day to 50% flowering	P	-0.2353	0.3316	0.0562	-0.1480	-0.1498	-0.0764	0.1878	-0.3727	0.0454	0.0232	-0.337**
	G	0.1669	-0.7335	0.9634	0.0540	-0.0670	-0.5328	-0.1898	-0.1610	0.0920	0.0523	-0.355**
Day to maturity	P	-0.2213	0.3525	0.0563	-0.1382	-0.1188	-0.0787	0.1464	-0.3552	0.0354	0.0172	-0.304*
	G	0.1649	-0.7422	0.9653	0.0471	-0.0501	-0.5257	-0.1412	-0.1433	0.0751	0.0315	-0.318*
Plant height (cm)	P	-0.1583	0.2375	0.0835	0.0384	0.0558	-0.1455	-0.0586	0.0747	0.0557	-0.0296	0.153
	G	0.1175	-0.5234	1.3689	-0.0138	0.0247	-0.9580	0.0584	0.0305	0.1062	-0.0548	0.155
Number of productive tillers per plant	P	0.1099	-0.1539	0.0101	0.3167	0.3796	-0.0336	-0.4713	0.7779	0.0061	-0.0769	0.864**
	G	-0.0912	0.3534	0.1918	-0.0988	0.1619	-0.2122	0.4738	0.3229	0.0074	-0.1668	0.942**
Number of panicles/ m ²	P	0.0777	-0.0924	0.0103	0.2651	0.4535	-0.0388	-0.5505	0.8206	0.0246	-0.0782	0.892**
	G	-0.0608	0.2020	0.1836	-0.0870	0.1840	-0.2478	0.5174	0.3266	0.0488	-0.1529	0.914**
Panicle length (cm)	P	-0.1106	0.1707	0.0748	0.0655	0.1084	-0.1625	-0.1335	0.1789	0.0664	-0.0295	0.225
	G	0.0860	-0.3774	1.2684	-0.0203	0.0441	-1.0339	0.1292	0.0713	0.1314	-0.0588	0.240
Number of grains/ panicle	P	0.0765	-0.0894	0.0085	0.2586	0.4324	-0.0376	-0.5773	0.8597	0.0249	-0.0853	0.871**
	G	-0.0599	0.1982	0.1512	-0.0886	0.1800	-0.2524	0.5287	0.3503	0.0558	-0.1671	0.896**
Test weight (g)	P	0.0950	-0.1356	0.0068	0.2668	0.4030	-0.0315	-0.5376	0.9233	0.0276	-0.890	0.928**
	G	-0.0747	0.2958	0.1162	-0.0888	0.1672	-0.2050	0.5153	0.3595	0.0483	-0.1782	0.956**
Amylose content (%)	P	0.0865	-0.1010	-0.0377	-0.0156	-0.0903	0.0874	0.1165	-0.2067	-0.1234	0.0169	-0.267*
	G	-0.0687	0.2494	-0.6505	0.033	-0.0402	0.6076	-0.1320	-0.0777	-0.2236	0.0296	-0.303*
Protein content (%)	P	0.0493	-0.0549	0.0223	0.2203	0.3206	-0.0433	-0.4449	0.7429	0.0188	-0.1107	0.720**
	G	-0.0443	0.1187	0.3806	-0.0837	0.1427	-0.3085	0.4483	0.3250	0.0336	-0.1971	0.815**

Phenotypic residual effect = 0.2566, Genotypic residual effect = 0.2403.

provide the clear picture about whether the association of a character with grain yield is because of direct

effect or because of indirect effect through other component traits and hence useful in indirect selection.

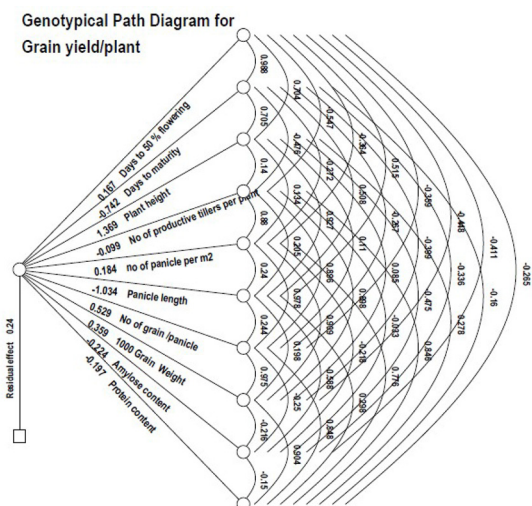


Fig. 1. Genotypical path diagram for grain yield/plant.

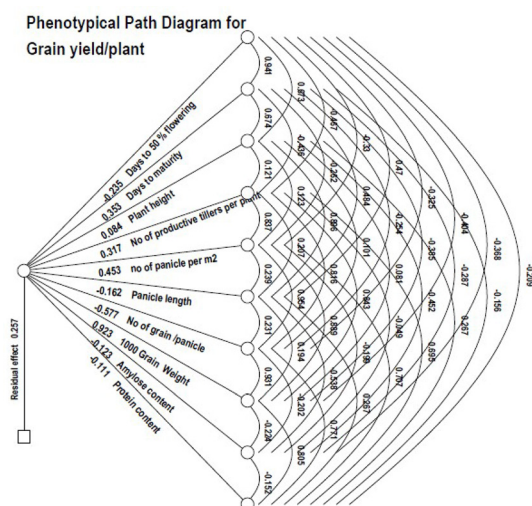


Fig. 2. Phenotypical path diagram for grain yield/plant.

Path coefficient analysis was used to compute direct and indirect effects of ten characters on grain yield in the present study. The characters viz., test weight, number of productive tillers per plant, number of panicles/ m², number of grains/ panicle and protein content exhibited highest positive direct effects on grain yield at both the levels (Table 5). Hence, selection for these character could bring improvement in yield and yield components. These results are in agreement to the earlier finding of Rashmi *et al.* (2017), Lakshmi *et al.* (2017), Behera *et al.* (2017), Saha *et al.* (2019), Nanda *et al.* (2019) and Perween *et al.* (2020). The dimensions of residual effect were very low, which indicated the consideration of most of the yield contributing characters. Moreover, majority of values were less than unity, which indicated that inflation due to multicollinearity was minimal (Gravois and Helms 1992).

CONCLUSION

From the study, it is clear that the traits like number of productive tillers per plant, number of panicle/ m², panicle length, number of grains per panicle, test weight and spikelet per panicle, exhibiting highest values of PCV, GCV, heritability and genetic advance. It is highly recommended to select these traits to attain increased yield. While days to 50% flowering, days to maturity, amylose content (%), protein content (%) exhibiting low values of variance, heritability and genetic advance and hence these traits are ineffective to attain gain by practicing selection. The correlation and path studies revealed that the traits viz., number of productive tillers per plant, number of panicles/ m², panicle length, number of grains/ panicle, test weight (Fig. 1 and 2) positive direct effect on grain yield per plant indicating the usefulness of these trait in selection for enhancing the grain yield among genotypes. Thus a genotype with higher magnitude of these traits could be either selected from existing genotypes or evolved by breeding program for genetic improvement of yield in rice.

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